THE INFLUENCE OF PALGHAT GAP FEATURES ON GENETIC VARIATION AND SPECIATION OF SELECTED TAXA IN SKY ISLANDS OF SOUTHERN WESTERN GHATS, KERALA, INDIA

Thesis
Submitted to the University of Calicut
for the award of the Degree of
DOCTOR OF PHILOSOPHY IN BOTANY

BY
MAYA AMMATHIL MANOHARAN
Under the guidance of
Dr. Suresh V

DEPARTMENT OF BOTANY
GOVT. VICTORIA COLLEGE PALAKKAD FEBRUARY 2024

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CERTIFICATE FROM THE HEAD OF THE INSTITUTION

This is to certify that the thesis entitled **"THE INFLUENCE OF PALGHAT GAP FEATURES ON GENETIC VARIATION AND SPECIATION OF SELECTED TAXA IN SKY ISLANDS OF SOUTHERN WESTERN GHATS, KERALA, INDIA"** submitted to the University of Calicut by Ms. Maya Ammathil Manoharan, in partial fulfillment for the Degree of Doctor of Philosophy in Botany. This thesis is hereby acknowledged as a bonafide record of the research work conducted by the candidate under the guidance of Dr. Suresh V, Associate Professor of the Research Department of Botany, Govt. Victoria College Palakkad. I affirm that this thesis represents the independent work of the candidate under his supervision, and no part of it has been submitted previously for the award of any other degree, or diploma in any other university.

Place: Palakkad
Date: 22/06/2024

Principal

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This is to certify that the corrections suggested by the adjudicators for the Ph.D. thesis entitled **"THE INFLUENCE OF PALGHAT GAP FEATURES ON GENETIC VARIATION AND SPECIATION OF SELECTED TAXA IN SKY ISLANDS OF SOUTHERN WESTERN GHATS, KERALA, INDIA"** submitted to the University of Calicut by Ms. Maya Ammathil Manoharan in partial fulfillment of the requirements for the award of the Degree of Doctor of Philosophy in Botany (Research Scholar, Department of Botany, Govt. Victoria College, Palakkad) have been incorporated into the revised soft copy and hard copies of the thesis being submitted. I hereby certify that the content of both the hard copy and the soft copy of the thesis are identical, and the revised copy may be uploaded to the respective repositories.

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DECLARATION

I hereby declare that the work presented in the thesis entitled " **THE INFLUENCE OF PALGHAT GAP FEATURES ON GENETIC VARIATION AND SPECIATION OF SELECTED TAXA IN SKY ISLANDS OF SOUTHERN WESTERN GHATS, KERALA, INDIA***" is a genuine record of research work carried out by me at P. G. & Research Department of Botany, Govt. Victoria College, Palakkad under the guidance and supervision of* ***Dr. Suresh V, Associate Professor,*** *P. G. & Research Department of Botany, Govt. Victoria College, Palakkad. No part of this thesis has been previously submitted for the award of any degree or diploma in any other University and the thesis is free from AI generated content.*

Place: Palakkad
Date: 22/06/2024

Maya Ammathil Manoharan

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ABBREVIATIONS

ACCURACY	- Accuracy (fraction correct).
ANN	- Artificial Neural Network.
ANOVA	- Analysis of variance.
ANPP	- Aboveground net primary productivity.
AUC	- Area under the ROC curve.
BHL	- Biodiversity Heritage Library.
BIAS	- Bias score (frequency bias).
Boot	- Bootstrapping.
BRT	- Boosted Regression Tree.
BVOCs	- Biogenic volatile organic compounds.
CV	- Cross Validation.
CEPF	- Critical Ecosystem Partnership Fund.
CMIP5	- Coupled Model Intercomparison Project Phase 5.
CMIP6	- Coupled Model Intercomparison Project Phase 6.
CNI	- The Close-Neighbour-Interchange.
COR	- Correlation.
CSI	- Critical success index (threat score).
CTA	- Classification Tree Analysis.
CTAB	- Cetyl trimethyl ammonium bromide.
CWG	- Central Western Ghats.
DEM	- Digital elevation model.
DTPA	- Diethyl triamine Penta acetic acid.
EDTA	- Ethylenediaminetetraacetic acid.
EM	- Ectomycorrhizal.
ENFA	- Ecological niche factor analysis.
ENM	- Ecological niche modelling.
ENVIS	- Environmental Information system.
ETS	- Equitable threat score (Gilbert skill score).
FAR	- False alarm ratio.
FDA	- Flexible Discriminant Analysis.
G×E	- Genotype-by-environment interactions.
GAM	- Generalised Additive Model.
GARP	- Genetic Algorithm for Rule Set Production.
GBIF	- Global Biodiversity Information Facility.
GBM	- Gradient Boosting Model.
GCC	- Global climate change.
GCM	- Global Climate Model.
GDEM	- Global Digital Elevation Model.
GHG	- Green House Gas Emission.
GIS	- Geographic Information Systems.
GLM	- Generalized Linear Model.
GPS	- Global position system.
IBP	- International Biological Program.
IBD	- Isolation by Distance
IBE	- Isolation by Environment
IPNI	- International Plant Names Index.
IPP	- Isopentenyl pyrophosphate.

ITS	- Internal transcribed spacer.
ITV	- Intraspecific trait variability.
IUCN	- International Union for Conservation Status.
KAPPA	- Cohen's Kappa (Heidke skill score).
LR	- Logistic Regression.
MARS	- Multiple Adaptive Regression Splines.
MAT	- Mean annual temperature.
MAXENT	- Maximum Entropy.
MCMC	- Markov chain Monte Carlo.
ME	- Minimum Evolution.
ML	- Maximum Likelihood.
NASA	- National Aeronautics and Space Administration.
NCAS	- National Centre for Atmospheric Science.
Ne	- Effective population size.
NERC	- Natural Environment Research Council.
NJ	- Neighbour-joining method.
NWG	- Northern Western Ghats.
OK	- Ordinary Kriging.
OTU	- Operational taxonomic unit.
PCA	- Principal component analysis.
PFT’s	- Plant Functional Traits.
POD	- Probability of detection (hit rate).
POWO	- Plants of the World Online.
PSM	- Plant Secondary Metabolites.
PVP	- Polyvinylpyrrolidone.
QA	- Quality assessment.
RCP	- Representative Concentration Pathway.
RF	- Random Forest.
RLTBs	- Red-lined torpedo barbs.
ROC	- Receiver Operating Characteristics.
SDM	- Species distribution modelling.
sdmTMB	- sdm Template Model Builder.
SILC	- Sensor Information Laboratory Corporation.
SLA	- Specific leaf area.
SR	- Success ratio.
SRE	- Surface Range Envelop.
SSP	- Socioeconomic pathway scenarios.
Sub	- Sub-Sampling.
SVM	- Support Vector Machine (SVM).
SWCC	- Soil Water Characteristic Curve.
SWG	- Southern Western Ghats.
SWMS	- Southwest Monsoon Seasons.
TBE	- Tetrabromoethane.
TSS	- True Skill Statistics.
UPGMA	- unweighted pair group method with arithmetic mean
USDA	- The United States Department of Agriculture
VIF	- Variation Inflation Factor
WG	- Western Ghats
WGEEP	- Western Ghats Ecology Expert Panel
WPGMA	- Weighted Pair Group Method with Arithmetic Mean.

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This study deals with the species diversity and ecological dynamics of sky islands in the Western Ghats, which are renowned for their unique biodiversity and susceptibility to climate change. The primary focus was to understand the influence of the geographical features of the Palghat Gap, in shaping ecological characteristics, speciation and the prevalence of endemic species.

The thesis comprises of twelve chapters. The chapter one has an in-depth introduction to the research topic, highlighting its significance. It deals with the interdisciplinary nature of the study, exploring its connections with various other scientific field. Chapter two provides a review of relevant research literature, addressing the floristic diversity of the Western Ghats, the biogeographic gap in the region, the significance of sky islands, the influence of climate and edaphic factors, and the utilization of various modelling techniques to solve challenges related to habitat restructuring and biodiversity conservation.

The third chapter includes the preliminary floristic diversity analysis done over the sky islands across the Palghat Gap and analysed floristic divergence of sky islands across the Palghat Gap and emphasised the role of Palghat Gap features over the floristic diversity of Western Ghats.

In the fourth chapter of this study, we included the ensemble ecological niche modelling done to forecast the future distribution of the selected sky island tree species. Where we explored the impact of the gap on the distribution of these species, and the declines in suitable habitat areas of these species over time. This underlined the immediate need for conservation actions over these habitats, and thereby putting forward the important role of the utilisation of ensemble forecasting in species conservation. Then in the fifth chapter, our study focused on intraspecific morphometric variations within populations of *Elaeocarpus gadgilii*. Here we correlated these intraspecific morphometric variations to geographical factors, and thereby underlined the importance of this study in comprehending population dynamics and adaptive strategies of sky island species in such habitats.

In the sixth chapter of our research, the detailed intricate relationships between climate variability over the sky islands across the Palghat Gap and their association with the morphological characteristics of *Elaeocarpus gadgilii* were included. Here

we carefully examined how the climatic conditions in this region influenced the physical traits of the species. This study showed the ecological interactions between climate and intraspecific morphological divergence of concerned species. The seventh chapter, our attention shifted towards an in-depth investigation of the soil parameters of the study area. This led to the understanding of the vital role played by soil parameters in shaping the growth and development of this plant species within the sky island habitat. Next in the eighth chapter, the study dealt with the genetic divergence of the *E. gadgilii* populations within and between the sky islands across the Palghat Gap. This vividly demonstrated the noticeable genetic divergence among *E. gadgilii* populations, which thereby emphasised the impact of geographical gaps over it. In chapter nine, we had an overall discussion over the findings from earlier chapters. There by unravelling the interrelation and efficacy of the Palghat Gap in influencing the floristic diversity of sky islands of the Western Ghats, considering the implications of climate parameters, edaphic factors, as well as morphometric and genetic intraspecific variation of *E. gadgilii* of sky islands across the Palghat Gap region. Our in-depth analysis emphasised the gap's crucial role in shaping the sky island habitat, leading to speciation, and highlighting its vital importance for biodiversity conservation in the region.

In the tenth chapter, an overview of our study was given. This section detailed the interrelationship between floristic diversity, climate, soil, and intraspecific morphological and genetic diversity of *E. gadgilii* populations in the sky islands of the Western Ghats. It described how the Palghat Gap features would have influenced the sky island and its inhabitants at the population level. Our work contributed valuable insights into the ecological dynamics of these unique ecosystems, serving as an important resource for researchers, biogeographers, and conservationists. The study highlighted the importance of sky islands, their exceptional environments, and their diverse inhabitants. Then, the recommendations for the future perspectives of the given study are mentioned in chapter 11. Finally, all the references cited in the thesis are listed in Chapter 12.

ABSTRACT

This study investigates the ecological dynamics and species diversity of sky islands in the Western Ghats, with a focus on the critical role of the Palghat Gap. Sky islands in this region are noted for their rich biodiversity and susceptibility to climate change. The research found considerable divergence between sky islands located on the southern and northern sides of the Palghat Gap, highlighting the significant impact of geography on their ecological characteristics. Geographic isolation in these sky islands was identified as a crucial factor promoting species diversification and the emergence of neo-endemism.

The research investigated the interconnections among various habitat components, concentrating on the sky islands of the Western Ghats across the Palghat Gap. It uncovered significant differences in floral diversity between sky islands on the northern and southern sides of the Palghat Gap. Additionally, the investigation assessed the habitat suitability of selected sky island species using advanced ensemble model forecasting techniques, revealing the impact of the geographical gap on the distribution of sky island species throughout the Western Ghats.

The findings highlight the critical necessity of preserving species in their natural habitats, emphasizing the pivotal role of modelling in biodiversity conservation within the Western Ghats region. Ensemble forecasting analysis underscored the urgent need for conservation measures across the Western Ghats, employing both in-situ and ex-situ strategies. Additionally, an analysis of intraspecific morphometric variation in the *Elaeocarpus gadgilii* populations across the sky islands on the northern and southern sides of the Palghat Gap revealed statistically significant differences. These results suggest that the biogeographical gap and associated geographical factors may have influenced the species, leading to natural selection favouring traits that enhance survival and reproduction in diverse environments.

The research highlighted the intricate interdependencies between sky island climate variables and intraspecific morphological trait variations of *E. gadgilii* in the processes of natural selection. It revealed a significant statistical correlation between annual precipitation and the morphometric variables of *E. gadgilii* populations.

The research delved into the impact of soil parameters on *E. gadgilii* populations within and between the sky islands of the Western Ghats across the Palghat Gap.

This investigation unveiled statistically significant variations in edaphic parameters within and between the sky islands, highlighting their importance as factors contributing to habitat isolation.

The interrelationships among populations of *E. gadgilii* species inhabiting different sky islands of the Western Ghats were explored at the genetic level. The results demonstrated a clear-cut divergence existed between populations of *E. gadgilii* from sky islands on the Southern and northern sides of the Palghat Gap. Based on the phylogenetic and intraspecific divergence analysis done between *E. gadgilii* populations, it is inferred that the geographical features of the Palghat Gap found to have a significant influence not only at morphometric level but also at the molecular-level characteristics of *E. gadgilii* populations.

Research on these isolated ecosystems was crucial for delineating conservation priorities and devising protection strategies. It provided valuable insights into species adaptive responses to diverse environmental conditions, informing the formulation of effective conservation methodologies. Such investigations are indispensable for elucidating intraspecific variability, the role of geographical barriers in speciation, and the influence of environmental factors on population dynamics and adaptation. Consequently, sky islands constitute focal points in biodiversity conservation endeavours.

ABSTRACT IN MALAYALAM

സംഗ്രഹം

പാലക്കാട് ചുരത്തിന് ചുറ്റുമുള്ള ഉയർന്ന ആകാശദീപുകളിൽ ശ്രദ്ധ കേന്ദ്രീകരിച്ചുകൊണ്ട് പശ്ചിമഘട്ടത്തിലെ പാരിസ്ഥിതിക ചലനാത്മകതയും ജൈവവൈവിധ്യവും അതിൽ പാലക്കാട് ചുരത്തിന്റെ പങ്കും പഠനവിധേയമാക്കി. ഈ മേഖലയിലെ പാരിസ്ഥിതിക സവിശേഷതകളും, ഭൗമ പ്രക്രിയകളും ഭൗമശാസ്ത്രപരമായ ഒറ്റപ്പെടലുകൾക്ക് നിദാനമാവുകയും അതുവഴി ആകാശദീപുകളിലെ ജീവി വർഗ്ഗങ്ങൾക്ക് കൂടുതൽ വൈവിധ്യവൽക്കരണത്തിന് അവസരം നൽകുകയും, തദ്വാരാ പുതിയ തനത് ജീവി വർഗ്ഗങ്ങളുടെ ഉദയത്തിനും കാരണമാവുന്നതായി കണ്ടെത്തി.

ഈ പഠനത്തിൽ വ്യത്യസ്ത പാരിസ്ഥിതിക പ്രക്രിയകളുടെ പരസ്പര ബന്ധം അവലോകനം ചെയ്യുകയുണ്ടായി. പാലക്കാട് ചുരത്തിന് തെക്കുഭാഗത്തുള്ള മേഖലയും വടക്കുഭാഗത്തുള്ള മേഖലയും തമ്മിലുള്ള പാരിസ്ഥിതിക അന്തരം ഇതിൽ നിന്നും വ്യക്തമായി. പാരിസ്ഥിതിക മാത്യകാ പഠനത്തിലെ ഏറ്റവും നൂതന മാർഗമായ സമഗ്ര മാത്യകാ പ്രവചനം ഉപയോഗിച്ച് വ്യത്യസ്ത സസ്യ വർഗ്ഗങ്ങളുടെ പാരിസ്ഥിതിക മുൻഗണന ക്രമം കാലാവസ്ഥ വ്യതിയാനത്തിനിടയിൽ എങ്ങനെയായിരിക്കും എന്ന് പ്രവചിക്കാൻ ശ്രമിച്ചു. തിരഞ്ഞെടുക്കപ്പെട്ട ചില സസ്യങ്ങളുടെ ഇപ്രകാരത്തിലുള്ള പാരിസ്ഥിതിക മുൻഗണന പഠനവിധേയമാക്കുകയും അവയുടെ സംരക്ഷണത്തിന് ആവശ്യമുള്ള മാർഗങ്ങൾ അവലംബിക്കാനുള്ള അടിസ്ഥാന വിവരങ്ങൾ പ്രസ്തുത പഠനം പ്രദാനം ചെയ്യുകയും ചെയ്തു.

ഇപ്രകാരം തെരഞ്ഞെടുക്കപ്പെട്ട ഇലയോകാർപ്പസ് ഗാഡ്ഗിലി എന്ന സസ്യത്തിന്റെ രൂപസ്വഭാവങ്ങളിൽ ഉള്ള വ്യതിയാനങ്ങളും സാമ്യതകളും പാലക്കാട് ചുരത്തിന് തെക്കും വടക്കും അടിസ്ഥാനമാക്കി എങ്ങനെ ആയിരിക്കും എന്നതും വിശദമായി പഠിച്ചു. ഇതിൽ വരുന്ന വ്യതിയാനങ്ങൾക്ക് പാലക്കാട് ചുരത്തിലെ കാലാവസ്ഥ സ്വഭാവ സവിശേഷതകൾ എങ്ങനെയൊക്കെ സ്വാധീനം ചെലുത്തുന്നു എന്നതും പഠനവിധേയമാക്കി. ഇതിൽ നിന്നും പാലക്കാട് ചുരത്തിലെ കാലാവസ്ഥ, ഭൗമശാസ്ത്ര സ്വഭാവ സവിശേഷതകൾ എന്നിവ വലിയ രീതിയിൽ സസ്യ വൈവിധ്യവൽക്കരണത്തിന് ആക്കംനൽകുന്നതായി കണ്ടെത്തി. ഇതിൽ പ്രധാനമായും വാർഷിക മഴയുടെ അളവ് വലിയ രീതിയിൽ സ്വാധീനം ചെലുത്തുന്നുണ്ട്. പ്രസ്തുത സസ്യത്തിന്റെ തന്നെ ജനിതകഘടനയിൽ പാലക്കാട് ചുരത്തിന്റെ സ്വാധീനം ഡിഎൻഎ ഘടനയുടെ സാമ്യതകളും വ്യതിയാനങ്ങളും അപഗ്രഥിച്ചുകൊണ്ട് പഠനവിധേയമാക്കി. രൂപ വൈവിധ്യത്തിൽ മാത്രമല്ല അതിനു അടിസ്ഥാനമാകുന്ന ജനിതകഘടനയിലും പാലക്കാട് ചുരത്തിലെ സവിശേഷതകൾ സ്വാധീനം ചെലുത്തുന്നതായി ഇതിൽ നിന്നും മനസ്സിലാക്കി. തിരഞ്ഞെടുക്കപ്പെട്ട തനത് സസ്യങ്ങളിൽ ആണ് പഠനം കൂടുതൽ നടത്തിയത് എന്നിരുന്നാലും ഇത് ഈ മേഖലയിലെ മറ്റു സസ്യവിഭാഗങ്ങളുടെയും ഈ മേഖലയുടെ തന്നെയും സംരക്ഷിത പ്രവർത്തനങ്ങൾക്ക് ആവശ്യമുള്ള സാമ്പ്രദായിക മാർഗ്ഗങ്ങൾക്ക് രൂപീകരണം നൽകുന്നതിനുള്ള അടിസ്ഥാന വിവരങ്ങൾ നൽകുകയുണ്ടായി. ഇത് ആകാശദീപുകളുടെയും മറ്റ് പശ്ചിമഘട്ട മേഖലകളുടെയും ഭാവിയിലുള്ള സംരക്ഷണ പ്രവർത്തനങ്ങൾക്ക് ഊർജ്ജം പകരുന്നതാണ്.

CHAPTER 1:
GENERAL INTRODUCTION

1.1. Sky islands

"Sky islands" are isolated geological formations of mountainous regions that are insulated from other habitats by their elevated topography, geographical distance, climate and other natural barriers (Warshall 1995, Love *et al*., 2023b). In contrast to the surrounding areas, these terrestrial sky islands are the one known for their high species diversity and endemism. The sky island habitat features play a pivotal role in driving morphological, physiological, and genetic variation in species inhabiting this habitat. These landscape insulation features, in turn, promote genetic drift, natural selection, and limited gene migration in this habitat. These habitats are the zones where climate variability is at its extreme with complex topography. Consequently, sky islands became hotspots for diversification and often exhibited niche conservatism, where species retain ancestral traits.

Several studies on sky islands highlighted the significant isolation mechanism acting over it, and they were the mechanism of isolation by distance, isolation by environment and habitat contraction of sky island species under unpredictable climate change. One of the important among them is isolation by distance like the one caused by geographic isolation introduced by natural barriers, and which initiates allopatric speciation in these habitat. The connection between allopatric speciation and niche conservatism contributed significantly to the evolution in these regions. The concept of niche conservatism further enhanced our understanding of the processes that govern these exceptional ecosystems, shedding light on their distinct evolutionary mechanisms (McLaughlin 1995, Warshall 1995, Love *et al*.,2023b).

The ecological and evolutionary characteristics of sky islands are influenced by a range of factors. These factors include the geological composition of the bedrock, the topographical features of both mountains and valleys, and the establishment and modification of migration barriers and corridors (Mani and Giddings 1980). The species inhabiting sky islands aligned along the north-south axis exhibited to have more pronounced evolutionary potential compared to those in the sky islands oriented along the east-west axis. This observed disparity in evolutionary potentiality is due to the heightened diversity of climates of the Western Ghats on the north-south axis (Larsen 2013).

The colonisation in sky islands occurs through niche transitions from habitats at lower elevations and relatively short migrations to nearby sky islands. In the case of newly colonised sky islands, the time got for them to adapt will be less, so it is expected that the extent of divergence in it to be less pronounced. Successful establishment in a new environment requires adaptive mechanisms. Without these adaptations and subsequent divergence, the eventual fate of species is likely extirpation. The evolutionary processes occurring on each individual island, combined with the element of time, will inherently lead to distinct outcomes, resulting in unique gene pools for each respective island (Bowie *et al*., 2006, Fazalova *et al*., 2010).

All over the world, roughly 20 distinct sky Island complexes are reported. These sky island complexes are classified into five distinct categories based on its isolation nature, and they are namely the Stepping Stone Archipelago between two mountain chains, Isolated massifs with outliers, Cordillera with outliers, Isolated sky island chains, and High-altitude sky islands. The Western Ghats are one among them and are classified under the isolated sky island chain type. Sky islands are a significant source of new species due to their limited migration options and harsh environment (Warshall 1995, Robin *et al*., 2010).

Biodiversity is concerned with several components, like the climate variables, spatial area size and other parameters like speciation rate, extinction rate, the ecotone effect, mutualism, competition and soil components (physical and chemical properties). The change in climate variables affects energy availability, productivity, and other parameters of an ecosystem (McCain and Grytnes 2010). Tropical mountains are zones with greater biodiversity, and they encourage speciation and long-term population persistence, even though such habitats are at risk due to anthropogenic alterations. The sky islands of the Western Ghats have got little attention in India in terms of conservation and research. Therefore, it is vital to raise awareness of the hazards faced by such habitats (Robin and Nandini 2012). Most of these biodiverse tropical highland forests are found to be under constant threat of fire and exotic plant invasions. Therefore, such areas have recently gained more attention in conservation projects (Bubb *et al*., 2004). The devastating adverse effects on the montane forests are mainly caused by unpredictable temperatures and fluctuating precipitation patterns, which in turn affect the biodiversity of such montane forests (Bruijnzeel *et al*., 2010).

Even now, there exists insufficient knowledge on the spatial variation of species richness in relation to a variety of aspects such as the carbon cycle and nutrient

dynamics. Most of the Western Ghats regions, known for biodiversity have not yet been fully investigated. So, it is challenging to determine the conservation and restoration status of such species located exclusively in undiscovered places, which may be endemic, vulnerable, threatened, or maybe even on the verge of extinction. Hence, the uncovering species composition of habitats like sky islands has become essential. Floristic research on areas like geographically remote sky islands in the highest reaches of the mountains will provide important insights into the biogeography and species evolution in these islands. The abundance of endemic species and variation at the species level are found to be crucial in such sky island habitats (Storey 1995, Gunnell *et al*., 2003). The conservation of rare and endangered plants of sky islands is possible only after a thorough investigation of the sky island species population dynamics, genetic potential for evolution, reproduction and spatial distribution (Botsford *et al*., 2019).

According to recent surveys, there are about 36 biodiversity hotspots around the world, and all are known for their endemic status (Bellard *et al*., 2014). The Western Ghats, also known as the Sahyadri Mountain range, are recognized as one of India's biodiversity hotspots, spanning six Indian states and are renowned for their rich biodiversity and numerous unique species. According to the Western Ghats Ecology Expert Panel (WGEEP), 64% of the total Western Ghats area is designated as ecologically sensitive, where human interference should be restricted to maintain ecological balance. Unfortunately, many of these areas have already been impacted by activities such as mining, industrialization, human settlements, and agriculture. If these trends persist, the Western Ghats may face significant threats to its existence in the future. As the Western Ghats were found to have lost a major part of the forest area, the government established committees to study protection measures to safeguard the Western Ghats, which include the Gadgil Committee, followed by the Kasturirangan Committee (Gurusamy and Basil 2021).

Palghat Gap is a low land area traversing the Western Ghats, and the widest gap measuring 30 to 40 km at 10° 45′ latitude. The Palghat Gap is the one that connects Palakkad in Kerala with Coimbatore and Pollachi in Tamil Nadu. South India’s climate is largely influenced by this Gap, and the southwest monsoons as well as storms from the Bay of Bengal cross the mountains through this gap opening. A remnant plateau landform from the Jurassic age is found from this gap (Subramanian and Muraleedharan 1985). This gap is flanked on the north by the Nilgiri Hills and on the

south by the Anamalai Hills. As this gap is the oldest and widest, its impact on the biodiversity of the sky islands of the Western Ghats on its northern and southern flanks is probably high. So, it's expected to have a profound influence on the evolution of species inhabiting the sky islands (Soman *et al*., 1990, Biswas and Praveen Karanth 2021). These gaps, which isolate the ecological habitats, prompt significant changes in the diversity of species that adapt to these new environments. Some species successfully adapt and evolve with new characteristics, while others face extinction. However, it's crucial to note that each species follows a unique evolutionary path due to variations in timing, habitat, and unpredictable climatic fluctuations to which it is exposed (Johnson and Stinchcombe 2007). A study on the status and spatial distribution of the endangered White-bellied Shortwing (*Brachypteryx majo*r) across the sky islands clearly demonstrated the mechanism of sky islands and the effect of the Palghat Gap over its populations (Robin *et al*., 2006). If changes took place rapidly within populations of a species at its phenotypic level, this would probably affect the behaviour of other populations in the community and then later it affects the community structure (Vellend 2006).

The features of these gaps like altitude, gap distance, wind (blowing west to east during monsoon and east to west during retreat monsoon) and other features may also act as natural barriers. These features of the Palghat Gap can render the dispersal of propagules across it nearly impossible, resulting in the development of unique isolation mechanisms. These mechanisms may reduce gene flow between populations in the sky islands of the Western Ghats across these gaps. Such processes may have facilitated the emergence of isolated populations within the sky islands of the Western Ghats, potentially leading to the evolution of new species over time.

The present world's climate changes unpredictably, therefore the species in such vulnerable habitats must have to adapt rapidly to survive. If a species is unable to adapt to these rapid changes, it may face extinction. In some cases, migration can be a solution to avoid extinction. But this is not always possible, especially for species that are separated geographically by great distances from other habitats. In such cases, the species is trapped in an environment that no longer supports its survival, ultimately leading to its extinction. When the physical distance between sky island habitats increases, the likelihood of migration becomes limited. So, it's better to understand the interdependencies within and between the ecological components of sky islands, and

that would be possible through comparative analysis of ecological factors of sky islands of Western Ghats across the Palghat Gap.

1.2. Ecological niche modelling (ENM)

Recent development in modelling tools have introduced several advancements in species conservation, under such unpredictable changing climates. These modelling techniques are called as Species Distribution Models (SDMs), or Ecological Niche Models or Habitat Suitability Models. It works based on the relationship between species geographical occurrences and corresponding environmental variables. These models find applications in various fields, including biodiversity conservation, biodiversity assessments, evolutionary biology, epidemiology, global change biology, and wildlife management. It is important to note that different SDMs exist, and their effectiveness varies depending on factors such as the type of response variable, predictor variables, output type, assumed species-environment relationships, estimation methods for species distribution and the selection of relevant predictor variables. These models represent a valuable tool for predicting and summarising species distributions in response to changing environmental conditions, ultimately contributing to species protection and conservation efforts (Guisan and Zimmermann 2000, Naimi *et al*., 2011, Araujo and Peterson 2012, Peterson and Soberon 2012),

Ecological niche models forecast species high probable habitat-suitable areas, thereby allowing us to predict the distribution, population structure and the risk of extinction of the species. Yet, all of these are more on the concept of habitat loss rather than the components of species fitness (Kearney *et al*., 2010a). Whereas physio-demo genetic models appear to be more beneficial because they predict not only habitat loss but also physiological, demographic, and genetic parameters (Kramer *et al*., 2010). However, these models cannot prevent co-extinction due to a lack of population dynamics and interspecific interaction data (Brook *et al*., 2008). All the ENM models have their advantage and disadvantage.

Bioclimate modelling works based on niche-specific bioclimatic variables as well as current occurrence data of the species. Modelling techniques uses occurrence data of the species under study to correlate existing climate data of their present niche with the expected future climate data, to forecast future habitat suitability zones of the species (Akaike 1974). Through this advanced ecological niche model forecasting technique several endemic and threatened species future spatial distribution patterns were predicted using their occurrence data (Babar *et al*., 2012). The predictability of

the model is determined by the accuracy of the occurrence data and the amount of occurrence data provided. BIOCLIM, Euclidean distance, Gower distance, Mahalanobis distance, GLM, Maxent, Random Forest, DOMAIN, GARP, GAM, FDA, MARS, ENFA, Artificial Neural networks, SVM are some of the models available in this field. These distribution models are also impacted by temporal errors in incidence and climatic baseline and are unavoidable (Roubicek *et al*., 2010). This modelling science keeps evolving with new ways to model things. It uses key environmental factors to predict where certain species are likely to thrive. This helps us to understand the risk of extinction of several species and estimate where they might be found. It also lets us see how certain ecological factors affect the distribution of these species. These finding mainly favours to develop strategies for in-situ biodiversity conservation.

1.3. Climate change

The impact of climate change on species, biodiversity, biomes, and habitat is significant. The effects of climate change on high-elevation habitats are unpredictable because they are temperature-sensitive zones that are vulnerable to small changes. According to the pieces of evidence from several fossil records and several forecasting studies, the risk posed by climate change over the ecosystem is very high (Bellard *et al*., 2012).

In this unpredictable rapidly changing climate condition, the response of a species depends on multiple factors like the geographic location where it exists, pollination methods it adopts, its growth rate, reproductive strategy, spatial mobility and more (Jackson and Overpeck 2000). The modification that the species undergoes due to climate change causes changes in its community structure, as all the components of each ecosystem are in the web of interaction. Under extreme condition these changes in community structure can result in speciation or extinction (Koh *et al*., 2004, Walther 2010). The rapid adaptations of species under adverse climate conditions are made possible through mutation, natural selection in existing genotypes, plasticity as a short-term response, inter or intraspecific variation in morphology or behavioural patterns and genetic drift. Plasticity is a more noticed phenomenon than genetic level modifications because survival under an unpredictable climate shift needs a quick response (Botkin *et al*., 2007, Chevin *et al*., 2010, Hoffman and Sgro 2011).

Climate change affects the spatial distribution and existence of native species and promotes the invasion of invasive species. These invasive species have a wide range of adaptability in harsh environmental conditions, and this thereby increases the

risk of the existence of native species and later causes biodiversity loss (Walther *et al*., 2009).

The plant's response to the changing environment takes place in three dimensions, namely spatial, temporal, and self-regulation. Where the spatial and temporal responses are easily observable. The third dimension is self-regulation, which includes behavioural and physiological adjustments and are not easily observed. If a species under the threatened category is unable to respond and adapt along any of these above mentioned three dimensions the species would be at risk of extinction. There are various components in climate and their impact on biodiversity is at different levels, like directional selection, rapid migration, or extinction. All of which lead to a reduction in biodiversity (Parmesan 2006, Botkin *et al*., 2007). Most of the species bear such ability to reflect rapidly to such changes, but this depends on several features of the species like sensitivity to exposure, adaptive capacity, migration potential, as well as the species existing habitat. Therefore, before studying the response of each species to ecological change, it is important to study the features that are associated with its response must be evaluated (Dawson *et al*., 2011).

To introduce the best strategies to conserve present biodiversity, the macroecological and biogeographic factors influencing species distribution must be studied. Currently studies on climate change and its impacts have increased awareness about the threats caused by unpredictable climate change on biodiversity (Parmesan *et al*., 2011). Some of the studies have mentioned the significance of IUCN status analysis, species-area relationships model, bioclimatic envelope model, dynamic vegetation model and dose-response model to analyse the risk of biodiversity loss (Thomas *et al*., 2004).

Studies on climate change and its impacts on species distribution and adaptation of sky island species unravel the role of climate as a driving factor in speciation and evolution in such vulnerable sky island habitats. So, investigating the sky islands climate is essential for understating the role it played in isolating the habitat, this raises the significance of the study. So, to protect the biodiversity of the sky islands habitat one of the ecological components that has been given a significant spot is its unpredictable climate.

1.4. Soil biome

The effects of climate change on soil is understood only if we understand the interdependencies between them. Soil, climate and atmosphere are all linked by car-

bon, nitrogen and hydrogen cycles. Where the soil is one of the significant factors in the global nutrient cycle (IPCC 2007, Brevik 2012, IPCC 2013, Allen *et al*., 2018). Each component of the soil has paramount importance, and the interconnection and balance between them are fundamental. However, the interference of human activities exerted a significant influence on the C, H, and N content of the soil. Among other components of Soil, phosphorus stands out. Even though the effect of climate on vegetation growth and physiological development is significant, its effects remain relatively minor compared to other ecological component effects (Beadle 1966, Brevik 2012).

Carbon and nitrogen play a significant role in the physical and biological functioning of the soil, and climate change adversely affects it. This causes an imbalance in the global nutrient cycle, and thereby the soil quality changes, and in turn disrupts the entire ecosystem. This in turn affects the inhabitants of the ecosystem and which adversely affects the individual that cannot adapt, ultimately causing its extinction (Brevik 2012). Several forecasting climate model studies mentioned that major fluctuations are found in soil carbon, either decreasing or increasing in future time periods. Soil microbes are the one that maintain the equilibrium in atmospheric carbon and organic carbon within the soil. The quantity of soil organic matter (SOM), the C/N ratio reflects the organic carbon content of the soil. This is directly linked to the diversity of microbial communities present in the soil. One of the important climate components that alters the carbon content of soil is the atmospheric temperature. The temperature varies with changes in latitude and elevation, and this vicariance reflects the plant community diversity (Wieder *et al*., 2013).

Due to global warming, the future climate is anticipated to have high temperature and more frequent fluctuations in climate. Therefore, the increase in temperature causes a decrease in the soil carbon level which adversely impacts the global carbon cycle. The elevated temperature not only has an effect on carbon level but also affects soil organic matter and enhances nitrification. These all are in turn tied to the vegetation of the ecosystem. The soil structure, formation, water retention capacity and ion exchange are defined by the soil organic matter content. That is the disturbance in one factor affects the other, as all ecological components are interconnected. Such disturbances will affect the vegetation in the ecosystem and will later drive processes like adaptation, selection, and in severe cases, migration or extinction (Niklinska *et al*., 1999, Gorissen *et al*., 2004, Reich *et al*., 2006).

Understanding the interconnection between the fundamental ecological elements is significant. This knowledge is crucial, as the ability to predict the faith of biodiversity through modelling is connected to the correctness of edaphic parameters used in it. So, to protect biodiversity, it is crucial to understand the importance of each edaphic component. This thereby unveils the role of each edaphic parameter in isolating the sky islands and the influence of it over the floristic diversity of these habitats. So, the challenges posed by these ecological components over the biodiversity of the habitat can be forecasted. This would aid in devising substantial conservation strategies to preserve and protect biodiversity of sky islands.

1.5. Morphological variation

The ecological niche of a species defines the favourable environmental conditions it thrives. When a species encounters unfavourable conditions, through adaptive capability the species can survive with various adaptive modifications. One such significant modification is the alteration of functional traits, which can be observed in visible characteristics related to its function (Poorter and Garnier 2007). That is the leaf of plants expands with high nutrient availability, and with low nitrogen availability the roots will be dense, and thinner with high lignin content. Species which are characterised by their rapid growth often exhibit a substantial increase in leaf area and an extended root length. However, these attributes are juxtaposed with diminished carbon and nitrogen content in their leaves, alongside reduced specific root and leaf lengths when a species under depleted nutrient levels. That is both biotic and abiotic factors exert their influences on each individual species inhabiting the associated habitat (Eissenstat *et al*., 2000, Comas and Eissenstat 2004). However, the examination of such variations on each individual trait in response to distinct climate or niche component change is challenging. The ability of the ecological component to affect multiple traits at the same time makes a single-trait analysis complex (Lavorel and Garnier 2002).

As told in the Holy Grail hypothesis, the changes in the environment are predicted and understood through the change in functional traits of the species, like leaves undergoing modification in shape, size, and other features due to unfavourable and disturbed ecosystems. The leaf characteristics are the major trait that are used to study the response of species to shifts in the environment. Among the leaf traits leveraging leaf length and width are preferable than measuring the leaf area. The morphological attributes are the one that reflect the environmental change. The changes in

morphological parameters of the inhabitants in a habitat acts as indicators for the unpredictable changes in climate and other ecological factors to which it is exposed. These attributes that acts as indicators of environmental change hold important value in biodiversity conservation. The adaptation of plants with respect to environmental variation is crucial for species survival (Lavorel and Garnier 2002, Diaz *et al*., 2007, Li *et al*., 2020, Liu *et al*., 2022).

The response of plants to climate for short-term and long-term adaptation differs (Zhu *et al*., 2012). When a plant is exposed to adverse environmental conditions the response of the species varies. The impact of the plant's response reflects on its morphological traits, and these trait variations are not uniform. Such variability in traits may yield localised adaptations compatible with the exposed environmental condition. The introduction of genetic modifications invariably triggers alterations, irrespective of whether they are confined to a specific geographical scope or are temporary in nature. Consequently, the mechanism of phenotypic plasticity consistently assumes a pivotal role within the broader framework of adaptive evolution. In the process of speciation, the first step is the change in phenotypical traits of species (Frank 2011, Fan *et al*., 2020). The intensity of variation in morphological traits depends on the severity of adverse environmental conditions to which it is exposed to. To adapt and succeed in natural selection, species respond to such adverse environmental change with phenotypic plasticity, either through interspecific or intraspecific variation. (Nicotra *et al*., 2010, Franks *et al*., 2014). Phenotypic plasticity refers to the idea that plants behave differently in different environments (Bradshaw 1965).

These adaptive responses are observed through variations in the physical characteristics especially over the leaves both in terms of their quality (features that can be described, like colour or shape) and quantity (measurable traits, like size or number). By studying these variations in leaf traits, the interconnectedness of different elements within an ecosystem can be analysed. This involves examining how changes in one ecological component can lead to observable changes in leaf morphology. By understanding these relationships, we can predict how each species within the ecosystem will react and adapt to alterations in various components of their environment. This predictive ability can then be harnessed to develop strategies for conserving biodiversity, by foreseeing how each species might respond to potential future changes in their environment. Ultimately, this scientific approach allows for the prediction of how species will adapt and change in response to shifts in their ecosystem. By compre-

hending the processes of adaptive evolution and acclimation (how organisms adjust to their environment) and studying the range of changes across various ecological components, researchers can contribute to the conservation of biodiversity and the prevention of species loss.

1.6. Genetic variation

The impediments in gene flow between individuals within a population can be either biotic factors or abiotic factors. The reduction in gene flow between populations contributes to the increased divergence between them (Van Der Velde and Bijlsma, 2003). In intraspecific variability analysis, the rate of genetic variation within a genome differs based on the type of genome (chloroplast, mitochondrial, or nuclear) and the specific gene region under which analysis was done. The divergence of each gene depends on its vulnerability, it differs with respect to gene, genome, the species and the genus. This genetic divergence is the basis for phylogenetic analysis, and the rate of evolution can impact the accuracy and interpretation of phylogenetic analysis (Zurawski and Clegg 1987).

Among different genetic materials mitochondrial DNA, chloroplast DNA and micro-satellite DNA are generally used in most intraspecific genetic variability analysis. Chloroplast DNA is haploid and is a stable genetic material with highly conserved gene content and arrangement. The mitochondrial DNA evolves at a slower pace compared to the chloroplast genome. This slower evolution of the mitochondrial genome might cause implications for understanding the evolutionary history of organisms and their relationships. The Chloroplast DNA is non-recombinant, and it also has a high copy number. These characteristics make chloroplast DNA suitable for the study of evolutionary relationships (phylogeny) within plant systems. Then the nuclear genes, found within the cell nucleus, evolve at a faster rate. This contrasts with the slower evolution of mitochondrial genomes and the characteristics of chloroplast DNA (Small *et al*., 2004).

Darwin's theory of natural selection provides a clear explanation of how species evolve through the process of variation. The intraspecific divergence analysis of species unveils the genetic variability between the populations of a species, to adapt to adverse environmental conditions to which it is exposed. The impact of adverse environmental conditions on the species either remains within morphological traits or may have impacted the gene level. In the majority of intraspecific variability studies, the variation remains within the morphological traits, and that means this variation will be

a temporary adaptation. These adaptations can later become permanent or not. If the adaptation has an impact on the gene, the extent to which they are varied and the transferability of this adaptation to the next generation can easily be understood. The long-term adaptations can generally be considered to generate new species through the acquisition of variations. As per Darwin, the inheritance of variations can result in the collection of advantageous traits or adaptations, offering the emergence of new species (Darwin 1896).

The sky islands are unique habitat that plays a crucial role in the biodiversity of their surrounding habitat. These habitats are highly vulnerable areas, more prone to variations due to their isolated nature and less gene flow. This nature of the habitat increases the potentiality of its inhabitants to undergo speciation. These features of this habitat make them a major repository of diverse species, and a major source of new species to biodiversity. Investigating the ecological components of such habitats unravels the impact of the biogeographical gap over such habitats. The effect of this gap over these habitat features vary in different fields. This can be unveiled only through a detailed study of its components. This study clearly demonstrates the interaction between each ecological component. The extent to which each component of the sky islands is impacted by this geographical gap can be understood. The sky islands of Western Ghats are especially high elevated zones. These high elevated mountains are more prone to small changes. To cope with changing conditions at higher elevations where temperature drops, the plants undergo various changes in their traits, including phenology, physiology, anatomy, and morphology. These adaptations help them to thrive in challenging conditions, which also affect nutrient cycles and soil characteristics (Ahmad *et al*., 2016).

There are several studies on the floristic diversity, endemism and biodiversity of the Western Ghats that are completed, and many of such studies are ongoing. However, research specifically addressing isolation mechanisms within the sky islands remains limited. Additionally, there are a few populations genetic studies examining the relationship between island structures and the evolutionary processes shaping species within this region (Robin *et al*., 2010, Young 2003). There are some studies that showed the importance of geographical distance and its positive correlation with genetic distance between populations (Whitlock and McCauley 1999). The studies on the floristic diversity of sky islands and intraspecific variability of sky island plants are merely negligible. Moreover, the sky islands experience exceptionally challenging

environmental conditions, and even narrow shifts in climate have a notable impact on its floristic diversity. Phenomena such as isolation-by-distance or isolation-by-resistance can create a strong spatial genetic population pattern because of specific mating behaviours in nearby populations, non-uniform movement and increased genetic changes within local genetic groups (Wright 1943, Landguth *et al*., 2010).

The impact of natural barriers on the population of a species depends on the altitude range where the species exists, and the capacity of the species to disperse. That is the species that inhabit the lower elevation are expected to have a large population size and less fragile than the species on the higher altitudes. The species on the higher altitude seem to be much more vulnerable and are the one with small population size. So, the impact of environmental change over higher altitudes will be higher than that of lower altitude inhabitants (Robin *et al*., 2010). Conducting a study focusing on the intraspecific genetic and morphological variations over the sky islands species across the Palghat Gap would provide an opportunity to unveil the potential influence exerted by this distinctive geographical feature on speciation events within the region. By doing so, we can gain insights into whether the Palghat Gap plays a pivotal role in shaping the diversity of plant species found within the sky islands of the Western Ghats, particularly in the context of the presence of the Palghat Gap.

Furthermore, this investigation allows us to assess the extent of the Palghat Gap's impact on both the speciation and distribution patterns of plant species in this region. To get a clear-cut understanding of the influence of Palghat Gap features, it is important to consider the major components of the habitat like edaphic factors and climate data of the habitat. Accordingly, each ecological component assumed to have a crucial role in defining the sky island habitat.

1.7. Aim of the study

The study addresses the influence of the Palghat Gap features in speciation, genetic diversity, and endemism in the selected taxa.

1.8. Objectives of the study

1) To study the detailed phytogeography of sky islands in the Western Ghats based on secondary data and selecting a few taxa restricted to sky islands and an extensive collection of these species from the study area.
2) Ensemble forecasting of the selected sky island species, to study the effect of the Palghat Gap features in their distribution.
3) To study the effect of climate on the intraspecific morphometric variation of the selected species.
4) To study the effect of edaphic factors on the intraspecific morphometric variation of the selected species.
5) To analyse the genetic variation in the selected species by morphometric analysis, followed by confirmation of the data by utilising molecular data on selected genes.
6) To analyse the correlation of the extent of similarities and dissimilarities within each plant species; both between populations and within populations by considering the northern and southern sides of the Palghat Gap.

CHAPTER 2:
REVIEW OF LITERATURE

2.1. Sky islands

Sky islands are habitats situated on elevated peaks and ridges of mountains. These habitats serve as the cradle for unparalleled and exclusive ecosystems. Within the spectrum of diverse sky islands, cloud forests stand out due to their high vulnerability attributable to their extreme dimensions and their heavy dependence on water vapour as an important factor for their respective habitats (Hayward 2022). These geographical formations are vulnerable biotic systems highly susceptible to climate change. The concept of terrestrial islands was first described in the 1940 and has gained attention through the herpetologist Edward H. Taylor. The term "sky island" was later popularised by Weldon Heald in his book in 1967. Following Heald's work, researchers like Brown and Vuilleumier tested island biogeographical theory using sky island populations of mammals and birds in North and South America. Sky islands play an important role in promoting genetic diversity, which highlight the importance of sampling and the use of rapidly mutating genetic markers in investigating recent genetic divergence (McCormack *et al*., 2009, Love *et al*., 2023b).

Tropical montane forests over such habitats are often endangered ecosystems with persistent cloud cover. Investigating the structural, functional, and distributional aspects of these ecosystems, substantiated their liability to edge effect and the potential risk of fragmentation. The tropical montane forests found in peninsular India, are commonly called as shola forests. The shola-grassland ecosystem plays a crucial role in hydrology, biogeochemistry, and the conservation of diverse species. However, anthropogenic activities and climate change pose significant threats to the ecological balance between the forest and grassland components, which increases the concerns about the long-term sustainability of these ecosystems (Bunyan *et al*., 2012). In young tropical forests, the rate and direction of succession are influenced by various factors, including liana competition, edaphic factors, and other conditions (Estrada Villegas 2019).

The increase in the size of shola habitats causes the heightened species richness, basal area, and the proportion of large trees. Conversely, as the shola size decreases, there will be a decline in the number of rare species specifically associated with transitional ecological zones. The smaller sholas include some of the species observed in larger sholas, suggesting a nested pattern. These substantiate the fact that

shola forests exhibit a high degree of structural organisation within their plant communities, which may be influenced by ecological succession (Mohandass and Davidar 2010). Species when they move from larger to smaller areas, they gradually disappear. This leads to species loss in successive sub-areas or depressions within the overall habitat (Anderson *et al*., 2012).

The phylogeographic studies on species within the sky islands displayed that their genetic structures are found to be impacted by the topography and climate of their habitat. This showed the influence of global climate change on shaping biodiversity and species adaptive responses. Therefore, future research demands to incorporate interdisciplinary data and employ comparative phylogeography studies to gain a better understanding of geographic patterns, diversification processes, and the preservation of species over such habitats (He and Jiang 2014). The study on genetic diversity and evolutionary patterns of the beetle *Rhantus suturalis* in the Australasian archipelago was assessed through phylogenetic and demographic methods. That revealed the phylogenetic relationships and population structures of *R. suturalis* and the ongoing speciation in its populations from New Guinea and New Zealand. This study on *R. suturalis* was a means of evidence for peripatric speciation and substantiated the significance of sky island's features in its evolutionary process (Toussaint *et al*., 2013).

The breakup of the supercontinent Gondwana, followed by various geological processes such as rifting, passive margin development, sedimentation, uplift and erosion led to the formation of the Western Ghats. The origin of the Western Ghats has raised several arguments, as it cannot be formed by a single mechanism like lithosphere-asthenosphere interactions or surface processes (Sinha-Roy 2018). The formation of the Western Ghats involved various geological processes, including rifting, extensive faulting, initial uplift, and eastward tilting. All through the tertiary period, the west coast of India went through multiple phases of uplift due to the erosion of large rock masses from the onshore area and their subsequent deposition in the offshore basins. The present Western Ghats is situated in the east of two basins in the western offshore region of India, namely the Mumbai offshore basin and the Konkan-Kerala offshore basin. These basins originated during the Cretaceous period when Madagascar and Seychelles separated from India (Singh *et al*., 2007).

The Western Ghats are the sky islands under the isolated chains type (Warshall 1995), with their vegetation composition primarily shaped by the quantity of seasonal rainfall, rather than fluctuations in atmospheric temperature. The major soil

types in the region are red, laterite, black, and humid soils. The tropical rainforests within the Western Ghats on the windward side of the southern region of the mountain range are typically found at elevation ranges from 500 to 1500m (Subramanyam and Nayar 1974). These tropical rainforests lack distinct summer and winter seasons, instead, they go through wet and dry seasons. The temperature fluctuations during these seasons are relatively minor compared to the significant variations in rainfall patterns (Richards 1952). The biogeographic patterns and species distribution within the Western Ghats highlighted its notable levels of biodiversity and endemism (Kuriakose and Sebastian 2016).

According to Hora's Continuous Range Hypothesis, there was an ecological connection along the Vindhya-Satpura range, that linked the eastern Himalayas to the west coast of India. The study done over the tropical fauna of the Western Ghats, Eastern Himalayas, Assam, Burma, and Malaya showed similarity, indicating a historical association instead of their current geographic separation of around 1,500 miles. The species populations in the Western Ghats exhibited limited divergence compared to their eastern counterparts, suggesting a recent separation between these regions. So further research is needed for better understanding of the distribution, taxonomy, and precise relationships among these areas (Dilger 1952).

The Western Ghats continuity is interrupted by three gaps of which the Palghat Gap is the oldest and widest with a maximum of 40 kilometres of gap distance (Robin *et al*., 2010). The exact origin of the Palghat Gap within the Western Ghats is under argument, and to develop to its current topography it seems to have undergone several shearing processes and erosion (D'Cruz *et al*., 2000). The impact of the Shencottah and Goa gaps on several taxa was found to be lesser, compared to the impact of the Palghat Gap. The distribution patterns of several species across these gaps correspond to the dimensions of the respective gaps. The studies across such gaps suggested that geographic features are not the only the primary cause of vicariance, instead, ecological factors, life history traits, and historical biogeography also have a significant role in it (Biswas and Praveen Karanth 2021).

The elevated zones of sky islands of the Western Ghats in southern India include unique shola habitats and are renowned for their endemism, which are not yet completely explored. The studies that have taken place over the Western Ghats especially included its floristic elements, where several of its sky island areas remain unexplored. The studies on the sky islands of the Western Ghats are minimal, especially

on its shifting climatic patterns, and the conservation necessity over these areas (Robin and Nandini 2012). The impact of geographic features of the Palghat Gap in shaping the population structure of White-bellied Shortwing bird species (*Brachypteryx major*) and the genetic differentiation over its population from sky islands of Western Ghats was examined by Robin. In addition to that, this study investigated the impact of past climate fluctuations on the genetic diversity and connectivity of White-bellied Shortwing populations across the sky islands. By combining genetic data with geological and climatic information, the research gave insights into the evolutionary history of this endemic bird in the sky islands of southern India (Robin *et al*., 2010).

The studies done over the *Populus angustifoiliius* across intermountain of Western US showed a prominent change in reproductive and productivity traits, which were a means of reflectance to natural selection and genetic drift. These traits shift found to aid in their persistence in climate change. This ensures that sky islands mountain chain is a natural laboratory to study the long-term response to climate change (Love *et al*., 2023a). Majority of such studies on sky islands took place on American sky islands, and there were only a few studies over Western Ghats sky islands that too with little study over plant species. As per several studies the sky islands are considered to be a powerful tool to study evolutionary process, as they are habitats with limited gene flow due to climatic or geographical barriers. Several studies on sky islands in United States highlighted its vulnerability amplified by a decline in populations of nearby ecosystems, limited habitat, and the adverse impact of climate change over such habitat. The United States found to have already established "sky island alliance and the national fish and wildlife foundation's sky islands grasslands conservation program" to conserve the sky islands (Love *et al*., 2023b). This raises the importance of the introduction of conservation measures over the sky islands all over the globe.

Several studies in plant ecology have integrated ecological experiments with epigenetic analyses to understand the impact of epigenetics on plant phenotypes, stress responses, habitat adaptation, and range distributions. Majority of studies were focused on the model species with well-established genomic resources, so these lack ecological realism. So, introducing this concept to non-model species is essential for understanding epigenetics in plant ecology in the real world. However, adapting genomic tools of non-model species would pose challenges because of their large and complex genomes. To understand the genome functioning with respect to ecological

process of the real world, such collaborative studies considering together molecular geneticists, ecologists, and bioinformaticians are crucial (Richards *et al*., 2017). The combination of population genetic analyses with organism based studies, allowed the validation of gene identifications which provided an in-depth understanding of the evolutionary processes (Tiffin and Ross-Ibarra 2014). The potential of genetic rescue to improve fitness in small and endangered populations is a well-known fact. However, it remains untouched in conservation practices, which are aimed at protecting threatened populations. Future research directions are proposed to guide the development of genetic rescue strategies. Genetic rescue is an important tool that can efficiently address biodiversity loss, improve population resilience, and highly benefit from the integration of molecular advancements in population genomics (Whiteley *et al*., 2015).

2.2. Floristic diversity of Western Ghats

Hooker, Chatterjee and Clarke called the Western Ghats as Malabar province and Prain named it India aquosa. This phytogeographical region is the wet forest area that experiences the impact of the southwest monsoon (Clarke 1898, Hooker 1904, Prain 1857-1944, Chatterjee 1940). The Portuguese settlement in Goa and the Dutch possessions in Malabar played a pioneering role in the scientific exploration of the regional flora. Garcia De Orta created "Coloquis dos Simples", a catalogue of indigenous medicinal plants in India (Garcia de Orta 1563). Later, between 1678 and 1693 Van Rheede published “Hortus Malabaricus”, a monumental work dedicated to the plants of Malabar (Van Rheede 1678-1693). In the mid-nineteenth century, British botanist Robert Wight made significant contributions to floristic studies in Peninsular India. He published a series of illustration books focusing on plants from South India. Among them, the notable publications include "Illustrations of Indian Botany" (Wight 1840-1850) and "Icones Plantarum Indiae Orientalis" (Wight 1838-1853). Together with Walker-Arnott and George-Arnott, Wight published "Prodromus Florae Peninsulae Indiae Orientalis" (Wight *et al*., 1834), describing several new taxa. Other important works in the 19th century include “Genera Plantarum” by Betham and Hooker (Betham and Hooker 1862-1883), “The Flora Sylvatica for Southern India" (Beddome 1869-1873), and "Flora Indica" (Roxburgh 1820-1824). From 1872 to 1897, with the assistance of numerous botanists, Hooker published “The Flora of British India” covering Phanerogams of India (Hooker 1872-1897). “The Flora of the Presidency of Madras" (Gamble and Fischer 1915-1936) and "The Forest Trees of Travancore"

(Bourdillon 1908) are other essential works. Other notable publications include "Flowering Plants of Travancore" (Rama Rao 1914), "Flora of Anamalai Hills" (Fischer 1921), "Flora of South Indian Hill Stations" (Fyson 1932), and Rare and threatened plants of South (Henry *et al*., 1979). In 1940, Chatterjee conducted an examination of the floristic divisions based on the presence of endemic species, and the Western Ghats alone he reported1500 endemic species (Chatterjee 1940).

Botanical Survey of India published "Flora of India". It has five volumes covering various plant families published so far (Sharma *et al*., 1993, Sharma and Balakrishnan 1993, Sharma and Sanjappa 1993, Hajra *et al*., 1997, Singh *et al*., 2000). Floristic studies have been carried out in several districts and protected areas of Kerala, with some being completed and others currently ongoing. Notable publications on the flora of Kerala include "Flora of Calicut" (Manilal and Sivarajan 1982), "Flora of Cannanore" (Ramachandran and Nair 1988), "Flora of Silent Valley tropical rain forests of India" (Manilal 1988), "Flora of Palghat district including silent valley National Park Kerala" (Vajravelu 1990), "Flora of Thiruvananthapuram" (Mohanan and Henry 1994), "Flora of Thenmala (i.e. Environs)" (Subramaniyan 1995), "Flowering Plants of Thrissur Forest (Western Ghats, Kerala)" (Sasidharan and Sivarajan, 1996), "Flora of Nilambur (Western Ghats, Kerala)" (Sivarajan and Mathew, 1997) and "Flora of Agasthyamala" (Mohanan and Sivadasan, 2002). "Flora of the Palni Hills, South India" (Mathew 1999), The flora of Palakkad district encompasses the identification and detailed study of 1,355 species from 732 genera representing 146 families of flowering plants. Notably, it was found that 25% of the flowering plant species listed in the Palakkad flora were already included in the Flora of the Presidency of Madras. A significant publication by Gamble and Fischer which documented a total of 4,516 species (Vajravelu 1990).

There were many flora of protected areas such as Shenduruny Wildlife Sanctuary (Sasidharan 1997), Periyar Tiger Reserve (Sasidharan 1998), Chinnar Wildlife Sanctuary (Sasidharan 1999), and Parambikulam Wildlife Sanctuary (Sasidharan, 2002). The "Checklist on the Flowering Plants of Kerala" was published in 2004 (Sasidharan 2004) and 734 taxa were recorded in it. Several other thesis studies about multiple hillocks within the Western Ghats have been completed, encompassing the Nelliyampathy forest area, while certain investigations are in progress.

In addition to all this, there are many new species discovered from the Western Ghats region, and of that, some were listed including *Litsea megamalayana*, a

species of the Lauraceae family, was found in the Megamalai Wildlife Sanctuary (Karuppusamy *et al*., 2023). *Strobilanthes scopulicola* was discovered in the high-altitude montane grasslands of the Nilgiri Biosphere Reserve (Thomas *et al*., 2020). *Ceropegia paulsamii*, a species of the Apocynaceae family, was found in the Megamalai Wildlife Sanctuary (Karuppusamy and Ravichandran 2017). *Impatiens kotebettii* and *Impatiens madapurae* were discovered from the Kotebetta and Bramhagiri mountains (Bhaskar and Sringeswara 2017). *Eriocaulon vamanae*, documented from the southern region of the Western Ghats in Kerala (Francis *et al*., 2020). *Strobilanthes malabarica* is a new species of *Strobilanthes* (Josekutty *et al*., 2016), *Myristica trobogarii*, a species of the Myristicaceae family, discovered from the southern region of the Western Ghats (Govind *et al*., 2020). *Hedyotis recurvata*, a species of the Rubiaceae family, described from the southern Western Ghats (Jiji *et al*., 2023). *Ardisia anamalaiana* found from the Anamalai Hills of the southern Western Ghats (Ravichandran *et al*., 2023). *Impatiens periyarensis*, species was documented from the Western Ghats region (Mani *et al*., 2020). *Elaeocarpus gadgilii* (Manoharan *et al*., 2021a) belonging to the Elaeocarpaceae family, and *Eugenia pokkudanii* (Manoharan *et al*., 2021b), a Myrtaceae member, *Glycosmis nelliyampathiensis* (Jabeena *et al*., 2021), *Tripogon sugathakumariae (*Jabeena *et al*., 2022), *Ischaemum sunilii (*Jabeena *et al*., 2022) are some of the new species reported from Nelliyampathy hill ranges of southern Western Ghats. These were some of the new discoveries from the Western Ghats, and there are many more species reported. This reflects over the high probability of speciation over the Western Ghats, especially over such insulator habit like sky islands. The sky islands of Western Ghats are isolated regions with complex topography and insulator features, that provides opportunities for speciation to occur. Therefore, the sky islands of Western Ghats are a hotspot for speciation, and are a resourceful area for studying the processes of evolutionary diversification.

2.3. Topographic features are drivers of species divergence.

A multidisciplinary approach is needed to understand the influences of geographic and ecological factors on species performance and distribution (Pironon *et al*., 2015). Landscape features, such as steep mountains and valleys act as barriers affecting dispersal patterns. The phylogeographic study of Chinese yew (*Taxus wallichiana*), a tree species, unveiled its population differentiation and phylogeographic patterns. Additionally, the study also suggested that localised refugia played an important role during the last glaciation in shaping the current distribution of Chinese yew (Gao

et al., 2007). Landscape fragmentation has relevant effects on ecological and evolutionary processes, thereby impacting various levels of biological organisation (Legrand *et al*., 2017). The limited dispersal of the night frog family (Nyctibatrachidae) across specific gaps within the mountain ranges of the Western Ghats of southern India, has led to clade endemism (Van Bocxlaer *et al*., 2012).

This geographic isolation within the Western Ghats has led to the diversification in two recently identified genera, *Sholicola* and *Montecincla*. The divergence of these montane bird groups from their Himalayan counterparts took place in the Miocene epoch, with the fragmentation of the previously uninterrupted moist forests in Peninsular India due to arid climatic conditions (Robin *et al*., 2017). There exists a direct link between species diversification and earth's history. The phylogenetic and biogeographic analyses on the parrot genus *Pionus* unveiled its montane diversification pattern. The distinct biogeographic differences between montane and lowland lineages are directly linked to the lineage diversification time (Ribas *et al*., 2007). Local adaptation has been observed in *Stylidium armeria*, across a narrow altitudinal gradient in the Bogong High Plains in Victoria. The findings revealed linear changes in leaf length, floral scape height, flower number, and an increase in abnormal flowers with increasing altitude. In a conditioned garden environment, the altitudinal pattern for flower abnormalities disappeared, but patterns for leaf length and scape height remained, but weaker. This shows that the heritable variation in these traits is caused by selection pressures from environmental factors varying with altitude. The unique selection pressures are yet to be identified, resulting in both co-gradient and countergradient patterns of variation (Hoffmann *et al*., 2009). The plant response features differ as per the habitat it exists and several other causes like glacial survival, in-situ survival, refugial isolation and allopatric-vicariant processes (Qiu *et al*., 2011).

The pattern of diversification differs between lowland and highland regions. Lowland diversification rates declined, possibly due to density-dependent cladogenesis, while highland diversification rates raised significantly during the Pleistocene. This is likely caused by habitat fragmentation and altitudinal migration (Weir 2006). The study on the flour beetles (*Tribolium castaneum*) displayed that the evolution at the expansion edge led to increased dispersal ability and decreased intrinsic growth rates. This evolutionary process results in both higher mean expansion speed and greater stochastic variation in speed among different population expansions. This showed that the rapid evolution of traits at the expansion edge of a population can

have significant effects on the speed and variability of range expansions. (Weiss-Lehman *et al*., 2017). Elevational gradients play a crucial role in facilitating speciation and are factors contributing to the maintenance of parapatric ranges. The montane regions act as "species pumps" and lowland regions as "museums" of wild species. The above concept is justified in the study on the riodinid butterfly genus *Ithomiola*, which challenges the traditional view. It reveals the strict distribution patterns based on geography and elevation, with upward parapatric speciation along elevational gradients. Young derived species are predominantly found in montane regions, while older basal species are confined to lowland areas (Hall 2005).

Guayana Highlands, noted for their remarkable biodiversity and endemism, the mountain peaks within this region found to harbour unknown taxa adapted to cold environments with high vicariance. The complex topography and diversity of this habitat contributed to its high levels of species diversity and endemism. This facilitated speciation in this habitat and has caused the dispersion of species into the surrounding lowland regions (Rull 2005). Multiple dispersal events and range expansions occurred with significant diversification in the Eocene-Miocene period. Molecular phylogenetic analysis of *Digitipes* revealed that the southern Western Ghats acted as a refuge for it during Cretaceous volcanism (Joshi and Karanth 2013). The complexity in intraspecific variation in *Populus tremula* and *P. tremuloides* in both their leaf and root morphological traits, implied its local adaptation and natural selection (Hajek *et al*., 2013).

Local adaptations happen even when gene flow is high, and the genetic makeup of a species has an important role in influencing local adaptation in the presence of gene flow. Advancements in genomics have notified the genetic basis of adaptation through gene flow. The three key features that control adaptation in relation to gene flow are the sources of adaptive variation influenced by gene flow, the impact of selection on migration and gene flow and the mechanisms that enable local adaptation to persist despite gene flow (Tigano and Friesen 2016).

Population genomics and genome-wide association studies are valuable tools for finding genes associated with functional traits and speciation (Ellegren 2014). The importance of geographic isolation in inducing genetic divergence in alpine plants is unveiled by studying the origin and migration patterns of *Hippophae tibetana*, an alpine shrub species in the Qinghai-Tibetan Plateau (Jia *et al*., 2011). The genetic divergence in *Kingiodendron pinnatum* from the Western Ghats of India is found to be

influenced by paleoclimatic conditions and the Palghat Gap which acted as a geographic barrier (Nair *et al*., 2019). The study on *Kalmia procumbens* genetic divergence unveiled that the long-term isolation of a species throughout the pleistocene is not necessary to explain its current genetic structure and to understand its biogeographic history (Ikeda *et al*., 2017). The geographic gap distance was found to have shaped the population genetic structure of the endemic frog species, *Indirana beddomii*, with significant genetic diversity between its populations (Nair *et al*., 2012). *Indirana semipalmata,* another endemic frog from the Western Ghats, showed intraspecific genetic variability, thereby reflecting the role of the geographical gap over its population. High genetic diversity was observed in its populations from the southern Western Ghats. The Shencottah gap was the one that was found to have played a crucial role in shaping the genetic structure of this frog species, through restricted gene flow and genetic clustering on either side of this gap (Kumar *et al*., 2020).

The ancestral divergence in the lion-tailed macaque population, dates back approximately 2.11 million years ago, across the Palghat Gap. Lion-tailed macaque troops inhabiting isolated forest patches within the Anamalai hills display reduced mitochondrial DNA diversity compared to troops residing in larger contiguous forests. The small populations in fragmented and isolated landscape found to have low genetic variability (Ram *et al*., 2015). A nested pattern of genetic diversification was observed within the montane bird community in the Western Ghats, reflected the influence of the Palghat Gap over it (Robin *et al*., 2015). The Palghat Gap in the Western Ghats, which separated the Nilgiri and the southern populations of Asian Elephants, along with the Brahmaputra River in northeastern India, are believed to have acted as barriers to genetic exchange in Asian elephants (Vidya *et al*., 2005). The study conducted on three montane plant species *Symplocos laurina, Gaultheria fragrantissima,* and *Eurya nitida* from the Western Ghats, found to have high level of genetic diversity within their populations (Deshpande *et al*., 2001). In the case of *Eurya nitida,* there was moderate genetic differentiation among populations in the Northeastern and Western Ghats regions, indicating strong geographic structuring and limited gene flow (Bahulikar *et al*., 2004). Despite the absence of morphological differences, *Gaultheria fragrantissima* exhibited significant genetic variation between the Western Ghats and Northeastern Himalayas (Apte *et al*., 2006).

The geographical isolations are major factors that introduce high genetic diversity between populations, thereby introducing several lineages. The red-lined tor-

pedo barbs (RLTBs), endemic to the Western Ghats, faced threats from habitat degradation, overexploitation, and fragmentation. Analysis of morphometric and genetic data of RLTB led to the identification of its distinct populations, with 12 lineages identified through multivariate analysis and eight evolutionarily distinct lineages identified through mitochondrial DNA analysis. Divergence time analysis of RLTB populations indicated that these lineages were separated over 5 million years ago through geographical isolation (John *et al*., 2013). Nine highly divergent lineages of *Raorchestes* bush frogs with significant genetic divergence were found from the Western Ghats. The findings highlighted the significance of sampling and genetic analysis in uncovering unknown diversity in tropical hotspots (Vijayakumar *et al*., 2016).

The analysis of the cytochrome-b gene from mitochondrial DNA was conducted on two Nilgiri tahr populations situated on either side of the Palghat Gap. The two variable sites identified within it revealed a small genetic distance between the populations. Phylogenetic analysis showed a clear clustering of samples based on their geographic location. The formation of the Palghat Gap in the Pleistocene period is believed to have played a role in the diversification of these populations (Joshi *et al*., 2018). The genotypic diversity within the populations of the dominant plant species *Solidago altissima* has a significant impact on arthropod diversity, community structure, and aboveground net primary productivity (ANPP). This notified the need to incorporate population genotypic diversity in addition to species diversity for a clear understanding of ecological dynamics and functioning (Crutsinger *et al*., 2006). Intraspecific gene sequencing analysis unveiled the genetic basis of phenotypic evolution and the evolutionary aspect of genetic variation (Messer *et al*., 2016).

The genetic structure of *Lupinus alopecuroides* across 10 isolated locations was examined through microsatellite DNA markers. Most populations showed low variation, some being monomorphic. However, significant genetic differentiation existed between populations. Founder effects, limited gene flow, and autogamy contributed to this pattern. Genetic relationships and lack of genetic-geographic correlation highlight founder effects and colonisation history shaping population differentiation (Vasquez *et al*., 2016). The phylogeographic patterns of *Avicennia germinans* and *Rhizophora mangle* in Florida were studied based on the genetic data from its 150 individuals. The aim of the study was to assess genetic diversity, potential phylogeographic breaks and quantify gene flow. Surprisingly, no significant phylogeographic

breaks were observed in either species, with a high level of genetic connectivity and limited geographic structure (Hodel *et al*., 2016).

The tropical mountains are found to be an important biodiversity hotspot, due to high hidden differentiation and constrained gene flow (Mastretta-Yanes *et al*., 2018). Genomic analysis of five diploid species within the *Eutrema* genus in the biodiversity hotspot of the Himalaya-Hengduan Mountains, including three species exclusively found in sky islands, uncovered the substantial genetic divergence within the species. The limited gene flow by geographical isolation has played a significant role in their diversification (Zhang *et al*., 2019a). Cape Rockjumper birds within the sky islands of southwest South Africa were found to exhibit minimal genetic diversity due to continuous dispersal across isolated mountain ranges, and no geographical differentiation (Oswald and Lee 2021).

The underlying genetics of plant adaptation are the areas where further investigation is needed. These include the need to validate gene function, understand molecular mechanisms, extend the research to non-model species, evaluate allele fitness in natural settings, and develop multifactorial studies. By addressing these research gaps, our understanding of plant adaptation can be enhanced (Anderson and Song 2020).

Genetic structures of Western Ghats butterfly species, *Heteropsis oculus* (high-elevation specialist) and *Mycalesis patnia* (lower elevations), were compared using Amplified Fragment Length Polymorphisms. *H. oculus* in sky islands, was found to have a stronger genetic structure with restricted gene flow in fragmented landscape. These are due to features of sky islands habitat isolation arising from habitat gaps and factors like temperature and rainfall, beyond habitat continuity (Sekar and Karanth 2013).

Canarina eminii an epiphytic plant from afromontane forest, the study of its population genetic structure unveiled the role of change in climate and geographical barriers in shaping its population (Mairal *et al*., 2017). The study on *Ficus tikoua* and its pollinator, *Ceratosolen* fig wasps, within the sky islands of southwest China, unveiled that there were three genetically distinct pollinator groups that had overlapping distributions and were found to be influenced by the region's complex topography and climate oscillations. This genetic variability in pollinators aligned with the morphological differences observed in male figs of their host plants. The spread of one pollinator group after the last glacial period does not align with the dissemination of its

associated plant phenotype, possibly due to the presence of significant natural barriers. These finding highlighted the interconnectedness between topography, climate change, and intraspecies differentiation, which contributed to the remarkable diversity within its population observed in southwest China (Deng *et al*., 2020).

2.4. Ecological niche modelling as a pioneering step in Biodiversity Conservation

Species distribution models (SDMs) has become popular in the field of forecasting the faith of biodiversity under unpredictable conditions caused by adverse human activities. The recent improvement in SDM highlighted its use in finding the impacts of climate change on various levels of biodiversity and in strategising conservation management. Collaboration of SDMs with ecological theory is necessary. That is to incorporate species migration, population dynamics, biotic interactions, and community ecology at various spatial scales of analysis of SDM (Guisan and Thuiller 2005). Precise forecasting of species spatial distribution ranges is essential for a wide range of application in ecological, evolutionary, and conservation purposes (Elith *et al*., 2006). The size of the sample and the traits of the species impact the precision and dependability of the bioclimatic model when predicting spatial distribution patterns (Shao *et al*., 2009). To evaluate models using presence-only data, multiple assessment measures are required. The models showed greater precision over species with narrow ranges, restricted environmental tolerance, and common characteristics of rare species. This showed the effectiveness of species distribution modelling for rare species and suggests its significance in devising conservation strategies (Hernandez *et al*., 2006). To predict species spatial distribution range shifts under future climate scenarios, bioclimatic models are usually employed to study the impact of climate change on biodiversity. However, the variability among projections from different models has raised concerns about their reliability in decisions. This raised the importance of using multiple models together within an ensemble forecasting framework (Araujo and New 2007).

The present context of adverse and unpredictable environmental change and other related ecological consequences has raised the significance of species distribution models (SDMs) in mapping and monitoring the distributions of animals and plants (Miller 2010). To raise the precision in prediction accuracy of species distribution models (SDMs), incorporating intraspecific variation data into it is the best method and this would provide valuable insights for population-focused conservation ap-

proaches (Biaou *et al*., 2023). To understand the distribution pattern of different taxa, continuous assessment through statistical models is essential under the present and future climate change and that would aid in devising better conservation management strategies. The combination of ecological knowledge with statistical methodology holds paramount importance over the mere usage of a particular statistical method. So, combining various approaches based on ecological insights to modelling techniques showed promising results in the field of applied ecology (Austin 2007). SDMs importance is raised while they are employed in evaluating the risk of extinction of species (Benito *et al*., 2009). Precise predictions of the impacts of climate change on species under extinction risks are crucial for the effective implementation of conservation (Kearney *et al*., 2010b). The utilisation of species distribution models in assessing the impacts of climate change has recently increased. However, their effectiveness in guiding large-scale conservation projects is yet questioned unless and until they offer more precise predictions beyond the basic ecological concept (Sinclair *et al*., 2010). SDMs are also important in predicting biodiversity losses, and invasion risks under future climates. The limited availability of high-resolution input data for future climate scenarios has limited its application. The BioPlant dataset serves as a standardised platform for ensemble modelling and serves as an example for developing high-defined regional datasets (Xiaojun *et al*., 2011). R packages provide a wide platform for modelling using several models and are important in devising the spatial coverage of samples and random sampling in various environmental research applications (Walvoort *et al*., 2010).

Spatial distribution analysis of *Zygophyllum eurypterum* from the northeast of Semnan Province was done with the Ecological Niche Factor Analysis (ENFA) method and where presence-only data was used for the analysis. In the study, the models used were the Artificial Neural Network (ANN) and Logistic Regression (LR)models. The obtained prediction outcomes were with high accuracy in predicting its spatial distribution, as they were closely aligned with actual vegetation maps of the species concerned. As per the prediction, *Z. eurypterum* was found to primarily occur in rangelands with specific soil characteristics in specific elevation ranges (Chahouki *et al*., 2012). So ENM-based approaches are found to be effective in exploring ecological, biogeographical, and conservation fields (Babar *et al*., 2012). However, ENM studies found to be limited in developing countries and aquatic environments (Barbosa *et al*., 2012).

Brainea insignis, a rare and endangered species, modelling done over it was efficient as it was able to effectively detect its high probable habitat suitable areas. This study also put forward the fact that the predictive models rely especially on topographic variables and may not accurately extrapolate spatial patterns over long distances to larger regions (Wang *et al*., 2012). So standardised modelling methods are important in modelling (SDM) and are important for ensuring comparability with the concerned species. An assessment of recent publications applying SDMs revealed that the majority did not ensure comparability, such as disclosing maximum probability ranges and the number of species occurrences used. The predictions of future distribution showed variation, with 80% of the species experiencing range contraction, while the best model suggested no net loss of habitat. This highlighted the importance of reporting and evaluating all decisions made during SDM generation to provide reliable management recommendations based on species biology and ecology (Rodriguez-Castaneda *et al*., 2012). Forecasting the spatial distribution of species in future with its co-occurrent ecological components was challenging in the field of ecology. This increases the need for incorporating the species interaction data, abiotic factors and biotic factors at various scales of modelling (Wisz *et al*., 2013).

The advancement in spatial data analysis and species distribution modelling in phylogeography has improved and widened its scope. ENMs have become a common tool in phylogeographic analysis, which included species-specific information on environmental tolerances (Alvarado-Serrano and Knowles, 2014). In *Tsuga chinensis* spatial distribution modelling was done using the BIOMOD package in R platform with nine different models. The findings of this study showed the efficiency of BIOMOD in reducing error and enhancing forecasting accuracy (Bi *et al*., 2013). Currently, BIOMOD-based ensemble modelling studies popularised in learning the spatial distribution of various taxa, especially done on terrestrial plants in Europe (Hao *et al*., 2019). The precision of ensemble modelling depends on three major features, and they were sub-model accuracy, diversity between subsample sets, and optimal ensemble method selection. This modelling method in the R platform employs a set of algorithms to generate multiple subsample sets, which are then selected based on clustering results to maximise diversity (Wang and Yan 2019).

SDM techniques have been developed since the mid-1980s and have become increasingly important tools in devising forest management strategies, particularly in the context of adverse climate change (Pecchi *et al*., 2019). Species distribution mod-

els (SDMs) are valuable tools for understanding and assessing the distribution of rare and endangered species, particularly for conservation purposes. In the case of *Veronica micrantha*, a vulnerable plant species, SDM aided in forecasting its distribution for devising effective strategies to conserve it. This method of study provided more details on species distribution and the underlying pressures they face, compared to the traditional methods (Sousa-Silva *et al*., 2014). The ensemble modelling strategy incorporates the sequential nature and inherent characteristics of the two data types and it utilises a constrained likelihood approach. This method showed improved estimation and prediction capabilities compared to conventional approaches (Jin and Deng 2015). Species-biotic interactions in ecological models are crucial, particularly for species-level to community-level distribution studies (Dormann *et al*., 2018). Edaphic factors in species distribution models (SDMs) also raise the effectiveness of prediction, especially for species with specific habitat requirements and ecological associations, as notified in the SDM study done over endangered orchid species *Spiranthes parksii* (Wang *et al*., 2019). SDM was found to be successful in discovering unknown populations of rare plants to relocate them (Dyakov 2015).

ENM precision in predicting the distribution of the species was confirmed by overlaying with the IUCN map in several cases (Valencia-Rodriguez *et al*., 2021). S-SDMs (Spatially Structured Species Distribution Models) are other modelling tools found to be effective and accurate in locating the occurrences of rare species (Rosner-Katz *et al*., 2020). The sdmTMB (Template Model Builder) in R, was found to have improved the accessibility of these models in species distribution modelling and other fields (Anderson *et al*., 2022). SDMtune, a software package, supported by three evaluation metrics and with four statistical methods, were artificial neural networks, boosted regression trees, maximum entropy modelling, and random forest. The package also aids in visualising the output. SDMtune has a unified and user-friendly framework, thereby showing the challenge of balancing model complexity (Vignali *et al*., 2020). Several studies showed that climate and environmental heterogeneity were the main drivers of plant diversity, whereas past environmental conditions were found to have a lesser impact. Machine learning models nowadays found to have a strong background in predicting species richness and phylogenetic divergence, highlighting their potential for understanding the intricate relationships between the environment and plant diversity (Cai *et al*., 2023).

Understanding the potential impacts of climate change on biodiversity is necessary to prevent species mass extinction under extreme scenarios, and is made possible through diverse model projections (Bellard *et al*., 2012). Analysis of the habitat models and their efficiency in predicting climate-driven range changes are done in different Australian plant species, which highlighted the choice of habitat model has a significant impact on projected outcomes (Fordham *et al*., 2012). Advancements in modelling techniques have the potential to enhance conservation strategies in a changing environment (Thuiller *et al*., 2008).

The constraints of species spatial distribution patterns in model predictions heighten their susceptibility to extinction. So, while evaluating the spatial distribution of the species, the extent to which it is distributed is pivotal when assessing the threat of extinction and devising effective conservation strategies in the challenges posed by the global warming (Schwartz *et al*., 2006). Studies on local adaptation indicate that certain species can quickly undergo evolutionary processes to avoid extinction, even in the face of rapid environmental changes, despite distribution and phenotypic plasticity constraints (Skelly *et al*., 2007).

2.5. Impact of climate variables on intraspecific variability

The plant response varies with climate variables. *Acer rubrum* leaf shapes were found to be correlated with mean annual temperature (MAT), and its leaves from colder climates exhibited a toothier and more dissected morphology. Such patterns of relationships between leaf traits and climate can provide valuable insights for reconstructing past climates. Conversely, *Quercus kelloggii* showed less sensitivity to MAT, and its leaves with small teeth were more common at high-elevation sites due to windy conditions and sufficient water availability (Royer *et al*., 2008). The study on the intraspecific variation of *Helleborus foetidus* in functional leaf traits of its 138 populations from various locations revealed that its eight leaf traits showed significant variation. This suggests that such variation in population holds paramount implications in broadening its ecological range, enhancing the stability and persistence of plant populations and communities, and offering valuable contributions to trait-based community ecology models (Herrera *et al*., 2015). The investigation on *Phragmites australis* unveiled its intraspecific variation and adaptation strategies in response to climate and environmental changes. There was substantial variation in functional traits within the species across different regional scales (Zhichao *et al*., 2022). Biotic and abiotic factors appear to have control over the traits within a species. A study

done over three important functional traits (plant height, leaf area, and specific leaf area) in dominant plant species within Mediterranean shrublands, revealed that abiotic factors, such as rainfall, and biotic factors, such as the traits of neighbouring plants and crowding, had notable impacts on the observed ITV (Le Bagousse-Pinguet *et al*., 2015).

Intraspecific leaf anatomical trait variability analysis was done over *Sesleria rigida* in Serbia. Among the traits, the leaf's anatomical traits were found to have a significant correlation with precipitation and humidity and no correlation with temperature. So not all climate variables are ubiquitously responsible for the vicariance shown by population, the impact of each varies with species and habitat (Kuzmanovic *et al*., 2012). Life history, plasticity and local adaptation have been found to play an important role in the tundra plants. Remedial plant responses to warming are observed across their species population range. Thereby they adapt to local climates, especially in terms of growing season temperature, but may experience more decline in population size due to rapid climate change rates and local adaptation. So as per the study the importance of considering the entire species range was put forward, instead of aiming just on trailing edge populations, especially in forecasting the distribution of species to study the impacts of climate change on its abundance and distribution. It also highlighted the need to consider demographic mechanisms and local adaptation when assessing the effects of climate change on biodiversity (DeMarche *et al*., 2018). Leaf width of *Dodonaea viscosa* subsp. *angustissima* was found to be influenced by regional maximum temperature and then its leaf area was influenced by minimum temperature (Guerin *et al*., 2012). *Quercus variabilis* morphological variabilities were found to be a means of adaptation to climate change, where its leaf area and width were more sensitive to temperature (Wu *et al*., 2010). Furthermore, the leaf size and shape of plants are the two morphological traits that were found to have changed over several decades in response to climate change (Li *et al*., 2020, Peppe *et al*., 2011).

Morphological parameters of a species are the one which have the potential to reflect on changes in population processes, as these traits are readily observable and quantifiable. This enables the researchers to gain a better understanding of how various species respond to environmental changes. Climate shifts were found to be primarily affecting the quantitative morphometric characteristics rather than qualitative ones (Khan *et al*., 2020). The investigation on the distribution and origin of a montane lizard, *Sceloporus jarrovii*, in the Madrean sky islands revealed its future warming

response. In the study, they used field surveys, climate data, genomics, and physiology data to compute the influences of climate on its distribution and found that past climate change affected their current range, with warm winters surprisingly linked to its absence at lower elevations. Lizard body temperature was found to have a negative correlation with climate. Different range populations diverged millions of years ago, remaining distinct despite glacial dispersal chances (Wiens *et al*., 2019).

Morphological variability in Five *Jatropha* species from the Tehuacan-Cuicatlan Biosphere Reserve was found to have a positive correlation with altitude and temperature gradient. These interspecific morphological variations between *Jatropha* species enabled it to adapt and thrive in diverse altitude and temperature conditions (Hernandez-Nicolas *et al*., 2017). The impact of climate on intraspecific trait variation within local areas, suggests that plant populations from different locations may exhibit variability in responses to climate change (Iozia *et al*., 2022). Intraspecific variability in *Copaifera langsdorffii* is a means of adaptation to a changing environment and for escaping from the risk of local extinctions. The morphological and physiological characteristics of this species, such as leaf area, petiole length, and quantum yield, are significantly influenced by the climate of the local environment. Populations living in a wide range of diverse environments found to have greater plasticity, thereby indicating their ability to adapt to different conditions. The ability of this species to modify its traits in response to varying climates is a relevant factor, which showcases its ability to withstand and persist in different habitats, thereby coming across the challenges posed by climate change (Souza *et al*., 2018). An investigation on the carbon and water cycling dynamics of a forest ecosystem within the Madrean sky islands using the Eddy covariance method unveiled that this forest has functioned as a net carbon sink. These are sourced with more carbon content in comparison with other montane forests of the western USA. Mild winter temperatures and a bimodal precipitation pattern supported the activity of the forest. Additionally, the study mentioned the impact of climate change on water and carbon cycling within montane forest ecosystems (Knowles *et al*., 2020). To have an in-depth understanding of plant distribution patterns and to identify the populations which have the ability to survive in the changing environment, are made possible by introducing both the concepts of genetic and morphological trait variation together in research (Van Nuland *et al*., 2020).

Boechera stricta, a perennial forb species from the Rocky Mountains showed micro-geographic genotypic variation, indicating its genotypic local adaptation among different environments and also showed varying levels of adaptation in garden conditions. This was due to the influence of temperature, elevation, and herbivory on the species important fitness components including germination success, survival, and fecundity (Anderson *et al*., 2015).

The changing rainfall patterns made the tropical montane cloud forest in the southern Western Ghats more vulnerable (Murugan *et al*., 2009). Tropical species seem to exhibit narrower thermal tolerances, reduced dispersal, greater population structure, increased cryptic diversity, and higher rates of speciation when compared to temperate species. The influence of rapid climate variability plays a crucial role in shaping global diversity patterns and that significantly impacts the vulnerability of tropical montane species (Sukumar *et al*., 1995). This raised the urgent need for research on thermal tolerances and acclimation potentials of the species to devise effective conservation strategies in such areas. Modelling was used in testing the vulnerability of tropical mountaintop plant species in northeast Queensland, Australia. The resultant projection depicted that there would be a substantial decline in the best suitable climate niche of the species, potentially anticipating the gradual contraction in its current distribution (Costion *et al*., 2015).

The populations in different habitats within a region undergo adaptation depending on the environmental conditions. The phenology, leaf size, and survival of plants are influenced by average annual precipitation and temperature. Therefore, to understand this it is essential to study the plant materials sourced from local populations, as they are more likely to undergo adaptations crucial for its survival (Baughman *et al*., 2019). A study on pollen flora of endemic plants in the Western Ghats notified that rainforest vegetation was once widespread across the subcontinent but is now confined to a small region of Southern Western Ghats. The abundant rainfall and reduced dry periods of the southern Western Ghats, despite climate change, have created a favourable environment for the persistence of ancient tropical vegetation lineages (Prasad *et al*., 2009). The expected future climate scenario is reported to cause significant alterations within ecological systems and their processes (Belant *et al*., 2010).

The phenotypic plasticity of a species is its capacity to modify its physical traits in response to changing environmental conditions and is vital for its survival.

The diverse range of characteristic traits of a species maintains its heterogeneity and enables it to survive under a wide range of environmental pressure. Among the various traits, a specialised morphological trait is retained under an environmental condition and that is called phenotypic specialisation (Gratani 2014). In demographic models, the influence of phenotypic plasticity on a population's adaptive response to varied environments is assessed. This raised the understanding of how plasticity affected population dynamics and improved predictions of population persistence in changing environments (Reed *et al*., 2010). Several studies showed the impacts of climate change on ecological networks and ecosystem services. The complex and nonlinear nature of climate change responses necessitate the need for advanced research in this to have a core understanding of the effects of climate change on ecological systems (Walther 2010). A common milkweed, *Asclepias syriaca*, was investigated to study its adaptation, growth and defence traits along its latitudinal range. The findings indicated that climate-driven variations were found in growth traits and this was thereby found to have played a role in the development of defencive traits in milkweed in response to herbivory (Woods *et al*., 2012).

The plant population adaptability depends on the rate and the potential of the plant for adaptive evolutionary responses (Shaw and Etterson 2012). Dominant tree diversity analysis has a broader applicability in forest management (Dale *et al*., 2010). Understanding the drivers of evolutionary change and identifying species with varying adaptive capacities are vital for assessing their ability to thrive or decline. Collaboration of evolutionary processes into management strategies is critical for minimising biodiversity loss in the context of rapid climate change (Hoffmann and Sgro 2011).

The rapid climate change in fragmented landscapes overcomes adaptation capacity, leading to substantial genetic changes in plant populations. This results in unexpected alteration in species presence and abundance, reduced persistence to environmental disturbances and an increased risk of extinction. So, in such landscapes, extensive research is needed to understand the causes and consequences of maintaining or losing climate-related genetic diversity in plants (Jump and Penuelas 2005). Phylogeographic studies help to understand the genetic exchange history, differentiating between gene flow and common ancestry. Plant populations are affected by shared ancestry and patterns of genetic exchange. The interconnection between plants

is particularly complex due to diverse reproductive ecology and weak reproductive barriers between morphologically diverse species (Schaal *et al*., 1998).

The effect of global climate change (GCC) on genetic diversity is important for predicting species future distributions. It is a potential research direction that puts forward the importance of cryptic diversity and conservation efforts for biodiversity by understanding the implications of GCC in it (Pauls *et al*., 2013). *Artemisia californica*, a shrub showed clinical variation in most of the traits with respect to varying precipitation. The labile responses of plants to environmental diversity varied among populations, and were found to be strongly correlated with the source site's precipitation patterns. The findings suggest the importance of integrating evolutionary processes with global change models for accurate predictions of plant responses to climate change (Pratt and Mooney 2013). To understand how species respond to climate change, an interdisciplinary approach of study that considers habitat changes, population dynamics, and ecological interactions is necessary. The connection between life history, disturbance regime, and distribution pattern, plays a critical role in determining the risk of species extinction under climate change (Keith *et al*., 2008).

Natural selection, in collaboration with genetic linkage, shapes the genomic pool of nucleotide polymorphism (Cutter and Payseur 2013). Epigenetic mechanisms in forest trees are a major source of adaptive traits, and that can be adopted in biotechnology, plant breeding, and ecosystem conservation. Genotype-by-environment interactions (G×E) are relevant in unveiling the alterations in genetic effects influenced by the environment, which include diverse genetic factors and molecular variations. Transcriptome studies and the identification of genes involved in G×E provide further understanding of this phenomenon (Des Marais *et al*., 2013). Genetic mechanisms play an important part in introducing plant adaptation in natural populations (Anderson *et al*., 2013).

Using genomic data and species interactions in predicting the species response to climate change increases the prediction accuracy. The studies on forest trees in research made a significant contribution in understanding the response of plants to climate change, as they offer an extended timeframe for interpretation (Alberto *et al*., 2013). To understand the response of populations to changing environment in natural settings a theoretical and empirical approach to the study is necessary (Chevin *et al*., 2013). Plant species may encounter challenges to cope with climate-driven range shifts due to dispersal limitation. Here the significance of animals rose as they are

plant dispersal agents in an extensive range. In contrast, wind dispersal (anemochory) is significant for a small subset of plant species (Cunze *et al*., 2013). In a study of great tits (*Parus major*) in Wytham Woods, the authors parameterised a mechanistic model to estimate the rate of environmental change allowing for in situ adaptation. The focus was on the role of phenotypic plasticity in population survival, particularly in response to changes in early spring temperature affecting temporal synchrony between birds and food resources. While conservative estimates suggest a low risk of population extinction under expected temperature change, the importance of phenotypic plasticity varies with life histories, raising the need to understand its determinants and constraints for assessing risks in changing environments (Vedder *et al*., 2013).

Phenotypical plasticity was observed in 72 individuals of Afrotropical butterfly that exhibited different phenotypes in response to variations in dry and wet seasons. By knowing the gene expression patterns, the researchers discovered that there was significant variation in gene expression of phenotype variants between populations (Oostra *et al*., 2018). Theoretical studies and quantitative genetics, aid in predicting the complex interactions between genetics, demography, and evolution (Shaw and Etterson 2012). The increase in flowering time remarks the increased strength of selection and evolutionary responses under present climatic conditions (Anderson *et al*., 2012). The rugged alpine terrains play an important role in creating small-scale microclimatic variation, which increases species diversity and this potentially enables plant migration to local micro-refugia in response to climate change. The presence of microclimate variation and ecological disturbance contributes to the promotion of species diversity and adaptation (Opedal *et al*., 2015). Abiotic factors play a relevant role in shaping plant defences independent of herbivory (Abdala-Roberts *et al*., 2016). The impact of genetic variation on ecological interaction networks potentially impacts community stability, and evolution within the community (Lau *et al*., 2016). The rapid rate of environmental change poses significant challenges in conservation initiatives (Jackson and Sax 2010).

2.6. Impact of edaphic factors on intraspecific variability

Spatial heterogeneity in resource availability, such as soil characteristics, topography, and environmental disturbances significantly impact the composition, structure, and dynamics of forest ecosystems. The interconnection between soil, topography, and environmental disturbance is of particular importance in understanding

the patterns and processes shaping tropical forest ecosystems (Bunyavejchewin *et al*., 2019). Intraspecific variation in vegetative height was observed in taxa in response to changes in edaphic factors. However, individual species exhibited diverse trait responses that did not ubiquitously affect the entire community (Siefert *et al*., 2014). Soil resources and topography are key factors promoting the variation in tree community composition (Baldeck *et al*., 2013).

The plant *Eriogonum calcareum*, from volcanic outcrops in Idaho and Oregon, has two distinct varieties: *Eriogonum calcareum* var. *calcareum* and *Eriogonum calcareum* var. *sceptrum*. These varieties differ in morphology, niche geography and ecology. *Eriogonum calcareum* var. *calcareum*, in the northwest, has sessile involucres with hairy tubes, shorter scapes, and narrower leaves. *Eriogonum calcareum* var. *sceptrum*, in the southeast, has pedunculate involucres, longer scapes, and wider leaves. *Eriogonum calcareum* var. *calcareum* found in soil with higher Mg and K, lower pH and Ca/Mg ratio, compared to *Eriogonum calcareum* var. *sceptrum*. The morphological and ecological divergence between two varieties of *Eriogonum calcareum* was investigated and the findings showed that population differentiation was likely driven by geographic isolation and edaphic selection (Brown and Mansfield 2017). *Eriogonum crosbyae*, showed phenotypic plasticity in associations with soil properties and was found to display edaphic specialisation. The species showed high genetic and phenotypic diversity within their three distinct genetic groups. The predictive power of soil properties was found to be limited (McClinton 2019).

Environmental factors play a crucial role in shaping the ecological characteristics of plant communities and their spatial patterns. Potassium concentration, electrical conductivity, organic matter content, soil condition, human activities, and grazing pressures are some of the features that found to have a substantial impact on the distribution, composition, abundance and formation of vegetation in each landscape (Iqbal *et al*., 2021). Habitat differentiations are more evident in savannic formations, while plant diversity does not exhibit significant differences among forest habitats. Soil analysis and vegetation assessment done over savannic and forest formations showed that soil variables have a notable impact on both the structure and diversity of vegetation, particularly in savannic formations. (Rodrigues *et al*., 2018). In high-elevation Tibetan alpine meadow communities, intraspecific trait variation is found to be the key factor that shaped their populations. The study illustrated that as environmental conditions become more challenging, intraspecific trait variation in multiple

traits becomes increasingly important. These variations are influenced by both inter and intraspecific responses to limited soil resources, particularly to phosphorus deficiency. The intraspecific trait variation reduces the impacts of environmental filtering and offers a new perception of eco-evolutionary processes that improves and maintain community stability and ecological function (Niu *et al*., 2020).

Quercus cerris and *Quercus frainetto*, are two tree species in the Sumadija region. Among them *Quercus cerris* displayed greater intraspecific variability compared to *Quercus frainetto*. The observed patterns of population differentiation also differed between the two species, indicating the diversity in the factors that contributed to the intraspecific variability (Jovanovic *et al*., 2022). Understanding the role of each environmental factors is crucial in apprehending the process of forest succession. Collaborating edaphic variation with climate change research and incorporating it into species distribution models increases its potential. Identifying climate refugia and recognising the species with adaptability that buffer against climate change impacts. Like climate variables, edaphic variation also provides valuable contributions to managing and conserving ecosystems (Hulshof and Spasojevic 2020)

It is relevant to consider multiple ecological factors when studying the local adaptation of a species. The investigation on *Ruellia nudiflora*, gave fruitful evidence for local adaptation influenced by soil source at one site, indicating its specialisation to specific soil characteristics (Ortegon-Campos *et al*., 2012). A study was conducted on the Horqin Sand Land of northern China on 34 plant species along a gradient of restored sand dunes. There in the study soil characteristics and plant functional traits were considered as baseline data. As per the study it is found that the intraspecific variation in the studied species found to have played a role in plant coexistence and the persistence of herbaceous plants in sandy grassland habitats. However, the impact of intraspecific variation in response of community traits to habitat changes was limited (Zuo *et al*., 2017). Additionally, the presence of tree species in humid tropical environments was found to be influenced by the properties of the soil (Montagnini and Sancho 1990).

Nutrient availability is another factor that causes interspecific competition among plants. In environments with high nutrient levels, the competition for nutrients becomes irrelevant and there the competition remains over the other factors like light, thereby favouring the dominance of fast-growing perennial species with traits that facilitate nutrient retention. In contrast, in nutrient-poor environments, traits that mini-

mise nutrient losses are recommended, leading to lower growth rates. These distinct traits exhibited by species from nutrient-poor and nutrient-rich habitats prevent them from successfully colonising each other's environments. These trait differences also impact litter decomposition and nutrient cycling, where plant species dominance and nutrient availability reinforce each other, ultimately contributing to ecosystem stability (Aerts 1999). Research undergone in the Pe-de-Gigante Reserve located in Sao Paulo, Brazil, highlighted the significance of soil properties in shaping the distribution and characteristics of vegetation within the study area (Cruz Ruggiero *et al*., 2002). The divergence in Lasthenia species is found to be influenced by soil-related factors. This study revealed that there exist variations in the tolerance level of closely related and reproductively isolated taxa in different soil conditions. This substantiated the role of soil-related factors in the diversification of the *Lasthenia* genus. *Lasthenia* was found to be a valuable model for studying the interplay between adaptation, reproductive isolation, and speciation (Rajakaruna 2003). The impact of small-scale edaphic gradients on adaptation, reproductive isolation, and coexistence of *Lasthenia californica* and *L. gracilis*, the two closely related wildflower species was examined. It was found that the edaphic factors such as soil water content and mineral concentrations contributed to diversity in fitness. Limited dispersal and early-season mortality of migrants may have contributed to the reproductive isolation of *Lasthenia*. Continuous habitats support closely related but differently adapted taxa, providing a perception of the generation and maintenance of species in natural environments (Yost *et al*., 2012). *Protium alvarezianum* and *Protium subserratum* are two tree species found in the Amazon and exhibited differences in the edaphic specialisation. The *P. alvarezianum* has stronger population differentiation with respect to geographic distance. In contrast, the species with broader soil tolerance *P. subserratum* exhibited less population differentiation, unless specific habitat features acted as barriers (Fine *et al*., 2013).

A study was done on 550 tree species in central Panama to understand their response to environmental factors. As per the study, it was found that dry-season intensity and soil phosphorus strongly influenced the distribution of more than half of the species. These findings highlighted the role of soil phosphorus in limiting the distribution of tropical trees. This understanding played a vital role in understanding species distribution limits and in predicting changes in forest composition (Condit *et al*., 2013). The effect of phylogenetic signals in local habitat niches on the phylogenetic

structure of forest communities varies depending on the study site (Baldeck *et al*., 2013).

A study conducted in the semiarid region of Brazil underlined the interconnection between landscapes, soils and vegetation. In this study, the pedological similarities within catenas and the important soil attributes that influenced the segregation of plant communities were identified. Also noted that there existed a fertility gradient, where plant communities grouped based on similar landforms. Important soil features such as sodium saturation, phosphorus, aluminium saturation, and sand content, played vital roles in segregating plant communities along the gradient, with uplands and cerrado vegetation at one extreme and slopes with dry forests at the other, while lowlands occupied the central position (Arruda *et al*., 2015).

The impact of soil variables on phylogenetic beta diversity was more significant than that of topographic variables. The observed patterns of phylogenetic beta diversity are supported by previous findings of niche similarity among closely related species. This showed the importance of phylogenetic signals in shaping the phylogenetic structure of tropical tree communities, particularly among closely related species that share similar habitat niches (Baldeck *et al*., 2016). Plants adapted to specific soil types provided an important perception of evolutionary processes, local adaptation and phenotypic plasticity playing important roles in soil specialisation. The rapid evolution within lineages enabled the study of parallel evolution and pinpointed the involvement of genetic diversity in soil adaptations and contributions to reproductive isolation. However, edaphic specialists may experience less competitiveness and high vulnerability to herbivory in diverse soils, indicating a high cost of tolerance and strong divergent selection. Interactions with microbes, herbivores, and pollinators influence soil specialisation by affecting tolerance and gene flow between populations. Furthermore, climate change has implications for edaphic specialists, as it alters competition dynamics and can expand or limit their ranges based on pre-adaptations to stressors (Rajakaruna 2018). Soil heterogeneity is a relevant factor in raising the diversity of ectomycorrhizal (EM) fungi (Mujic *et al*., 2016). Taxonomic and functional composition of premontane forests found to be influenced by soil nutrients and rainfall seasonality resulted in species richness differences similar to those observed across elevation gradients. Therefore, in-depth knowledge of the local edaphic conditions has become vital for predicting the response of premontane forests to climate change (Prada *et al*., 2017). The relevant environmental driver of speciation in the

Mediterranean Basin was found to be the high soil pH and dry-seasonal climate conditions (Buira *et al*., 2021). In addition to that, the variation in species composition and basal area can be substantiated by soil nutrients and its topography (Vincent *et al*., 2018).

The effect of edaphic factors on the spatial distribution of African mahogany in the Dzanga-Sangha Dense Forest Reserve, unveiled that its non-random distribution was potentially due to specific soil characteristics. Here no topographic preferences were observed, and three of the four species showed significant associations with soil parameters (Hall *et al*., 2004). Investigation on habitat specificity of 35 plant species of *Protium*, *Crepidospermum*, and *Tetragastris* genera in the western Amazon region, showed specialisation in different soil types (white-sand, clay, and terrace soils) across the region. The evolutionary process within the *Protieae* tribe in the Amazon basin was with respect to soil specificity, indicating the significant role of edaphic heterogeneity in speciation (Fine *et al*., 2005). Diversity in character traits was found in closely related gastropod species that coexisted in the same habitat. The investigation was done on these gastropod species to justify the two hypotheses, namely ecological character displacement and allopatric adaptation. The findings suggested that the differences between the species are likely caused by interspecific competition, which supported the idea of character displacement. The study thereby demonstrated that both local adaptation and demographic processes contributed to the development of distinct character traits in sympatric gastropod species (Marko 2005).

The study on the influence of edaphic factors over seven fern species in northwestern Amazonia revealed that each fern had its own realised niches that differed based on its soil characteristics and inundation gradients. The variations were found in their distribution along these gradients, with some rarely co-occurring and others showing different abundance patterns. The divergence in distribution patterns suggests that ecological speciation played a significant role in the radiation of the *Polybotrya* genus, indicating the independent adaptation to different habitats by distinct evolutionary lineages (Tuomisto 2006). The relationship between soil characteristics and plant distribution in a tropical rainforest in Ecuador was investigated. The distribution patterns of pteridophytes, angiosperm ground herbs and palms exhibited a correlation with geographical distances. Soil and topographic characteristics were found to have an impact on the floristic patterns. Elevation differences, soil calcium, and sand content had an important role in terrestrial pteridophytes and palms distribu-

tion. These findings enumerated the vital role of soil factors in plant distribution and beta diversity, even at a local scale (Poulsen *et al*., 2006). The environmental variables were correlated with the spatial distribution of a few tree species in a tropical seasonal forest fragment in Luminarias, SE Brazil, unveiled its strong associations with soil pH and texture (Rodrigues *et al*., 2007).

The research on spatial distribution of species of neotropical forest plots in Colombia, Ecuador and Panama, showed that a significant portion (36-51%) of tree species found to have a strong association with soil nutrient content of that area. These associations underscored the crucial role of belowground resources in shaping tropical tree communities (John *et al*., 2007). Soil elements are found to be key factors influencing species selection and diversification in vegetation structures in the cerrado communities located in the Serra Negra Mountain range in Brazil (Abreu *et al*., 2012). Genetic drift and divergent selection have vital roles in driving population differentiation in edaphic specialist species. The study on *Primulina juliae*, a perennial herb from the Nanling Mountains, had a limited population in the eastern Chinese provinces of Jiangxi and Fujian. In the Gesneriaceae family, *Primulina* stands out as the most diverse genus, comprising approximately 180 species in China. The genetic variability was between the species and found to have a strong association with edaphic and climatic factors of the habitat. It was independent of spatial effects, thereby highlighting the importance of local adaptation (Wang *et al*., 2017).

Intraspecific variability and interspecific variability studies in diverse soil conditions provide a valuable perception of the role of edaphic factors in natural selection and evolution. Studies over the past five decades showed that the vital cause of plant diversification is its response to heterogeneous soil conditions, such as serpentinite outcrops, mine tailings, guano deposits, and salt flats. These studies highlighted the adaptive differentiation of plants in relation to edaphic features and showed the connection between adaptive traits and reproductive isolation among taxa. Advancements in genetic techniques and understanding of substrate tolerance genetics will advance our understanding of the vital role of soil factors in plant evolution (Rajakaruna 2004).

2.7. Intraspecific variability as the driver of speciation and evolution.

Organisms and the environment are interconnected and evolve together at various levels. Organisms display adaptations at both physiological and behavioural levels, and that enable them to subsist with short-term and long-term environmental fluc-

tuations. These adaptations have a high impact on how populations respond to both ecological changes and geographical variations. These responses have a vital role in shaping species distribution patterns within communities and understanding the coexistence of multiple species. The interlinkage between organisms and environmental variables has a high effect on the complex patterns of biodiversity and ecological dynamics observed in natural systems (Levins 1968). Intraspecific variation has the potential to influence ecological dynamics (Bolnick *et al*., 2011). While interspecific variation generally has a stronger impact on community-level trait responses, except for specific leaf areas, intraspecific trait variation can also have important effects on species interactions, population dynamics, and community dynamics (Griffiths *et al*., 2018). The responses of traits to intraspecific variation vary among species, leading to contrasting effects on community-level trait values (Kichenin *et al*., 2013). Species trait data, particularly focusing on intraspecific trait variability (ITV), are valuable tools for ecological reasoning and prediction in biological communities (Alofs 2016). Intraspecific variations play a significant role in moulding the relationships between variable traits and environmental gradients, such as leaf area and height influenced by many environmental variables (Jung *et al*., 2010).

The variability within a species plays a crucial role in the survival of that species in ever-changing environments. The interspecific variability has a greater effect on the overall response of the plant community with elevation change. This indicates that how plant species adapt to their environment is complex, so more focus should be paid to the role of intraspecific variability in moulding plant community structure (Kichenin *et al*., 2013). The importance of considering intraspecific functional variability using a single trait value to describe a species can mask significant variation along environmental gradients (Albert *et al*., 2010). The intraspecific responses on community level traits can be influenced by various factors such as dominant species and variations in trait-environment responses among species. Consequently, the contribution of intraspecific trait variability (ITV) at the community level may not always be vital. However, it is important to discern the role of local adaptation and phenotypic plasticity in carving community level trait responses to environmental changes (Lajoie and Vellend 2015).

Phenotypic diversity and variation within natural populations highlight its ecological dynamics. Traditional ecological models focus solely on trait, this means that total population density may overlook the ecological implications of trait variation.

Therefore, introducing trait variation into ecological models is needed for an effective understanding of ecological dynamics (Bolnick *et al*., 2011). A large range of variation in traits led to better alignment between traits and the environment, enumerating that trait variability contributes to adaptation under specific environmental gradients and the assemblage of communities based on trait characteristics (Mitchell *et al*., 2017). Epigenetic markers show a stronger relationship with functional traits compared to genetic markers. *Helleborus foetidus* showed epigenetic variation that contributes to its intraspecific functional diversity, and enabled it to adapt to diverse ecological conditions, despite limited genetic diversity (Medrano *et al*., 2014). Epigenetic variation is specifically important for long-lived organisms like forest trees, which have complex life cycles and exhibit traits such as extended lifespans, ecological dominance, wide geographic distribution and clonal propagation. Understanding the role of epigenetic variation in phenotypic plasticity and adaptive capacity provides an important perception of the conservation and management of plant species (Brautigam *et al*., 2013).

The rate of environmental change, the strength of natural selection, population characteristics, and genetic factors, influence the time taken by a species to become extinct. In a changing environment, the average characteristics of a population may lag behind the optimal traits but evolve concurrently. The extent of this lag plays a crucial role in determining the vulnerability of a species to extinction. So, it is important to consider the rate and magnitude of environmental changes in conservation efforts (Burger and Lynch 1995).

Recently speciation has been remarkably observed in tropical montane areas, while wild species are primarily found in lowland regions. Study on African greenbuls *Andropadus*, a montane species that has gone through extensive speciation events in the past 2.8 million years when compared to their lowland counterparts. These findings provide evidence supporting the idea that montane regions have served as a vital centre for speciation, particularly during climatic instability (Roy 1997). The concept of coextinction involves the vanishing of a species due to the disappearance of another species on which it depends. This phenomenon is observed in various interdependent systems, such as pollinating fig wasps and fig trees, parasites and their hosts, butterflies and their larval host plants, and butterflies and their host ants. Through the study, the researchers gauged that around 6,300 associated species are at risk of coextinction, as they rely on host species and are currently classified as endangered. These

findings exemplify the need to consider the potential impact of co-extinctions when estimating the high extinction risk of species (Koh *et al*., 2004). The migration rate of plant species, population growth rate, vegetation productivity, and the probability of extinction are interlinked with the rate of environmental change (Davis 2005). Two frog species from Australia, *Limnodynastes tasmaniensis* and *L. peronii*, showed variations in body size and sexual size dimorphism (SSD) with respect to climate and latitude (Schauble 2004). The diversity of pollinator communities was strongly influenced by landscape heterogeneity. This showed the interplay between landscape characteristics, climate change and land management practices and their vital impact on the abundance and diversity of pollinators (Senapathi *et al*., 2017). Comparing the ecological impacts of climate change in diverse environments such as polar regions and tropical marine ecosystems, showed that both plant and animal species respond to climate change at different levels, from individual species to entire community level. Despite the uncertainties over the surrounding future outcomes of communities and ecosystems under global change, it is evident that climate change has vital implications across various ecosystems (Walther *et al*., 2002).

Populations in small sizes are at risk of demographic stochasticity, as well as random and directional environmental changes. The influence of mutation and genetic variability is evaluated by estimating the critical rates of environmental change that led to extinction within a few tens to a few thousand generations (Burger and Lynch 1997). Throughout history, tree species found to have relocated their distribution ranges in response to climatic changes. This suggests that ancestral tree populations likely underwent adaptive differentiation in relation to latitude or elevation and acquired environmental sensitivities as they migrated (Davis and Shaw 2001). The response of species to environmental gradients varies, and that depends on the type of environmental predictors, and whether they influence indirectly or directly. It is thereby vital to critically evaluate the assumption of linear relationships between organisms and their environment (Austin 2002). Plants and animals experience various impacts in diverse ecosystems, at different levels of organisation, such as species and communities. Although the future evolution of communities and ecosystems under global change remains uncertain, the analysis consistently demonstrated a pattern of ecological transformations across different ecosystems (Walther *et al*., 2002).

The nature of the adaptive response and the extent of adaptation vary across different contexts and habitats, thereby reducing the effectiveness of general ecologi-

cal rules. Environmental variations can lead to both short-term and long-term morphological changes in organisms, improving their survival capacity. The terms "exposure", "experiences", "development", and "adaptations" are natural phenomena of morphological changes in organisms. These morphological variations are a response to environmental fluctuations (Millien *et al*., 2006). As per several studies, there found to be a positive correlation between specific leaf area (SLA) and the elevational range of species. Intraspecific variations in SLA generally align with the changes observed in the community mean SLA, although to a lesser range (Adamidis *et al*., 2021). The investigation done on the biodiversity patterns of endemic tree species in the Western Ghats at a large spatial scale yielded important insights into the diversification in the distribution pattern of endemics in the environmental gradient (Gimaret-Carpentier *et al*., 2003).

Various computational techniques exist to examine the intraspecific variability of species. Maximum likelihood methods are computational methods for deducing evolutionary trees based on nucleic acid sequence data. This approach offers advantages over traditional parsimony algorithms, as they consider potential variations in evolutionary rates among lineages. It also allows hypothesis testing on the constancy of evolutionary rates through likelihood ratio tests and provides an approximate estimation of the associated error in the inferred tree (Felsenstein 1981). The neighbour-joining method is a distance-based approach for constructing phylogenetic trees based on evolutionary distances. It involves clustering operational taxonomic units (OTUs) to minimise total branch length, starting from a starlike tree. This method provides a quick estimation of branch lengths and tree structure. Computer simulations were used to compare the efficiency of the neighbour-joining method with five other tree-building methods (Saitou and Nei 1987). The BEAST software package version 1.7 is a computational tool used for evolutionary biology, statistical phylogenetics, and population genetics. It employs Markov Chain Monte Carlo (MCMC) algorithms for Bayesian phylogenetic inference, divergence time estimation, coalescent analysis, phylogeography, and other molecular evolutionary investigations. The package includes the user-friendly program BEAUti, which offers advanced models for sequence and trait evolution. Additionally, it provides visualisation and summary tools for multispecies coalescent and phylogeographic analyses. BEAST 1.7 and BEAUti are open-source and can be accessed through the provided URLs (Drummond *et al*., 2012). The widely used BEAST software package facilitates Bayesian

phylogenetic and phylodynamic inference using genetic sequence data. It incorporates diverse evolutionary models, such as trait evolution and coalescent demographic models, through efficient Markov Chain Monte Carlo integration. With a user-friendly graphical interface, the software enables the construction of complex evolutionary analyses in a user-friendly manner (Suchard *et al*., 2018).

Advancements in population genomics have provided perception into the factors driving genetic variation, including the role of effective population size (Ne) in shaping genetic diversity and resolving "Lewontin's paradox". Linked selection influences overall genetic diversity and diversity variation within the genome. Additionally, a species life history can serve as a predictor of genetic diversity (Ellegren and Galtier 2016). In lowland Bolivia, species distribution patterns of woody species in tropical forests pinpointed their response to environmental gradients. Climate, particularly rainfall and temperature, was found to have a stronger influence on its species distribution compared to soils (Toledo *et al*., 2012). The high intraspecific variation in plant secondary metabolites (PSMs) enabled rapid evolution, and these trait variances were associated with environmental factors, which strongly respond to selection. PSM polymorphisms are important, and studies considering plant population diversity are indeed needed to understand the causes and consequences of intraspecific variation in PSMs. This showcased the benefits of plant diversity and suggested the directions for future research (Moore *et al*., 2014).

DNA barcoding is a valuable and efficient technique for accurately identifying plant species. However, the use of single-locus DNA barcodes has limitations in their effectiveness across all species. Recent studies suggested the utilisation of complete chloroplast genome sequences as a "super-barcode," although its widespread implementation is currently hindered by cost-effectiveness and efficiency constraints in standard laboratory settings. Nevertheless, the adoption of specific barcodes has the potential to enhance species and population-level discrimination (Will and Rubinoff 2004, Li *et al*., 2015). DNA barcoding has improved the field of species identification, but the optimal sample sizes to capture intraspecific haplotype variation yet remains a complex task (Phillips *et al*., 2019). Insufficient investigation of underlying processes has weakened the evidence supporting coevolutionary diversification, a key cause of plant and insect diversity. Current studies are predominantly focused on macroevolutionary patterns, overlooking the mechanisms and challenges associated with coevolution-driven speciation at various evolutionary scales. This highlights the po-

tential mechanisms, approaches, and essential criteria for demonstrating coevolutionary diversification, intending to inspire extensive research in this field (Althoff *et al*., 2014).

Climate change affects plant development through factors like increased CO_2 levels, higher temperatures, and drought stress. While some responses are common across species, others are specific to certain species and developmental stages. Leaf growth, reproduction and growth rate were found to vary with specific thresholds. However, the understanding of the molecular mechanisms behind these responses is limited, with only a few identified genes and unknown conservation status. Further research is needed to uncover the molecular mechanisms driving plant responses to climate change, particularly the combined effects of multiple factors. This research is crucial for mitigating the negative impacts of climate change on global agriculture (Gray and Brady 2016). Biodiversity plays a vital role in climate regulation and ecosystem stability. However, human activities and climate change have negatively affected biological resources. This review highlights the significance of biodiversity and puts forward the consequences of climate change on plants, animals, humans, and ecosystems. It also substantiated the necessity of effective conservation measures to overcome the impacts and safeguard the planet (Sadguru and Seema 2019).

Phylogeographic studies have shown that the genetic structures of species in isolated islands are influenced by interactions between topography, climate, and habitats. Global climate change, including Pleistocene climate fluctuations and the uplift of the Qinghai-Tibetan Plateau, had a significant impact on biodiversity and geographic patterns. Species that have exhibited specific responses, adjusted their distributions accordingly and thereby adapted to changing environments. To enhance the understanding of sky islands, future research should focus on interdisciplinary data, comparative phylogeographic studies and collaborative methodologies from various disciplines. This multidisciplinary approach will help to investigate the role of geography, climate, and biological factors in moulding biodiversity patterns, diversification and speciation, as well as in protecting species and genetic diversity (He and Jiang 2014).

Habitat destruction and overexploitation directly contribute to species loss, but extinction is often intensified by synergistic processes. Recent research estimates that the rate of extinction risk is more severe due to these ecological interactions (Romero-Munoz *et al*., 2021). Conservation efforts targeting individual threats may

be insufficient to face challenges posed by uncontrollable cascading effects of the environment. Plants experience several environmental stressors like climate change, land use, fragmentation, invasiveness, and biotic and abiotic stress. Plants respond to these stresses through local adaptation and phenotypic plasticity. The Role of Phenotypic plasticity in survival and ecological implications remains uncertain but is essential for responding to global change, particularly in the competition between native and invasive species. Species with higher adaptive plasticity thrive in new and unknown environments. Studies on phenotypic and genetic variations within species are particularly important for endemic and rare species to understand their impacts on ecosystem dynamics (Gratani 2014, DeMarche *et al*., 2018). Sky islands are a type of oceanic island. These oceanic islands are important in terms of their unique habitat with high biodiversity and endemism, in comparison to the mainland ecosystem. Moreover, significant differences in historical and projected human impact and land cover change are identified between islands and terrestrial areas. Islands are found to be more susceptible to current and future threats, indicating greater vulnerability. In addition to that, as the sky islands are on elevated mountains, it increases their vulnerability to environmental change. High endemism, rich biodiversity, smaller land areas and conservation risks of sky islands, rose their importance in global biodiversity conservation initiatives (Kier *et al*., 2009).

CHAPTER 3:
PRELIMINARY FLORISTIC DIVERSITY SURVEY ON SKY ISLANDS ACROSS PALGHAT GAP: AN IN-DEPTH ASSESSMENT FOR TAXA SELECTION

CHAPTER 3: - Preliminary Floristic Diversity Survey on Sky Islands across Palghat Gap: an in-depth assessment for Taxa Selection.

3.1. Introduction

Islands are unique ecosystems with clear boundaries that separate them from other ecological regions, these islands are broadly categorised into two primary groups: "Real islands" and "Terrestrial islands". Real islands are defined as land-masses surrounded by water, with no connection to a mainland. An example of this category is the oceanic island. Oceanic islands provide ideal environments for conducting experimental research and detailed investigations into ecologically driven evolutionary processes. Terrestrial islands, on the other hand, are identified by distinct environmental characteristics, often associated with variations in elevation. A distinct variant within the terrestrial island is the "sky island", where isolation arises not solely from elevation differentials, but from additional physical impediments. This unique isolation makes sky islands an ideal and controlled experimental context for the examination of various ecological facets, encompassing biodiversity and evolutionary dynamics through the lens of natural selection, community structure and dispersal mechanisms (Carvajal-Endara *et al*., 2017). So, research conducted on such islands is of higher importance, as adaptations displayed by species inhabiting these ecosystems were unique. These adaptations are through changes in plant functional traits (PFTs). These trait variations are responses either to isolation or in association (positively or inversely) with other ecological elements. So, variations in PFTs serve as valuable tools for anticipating how species will respond to environmental filters. So, to understand how evolution, colonisation and connectivity work, it's really important to have a good understanding of the whole island ecosystem (Whittaker *et al*., 2010, Swenson *et al*., 2012, Whittaker *et al*., 2017).

Biodiversity hotspots are such areas recognised for their rich diversity and endemism. One among them is the Western Ghats which stands out as an exceptional example even predating other hotspots of India. The Western Ghats region, owing to its distinctive geological history, vegetation cover, soil composition, edaphic characteristics, precipitation patterns, and other contributing factors creates a favourable environment that supports a wide variety of species. Specifically, the southern sector of the Western Ghats is renowned as an optimal ecological niche boasting a remarkable abundance of species and notably elevated levels of biodiversity. The significant areas

of heightened biodiversity are primarily identified to be in mid to high-elevation zones (Pascal 1988, Ramesh *et al*., 1991, Irl *et al*., 2020).

The Western Ghats, are estimated to harbour a significant portion of India's biodiversity, encompassing approximately 20% of the country's flora and fauna. This ecologically valuable region also accounts for approximately 6% of India's total geographical expanse. Notably, the Western Ghats is home to two biosphere reserves, 68 sanctuaries and 20 national parks, collectively contributing to its protected status (MacKinnon and MacKinnon 1986, Myers 1988). As per the evaluation conducted by Menon and Bawa on the Western Ghats from the year 1920 to 1990, it is found to have already lost 40% of its forest cover (Menon and Bawa 1997). Over the same period, the phenomenon of habitat fragmentation caused a fourfold increase in habitat reduction, which would have significantly impacted the spatial continuity of ecological domains within this region. Furthermore, there are reports of a remarkable decline in 83% of the coverage of its forest patches, underscoring the considerable transformation and depletion of the Western Ghats forested landscape (Cincotta *et al*., 2000). The above-mentioned historical records may have nearly surpassed at the presently evident stress of environmental pressures and heightened population demands resulting in reduced species persistence. The looming threats of deforestation and climate change further exacerbate the vulnerabilities faced by the Western Ghats (Simberloff and Abele 1976).

The vegetation of the Western Ghats (WG) is notably influenced by three prominent environmental gradients, and they are the reduction in rainfall from west to east, an augmentation in seasonality from south to north, and a temperature gradient in relation to elevation. The orographic impact of wind over the Western Ghats slopes causes the west-to-east rainfall gradient. So, the western slopes of the Western Ghats receive 7000 mm or more rainfall than the eastern slopes. The rainfall on the eastern slopes of the Western Ghats base drops to 1000-2000 mm. That is, the western slopes of WG experience dry seasons lasting about two to three months, and then towards the eastern slopes, the duration of the dry season gradually increases. Therefore, the endemism of WG conspicuously prevails along the western slopes of the Western Ghats. Then about the southwest monsoon on which WG relies, as it arises from the south, the rainfall decreases towards the north, causing variation in climatic conditions across the Ghats in north-to-south axis. The other major gradient is temperature, which drops with elevation of the Western Ghats. So, under such unpredictable cli-

matic conditions, the chance of WG species becoming extinct is high (Pascal 1982, 1988). Species extinctions and structural deterioration of habitat have a major impact on the ability of the concerned habitat to function (Anitha *et al*., 2010). So, to evade such extinctions, species are compelled either to uphold a substantial fundamental niche or rapid adaptability or swiftly respond to shifting environmental conditions, thereby effectively checking the dynamic alterations in the actual environmental space (Pascal 1982, 1988, 1990, Bose *et al*., 2016).

Temperature gradients are not only caused by elevation but also by biogeographic barriers, which in turn influence the structure, habitat and distribution of species. The Western Ghats are a continuous mountain range, where the continuity is breached by three such geographical barriers, among which the Palghat Gap holds significance of being the widest, and oldest and is also well-known for influencing the distribution of species in the Western Ghats. These biogeographical openings probably exert a formative influence on the arrangement of ecological communities and the constitution of species over the habitats within it and its surroundings. It may even have impacted the adjacent mountainous areas, thereby exhibiting distinct patterns of species distribution and community organisation. So, these gaps emerged to act as pivotal factors, driving the processes of speciation, and fostering biodiversity in the habitat under its vicinity (Robin *et al*., 2010, Fjelds *et al*., 2012, Ramachandran *et al*., 2017).

Unravelling the intricate interplay between geodiversity, edaphic diversity, climate change and plant diversity, poses a formidable challenge. Within this complex web of interaction between ecological components, the fundamental ecological dynamics that mould communities and biodiversity are species diversification, dispersal, ecological drift and niche selection (Abbasi-Kesbi *et al*., 2016, Vellend 2016). The impact of harsh environments on plants is ameliorated by their adaptation to stress, which in turn increases diversity. If edaphic heterogeneity influences and causes diversity in one trophic level, it will have an effect on the other trophic levels to which it is related (Van Nuland *et al*., 2016).

Soil and light availability are some of the major critical factors for preserving tree diversity over tropical ecosystems through niche differentiation (Silvertown 2004). Human activity, habitat fragmentation, and climate change also have a significant impact on the tropical tree ecosystems of the Western Ghats and its species composition (Nair 2019). The habitat disturbance reduces resource availability, which

would have an impact on the population and community dynamics (Denslow *et al*., 1998). According to Connell's theory, low or infrequent levels of disturbance result in the extinction of some species and a decrease in diversity due to competitive dominants, intermediate levels of disturbance result in an increase in diversity. When disturbances are frequent and severe, the chance of the local species becoming extinct is high because they cannot tolerate multiple disturbances (Wilson 1994). When disturbances stem from anthropogenic activities, the resultant degradation assumes a lasting and irreparable nature, potentially driving certain species within the affected region towards the brink of extinction (Hooper *et al*., 2004).

In a community, both biotic and abiotic components serve as filters, exerting influence over its functional attributes like morphological, physiological, and ecological traits. The manifestations of adaptation are evident in the organisms that manage to persist within the community's confines. An analysis of the plant life forms existing within an ecosystem unveils the intricate ways in which each form has undergone evolution in reaction to stressors and disruptions, alongside its reactions to shifts in climatic conditions (Shipley *et al*., 2016).

In recent years, there has been increased interest in utilising forest trees as a nonclassical model for studying population genetics, evolutionary genomics, and ecological genomics. These tree species possess several advantageous characteristics, including minimal domestication, extensive open-pollinated native populations, and abundant genetic and phenotypic variation. Consequently, they serve as excellent organisms for investigating the molecular mechanisms underlying adaptive divergence within natural populations (Gonzalez-Martínez *et al*., 2006). Tree populations, characterised by a comparatively sluggish pace of neutral evolution, demonstrate swift responses to natural selection. This feature renders the detection of selection signals potentially more straightforward in tree populations compared to numerous other groups (Savolainen and Pyhajarvi 2007). The floristic diversity within the Western Ghats, especially within the realm of sky island flora, presents an inexhaustible wellspring of novel species within a context where the genuine threat of species extinction looms. Therefore, the sky islands, particularly those situated proximate to the Palghat Gap, are assumed to have undoubtedly exerted a discernible influence upon their unique floral assemblages. So, the present chapter dealt with an in-depth assessment of the preliminary survey of floristic diversity of sky islands, to select the taxa which reflect over the environmental filters, thereby substantiating the hypothesis that the Palghat

Gap features has influence over the speciation, intraspecific morphometric and genetic variability on sky islands across it.

3.2. Methodology

3.2.1. Study area

The preliminary floristic survey was done on the sky islands of the Western Ghats encircling the Palghat Gap, situated within the Palakkad district. The designated study zone spanned a geographical expanse of 30 kilometres, extending from the Palakkad gap's vicinity to the northern periphery of the Western Ghats and a corresponding 30 kilometres to the southern boundary. Employing GIS tools and ArcMap, a polygon of 30 kilometres in width and approximately 60 kilometres in length was meticulously demarcated to define the research area. The primary objective of this study was to evaluate the influence exerted by the Palghat Gap on the floristic diversity within the sky islands of the Western Ghats, within the vicinity of the Gap. The floristic survey exclusively focused on the distinct ecological realm of sky islands, especially the elevated terrain beyond 800 metres in elevation (Plate 3.1). The defined study area is delimited to the north by the Mannarkkad division and to the south by the Nenmara division.

An initial analysis of floristic attributes was undertaken individually for each of these divisions. Owing to the focus on high-altitude regions during field surveys, the count of hillocks included within the designated polygon was restricted. While the number of hillocks on the northern side was limited, the geographical extent encompassed by these formations was more expansive compared to the southern sky islands. Although constrained in size, the southern sector featured a comparatively higher number of hillocks. The study area was specifically centred on the Nelliyampathy range and Kollengode range under Nenmara division (Working plan of Nenmara forest division 2015-2016 to 2024-2025) and Agali range of Mannarkad division of the Western Ghats (Working plan of Mannarkad forest division 2012-2013 to 2022-2023). Specifically, the Agali range, situated on the northern perimeter of the Palghat Gap, was deliberately selected from the Mannarkad division. This judicious selection was guided by the inherent objective of scrutinising exclusively the high-altitude sky islands within this domain. Concurrently, the study encompassed the southern sector of the region of Western Ghats, particularly embracing the Nelliyampathy and Kollengode ranges within the Nenmara division. In accordance with stringent selection criteria, a judicious compilation of four principal hillocks was meticulously selected

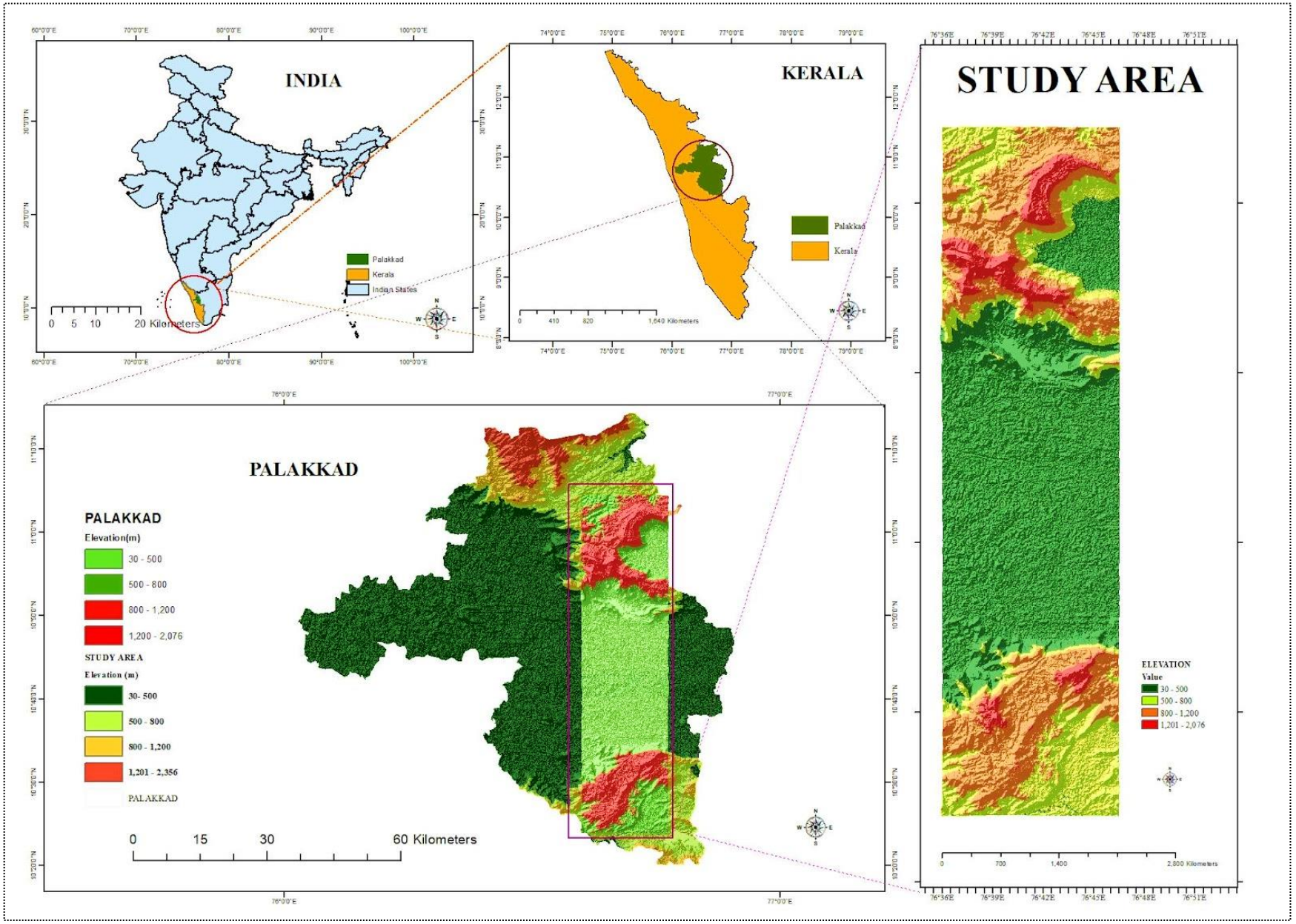


Plate 3.1: DEM (Digital Elevation Map) of the study area over the sky islands of Western Ghats across the Palghat Gap.

from the Agali range. Similarly, additional hillocks were systematically chosen from the Kollengode range and Nelliyampathy range.

The primary hillocks earmarked within the Agali range encompass Keralamedu, Muthikulam, Varadimala and Amandam. Shifting attention to the Nenmara division, the elevated eminences encompass the Nelliyampathy Hilltop, Valiyamanpara, Pothumala, Keshavanpara, Minnampara, Sisilimala, Karimala, Karasurimala, Anamedu and Mattumala (Table 3.1). The empirical survey and subsequent analyses were executed between 2018 and 2020, involving meticulous field excursions. The study primarily involved the comparative evaluation of floral diversity exhibited by the Western Ghats sky islands positioned across the Palghat Gap.

Table 3.1. The selected sky island locations of the Western Ghats across the Palghat Gap within the study area for preliminary floristic survey.

SL. No	Altitude	Lat-Long	Location
1	1407.87m	11°2'23" N, 76°42'32" E	Keralamedu
2	923.5m	11° 01' 34.86"N, 76° 38' 31.38"N	Amandam
3	1498.092m	10°56'26" N, 76°38' 9" E	Muthikulam
4	1397.813m	11°2'32" N, 76°42'43" E	Varadimala
5	1458m	10°31'57.67"N, 76°40'42.88"E	Nelliyampathy hilltop
6	1264.8m	10°33'22" N, 76°45'42.10" E	Valiyamanpara
7	1201m	10°26' 7" N, 76° 39'17" E	Pothumala
8	1002m	10°32'30.305" N, 76°40'40.23"E	Keshavanpara
9	1336.5m	76°43'6" E, 10°31' 59" N	Minnampara
10	1216.9m	10°30' 43.636" N, 76°42'44.935" E	Sisilimala
11	1390.7m	10°32'13.045" N, 76°44' 38.963" E	Karimala
12	1412.8m	10°31' 29.451" N, 76° 44' 21.177" E	Karasurimala
13	1200m	10°30'7.416" N, 76° 42' 11.7426" E	Anamedu
14	1299.7m	10°31' 34.86" N, 76°43'13" E	Mattumala

3.2.1.1. Digital elevation mapping and spatial mapping

The ASTER Global Digital Elevation Model (GDEM) Version 3, known as ASTGTM, offers a global digital elevation model (DEM) covering terrestrial regions of Earth. This model boasts a spatial resolution of 1 arc second, equivalent to approximately 30m of horizontal posting at the equator. The collaborative efforts of the National Aeronautics and Space Administration (NASA) and Japan's Ministry of Economy, Trade, and Industry culminated in the development of the ASTER GDEM data sets (METI). The generation of ASTER GDEM data products was entrusted to the

Sensor Information Laboratory Corporation (SILC), headquartered in Tokyo. This version of ASTER GDEM, denoted as Version 3, was meticulously constructed utilising a staggering 1,880,306 Level-1A scenes acquired between March 1, 2000, and November 30, 2013 (V3) (Fujisada *et al*., 2005, *2011*, 2012).

Each individual ASTER GDEM tile is associated with a pair of files: a quality assessment (QA) NUM file and an elevation data DEM file. Both files possess dimensions of 3601 samples by 3601 lines, thereby covering a data area of 1 degree by 1 degree. For the purpose of this study, DEM GeoTIFF files were sourced from ASTER GDEM v003. These DEM files, in conjunction with the respective study area shapefiles, were imported into ArcMap. The process involved importing both the DEM file and the .shp file delineating the study area, followed by the extraction of the DEM for the designated study area. Subsequently, modifications were done over the DEM of the study area and the Hill shade effect was employed. The resultant DEM of the study area underwent reclassification, involving the division of elevations into four distinct intervals measured in metres, where the intervals were demarcated as follows, 30-500m, 500-800m, 800-1200m, and 1200-2000m. The precise upper limit of the last elevation range is subject to variation contingent upon the specific characteristics of the study area. The delineation of the study area was accomplished through the conversion of the reclassified raster to a vector format, allowing for the computation of the study area's extent in terms of square kilometres.

The Digital Elevation Model (DEM) of the designated study area was meticulously generated, serving as the foundational cartographic framework for subsequent analytical endeavours. In tandem, the precise GPS coordinates corresponding to the targeted plant specimens under scrutiny were judiciously overlaid upon this spatial framework. This integration engendered a spatial visualisation wherein the locations of these specific plant specimens were graphically marked. A pivotal facet of this investigation was the deliberate emphasis on the profound ecological value encapsulated within the unique realm of the sky islands. These habitats renowned for their remarkable endemism and occupy a pivotal ecological niche within the broader landscape of study. Special attention was vested in species that exhibit an exceptional level of endemism, notably those exclusive to the Western Ghats and further delineating those exclusively confined to the Southern Western Ghats.

3.2.2. Plant collection and identification

After demarcating the study area, an extensive field visit was done, continuously for about two years (2018 to 2020), over the sky islands of Western Ghats. Where the focus was mainly over the tree species found exclusively over the sky islands, and the one clearly reflects over the change in environmental filters. During the survey we came across several species including herbs, shrubs and even trees, where survey was done with more focus on trees. The species came across the survey especially trees were documented, photographed and few plant specimens were preserved. After the two years preliminary floristic survey, taxa best fit to the study was selected. After that further extensive field visits were done from 2020 to 2023 for extensive collection of populations of the selected taxa from different locations within the study area. After locating maximum populations of the selected taxa, replicative field visit was done over the study area for about three years. Each year the specimen samples of the populations of selected taxa were collected repeatedly during the flowering time.

The plant material obtained during field collection was carefully stored within zippered covers. A portion of these collected specimens was utilised for the preparation of herbarium specimens, while others were earmarked for the purpose of identification. The identification of the amassed plant material was accomplished through reference to established floras and revisionary publications, including works authored by Hooker (1872-1897), Gamble and Fischer (1915-1936), Manilal (1988), Manilal and Sivarajan (1982), Vajravelu (1990) and Sasidharan (2002). In addition to these primary sources, supplementary online references were drawn during the identification process. Notably, resources such as POWO, BHL from the New York Botanical Garden, Tropicos, IPNI, and the Kew Library were extensively consulted to ensure accurate taxonomic determination (BHL 2023, IPNI 2023, Kew 2023, POWO 2023, Tropicos 2023).

3.2.3. Herbarium preparation

After the collection, most specimens were given formaldehyde treatment, followed by the implementation of a wet herbarium preparation technique (De Vogel 1987, Forman and Bridson 1989). The specimens subjected to formalin treatment were subsequently compressed within blotting paper, facilitating moisture absorption. Following this, the meticulously prepared specimens were affixed onto standardised herbarium sheets measuring 42 x 28 cm. Each specimen was accompanied by a label adhering to standardised dimensions of 14.5 x 11 cm.

3.2.4. Floristic survey analysis

The collected plant specimens underwent a sequence of procedures, including cataloguing, photography, and diverse analytical examinations. The analysis includes spatial distribution analysis, a comparative appraisal of endemicity, an evaluation of family distribution patterns across the sky islands, and an assessment of species habitat preferences. These analyses were done by referring to significant floristic literature (Sasidharan 2004, ENVIS 2016). In addition to these analyses, the classification of each species under specific conservation criteria were determined by referencing the IUCN Red List, Version 2022-2 and IUCN 2023-1 (Sasidharan 2003, IUCN 2022, IUCN 2023).

3.2.5. Selection of Taxa

Nonetheless, antiquated secondary data were excluded due to their inadequacy in pinpointing the specific taxa aligning with the hypothesis. Consequently, significant emphasis was placed on executing direct field surveys. Therefore, determination of taxa was made upon the insights garnered through these first-hand field investigations. In accordance with that the preliminary floristic survey done over sky islands spanning across the Palghat Gap, the taxa specific for the study were selected. The survey was conducted in a randomised manner, confined to the sky islands situated within the Western Ghats of Palakkad, across the Palghat Gap. During the selection of taxa, trees were prioritised due to their heightened genetic stability in ecological contexts. The survey was done devoid of sedges, grasses, and small herbs. The survey's primary objective was the identification of species that substantiated the study's focal hypothesis: "The influence of Palghat Gap features on intraspecific variation within the designated taxa". Supplementary data from the Kerala flora were also employed to facilitate this selection process. The selection of the taxa was done based on the following criteria. The selection criteria include the plant species displaying a limited geographic range primarily within the sky islands of the Western Ghats, situated on both the sky islands on the south and north of the Palghat Gap, but notably absent within the gap itself. The species falling under the category of endemism, indicating their exclusivity to Western Ghats. The chosen species should hold particular significance in conservation efforts due to their unique ecological attributes. Included taxa were recognised for their diverse applications like pharmaceuticals, medicinal applications, and beyond. The selection criteria encompass species that exhibit adaptability to changing environmental conditions, serving as indicators of ecological responsive-

ness. Emphasis is placed on taxa demonstrating resilience against unfavourable environmental circumstances, thereby maintaining consistent distribution patterns unaffected by external factors. Furthermore, the species susceptibility to habitat modification highlights the pressing issue of habitat transformation. The species which are endemic, and the species requiring immediate conservation of biodiversity measures, and those best exemplifying this specialised habitat. The species serve as indicators that reflect the dynamic shifts occurring in the environmental determinants within their respective habitats.

During the field visits, a comprehensive analysis of the phenological temporal variations among species inhabiting the sky islands spanning the Palghat Gap was conducted. The primary objective was to assess the degree of reproductive isolation exhibited by each species as influenced by this geographical gap. To achieve this, meticulous observations were made to document the phenological stages of the selected taxa, thereby providing insights into the timing and synchronization of key reproductive events. Furthermore, a critical examination of seed dispersal agents associated with the identified taxa was undertaken during the field investigations. This supplementary analysis aimed to verify and cross-reference the potential for gene flow between the sky islands situated in the Western Ghats, particularly across the Palghat Gap. By scrutinizing the mechanisms and agents responsible for seed dispersal, the study sought to elucidate any patterns or constraints that may impact genetic exchange between these distinct ecological entities. The combined assessment of phenological variations and seed dispersal dynamics constitutes a robust methodology for evaluating the reproductive isolation and potential gene flow among species inhabiting the sky islands across the Palghat Gap in the Western Ghats.

3.3. Results and discussion

The preliminary floristic survey was systematically conducted over the sky islands located within the predefined study area. It is important to note that this survey was carried out without the inclusion of sedges, grasses, and small herbs. Over the span of five years, despite the inherent challenges posed by natural calamities, a total of 14 hillocks, distributed across the selected ranges, were subjected to systematic and repeated visits.

3.3.1. Study area

The study area covered over the expanse of the sky islands of Western Ghats across the Palghat Gap. This included the sky islands of Western Ghats flanking on

the northern and southern sides of the Palghat Gap. The fieldwork over the study area robustly captured the floristic diversity exhibited within these ecologically pivotal sky islands of Western Ghats (Plate 3.1). A total of 14 hillocks were surveyed and spatially mapped over the DEM of the study area (Plate 3.2, Table 3.1).

3.3.1.1. Digital elevation mapping and spatial mapping

To demarcate the area of study, Digital Elevation Mapping was utilized to delineate the sky islands within the specified study region. Where the study area was delineated into 4 altitudes ranges, which include 30-500m, 500-800m, 800-1200m and 1200 to 2076m (Plate 3.2). As per the spatial analysis, the total area of the rectangular polygon of study area was 1448.334455 km². The study was especially done over the sky islands of the Western Ghats on the northern and southern of Palghat Gap. Towards northern side of Palghat Gap the study area was about 695.058175 km², while on the Southern side the study area covering roughly about 753.237628 km².

Towards the southernmost side of Western Ghats, the maximum elevation range was 1614m and towards the northernmost side the maximum elevation range was 2076m. Among this altitude range within the study area, only the area above the elevation range of 800m was considered for the study. The study area of sky Island above 800m towards the south was about 179.048657 km^2 and towards the northern side of sky island it was about 243.741834 km^2, even though the area over the northern side was larger, the number of hillocks compared to the Southern side was limited.

3.3.2. Plant collection and identification

As per the floristic survey done over the sky island of Western Ghats in a two-year time period, about 186 taxa were documented (Table 3.2). The specimens were photographed and were collected and preserved for identification and herbarium preparation. The majority of the species documented were tree, with few herbs and climbers. There were about 61 trees documented, of that few were found over the sky islands on the northern and southern sides of the Palghat Gap, some were unique to each side.

After the survey the taxa specific to the study were selected. Then an extensive field visit was done over the study area for about 3 years to locate the populations of the selected taxa from different locations and to collect the specimens of the population separately. The samples of the populations of the selected taxa were collected and preserved separately. Repeated and systematic field visit and specimen collection were done over these fields, especially during the flowering time. During the survey

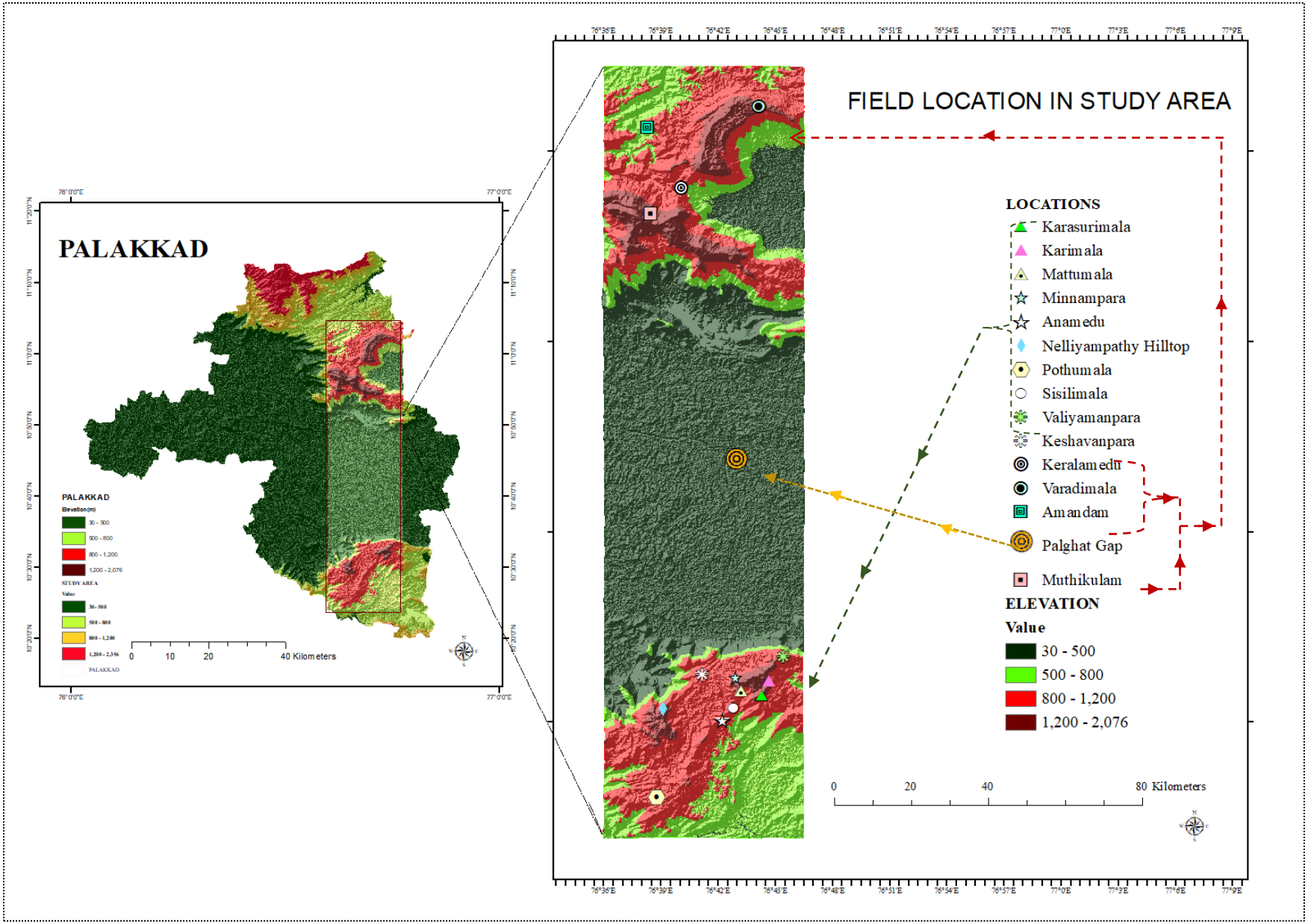


Plate 3.2: Location mapping of selected hillocks on DEM of sky islands of the Western Ghats within the study Area.

Table 3.2: List of plants documented (APG) as per the preliminary floristic survey done over the sky islands of the Western Ghats across the Palghat Gap, within the study area.

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
1	*Peperomia heyneana* Miq.	Magnolids	Piperales	Piperaceae	NE	Evergreen forests	Herb	No	Indian Subcontinent to South China and Indo-China	64	GVCH001858
2	*Peperomia tetraphylla* (G.Forst.) Hook. & Arn.	Magnolids	Piperales	Piperaceae	NE	Evergreen, moist deciduous and shola forests	Herb	No	Pantropical	22	GVCH001857
3	*Piper umbellatum* L.	Magnolids	Piperales	Piperaceae	NE	Semi-evergreen and evergreen forests	Shrub	No	Paleotropics	57	GVCH001859
4	*Thottea sivarajanii* E.S.S.Kumar, A.E.S.Khan & Binu	Magnolids	Piperales	Aristolochiaceae	NE	Evergreen and semi-evergreen forests	Shrub	Yes	Southern Western Ghats (Kerala)	138	GVCH001860
5	*Thottea siliquosa* (Lam.) Ding Hou	Magnolids	Piperales	Aristolochiaceae	NE	Evergreen and semi-evergreen forests	Shrub	No	Penninsular India and Srilanka	1202	GVCH001861
6	*Meiogyne pannosa* (Dalzell) J.Sinclair	Magnolids	Magnoliales	Annonaceae	NT	Evergreen forests	Tree	Yes	Western Ghats	139	GVCH001862
7	*Orophea thomsonii* Bedd.	Magnolids	Magnoliales	Annonaceae	EN	Evergreen and semi-evergreen forests	Shrub	Yes	Western Ghats	177	GVCH001863
8	*Monoon coffeoides* (Thwaites ex Hook.f. & Thomson) B.Xue & R.M.K.Saunders	Magnolids	Magnoliales	Annonaceae	NE	Evergreen and semi-evergreen forests	Tree	No	South India and Sri Lanka	140	GVCH001864
9	*Actinodaphne campanulata* Hook.f.	Magnolids	Laurales	Lauraceae	VU	Evergreen forests	Tree	Yes	Southern Western Ghats	86	GVCH001865

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
10	*Actinodaphne bourdillonii* Gamble	Magnolids	Laurales	Lauraceae	NT	Evergreen forests	Tree	Yes	Southern Western Ghats	103	GVCH001866
11	*Cinnamomum malabatrum* (Burm.f.) J.Presl	Magnolids	Laurales	Lauraceae	LC	Evergreen and semi-evergreen forests, also in the plains	Tree	Yes	Southern Western Ghats	176	GVCH001867
12	*Cinnamomum wightii* Meisn.	Magnolids	Laurales	Lauraceae	EN	Shola forests	Tree	Yes	Southern Western Ghats	141	GVCH001868
13	*Cryptocarya anamalayana* Gamble	Magnolids	Laurales	Lauraceae	EN	Evergreen forests	Tree	Yes	Southern Western Ghats	102	GVCH001869
14	*Litsea coriacea* (B.Heyne ex Nees) Hook.f.	Magnolids	Laurales	Lauraceae	NT	Semi-evergreen forests and sacred groves	Tree	Yes	Peninsular India	112	GVCH001870
15	*Litsea bourdillonii* Gamble	Magnolids	Laurales	Lauraceae	NT	Evergreen forests	Tree	Yes	Southern Western Ghats	32	GVCH001871
16	*Litsea ghatica* Saldanha	Magnolids	Laurales	Lauraceae	VU	Evergreen forests	Tree	Yes	Western Ghats	26	GVCH001873
17	*Litsea stocksii* (Meisn.) Hook.f.	Magnolids	Laurales	Lauraceae	NT	Shola forests	Tree	Yes	Southern Western Ghats	34	GVCH001874
18	*Litsea anamalayana* Robi and Udayan	Magnolids	Laurales	Lauraceae	CR	Shola forests	Tree	Yes	Southern Western Ghats	33	GVCH001872
19	*Litsea wightiana* (Nees) Wall. Ex Hook.f.	Magnolids	Laurales	Lauraceae	NT	Evergreen forests	Tree	Yes	Southern Western Ghats	58	GVCH001875

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
20	*Phoebe wightii* Meisn.	Magnolids	Laurales	Lauraceae	LC	Evergreen and shola forests	Tree	Yes	Peninsular India	175	GVCH001876
21	*Phoebe lanceolata* (Nees) Nees.	Magnolids	Laurales	Lauraceae	LC	Semi-evergreen and evergreen forests, also in secondary forests	Tree	No	India and Myanmar	49	GVCH001877
22	*Anaphyllum wightii* Schott.	Monocots	Alismatales	Araceae	NE	Evergreen and semi-evergreen forests	Herb	No	Western Ghats and Laccadiv Islands.	1204	GVCH001878
23	*Coelogyne mossiae* Rolfe.	Monocots	Asparagales	Orchidaceae	NE	Grasslands, evergreen and shola forests	Herb	Yes	Southern Western Ghats	9	GVCH001879
24	*Habenaria furcifera* Lindl.	Monocots	Asparagales	Orchidaceae	NE	Moist deciduous and semi-evergreen forests, also in grasslands	Herb	Yes	Western Ghats	10	GVCH001880
25	*Habenaria heyneana* Lindl.	Monocots	Asparagales	Orchidaceae	NE	Grasslands	Herb	Yes	Peninsular India	11	GVCH001881
26	*Habenaria longicorniculata* J. Graham.	Monocots	Asparagales	Orchidaceae	NE	Grasslands and moist deciduous forests	Herb	No	Western Ghats and Sri Lanka	178	GVCH001882
27	*Habenaria perrottetiana* A. Rich.	Monocots	Asparagales	Orchidaceae	NE	Grasslands	Herb	Yes	South India	12	GVCH001883
28	*Porpax braccata* (Lindl.) Schuit., Y. P.Ng & H.A.Pedersen	Monocots	Asparagales	Orchidaceae	NE	Evergreen and shola forests, also in grasslands	Herb	No	South India, Sri Lanka and Eastern Himalayas	36	GVCH001884

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
29	*Thrixspermum filiforme* (Hook.f.) Kuntze.	Monocots	Asparagales	Orchidaceae	NE	Evergreen and shola forests	Herb	No	South India and Sri Lanka	174	GVCH001885
30	*Satyrium nepalense* D. Don	Monocots	Asparagales	Orchidaceae	NE	Grasslands	Herb	No	Sri Lanka, India, Bhutan and Myanmar	13	GVCH001886
31	*Chlorophytum indicum* (Willd. Ex Schult. & Schult.f.) Dress	Monocots	Asparagales	Asparagaceae	NE	Grasslands	Herb	Yes	Western Ghats	4	GVCH001887
32	*Commelina clavata* C.B. Clarke	Monocots	Commelinales	Commelinaceae	LC	Wet areas in moist deciduous forests	Herb	No	India, Sri Lanka and Java	179	GVCH001888
33	*Cyanotis burmanniana* Wight	Monocots	Commelinales	Commelinaceae	NE	Wastelands	Herb	Yes	Western Ghats	212	GVCH001889
34	*Cyanotis cristata* (L.) D.Don	Monocots	Commelinales	Commelinaceae	LC	Grasslands	Herb	No	Paleotropics	291	GVCH001890
35	*Cyanotis thwaitesii* Hassk.	Monocots	Commelinales	Commelinaceae	NE	Evergreen forests and margins of grasslands	Herb	No	India, Sri Lanka and Indo-China	180	GVCH001891
36	*Murdannia semiteres* (Dalzell) Santapau	Monocots	Commelinales	Commelinaceae	LC	Among sedges and grasses	Herb	Yes	Peninsular India	300	GVCH001892
37	*Meistera masticatorium* (Thwaites) Škorničk. & M.F.Newman	Monocots	Zingiberales	Zingiberaceae	LC	Evergreen forests	Herb	No	South India and Sri Lanka	136	GVCH001893
38	*Curcuma decipiens* Dalzell	Monocots	Zingiberales	Zingiberaceae	NE	Exposed laterite soil and rocky hill slopes	Herb	Yes	Peninsular India	299	GVCH001894

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
39	*Hedychium venustum* Wight	Monocots	Zingiberales	Zingiberaceae	NE	Banks of streams in evergreen forests	Herb	Yes	Western Ghats	23	GVCH001895
40	*Zingiber anamalayanum* Sujanapal & Sasidh.	Monocots	Zingiberales	Zingiberaceae	NE	Grasslands	Herb	Yes	Southern Western Ghats	37	GVCH001896
41	*Zingiber neesanum* (J.Graham) Ramamoorthy	Monocots	Zingiberales	Zingiberaceae	NE	Moist deciduous, semi-evergreen and evergreen forests, also in the plains	Herb	Yes	Western Ghats	298	GVCH001897
42	*Zingiber nimmonii* (J.Graham) Dalzell	Monocots	Zingiberales	Zingiberaceae	LC	Moist deciduous forests, also in the plains	Herb	Yes	Western Ghats	38	GVCH001898
43	*Schoenoplectiella mucronata* (L.) J.Jung & H.K.Choi	Monocots	Poales	Cyperaceae	LC	Grasslands, wet fallow fields, banks of streams and pools	Herb	No	Eurasia, from Central and South Europe east to Japan	59	GVCH001899
44	*Diploclisia glaucescens* (Blume) Diels.	Eudicots	Ranunculales	Menispermaceae	NE	Evergreen, semi-evergreen and moist deciduous forests	Climber	No	Indo-Malesia and China	131	GVCH001800
45	*Leea indica* (Burm. F.) Merr.	Eudicots-rosids	Vitales	Vitaceae	NE	Degraded semi-evergreen and evergreen forests, also in the plains	Shrub	No	Indo-Malesia, China and Australia	108	GVCH001901
46	*Crotalaria nana* Burm.f.	Eudicots-rosids	Fabales	Leguminosae	NE	Grasslands	Herb	No	Indo-Malesia	276	GVCH001902

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
47	*Crotalaria multiflora* (Arn.) Benth.	Eudicots-rosids		Leguminosae	NE	Grasslands	Herb	No	Peninsular India and Sri Lanka	208	GVCH001903
48	*Crotalaria spectabilis* Roth.	Eudicots-rosids	Fabales	Leguminosae	NE	Deciduous forests and shola margins	Shrub	No	Paleotropics	275	GVCH001904
49	*Flemingia strobilifera* (L.) W.T.Aiton.	Eudicots-rosids	Fabales	Leguminosae	NE	Deciduous and semi-evergreen forests, also in the plains	Shrub	No	Indo-Malesia	273	GVCH001905
50	*Senna didymobotrya* (Fresen.) H.S.Irwin & Barneby	Eudicots-rosids	Fabales	Leguminosae	LC	Grown as garden plant, also as an escape in the High Ranges	Tree	No	Native of tropical east Africa, introduced elsewhere	173	GVCH001906
51	*Tephrosia tinctoria* (L.) Pers.	Eudicots-rosids	Fabales	Leguminosae	LC	Savannahs and moist deciduous forests, also in the plains	Shrub	No	Peninsular India and Sri Lanka	217	GVCH001907
52	Vigna vexillata var. Wightii (Bedd.) Babu & S.K.Sharma	Eudicots-rosids	Fabales	Leguminosae	NE	Moist deciduous forests	Climber	Yes	Southern Western Ghats	216	GVCH001908
53	*Polygala glaucoides L.*	Eudicots-rosids	Fabales	Polygalaceae	NE	Among sedges and grasses in scrub jungles	Herb	No	India and Sri Lanka	235	GVCH001909
54	*Xanthophyllum flavescens* Roxb.	Eudicots-rosids	Fabales	Polygalaceae	NE	Evergreen and semi-evergreen forests, also sacred groves in the plains	Tree	Yes	Western Ghats	123	GVCH001910

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
55	*Rubus niveus* Thunb.	Eudicots-rosids	Rosales	Rosaceae	NE	Evergreen and moist deciduous forests, also in grasslands	Climber	No	Indo-Malesia and China; in India temperate Himalayas and South India	55	GVCH001911
56	*Elaeagnus conferta* Roxb.	Eudicots-rosids	Rosales	Elaeagnaceae	LC	Semi-evergreen and evergreen forests	Climber	No	Indo-Malesia and China	87	GVCH001912
57	*Elaeagnus indica* Servett.	Eudicots-rosids	Rosales	Elaeagnaceae	NE	Semi-evergreen forests	Climber	No	Indo-Malesia	60	GVCH001913
58	*Ziziphus mauritiana* Lam.	Eudicots-rosids	Rosales	Rhamnaceae	LC	Dry deciduous forests, also planted in the plains	Tree	No	Paleotropics	172	GVCH001914
59	*Celtis timorensis* Span.	Eudicots-rosids	Rosales	Cannabaceae	LC	Evergreen forests	Tree	No	Indo-Malesia	132	GVCH001915
60	*Gonostegia bennettiana* (Wight) Pusalkar & Ingle	Eudicots-rosids	Rosales	Urticaceae	NE	Evergreen forests	Shrub	No	Peninsular India and Sri Lanka	181	GVCH001916
61	Gonostegia wightii (Benn.) Pusalkar & Ingle.	Eudicots-rosids	Rosales	Urticaceae	NE	Grasslands	Herb	Yes	South India	219	GVCH001917
62	Ficus exasperata Vahl	Eudicots-rosids	Rosales	Moraceae	LC	Moist deciduous forests, also in the plains	Tree	No	East Africa, Arabia, India and Sri Lanka	130	GVCH001918
63	*Begonia malabarica* Lam.	Eudicots-rosids	Cucurbitales	Begoniaceae	NE	Semi-evergreen forests	Herb	Yes	Peninsular India and Sri Lanka	297	GVCH001919
64	*Celastrus paniculatus* Willd.	Eudicots-rosids	Celastrales	Celastraceae	NE	Moist deciduous and semi evergreen forests	Climber	No	South Asia and Australia	151	GVCH001920

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
65	*Euonymus angulatus* Wight	Eudicots-rosids	Celastrales	Celastraceae	VU	Evergreen foreats	Shrub	Yes	Southern Western Ghats	66	GVCH002070
66	*Euonymus indicus* B.Heyne ex Wall.	Eudicots-rosids	Celastrales	Celastraceae	LC	Evergreen forests	Tree	Yes	Western Ghats	54	GVCH001921
67	*Euonymus laxiflorus* Champ. Ex Benth.	Eudicots-rosids	Celastrales	Celastraceae	LC	Evergreen forests	Shrub	Yes	South India, South China, Taiwan and Indo-China.	145	GVCH001922
68	*Rourea minor* (Gaertn.) Merr.	Eudicots-rosids	Oxalidales	Connaraceae	NE	Semi-evergreen and moist deciduous forests, also in sacred groves in the plains	Climber	No	India, Sri Lanka, Bangladesh and Malesia	137	GVCH001923
69	*Elaeocarpus munroi* (Wight) Mast.	Eudicots-rosids	Oxalidales	Elaeocarpaceae	NT	Evergreen and shola forests	Tree	Yes	Southern Western Ghats	265	GVCH001924
70	*Elaeocarpus gadgilii* A.M.Maya, V.Suresh & K.M.P.Kumar	Eudicots-rosids	Oxalidales	Elaeocarpaceae	NE	Moist deciduous and evergreen forests	Tree	Yes	Western Ghats	183	GVCH001925
71	*Mesua ferrea L.*	Eudicots-rosids	Malpighiales	Calophyllaceae	NE	Evergreen forests	Tree	No	Indo-Malesia	184	GVCH001926
72	*Drypetes oblongifolia* (Bedd.) Airy Shaw.	Eudicots-rosids	Malpighiales	Putranjivaceae	NE	Evergreen forests	Tree		Indo-Malesia	171	GVCH001928
73	*Hydnocarpus alpinus* Wight	Eudicots-rosids	Malpighiales	Achariaceae	VU	Evergreen and semi-evergreen forests	Tree		South India and Sri Lanka	110	GVCH001927
74	*Hydnocarpus sp.*	Eudicots-rosids	Malpighiales	Achariaceae	-	-	Tree	-	-	185	GVCH001929

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
75	*Agrostistachys indica* Dalzell	Eudicots-rosids	Malpighiales	Euphorbiaceae	LC	Evergreen and shola forests	Tree	Yes	Indo-Malesia	146	GVCH001930
76	*Croton klotzschianus* (Wight) Thwaites	Eudicots-rosids	Malpighiales	Euphorbiaceae	NE	Evergreen forests	Shrub	No	Peninsular India and Sri Lanka	67	GVCH001931
77	*Croton zeylanicus* Müll.Arg.	Eudicots-rosids	Malpighiales	Euphorbiaceae	NE	Evergreen forest margins	Shrub	No	Peninsular India and Sri Lanka	170	GVCH001934
78	*Euphorbia rothiana* Spreng.	Eudicots-rosids	Malpighiales	Euphorbiaceae	NE	Margins of evergreen forests and grasslands	Shrub	No	India and Sri Lanka	39	GVCH001932
79	*Excoecaria oppositifolia* var. *Cr enulata* (Wight) Chakrab. & M.Gangop.	Eudicots-rosids	Malpighiales	Euphorbiaceae	NE	Evergreen and shola forests	Shrub	No	Peninsular India and Sri Lanka	147	GVCH001933
80	*Mallotus tetracoccus* (Roxb.) Kurz	Eudicots-rosids	Malpighiales	Euphorbiaceae	NE	Evergreen, semi-evergreen and shola forests, also in the plains	Tree	No	India, Sri Lanka and China	169	GVCH001935
81	*Mallotus sp.*	Eudicots-rosids	Malpighiales	Euphorbiaceae	0		Tree	0	0	188	GVCH001936
82	*Paracroton integrifolius* (Airy Shaw) N.P.Balakr. & Chakr.	Eudicots-rosids	Malpighiales	Euphorbiaceae	NE	Evergreen forests	Tree	No	Peninsular India and Sri Lanka	124	GVCH001937
83	*Antidesma alexiteria* L.	Eudicots-rosids	Malpighiales	Phyllanthaceae	NE	Evergreen forests	Tree	No	South India and Sri Lanka	148	GVCH001938
84	*Antidesma montanum* Blume	Eudicots-rosids	Malpighiales	Phyllanthaceae	LC	Evergreen and shola forests, also in sacred groves	Tree	No	Indo-Malesia and East Himalayas	189	GVCH001939

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
85	*Bridelia stipularis* (L.) Blume	Eudicots-rosids	Malpighiales	Phyllanthaceae	LC	Semi-evergreen and moist deciduous forests and sacred groves		No	Tropical & Subtropical Asia	278	GVCH001940
86	*Glochidion ellipticum* Wight	Eudicots-rosids	Malpighiales	Phyllanthaceae	EN	Evergreen and shola forests	Tree	Yes	Indian Subcontinent to Indo-China.	149	GVCH001941
87	*Glochidion zeylanicum* (Gaertn.) A.Juss.	Eudicots-rosids	Malpighiales	Phyllanthaceae	LC	Evergreen and semi-evergreen forests, also in the plains	Tree	No	Indo-Malesia	292	GVCH001942
88	*Eugenia pokkudanii* A.M.Maya, K.M.P.Kumar & V.Suresh	Eudicots-rosids	Myrtales	Myrtaceae	CR	Shola forests	Shrub	Yes	Southern Western Ghats	113	GVCH001943
89	*Syzygium cumini* (L.) Skeels.	Eudicots-rosids	Myrtales	Myrtaceae	LC	Evergreen forests, also in the plains	Tree	No	Indo-Malesia to Australia	68	GVCH001944
90	*Syzygium densiflorum* Wall. Ex Wight & Arn.	Eudicots-rosids	Myrtales	Myrtaceae	VU	Evergreen and shola forests	Tree	Yes	Southern Western Ghats	90	GVCH001945
91	*Syzygium laetum* (Buch.-Ham.) Gandhi	Eudicots-rosids	Myrtales	Myrtaceae	NE	Evergreen forests	Tree	Yes	Southern Western Ghats	61	GVCH001946
92	*Memecylon sessile* Benth. Ex Wight & Arn.	Eudicots-rosids	Myrtales	Melastomataceae	NE	Evergreen and semi-evergreen forests, and also in sacred groves	Tree	Yes	Southern Western Ghats	150	GVCH001947
93	*Memecylon wightii* Thwaites	Eudicots-rosids	Myrtales	Melastomataceae	NE	Evergreen forests	Tree	No	Western Ghats and Sri Lanka	134	GVCH001948

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
94	*Memecylon umbellatum* Burm.f.	Eudicots-rosids	Myrtales	Melastomataceae	-	Semi-evergreen, shola and moist deciduous forests, also in the plains	Tree	No	Peninsular India, Sri Lanka, Jawa, Malasia, Myanmar, Vietnam	133	GVCH001949
95	*Osbeckia aspera* (Meerb. Ex Walp.) Blume	Eudicots-rosids	Myrtales	Melastomataceae	NE	Evergreen forests and grasslands, also in the plains	Herb	No	Peninsular India and Sri Lanka	40	GVCH001950
96	*Sonerila versicolor* Wight	Eudicots-rosids	Myrtales	Melastomataceae	NE	Evergreen forests	Herb	Yes	Southern Western Ghats	80	GVCH001951
97	Staphylea cochinchinensis (Lour.) Byng & Christenh.	Eudicots-rosids	Crossosomatales	Staphyleaceae	LC	Evergreen forests	Tree	No	Indo-Malesia and China	69	GVCH001952
98	*Allophylus cobbe* (L.) Forsyth f.	Eudicots-rosids	Sapindales	Sapindaceae	NE	Moist deciduous and semi-evergreen forests, also in sacred groves	Shrub	No	South India, Sri Lanka and South East Asia	6	GVCH001953
99	*Acronychia pedunculata* (L.) Miq.	Eudicots-rosids	Sapindales	Rutaceae	LC	Semi-evergreen forests, also in the plains	Tree	No	Tropical & Subtropical Asia	41	GVCH001954
100	*Atalantia wightii* Yu.Tanaka	Eudicots-rosids	Sapindales	Rutaceae	NE	Semi-evergreen and evergreen forests	Shrub	No	South West India	114	GVCH001955

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
101	*Murraya paniculata* (L.) Jack	Eudicots-rosids	Sapindales	Rutaceae	NE	Evergreen and semi-evergreen forests, also grown in the plains	Shrub	No	Indo-Malesia and Australia	135	GVCH001956
102	*Glycosmis nelliyampathiensis* Jabeena & Maya			Rutaceae	NE	Evergreen forests	Shrub	Yes	Southern Western Ghats	142	GVCH001957
103	*Zanthoxylum ovalifolium* Wight	Eudicots-rosids	Sapindales		LC	Evergreen forests	Shrub	No	Indo-Malesia to Australia	27	GVCH001958
104	*Heynea trijuga* Roxb. Ex. Sims.	Eudicots-rosids	Sapindales	Meliaceae	LC	Evergreen, semi-evergreen and shola forests	Tree	No	Indo-Malesia	152	GVCH001959
105	*Firmiana colorata* (Roxb.) R.Br.	Eudicots-rosids	Malvales	Malvaceae	NE	Semi-evergreen and moist deciduous forests	Tree	No	Indian Subcontinent to China	165	GVCH001960
106	*Leptonychia caudata* (Wall. Ex G.Don) Burret	Eudicots-rosids	Malvales	Malvaceae	NE	Evergreen, semi-evergreen forests	Tree	No	Indo-Malesia	1201	GVCH001961
107	*Capparis brevispina* DC.	Eudicots-rosids	Brassicales	Capparaceae	NE	Dry deciduous forests	Shrub	No	Peninsular India and Sri Lanka	104	GVCH001962
108	*Capparis moonii* Wight	Eudicots-rosids	Brassicales	Capparaceae	NE	Evergreen forests, also in sacred groves in the plains	Shrub	No	South West India and Sri Lanka	127	GVCH001963
109	*Cleome gynandra* L.	Eudicots-rosids	Brassicales	Cleomaceae	NE	Grown as garden plant, also getting naturalised	Shrub	No	Pantropical	116	GVCH001964

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
110	*Erythropalum scandens* Blume.	Eudicots	Santalales	Erythropalaceae	LC	Evergreen and semi-evergreen forests	Climber	No	Indo-Malesia to South West China	257	GVCH001965
111	*Viscum angulatum* B.Heyne ex DC.	Eudicots	Santalales	Santalaceae	NE	Semi-evergreen forests	Shrub	No	Indo-malesiaasia and Australia	153	GVCH001966
112	*Taxillus recurvus* (Wall. Ex DC.) Tiegh.	Eudicots	Santalales	Loranthaceae	NE	Shola forests	Shrub	No	Western Ghats	91	GVCH001967
113	*Drosera peltata* Thunb.	Eudicots	Santalales	Droseraceae	LC	Grasslands, in moist localities	Herb	No	Indo-Malesia to Australia and East Asia	237	GVCH001968
114	*Drosera indica* L.	Eudicots	Caryophyllales	Droseraceae	NE	Moist deciduous forests, also in the plains	Herb	No	Paleotropics	224	GVCH001969
115	*Impatiens parasitica* Bedd.	Eudicots-asterids	Ericales	Balsaminaceae	NE	Shola forests	Herb	Yes	Southern Western Ghats	28	GVCH001970
116	*Palaquium ellipticum* (Dalzell) Baill.	Eudicots-asterids	Ericales	Sapotaceae	NE	Evergreen forests	Tree	Yes	Western Ghats	106	GVCH001971
117	*Xantolis tomentosa* (Roxb.) Raf.	Eudicots-asterids	Ericales	Sapotaceae	NE	Evergreen forests	Tree	No	India, Sri Lanka and Indo-China	164	GVCH001972
118	*Maesa indica* (Roxb.) Sweet	Eudicots-asterids	Ericales	Primulaceae	LC	Evergreen, moist deciduous and shola forests and grasslands	Shrub	No	Indo-Malesia and Pakistan	117	GVCH001973
119	*Myrsine daphnoides* (Mez) Ricketson & Pipoly	Eudicots-asterids	Ericales	Primulaceae	NE	Shola forests	Shrub	Yes	Southern Western Ghats	93	GVCH001974
120	*Symplocos macrophylla* Wall. Ex DC.	Eudicots-asterids	Ericales	Symplocaceae	NE	Evergreen forests	Tree	Yes	Southern Western Ghats	94	GVCH001975

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
121	*Symplocos cochinchinensis* (Lour.) S.Moore	Eudicots-asterids	Ericales	Symplocaceae	NE	Evergreen, semi-evergreen and shola forests	Tree	No	Indo-Malesia and China	191	GVCH001976
122	*Mappia nimmoniana* (J.Graham) Byng & Stull	Eudicots-asterids	Icacinales	Icacinaceae	NE	Moist deciduous, evergreen and shola forests, also in the plains	Shrub	No	Indo-Malesia and China	7	GVCH001977
123	*Canthiumera neilgherrensis* (Wight) K.M.Wong	Eudicots-asterids	Gentianales	Rubiaceae	VU	Evergreen forests	Tree	Yes	Southern Western Ghats	186	GVCH001978
124	*Hedyotis leschenaultii DC.*	Eudicots-asterids	Gentianales	Rubiaceae	NE	Grasslands	Herb	Yes	Peninsular India	97	GVCH001979
125	*Lasianthus oblongifolius* Bedd.	Eudicots-asterids	Gentianales	Rubiaceae	NE	Evergreen forests	Shrub	Yes	Southern Western Ghats	82	GVCH001980
126	*Lasianthus parvifolius* Wight	Eudicots-asterids	Gentianales	Rubiaceae	NE	Evergreen forests	Shrub	Yes	Southern Western Ghats	71	GVCH001981
127	*Mitracarpus hirtus* (L.) DC.	Eudicots-asterids	Gentianales	Rubiaceae	NE	Degraded moist deciduous forests and wastelands	Herb	No	Tropical America; now common in South India	287	GVCH001982
128	*Neanotis indica* (DC.) W.H.Lewis	Eudicots-asterids	Gentianales	Rubiaceae	NE	Evergreen and shola forests	Herb	No	South west India, Indonesia	192	GVCH001983
129	*Exallage auricularia* (L.) Bremek.	Eudicots-asterids	Gentianales	Rubiaceae	NE	Degraded forests and in the plains	Herb	No	Indo-Malesia to Pacific Islands	259	GVCH001984
130	*Psychotria globicephala* Gamble	Eudicots-asterids	Gentianales	Rubiaceae	EN	Evergreen forests	Shrub	Yes	Southern Western Ghats	163	GVCH001985

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
131	*Pavetta indica* L.	Eudicots-asterids	Gentianales	Rubiaceae	NE	Evergreen forests, scrub jungles and sacred groves	Shrub	No	India and Sri Lanka	154	GVCH001986
132	*Psydrax umbellatus* (Wight) Bridson	Eudicots-asterids	Gentianales	Rubiaceae	NE	Moist deciduous forests and sacred groves	Tree	No	Indo-Malesia and China	51	GVCH001987
133	*Rubia cordifolia* L.	Eudicots-asterids	Gentianales	Rubiaceae	NE	Semi-evergreen and moist deciduous forests	Climber	No	Asia, Africa and Europe	42	GVCH001988
134	*Richardia scabra* L.	Eudicots-asterids	Gentianales	Rubiaceae	NE	Degraded forest areas, also in the plains	Herb	No	Native of Tropical America; introduced in Africa and Asia	236	GVCH001989
135	*Wendlandia thyrsoidea* (Roth) Steud.	Eudicots-asterids	Gentianales	Rubiaceae	NE	Grasslands and shola forests	Tree	No	Peninsular India and Sri Lanka	128	GVCH001990
136	*Fagraea ceilanica* Thunb.	Eudicots-asterids	Gentianales	Gentianaceae	NE	Moist deciduous, evergreen, semi-evergreen and shola forests, also in sacred groves	Tree	No	Indo-Malesia	155	GVCH001991
137	*Swertia angustifolia* Buch.-Ham. Ex D. Don	Eudicots-asterids	Gentianales	Gentianaceae	NE	Grasslands	Herb	No	South Asia to Indo-China and China	43	GVCH001992
138	*Carissa spinarum* L.	Eudicots-asterids	Gentianales	Apocynaceae	LC	Evergreen and semi-evergreen forests	Shrub	Yes	Paleotropics	118	GVCH001993
139	Ceropegia bulbosa Roxb.	Eudicots-asterids	Gentianales	Apocynaceae	NE	Scrub jungles	Climber	No	India and Pakistan	286	GVCH001994

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
140	*Hunteria zeylanica* (Retz.) Gardner ex Thwaites	Eudicots-asterids	Gentianales	Apocynaceae	LC	Evergreen forests	Tree	No	Tropical Africa to Indo-Malesia	129	GVCH001995
141	*Rauvolfia verticillata* (Lour.) Baill.	Eudicots-asterids	Gentianales	Apocynaceae	NE	Semi-evergreen forests, shola openings and grasslands	Shrub	No	Indo-Malesia	17	GVCH001996
142	*Vincetoxicum hirsutum* (Wall.) Kuntze	Eudicots-asterids	Gentianales	Apocynaceae	NE	Shola forests	Climber	Yes	South India	220	GVCH001997
143	*Adelocaryum coelestinum* (Lindl.) Brand	Eudicots-asterids	Boraginales	Boraginaceae	NE	Degraded forests	Herb	No	Indo-Malesia and China	95	GVCH001998
144	*Argyreia hirsuta* Wight & Arn.	Eudicots-asterids	Solanales	Convolvulaceae	NE	Deciduous and shola forests, also in the plains	Climber	No	South India and Sri Lanka	193	GVCH001999
145	*Ligustrum robustum* (Roxb.) Blume	Eudicots-asterids	Lamiales	Oleaceae	NE	Evergreen forests	Tree	No	Sri Lanka and Peninsular India	194	GVCH002000
146	*Aeschynanthus perrottetii* A.DC.	Eudicots-asterids	Lamiales	Gesneriaceae	NE	Evergreen and shola forests	Shrub	Yes	Western Ghats	22	GVCH002001
147	*Henckelia fischeri* (Gamble) A.Weber & B.L.Burtt	Eudicots-asterids	Lamiales	Gesneriaceae	NE	On wet rocks in evergreen forests	Herb	Yes	Southern Western Ghats	223	GVCH002002
148	*Henckelia meeboldii* (W.W.Sm. & Ramaswami) A.Weber & B.L.Burtt	Eudicots-asterids	Lamiales	Gesneriaceae	NE	On wet rocks in grasslands	Herb	Yes	Southern Western Ghats	195	GVCH002003
149	*Torenia bicolor* Dalzell	Eudicots-asterids	Lamiales	Linderniaceae	LC	Marshy areas	Herb	Yes	Western Ghats	44	GVCH002004
150	*Barleria courtallica* Nees	Eudicots-asterids	Lamiales	Acanthaceae	NE	Evergreen and semi-evergreen forests	Shrub	No	Western Ghats	72	GVCH002005

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
151	*Barleria involucrata* Nees	Eudicots-asterids	Lamiales	Acanthaceae	LC	Evergreen forests	Shrub	Yes	Peninsular India	261	GVCH002006
152	*Dicliptera cuneata* Nees	Eudicots-asterids	Lamiales	Acanthaceae	NE	Evergreen forests and wet areas in deciduous forests	Shrub	Yes	Peninsular India	260	GVCH002007
153	*Dicliptera foetida* (Forssk.) Blatt.	Eudicots-asterids	Lamiales	Acanthaceae	NE	Evergreen forests	Shrub	No	SW. Arabian Peninsula, South India and Sri Lanka	96	GVCH002008
154	*Rostellularia procumbens* (L.) Nees	Eudicots-asterids	Lamiales	Acanthaceae	NE	Grasslands and waste places	Herb	No	Indo-Malesia and East Africa	196	GVCH002009
155	*Justicia santapaui* Bennet	Eudicots-asterids	Lamiales	Acanthaceae	NE	Evergreen and semi-evergreen forests	Shrub	Yes	Western Ghats	162	GVCH002010
156	*Justicia*.sp	Eudicots-asterids	Lamiales	Acanthaceae	-	-	Shrub	-	-	84	GVCH002011
157	*Strobilanthes sp.*	Eudicots-asterids	Lamiales	Acanthaceae	-	-	Shrub	-	-	74	GVCH002012
158	*Strobilanthes* .sp	Eudicots-asterids	Lamiales	Acanthaceae	-	-	Shrub	-	-	3	GVCH002013
159	Thunbergia fragrans Roxb.	Eudicots-asterids	Lamiales	Acanthaceae	NE	Deciduous forests, also in the plains grown as garden plant	Climber	No	Indo-Malesia and Australia	182	GVCH002014

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
160	*Callicarpa tomentosa* (L.) L.	Eudicots-asterids	Lamiales	Lamiaceae	LC	Semi-evergreen and moist deciduous forests, also in the plains	Tree	No	Peninsular India and Sri Lanka	156	GVCH002015
161	*Colebrookea oppositifolia* Sm.	Eudicots-asterids	Lamiales	Lamiaceae	LC	Grasslands	Shrub	No	South and South East Asia to China	144	GVCH002016
162	*Leucas nubica* Benth.	Eudicots-asterids	Lamiales	Lamiaceae	NE	Moist deciduous and semi-evergreen forests	Shrub	No	Indian Subcontinent to South China	226	GVCH002017
163	*Leucas chinensis* (Retz.) Sm.	Eudicots-asterids	Lamiales	Lamiaceae	NE	Grasslands	Herb	No	Peninsular India, China, Japan to Philippines	197	GVCH002018
164	*Leucas lamiifolia* Desf.	Eudicots-asterids	Lamiales	Lamiaceae	NE	Shola forests and grasslands	Shrub	Yes	Western Ghats	198	GVCH002019
165	*Coleus fruticosus* Wight ex Benth.	Eudicots-asterids	Lamiales	Lamiaceae	NE	Often grown as live fence in the high ranges	Shrub	No	Peninsular India	161	GVCH002020
166	Coleus barbatus (Andrews) Benth. Ex G.Don	Eudicots-asterids	Lamiales	Lamiaceae	NE	Grasslands and dry deciduous forests	Herb	No	India, Sri Lanka and Tropical East Africa	272	GVCH002021
167	*Premna paucinervis* (C.B.Clarke) Gamble	Eudicots-asterids	Lamiales	Lamiaceae	NE	Semi-evergreen forests	Climber	Yes	South India	157	GVCH002022

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
168	*Teucrium heynei* V.S.Kumar & Chakrab.	Eudicots-asterids	Lamiales	Lamiaceae	NE	Grasslands and moist deciduous forests	Shrub	No	Peninsular India and Sri Lanka	160	GVCH002023
169	*Aeginetia acaulis* (Roxb.) Walp.	Eudicots-asterids	Lamiales	Orobanchaceae	NE	Moist deciduous forests and grasslands	Herb	No	Tropical Asia and China	203	GVCH002024
170	*Parasopubia delphiniifolia* (L.) H.-P. Hofm. & Eb. Fisch.	Eudicots-asterids	Lamiales	Orobanchaceae	NE	Grasslands, laterite hillocks and moist deciduous forests	Herb	No	India and Sri Lanka	209	GVCH002025
171	*Striga asiatica* (L.) Kuntze	Eudicots-asterids	Lamiales	Orobanchaceae	NE	Grassy areas in deciduous forests, also in the plains	Herb	No	South East Asia and Africa	30	GVCH002026
172	*Solanum giganteum* Jacq.	Eudicots-asterids	Solanales	Solanaceae	LC	Semi-evergreen, evergreen and moist deciduous forests	Shrub	No	Native of Tropical & S. Africa	125	GVCH002027
173	*Gomphandra tetrandra* (Wall.) Sleumer	Eudicots-asterids	Aqulifoliales	Stemonuraceae	LC	Evergreen and Semi-evergreen forests	Tree	No	South and South east Asia, also in china	1203	GVCH002028
174	*Lobelia heyneana* Schult.	Eudicots-asterids	Asterales	Campanulaceae	LC	Wet areas in evergreen forests and moist grassy places	Herb	No	Indo-Malesia, China and Africa	229	GVCH002029

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
175	*Lobelia nicotianifolia* Roth	Eudicots-asterids	Asterales	Campanulaceae	NE	Grasslands, shola and evergreen forests	Shrub	No	Indo-Malesia and China	45	GVCH002030
176	*Anaphalis subdecurrens (DC.) Gamble*	Eudicots-asterids	Asterales	Asteraceae	NE	Grasslands	Herb	No	India and Sri Lanka	280	GVCH002031
177	*Anaphalis travancorica W.W.Sm.*	Eudicots-asterids	Asterales	Asteraceae	NE	Rocky slopes and grasslands	Herb	Yes	Southern Western Ghats	98	GVCH002032
178	*Crassocephalum crepidioides* (Benth.) S.Moore	Eudicots-asterids	Asterales	Asteraceae	NE	Deciduous forests, also in forest plantations and plains	Herb	No	India, Sri Lanka, China, Africa and Madagascar	120	GVCH002033
179	*Emilia scabra DC.*	Eudicots-asterids	Asterales	Asteraceae	NE	Semi-evergreen forests and grasslands	Herb	Yes	India	200	GVCH002034
180	*Erigeron karvinskianus DC.*	Eudicots-asterids	Asterales	Asteraceae	NE	Moist grasslands, road cuttings in the high ranges	Herb	No	Neotropics, Mexico to Venezuela, Chile and the Antilles	187	GVCH002035
181	*Laggera alata* (D.Don) Sch.Bip. Ex Oliv.	Eudicots-asterids	Asterales	Asteraceae	NE	Grasslands	Herb	No	India, Myanmar, China and Tropical Africa	99	GVCH002036

Sl.no	Binomial name	Clade	Order	Family	Conservation status	Habitat	Habit	Endemism	Distribution status	Collection No:	Accession No:
182	*Strobocalyx arborea* (Buch.-Ham.) Sch.Bip.	Eudicots-asterids	Asterales	Asteraceae	LC	Evergreen forests	Tree	No	Indo-Malesia	100	GVCH002038
183	*Viburnum punctatum* Buch.-Ham. Ex D. Don	Eudicots-asterids	Dipsacales	Adoxaceae	NE	Semi-evergreen forests	Tree	No	Indo-Malesia	31	GVCH002037
184	*Centella asiatica* (L.) Urb.	Eudicots-asterids	Apiales	Apiaceae	LC	Deciduous forests, also in wet places in the plains	Herb	No	Tropical Asia and Africa	46	GVCH002039
185	*Tetrataenium rigens* (Wall. Ex DC.) Manden.	Eudicots-asterids	Apiales	Apiaceae	NE	Grasslands	Herb	Yes	Southern Western Ghats	19	GVCH002040
186	*Tetrataenium ceylanicum* (Gardner ex C.B.Clarke) Manden.	Eudicots-asterids	Apiales	Apiaceae	NE	Grasslands	Herb	No	South India and Sri Lanka	20	GVCH002041

we were able to introduce two new species to science and they were *Elaeocarpus gadgilii* A.M.Maya, V.Suresh & K.M.P.Kumar (Manoharan *et al*., 2021b) and *Eugenia pokkudanii* A.M.Maya, K.M.P.Kumar & V.Suresh (Manoharan *et al*., 2021a). *Eugenia pokkudanii* shows morphological similarities with *E. discifera* Gamble (1918: 239) (Gamble 1918), but differs mainly by lateral nerves 6–8 pairs (vs. 10–15 pairs), petiole 2–5 mm long (vs. 6–10 mm long), flower 0.7–1 cm across (vs. up to 2 cm across), pedicel 0.3–0.55 cm long (vs. 0.5–0.9 cm long), bracteole oblong (vs. lanceolate), calyx tube 0.9–1.5 mm long (vs. 2–3 mm long), calyx lobes 1.6–2.5 mm wide (vs. 4–5 mm wide), petals broadly elliptic (vs. orbicular). It also showed distinct dissimilarity from *Eugenia indica* (Wight 1842: 523) Chithra (1983: 153) (Wight 1842, Chithra 1983). *E. gadgilii* a taxon resembling *E. variabilis* Zmarzty (2001: 429) (Zmarzty 2001) and showing some similarity also with *E. serratus* L. (1753: 515) (Linnaeus 1753), but differing in many features like coriaceous leaves with conspicuous venation on adaxial surface, margin crenate-serrulate, the outer tooth of anthers with very long shining setae, calyx red and the wider fruits with 3–5 cm long (Table 3.3).

Table 3.3. Morphological comparison of *Elaeocarpus gadgilii* with *Elaeocarpus variabilis*., *Elaeocarpus serratus* var. *serratus*. and *Elaeocarpus serratus* var. *weibelii*.

Characters	*E. variabilis*	*E. serratus var. serratus*	*E. serratus var. weibelii*	*E. gadgilii*
Leaf Texture	Chartaceous	Chartaceous	Chartaceous	Coriaceous
Leaf teeth distance	3–10 mm	2–10 mm	5–15 mm	3–17 mm
Main and mid veins on adaxial surface	not conspicuous	not conspicuous	not conspicuous	Conspicuous
Main vein Pairs	4–8	4–7	6–9	3–5
Sepal colour	pinkish to reddish brown	greenish white	greenish white	pink to reddish
Petal Size	4.5–7.7 mm long	5–9.5 mm long	7.8 mm long	6–9 mm long
Disk lobes	fused, orbicular with reniform base	free, orbicular to broadly ovate with truncate base	free, broadly ovate with reniform base	free, ovate disk lobes with round or truncate base
Setae	Absent	outer tooth with very short setae	outer tooth with very short setae	outer tooth with very long shining setae
Style	1–3 mm long	2–4.5 mm	1.34–1.61 mm	1.6–4.4 mm long
Fruit	2.1–3.1 cm long, ellipsoid, ovoid, base round or cuneate	2.1–3.9 cm long, ellipsoid, base round or cuneate	1.5–1.7cm long, globose, base reniform	3–5 cm long, ellipsoid, base round or cuneate
Stones over endocarp	ellipsoid to broadly obovoid	oblong, ellipsoid or obovoid	broadly ellipsoid to round,	Ovoid

3.3.3. Herbarium preparation

All the herbarium prepared were mounted over the labelled herbarium sheets. All the herbarium specimens are deposited in GVCH herbarium and accession number are provided in table 3.2 (acronyms according to Thiers, 2024 [continuously updated]).

3.3.4. Floristic survey analysis

The comparative evaluation was undertaken to assess floristic diversity and the distribution of each species across the diverse sky islands across the Palghat Gap. The findings from the survey revealed noteworthy patterns like certain species exhibited specificity to either the southern or northern sky islands, while some species demonstrated a shared presence. Despite the survey's constraints within a delimited spatial and temporal scope, a discernible divergence between the sky islands on the Southern and northern sides emerged distinctly. The imperative consideration of this distinctive habitat arises from its pronounced vulnerability to climatic shifts, propelling it into the ambit of this study. Among the documented 186 species, a notable 67 species were identified as endemic (Plate 3. 3, Plate 3.4 - 3. 14). The species were analysed based on its distribution.

Out of the 67 aforementioned species, 31 were endemic to the Southern Western Ghats, 1 were endemic to the Southern Western Ghats within the Kerala boundary, 17 species displayed endemism to the broader Western Ghats region, 8 species were confined to Peninsular India and 4 species to south India (Plate 3.15: a). Through meticulous preliminary survey analysis, it was determined that 36% of the species gathered from the sky islands fell under the category of endemism. Among these, majority of the species were endemic to the Western Ghats, particularly concentrated within the Southern Western Ghats. This notable concentration underscores the remarkable biodiversity of the Western Ghats sky islands. Despite the preliminary nature of the survey, the analytic results unequivocally underscore the endemic-rich nature of these terrestrial islands. This outcome underscores the heightened significance of these sky islands. The significance stems from the fact that out of the total 186 species collected 67 species displayed varying degrees of endemism.

The geographical feature of this habitat may have played a pivotal role as a pioneering catalyst in the process of speciation. Such speciation events could contribute to an escalation in the count of endemic species, driven by the phenomenon of neo-endemism. An organism is designated as endemic when its distribution is restricted to

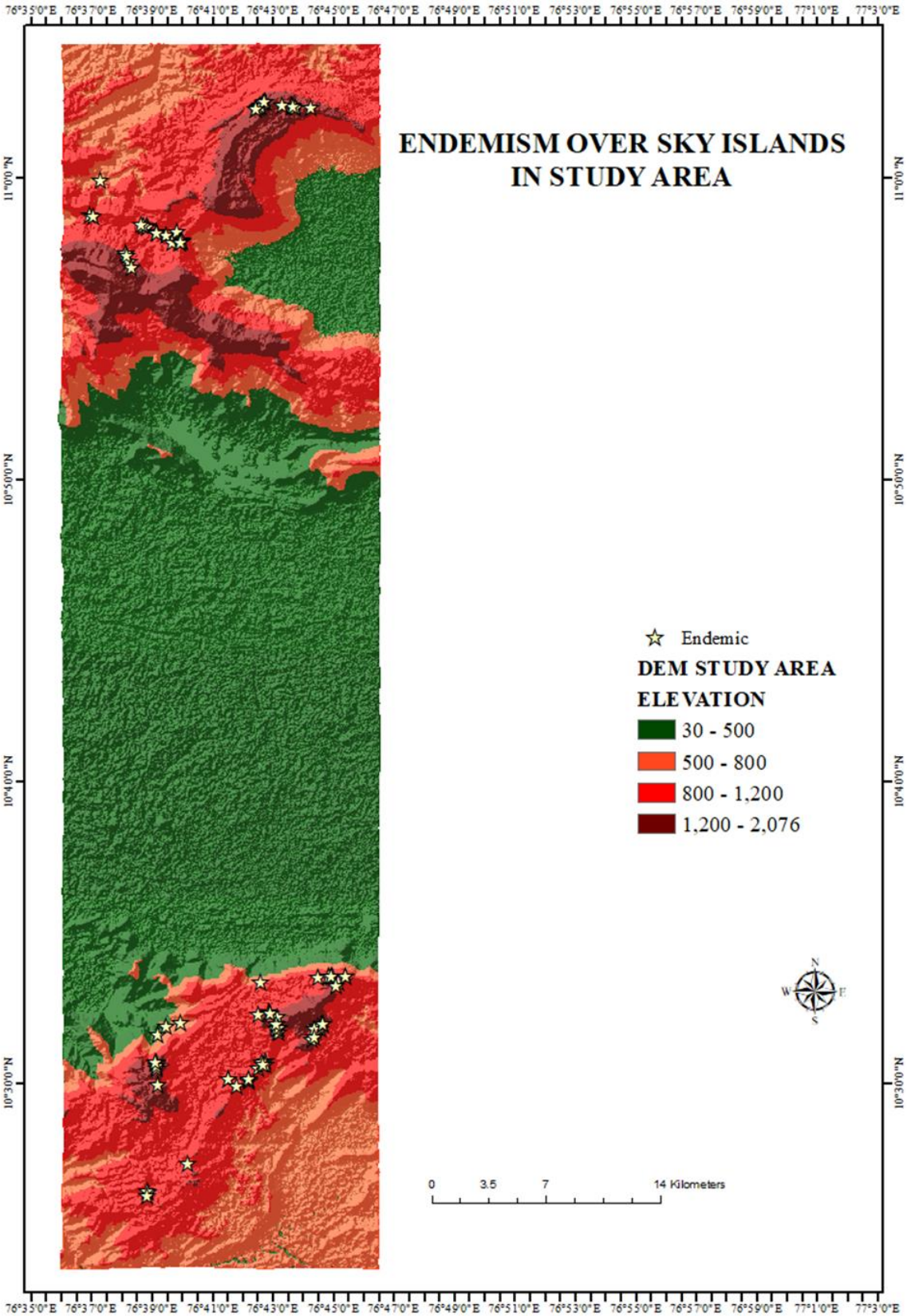
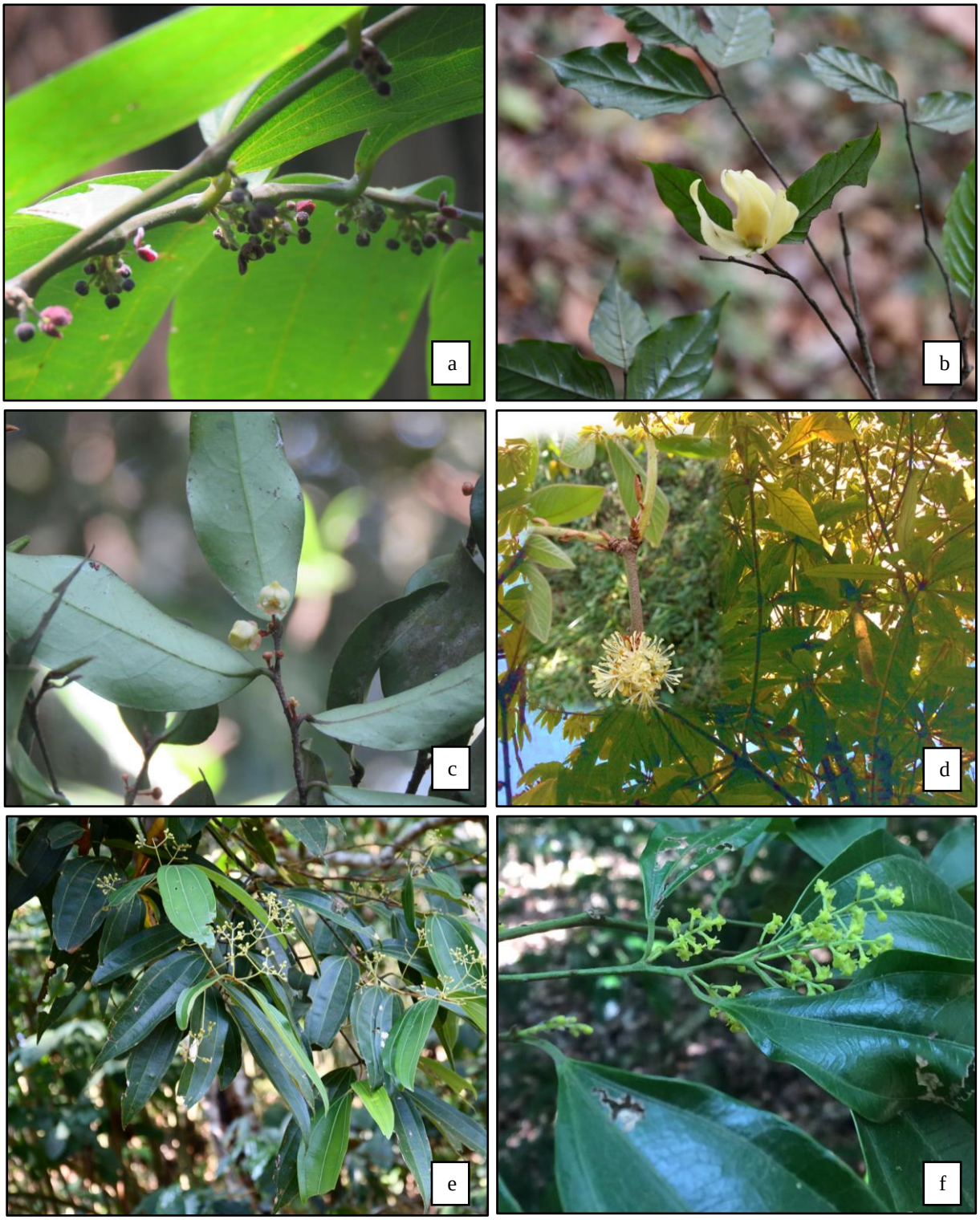


Plate 3.3: The spatial mapping of endemic plants over DEM of sky islands of the Western Ghats in the study Area.

Plate 3.4: Endemic plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Hedyotis leschenaultii* DC., b. *Dicliptera cuneata* Nees., c. *Lasianthus oblongifolius* Bedd., d. *Lasianthus parvifolius* Wight., e. *Justicia santapaui* Bennet., f. *Litsea ghatica* Saldanha.



Plates 3.5: Endemics plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Thottea sivarajanii* E. S. S. Kumar., A. E. S. Khan & Binu., b. *Meiogyne pannosa* (Dalzell) J. Sinclair., c. *Orophea thomsonii* Bedd., d. *Actinodaphne campanulata* Hook. f., e. *Cinnamomum malabatrum* (Burm. f.) J. Presl., f. *Cinnamomum wightii* Meisn.

Plate 3.6: Endemic plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Cryptocarya anamalayana* Gamble., b. *Litsea coriacea* (B. Heyne ex Nees) Hook. f., c. *Litsea bourdillonii* Gamble., d. *Litsea stocksii* (Meisn.) Hook. F., e. *Litsea anamalayana* Robi and Udayan., f. *Litsea wightiana* (Nees) Wall. ex. Hook. f.

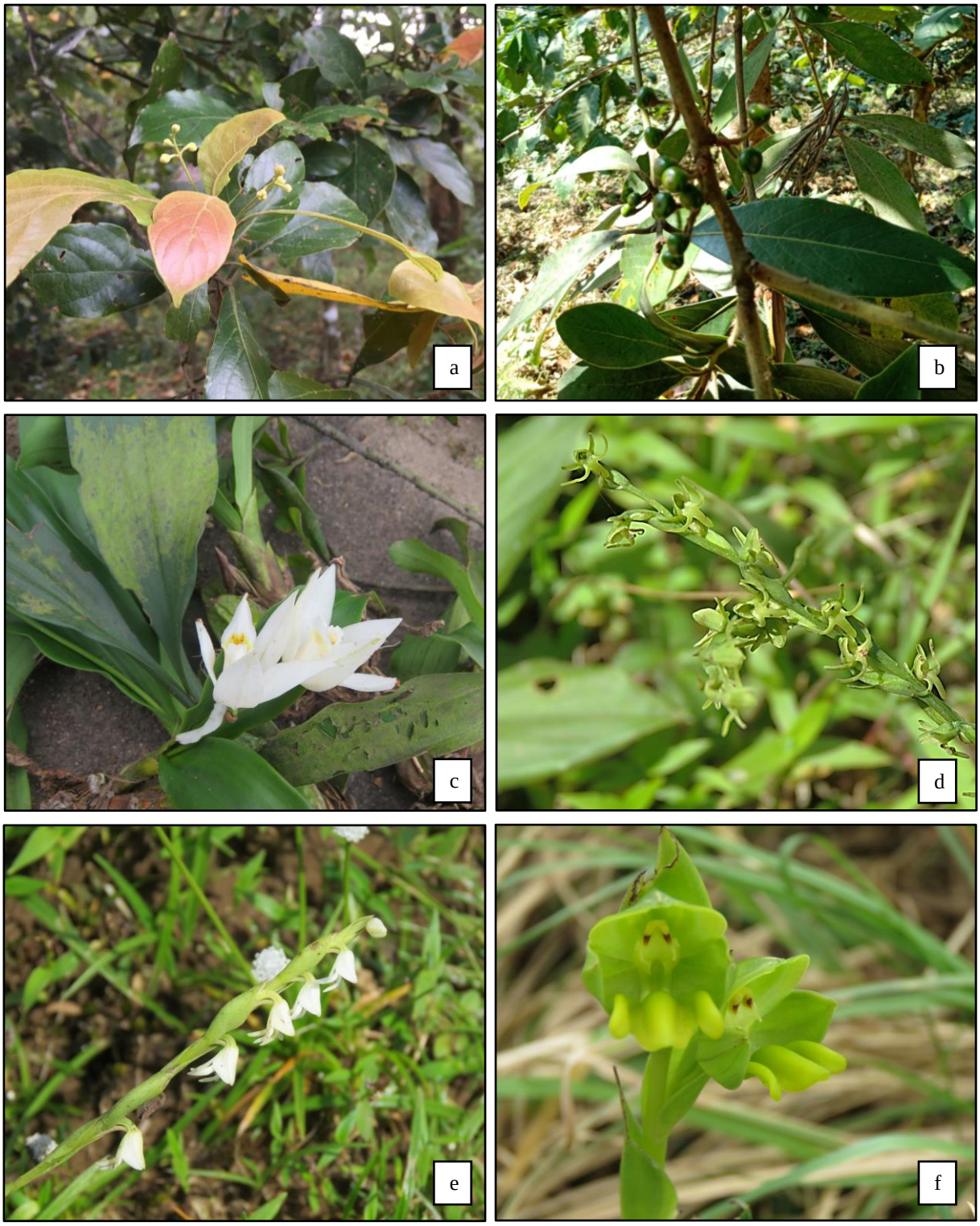


Plate 3.7: Endemic plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Phoebe wightii* Meisn., b. *Actinodaphne bourdillonii* Gamble., c. *Coelogyne mossiae* Rolfe., d. *Habenaria furcifera* Lindl., e. *Habenaria heyneana* Lindl., f. *Habenaria perrottetiana* A. Rich.

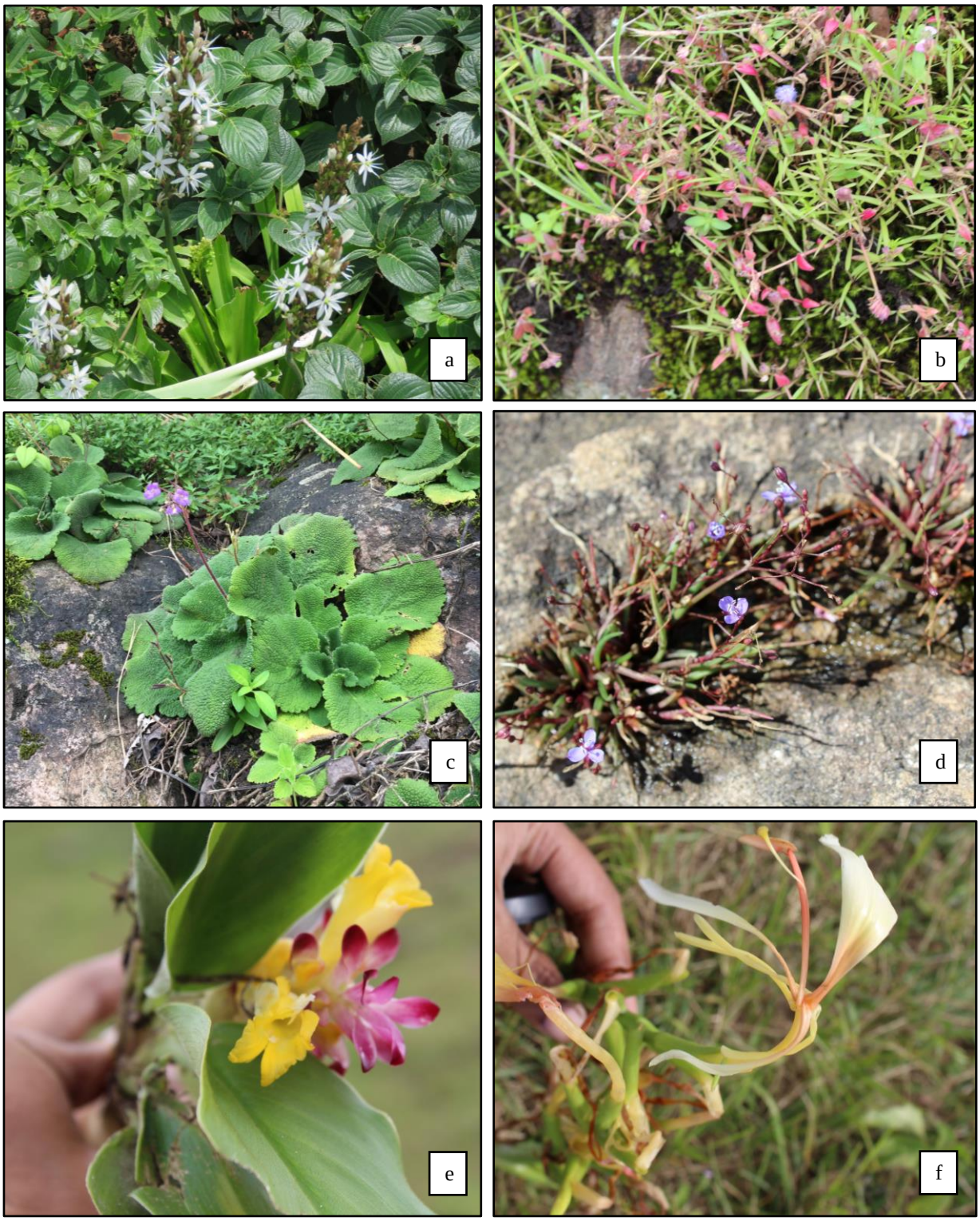


Plate 3.8: Endemic plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Chlorophytum indicum* (Willd. ex Schult. & Schult. f.) Dress., b. *Cyanotis burmanniana* Wight., c. *Henckelia meeboldii* (W.W.Sm. & Ramaswami) A.Weber & B.L.Burtt., d. *Murdannia semiteres* (Dalzell) Santapau., e. *Curcuma decipiens* Dalzell., f. *Hedychium venustum* Wight.

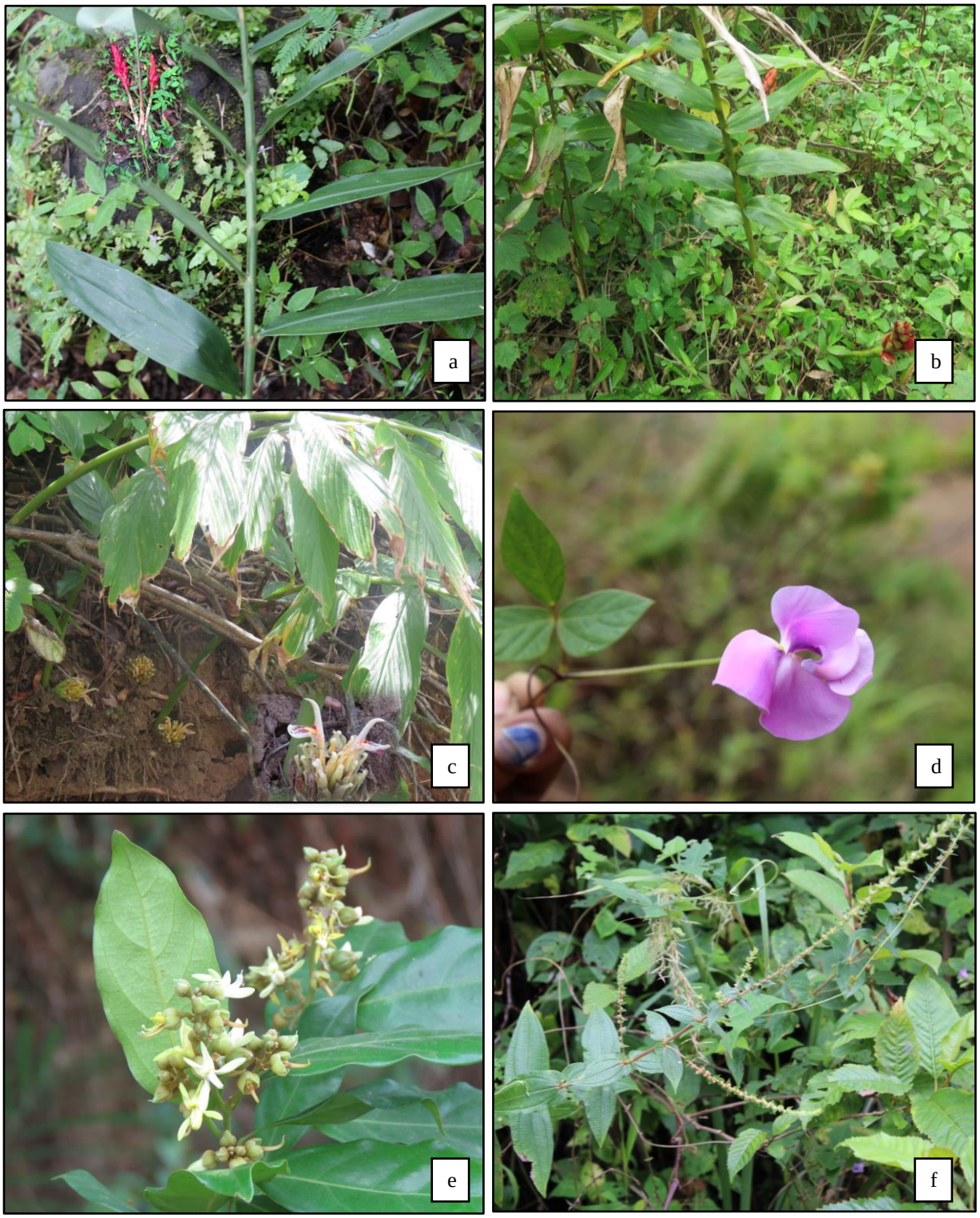


Plate 3.9: Endemic plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Zingiber neesanum* (J. Graham) Ramamoorthy., b. *Zingiber anamalayanum* Sujanapal & Sasidh., c. *Zingiber nimmonii* (J.Graham) Dalzell., d. *Vigna vexillata* var. *wightii* (Bedd.) Babu & S. K. Sharma., e. *Xanthophyllum flavescens* Roxb., f. *Gonostegia wightii* (Benn.) Pusalkar & Ingle.

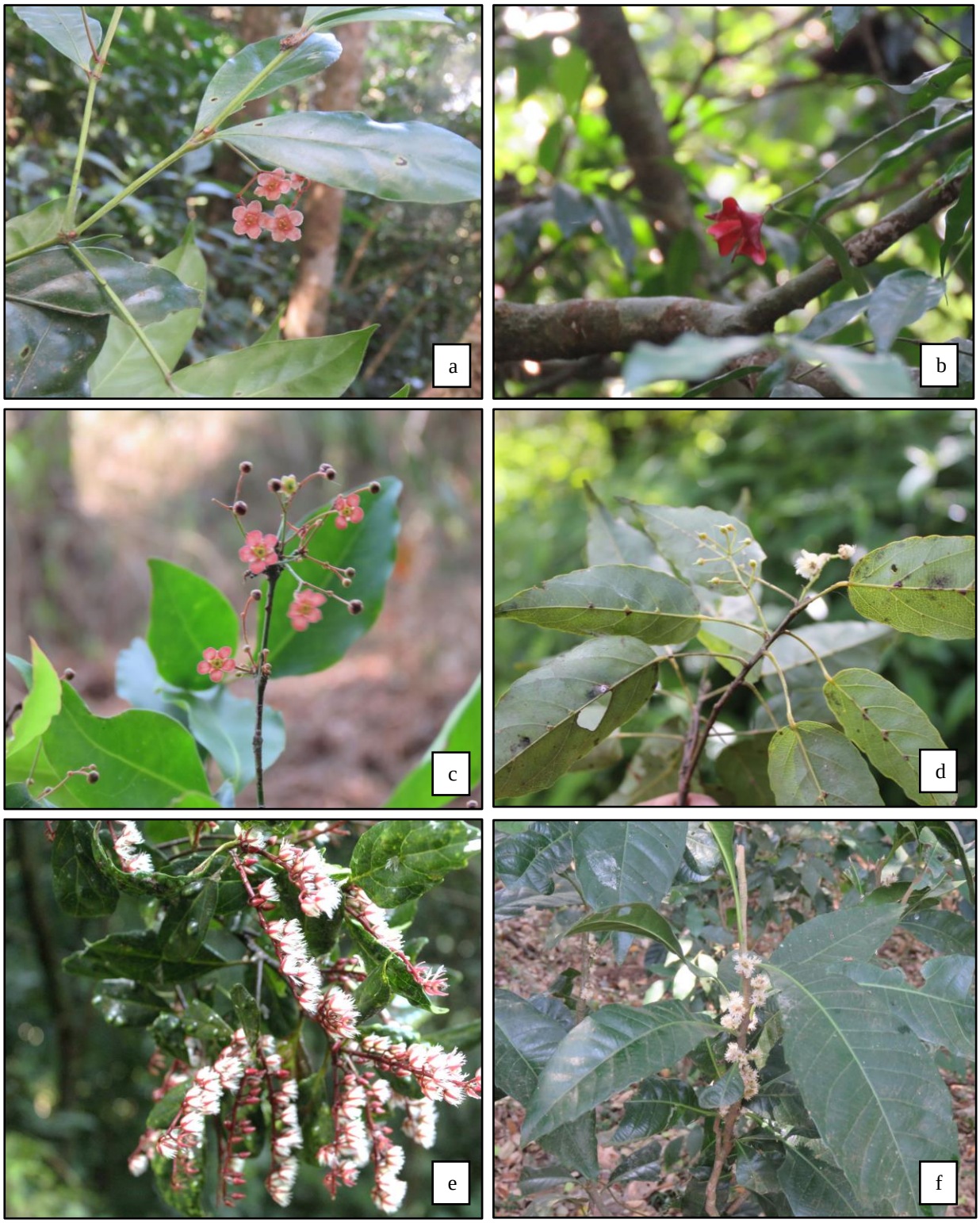


Plate 3.10: Endemics plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Euonymus angulatus* Wight., b. *Euonymus indicus* B. Heyne ex. Wall., c. *Euonymus laxiflorus* Champ. ex. Benth., d. *Elaeocarpus munroi* (Wight) Mast., e. *Elaeocarpus gadgilii* A. M. Maya, V. Suresh and K. M. P. Kumar., f. *Agrostistachys indica* Dalzell.

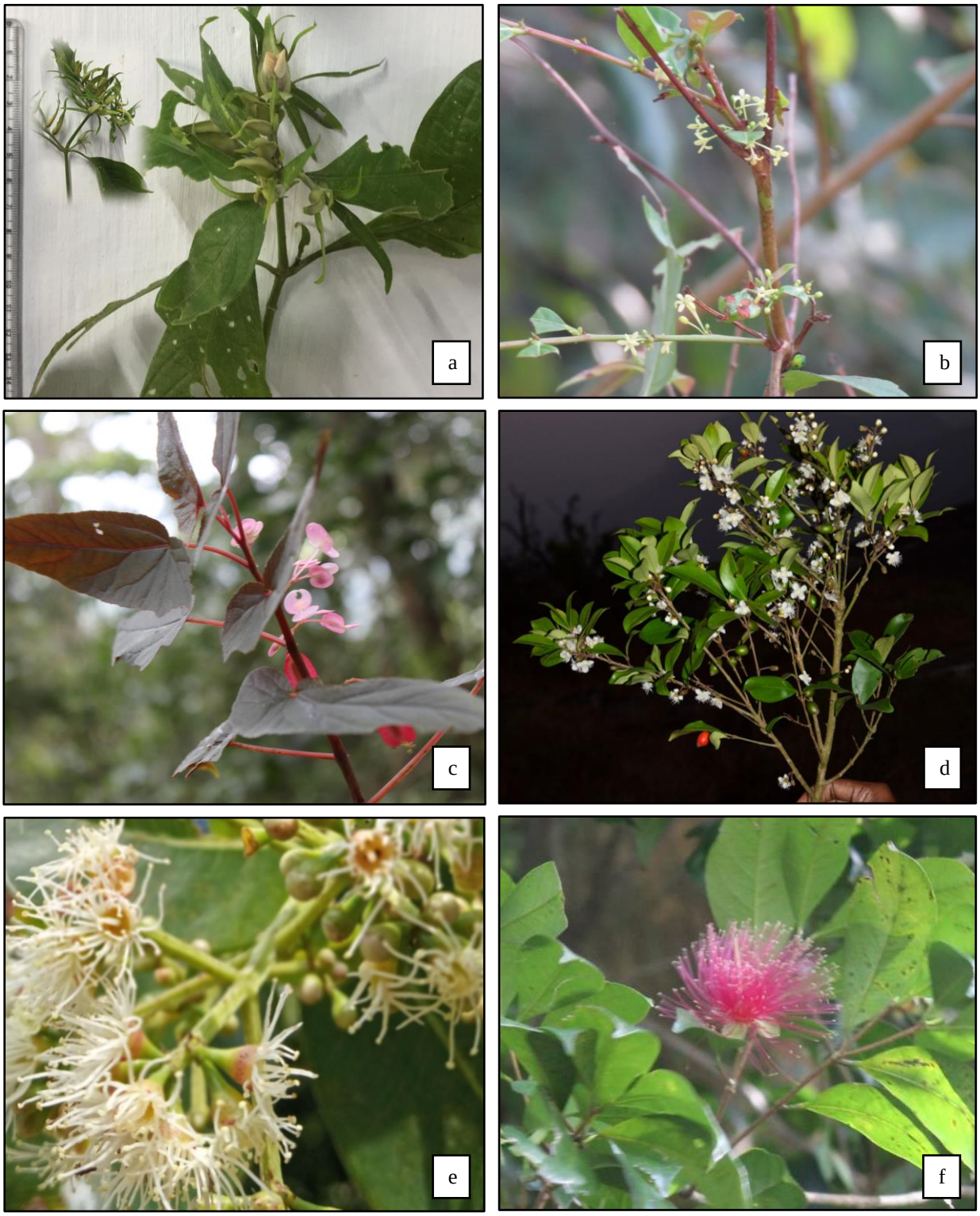


Plate 3.11: Endemics plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Barleria involucrata* Nees., b. *Glochidion ellipticum* Wight., c. *Begonia malabarica* Lam., d. *Eugenia pokkudanii* A. M. Maya, K. M. P. Kumar & V. Suresh., e. *Syzygium densiflorum* (Blume) Wall. ex Masam., f. *Syzygium laetum* (Buch.-Ham.) Gandhi.

Plate 3.12: Endemics plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Symplocos macrophylla* Wall. ex. DC., b. *Sonerila versicolor* Wight., c. *Memecylon sessile* Benth. ex Wight & Arn., *d. Impatiens parasitica* Bedd. e. *Palaquium ellipticum* (Dalzell) Baill., f. *Glycosmis nelliyampathiensis Jabeena & Maya ., g. Canthiumera neilgherrensis* (Wight) K.M.Wong.,

Plate 3.13: Endemics plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Myrsine daphnoides* (Mez) Ricketson & Pipoly., b. *Tetrataenium rigens* (Wall. ex. DC.) Manden., c. *Psychotria globicephala* Gamble., d. *Aeschynanthus perrottetii* A. DC., e. *Vincetoxicum hirsutum* (Wall.) Kuntze., f. *Carissa spinarum* L.

Plate 3.14: Endemics plants over the sky islands of the Western Ghats across the Palghat Gap in the study area: a. *Henckelia fischeri* (Gamble) A. Weber & B. L. Burtt., b. *Torenia bicolor* Dalzell., c. *Leucas lamiifolia* Desf., d. *Premna paucinervis* (C. B. Clarke) Gamble., e. *Anaphalis travancorica* W. W. Sm., f. *Emilia scabra DC.*

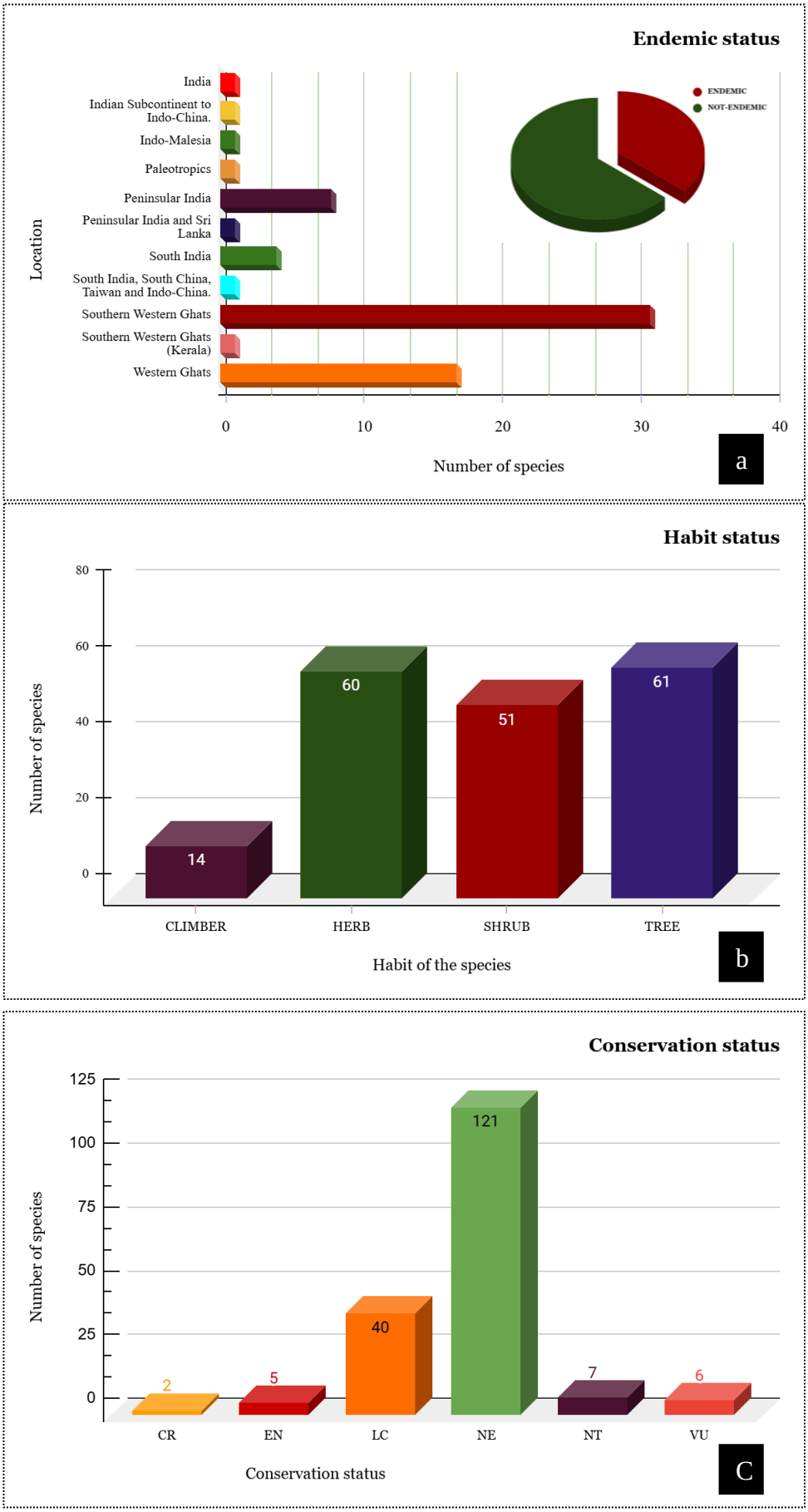


Plate 3.15: Floristic diversity analysis over plants collected from the sky islands within the study area: a. The endemic status, b. Habit status and c. Conservation status of the species collected from the sky islands.

a specific geographic area, which can range from expansive regions to more localised habitats. This classification gives rise to two distinct categories of endemics: neo-endemic and paleoendemic. The former pertains to species that have recently emerged as unique to a specific locale, whereas the latter refers to species that have ancient, enduring ties to a particular geographic region (Major 1988, Warshall 1995). Given that geographical isolation profoundly influences the process of speciation, thereby the potential for neo-endemism within the studied sky islands is notably heightened. This propensity is chiefly attributed to the pronounced separation of sky islands resulted from the presence of the Palghat Gap, an ancient and expansive geographical divide that disrupts the contiguous expanse of the Western Ghats.

Furthermore, the examination of the habit preferences of the documented species revealed that 61 out of the total 186 documented species were exclusively arboreal (Plate 3.15: b). The survey, being primarily concentrated on trees, offers a lens into the evolutionary dynamics of the species within their respective habitats. By focusing on this specific biological aspect, the survey stands out to illuminate the intricate evolutionary processes unfolding within the sky island ecosystems.

The conservation category of each documented species was analysed based on the IUCN 2023 version (Plate 3.15: c). As per the conservation status analysis of the species collected, among that the endemic species, 7 of the species were under the Nearly threatened category (NT) and they were *Meiogyne pannosa* (Dalzell) J.Sinclair, *Litsea coriacea* (B.Heyne ex Nees) Hook.f., *Actinodaphne bourdillonii* Gamble., *Litsea bourdillonii* Gamble, *Litsea stocksii* (Meisn.) Hook.f., *Litsea wightiana* (Nees) Wall. ex. Hook. f., and *Elaeocarpus munroi* (Wight) Mast. Six of the species under the Vulnerable category were *Actinodaphne campanulata* Hook.f., *Litsea ghatica* Saldanha., *Euonymus angulatus* Wight., *Hydnocarpus alpinus* Wight., *Syzygium densiflorum* Wall. ex Wight & Arn. and *Canthiumera neilgherrensis* (Wight) K. M. Wong. Five under the Endangered category included *Orophea thomsonii* Bedd., *Cinnamomum wightii* Meisn, *Cryptocarya anamalayana* Gamble, *Glochidion ellipticum* Wight., and *Psychotria globicephala* Gamble. *Litsea anamalayana* Robi and Udayan., *Eugenia pokkudanii* under Critically endangered category (CR), and 40 species are under the least concerned category. This observation underscored the vulnerability of the endemic species to the looming threat of extinction. Then the not evaluated category of species were about 121 out of the total of the 186 species documented, thereby intensifying the complexity of the scenario. The Not Evaluated category

signifies a state of uncertainty regarding the precarious status of these species, with the potential for being on the brink of extinction. This unpredictability accentuates the gravity of the situation. This underscores the significance of implementing robust conservation measures within these areas. The act of categorising species over the conservation status played a pivotal role in amplifying awareness of their vulnerability and the associated risks of loss of biodiversity. This categorisation acts as a catalyst, galvanising the impetus for conservation initiatives. In the absence of such systematic evaluation, the likelihood of species loss escalates. The adoption of the IUCN categorisation framework emerges as a fundamental stride towards enhancing awareness about the imperatives of conservation efforts. This increases the significance of the study area, underscoring its pivotal role in biodiversity preservation. Furthermore, this region emerges as a significant wellspring of endemic species, thereby emphasising its paramount importance in the broader context of biodiversity conservation efforts. This accentuates the heightened importance of conducting thorough analyses of floristic diversity across these sky islands. Consequently, these analyses serve as a conduit for elevating awareness and instilling the necessary impetus for conservation measures.

The family status analysis was conducted based on the floristic survey data of the sky islands in the Western Ghats across the Palghat Gap. For the sky islands positioned on the northern side of the Palghat Gap, the collected species belonged to 42 families. Notably, the two prominent families were Rubiaceae and Acanthaceae (Plate 3.16). On the southern side of the sky islands, there were approximately 58 distinct families, with Lauraceae standing out prominently (Plate 3.17). As per the analysis done over the occurrence status of the species over the sky islands across Palghat Gap, there were 33 species that exhibited a shared presence on both the sky islands on the northern and southern sides of the Palghat Gap. However, it is notable that a discernible contrast exists, with some species solely present on the sky islands on one side of Palghat Gap and absent on the other. Based on the comparative analysis of the initial survey, a total of 83 species were gathered from the sky islands located on the northern side of the Palghat Gap. Among these, 50 species were found exclusively within this northern sky islands segment. In contrast, from the sky islands on the southern side of the Palghat Gap, 111 out of 144 species that exclusively inhabited on this southern segment. This delineates a distinctive and divergent pattern of species diversity across the Palghat Gap.

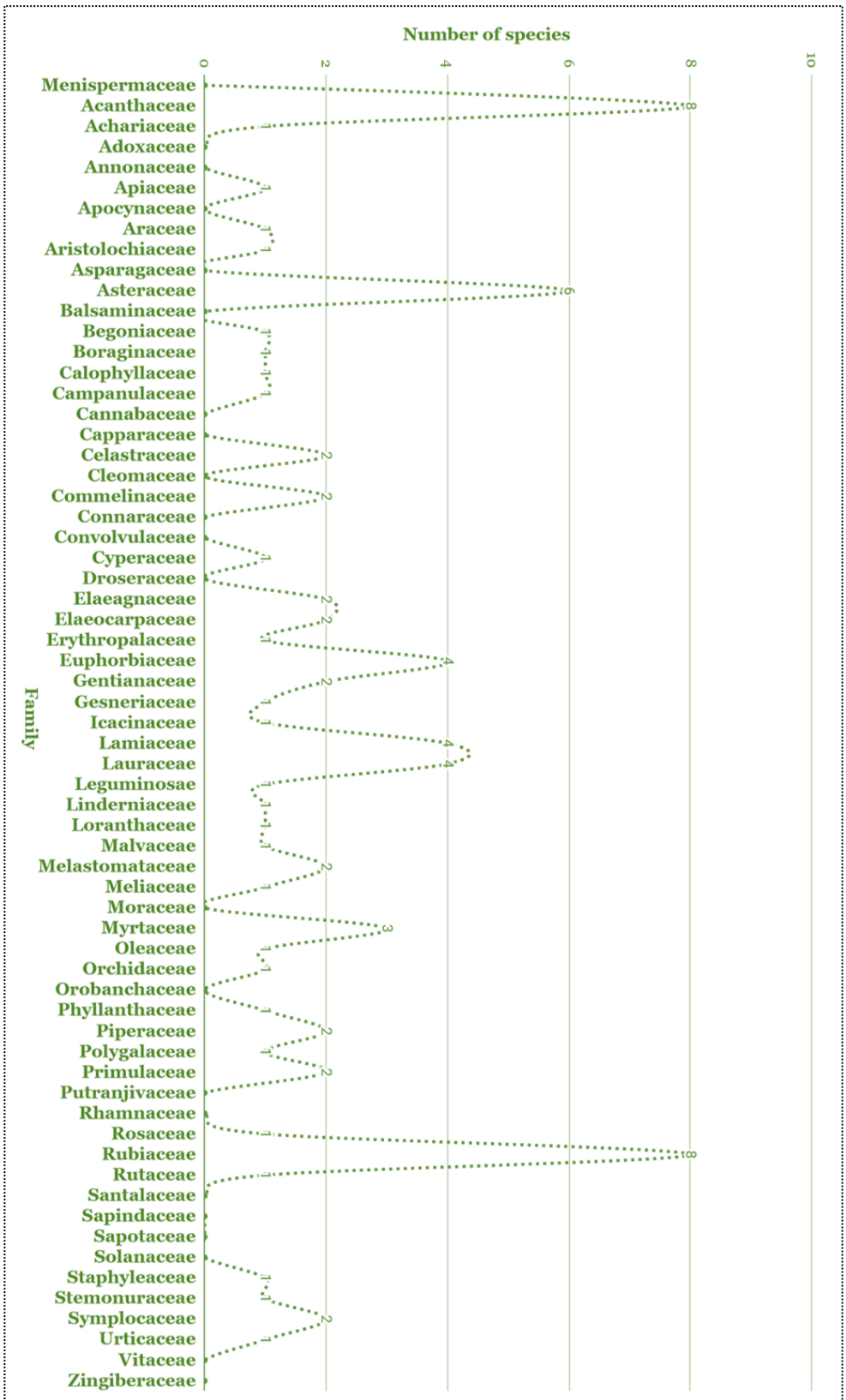


Plate 3.16: Family status of the species collected from the sky islands of the Western Ghats on the northern side of the Palghat Gap, with in the study area.

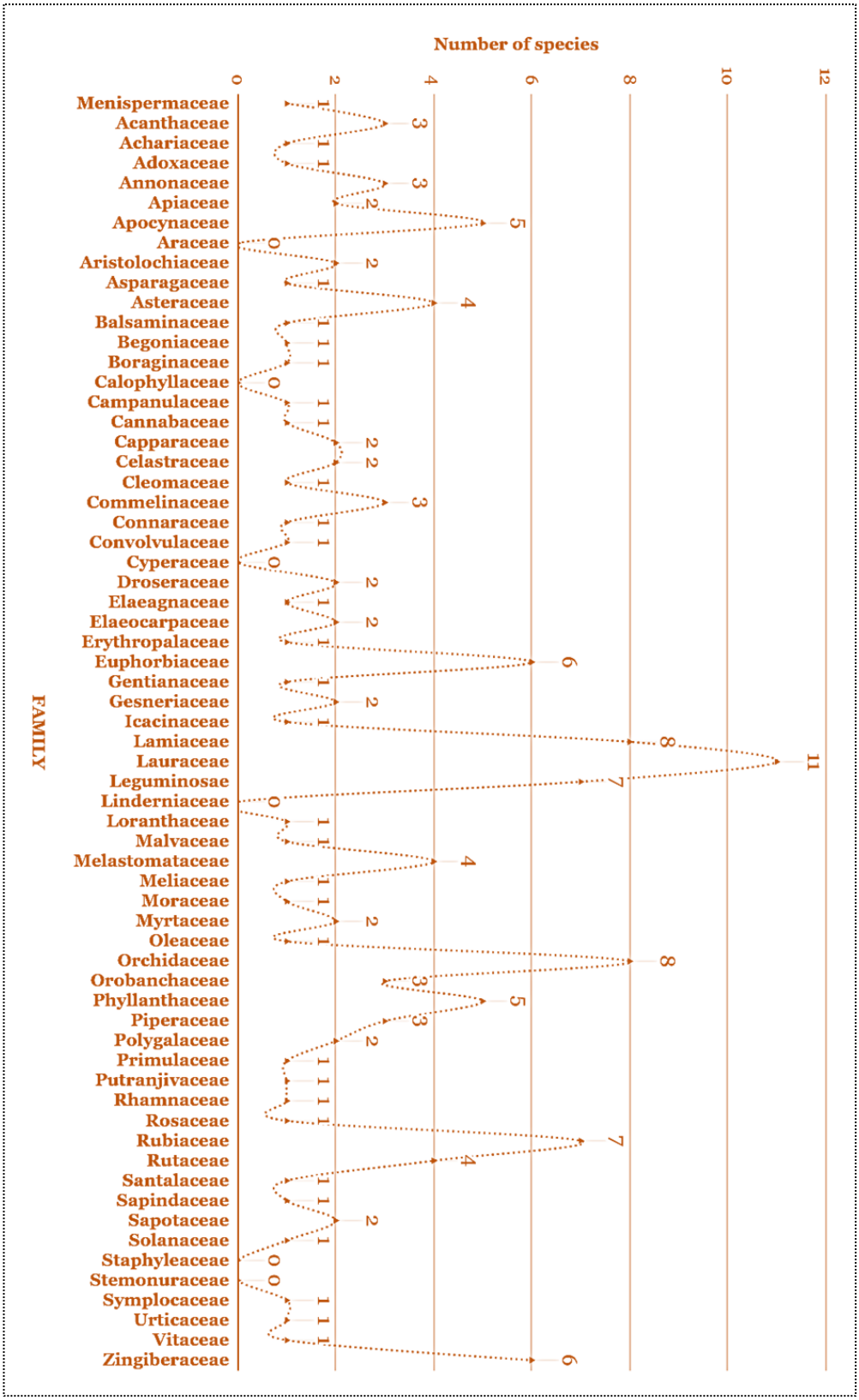


Plate 3.17: Family status of the species collected from the sky islands of the Western Ghats on the southern side of the Palghat Gap, with in the study area.

The comparative floristic survey analysis done over the sky islands of the Western Ghats, shows that the southern part of the Western Ghats appeared to be more diverse and biodiversity rich than the northern side sky islands. As discussed previously, the southern Western Ghats is mentioned to be the most biodiversity-rich region over the Western Ghats, which was substantiated by the fact that the Western Ghats depends on south-west monsoon. The climate and topographic variation across the Gap appeared to be the most probable cause that have resulted in the floristic diversification across the Gap.

As per the present analysis the floristic diversity of the sky islands of the Western Ghats on the southern side of Palghat Gap is found to be different from the sky islands of Western Ghats on the northern side, and southern side sky islands seems to be more diverse and biodiversity rich. The survey revealed that there were a few species that are specific to sky islands on the northern and southern part of the Palghat Gap, as well as some common species.

Despite the limited area and time period of the survey, it was found that there was a distinct variation in the floristic diversity observed over the sky islands of Western Ghats on the southern and northern sides of Palghat Gap. This shows that sky islands are highly diverse and distinct, and which are highly susceptible. The sky islands, harbouring a multitude of endemic species, strongly indicate that these regions likely boast a high probability of undergoing speciation. Here the geographical isolation are the one that found to have significantly influenced the diversification of species found in sky islands. This isolation of sky island habitat, combined with sporadic gene flow within it, may have contributed to the hybridisation and subsequent diversification of certain sky island species, like the patterns observed in species diversification (Zhang *et al*., 2019a).

3.3.5. Selection of taxa

The preliminary floristic survey carried out between 2018 to 2020 in the sky islands, served as the foundation for taxa. The survey involved a randomised approach across the designated sky islands, encompassing the random gathering, documentation, and analysis of species, with a specific focus on trees. Species selected for the present subject area of focus of the study were based on the criteria already mentioned. As per the criteria three distinct species were judiciously selected (Plate 3.18). The species selected were namely *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P. Kumar, endemic to the Western Ghats, *Elaeocarpus munroi* (Wight) Mast.

Plate 3.18: The three species selected from the sky islands of the Western Ghats, based on the preliminary floristic survey done over the sky islands across the Palghat Gap: a. *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P. Kumar., b. *Phoebe wightii* Meisn., and c. *Elaeocarpus munroi* (Wight) Mast.

endemic to the southern Western Ghats, and *Phoebe wightii* Meisn. endemic to the peninsular region of India.

Although all these three species met some of the selection criteria, but last two that is *Elaeocarpus munroi* (Wight) Mast. and *Phoebe wightii* Meisn., samples were insufficient and there was no prominent visible intraspecific morphometric variation to test the hypothesis at the morphometric level. The above-mentioned last two species population size was a little higher over the northern sky islands. This reflect that the changes in environmental variable fluctuation caused by Palghat Gap features may have affected their distribution. Therefore, the study over these two species were not extended to the morphometric variation analysis level. Instead, the effect of environmental variable change over the distribution of these two species were studied under a very limited population. This was made possible through the Ecological Niche Modelling (ENM) technique. Through this ENM technique, the effect of Palghat Gap features over the distribution of these species were studied. In addition to this, the distribution of *Elaeocarpus gadgilii* was also forecasted to analyse its faith. Ecological Niche Modelling (ENM) analysis for the aforementioned trio of species is elaborately presented in Chapter 4.

Amongst the triad of species under investigation, only "*E. gadgilii*" demonstrated adherence to the selection criteria for inclusion in the intraspecific morphometric variation analysis. This selection was motivated by the intention to scrutinise the morphometric reflectance of its population in relation to gradients of environmental variables. This species, hitherto not reported in floristic literature, exhibits endemism to the southern Western Ghats and a distinct affinity to sky island habitats. The notable morphological diversity exhibited exclusively within the confines of the designated study area further underscored its choice for inclusion in this study.

The alterations in environmental parameters typically set off a series of cascading effects. Initially, as per several direct field and literature observations, it is found that these environmental variables first reflect over the migration patterns and are then followed by the establishment through isolation mechanisms or the reduction in the population. These changes subsequently impact the overall distribution of the species. Those that have got the ability to endure and adapt to these environmental modifications tend to persist over time, often showcasing inherent morphometric variations. To understand the implications of these evolving environmental determinants, it is prudent to conduct an examination of the projected future distribution of species

that closely mirror the intricacies of their habitat. Such an approach enables a more nuanced understanding of the intricate relationship between species and their changing surroundings, shedding light on the potential consequences of these distributional shifts on the ecological dynamics of these sky island ecosystems.

The impact of topographic and environmental changes will be prominently evident in the alteration found in species distribution. When environmental conditions are conducive, species tend to expand their distribution range. Conversely, in cases of unfavourable environmental shifts, a gradual contraction of the area of natural habitat, potentially leading to its reduction from previously inhabited regions. In this context, drawing upon the data obtained from the floristic survey, specific species were identified as the subject of the study to substantiate the hypothesis under consideration, and the one that serves as an indicator of the environment's variants acted upon the sky island habitat.

During the field investigation, it was observed that the initial two species, *Phoebe wightii* and *Elaeocarpus munroi* (Plate 3.18), exhibit restricted and fragmented distributions in the sky islands within the Western Ghats flanking across the Palghat Gap over its northern - southern axis. This differential spatial distribution pattern poses a significant threat to their survival, as it places them in a precarious position with a heightened risk of extinction. The population sizes of both species were notably low, particularly over sky islands on the southern side of the Palghat Gap, with the lowest population numbers observed compared to the northern sky islands. The endemic nature of these species holds paramount importance in biodiversity conservation. Among the two species, *Elaeocarpus munroi* has been already designated as a "nearly threatened" species as per the IUCN 2023-1 version, indicating its highly vulnerable status. Therefore, the risk of extinction of these species is high, especially in the case of *E. munroi* and argues for conservation measures like in-situ or ex-situ.

While the conservation assessment for *Elaeocarpus gadgilii* (Plate 3.18) is still pending, owing to its recent discovery. This poses a question in research, as no conservation categorisation has been done over this species. So, the risk of its extinction is unknown, which makes it an important object in this field of study. Therefore, here in this study, the application of modelling techniques stand as a pivotal stride in this research. This technique holds the key to gauging the urgency of initiating conservation measures for these species. By evaluating the potential risk of extinction, these models aid in comprehending the magnitude of intervention required to avert the

threat. The integration of modelling methodologies offers a systematic approach to assess the risk, enabling informed decision-making and the implementation of targeted conservation strategies to safeguard these species from the looming danger of extinction. The primary objective of the present chapter was to select suitable taxa for justifying the present study. The survey was done to ease the selection process through direct observation. By considering different aspects of analysis three species found over the sky islands within the study area were selected

The present floristic diversity study over the sky islands across Palghat Gap show distinct diversification in floristic diversity across Palghat Gap. It is because the species found in sky islands encounter constraints in their distribution and movement due to the lack of continuous habitat connections. The fragmented nature of their habitat impedes dispersal and thereby limits gene flow between populations inhabiting different sky islands. This limitation significantly influences the ecological and genetic traits of sky island species (Sekar and Karanth 2013). The diversification process of sky island species has profoundly impacted this geographic isolation. And this isolation is clearly visible over the present study results, that the sky island across the gap appears to be separated through the presence of unique species over the sky islands. This signifies that the isolation of populations within separate mountainous regions, referred to as sky islands, plays a vital role in fostering the divergence and evolutionary development of distinct species. The geographic isolation hinders gene flow between populations, results in genetic differentiation and the emergence of novel species (Zhang *et al*., 2019a).

During the preliminary floristic survey, some of the species flowering times appeared to be different over sky islands across Palghat Gap, namely *Phoebe wightii* Meisn., *Litsea wightiana* (Nees) Wall. ex Hook.f., *Litsea anamalayana* Robi & Udayan, *Litsea stocksii* (Meisn.) Hook.f., *Elaeocarpus munroi* (Wight) Mast., *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P.Kumar. The observed variance in phenological timing currently remains minimal, yet there exists the potential for future augmentation. Notably, the flowering period of these species seems to exhibit some variations across Palghat Gap. A detailed study over the phenology was not done in this study. This could possibly be attributed to a later onset of the season on this specific side of the sky islands. The sky islands conditions are extreme, even a small environmental change would cause a wide range of variations at different levels of the ecosystem.

The Western Ghats (WG) is an extensive mountain range extending over 1600 kilometres along the western coast of the Indian Subcontinent, spanning from 8° to 21°N (Subramanyam and Nayar 1974, Ali and Ripley 1983). Additionally, a distinct north-south gradient is evident in terms of seasonality and rainfall patterns within the Western Ghats region (Pascal 1988). Studies focused on plant diversity in the Western Ghats have indicated that the southern areas exhibit exceptional richness and a greater prevalence of endemic species compared to the central and northern regions (Pascal 1988, Gimaret-Carpentier *et al.*, 2003, Davidar *et al.*, 2007). Many of recent floristic studies done over the Western Ghats mentioned the chance of floristic divergence on the Westrn Ghats across Palghat Gap. The present study was clearly able to analyse the floristic diversity of sky islands across Palghat Gap and through the in-depth assessment of the survey data the selection of taxa suitable for justifying further objectives of the study mentioned in the following chapter was hereby accomplished.

3.4. Conclusions

The floristic diversity and uniqueness exhibited by the sky islands within the Western Ghats highlight the significance of conservation measures over this habitat. The vitality of this habitat raises from its high susceptibility to the vicissitudes of climate change, coupled with the presence of species that are endemic to these ecologically distinct niches. The implications of climate change have the potential to disturb these delicate ecosystems thereby necessitating protective measures.

Moreover, upon meticulously analysing the Western Ghats sky islands, a notable distinction was observed. Especially in the biodiversity richness and that is the diversity of Western Ghats on the southern side of the Palghat Gap considerably higher than that observed on the northern side. This distinctiveness highlighted the strong interlink between geographical dynamics and biodiversity patterns. The endemics found over these unique habitats clearly demonstrate the fact that these habitats are prone to speciation, therefore neo-endemism is more probable here. These refined distinctions serve to signify the vital role of geographical factors of Palghat Gap in shaping biodiversity that characterises the Palghat Gap. This study also showed the pivotal significance of Digital Elevation Mapping techniques and spatial mapping methodologies in this field of study. Their utilisation enabled the illustration of the spatial distribution and topographic attributes that render sky islands susceptible to ecological disturbances.

CHAPTER 4:
FORECASTING THE DISTRIBUTION OF SELECTED TAXA IN SKY ISLANDS OF WESTERN GHATS USING ENSEMBLE MODELLING

4.1. Introduction

Niche Modelling infers the regions in which the species are more likely to be present by using species occurrence data including environmental variables such as temperature, precipitation, and topography. ENM (Ecological Niche Modelling) serves as a method for gathering the determinants influencing species distribution patterns and foreseeing the consequence of climate change on biodiversity in future times. In addition to that, it aids in framing conservation strategies, by outlining the pivotal areas for the survival of species. ENM enables to assess the reasonable consequences of alterations in land usage, including urbanisation and habitat fragmentation, on species distribution. It stands out as an important method for unravelling the interconnection between species and their niche environment. It provides valuable details to guide the decisions concerning conservation and management (McMahon *et al*., 2011, Peterson and Soberon 2012, Carrillo-Garcia *et al*., 2023).

The modelling approach uses computational algorithms to predict the occurrence of species within a designated environment, referred to as the realised niche, at precise temporal and spatial coordinates. Predictor variables such as climate (temperature and precipitation), soil composition, water depth, and land cover, can be used to generate the projections of spatial distribution (Beaumont *et al*., 2016). The species distribution models connect the dimensions of both its geographical and environmental space. Geographical space is graphically represented through species occurrence mapping, employing longitude and latitude coordinates on a cartesian plane. Environmental space encompasses the ecological niche occupied by a species. The environmental niche refers to the specific assemblage of environmental variables that facilitate the survival and thriving of a species. This niche is species-specific (Newsome *et al*., 2007, Franklin 2013).

George Hutchinson initially introduced this theory of ecological niche in 1957 (Hutchinson 1957). Two significant components of the niche concept is the fundamental niche and the realised niche, which are used to elucidate the distribution and abundance of species. The fundamental niche refers to the assemblage of environmental conditions under which a species can subsist and propagate. It encompasses the complete range of physical and biological circumstances that a species can cope with,

such as temperature, moisture, light, and other resources. In ecology, the concepts of fundamental niche and realised niche play a significant role in comprehending the abundance and distribution of various species. The former niche pertains to the hypothetical range of a species, while the latter refers to its actual distribution in nature. Biologically, the realised niche is typically smaller than the fundamental niche due to the influence of biotic factors like predation and competition. The fundamental niche is a theoretical concept that represents the potential distribution of a species at conditions where no constraints like biotic interactions like competition and predation exist. In contrast, the realised niche is the portion of the fundamental niche where a species inhabits nature with all conditions under which a species exists with all biotic and abiotic interactions. It is worth noting that the realised niche of a species can alter over time owing to changes in the environment or the introduction of new species. For instance, a non-native species outcompetes the native species and expands its realised niche at the expanse of native species (Elith and Leathwick 2009, Severtsov 2013).

Some models specifically concentrate on geographical space, but most models consider both geographical and environmental space for their analysis. The process of species distribution modelling starts with the collection of point-based species occurrences, which are used as data for modelling. These models used in modelling, in turn, use the occurrence data to project the possible distribution of the species within the environmental space by calibration and prediction. Then these outcomes are presented on geographical space maps (Van Moorter *et al*., 2023).

Recently, the R programme has become increasingly popular for its extensive functionality in statistical analysis and graphical visualisation, due to its high-level architecture and open-source nature. Furthermore, the language has witnessed a surge in its implementation in mathematical computing and modelling methodologies like GBM, GAM, and SVM (Naimi and Araujo 2016). The R encompasses a wide range of modelling packages, and many of these packages are developed and made accessible to the public is on the rise (Hijmans and Elith 2017, Thuiller *et al*., 2016). Every package comes with its unique set of strengths and limitations. However, Biomod2 and Sdm are novel R packages that stand out from the rest as they address the inadequacies of the already existing packages. Moreover, they facilitate the use of several models together and offer several evaluation approaches that enable the better projection of potential species distribution in both space and time. The R workspace acts as a platform that supports all the algorithms loaded and associated with this package.

When analysing species distribution, species occurrence data is usually presented in either a coordinate list or spatial point dataset format. Environmental variables are often available as geographic data, which can be in the form of spatial raster's or vectors. However, to use this type of data in species distribution modelling, it typically needs to be converted into a structure that is suitable for analysis. This conversion process often requires the use of GIS operations. To perform these operations in R, it is necessary to have the "rgdal" package installed to read the raster data. Therefore, it is crucial to import all necessary packages before starting any modelling runs in R. Additionally, for each run, the library function should be used to read the required package. By following these steps, we can ensure that their species distribution models are accurate and reliable (Naimi and Araujo 2016).

Subsampling and Bootstrapping are commonly used replication methods in SDM while running the models. Subsampling refers to the process of randomly dividing the data into training and testing sets without replacement and repetition. In contrast, K-fold cross-validation divides the data into K approximately equal subsets and fits the model K times, using a different subset as the test set and the remaining K-1 subsets as the training set each time. When K is set to the number of observations, the method is referred to as leave-one-out cross-validation, where only one observation is used to evaluate the model at a time (Syfert *et al*., 2014). Bootstrapping is a resampling technique that involves repeatedly drawing a sample of equal size to the original dataset with replacement and using it for training. The observations that are not selected are utilised for evaluation during each iteration.

Evaluation measures include both threshold-dependent statistics, such as TSS, Specificity, and Sensitivity, and threshold-independent statistics, such as AUC and COR. Additionally, jackknife methods are available to compute p-values for small sample-size datasets (Pearson *et al*., 2007). The environmental variables that define the habitat of each species are considered as the predictor variables (Gonzalez-Benito and Gonzalez-Benito 2006). Climate variables and bioclimatic variables are both measures of the physical and environmental conditions that exist within a particular geographic location. However, there are some key differences between the two concepts. Climate variables typically refer to the physical properties of the atmosphere, such as temperature, precipitation, wind and atmospheric pressure. These variables are important for understanding the climate of a particular region and can be used to model and predict weather patterns over time. Bioclimatic variables, on the other

hand, are a subset of climate variables that have been transformed or scaled to reflect their importance to biological processes. Bioclimatic variables are often used as predictors in ecological models because they provide important information about the biological and environmental conditions that can influence the distribution and abundance of species (Watling *et al*., 2012). Bioclimatic variables like water deficit and frost days are derived from precipitation and temperature data, but they reflect the conditions that are most limiting to plant growth and survival. Bioclimatic variables are generally considered to be more important than climate variables in understanding species distributions because they provide a more direct link to the environmental factors that can limit or promote the growth and survival of different organisms (Amiri *et al*., 2020). Climate variables provide an important context for understanding the overall climate of a region, whereas bioclimatic variables are more closely tied to the biological and ecological processes that determine which species can thrive in a particular environment. In essence, climate variables provide important information about the physical properties of the atmosphere, while bioclimatic variables are a subset of climate variables that have been transformed or scaled to reflect their importance to biological processes. Bioclimatic variables are generally considered to be more important than climate variables in understanding species distributions because they provide a more direct link to the environmental factors that can limit or promote the growth and survival of different organisms (Elith *et al*., 2006, Watling *et al*., 2012, Title and Bemmels 2018, Worldclim 2022).

Determining the importance of predictor variables in explaining the distribution is of great practical significance to researchers interested in interpreting model outputs. The Variables Importance Score was used to display the significance of each variable and is a well-known method for determining variable importance (Elith *et al*., 2005, Murray and Conner 2009). The ROC (Relative Operating Characteristics) curve is a graphical representation, to evaluate the prediction accuracy, that plots, the true positive rate also known as sensitivity on the y-axis and the false positive rate or 1-specificity on the x-axis, across a range of threshold probability values. The accuracy of the model is measured by the area under the curve (AUC), where a greater AUC indicates higher accuracy. A model run with an AUC value between 0.5 and 0.7 is of poor quality and performance, above 0.7 the performance is good and near to 1 means the prediction performance of the model is excellent (Fawcett 2006).

The idea of combining predictions from different models into an ensemble has gained considerable popularity in species distribution modelling (Hao *et al*., 2019). The SDM platform is a software tool for projecting species distribution over space and time. It supports various modelling approaches, has an object-oriented design, and can handle spatial and temporal data for single or multiple species. It also provides a standardised and unified structure for handling species distribution data and modelling techniques. Thereby allows scientists to modify and extend the framework. The modelling software implemented in R has a flexible and user-friendly interface (Naimi and Araujo 2016). BIOMOD is a freely available, open-source computer platform designed to enable ensemble forecasting of species distributions and consider the impact of various methodological uncertainties in models and examine species-environment relationships. This software offers a range of modelling techniques, enabling the projection of species distributions under different environmental conditions, such as climate or land use change scenarios, as well as dispersal functions. BIOMOD also provides features to assess species temporal turnover, plot species response curves and evaluate the strength of species interactions with predictor variables. The modelling software implemented in the R platform and its use is not restricted by licence fees. In 2009, a significant upgrade of BIOMOD was released, known as biomod2. This version is an object-oriented program in the R community. It integrates approximately ten distinct model algorithms and has the unique ability to compare or merge them using the data and parameterisation. Additionally, biomod2 takes advantage of R's robust features, which now incorporate geographic information systems and web-server data queries through packages such as “rgdal” and “raster” (Thuiller *et al.*, 2016). The package “sdm” and “biomod2" provide tools for modelling, calibrating, and evaluating species distribution. These tools are for creating an ensemble of models, forecasting and visualisation. The biomod2 package allows up to 10 individual models to consistently run on datasets that contain presence/absence or presence/pseudo-absence data. The models can be combined to create ensemble models and projections. The package also includes additional evaluation and visualisation tools. All these functions are in accordance with scientific standards (Thuiller *et al*., 2016).

The Species Distribution Modelling (SDM) framework is an essential tool for predicting species distribution. It involves a series of steps, such as pre-processing, processing, and post-processing, which are crucial for building accurate models. De-

pending on the chosen modelling approach, additional packages may need to be installed on an R platform before initiating the modelling process. One of the key advantages of the SDM framework over other modelling tools is that it is user-friendly and makes possible the inclusion of essential steps such as checking for multicollinearity, determining variable importance and model evaluation. These steps ensure that the model is both reliable and accurate, making it an invaluable tool for environmental scientists, conservationists and policymakers alike (Naimi and Araujo 2016). So present study makes use of R packages like BIOMOD2 and SDM to evaluate the faith of the three species under selection. Thereby evaluating each species high probable habitat suitable areas of the concerned species over the Western Ghats. Such evaluation may probably give a perception of the influence of the environmental factors over the future distribution of the three species selected in chapter 3 for the present analysis.

4.2. Methodology

The three notable sky island species selected for the present objective of this study were *Elaeocarpus munroi* (Wight) Mast., *Phoebe wightii* Meisn. and *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K.M.P. Kumar (Plate 3.18).

Data management and processing: -

The determination of their distribution patterns was accomplished through a combination of field visits and data sourced from the Global Biodiversity Information Facility (GBIF). These chosen species are representative of the unique ecological characteristics inherent to the sky island habitat and their distributional insights offer valuable understanding regarding the response of specialised species to the changing environmental context.

Modelling involves three major steps like Data management and processing, Model fitting and processing and finally projection and ensemble forecasting. The Data input given in modelling includes the environmental variable and occurrence data. The species occurrence data were acquired either through direct observation or through curated resources such as the Global Biodiversity Information Facility (GBIF 2022) and herbarium collections. The occurrence data derived from direct field visits were given priority, so as to ensure a first-hand understanding of species presence, and the Global Biodiversity Information Facility (GBIF) served as a supplementary source to enrich the dataset. To ensure the fidelity of species occurrence data, a approach was essential. This entails meticulous steps to validate the coordinate system format and to ensure the congruence of geographic coordinates. More species data are

collected especially from herbarium collections, which only recorded species presence data, but it becomes challenging to pinpoint the exact location of a species. However, analysing spatial autocorrelation in the predictors can help to understand how similar nearby locations are to the uncertain species location since areas with similar environmental conditions often exist in proximity. This suggests that the error in determining the species location may not be as significant. Moreover, it necessitates the resolution of any potential issues that may emerge during the process. Subsequently, each occurrence datum underwent meticulous accuracy verification.

A distinctive attribute of the employed modelling package lies in its object-oriented structure, which contributes to error mitigation during the execution of the species distribution model. This platform also incorporates functionalities designed to generate absence data when such information is lacking. Given that under the constraints of limited occurrence data presence-absence background data were utilised, where instances of absence were generated utilising the built-in function (Naimi *et al*., 2014).

The other major step to begin modelling is to choose the area of interest and determine the level of prediction expected for that area. This enables us to specify the training data set and the variables used as predictors. Additionally, if there is a separate independent dataset available for evaluating or validating the performance of the model, it can be included using the test argument. The modelling packages include an inbuilt function to add pseudo absence data from background ecological space. This function does not require a precise formula since it can automatically detect the dataset and predictors (Barbet-Massin *et al*., 2012). The present chapter considered the continuous mountain ranges of Western Ghats as study area.

Environmental data, the other major data required and that typically fall into four distinct categories: moisture, thermal, radiation and mineral nutrients. A plethora of online databases are now accessible for procuring such data spanning from local to regional scales. Notable resources encompass repositories like Worldclim and the Global Soil Database. The present study encompassed the inclusion of both historical and projected climate data. The climate data utilised here are sourced from Worldclim version 2.1. The latest version of Worldclim offers four shared socioeconomic pathway (SSP) scenarios (Fujimori *et al*., 2017, O'Neill *et al*., 2017, 2016, Riahi *et al*., 2017), namely SSP126, 245, 370, and 585. These scenarios were downscaled from the CMIP6 project (Eyring *et al*., 2016, O'Neill *et al*., 2016, Hausfather 2019, Watanabe

et al., 2019), which is an expansion of CMIP5 and incorporates the SSPs as an updated version of the representative concentration pathways (RCPs) (Meinshausen *et al*., 2011, Van Vuuren *et al*., 2011, 2012). The earlier version of Worldclim utilised climate data from CMIP5 (Taylor *et al*., 2012), which examined various potential greenhouse gas emissions scenarios (Nakicenovic *et al*., 2000, Carbon Brief 2019). Future climate data used for the present research were downscaled from the CMIP6 project, available in Worldclim and which include monthly values of minimum temperature, maximum temperature, and precipitation in four shared socioeconomic pathways (SSPs), in 23 global climate models (GCMs). The Worldclim available future climate data in SSPs were averaged over 20-year periods (2021-2040, 2041-2060, 2061-2080 and 2081-2100) and are available at resolutions of 10 minutes, 5 minutes, 2.5 minutes and 30 seconds.

The investigation of the present chapter centres on regions within the Western Ghats area that are vulnerable to erratic weather patterns resulted from the orographic effect. Among the pool of twenty-three global climate models (GCMs), the MIROC6 GCM model was chosen. MIROC6 model, recognised for its compatibility with the Western Ghats region (Konda and Vissa 2023). In alignment with this choice, the model was harnessed across four distinctive socioeconomic pathways namely SSP126, SSP245, SSP370, and SSP585. These downscaled data from CMIP6 were derived from Worldclim version 2.

The climate data available in Worldclim are four distinct temporal segments spanning from 2021 to 2100. Each time period was encapsulated within a 20-year interval, yielding an assessment of species distribution dynamics over the designated time span. The datasets for this assessment were made available through the Worldclim platform (Future climate data 2022). In essence, this approach amalgamated sophisticated climate data, optimal model selection and diverse socioeconomic pathways to produce projection of potential future habitats of the species on Western Ghats.

Amid the four variables available—minimum temperature, maximum temperature, precipitation, and bioclimatic parameters— in worldclim future climate data, the bioclimatic variables were accorded prominence, as they stand as the most biologically pertinent factors within the context of species distribution modelling (Worldclim 2022). There are about 19 bioclimatic variables (Table 4.1) available in different

resolutions, and one of the key determinants here was the utilisation of bioclimatic variables at a spatial resolution of 10 minutes as the predictor variable.

Collinearity is another issue that arises as a concern within modelling techniques, when two variables exhibit substantially high correlation. To effectively tackle this challenge, a predefined threshold, often denoted by a correlation coefficient value, is to be specified. Variables surpassing this threshold are systematically excluded from the modelling process through the utilisation of the "exclude" function. An alternative strategy to circumvent collinearity is to proactively eliminate the collinear variable prior to fitting the model in the context of species distribution modelling.

Table 4. 1. Bioclimate variables downscaled from Worldclim, future climate data (Future climate data 2022) for ensemble modelling.

Sl.No:	Bioclimatic variables	Description
1	BIO1	Annual Mean Temperature
2	BIO2	Mean Diurnal Range (Mean of monthly (max temp- min temp)
3	BIO3	Isothermality (BIO2/BIO7) (×100)
4	BIO4	Temperature Seasonality (Standards deviation ×100)
5	BIO5	Max Temperature of Warmest month
6	BIO6	Min Temperature of Coldest Month
7	BIO7	Temperature Annual Range (BIO5-BIO6)
8	BIO8	Mean Temperature of Wettest Quarter
9	BIO9	Mean Temperature of Driest Quarter
10	BIO10	Mean Temperature of Warmest Quarter
11	BIO11	Mean Temperature of Coldest Quarter
12	BIO12	Annual precipitation
13	BIO13	Precipitation of Wettest month
14	BIO14	Precipitation of Driest month
15	BIO15	Precipitation seasonality (Coefficient of variation)
16	BIO16	Precipitation of Wettest Quarter
17	BIO17	Precipitation of Driest Quarter
18	BIO18	Precipitation of Warmest Quarter
19	BIO19	Precipitation of Coldest Quarter

In the context of detecting multicollinearity among predictor variables, the SDM packages serve as a valuable tool. This entails assessing the correlation between variables, whereby highly correlated variables can be identified and subsequently excluded from the analysis. Techniques such as the variance inflation factor and pairwise correlation coefficients can be leveraged to quantify the degree of correlation. Furthermore, both Pearson (r) and Spearman correlation (p) coefficients offer insights into the nature and strength of relationships between variables. In essence, this ap-

proach underscores a methodical process of data validation, addressing diverse challenges, and harnessing advanced software capabilities to enhance the accuracy and reliability of the species distribution model (Naimi and Araujo 2016).

Here in this study for detecting and excluding high collinear variables, the Variance Inflation Factor (VIF) method was used (Graham *et al*., 2004, Naimi *et al*., 2014). The VIF technique was used to evaluate the correlation among predictors in a model. To calculate the VIF, multiple correlation coefficients are determined by regressing the predictor variable against all other predictors. The assessment of multicollinearity wherein a threshold of 10 was employed to identify variables exhibiting significantly high collinearity. One approach to address this issue was by calculating the VIF for each predictor and eliminating the one with the highest VIF, that is the one that surpasses the predefined threshold. This process was repeated until all highly correlated variables had been removed. Another method involves identifying the pair of variables with the highest correlation coefficient and excluding that variable. This procedure is then repeated until no highly correlated pairs remain (Naimi *et al*., 2011, 2014, Dorman *et al*., 2012).

In more detail, collinearity denotes a scenario where two or more predictor variables in a model are closely related, leading to challenges in interpreting the individual contributions of these variables to the model outcome. When variables are strongly correlated, it becomes difficult to distinguish the independent effects of each variable on the response variable, which can lead to unstable and unreliable model results. By excluding highly collinear variables, the model's accuracy and interpretability are enhanced and the risk of overfitting due to collinearity is mitigated. In this study, a total of nineteen bioclimatic variables were taken into consideration as potential predictor variables for the modelling process. To ensure the reliability of the model, a test for multicollinearity was conducted using the Variance Inflation Factor (VIF). This analysis aimed to identify any problematic collinearity patterns among the predictor variables. As a result of the VIF multicollinearity test, it was observed that ten variables exhibited significant collinearity issues. After addressing the collinearity concerns, the linear correlation coefficients were recalculated for these variables. These coefficients ranged from a minimum of -0.06113752 (between bio14 and bio8) to a maximum of 0.813837 (between bio9 and bio3), thus reflecting the degree of correlation between these variables after eliminating collinear ones. Importantly, the consistency of the VIF test outcomes was evident across all three species studied, indicat-

ing that the issue of multicollinearity was addressed uniformly in the modelling process for each species. By meticulously addressing collinearity, the study enhances the reliability and accuracy of the subsequent species distribution models. Consequently, these ten variables were excluded from further analysis, as their interdependence could potentially lead to unreliable and unstable model outcomes. The remaining nine bioclimatic variables selected for the study were bio2, bio3, bio8, bio9, bio13, bio14, bio15, bio18, and bio19.

Model fitting and processing: -

As the species occurrence data were managed and processed, the study area and predictor variables were set, the next step was to find the model that fit the object, and this was done through model fit runs. Once a data object has been created with all the processed input data, the subsequent step is to fit models to the object and select the optimal model for the data. In species distribution modelling, evaluating the best-fit models was crucial. The majority of modelling methods are designed to estimate the probability of species occurrence at a particular location. Evaluation statistics, such as TSS, Kappa, and AUC/ROC are the ones commonly used to assess the performance of a model (Araujo *et al*., 2005).

AUC is threshold-independent metrics and are not affected by specific thresholds. Once the models are established, additional tasks are necessary, including variable importance identification and model evaluation. To mitigate the potential for biased parameter estimation, several methods were used, such as random subsampling, K-fold cross-validation, Leave-one-out (Jackknife) and bootstrapping (Liu *et al*., 2009).

The model that fits the data best was determined through multiple attempts. The performance of each model run was determined by the success rate and the overall model performance and was assessed by calculating evaluation metrics such as AUC/ROC, TSS, Kappa and Deviance. To achieve a good fit model, a model should have minimal deviation 0 and high values for all other statistics value near to 1. Once a suitable model was identified, modelling was done, and its performance was evaluated. Predictions can then be generated based on the model.

Currently, SDM and Biomod2 are two packages that support multiple models and were considered for the study. This was to generate more accurate predictions, as multiple instances of a model be used with different settings or ensembles of several models create a consensus of predictions. The variables and models used for model-

ling are specified in the argument of modelling function. If there were fewer occurrence data available, the performance statistics were estimated using the training dataset. If there are enough datasets, then they can be split, and the replication duration can be increased to make model fitting easier. In SDM, the data partitioning techniques available are sub-sampling function ("sub"), bootstrapping ("boot") and cross-validation ("cv"). The test percent, number of replications and list of models were to be mentioned in the model fit argument in SDM. These settings were mentioned only in SDM package run, not in BIOMOD2, as its pathway was different, but each step aim is the same as in SDM.

The initial modelling endeavour employed in the three distinct species was the "biomod2" package, to analyse the distribution patterns spanning both historical and future periods. The limited available presence records necessitated the incorporation of pseudo-absence data and was achieved through the utilisation of the package's built-in functions. Within this framework, an ensemble forecasting approach was adopted to project the species distributions across varying time spans. Multiple models were employed for this ensemble approach, and each was tailored to the specific requirements of the individual species. Notably, the ensemble forecasting procedure was conducted 40 times per model, with a predetermined threshold of 0.8 being employed to enhance the precision of predictions. The selection of the optimal model for each species was contingent upon the unique nature of species distribution, which is influenced by bioclimatic variables. This dependency underscores the variation in the choice of model that best captures the distributional dynamics of each species. Furthermore, the assessment of variable importance played a pivotal role in comprehending the predictive power of individual predictor variables. This metric elucidates the degree to which species distribution hinges upon specific environmental variables. The "biomod2" package offers an array of ten pre-built models, encompassing Maxent, GLM, GBM, GAM, CTA, ANN, SRE, FDA, RF, and MARS thereby enabling a diverse and robust modelling approach was used to uncover the intricacies of species distribution.

In BIOMOD2, replication methods were not mentioned and were set as default, instead in the settings prevalence, metric evaluation (stat values considered for evaluation), the variable importance number and all the models to be considered are to be specified in the model fit run argument. As per the model fit run, the best model for each species was selected, based on evaluation statistics. Then through the

“getEvaluation” function, the mentioned stat value measures score mentioned in the argument can be obtained and based on which each model was evaluated.

In the SDM package, the major stat values considered for selecting the best model fit were AUC, TSS, Deviance and Kappa. In BIOMOD2, the available evaluation stats were ROC, TSS, Kappa, SR, FAR, POD, CSI and ETS. In all the above mentioned modelling these stat values range from 0 to 1. Where if Deviance is near zero and remaining all other stat values near 1, means that the model considered in modelling were the best fit to the object under concern.

The subsequent procedural stage encompassed the examination of the best-fit models tailored to each specific species within the designated modelling packages. The assessment of model fit involved the application of diverse statistical metrics. Specifically, we considered the True Skill Statistic (TSS), the Receiver Operating Characteristic (ROC) curve and the Kappa coefficient within the BIOMOD2 package. In alignment with the model fit assessment, the model that yielded the optimal performance was singled out for further analysis. Then the final model run was done with the selected model. In BIOMOD2, the final model run was done with the function “BIOMOD-Modelling” function, where in the argument the prevalence given was 0.5, split percent as 100, metric. eval where stats are mentioned, number of replications given was 40, var. import (number of variable importance) given was 3 and selected best models were mentioned, and it changes in accordance with species data.

In the SDM package, the final model run was done with “sdm" function, where in the argument, the number of replications raised from 1 to 40, the test percentage (test. p) given was 30 and the best replication method was also mentioned. Here the best replication method was also selected based on evaluation stat. Then the prediction was done as per the fit models.

Prediction and Ensemble forecasting: -

In order to predict the habitat-suitable areas for the species, in SDM, the "predict" function was employed during the model run. The prediction argument included the final model fit object, predictor variable and predicted output name. The resulting output was a raster projection of the predicted suitable habitat areas. The prediction using the BIOMOD2 software package, where the "BIOMOD_Projection" function was utilised, where in the argument the model object, predictor variable and chosen best-fit models were specified.

The results of the prediction were presented in the form of a raster object that provided a visual map of the suitable habitats for concerned species throughout the entire study area, the Western Ghats. The study highlighted the potential problems that can arise when relying on a single model for predictions or projections since different models can produce varying outcomes. To address this issue, the present study employed an ensemble approach that utilised multiple models and techniques to explore a range of projections. By appropriately analysing the results of this approach, we were able to achieve significant improvements in forecast robustness.

Employing an ensemble forecasting technique, these predictions were amalgamated into a unified output prediction. This outcome was represented visually through a raster image, wherein a spectrum of colour was employed to signify the probability of species occurrence in future scenarios. Overall, this systematic process advanced the modelling endeavour by selecting the best-fit models, assessing their performance efficiency and synthesising predictions into an output, enhancing our understanding of species distribution dynamics across various time periods. The colour scale was incorporated within the raster image to provide a visual representation of the probability distribution. Notably, this scale served to delineate habitats with high to low probabilities of suitability for the species in the projected future scenarios.

These species distribution modelling packages provide an ensemble function that can be utilised to create an ensemble forecast or prediction based on several models available within the SDM and BIOMOD2. The user can take advantage of various techniques implemented in a flexible manner (Araujo and New 2007, Sharma *et al*., 2023). Ensemble forecasting technique, where multiple models were used to generate an ensemble of several projections of predictions. This approach was advantageous over single model predictions, as it helps to reduce inaccuracies.

The ensemble run produces a consensus of predictions using multiple models by specifying these multiple selected models in the species distribution model object. The BIOMOD2 package employs ensemble modelling using the "BIOMOD_EnsembleModelling" function. In this function argument the predicted object, selected models, threshold, metric evaluation threshold, and variable importance were specified. The prevalence was set at 0.5 in “BIOMOD_EnsembleModelling”, and the TSS was used for metric evaluation with a variable importance of 3. The ensemble modelling used a threshold of 0.8, that is TSS value above 0.8. The models that best fit are selected through the model fit run, are specific to each species and were speci-

fied in the settings argument for ensemble modelling. Then ensemble models were projected separately in BIOMOD2 and then the prediction output was obtained as a single raster through the function “BIOMOD EnsembleForecasting", where in this function argument the ensemble modelled object was given as an object. Then this ensemble output was used for further assessment.

In the SDM package, there is no need for an additional projection of the ensemble, as the ensemble function performs the projection, and the ensemble is done in a single run. In the SDM package, the ensemble is performed using the "ensemble" function, where in the argument the model object, predict object, output name, and selected method (weighted or unweighted) were mentioned. If ensemble forecasting with threshold-based statistics is selected, the "opt" argument can be used, where the threshold ID has to be specified and there are several other criteria for optimising the threshold. The threshold is selected based on evaluation statistics and the model ID. If threshold-independent AUC was chosen, the threshold ID is not required in the argument for the ensemble.

When the occurrence data is limited, in the SDM package the methods employed were either the weighted or unweighted method. If the weighted method was used, then the "stat" parameter should either set to AUC or TSS stat as evaluation stat for analysis. TSS statistics are threshold-dependent and AUC threshold-independent. Therefore, in SDM modelling, the "opt" argument must be filled with the ID number of the model that has high specificity + sensitivity, max (Kappa), Max (TSS) etc... On the other hand, if AUC stat was used, as it was threshold-independent, no need to mention the threshold ID in the argument for the weighted method. Alternatively, the unweighted method, where there is no necessity to mention any evaluation stat.

The predictions here in the study were done over future time periods (2021-2040, 2041-2060, 2061-2080, 2081-2100) in four SSPs and also for Past and Near present (1970-2000) periods of climate data. The past and near present climate data were downscaled from Historical climate data in Worldclim site. For each ensemble run, the predictor variables are to be extracted to the R workspace for each time period, to get the predictions over different time periods.

Ensemble analysis combines the results of multiple models, reducing the uncertainty of a single model or emission scenario. An ensemble analysis experiment produces visual outputs based on statistics, including the mean, minimum, maximum, variance, and percentiles across multiple algorithms or climate scenarios. Predictions

are evaluated based on the high habitat suitable areas within the study area at different time periods. Evaluation of the prediction of the habitat-suitable areas of concerned species is depicted through a colour scale map. To analyse it is converted into a vector format, then processed and then the high probable habitat-suitable areas for each species were measured in square kilometres, with the aid of ArcMap 10.8.

4.2.1. Modelling on *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P. Kumar

The species *Elaeocarpus gadgilii* is endemic to the southern Western Ghats region. It is a tree species belonging to the family Elaeocarpaceae. As recently discovered, there is a lack of prior scientific data, like its occurrence data, conservation status etc.

Data management and processing: -

The data concerning the occurrence *E. gadgilii* was directly acquired through field visits (Plate 4.1), as this information was not available in the GBIF database or other online sources. To complement this dataset, supplementary absence data was sourced from the background geographical space (Plate 4.2). Notably, the modelling process relied on a presence-absence background dataset. This was meticulously integrated through the utilisation of an inherent function within the BIOMOD2 package, ensuring a dataset for the modelling process. The study area over which the prediction done, was over the mountain ranges of the Western Ghats. The bioclimate variable selected for the study, after the VIF test were bio2, bio3, bio8, bio9, bio13, bio14, bio15, bio18, and bio19 after excluding the remaining 10 high collinear variables. Then the data object was set and was imported to the R workspace.

Model fitting and post processing: -

Then the model fitting test run was done with ten distinct models within the biomod2 package. The process of model selection was underpinned by a meticulous evaluation of model performance metrics, encompassing ROC, TSS and Kappa score. The paramount aim of this was to identify the best-fit model which most accurately captures the species distribution patterns of *E. gadgilii*.

Through this rigorous evaluation, the models that stood out as the optimal choice for the present species were Random Forest (RF) and Gradient Boosting Machine (GBM) (Plate 4.3). These selections were substantiated by the attainment of high ROC, TSS, and Kappa values indicating a robust fit of these models to the data and their potential efficacy in predicting the distribution of *Elaeocarpus gadgilii*. The

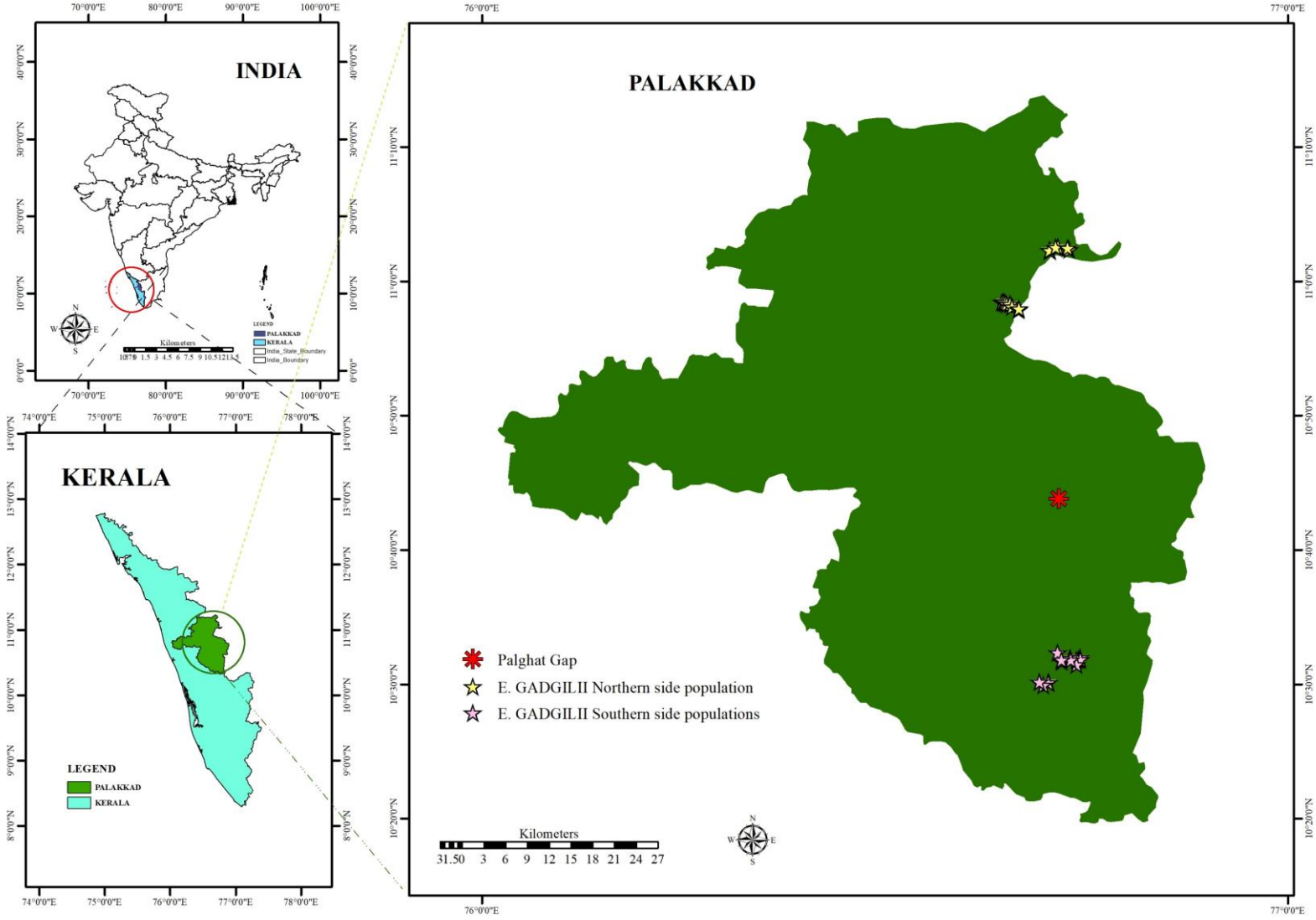


Plate 4.1: Distribution map of *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P. Kumar collected from the sky islands within the study area.

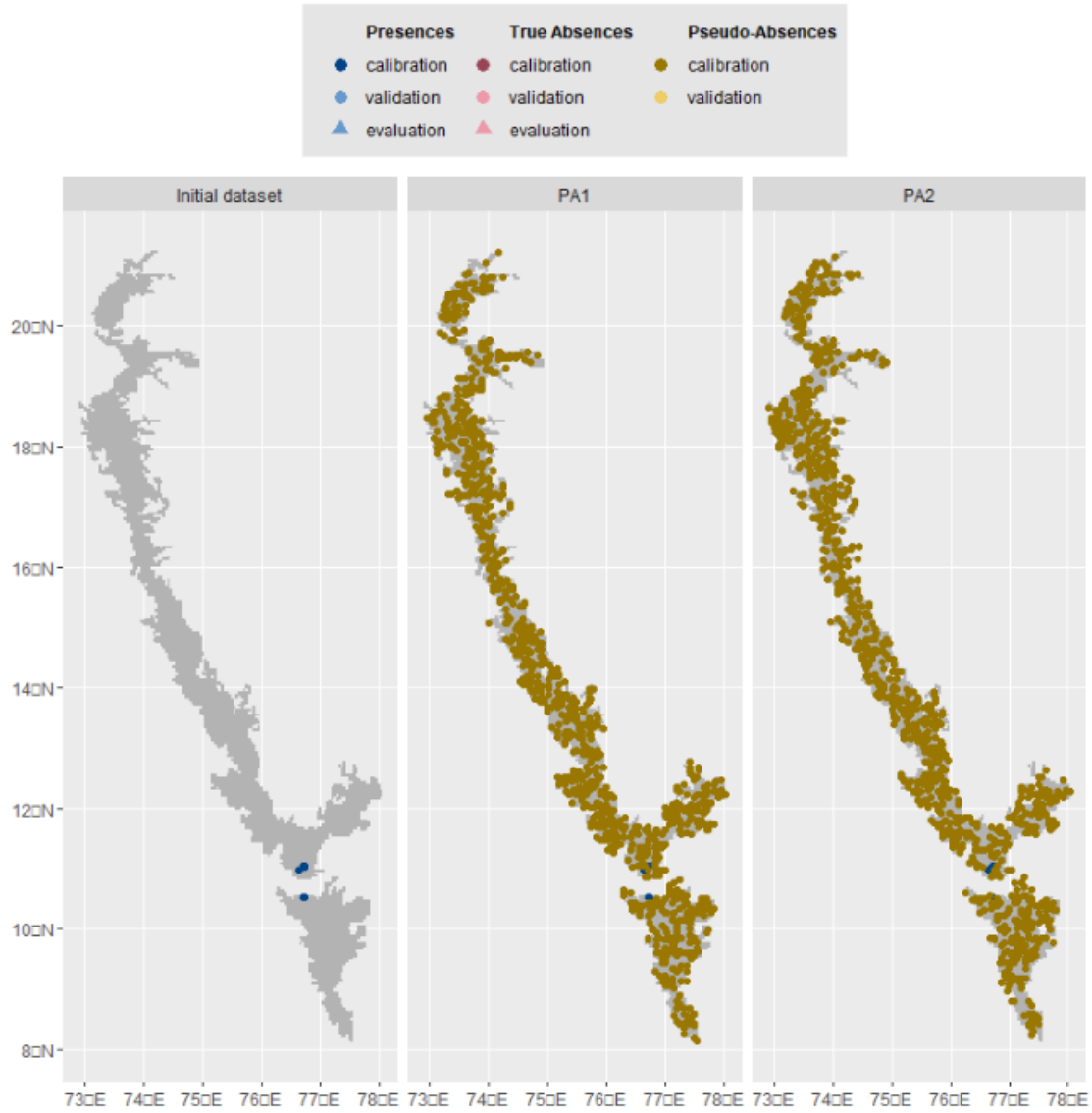


Plate 4.2: Spatial distribution mapping of *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P. Kumar based on presence-absence occurrence data in BIOMOD2 modeling.

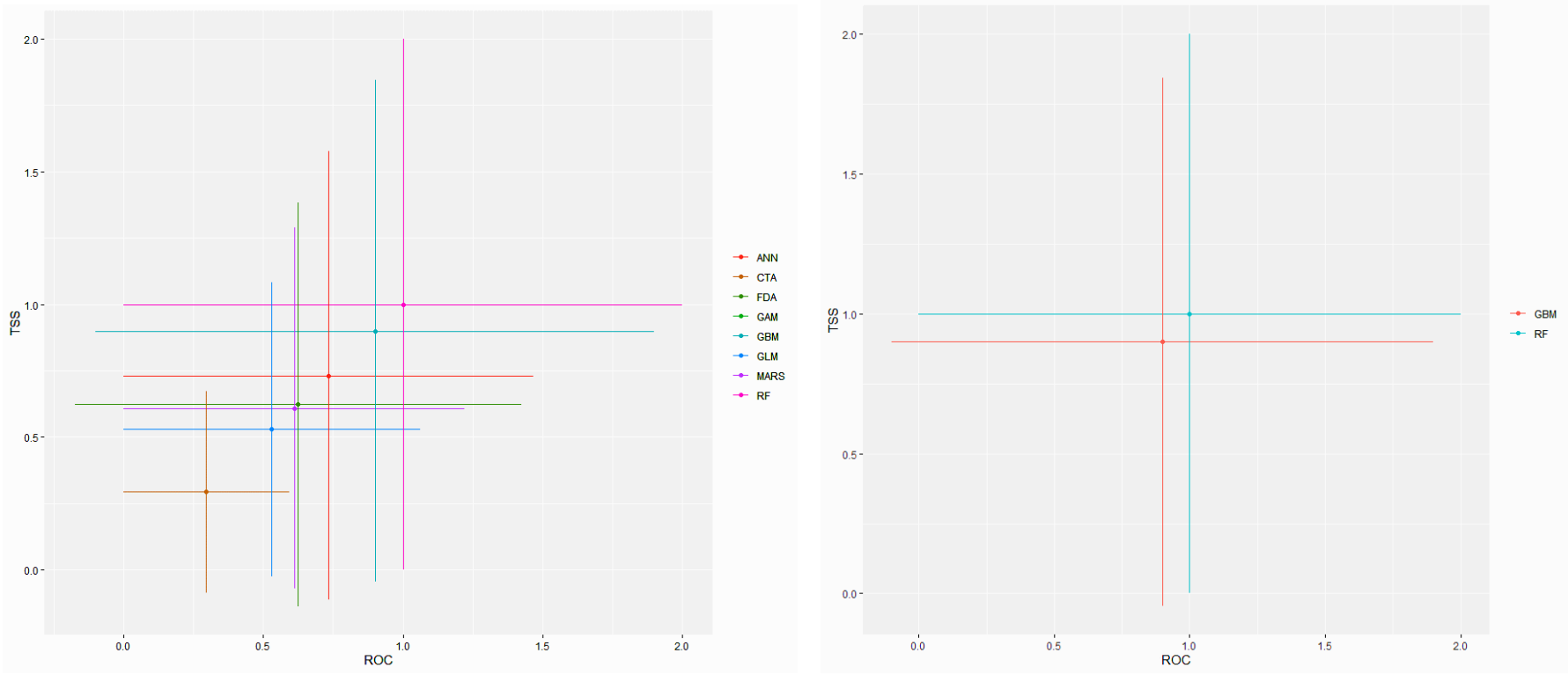


Plate 4.3: Model fit evaluation conducted using 10 models in BIOMOD2 modeling for *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P. Kumar (The model evaluation stat used were ROC and TSS).

ultimate phase of the modelling process involved the execution of the chosen best-fit models, namely GBM and RF.

These models were meticulously selected based on their superior alignment with the species distribution patterns. The specific configurations adopted for the model execution encompassed various parameters. For the final model run the argument was set accordingly where a total of 40 replications were carried out to enhance the robustness of predictions. A prevalence value of 0.5 was set, signifying the proportion of species presence data. Additionally, a minimum variable importance threshold of 3 was set in the argument to ensure the significance of predictor variables. Then the data split percentage of 100 was employed, where this parameter governs the division of the dataset into training and testing subsets, which influences the accuracy assessment of the model predictions. The predictive outputs generated through the biomod2 package's forecasting functionalities were leveraged for subsequent ensemble forecasting. Variable importance analysis was also done to evaluate the bioclimate variable that control the distribution of *E. gadgilii* across the Western Ghats.

Projection and Ensemble forecasting: -

This ensemble technique consolidated the individual predictions produced by the GBM and RF models. Notably, a threshold value of 0.8 was employed to refine the ensemble forecasting process, ensuring a judicious integration of predictions to yield a refined output.

After the final model run, predictions were made for the time range extending from 1970 to 2100, covering both past and future time frames, in four SSP scenarios. Following the execution of the final model run encompassing both best fit models, that is the GBM and RF models, the outcome was materialised in the form of ensemble forecast output raster's. These raster's vividly illustrated high probable habitat suitable areas for the species from past to future. Employing a colour spectrum of regions of varying habitat suitability were differentiated. Within this visual representation, areas with a heightened probability of serving as suitable habitats were distinctly highlighted, juxtaposed with those displaying lower likelihoods. Upon completion of the ensemble run, the investigation proceeded to scrutinise the individual significance of each selected variable that contributed to the model's performance, ultimately influencing the distribution patterns of *Elaeocarpus gadgilii*.

The ensemble forecasts generated a series of output raster's, each uniquely informative and collectively offering insights into the potential trajectory of *Elaeocarpus gadgilii*. Through the systematic evaluation of these output rasters, an enhanced comprehension of the species future prospects on habitat distribution patterns and suitability across diverse scenarios. This ensemble forecasting was explored within the context of four different Shared Socioeconomic Pathway (SSP) scenarios, in four-time intervals to meticulously analyse the high probable habitat-suitable areas of *E. gadgilii*, Arcmap 10.8 was employed. Then each SSP scenario of the future time period was evaluated and compared to the area of high probable habitat suitable in past distribution of *E.gadgilii*.

4.2.2. Modelling in *Elaeocarpus munroi* (Wight) Mast.

Elaeocarpus munroi is a tree belonging to the Elaeocarpaceae family and grows primarily in the wet tropical biome.

Data management and processing: -

This process employed 9 bioclimatic variables out of the total 19 predictor variables after VIF test. The occurrence data necessary for modelling was acquired from both direct field visits and the GBIF (GBIF 2022) source. Through direct field visit the occurrence data was limited (Plate 4.4), so major part of occurrence data was from GBIF.

Model fitting and processing: -

Subsequent to data preparation, a rigorous model fit test was executed. The initial phase of this study involved the implementation of modelling through the BIOMOD2 package. This test encompassed the deployment of 10 distinct models. The dataset was divided using a split percentage of 100%, alongside a prevalence level set at 0.5. The assessment of model performance hinged on metric evaluation statistics, culmination of the modelling procedure using the BIOMOD2 package, it became evident that solely the "RF" model exhibited the ability to fittingly capture the data pertaining to *Elaeocarpus munroi*. The study was oriented towards the implementation of ensemble modelling. Notably, the model fitting endeavours conducted within the BIOMOD2 package underscored a noteworthy observation – exclusively the Random Forest (RF) model exhibited compatibility with the species *Elaeocarpus munroi* data.

Given that the primary thrust of the study was centred on the utilisation of ensemble modelling, the outcomes derived from the model run conducted within the BIOMOD2 framework were deemed inadequate. This perception was rooted in the

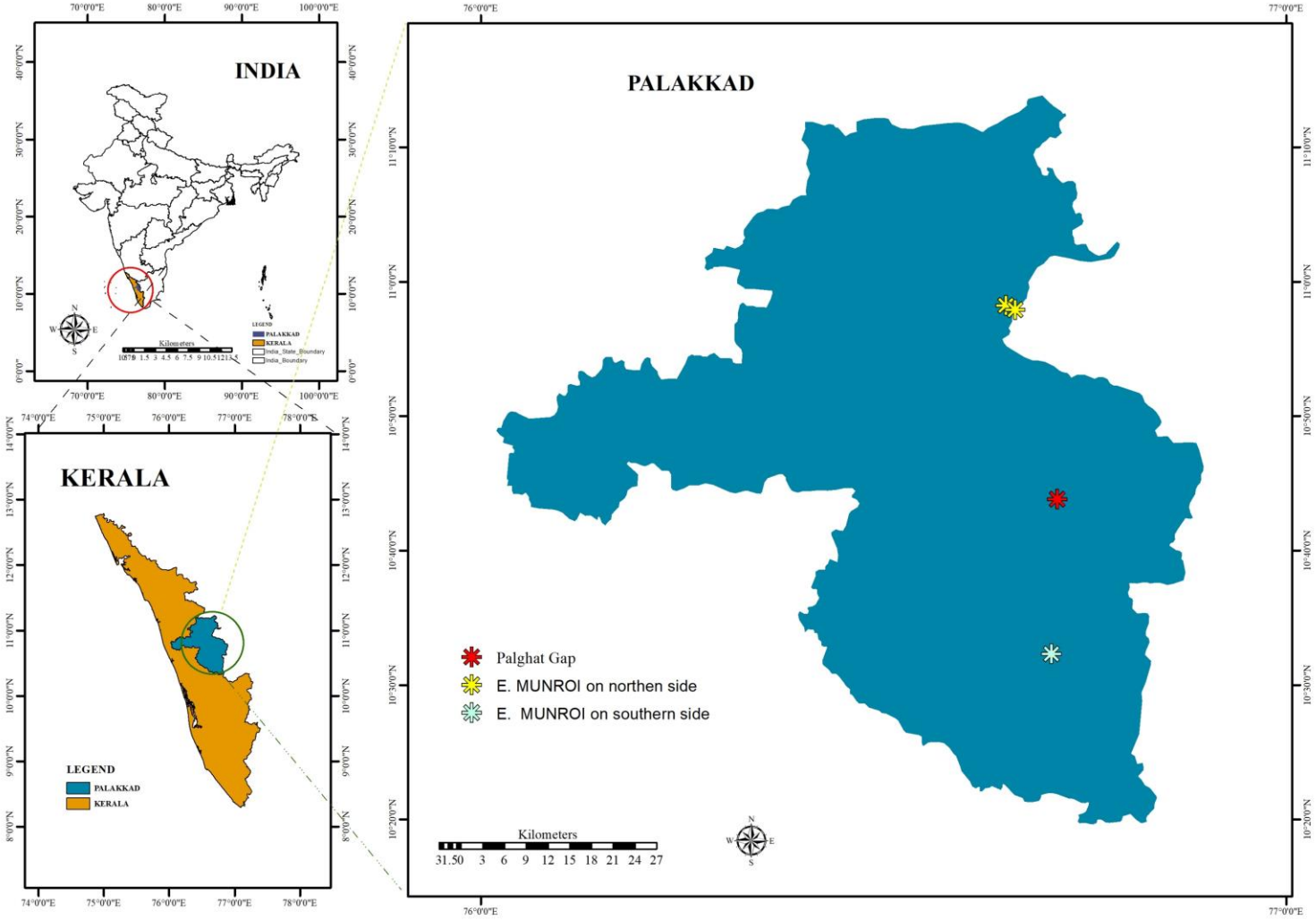


Plate 4.4: Distribution map of *Elaeocarpus munroi* (Wight) Mast. collected from the sky islands of the Western Ghats within the study area.

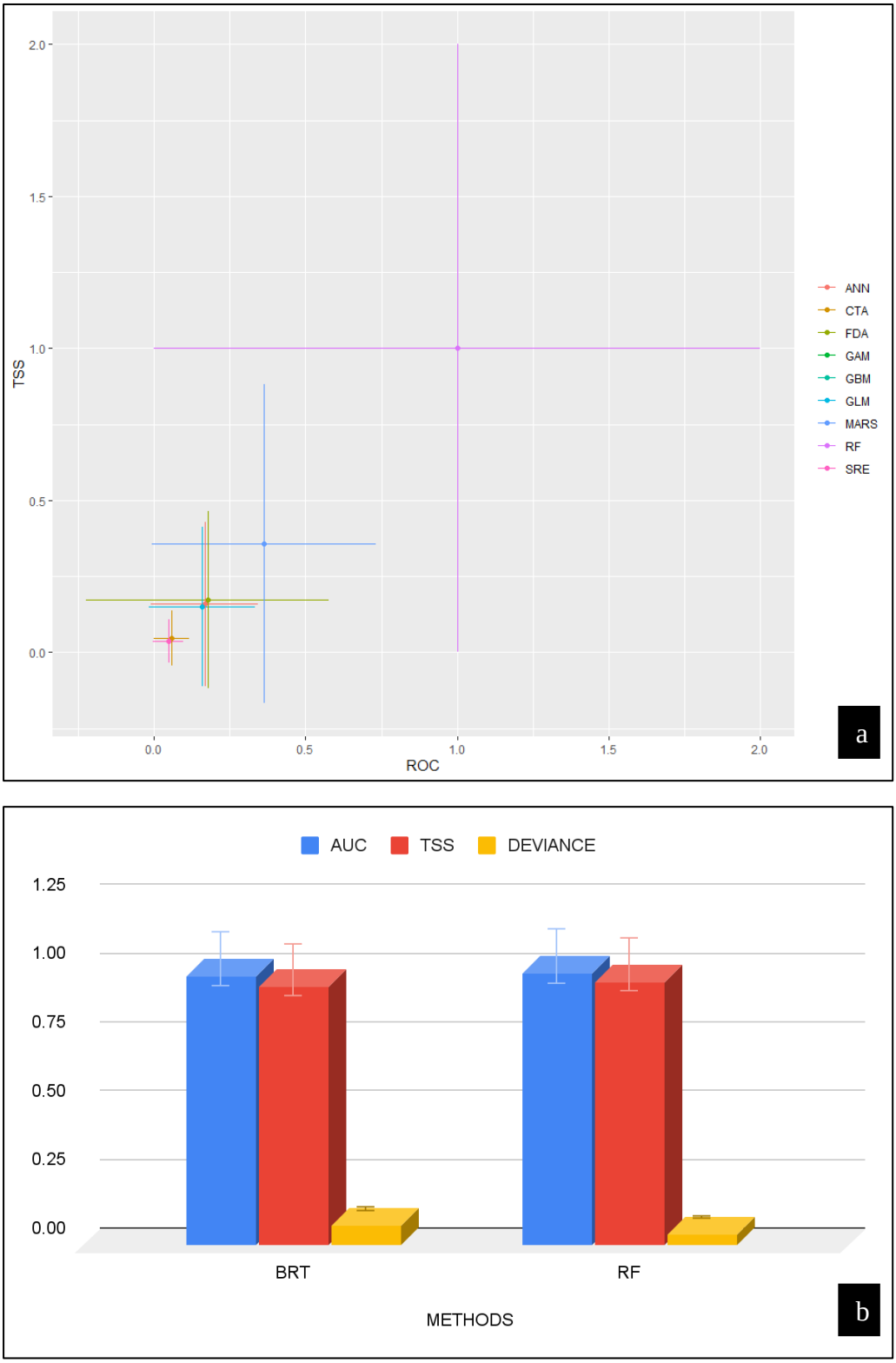


Plate 4.5: a. Model fit evaluation conducted using 10 models in BIOMOD2 modeling for *Elaeocarpus munroi* (Wight) Mast. (The model evaluation stat used were ROC and TSS), b. Model fit evaluation done over selected two best fit model, after final model run done using 15 models in SDM modeling for *Elaeocarpus munroi* (Wight) Mast. (The model evaluation stat used were AUC, TSS and Deviance).

fact that the BIOMOD2 framework yielded only a solitary model demonstrating alignment with the target species. To address this limitation and to fulfil the study's objective of ensemble modelling, an alternative approach adopted was SDM. Species Distribution Modelling (SDM) package holds intrinsic capabilities for ensemble modelling, aligning well with the research's overarching focus. The SDM package encompasses a built-in repository comprising 15 distinct model algorithms tailored for species distribution modelling.

Although the fundamental methodology behind both ensemble modelling approaches remained consistent, a crucial point of departure lay in the distinct array of models inherent to each respective package. In the case of *Elaeocarpus munroi*, the SDM package was employed. A model fit test was undertaken utilising 10 out of the available 15 models. Numerous iterative runs were conducted, aimed at identifying the models that exhibited the most apt alignment with the provided object data. Each model run algorithm was set with a 30% test proportion, a solitary replication, and with the incorporation of the selected 9 bioclimatic predictor variables based on VIF. In the initial model fit the mahal.dismo model failed to yield satisfactory outcomes, prompting its subsequent removal. Following this refinement, the model fit procedure was reiterated. The evaluation of model suitability rested on a diverse array of statistical evaluation metrics AUC, TSS and Deviance. The numerical range for these evaluation metrics spans from 0 to 1, with an optimal model characterised by Deviance values proximate to 0 and all other metrics converging towards 1. Upon completion of the exhaustive modelling iterations, BRT and RF emerged as the most fitting model for E. munroi (Plate 4.5: b) in SDM package.

Preceding the definitive model execution, an exhaustive evaluation of the optimal replication methods encompassing sub-sampling, bootstrapping, and cross-validation was undertaken. This assessment hinged on the analysis of pertinent statistical indicators. As a result, Bootstrapping emerged as the most suitable replication approach, manifesting superior attributes. For the ultimate model run, a replication counts of 40 was designated. Within this context, the chosen replication method was bootstrapping. This culminating endeavour entailed the utilisation of two distinct models, namely BRT and RF.

In the preceding model run of *E. munroi* in the BIOMOD2 package, RF was the sole model that was the best fit. As per SDM model fit run BRT and RF were the models that were proved to be best fit. In BIOMOD2, BRT was not available, but in

both packages, RF was present and was proved to be the best fit for the species. This is a noteworthy indication of the accuracy inherent within both modelling packages SDM and BIOMOD2. This observation underscores the robustness of the modelling methodologies utilised. Within the context of the SDM package, the model fit run exhibited the emergence of two models that best aligned with the species under consideration. This outcome serves as a promising testament to the potential efficacy of the SDM approach, further bolstering the credibility and potential utility of the package.

Projection and Ensemble forecasting: -

There after the final model run was done, thereby the prediction made by each model was projected as a raster. This facilitated the anticipation of species distribution predicated upon the outputs generated by each model. After completing the final model run, predictions were made for the time period ranging from 1970 to 2100, in four SSP scenarios. This covered both historical and future time frames.

The resultant outcome was articulated through a raster visualisation, with the distinct hues denoting areas of high and low probable habitat suitable area for the species. Then the ensemble run was done were all the projections made by every model were ensembled to a single raster. As projected ensemble raster demonstrated the high probable to least probable habitat suitable areas of *Elaeocarpus munroi* in a colour scale. Then the ensemble raster output was meticulously evaluated by using the Arcmap 10.8, and a spatial data analysis was executed.

4.2.3. Modelling in *Phoebe wightii* Meisn.

Phoebe wightii, is a tree belonging to Lauraceae, that is showing its exclusive presence in sky islands of the Southern Western Ghats and are endemic to Peninsular India.

Data management and processing: -

Field visits were conducted in the sky islands of the Western Ghats, specifically surrounding the Palghat Gap, where the species was observed to have a limited distribution. Direct field visit species occurrence data (Plate 4.6) was collected, and additional occurrence data were sourced from GBIF (GBIF 2022). The predictor variables employed here were chosen after the VIF multicollinearity test. Thereby 10 bioclimate variables with high collinearity were excluded and remaining 9 variables were selected, and they were bio2, bio3, bio8, bio9, bio13, bio14, bio15, and bio19.

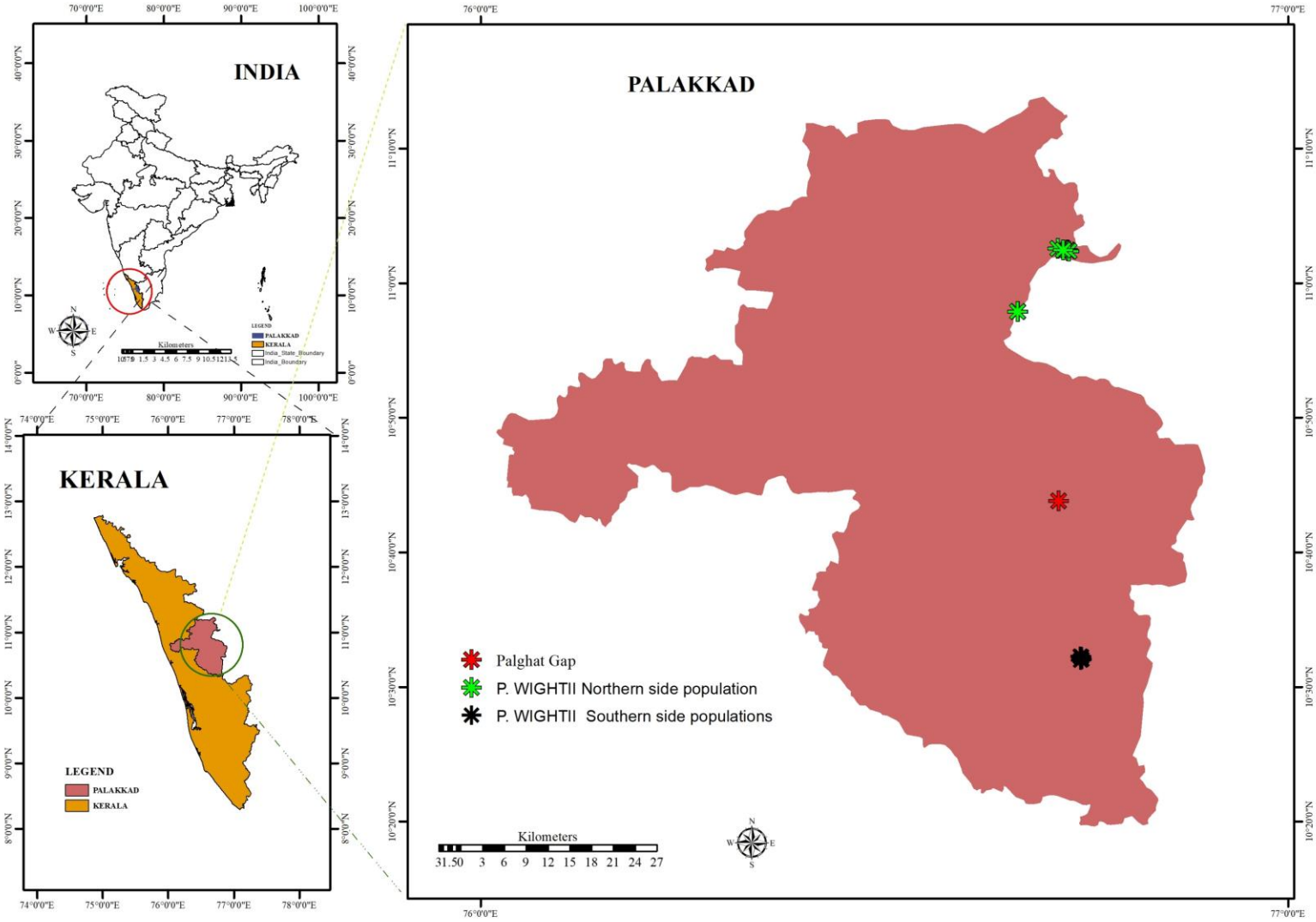
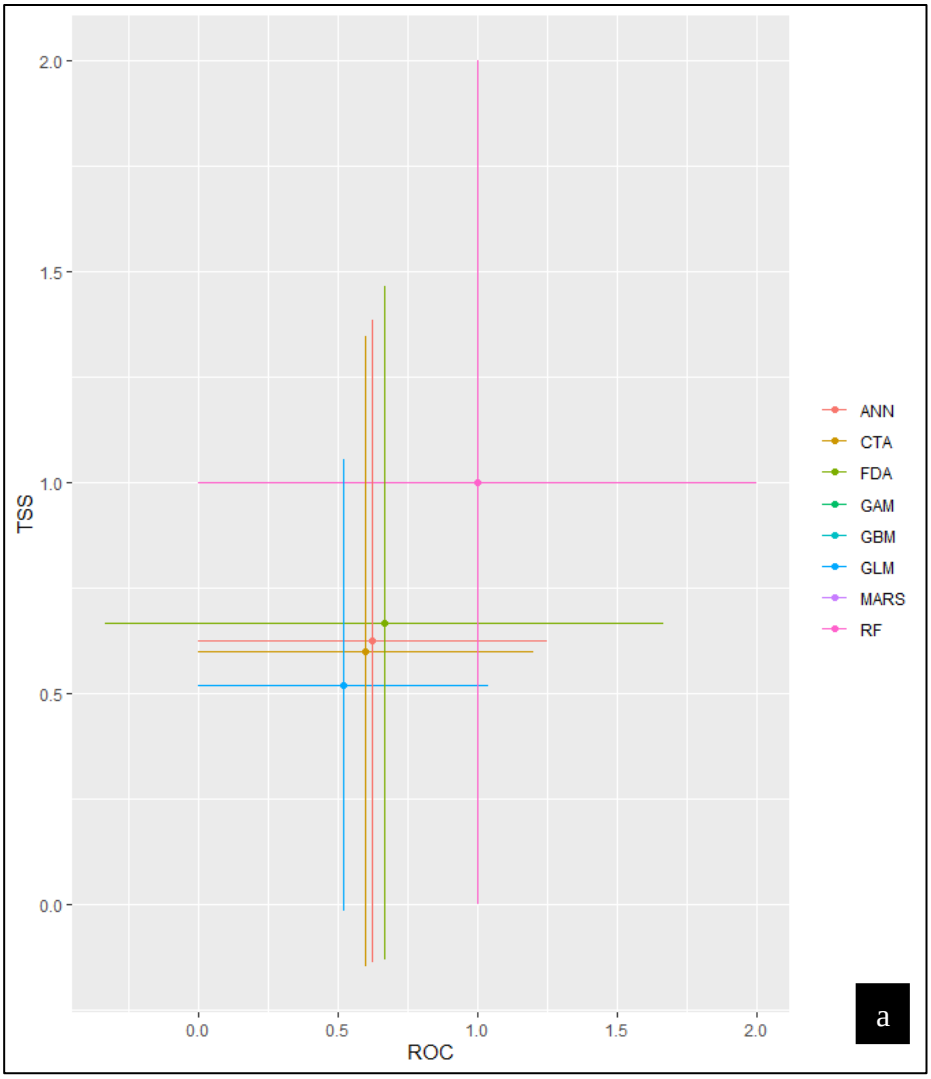


Plate 4.6: Distribution map of *Phoebe wightii* Meisn. collected from the sky islands within the study area.



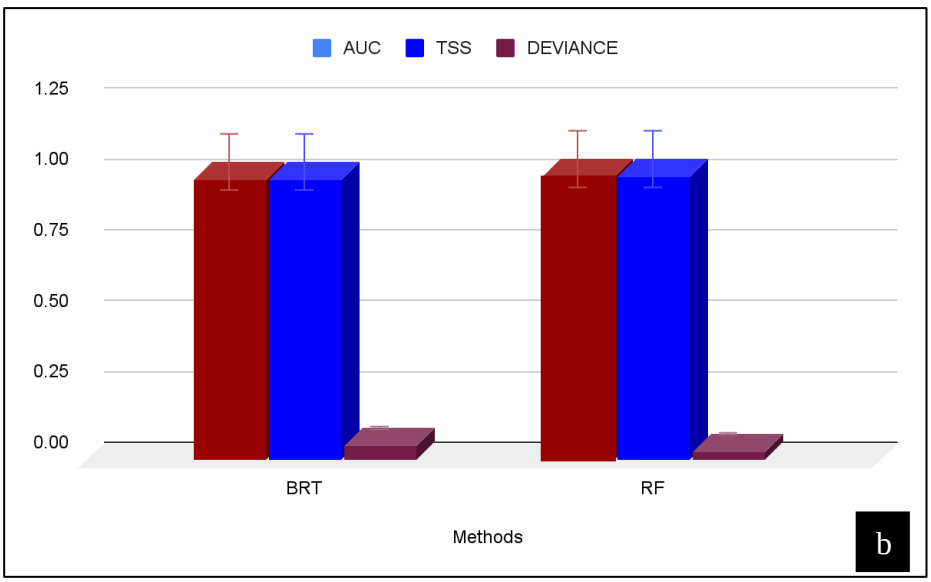


Plate 4.7: Model fit evaluation conducted using 10 models in BIOMOD2 modeling for *Phoebe wightii* Meisn. (The model evaluation stat used were ROC and TSS), b. Model fit evaluation done over selected two best fit model, after final model run done over 15 models with in SDM modeling for *Phoebe wightii* Meisn. (The model evaluation stat used were AUC, TSS and Deviance).

Model fitting and processing: -

This data object was subjected to a model fit test using the BIOMOD2 package in the R platform. As previously mentioned, the package includes ten built-in models, and all models were tested. The process of model fitting was meticulously executed, where the argument for the model fit run was set with a prevalence point at 0.5 and a data split percentage of 100%. Notably, a singular replication number was employed to ensure consistency and reliability throughout the procedure. Upon rigorous evaluation, it was unequivocally determined that only one optimal model fit with this species under investigation within the BIOMOD2 package. Specifically, the RF model (Plate 4.7: a) exhibited a commendable degree of suitability and precision. Regrettably, the pursuit of ensemble forecasting was hindered by the constraint that the BIOMOD2 package exclusively permitted the utilisation of a single best fit model for the species *Phoebe wightii*. To circumvent this limitation and broaden the spectrum of analytical exploration, an alternative path was pursued. That is the SDM package, and was utilised here as a robust option, granting access to a diverse array of 15 distinct models. Embracing this opportunity, the model-fitting endeavour was seamlessly transitioned to SDM package, thereby facilitating rigorous analytical process. Each replication technique was performed singularly. Out of the total pool of 15 models accessible within the SDM package, a subset of 11 models was designated for the testing process. These selected models encompassed a range of models including CART, GAM, RF, BRT, MAXENT, BIOCLIM, FDA, MARS, SVM, mahal.dismo, and GLM. The assessment of model performance encompassed an array of metrics, notably encompassing AUC, TSS, and DEVIANCE. The process of model selection involved a rigorous evaluation of various fits through multiple iterations. In the first evaluation utilising the aforementioned primary evaluation criteria. Following an in-depth analysis of model fitting, it was ascertained that the BRT and RF models exhibited the highest degree of suitability for *P. wightii* (Plate 4.7: b).

After a thorough examination of evaluation statistics, the bootstrap replication method emerged as optimal choice among the three replication techniques. Employing the chosen models in tandem with the selected replication technique, a conclusive iteration encompassing 40 replications per model was executed. Subsequent to the conclusive model run, prognostications were generated for the temporal span spanning from 1970 to 2100, thereby encompassing historical and prospective time raster frames.

The Variable Importance metric assesses the degree of significance associated with each individual predictor variable in relation to the spatial distribution of the species across the Western Ghats region. Thereby the importance of variables in the distribution of *Phoebe wightii* was also evaluated.

Ensemble forecasting: -

Ensemble forecasting of high-probable habitat suitable areas raster output was assessed and analysed. Ensemble forecasting, where the projected data of each species were used. There the projected data of each model fit output were ensembled through ensemble forecasting. The ensembled forecasted distribution data of each species over the Western Ghats were spatially evaluated by ArcMap 10.8, and area of high probable to least probable habitat suitable area of *Phoebe wightii* was measured in square kilometres.

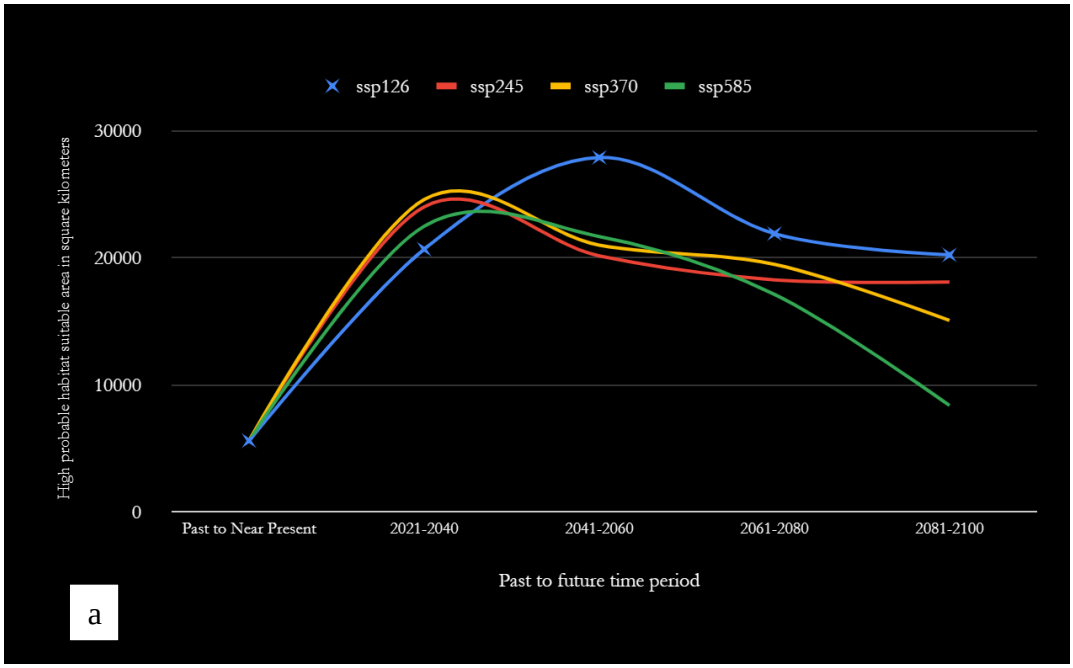
4.3. Results and discussion

The ensemble modelling was done here over three selected taxa. To forecast and evaluate the high probable habitat suitable area of these species all over the Western Ghats, from past to future time period. Here the predictions were made in four time periods in four SSP scenarios.

4.3.1. Modelling in *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P. Kumar

Throughout the model run, a standout variable emerged as the chief influencer regulating the distribution of the species was assessed. It was thereby found that the bio14, the bioclimatic variable associated with the precipitation levels during the driest month, wielded the most pronounced impact on the distribution dynamics of *Elaeocarpus gadgilii*. This variable reflects the precipitation (mm) magnitude during the period of driest month, thereby underlining its vital role in shaping the species distribution. A secondary determinant that surfaced as a notable factor in shaping the distribution patterns of this species *E. gadgilii* was bio3. Bio3 represents isothermality (%), Isothermality measures the extent of temperature fluctuation between day and night compared to the seasonal variations between summer and winter. Its significance lies in illuminating the interplay between environmental conditions and the species distribution during different seasons.

The depicted findings epitomise the intricate relationships between these variables and the species distribution across different temporal and environmental contexts. As per biomod2 ensemble forecasting done on *E. gadgilii*, several output rasters



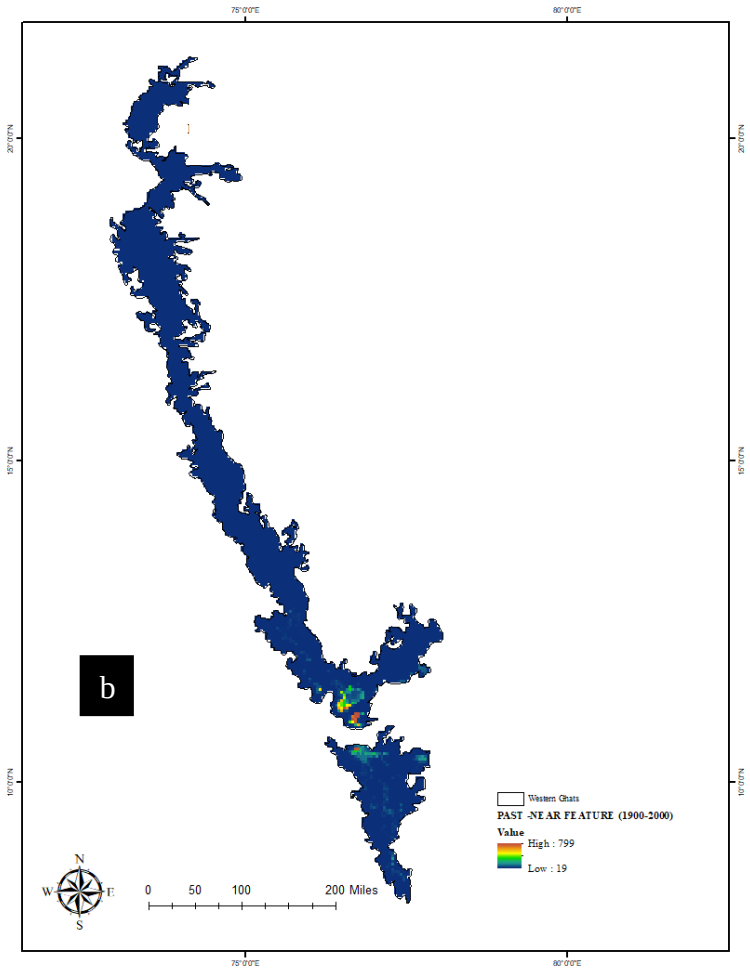


Plate 4.8: a. Comparing the predicted high probable habitat suitable area of *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P. Kumar on the Western Ghats in square kilometers from Past to Near present (1970-2000) to future time periods (2021 to 2100) in four SSP scenarios, as per Biomod2 Ensemble modeling, b. The low to high probable habitat suitable area of *E. gadgilii* on the Western Ghats during 1970-2000 are represented in a color scale from blue to red respectively, as per Biomod2 Ensemble modeling.

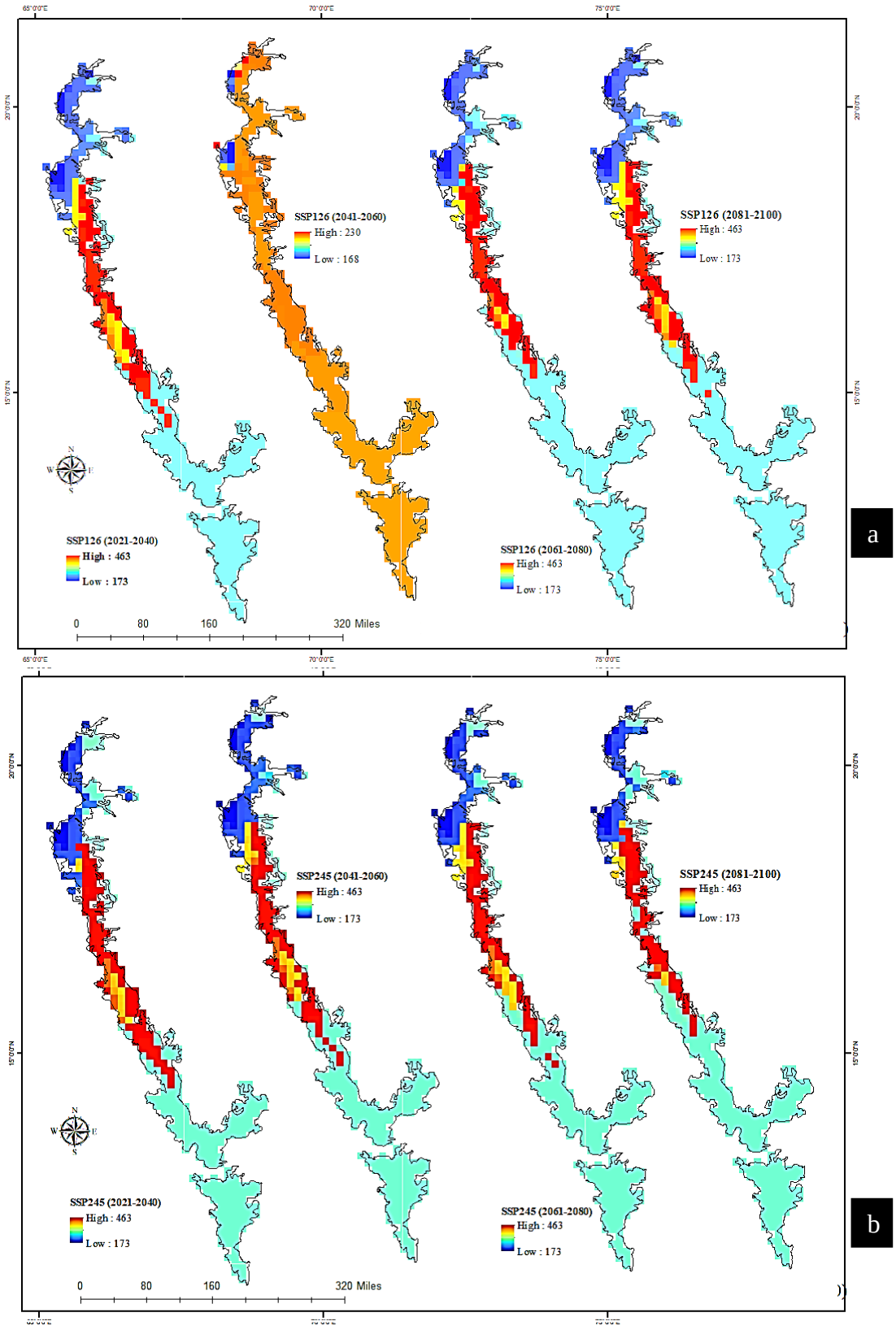
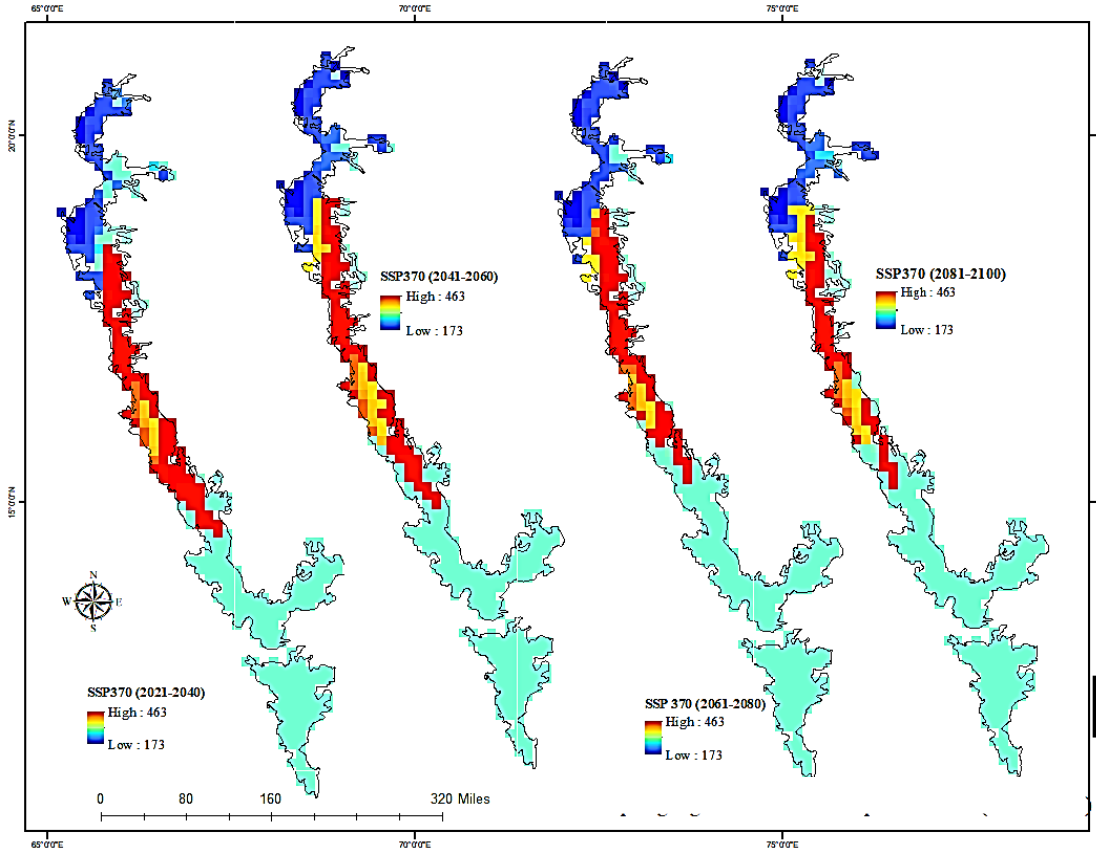


Plate 4.9: a. The low to high probable habitat suitable area of *E. gadgilii* on the Western Ghats during 2021-2100, according to SSP126 scenario, are represented in color scale from blue to red respectively, as per Biomod2 Ensemble modeling, b. The low to high probable habitat suitable area of *E. gadgilii* on the Western Ghats during 2021-2100 according to SSP245 scenario, represented in color scale from blue to red respectively, as per Biomod2 Ensemble modeling.



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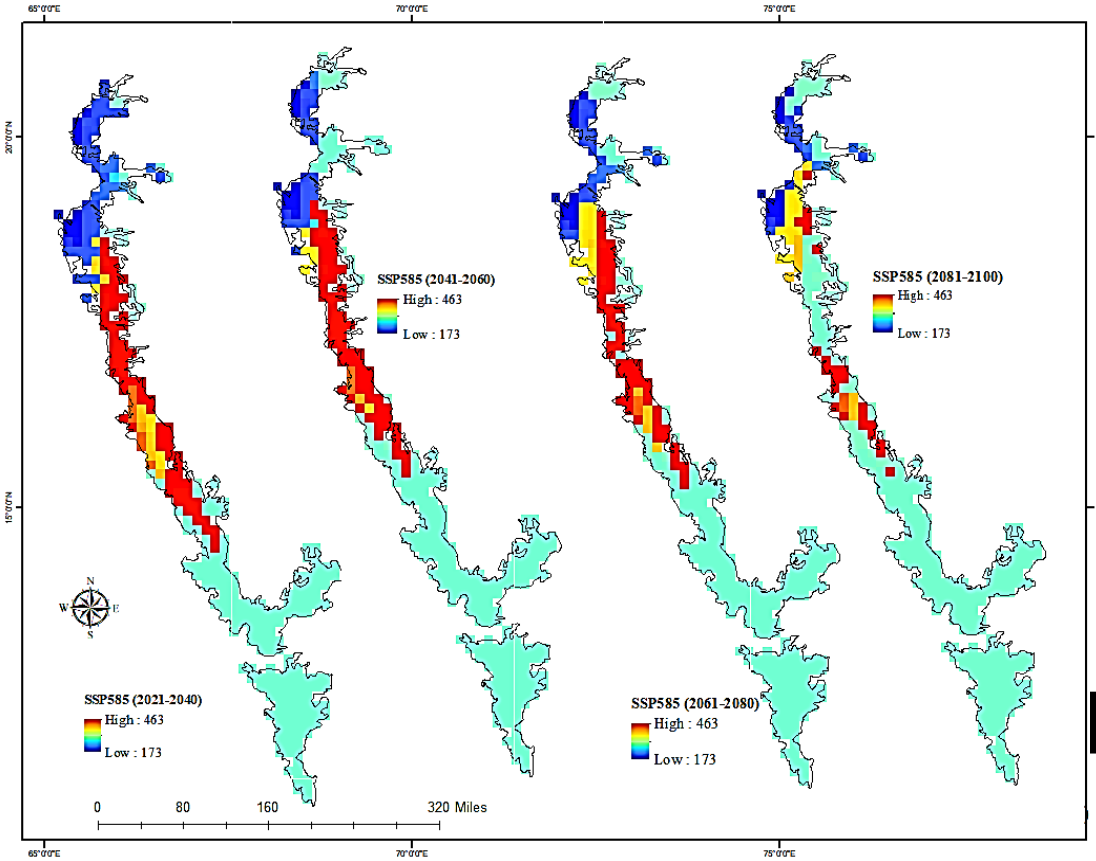


b

Plate 4.10: a. The low to high probable habitat suitable area of *E. gadgilii* on the Western Ghats during 2021-2100, according to SSP370 scenario are represented in color scale from blue to red respectively, as per Biomod2 Ensemble modelling, b. The low to high probable habitat suitable area of *E. gadgilii* on the Western Ghats during 2021-2100, according to SSP585 scenario, represented in color scale from blue to red respectively, as per Biomod2 Ensemble modelling.

were obtained, which clearly demonstrated the high probable habitat suitable area of *E. gadgilii* all over the Western Ghats from 1970 to 2000, in four SSP scenarios. As per the forecasting done for 1970 to 2000 time period, that is in past and present time period a small part of northern and southern Western Ghats surrounding the Palghat Gap appeared to the high probable habitat suitable area of *E. gadgilii*, over covering around 5604 km² of Western Ghats (Plate 4.8: a). The raster output with hue variants clearly depict the high probable habitat suitable area of *E. gadgilii* on Western Ghats with dark red pixels, where blue hue represents the least probable habitat suitable areas (Plate 4.8: b).

As per the SSP126 scenario, the habitat is expected to experience minimal greenhouse gas emissions. Ensemble forecasting was conducted for four time periods: 2021-2040, 2041-2060, 2061-2080, and 2081-2100 (Plate 4.9. a). According to the SSP126 predictions for these periods, the high probable habitat suitable area for *E. gadgilii* seems to shift from the southern to the northern and central parts of the Western Ghats. Specifically, during 2021-2040, approximately 20,677 km² of the Western Ghats is predicted to be a high probable habitat suitable area for *E. gadgilii*. This area increases to 27,905 km² during 2041-2060, decreases to 21,901 km² during 2061-2080, and further reduces to 20,235 km² during 2081-2100 (Plate 4.8: a). The shift in high probable habitat suitable area from the southern to the northern Western Ghats is evident, with a notable decrease in the southern region. Notably, during the 2041-2060 period, the least probable habitat suitable area for *E. gadgilii* appears to be negligible. This shift indicates a significant change compared to the forecast for the past to near-present time period. The overall trend suggests a favorable expansion of *E. gadgilii* towards the northern Western Ghats.

While the probability of its presence in the southern Western Ghats diminishes, potentially leading to the species' complete disappearance from this region by 2100 (Plate 4.9. a). In the context of SSP245 (Plate 4.9: b), 370 (Plate 4.10: a), and 585 scenarios (Plate 4.10: b), the habitat is anticipated to experience varying levels of greenhouse gas (GHG) emissions, ranging from intermediate to very high. Ensemble forecasting raster for *E. gadgilii* was conducted across these three SSP scenarios in four time periods: 2021-2040, 2041-2060, 2061-2080 and 2081-2100. These forecasts clearly illustrate the impact of GHG emissions on the distribution of *E. gadgilii*. Across all three scenarios, the northern Western Ghats consistently emerges as the high probable habitat suitable area for *E. gadgilii*. This suggests that the population of

E. gadgilii in the southern Western Ghats are at high risk. As GHG emissions increase, the high probable habitat area of *E. gadgilii* in the northern Western Ghats will undergo a significant reduction. This observation underscores the adverse effects of GHG emissions and raises concerns about the potential disappearance of *E. gadgilii* from the Western Ghats, particularly the southern region (Plate 4.8-4.10).

Comparing the high probable habitat suitable area of *E. gadgilii* on the Western Ghats from past to future scenarios reveals significant changes. In the past scenario, the high probable habitat suitable area of the Western Ghats was approximately 5604 km², indicating an area below 10000 km². However, between 2021 and 2060, the high probable habitat suitable area increased substantially above 20000 km². In contrast, during the 2061-2100 time period, there were variations in output across all four scenarios. According to SSP126, during 2061 to 2080, the high probable habitat suitable area did not fall below 20000 km². In SSP245 and 370 scenarios, however, the high probable habitat suitable area ranged from 20000 km² to 10000 km². On the other hand, SSP585, were very high greenhouse gas emissions are expected, demonstrated a decrease in the high probable habitat suitable area, going below 10000 km² (Plate 4.8: a). This clearly illustrates the drastic impact of increased greenhouse gas emissions on *E. gadgilii*. Among the four scenarios SSP126 is the least expected and SSP585 scenario is the more expected condition in future with the present scenario. So urgent conservation measure must be introduced over the Western Ghats to safeguard the prevailing populations of *E. gadgilii* and preparing the areas of Western Ghats where it expected to appear in future.

As per model forecasting on *E. gadgilii*, the species where it is now found seems to be a less probable habitat suitable area in future. This increases the likelihood of its disappearance, from the present habitat in future. The conducted modelling was done across historical and near present and future timeframes (2021-2100). As per ensemble forecast projections of *E. gadgilii* distribution, the location where it is found now was a high probable habitat suitable in the past and near present, later in future these areas predicted to become least probable.

Therefore, conservation efforts are very essential to prevent the species from becoming endangered or extinct from where it exists now. The conservation status of the species is unknown since it is newly discovered, and no efforts were done to document its conservation statistics. Modelling techniques are hereby beneficially used to assess and emphasize the probable risk of existence of the species. Thereby the pre-

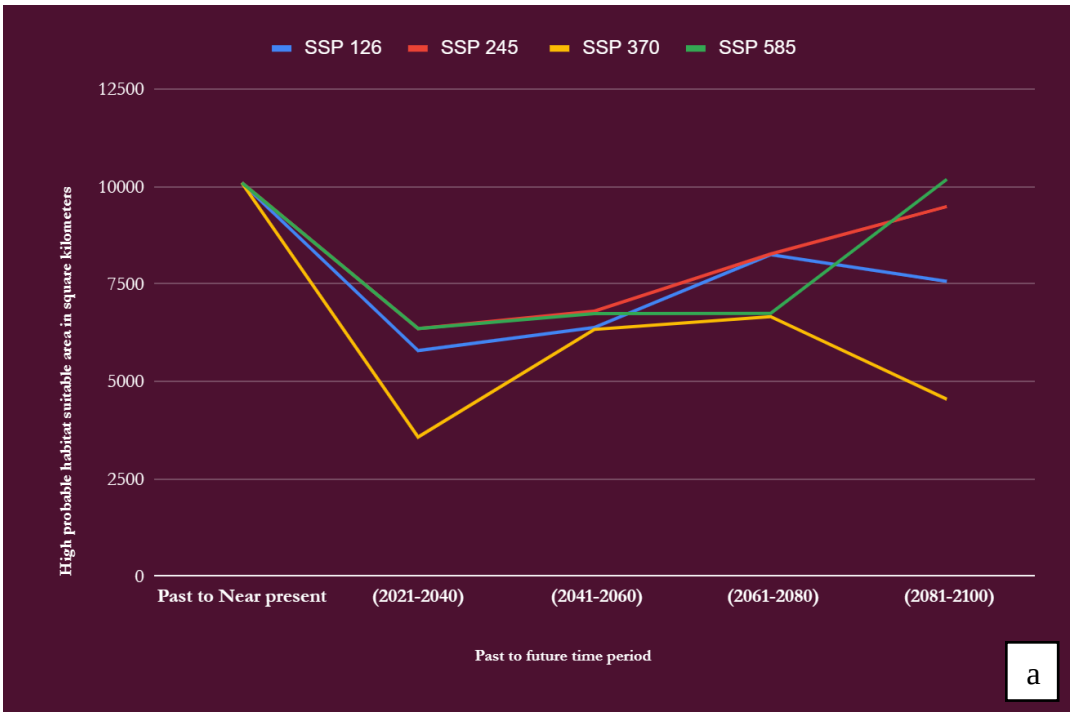
sent forecast analysis raises the significance and the need for introducing ex-situ or in-situ conservation measures over these species.

4.3.2. Modelling in *Elaeocarpus munroi* (Wight) Mast.

A meticulous examination of the raster data unveiled the distribution pattern of the species *Elaeocarpus munroi* across the expanse of the Western Ghats. Utilising ArcGIS, the high probable habitat regions were quantitatively assessed, subsequently paving the way for an ensemble run integrating the selected models. The threshold value that guided the prediction of habitat suitability regions was determined to be 0.450688993. This pivotal threshold was established through judicious reference to the conclusive model fit run report involving the chosen BRT and RF models in SDM package. With this threshold in place, a precise calculation of the expanse encompassing high probable habitat suitability zones were performed.

It is of paramount importance to underscore that the process of ensemble forecasting was conducted to prognosticate the distributional pattern of *E. munroi* across both historical and future timeframe. The assessment of bioclimatic variable significance was conducted through the lens of variable importance measures. This analysis hinged on the quantification of variable importance percentages, revealing a distinct hierarchy. Notably, it was discerned that the primary significant bioclimatic variable that controls the distribution of the species *E. munroi* was bio13. Bio13 provides information about the amount of precipitation(mm) during the wettest month of the year, which helps to understand seasonal precipitation patterns. Subsequently, bio19 the precipitation in the coldest quarter, the second most influential factor. It quantifies the total precipitation in the coldest three-month period. The pivotal influence of these two bioclimatic variables, bio13 and bio19 resonates in their profound impact on shaping the distributional dynamics of *E. munroi*. This observation accentuates their critical role in governing the habitat suitability and ecological niche preferences of the species under consideration.

Predictions were conducted across various scenarios, encompassing four Shared Socioeconomic Pathways (SSPs) in four distinct time intervals: 2021-2040, 2041-2060, 2061-2080, and 2081-2100 (Plate 4.11-4.13). The outcomes, depicted as raster images, showcased regions of elevated probable habitat suitable area for *E. munroi* through conspicuous dark red hues. Each map's graduated scale effectively conveyed varying degrees of likelihood of high probable habitat suitable area. As per



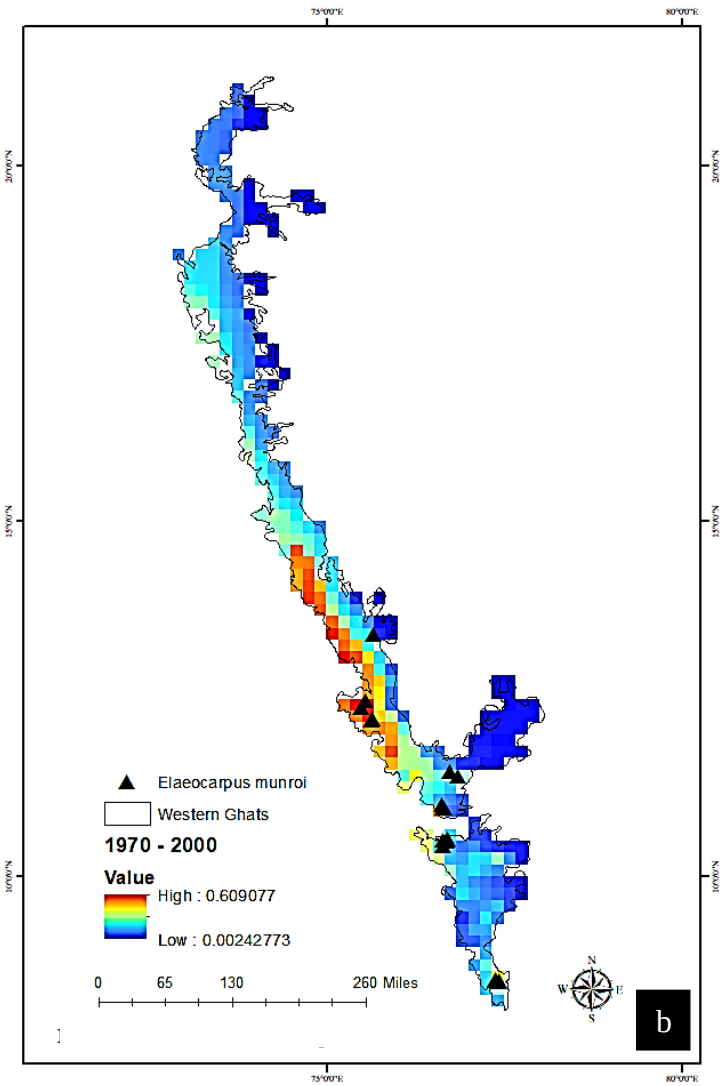
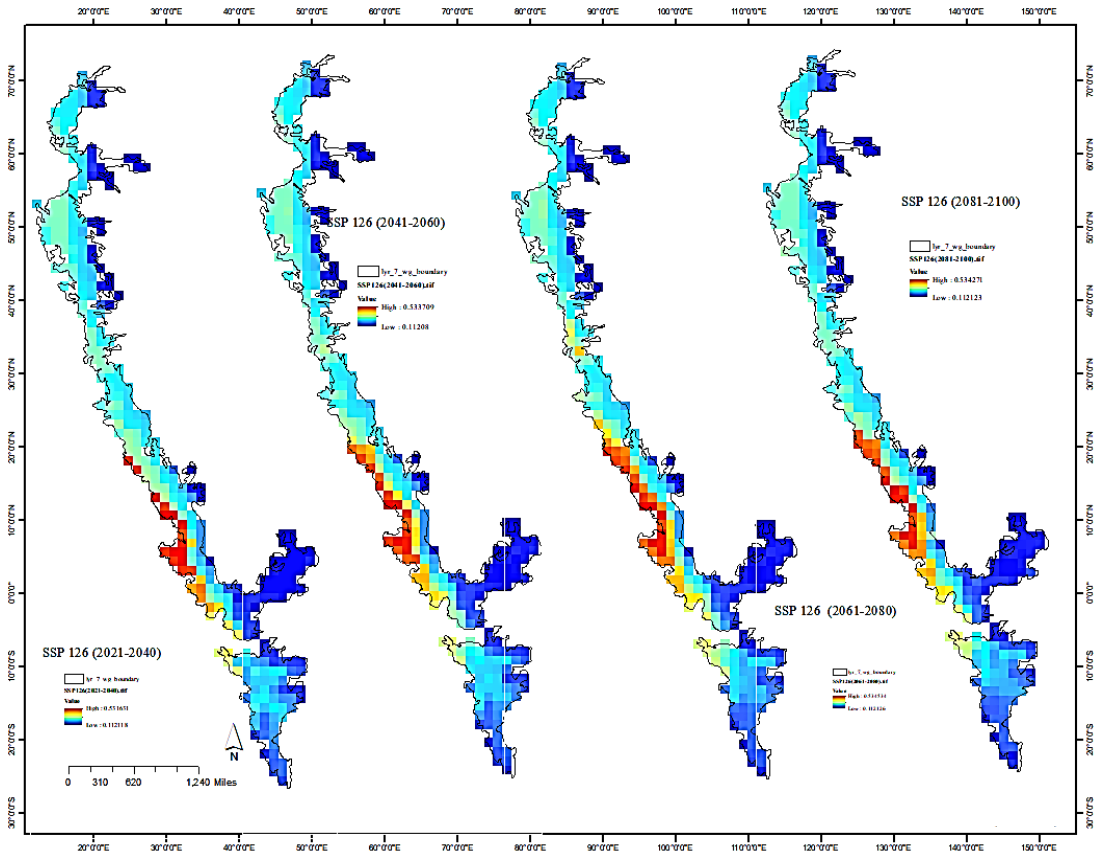


Plate 4.11: a. Comparing the predicted high probable habitat suitable area of *Elaeocarpus munroi* (Wight) Mast. on the Western Ghats in square kilometers from Past to Near present (1970-2000) to future time periods (2021 to 2100) in four SSP scenarios, as per SDM Ensemble modelling, b. The low to high probable habitat suitable area of *E. munroi* on the Western Ghats during 1970-2000 are represented in a color scale from blue to red respectively, as per SDM Ensemble modelling.



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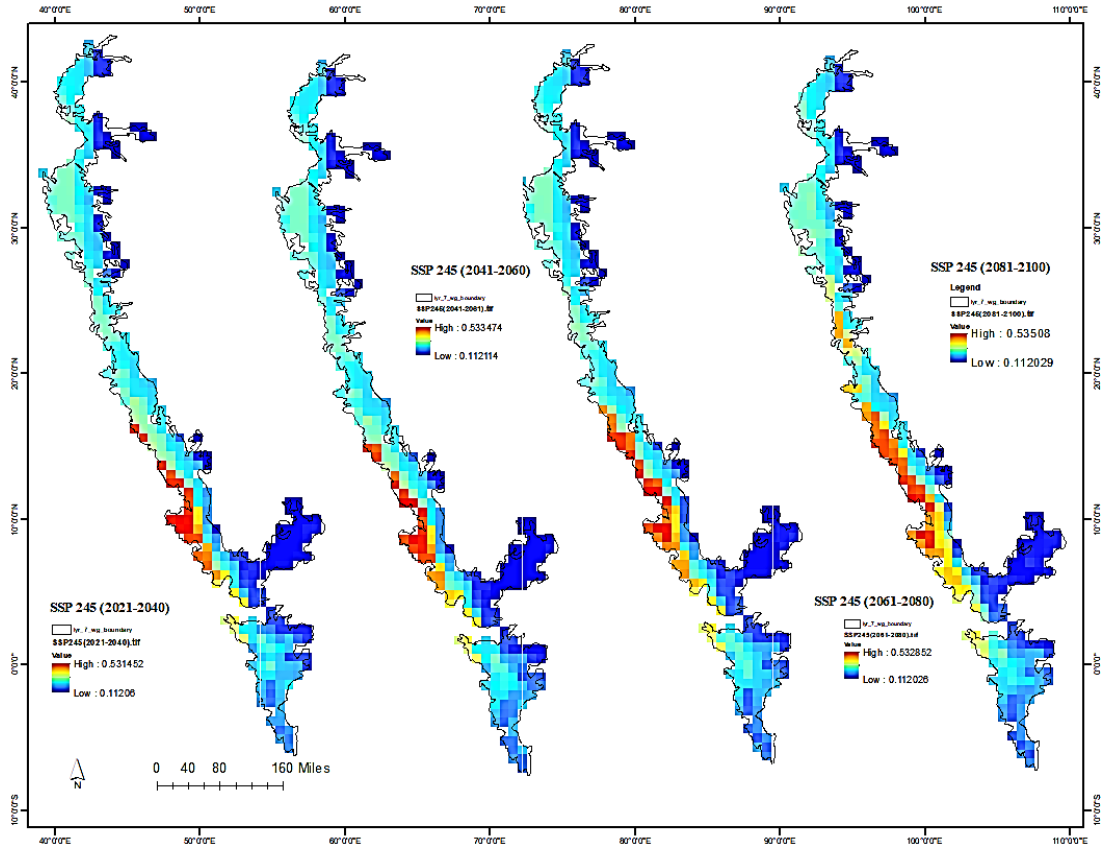


b

Plate 4.12: a. The low to high probable habitat suitable area of *E. munroi* on the Western Ghats during 2021-2100, according to SSP126 scenario, are represented in color scale from blue to red respectively, as per SDM Ensemble modelling, b. The low to high probable habitat suitable area of *E. munroi* on the Western Ghats during 2021-2100, according to SSP245 scenario, represented in color scale from blue to red respectively, as per SDM Ensemble modelling.

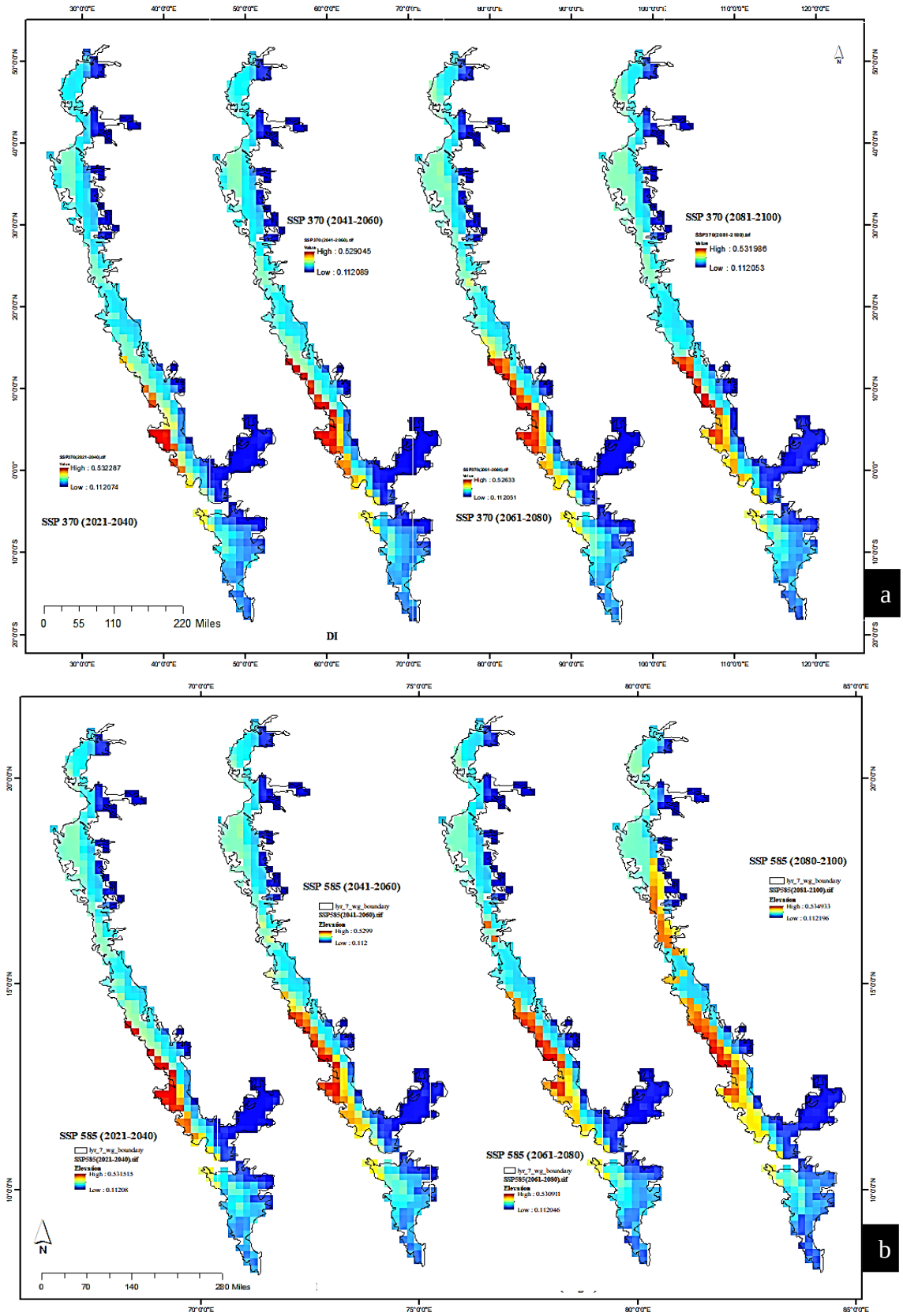


Plate 4.13: a. The low to high probable habitat suitable area of *E. munroi* on the Western Ghats during 2021-2100, according to SSP370 scenario, are represented in color scale from blue to red respectively, as per SDM Ensemble modelling, b. The low to high probable habitat suitable area of *E. munroi* on the Western Ghats during 2021-2100 according to SSP585 scenario, are represented in color scale from blue to red respectively, as per SDM Ensemble modelling.

ensemble forecasting, during the past era of 1970-2000, the landscape of high probable habitat-suitable areas were primarily concentrated within the central Western ghats (Plate 4.11: b). In contrast, the projections for future scenarios spanning 2021-2060 indicated a reduction in the area of high probable habitat suitable areas (Plate 4.11: a). However, an intriguing reversal manifested during the interval of 2081-2100, with the projected area resurging to levels closely resembling the area of habitat suitable for those witnessed in the past (1970-2000) (Plate 4.11: a).

The focus of assessment was on quantifying high probable habitat suitable areas for *E. munroi* over the Western Ghats, expressed in square kilometers, across discrete time periods and varied SSP scenarios. In the past scenario, the prediction indicated approximately 10094 km² of the Western Ghats as high probable habitat suitable for *E. munroi* (Plate 4.11: a). The SDM ensemble raster outputs for *E. munroi* on all scenarios clearly illustrated the distribution pattern of *E. munroi* from the past to the future, with high probable habitat suitable areas consistently appearing in the central Western Ghats from 1970 to 2100 (Plates 4.11: b, 4.12, 4.13). However, there was a reduction in high probable habitat suitable area over time.

The adverse impact of greenhouse gas (GHG) emissions was notably high in SSP370 and SSP126 scenarios, while SSP245 and 585 showed less adverse effects, though not favouring expansion. The expected high probable habitat suitable area of Western Ghats during 2021-2040 for *E. munroi* ranged between 7500 km² to 5000 km² in SSP126, 245, and 585. In SSP370, during 2021-2040, the area went below 5000 km². Between 2041-2060, the high probable habitat suitable area increased and ranged between 7500 - 5000 km² in all SSP scenarios. From 2061-2080, based on SSP370 and SSP585, the high probable habitat suitable area of Western Ghats for *E. munroi* ranged below 7500 km², while SSP245 and 126 indicated areas above 7500 km² as high probable habitat suitable area. By 2081-2100, based on SSP585 it is anticipated that the high probable habitat suitable area to reach near 10000 km², similar to the past scenario. With respect to SSP 370, indicated an area below 5000 km² to be highly suitable, and the other two SSPs suggested an area ranging between 7500-10000 km² (Plate 4.11: a).

Among the examined scenarios, only SSP585 in the 2081-2100 timeframe demonstrates a marginal expansion of suitable habitat area compared to historical distribution (Plate 4.13: b). It is noteworthy that this resurgence did not surpass the extended reduction observed during the previous historical epoch. That is all other sce-

narios exhibit a decrease in habitat, spanning from minor to substantial reductions. Consequently, the threat of species decline becomes substantial, underscoring the significance of conservation efforts and the urgency surrounding this issue. The current situation presents a less favourable outlook, primarily due to the projected decline in suitable habitat areas for the species in the future compared to the past. This reduction in high probable habitat suitable areas availability raises concerns about an elevated likelihood of species extinction. Consequently, it becomes imperative to undertake conservation efforts to safeguard the survival of *Elaeocarpus munroi*. This highlights a worrisome trend of diminishing suitable habitat areas for the species over time, indicating

an increased risk of extinction. It emphasises the importance of ex-situ conservation measures to prevent the potential loss of *E. munroi* from the present habitat.

So, the ensemble forecasting for *E. munroi* suggests that a higher likelihood of reduction in high probable habitat suitable areas in the Western Ghats is expected rather than expansion. This species is already classified as Nearly Threatened (IUCN 2023), this necessitates for the urgent measures to safeguard existing populations of *E. muroi*. Then Introducing or replanting seedlings in its suitable habitats and maintaining current populations are crucial steps to conserve its prevailing population and to prevent its extinction.

This species is endemic to the southern Western Ghats. As per the analysis it is evident that the *Elaeocarpus munroi* species, which is indigenous to the southern Western Ghats, is confronted with a substantial risk of disappearing from its existing ecological niches. The preservation of the unique biodiversity intrinsic to the southern Western Ghats necessitates the prompt execution of conservation strategies. Our prospective ensemble forecast predictions for *E. munroi* have indicated that potentially favourable habitats will predominantly manifest within the confines of the central Western Ghats region. However, here the crucial observation made over the modelling of species *E. munroi* as per ensemble forecast was that the chance of its disappearance from historically favourable high probable habitat suitable area from the southernmost Western Ghats. This region, once the prime habitat, is predicted to become unsuitable for the species regardless of climate scenarios. The geographic influence of the Palghat Gap on the region's ecology may have contributed to the observed distribution shift or may be due to the changing environmental conditions. These predictions hold valuable insights in preventing such endemic species extinction from the

Western Ghats, emphasising the significance of proactive conservation strategies. The potential risk of species extinction in their present locations outweighs the benefits of their appearance in the central Western Ghats. It is prudent, however, to acknowledge that the presence of the species in the central Western Ghats in the future remains probabilistic in nature. Consequently, the more judicious course of action involves directing conservation endeavours towards the existing populations within their current habitat. Consequently, strategies to safeguard the species *E. munroi* within their existing suitable habitat areas become pivotal.

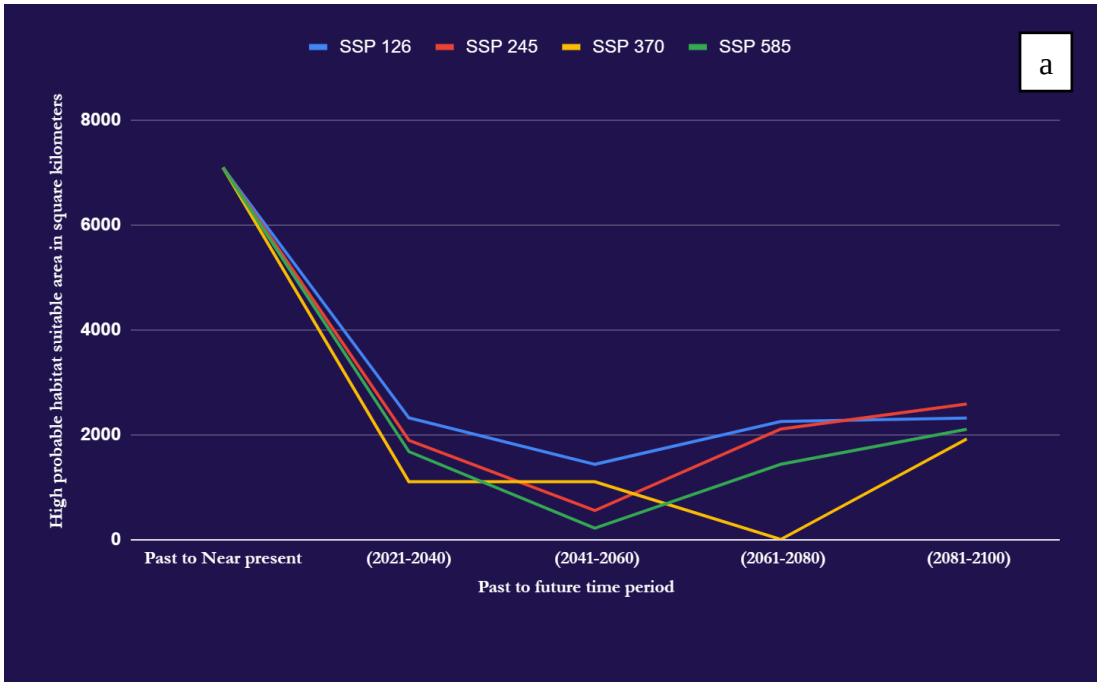
4.3.3. Modelling in *Phoebe wightii* Meisn.

Through the application of species distribution modelling, the analysis over variable importance metric pinpointed that the two pivotal variables that determine the distribution of *Phoebe wightii* were BIO13 (Precipitation of the wettest month) and BIO19 (Precipitation of the coldest Quarter). The former variable encapsulates the cumulative precipitation during the period of highest rainfall, offering insights into the potential influence of extreme precipitation events on the species plausible range. BIO19, characterises the total precipitation during the coldest quarter of the year, spanning over a three-month period. This specific environmental descriptor holds the potential to unravel how various ecological factors interplay in shaping the species distribution across different seasons.

As per the ensemble forecasting done for *Phoebe wightii*, the probable habitat for *P. wightii* in the Western Ghats has significantly diminished, based on predictions across various future scenarios compared to the past. In the period 1970-2000, approximately 7064 km^2 of the Western Ghats was deemed as high probable habitat suitable area for this species (Plate 4.14: a & b). However, in the future (2021-2100), under all scenarios, this area has decreased to less than 2600 km^2.

For instance, under SSP126, the habitat suitable area has dropped to a range of 2318 km^2 to 1433 km^2. Meanwhile, in SSP245 (2021-2100) the suitable area found to be within a range of 2583 to 551 km^2. With respect to SSP370 it ranged from 1915 km^2 to complete disappearance, and as per SSP585 prediction the area ranged from 2103 – 215 km^2 as the high probable habitat area for *P. wightii* in the Western Ghats (Plate 4.14a).

The SDM ensemble output rasters for *P. wightii*, spanning from the past to the future timeframe under all scenarios in the Western Ghats, vividly illustrate the area's



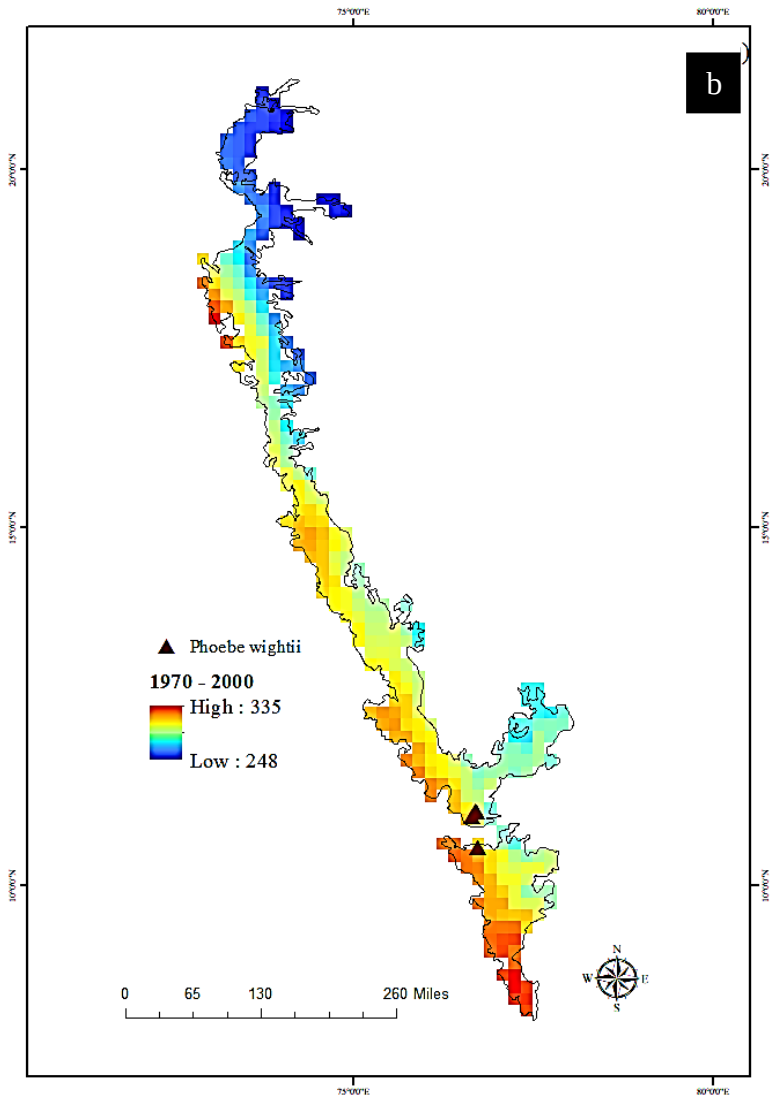


Plate 4.14: a. Comparing the predicted high probable habitat suitable area of *Phoebe wightii* Meisn. on the Western Ghats in square kilometers from Past to Near present (1970-2000) to future time periods (2021 to 2100), in four SSP scenarios, as per SDM Ensemble modelling, b. The low to high probable habitat suitable area of *P. wightii* on the Western Ghats during 1970-2000, are represented in a color scale from blue to red respectively, as per SDM Ensemble modelling.

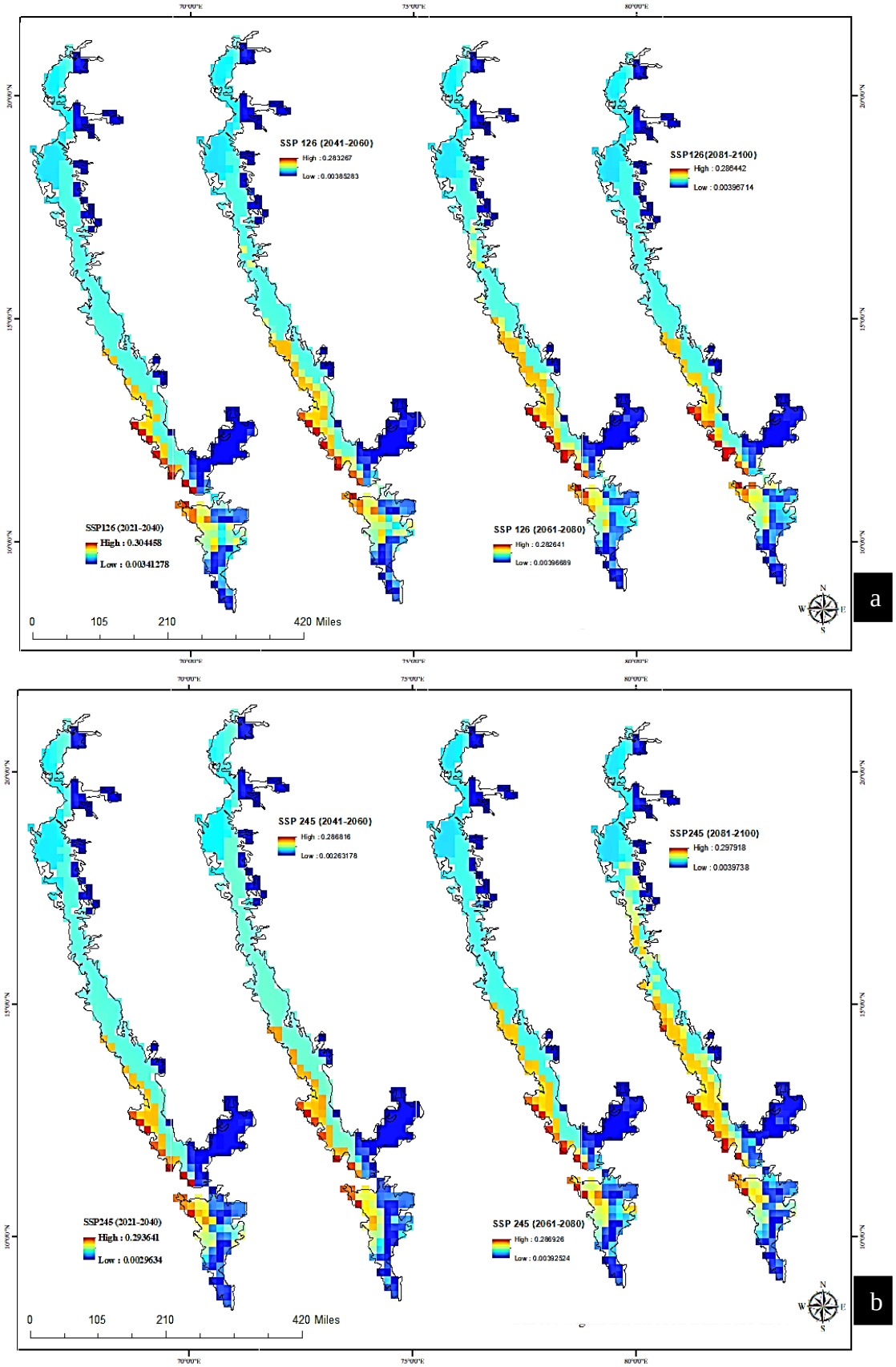


Plate 4.15: a. The low to high probable habitat suitable area of *P. wightii* on the Western Ghats during 2021-2100, according to SSP126 scenario are represented in color scale from blue to red respectively, as per SDM Ensemble modelling, b. The low to high probable habitat suitable area of *P. wightii* on the Western Ghats during 2021-2100 according to SSP245 scenario, represented in color scale from blue to red respectively, as per SDM Ensemble modelling.

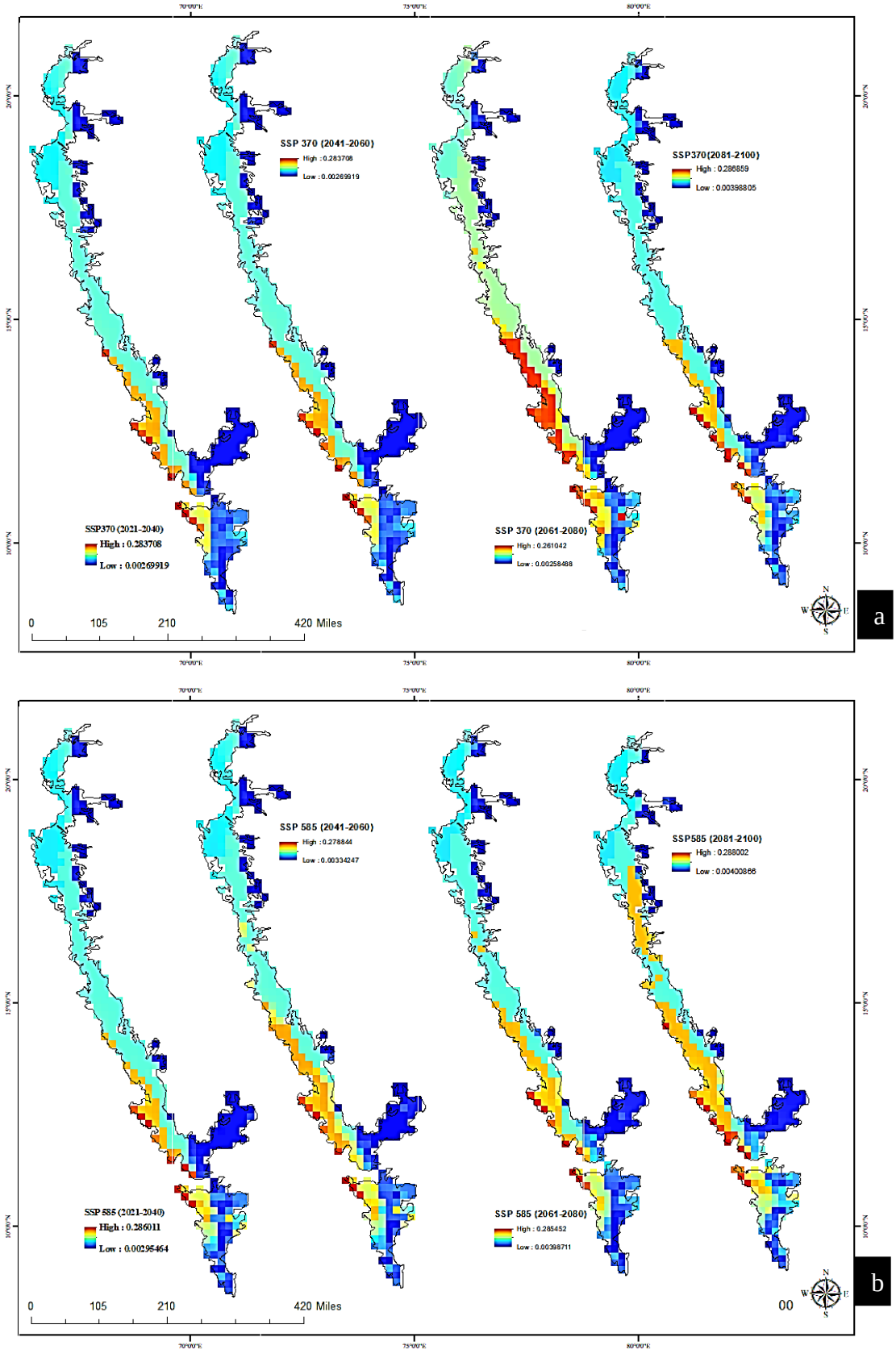


Plate 4.16: a. The low to high probable habitat suitable area of *P. wightii* on the Western Ghats during 2021-2100, according to SSP370 scenario are represented in color scale from blue to red respectively, as per SDM Ensemble modelling, b. The low to high probable habitat suitable area of *P. wightii* on the Western Ghats during 2021-2100 in SSP585 scenario, represented in color scale from blue to red respectively, as per SDM Ensemble modelling.

best suited for the species with a distinct red hue. In the past the presence of *P. wightii* was found to be in the northern, central, and southern regions of the Western Ghats. Notably, the Southern Western Ghats encompassed a significant area best suited for this species (Plate 4.14: b).

Moving forward to the future timeframe from 2021-2100, under all SSP conditions, the high probable habitat remained restricted to a small portion of the southern Western Ghats and some parts of the central Western Ghats. This starkly indicates a substantial loss of the best suitable area in the Western Ghats, particularly from the Southern Western Ghats. The majority of SWG region is projected to be the least suitable area for *P. wightii* (Plate 4.14 - 4.16). The adverse impact of greenhouse gas emissions is portrayed through these predictions made across four SSP scenarios, ranging from the least GHG to very high GHG. These emissions found to have adversely affected the distribution of *P. wightii*, with a pronounced adverse effect observed in the Southern Western Ghats, where the majority of its area is expected to become least suitable for the existence of *P. wightii*. That is in the future, the high probable habitat suitable areas for the species *Phoebe wightii* in the Western Ghats will be tremendously decreased (Plate 4.14 - 4.16).

This alarming decline in suitable habitat areas for *Phoebe wightii* raises significant concerns regarding the long-term viability and persistence of this species. The observed changes in habitat distribution patterns underscore the heightened risk faced by this species in terms of its continued existence (Plate 4.14a). Analysis of the high probable habitat-suitable area of the species *Phoebe wightii*, extending across the historical to present to future time frame, has divulged a notable and substantial decline.

In light of environmental transformations, the understanding of habitat suitable areas shifts and changes holds paramount significance for effective species conservation. This study delved into the alterations in habitat suitability area of the species across the expanse of the Western Ghats region. Here an alarming habitat shift was also observed, alongside the stark reduction in high probable habitat-suitable areas. This underscores the urgency of conserving the species and safeguarding it from disappearance. The Western Ghats region in India is encountering significant hurdles in species conservation due to changes in habitat and decrease in suitable areas (Kumar and Devi 2013). Human activities, including habitat loss, fragmentation, fires, and invasive species, worsen these challenges (Thomas and Palmer 2007). To tackle these issues, Das (Das *et al*., 2006) proposed thar identifying high conservation value areas

is the best way and he did it specifically focusing on amphibian richness and endemic tree species. Whereas Anand (Anand *et al*., 2010) stressed the importance of preserving and restoring remnant forests in human-altered landscapes to uphold biodiversity. These studies collectively highlight the pressing need for conservation efforts in the Western Ghats region.

As per the IUCN 2023 the *P. wightii* is placed under least conserved category, but as per ensemble forecast analysis the chance of it to enter to endangered or nearly threated category is high. So, to avoid the risk of its disappearance, an immediate conservation status analysis must be done over the species on Western Ghats. This research underscores that immediate conservation measures are imperative to protect the remnants of the wild varieties of *Phoebe wightii* within the Western Ghats. The observed concentration of suitable regions predominantly within the Central Western Ghats accentuates their pivotal role in ensuring this species future survival. This emphasises the importance of perpetual monitoring and proactive conservation strategies, aimed at mitigating the adverse repercussions of habitat loss. In conclusion, this study accentuates the critical need to preserve the habitat and diversity of *P. wightii* in the face of rapid changes in environmental elements, underscoring the invaluable contribution of ongoing research and concerted conservation efforts in sustaining the Western Ghats ecosystem.

In this study, we examined the habitat preferences and expected potential shifts in distribution of three sky island species. Here we investigated both historical and future projections to ascertain the high probable habitat-suitable regions for these species on Western Ghats. Our findings highlight a noteworthy decline in the suitable high probable habitat areas for *P. wightii* and *Elaeocarpus munroi*, spanning from past to future periods. Specifically, the suitable habitat area for *P. wightii* becomes limited, predominantly concentrating within the central and southern regions. Meanwhile, *E. munroi* displays a varied response, exhibiting potential habitat recovery under certain scenarios while facing decline under others. Furthermore, we observe a noteworthy expansion in the high probable habitat-suitable area for the species *E. gadgilii*. However, this expansion is accompanied by a concerning shift in the distribution of suitable habitats towards the northern Western ghats. This shift poses a substantial threat to the species, jeopardising its current existence and rendering its present habitat areas less suitable for its future survival. So, it is thereby evident that the impending loss of these species necessitates the implementation of conservation strat-

egies. Taking these all into consideration the observed shifts and reductions in high probable habitat-suitable areas, proactive measures are imperative to mitigate potential species loss and preserve the ecological balance of the studied sky island ecosystem.

Highlighting the importance of preserving species in their natural environments, ensemble forecasting is employed to predict suitable habitats for conservation efforts. This becomes particularly crucial for species like *Elaeocarpus munroi* and *Phoebe wightii*, characterized by fragmented distribution and this puts them at a heightened risk of extinction (Gaston and Fuller 2007). In the context of climate change and human land use, species distribution models become indispensable for successful biodiversity conservation. These models can forecast future biotic responses and guide proactive conservation strategies (Kharouba *et al*., 2008). In the field of biodiversity conservation and the ever-growing concerns about the impact of climate change on habitats and their inhabitants raises, where ensemble modelling takes centre stage. In the northwestern U.S.A., ecologists face the challenge of conserving habitat for disturbance specialist species, such as the Black-backed Woodpecker. To predict suitable nesting sites in recently burned areas, habitat suitability models were developed using data from three locations in Washington, Oregon, and Idaho. Ensemble predictions, considering multiple models, demonstrated consistency in 40% of east side Montana wildfires, providing robust insights for balancing salvage logging and habitat conservation in burned-forest landscapes. This approach showcases the potential of ensemble modelling in guiding conservation efforts for large-scale disturbance specialists, offering a valuable tool for ecological management (Latif *et al*., 2013).

These ensemble forecasting done over all these three species in the present study, lead to a conclusive assumption that the SWG would be least probable habitat for these species. This showed that biodiversity of SWG is under high risk. That is this environmental and geographical gap that separates it from other parts of Western Ghats would have obviously caused the SWG to be least suitable area in future, and thereby the loss of its biodiversity is unavoidable. So, measures must be introduced over GHG emissions to control climate change and thereby protect biodiversity of SWG. This fact is substantiated in a study on the contrasting rainfall trends in the southern Western Ghats. That is the unusual increase in surface temperature in the northern Arabian Sea and tropospheric temperature in northern India in recent decades has led to a distinct rainfall pattern. This shift is attributed to the movement of

the low-level jet stream towards the north, weakening the westerly winds over the southern Western Ghats and significantly altering the southwest monsoon rainfall pattern. The combined warming of the northern Arabian Sea and northern land troposphere causes the core position of the low-level jet stream to shift northward. The sea surface temperature over the Oman upwelling region and tropospheric temperature over the northern Indian landmass are correlated with rainfall in the north regions of the Western Ghats. These findings indicate a gradual climate change in the peninsular region, emphasizing the influential role of the Western Ghats Mountain chain in modulating monsoon rainfall in southern India. Therefore, the study cautions against overlooking the potential changes in regional precipitation and climate patterns. There by the rainfall in north will increase and that in south will decrease (Varikoden *et al*., 2019). This substantiates the present study's findings, indicating that the southern Western Ghats will be the least probable habitat suitable area for the three species in the future. This is due to the anticipated decrease in precipitation in the southern Western Ghats, gradually leading to a reduction in the diversity of the Western Ghats. Therefore, under the present and predicted future climate scenarios, the Southern Western Ghats are at risk of losing their biodiversity. This study thereby raised the importance of ensemble habitat modelling as a powerful tool for analysing the distribution of species in different scenarios.

In a study to anticipate the impacts of climate change on microalgae biomass production in polar regions, showcased the crucial role of environmental factors in it. Where the use of ensemble species distribution modelling proved useful in understanding and establishing links between controlling factors and the effects of climate-induced changes in Antarctic coastal communities (Jerosch *et al*., 2017). The modelling technique enables the examination of how environmental factors influence the distribution of various species (Kocev and Dzeroski 2013).

One notable strength of ensemble modelling lies in its ability to minimize uncertainty arising from variations in predictions among modelling techniques, ultimately enhancing the accuracy of predictions. This is not just a theoretical advantage; it found practical application in the U.S. Fish and Wildlife Service species assessment, guiding conservation decisions and informing recovery activities (Ramirez-Reyes *et al*., 2021). The integration of ensemble modelling into species status assessments and comparable frameworks emerges as a powerful tool. By doing so, it not only refines conservation strategies but also yields more robust status assessments for at-risk spe-

cies. This approach is pivotal in comparing both statistical and theoretical habitat models, underscoring the effectiveness of ensemble prediction in diminishing uncertainty (Jones-Farrand *et al*., 2011).

Biodiversity plays a critical role in maintaining the stability of the earth, as it provides indispensable ecosystem services necessary for our survival and overall quality of life. Therefore in-situ (on-site) and ex-situ (off-site) strategies of conservation become important and should be employed here to protect the species at risk of extinction. Additionally, the utilisation of ensemble forecasting can assist in identifying appropriate models for effective species conservation. The research underscores the immediate need to conserve these species in their natural habitats and emphasises the significance of employing modelling techniques to preserve biodiversity (Brooker *et al*., 2007). Recently several such in-situ conservation strategies are already implemented, but as the distribution of species affected by environmental factors, the Ex-situ, a means of conservation, is more advantageous.

The value of ensemble modelling lies in its capacity to unravel the intricate relationship between the environment and habitat, offering a foundation for effective conservation strategies. The present study underscores the pioneering role of modelling concepts in evaluating the impact of global climate change on the species of sky islands in the Western Ghats, emphasizing the broader applicability and significance of ensemble forecasting in understanding and addressing environmental challenges.

4.4. Conclusions

The present study used advanced modelling techniques to evaluate the spatial distribution of selected taxa and its potential risks of loss from the Western Ghats region. The study highlighted the diverse and substantial threats faced by these species, and the raising concerns in their extinction. The findings enumerated the expected high probable habitat suitability areas for *Phoebe wightii* from past to future scenarios, thereby revealed the pronounced reduction of its suitable habitat from the Western Ghats. Modeling on *Elaeocarpus munroi*, unveiled that this species would encounter decline in high probable habitat suitable area from the Western Ghats, with a potential recovery in 2081-2100 under scenarios SSP585 and 245, but a decline under scenarios SSP126 and 370. These indications collectively accentuate the high likelihood of species loss and its potential extinction.

SDM on *Elaeocarpus gadgilii* unveiled that this species is expected to expand its spatial distribution on the Western Ghats in the future, but not on the area where

they appeared in the past. A novel threat that emerged on this species as per the study was that it is currently located in areas that are projected to be least suitable for its survival in future. The tremendous shift in the spatial distribution of this species raises the urgency of preserving these species within their current habitats to overcome the expected risk of extinction from its present habitat. As per the findings of the study, the execution of targeted conservation strategies for these three representative species are vital. Both in-situ and ex-situ conservation approaches are recommended to safeguard the biodiversity of sky island. The advanced in modelling method provides a platform for identifying the most accurate models for specific species. This enables to cope with the potential errors in modelling, improves the selection of optimal models, and improving the precision in devising conservation measures. The recent developments in ensemble forecasting modelling have remarkable promise in the present field of study.

CHAPTER 5:
EXPLORING INTRASPECIFIC MORPHOMETRIC VARIATION IN *ELAEOCARPUS GADGILII* POPULATIONS ACROSS SKY ISLANDS OF THE WESTERN GHATS: INVESTIGATING THE ROLE OF GAP FEATURES ON SPECIATION

CHAPTER 5: - Exploring Intraspecific Morphometric Variation in *Elaeocarpus gadgilii* Populations across Sky Islands of the Western Ghats: Investigating the Role of Gap Features on Speciation

5.1. Introduction

The historical age of a habitat is evident through its phylogenetic structure. Functional, phylogenetic, and taxonomic diversities are significant dimensions shaped by abrupt ecological shifts. These components enable to predict the ecological and evolutionary responses (Swenson 2011). An island's insularity is shaped by its climate, geology, topography, pedogenesis age, and biotic interactions. The climatic variations in between sky islands contribute to their exceptional species diversity and distribution patterns. The significance of elevation and precipitation on diversity and distribution cannot be inflated. Biodiversity is also affected by eco-evolutionary processes in concomitance with various environmental factors (Steinbauer *et al*., 2017). But understanding how temperature, precipitation, and different living things interact is complex. So, figuring out how a single parameter like climate influences over biodiversity patterns is simple and that would help to predict ecosystem functions better and improve strategies for managing biodiversity in the future (Hakkenberg and Goetz 2021). The structure of communities is found to be significantly affected by climate change, which underscores the paramount significance of functional trait diversity (Newbold 2018), as it functions as an indicator of climate change, inducing observable and anticipatable shifts within ecosystems.

The "escalator to extinction" phenomenon posits that species respond to climate shifts via morphological, physiological, anatomical, or migratory adaptation, potentially culminating in extinction under severe circumstances. This phenomenon is particularly accentuated in mountainous regions (Urban 2015, 2018). The heightened risk of species extinction arises from population fragmentation, habitat destruction, reduced geographic niche ranges and geographical barriers, where endemic species are particularly vulnerable (Warren *et al*., 2013). Notably, distinctive species possess unique morphological adaptations that hold essential ecological significance (Cadotte *et al*., 2008). Although edaphic variation exerts a limited influence on plant dispersal, geology significantly shapes plant diversity through its connection to soil chronosequences. These sequences dictate soil's chemical and physical attributes. Climate-driven alterations in soil nutrient availability trigger biotic interactions like competi-

tion, facilitating niche selection and the persistence of thriving species (Rajakaruna 2004, 2018, Fine *et al*., 2005).

Phenotypic plasticity or local adaptations enable plants to surpass the effects of edaphic or climatic shifts. This is driven by edaphic heterogeneity fostering speciation. The process begins with edaphic tolerance, disruptive selection, and self-replicating populations with limited gene flow, culminating in reproductive isolation and speciation. Furthermore, edaphic variation triggers species-specific dispersal, which in turn, can cause extinction (Sultan 2004, Lankau 2011).

Climate change also exerts a pronounced influence on both floristic distribution and Plant Functional Traits (PFTs) in comparison to topographic alterations. PFTs are intrinsic as they underpin ecosystem functioning and stability. These traits encompass morphological, anatomical, or physiological attributes that enable plants to adeptly respond to environmental cues (Swenson *et al*., 2012, Whittaker *et al*., 2017, Bruelheide *et al*., 2018). Plants respond to shifts in climate, soil, and other environmental factors through migration or through the introduction of physiological, morphological, or genetic adaptations. Extreme environmental changes manifest initially in the plant's phenotypic traits, temporarily or across generations. As the initial response occurs at the morphological level, studying morphometric changes in plants subjected to environmental shifts aids in understanding biotic-abiotic interactions and predicting plant responses. Morphometric variation analysis examines shape and size changes in organisms due to environmental shifts. This approach unveils how factors like temperature, precipitation, or altitude impact species traits. By comparing traits among individuals from diverse locations, scientists identify trait diversity patterns reflecting the environmental influences on species evolution, adaptation mechanisms, and distribution constraints. Furthermore, morphometric variation analysis explores the impact of human activities, including habitat degradation and pollution, on species morphology (Lenoir *et al*., 2010). Here the study deals with intraspecific morphometric variation of *E. gadgilii* populations in sky islands of Western Ghats across Palghat Gap. To gain insights into the effect of the Palghat Gap features or other associated indirect factors on the morphometry of populations of *E. gadgilii*.

5.2. Methodology

5.2.1. Sample collection and herbarium preparation

Among the three tree species under selection *E. gadgilii* was selected for intraspecific morphometric variability analysis. *Elaeocarpus gadgilii* comes under the ge-

nus *Elaeocarpus* Burm ex L. (1753: 116) (Linnaeus 1753) is one of the largest genera with approx. 350 species, belonging to the Elaeocarpaceae family with various species of trees and shrubs worldwide (Coode 2004). It is a major tree genus found in the evergreen, secondary forest, roadside and riverbanks at high altitudes (Zmarzty 2001). The genus is represented in India by 29 taxa, most of which are restricted to the southern and northeastern parts of the country, with a few in the Andaman and Nicobar Islands (Zmarzty 2001, Meitei and Khuraijam 2019). Meitei and Khuraijam (2019) recently discovered 18 species of the genus in Northeast India. Zmarzty (2001) recorded 11 taxa (9 species and 2 variants) from Southern India and Sri Lanka, including four new taxa: *E. hedyosmus* Zmarzty (2001: 423), *E. taprobanicus* Zmarzty (2001: 427), *E. variabilis* Zmarzty (2001: 429), and *E. serratus* L. (1753: 515) var. *weibelii* Zmarzty (2001: 437). In 2021, *Elaeocarpus gadgilii* A.M.Maya, V.Suresh & K.M.P.Kumar, a new species was added to the genus, from the southern part of Western Ghats (Manoharan *et al*. 2021a).

The *Elaeocarpus gadgilii* are trees with coriaceous leaves slightly crowded at the branch tips, alternatively arranged. The inflorescence is hanging laterally or in axillary racemes, with vibrant bisexual flowers with pink or reddish sepals and white petals, this pink to reddish sepals attracts pollinators. The species morphological features found to prefer self-pollination and tree samples collected from different altitudes appears to be separate individuals of separate populations, as they appeared to have variations in their phenological time, altitude, geographical space and even in the climate. As this species is novel to science, its conservation status has not yet been evaluated, and is endemic to the Western Ghats (Manoharan et al., 2021). Samples of *Elaeocarpus gadgilii* were collected from the Sky Islands of the Western Ghats surrounding the Palghat Gap within the study area. Morphometric examination was performed on a subset of these specimens. In total, samples were collected from 43 different locations, with distances between sampling points ranging from 100 meters to over 40,000 meters. This species was found to be less abundant at individual locations, and its population density was low, like other species in this genus. The floral morphology indicated a preference for self-pollination. Among the samples collected from 43 location, specimens from 32 locations were selected for morphometric analysis, as the remaining 11 samples had not reached the flowering stage. These 32 samples varied in altitude and phenological periods and were from different geographical areas, thus they were treated as 32 separate populations of *E. gadgilii* (Table 5.1). The

remaining subset of each sample were preserved in formaldehyde, and herbarium specimens were prepared either using the standard wet or dry method (De Vogel 1987 and Forman and Bridson 1989). To remove excess moisture, formalin-treated samples were gently compressed using blotting paper. The meticulously prepared specimens were subsequently affixed onto herbarium sheets measuring 42 x 28 cm. Each specimen was accompanied by a standardised label of dimensions 14.5 x 11 cm.

Table 5.1. Total number of Samples of *Elaeocarpus gadgilii* located from sky islands of the Western Ghats within the study area.

Samples	Sample Id	Altitude	Lat-Long	Location	Southern side/Northern side of Palghat Gap	Collection No:	Accession no
1	SNLKRI-4	1324m	10°31' 55"N 76°43' 48"E	Karimala	Southern	1208	GVCH 002042
2	SNLKRI-5	1322m	10°31' 54"N 76°43' 49"E	Karimala	Southern	1209	GVCH 002043
3	SNLKSU-6	1278m	10°31' 48.072"N 76°44' 17.934"E	Karasurimala	Southern	1210	GVCH 002044
4	SNLKRI-7	1283m	10°31' 50.1492"N 76°44' 25.6704"E	Karimala	Southern	1211	GVCH 002045
5	SNLKSU-10	1289m	10°31' 58"N 76°44' 33"E	Karasurimala	Southern	1214	GVCH 002046
6	SNLKSU-12	1370m	10°31' 49"N 76°44' 35"E	Karasurimala	Southern	1215	GVCH 002047
7	SNLKSU-13	1429m	10°31' 27.114"N 76°44' 18.037"E	Karasurimala	Southern	1216	GVCH 002048
8	SNLMN-15	1308m	10°32' 20"N 76°42' 53"E	Minnampara	Southern	1218	GVCH 002049
9	SNLMT-16	1312m	10°31' 41"N 76°43' 11"E	Mattumala	Southern	1219	GVCH 002050
10	SNLKSU-17	1304m	10°31' 47"N 76°43' 52"E	Karasurimala	Southern	1220	GVCH 002051
11	SNLANMA-37	1205m	10°30' 7.6998"N 76°42' 12.027"E	Anamedu	Southern	1243	GVCH 002068
12	SNLANMA-38	1208m	10°30' 7.4232"N 76°42' 11.7426"E	Anamedu	Southern	1244	GVCH 002069
13	SNLANAMA-39	1211m	10°30' 5.187"N 76°42' 11.0514"E	Anamedu	Southern	1245	GVCH 002070
14	SNLANMA-40	1130m	10°29' 54.7836"N 76°41' 47.9322"E	Anamedu	Southern	1246	GVCH 002071
15	SNLANMA-41	1021m	10°30' 9.5688"N 76°41' 31.34"E	Anamedu	Southern	1247	GVCH 002072
16	SNLMT-42	1328m	10°31' 47.7402"N 76°43' 9.8322"E	Mattumala	Southern	1224	GVCH 002073
17	NVAR-19	1310m	11°2' 16"N 76°42' 19"E	Varadimala	Northern	1225	GVCH 002052
18	NVAR-20	1271m	11°2' 18"N 76°42' 17"E	Varadimala	Northern	1226	GVCH 002053
19	NVAR-21	1364m	11°2' 21"N 76°43' 44"E	Varadimala	Northern	1227	GVCH 002054
20	NVAR-22	1438m	11°2' 33"N 76°42' 54"E	Varadimala	Northern	1228	GVCH 002055
21	NVAR-23	1424m	11°2' 32"N 76°42' 44"E	Varadimala	Northern	1229	GVCH 002056

Samples	Sample Id	Altitude	Lat-Long	Location	Southern side/Northern side of Palghat Gap	Collection No:	Accession no
22	NVAR-24	1408.1m	11°2' 28"N 76°43' 38"E	Varadimala	Northern	1230	GVCH 002057
23	NKER-26	936m	10°58' 26.26"N 76°38' 43.95"E	Keralamedu	Northern	1231	GVCH 002058
24	NKER-27	919m	10°58' 24.97"N 76°38' 50.05"E	Keralamedu	Northern	1232	GVCH 002059
25	NKER-28	935.4m	10°58' 28.02"N 76°38' 52.62"E	Keralamedu	Northern	1233	GVCH 002060
26	NKER-30	919m	10°58' 23.12"N 76°38' 57.3504"E	Keralamedu	Northern	1235	GVCH 002061
27	NKER-31	936m	10°58'17.8674"N 76°39'5.2092"E	Keralamedu	Northern	1236	GVCH 002062
28	NKER-32	918m	10°58' 17.9652"N 76°39' 19.5804E	Keralamedu	Northern	1237	GVCH 002063
29	NKER-33	917m	10°58'18.2964"N 76°39' 19.4286"E	Keralamedu	Northern	1238	GVCH 002064
30	NKER-34	914m	10°58' 6.7398"N 76°39' 28.7172"E	Keralamedu	Northern	1239	GVCH 002065
31	NKER-35	974m	10°57' 51.7602"N 76°39' 58.2624"E	Keralamedu	Northern	1240	GVCH 002066
32	NKER-36	974m	10°57' 56.5596"N 76°39' 59.7918"E	Keralamedu	Northern	1241	GVCH 002067
Samples from 11 locations which has not reached reproductive stage							
33	SNLMN-1	1303m	10°32' 20"N 76°42' 51"E	Minnampara	Southern	1205	GVCH 002078
33	SNLMN-2	1302m	10°31' 52"N 76°43' 46"E	Minnampara	Southern	1206	GVCH 002077
34	SNLMN-3	1325m	10°31' 55"N 76°43' 47"E	Minnampara	Southern	1207	GVCH 002076
35	SNLKRI-8	1285m	10°31' 52"N 76°44' 27"E	Karimala	Southern		
36	SNLKRI-9	1288m	10°31' 54"N 76°44' 30"E	Karimala	Southern		
37	SNLKSU-14	1382m	10°31' 34"N 76°44' 20"E	Karasurimala	Southern		
38	SNLKSU-18	954m	10°32' 16.527"N 76°40' 36.726"E	Karasurimala	Southern		
40	SNLKSU-43	1302m	10°31'47.0"N 76°43'58.0"E	Karasurimala	Southern	1223	GVCH 002074
41	SNLKSU-44	1351m	10°31'41.34"N 76°44'28.24"E	Karasurimala	Southern		
42	NKER-25	915m	10°58'25.86"N 76°38'4.07"E	Keralamedu	Northern		
43	NKER-29	924m	10°58'27.0"N 76°38'52.8072"E	Keralamedu	Northern	1234	GVCH 002075

5.2.2. Morphometry data documentation and data Analysis

The subsequent examination of the specimen's morphological attributes was conducted through the utilisation of a Stereo microscope (Leica Sapo, Leica MC170 HD). Microscopic features were quantified employing the inherent technique integrated within the microscope. The morphological data encompasses a combination of qualitative and quantitative information, each of which underwent distinct procedures.

The resultant morphological data were bifurcated and documented in two distinct sets of qualitative and quantitative data. Specifically, the first set of morphometric data was prepared in a binomial format, with both qualitative and quantitative data in it, whereas the second of data set were exclusively prepared with quantitative data.

5.2.2.1. Binomial data Analysis

The binomial data encompassed a total of 42 qualitative traits (Table 5.2) and 57 quantitative traits (Plate 5.1-5.4), with reference to Zmarzty (2001) and Beentje (2010) (Table 5.3). These traits were subsequently documented and transformed into a binomial format. The binomial data representation delineated 32 populations as rows, with columns dedicated to each variable presented in a range class format. This endeavour yielded a cumulative consideration of approximately 529 variables.

Binomial data were analysed through statistical method, and these data has only two possible outcomes, such as success or failure, yes or no, or alive or dead. It is typically used in experiments where there are a fixed number of trials and binary outcomes, such as in medical trials or surveys. The binomial data of morphometric parameters underwent two sets of analysis: Factorial analysis and the phylogenetic tree construction method. These analyses were conducted using the Darwin6 software (Perrier and Jacquemoud-collect 2006).

The binomial data undergone dissimilarity analysis. Then the dissimilarity file saved in .dis format serves as the base for both the factorial analysis and the tree construction method. Factorial analysis and tree construction methods were the two different approaches used here to study the divergence and interrelation between the population of the species under analysis. The factorial method provides an overall representation of population diversity, while the tree method shows individual relationships. As an initial step of the analysis dissimilarity between each population indices were evaluated, where in the settings part the number of bootstraps can be selected by the user. The data nature selected was single data as the study was done over morphometric data. In the settings section, there were several methods to find the dissimilarity indices, and the methods were namely Continuous, Count, Modalities, and Presence/absence method. The present study employed the presence/absence indices in Binomial data analysis. In the presence-absence dissimilarity indices, different dissimilarity indices were available for analysing this binomial data.

Table 5.2. Qualitative morphometric parameters of *Elaeocarpus gadgilii* considered for intraspecific morphometric variability analysis.

SL.NO:	Qualitative parameters
1	Habit tree
2	Leaf shape elliptic
3	Leaf apex acute
4	Leaf apex obtuse
5	Leaf apex shortly acuminate
6	Leaf apex emarginate
7	Leaf base cuneate
8	Leaf base Oblique
9	Leaf base obtuse
10	Leaf margin narrowly crenately serrulate
11	Leaf margin crenately serrulate
12	Leaf teeth distance short
13	Leaf teeth distance distant
14	Domatia small Cup like with small pores
15	Domatia small Cup like with large pores
16	Domatia Poket like
17	Domatia large pocket like with small pore
18	Domatia Large pocket like large pores
19	Inflorescence axillary racemes
20	Inflorescence lateral racemes
21	Peduncle with adpressed hairs less
22	Peduncle with adpressed hairs moderate
23	Peduncle with adpressed hairs Dense
24	Pedicel indumentum moderate
25	Pedicel indumentum dense
26	Sepal indumentum on inner side other than margin and midvein moderate
27	Sepal indumentum on the inner side other than margin and midvein dense
28	Sepal indumentum on outer side moderate
29	Sepal indumentum on outer side dense
30	Disk lobes shape round
31	Disk lobe shape truncate
32	Disk lobe shape reinform
33	Filament straight
34	Filament slightly bent
35	Filament sigmoid
36	Petal margin hairs less
37	Petal margin hairs moderate
38	Domatia abundance less
39	Domatia abundance moderate
40	Domatia abundance high
41	Domatia prominent
42	Domatia less prominent

Plate 5.1: a. Habit of *Elaeocarpus gadgilii*. A. M. Maya, V. Suresh, and K. M. P. Kumar, b & c Twig of *E. gadgilii* with inflorescence, d. Fruit on the twig of *Elaeocarpus gadgilii.*

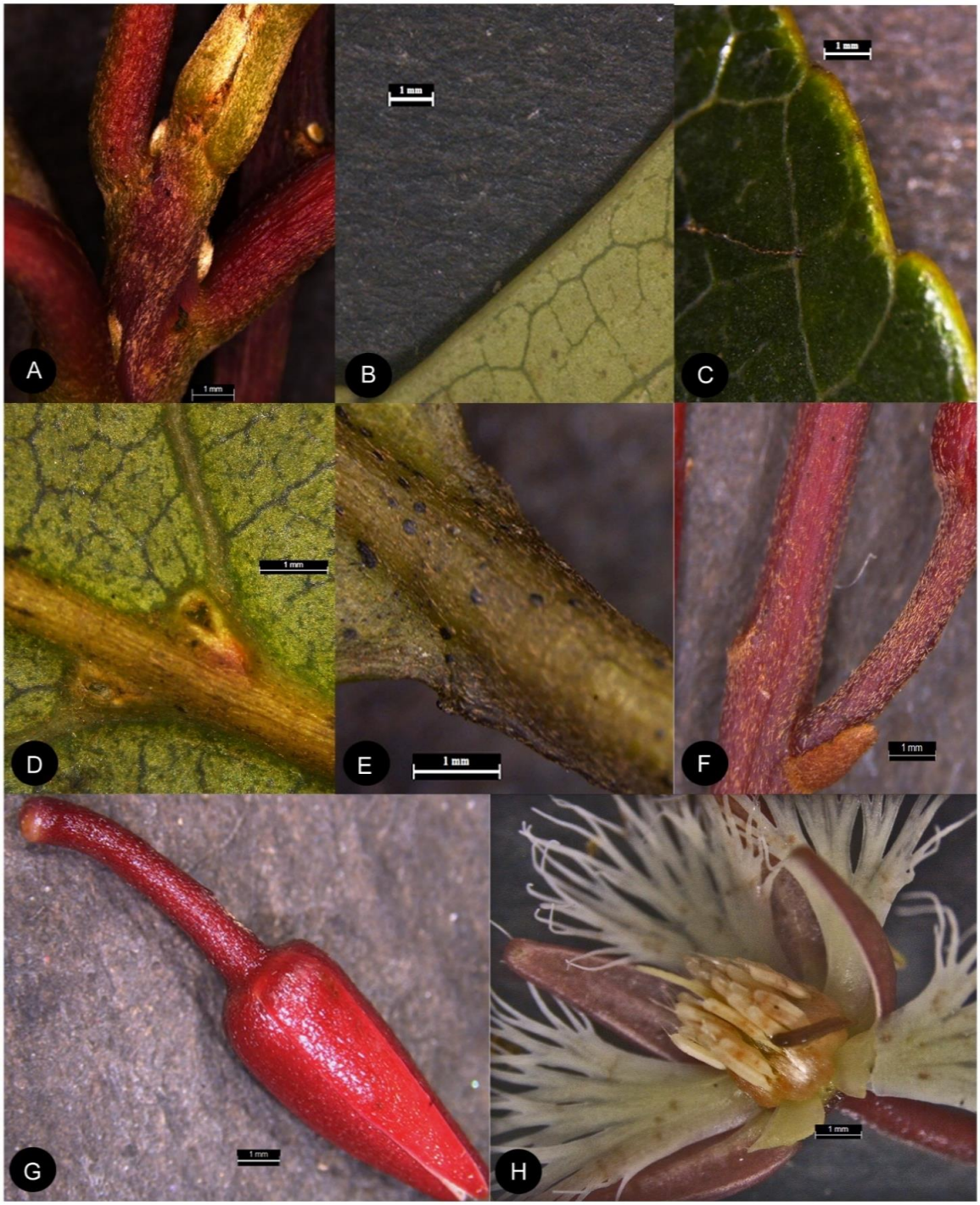


Plate 5.2: Morphometric parameters of *Elaeocarpus gadgilii*. A. M. Maya, V. Suresh, and K. M. P. Kumar: A. Twig tip apex, B. Leaf margin abaxial side, C. Leaf margin adaxial side, D. Domatia, E. A pair of pegs at petiole apex, F. Bract at the base of pedicel, G. Flower bud, H. Opened flower.

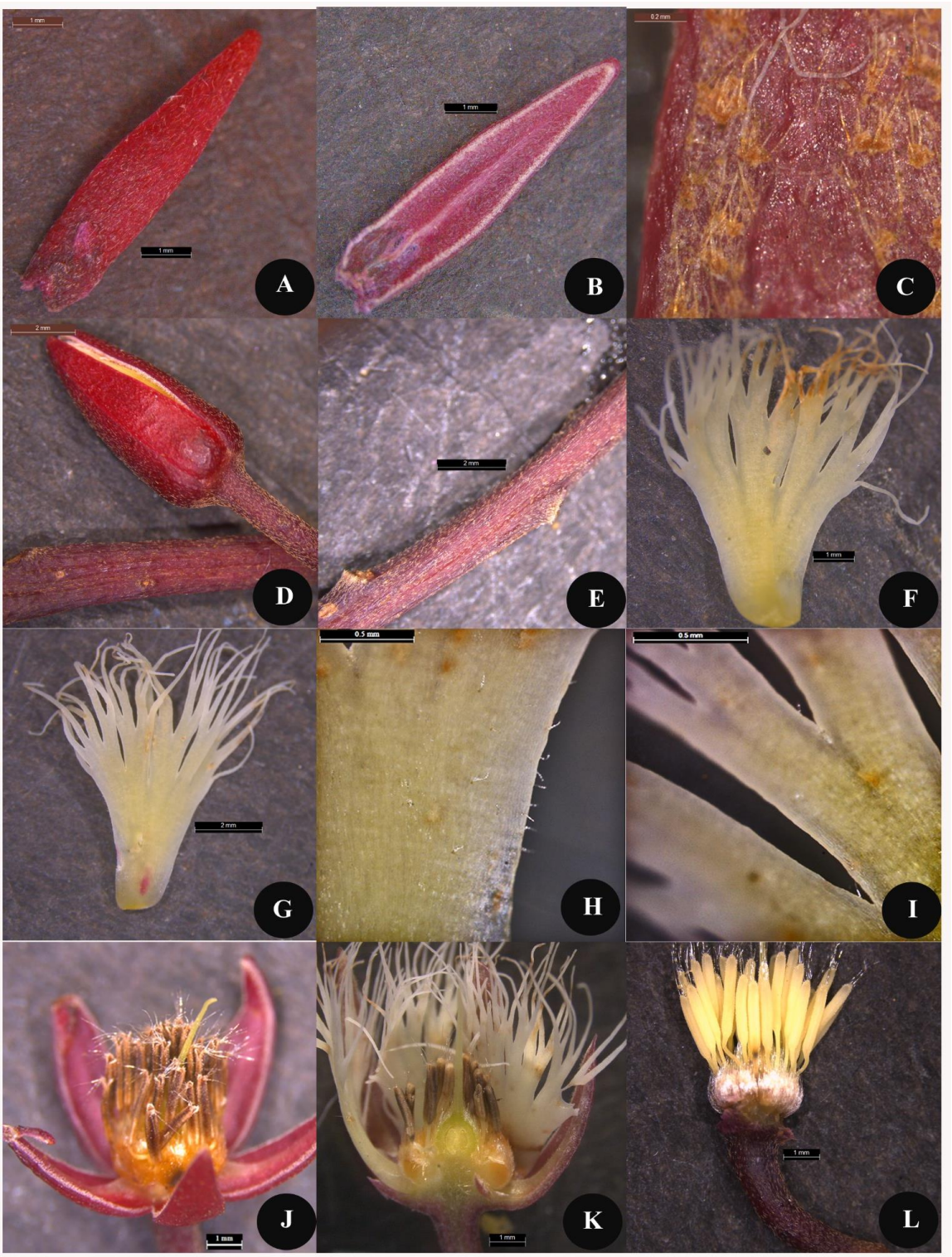


Plate 5.3: Morphometric parameters of *Elaeocarpus gadgilii*. A. M. Maya, V. Suresh, and K. M. P. Kumar : A. Outside of sepal, B. Inside of sepal, C. Indumentum on inner side of sepal, D. Indumentum on outer side of calyx and pedicel, E. Indumentum on rachis, F. Inner side of petal, G. Outer side of petal, H. Indumentum on margin and lower half of petal, I. Indumentum on margin of apical division of petal, J. Flower without petal, K. L. S. of flower, L. Flower without calyx and petal .

Plate 5.4: Morphometric parameters of *Elaeocarpus gadgilii*. A. M. Maya, V. Suresh, and K. M. P. Kumar: A. Flower without petal and sepal, B. Gynoecium over the disk, where disk lobes partially cover the base of ovary, C. Gynoecium without disk lobes, C.1. Ovary cover with dense shining glabrescent hairs, D. Disk lobes, D.1. Disk lobes covered with dense long hairs, E & E.1. Anther with setae at apex of outer tooth, F & F.1 Glabrous setae, very short to long at the tip of anther, G. Ovary C.S., H. Ovule, I. Fruit, I.1. Fruit base with disk remnants, I.2. Glabrescent fruit surface with short hairs, J. Endocarp surface, K. Seed C. S., L. Seed.

Table 5.3. Quantitative morphometric parameters of *Elaeocarpus gadgilii* considered for intraspecific morphometric variability analysis.

SL.NO:	Quantitative Parameter
1	Mature leaf length
2	Lamina length
3	Lamina breadth at middle
4	Lamina breadth at base
5	Petiole length
6	Petiole width
7	Midvein forks at the length
8	Distance between leaf teeth (Average variation within average leaf)
9	Number of vein pairs
10	Distance between veins
11	Petiole apex appendages at the length
12	Peduncle length
13	Peduncle width at apex
14	Peduncle width at middle
15	Peduncle width at base
16	No: of flowers in each peduncle
17	Pedicel length
18	Length b/w pedicel
19	Pedicel width
20	Floral length
21	Number of petals
22	Sepal length
23	Sepal width at apex
24	Sepal width at middle
25	Sepal width at base
26	Petal width at undivided part at apex
27	Petal width at undivided part at middle
28	Petal width at undivided part at base
29	Average range of length with in one average petal
30	Petal length
31	Major primary No: of division in each petal
32	Minor tertiary and Quaternary No: 0f divisions in each petal
33	Petal division length
34	Width of each division of primary divided part of petal
35	Number of Stamens
36	Length of stamens
37	Length of filament
38	Length of anther
39	Width of filament
40	Width of anther
41	No: of setae on anther
42	Length of setae on anther apices
43	No: of disk glands

SL.NO:	Quantitative Parameter
44	Disk glands length
45	Disk glands breadth
46	Carpel number
47	Locule number
48	Ovule number in each locule
49	Style length
50	Ovary length
51	Ovary breadth
52	Style breadth
53	Gynoecium length
54	Domatia length
55	Domatia breadth
56	Domatia pore diameter
57	Domatia pore size

Here, the Jaccard dissimilarity index was used for evaluating dissimilarity analysis.

Jaccard index (dij) = b+c/ a+ (b+c) (Real and Vargas 1996).

dij: dissimilarity between units i and j

xi, xj: variable values for units i and j

a: number of variables where xi = presence and xj = presence

b: number of variables where xi = presence and xj = absence

c: number of variables where xi = absence and xj = presence

The binomial dataset was imported into the Darwin6 platform (Perrier and Jacquemoud-collect 2006) for the purpose of conducting dissimilarity analysis. Within this context, the Jaccard dissimilarity index was computed for each iteration to quantify the dissimilarity between individual units. The primary objective of this analysis was to facilitate the comparisons among all 32 populations. To elucidate the interrelationships among these populations, two principal methodologies were harnessed, factorial analysis and tree construction. These approaches were selected as the core strategies to effectively depict the intricate relationships existing within the entirety of the studied populations.

5.2.2.1.1. Factorial analysis

This divergence analysis was conducted in scenarios where a substantial quantity of variables contributed to the assessment of dissimilarity among distinct populations. The factorial analysis was employed to reduce an extensive array of variables into a more concise set. This approach entails a multidimensional depiction of relationships among units (populations). The interrelations between these units are estab-

lished through the utilisation of eigenvectors and eigenvalues derived from the matrix W, representing scalar products between elements. The determination of these elements is based on the dij distances, calculated according to the Trogerson formula:

$$Wij = – (dij\ 2 – di.\ 2 – d.j\ 2 + d2\ )/2.$$

The factorial method, where interrelatedness between populations were graphically represented in two axes. The first axis includes several variable combinations and the second axis with several other combinations of variable information. Then, the information in each axis is shown by the percentage inertia (sum of all eigenvalues of all variables in the axis). The quality of the projector is evaluated by squared consinus. This cos^2 is used to avoid misinterpretation of the unit neighbourhoods on the planes (Perrier *et al*., 2003, Perrier and Jacquemoud-collect 2006)

5.2.2.1.2. Phylogenetic analysis

The tree methods serve as an approach to elucidate the inter-relationships among individual units, with these relationships being quantified in terms of distance. In this study, a hierarchical method was employed, systematically enumerating all conceivable tree topologies for a given number of units, denoted as 'n'. For each topology considered, a fitness criterion was computed based on edge length. Subsequently, an estimation process was undertaken, ultimately retaining the tree topology that optimises all the fitness criteria. To achieve this optimisation, multiple iterations were conducted. In each iteration, the units or groups of each element were defined as neighbours based on a matrix. These iterative processes encompassed updates to the connections between units using dissimilarity data. Ultimately, after several iterations, the final appropriate tree was created. In each iteration, the one with lesser similarity will be grouped.

In hierarchical clustering, the method available within it includes UPGMA, WPGMA, Ward (Minimum variance), Single linkage, and complete linkage. WPGMA (Weighted Pair Group Method with Arithmetic Mean) and the Ward method were used here in this study for hierarchical clustering, which is a technique used for grouping similar items into clusters. However, these two methods differ in how they cluster the units. At each iteration two closest clusters merged, and it went on to generate a tree (Perrier *et al*., 2003, Perrier and Jacquemoud-collect 2006). The ward method is a linkage-based method, here in each iteration, the populations with minimum variance are clustered. It is a method computationally more intensive than the WPGMA method. WPGMA focuses on the average similarity between the popula-

tions, while Wards, a linkage-based method focuses on minimum variance when forming clusters (Szekely and Rizzo 2005, Murtagh and Contreras 2012).

5.2.2.2. Quantitative data analysis

Quantitative analysis of 32 populations of *E. gadgilii* was performed here using IBM SPSS Statistics, version 22. A set of 57 quantitative parameters were initially documented, out of which 42 parameters were selected for analysis remaining were not considered due to small variance (Zmarzty 2001, Beentje 2010). To ensure robust statistical analysis, two non-parametric tests were employed at each level of analysis. Firstly, one set of non-parametric tests was conducted to assess the significance level of variance between all populations of *E. gadgilii*. Subsequently, the next set of analysis was carried out to examine the variation between populations across the Palghat Gap, based on the recorded quantitative morphometric parameters of of *E. gadgilii* between the populations located on sky islands on the southern and northern sides of the Palghat Gap.

5.2.2.2.1. Intraspecific morphometric variation of *Elaeocarpus gadgilii* at the population level

To ascertain the significance of degree of variability among variables of each population of *E. gadgilii*, the Kruskal-Wallis non-parametric statistical test was executed. This analytical tool operates akin to a one-way ANOVA, with the objective of detecting meaningful distinctions among the independent variables in question between populations. The application of this specific test was intended to evaluate the presence of statistically significant divergence between its populations in the sky islands of Western Ghats.

5.2.2.2.2. Intraspecific morphometric variation of *E. gadgilii* populations in relation to altitude

The topographic attributes like the altitude's and its relation to morphometric variability of *E. gadgilii* was analysed to find out the role of topography of the habitat over the sky island inhabited populations. So, each Morphological variables of each population of *E. gadgilii* in the sky island is related with altitude of mountain range where it exists and was done to find out the influence of the topographic features of the habitat over the population of *E. gadgilii*. The relation significance is evaluated using spearman correlation analysis. The spearman correlation analysis is a non-parametric statistical measure, to assess the significance of correlation.

5.2.2.2.3. Intraspecific morphometric variation of *E. gadgilii* across Palghat Gap

Next tier of analysis was executed across the populations of the species residing on the sky islands on the northern and southern sides of the Palghat Gap. This step aimed to scrutinise the hypothesis of the study. Therefore, a non-parametric assessment was conducted to evaluate the presence of statistically significant disparity between the populations inhabiting the sky islands of the Western Ghats on the opposite sides of the Palghat Gap. Here the comparison was done between the two groups of populations, that is each group with a wholesome population of each side. Here the magnitude of variance was gauged through the utilisation of the Mann-Whitney test, a non-parametric tool designed to assess the significance of variation. Furthermore, the evaluation of each variable's significance level of variance was conducted employing the Post Hoc test. This examination ensured the inclusion of quantitative parameters for subsequent analysis, with the overarching goal of determining the validity of the hypothesis (Siegel 1957, Whitney 1997, Conover 1999, John Gabrosek 2013).

5.3. Results and discussion

Study on *E. gadgilii* remains limited, owing to its novelty within the scope of this study. However, it is worth noting that insights gleaned from the broader genus *Elaeocarpus*, that they are economically and medicinally significant species, might be extrapolated to shed light on this species as well. The genus *Elaeocarpus* is known for its therapeutic attributes, particularly in the management of neurological and circulatory ailments. It also has promising potential in the modulation of blood pressure and heart rate (Swati *et al*., 2015). Several studies reported on the extraction of ethnomedicinal compounds from different vegetative parts of *Elaeocarpus* species. Fruits of certain species of *Elaeocarpus* fruits are edible and some of their seeds have commercial value and are used in the production of rosaries, bracelets and necklaces due to their religious importance. Additionally, some *Elaeocarpus* trees species have timber value. Presence of various phytoconstituents with medicinal significance have been reported from leaves, bark, seeds and fruits of some of the species of this genus *Elaeocarpus* (Weibel 1968, Murthi 1993, Hardainiyan *et al*., 2015a, Prasannan *et al*., 2020).

Multiple challenges confront various *Elaeocarpus* species, leading to their classification as threatened. These challenges encompass delayed fruiting, diminished seed viability and suboptimal germination rates attributed to the hardness of the seed coat. Within the genus, numerous species find themselves categorised as vulnerable,

endangered, or threatened. The issue of deforestation stands as a significant driver behind the decline of *Elaeocarpus* species, evident in instances such as the decline of the *Elaeocarpus* plant in northeastern India. The cultural significance of different *Elaeocarpus* species primarily steers their conservation narrative across diverse domains (Khan *et al*., 2004). The pronounced ethno-religious significance attributed to these species instigates an extensive practice of seed collection from the forest floor, thereby depleting the inherent natural seed bank. Additionally, the *Elaeocarpus* species exhibits an extended germination time frame coupled with modest germination rates. This situation is exacerbated by the commercial harvesting of seeds, consequently leading to a noteworthy diminution in the population of trees of this genus within their indigenous habitat (Khan *et al*., 2005, Kumari *et al*., 2018). Even though the above-mentioned facts are not specifically about the species under concern, but a general concept of this genus, most of it will be applicable to other species of this genus too. As this species is new to science, more facts about it are yet to be studied. The aforementioned facts provide an empirical foundation for the inclusion of *E. gadgilii* within the morphometric investigation. This study explicitly aimed to test the formulated hypothesis by focusing on the populations of *Elaeocarpus gadgilii*. The Important fact here is that, as *Elaeocarpus gadgilii* is a recently discovered species, the relative research concerning it is less.

5.3.1. Sample collection and herbarium preparation

The collection process involved the direct acquisition of specimens from all 32 *Elaeocarpus gadgilii* populations considered for the present study. Two to five twigs of samples specimens of each population were collected separately in polythene covers directly from the field. The collection was done in all seasons continuously for four years (2019 to 2023). Each location has a minimum of two to three mature tree individuals from each location. Sample specimens of all the populations morphometric parameters were measured and documented. Micro morphological data were assessed with the aid Leica sapo stereo microscope. Then the remaining specimens after morphometric analysis were processed and herbarium were prepared. All the herbarium specimens are deposited in GVCH herbarium and accession number are provided in table 5.1 (acronyms according to Thiers, 2024 [continuously updated]).

5.3.2. Morphometric data documentation and data Analysis

Subsequently, the morphometric qualitative and quantitative datasets were set in two forms, that is firstly by adopting a binary structure, by amalgamating both

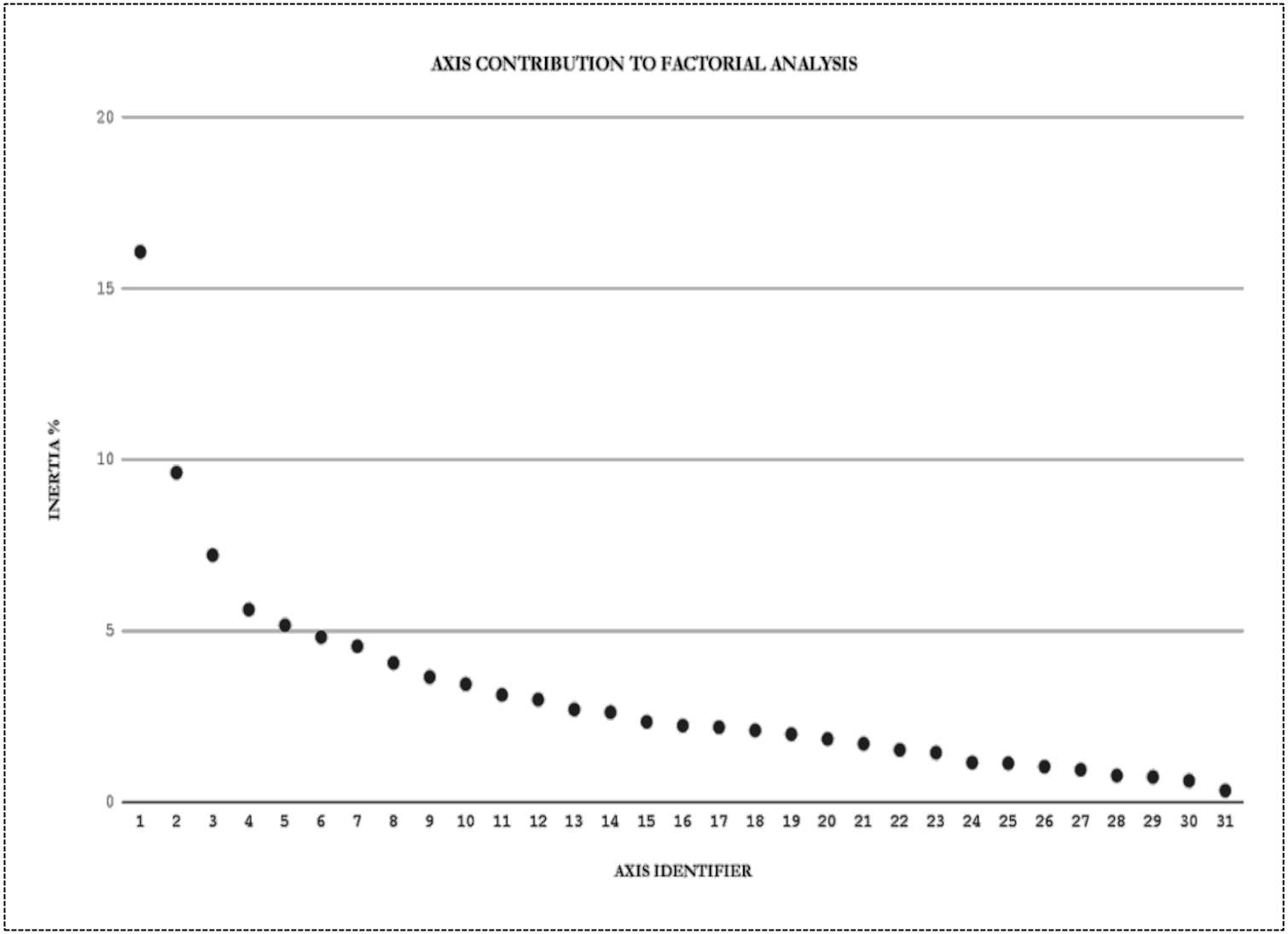


Plate 5.5. Axis (combination of variables) contribution to factorial analysis of the available 31 axes with positive percentage of inertia value, based on 529 morphometric variable combinations of *E. gadgilii* populations.

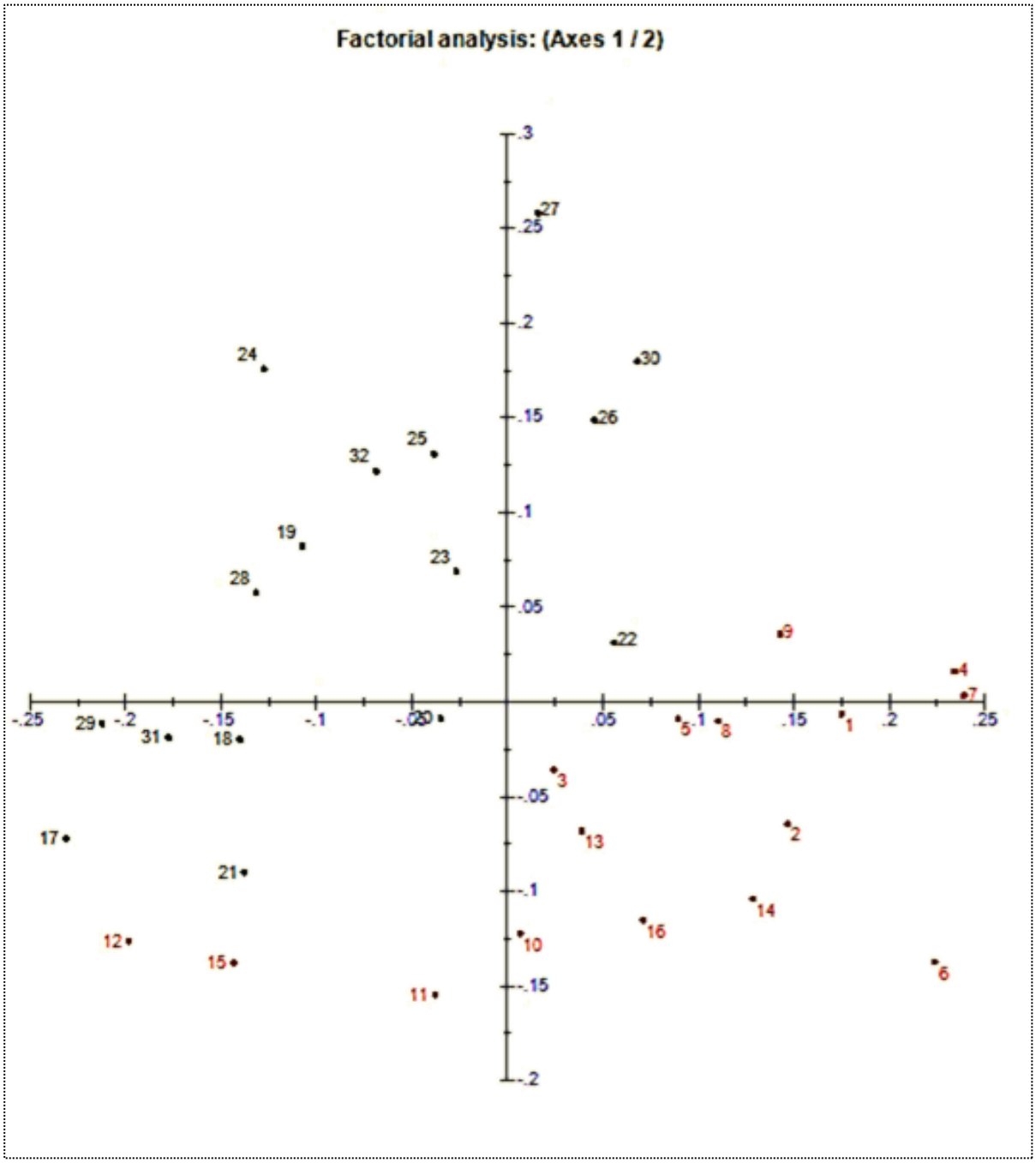


Plate 5.6: Factorial analysis comparing 32 *E. gadgilii* populations based on 529 morphometric (qualitative and quantitative) variables. Axes 1 and 2 are among the 31 axes with the highest percentage of inertia.

Footnote: (1 16 (Populations from the sky islands on the southern side of the Palghat Gap (Red color spot)), (17 32 (Populations from the sky islands on the northern side of the Palghat Gap (Black Color spot)). 1- SNLKRI- 4, 2 SNLKRI-5, 3. SNLKSU-6, 4. SNLKRI-7, 5. SNLKSU 10, 6. SNLKSU 12, 7. SNLKSU 13, 8. SNLMN 15, 9. SNLMT 16, 10. SNLKSU 17, 11. SNLANMA 37, 12. SNLANMA 38, 13. SNLANMA-39, 14. SNLANMA-40, 15. SNLANMA-41, 16. SNLMT-42, 17. NVAR-19, 18. NVAR-20, 19. NVAR-21, 20. NVAR-22, 21. NVAR-23, 22. NVAR-24, 23. NKER-26, 24. NKER-27, 25. NKER-28, 26. NKER-30, 27. NKER-31, 28. NKER-32, 29. NKER 33, 30. NKER 34, 31. NKER 35, 32. NKER 36.

qualitative and quantitative data, and secondly, the data were formatted exclusively comprising quantitative data, with numerical values being directly documented.

5.3.2.1. Binomial data analysis

Given that there was an extensive array of variables, the analysis strategy necessitated the application of two distinct dissimilarity techniques: factorial analysis and the Tree construction method. These approaches were adopted to effectively address the complexities stemming from the distinct distance between variables under scrutiny.

5.3.2.1.1. Factorial analysis

The initial phase of binomial data analysis entailed with the execution of factorial analysis on the population data encompassing 529 variables. This involved the projection of distinct combinations of variables onto each axis. The examination of the interplay between these axes facilitated the determination of associations between individual units, subsequently reflected in their projections on the axes. Each axis serves as a composite representation of multiple variables, with the extent of information encapsulated within an axis quantified by its corresponding inertia percent (Plate 5.5).

The inertia percent, an indicative of the proportion of information preserved by a given axis, is equated to its eigenvalue. In the context of analysis, the evaluation led to the identification of 31 axes characterised by positive eigenvalues, signifying their potential as distinct axis types. These axes stood as pivotal considerations throughout the course of our investigation. The determination of optimal axis combinations hinged upon a critical factor – the percentage inertia, as graphically represented in Plate 5.1.

To merit selection, an axis needed to surpass the 5% threshold in terms of its percentage inertia. Among the pool of 31 axes, attention was directed towards the selection of two axes distinguished by the highest eigenvalues and exhibiting the most substantial percentage inertia. This deliberate choice was instrumental in facilitating the illustration of intricate population relationships. The ensuing projection of population relationships found expression through the amalgamation of these two chosen axes, Axis 1 and Axis 2. The selected axes were then harnessed to visually portray the relationships between the various populations subsequent to the factorial analysis (Plate 5.6). This visualisation strategy was crafted with the intention of capturing and portraying the most plausible interconnections that underscore the entirety of the pop-

ulation set. Notably, the outcomes gleaned from the factorial analysis unveiled a distinctive pattern of interrelationships between populations in sky islands across the Palghat Gap. Within the graph, populations stemming from the northern sky island region are visually represented as black data points. This stands in notable distinction to the red data points employed for designating populations from the sky islands on the southern flanks across the Palghat Gap. This apparent divergence in colouration serves the purpose of accentuating the heightened interconnectedness that characterises the populations found within both the northern and southern sectors. This heightened interconnectedness is in stark juxtaposition to the comparatively weaker associations evident across the geographic gap. The visual contrast, as explicitly illustrated in Plate 5.5, fundamentally underscores a clear and distinguishable pattern in the dynamics of population interactions. Consequently, this visual representation effectively outlines well-defined groupings among the diverse population entities across the Palghat Gap.

Thereby, the interconnections among populations within sky islands of the Western Ghats situated on the opposing sides of the Palghat Gap, as well as the notable dissimilarity and reduced resemblance between populations on the sky islands across the Palghat Gap, was substantiated through the application of factorial analysis. As per the analysis there exists a distinct line of difference between population on sky islands of Western Ghats on southern and northern side of Palghat Gap.

5.3.2.1.2. Phylogenetic analysis

To distinctly outline these interrelationships between populations, the tree construction method within the Darwin6 software platform was employed here. The establishment of phylogenetic relationships among populations becomes attainable by leveraging morphological data, which encompasses the physical attributes of organisms. Through a comparative assessment of the morphological traits exhibited by diverse populations, researchers can infer the evolutionary associations that bind them together.

The phylogenetic tree was constructed utilising meticulously documented quantitative and qualitative morphological data from each individual population of *E. gadgilii*, to elucidate the intricate interrelations among it. This constructed phylogenetic tree assumes a pivotal role in facilitating the inference of evolutionary relationships existing between these populations. This inference is achieved through the identification of the most probable evolutionary scenario, shedding light on the historical

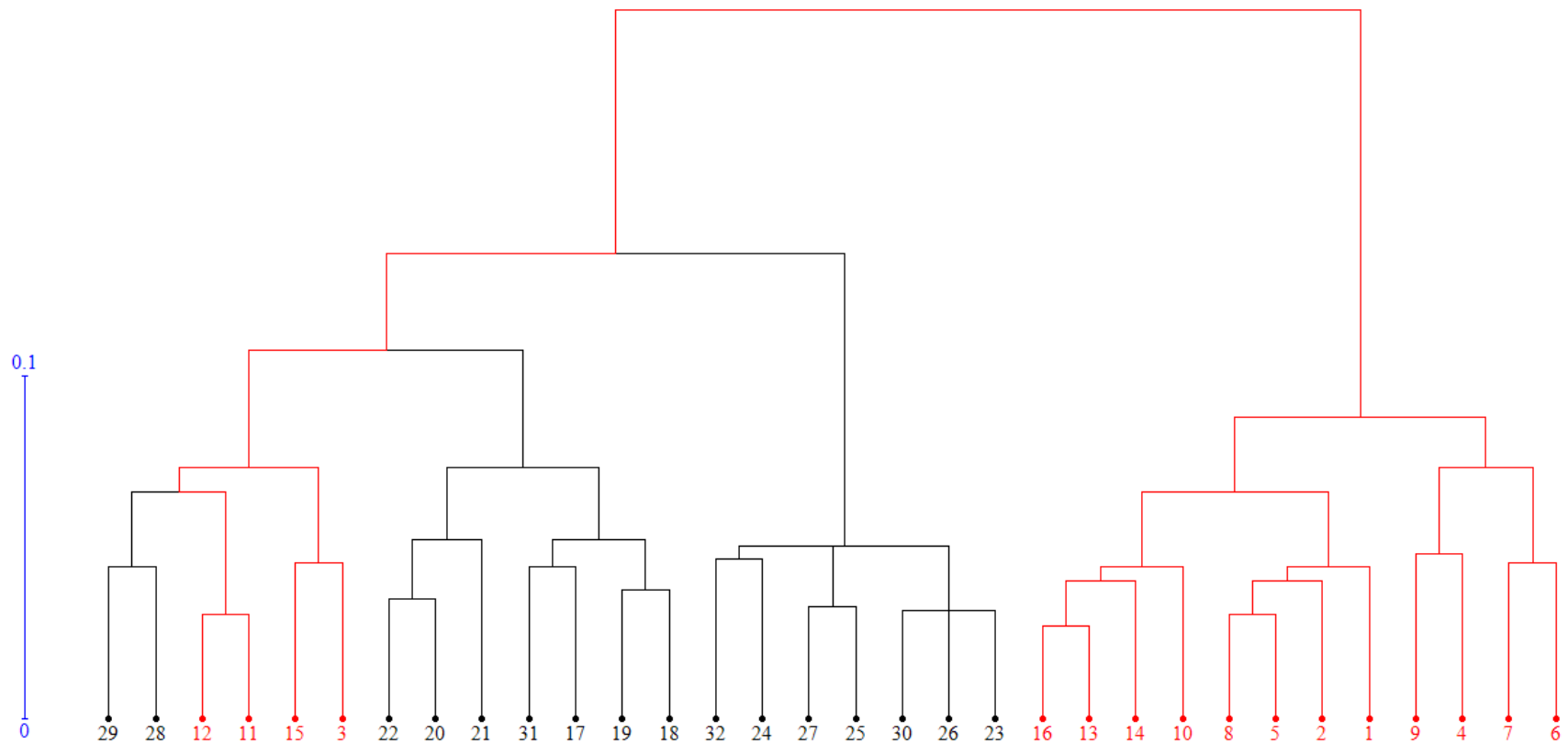


Plate 5.7: Phylogenetic tree constructed using the Ward (minimum variance) hierarchical clustering method based on the morphometric variables of *E. gadgilii*, analyzing the intraspecific relationships among populations in the sky islands across the Palghat Gap within the study area.

Footnote: (1-16 (Populations from the sky islands on the southern side of the Palghat Gap (Red color spot)), (17-32 (Populations from the sky islands on the northern side of the Palghat Gap (Black Color spot)). 1- SNLKRI- 4, 2 – SNLKRI-5, 3. SNLKSU-6, 4. SNLKRI-7, 5. SNLKSU-10, 6. SNLKSU-12, 7. SNLKSU-13, 8. SNLMN-15, 9. SNLMT-16, 10. SNLKSU-17, 11. SNLANMA-37, 12. SNLANMA-38, 13. SNLANMA-39, 14. SNLANMA-40, 15. SNLANMA-41, 16. SNLMT-42, 17. NVAR-19, 18. NVAR-20, 19. NVAR-21, 20. NVAR-22, 21. NVAR-23, 22. NVAR-24, 23. NKER-26, 24. NKER-27, 25. NKER-28, 26. NKER-30, 27. NKER-31, 28. NKER-32, 29. NKER-33, 30. NKER-34, 31. NKER-35, 32. NKER-36.

dynamics that have led to their current state. Moreover, this same phylogenetic tree serves as a valuable tool in unravelling evolutionary relation between these populations. The inclusion of mechanisms such as speciation, adaptation, and gene flow within the scope of the analysis allows for the understanding of the underlying forces that have driven the divergence and development of these populations over time.

In the current investigation, a hierarchical clustering approach was employed to construct a phylogenetic tree. Notably, two distinct methods were employed here, namely WPGMA and Ward (Minimum variance), which were utilised to execute this tree-building process. Through the application of these methods, the resultant phylogenetic tree effectively captured and portrayed the intricate relational patterns existing among individual populations. The analysis of the generated trees utilising both WPGMA and Among all the populations from the northern and southern sides of sky islands, the 4 populations (15, 3, 12 and 11) of the southern side and 2 the populations (29 and 28) of the northern side were found to have lesser variance, and among the 4 only two populations (12 and 11) of southern side populations where in a clade near to clade where the two populations (28 and 29) from northern side are placed. This analysis reveals a discernible variation among the majority of populations across the southern and northern sky Ward methods revealed a conspicuous differentiation between populations originating from the northern and southern regions. This study was done on 32 populations of *E. gadgilii*, with the initial set of 16 populations (designated as 1-16) representing the population of *E. gadgilii* from the southern sky islands. Subsequently, the next set of 16 populations (designated as 17-32) include the populations from the northern sky islands.

The tree depicted in Plate 5.7, was generated using the Ward (Minimum Variance) hierarchical method. That clearly illustrates the morphological variation and separation of populations *E. gadgilii* across the Palghat Gap. According to the tree there the population are placed in two major clades, of which the one on the right clade consists of 12 populations (16, 13, 14, 8, 5, 2, 1, 10, 9, 4, 7, 6) from Southern sky islands, while the other major clade on the left-hand side further branches into two secondary sub-clades, among them one sub-clade on the rightward side included 7 populations, and were 26, 23, 30, 27, 25, 32 and 24 from the sky islands on the northern side, while the other minor clade on leftward side comprises two tertiary subclades. There the tertiary subclade on the rightward side had 7 populations from the northern side and those populations were 22, 20, 21, 31, 17, 19 and 18. Towards

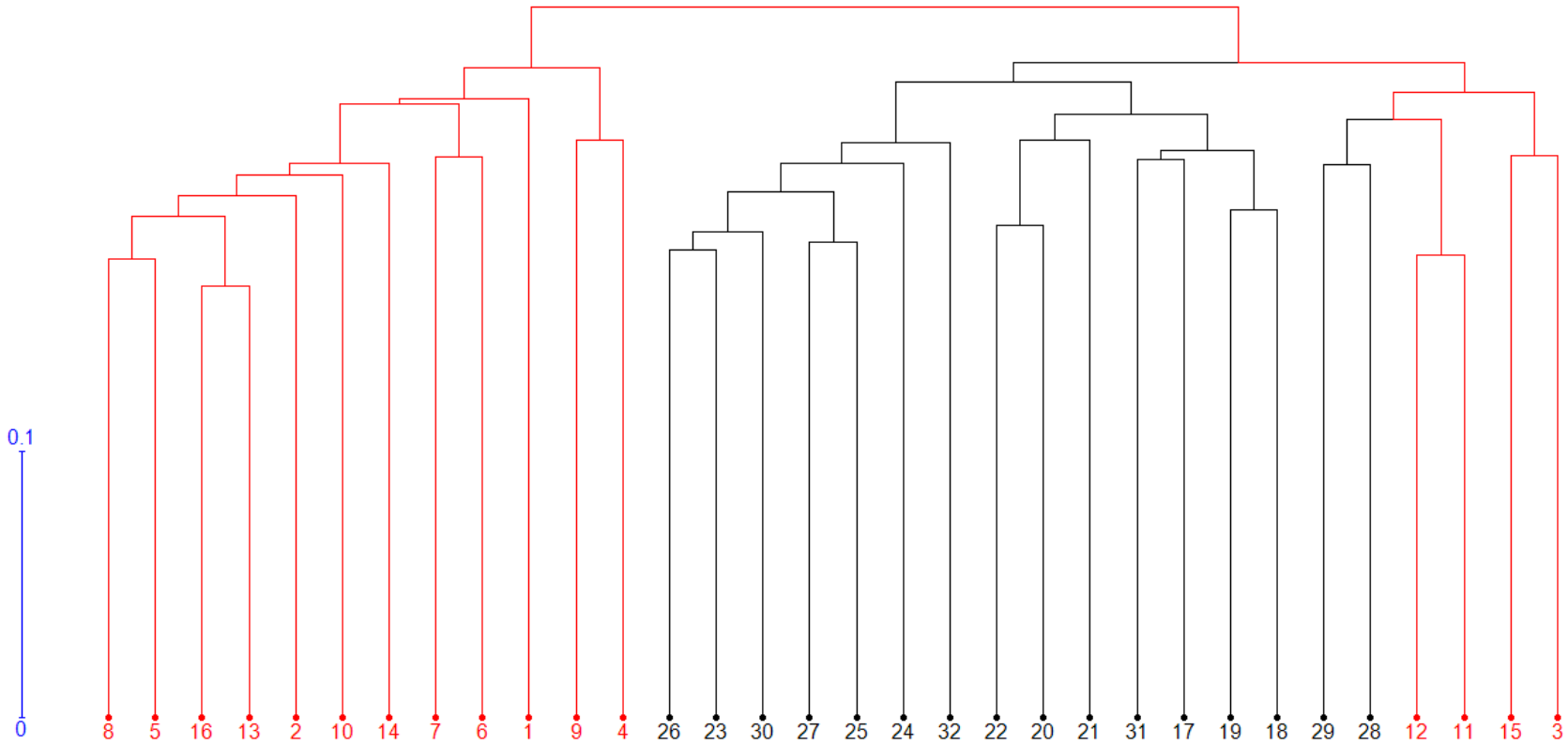


Plate 5.8: Phylogenetic tree constructed using the WPGMA hierarchical clustering method based on morphometric variables of *E. gadgilii*, analyzing intraspecific relationships among populations in the sky islands across the Palghat Gap within the study area.

Footnote: (1-16 (Populations from the Southern side (Red color spot)), (17-32 (Populations from the Northern side (Black Color spot)). 1- SNLKRI-4, 2 – SNLKRI-5, 3 – SNLKSU-6, 4 – SNLKRI-7, 5 – SNLYKSU-10, 6 – SNLKSU-12, 7 – SNLKSU-13, 8 – SNLMN-15, 9 – SNLMT-16, 10 – SNLKSU-17, 11 - SNLANMA-37, 12 - SNLANMA-38, 13 – SNLANMA-39, 14 – SNLANMA-40, 15 – SNLANMA-41, 16 - SNLMT-42, 17 NVAR-19, 18 – NVAR-20, 19 – NVAR-21, 20 – NVAR-22, 21 – NVAR-23, 22 – NVAR-24, 23 – NKER-26, 24 – NKER-27, 25 – NKER-28, 26 – NKER-30, 27 – NKER-31, 28 – NKER-32, 29 – NKER-33, 30 – NKER-34, 31 – NKER-35, 32 – NKER-36.

the leftward side the tertiary sub-clade again divided to quaternary sub-clade. The rightward quaternary subclade diverged into clade with two population that is 15 and 3 and both were from the southern side sky islands. Then the leftward quaternary clade subclade was again divided into two subclades, where one subclade with two populations 12 and 11 on the rightward side from the sky islands on Southern side of Palghat Gap. Then the leftward side subclade with two populations 29 and 28 and they were from the sky islands on northern side of the Palghat Gap (Plate 5.7). The presently defined phylogenetic tree clearly depicts the variance between the populations, where the populations with minimum variance are placed in single clusters. That is 14 populations of *E. gadgilii* from the Southern side of sky islands were found to be placed distantly from the clade where the northern population of *E. gadgilii* were placed. Even though the remaining 4 populations of *E. gadgilii* from Southern sky islands were placed near the northern side of populations but were placed in separate subclades.islands. However, these few populations that (29, 28) and (12, 11 clade) are within the closest clusters clearly demonstrates a significant ancestral link between these populations. This is substantiated by the relatively lower variance observed between two populations from the northern side (28 and 29) and two populations from the sky islands on the southern side (12 and 11) of the Palghat Gap, grouped within a single subclade. So as to ensure the population relation established by the above studied Ward method, an additional phylogenetic tree construction method used was WPGMA.

The phylogenetic tree depicted in Plate 5.8 was created through the WPGMA method, where the clustering was performed based on the simple average of distances between clusters determined by the similarity matrix. As per the analysis of the derived phylogenetic tree, the populations were divided into two major clades. One major clade on the leftward side of the tree, with 12 populations of *E. gadgilii* (8, 5, 16, 13, 2, 10, 14, 7, 6, 1, 9 and 4), were from sky islands on the southern side of Palghat Gap. The next major clade on the right-hand side of the tree was again divided into two minor secondary clades, were one clade placed on the leftward side was again subdivided into several subclades with all the populations (26, 23, 30, 27, 25, 24 and 32) from the sky islands on the northern side of the Palghat Gap and other secondary minor clade with 22, 20, 21, 31,17, 19 and 18th populations. Then next minor secondary clade on the rightward side, was divided into two tertiary sub-clade, one teritiary subclade with two populations from the southern side (15 and 3). Then the second

teritiary subclade on the leftward side of the tree again divided into two quaternary subclades. Each quaternary subclade with two populations each. That first quaternary sub clade with two populations from the southern side (11 and 12) and other one with two populations from the northern side (28 and 29) (Plate 5.8).

These two dendrogram generated through WARD and WPGMA methods depicted that six populations from 32 populations of *E. gadgilii* exhibited relatedness, encompassing four populations from the southern facet (3, 15, 11, 12) and two populations (28, 29) from the northern side of the Palghat Gap. However, it is imperative to acknowledge that beyond this set of six populations, the remaining 26 populations show distinct variation that is prominently discernible between the populations situated on the southern and northern sides across the Palghat Gap.

Upon analysis, these six populations manifest an interconnectedness, potentially stemming from an ancestral association predating their adaptation to environmental changes. This raises the prospect of an enduring lineage that they may have evolved over time and eventually diverge from neighbouring populations with that presently coexist. Here the small relatedness that prevails between some populations of *E. gadgilii* from sky islands separated from Palghat Gap probably reflecting the connectivity in geneflow remained before civilisation in the Palghat Gap, when the wild animals trespassing was possible across the Palghat Gap. As wide range of carnivores acts as secondary seed dispersal agents for the genus *Elaeocarpus*. So, before civilization, the species *E. gadgilii* may have probably experienced continuous gene flow across the Palghat Gap, as it is likely that the gap was traversed by seed dispersal agents.

Apart from this focal group of six populations, the residual 26 populations presented notable levels of variation, which stratify into two discernible clusters. Of these, 12 populations originate from the southern domain (8, 5, 16, 13, 2, 10, 14, 7, 6, 1, 9, 4), while the remaining 14 populations were from northern sky islands (26, 23, 30, 27, 25, 24, 32, 22, 20, 21, 31, 17, 19, 18). Remarkably, an analysis of the prevailing dataset substantiates that, at present, the data validates the distinction and dissimilarity characterising majority of populations of *E. gadgilii* from the sky islands across the Palghat Gap. This observed divergence serves as a validation of the underpinning hypothesis of the study. This distinctiveness is indicative of the evolutionary dynamics that would have played within this region, underscoring the complex interplay of geographical factors and historical events that would have led to the formation of dis-

crete population clusters of *E. gadgilii*. Therefore, it is more likely that gene flow was disrupted after the advent of civilization, as the movement of wild animals across the Palghat Gap became impossible. This disruption could explain the variations found between the populations from sky islands of the Western Ghats on either side of the gap. Gradually the population of *E. gadgilii* gets geographically separated as two distinct groups of its population on the sky islands on the northern and southern side of Palghat Gap. This would probably promote allopatric speciation, and the prolonged isolation may later lead to the evolution of new variants, and then to new species.

5.3.2.2. Quantitative data analysis

The analysis initially encompassed 57 quantitative morphometric parameters. However, only 42 were deemed suitable for further investigation due to the minimal variations observed among the remaining parameters, which included basic characteristics of the genus like petal number and sepal number. Subsequently, the variability of the selected quantitative parameters was evaluated from various perspectives. This evaluation encompassed assessing the significant level of variation among individual variables within populations within sky islands, as well as between sky islands across the Palghat Gap, while also examining the topographic influence on this variation.

5.3.2.2.1. Intraspecific morphometric variation of *Elaeocarpus gadgilii* at the population level

Non-parametric Kruskal-Wallis test, a statistical test like a one-way ANOVA that does not rely on assumptions of normality, was conducted to analyse the statistically significant variation between populations based on 42 different quantitative morphometric variables. As depicted in Table 5.4, the Kruskal-Wallis test yielded a calculated P-value of 0.00 for all parameters considered, at a significance level of 0.05. This P-value was significantly smaller than the chosen significance level, providing strong evidence of statistically significant variation in all 42 quantitative parameters among each of the 32 populations of *E. gadgilii*, indicating substantial diversity across the entire sample (Table 5.4). These findings suggest that the observed differences in the parameters were not random, but rather reflected meaningful distinctions between the populations. Consequently, the 42 parameters are considered as significant indicators of intraspecific morphometric variation in *E. gadgilii* populations. The obtained results support the notion that these parameters play a crucial role in characterising the variation within the populations of *E. gadgilii*.

Table 5.4. Kruskal-Wallis test statistics done on 42 selected quantitative morphometric parameters of *E. gadgilii* in between its 32 populations, at significance level of 0.05.

Sl. No:	Morphometric quantitative parameters	Chi-Square	df	Asymp. Sig.
1	Mature leaf length	655.909	31	0
2	Lamina length	856.396	31	0
3	Lamina Breadth at Apex	828.57	31	0
4	Lamina Breadth at Middle	884.692	31	0
5	Lamina Breadth at Base	992.671	31	0
6	Petiole length	1068.558	31	0
7	Petiole width	1061.201	31	0
8	Midvein fork at the length	445.456	31	0
9	Domatia length	1582.015	31	0
10	Domatia breadth	1462.925	31	0
11	Distance between leaf teeth	305.78	31	0
12	Distance between vein pairs	255.515	31	0
13	Peduncle length	1225.412	31	0
14	Peduncle width at apex	842.86	31	0
15	Peduncle width at base	935.674	31	0
16	Number of flowers in each peduncle	1007.838	31	0
17	Length between each pedicel	549.384	31	0
18	Pedicel length	1600.616	31	0
19	Pedicel width at middle	878.286	31	0
20	Floral length	1170.046	31	0
21	Sepal width at apex	904.795	31	0
22	Sepal length	1439.088	31	0
23	Sepal width at middle	989.072	31	0
24	Sepal width at base	1128.074	31	0
25	Petal width at undivided part at apex	1170.597	31	0
26	Petal width at undivided part at middle	1334.299	31	0
27	Petal width at undivided part at base	1462.807	31	0
28	Average range of length within one average petal	1285.876	31	0
29	Petal length	1462.838	31	0
30	Major primary number of divisions in each petal	692.739	31	0
31	Minor tertiary number of divisions in each petal	431.969	31	0
32	Petal division length	786.649	31	0
33	Number of stamens	1306.61	31	0
34	Length of stamens	929.027	31	0
35	Length of filament	955.634	31	0
36	Length of anther	1222.957	31	0
37	Width of filament	809.188	31	0
38	Width of anther	964.545	31	0
39	Number of setae on anther	704.487	31	0
40	Length of setae on anther apices	473.162	31	0
41	Disk glands length	1341.793	31	0
42	Disks glands breadth	1325.225	31	0

5.3.2.2.2. Intraspecific morphometric variation of *Elaeocarpus gadgilii* in relation to altitude

To explore the impact of altitude on intraspecific morphometric variation in the quantitative parameters of *E. gadgilii*, the correlation between each parameter and altitude was examined. Spearman correlation coefficient, a non-parametric statistical measure, was hereby employed to assess the statistical significance of correlations at significance level of 0.01 and 0.05. The statistical analysis revealed that certain quantitative morphometric parameters exhibited significant correlations with altitude. The correlation of each variable is detailed in table 5.5 (Table 5.5). Among these variables, the variable with statistically significant correlation with altitude were the one with least P value below significance level, and they were petal width at the undivided part of the base (r (30) = .481**, p = .005) and width of filament (r (30) = 0.398*, p = 0.024) and were positively correlated with altitude (p-value < 0.01). Other variables with significant negative correlation with altitude were lamina length (r (30) = -0.421*, p = 0.016), lamina breadth at the apex (r (30) = -0.619**, p = 0.000), lamina breadth at the middle (r (30) = -0.614**, p = 0.000), lamina breadth at the base (r (30) = -0.554**, p = 0.001), petiole length (r (30) = -0.394**, p = 0.026), petiole width (r (30) = -0.472**, p = 0.006), distance between vein pairs (r (30) = -0.432*, p = 0.013), and number of stamens (r (30) = -0.382*, p = 0.031).

Table 5.5. Spearman correlation statistics between Altitude of sky islands and selected 42 Quantitative morphometric variables of *Elaeocarpus gadgilii*, to analyse the influence of altitude over intraspecific morphometric variables, at significance level of 0.05 and 0.01.

Sl. No	Morphometric quantitative parameters	Spearman's rho-Correlation Coefficient with Altitude	Sig. (2-tailed)	N
1	Mature Leaf length	-0.339	0.058	32
2	Lamina length	-.421*	0.016	32
3	Lamina Breadth at Apex	-.619**	0	32
4	Lamina Breadth at Middle	-.614**	0	32
5	Lamina Breadth at Base	-.554**	0.001	32
6	Petiole length	-.394*	0.026	32
7	Petiole width	-.472**	0.006	32
8	Midvein fork at the length	-0.19	0.296	32
9	Domatia length	0.151	0.408	32
10	Domatia breadth	0.151	0.409	32
11	Distance between leaf teeth	-0.316	0.078	32
12	Distance between vein pairs	-.432*	0.013	32
13	Peduncle length	-0.098	0.595	32
14	Peduncle width at apex	-0.095	0.604	32
15	Peduncle width at base	0.271	0.133	32

16	Number of flowers in each peduncle	-0.047	0.797	32
17	Length between each pedicel	-0.033	0.856	32
18	Pedicel length	0.032	0.863	32
19	Pedicel width at middle	0.01	0.955	32
20	Floral length	-0.26	0.151	32
21	Sepal width at apex	0.074	0.689	32
22	Sepal length	-0.188	0.302	32
23	Sepal width at middle	0.073	0.69	32
24	Sepal width at base	0.115	0.53	32
25	Petal width at undivided part at apex	0.07	0.704	32
26	Petal width at undivided part at middle	0.13	0.478	32
27	Length of setae on anther apices	-0.063	0.733	32
28	Disk glands length	0.061	0.739	32
29	Disks glands breadth	-0.17	0.353	32
30	Petal width at undivided part at base	.481**	0.005	32
31	Average range of length within one average petal	0.173	0.343	32
32	Petal length	-0.001	0.998	32
33	Major primary number of divisions in each petal	-0.125	0.494	32
34	Minor tertiary number of divisions in each petal	0.099	0.589	32
35	Petal division length	-0.04	0.827	32
36	Number of stamens	-.382*	0.031	32
37	Length of stamens	0.09	0.624	32
38	Length of filament	0.119	0.517	32
39	Length of anther	0.186	0.308	32
40	Width of filament	.398*	0.024	32
41	Width of anther	0.044	0.813	32
42	Number of setae on anther	-0.002	0.993	32

*** Correlation is significant at the 0.05 level (2-tailed). ** Correlation is significant at the 0.01 level (2-tailed).**

These findings highlight that there exists a significant association between these above-mentioned intraspecific quantitative morphometric parameters of *Elaeocarpus gadgilii* with altitude, underscoring the influence of altitude on these morphometric parameters of *E. gadgilii* populations. The study revealed that the topographic features of the habitat significantly influenced its inhabitants. However, when comparing with other external features, topography is just one of the elements effecting the populations of *E. gadgilii*. The impact of altitude varies with species. Among the morphological variables of *E. gadgilii* only some of the morphometric parameters are linked to altitude, which shows its influence is relatively minimal. This showed that the effect of altitude over the populations of *E. gadgilii* at morphometric level was present, but it was not prominent.

Table 5.6. Mann-Whitney U test statistic on 42 quantitative morphometric parameters over the two sets of population from sky islands of the Western Ghats on the northern and southern side of the Palghat Gap, to analyse the significant level of variation at 0.05.

	Morphometric Parameters	Southern side (S)	Southern side (S) (Median)	Northern side (N)	Northern side (N) (Median)	Total (N)	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
1	Mature leaf length	1038	7.4	1003	8.1	2041	439534	978775	-6.088	0
2	Lamina length	1038	5.9	1003	6.7	2041	389867	929108	-9.821	0
3	Lamina Breadth at Apex	1038	1.9	1002	2.2	2040	342035.5	881276.5	-13.414	0
4	Lamina Breadth at Middle	1038	2.9	1003	3.2	2041	356188	895429	-12.361	0
5	Lamina Breadth at Base	1038	1.8	1003	2.3	2041	250799	790040	-20.314	0
6	Petiole length	1038	1.2	1003	1.7	2041	289266.5	828507.5	-17.406	0
7	Petiole width	1038	1.85	1003	2	2041	368009	907250	-11.462	0
8	Midvein fork at the length	1037	1.1	1001	1.2	2038	441945	980148	-5.822	0
9	Domatia length	1038	1.84	1003	1.13	2041	111474.5	614980.5	-30.735	0
10	Domatia breadth	1038	1.17	1003	0.77	2041	133651.5	637157.5	-29.07	0
11	Distance between leaf teeth	1038	0.8	1003	0.8	2041	512162.5	1015668.5	-0.634	0.526
12	Distance between vein pairs	1038	1.3	1003	1.3	2041	484685.5	988191.5	-2.703	0.007
13	Peduncle length	1038	4.4	960	4.9	1998	405034.5	944275.5	-7.236	0
14	Peduncle width at apex	1038	1.27	1003	1.4	2041	393286	932527	-9.563	0
15	Peduncle width at base	1038	2.04	1003	2.04	2041	516175.5	1055416.5	-0.329	0.742
16	Number of flowers in each peduncle	1038	13	1003	14	2041	481378.5	1020619.5	-2.968	0.003
17	Length between each pedicel	1038	0.5	1003	0.6	2041	453248	992489	-5.105	0
18	Pedicel length	1038	2.89	1003	0.5	2041	314233.5	817739.5	-15.634	0
19	Pedicel width at middle	1038	1.04	1003	1.08	2041	467386	1006627	-3.996	0
20	Floral length	1038	1.03	1003	1.2	2041	403694	942935	-8.86	0
21	Sepal width at apex	1038	0.82	1003	0.82	2041	514234	1017740	-0.475	0.635
22	Sepal length	1038	6.56	1003	6.57	2041	519090	1058331	-0.11	0.912

	Morphometric Parameters	Southern side (S)	Southern side (S) (Median)	Northern side (N)	Northern side (N) (Median)	Total	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
23	Sepal width at middle	1038	1.58	1003	1.53	2041	458310.5	961816.5	-4.677	0
24	Sepal width at base	1038	1.8	1003	1.79	2041	488498	992004	-2.409	0.016
25	Petal width at undivided part at apex	1038	2.73	1003	3.03	2041	385602.5	924843.5	-10.14	0
26	Petal width at undivided part at middle	1038	1.78	1003	1.81	2041	499065	1038306	-1.615	0.106
27	Petal width at undivided part at base	1038	1.21	1003	1.23	2041	510053.5	1049294.5	-0.789	0.43
28	Average range of length within one average petal	1038	3.7	1003	3.76	2041	456773.5	996014.5	-4.792	0
29	Petal length	1038	7.71	1003	8.09	2041	355340	894581	-12.413	0
30	Major primary number of divisions in each petal	1037	4	1003	3	2040	507855.5	1011361.5	-0.977	0.003
31	Minor tertiary number of divisions in each petal	1038	26	1003	23	2041	423480.5	926986.5	-7.305	0
32	Petal division length	1038	3.72	1003	3.99	2041	366552.5	905793.5	-11.571	0
33	Number of stamens	1038	22	1003	25	2041	416792	956033	-7.847	0
34	Length of stamens	1038	2.91	1003	2.82	2041	458782.5	962288.5	-4.641	0
35	Length of filament	1038	1.01	1003	0.89	2041	436831.5	940337.5	-6.291	0
36	Length of anther	1037	2.07	1003	1.91	2040	371492	874998	-11.17	0
37	Width of filament	1038	0.11	1003	0.1	2041	355019.5	858525.5	-12.53	0
38	Width of anther	1038	0.32	1003	0.29	2041	390760.5	894266.5	-9.766	0
39	Number of setae on anther	984	5	1003	5	1987	486517.5	971137.5	-0.563	0.574
40	Length of setae on anther apices	1038	0.64	1003	0.73	2041	434535	973776	-6.463	0
41	Disk glands length	1038	0.98	1003	1.08	2041	359806.5	899047.5	-12.08	0
42	Disks glands breadth	1038	1.11	1003	1.29	2041	358301.5	897542.5	-12.192	0

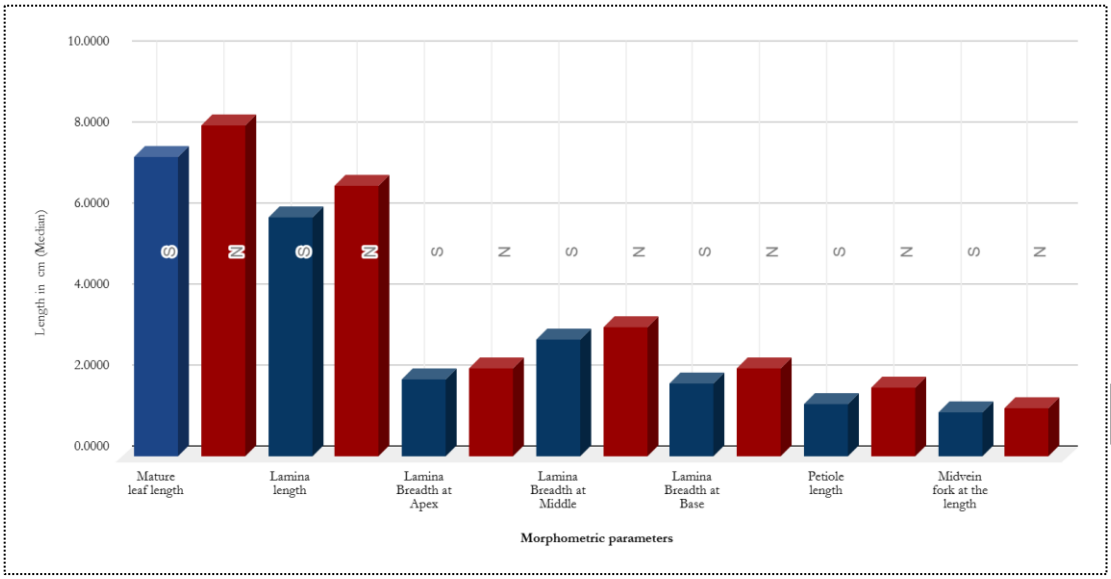
5.3.2.2.3. Intraspecific morphometric variation of *Elaeocarpus gadgilii* across Palghat Gap

The significance of variance in quantitative morphometric parameters of populations of *E. gadgilii* on the sky islands across the Palghat Gap was evaluated using the Mann-Whitney U test. As per Kruskal-Wallis test analysis it is already known that population of *E. gadgilii* with in the sky islands showed significant level of variation at morphometric level. The present analysis was done to compare the populations of *E. gadgilli* in sky islands across the Palghat Gap at morphometric level. For that the population was grouped into two, one group with populations from the sky islands on the southern side and the other group with the populations from the northern side of Palghat Gap. This approach facilitated the assessment of significant variations in each quantitative parameter between these two sets of populations of *E. gadgilii* in sky islands on the northern and southern sides of the Palghat Gap.

As per the analysis, among the 42 parameters examined, 7 parameters were found to lack statistical significance at the designated significant threshold level of 0.05. On the contrary, the remaining set of 35 parameters displayed noteworthy levels of variance, with a P-value of 0.00, underscoring pronounced and considerable statistical significance.

For each parameter, the statistical tests Mann-Whitney U test (U, W (Wilcoxon), Z, and P values) were conducted, and the results including the median, sample size (n), and the measure of significance level of variance is depicted in the table 5.6. Here two groups of population are represented as S and N, where S represents the set of populations from the sky Islands on the southern side, and N represents the set of populations from the northern side of sky islands. As per the Mann-Whitney U test results Distance between leaf teeth , Peduncle width at the base, Sepal width at apex, Sepal length, Petal width at the undivided part at middle, Petal width at undivided part at base and Number of setae on anther were the parameters that lacked significant level variance across Palghat Gap, as P-value > 0.05 (Table 5.6).

The remaining 35 quantitative parameters exhibited a high level of significant variance, and majority of them with P-values equal to or near to 0.00 (Table 5.6). However, among them there were three morphometric variables with P value >0.00, that is their significant level of variance was less compared to the one with P = 0.00.



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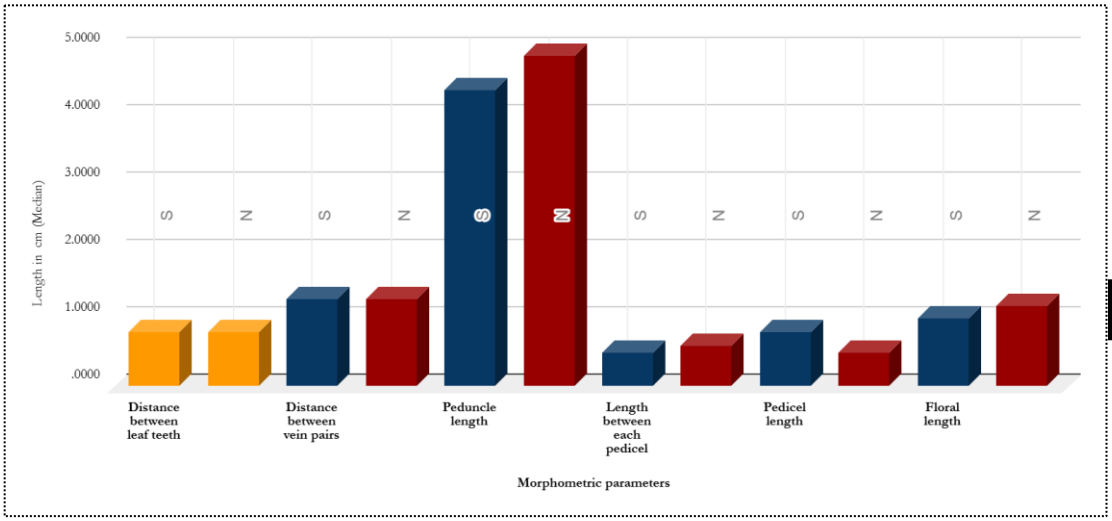

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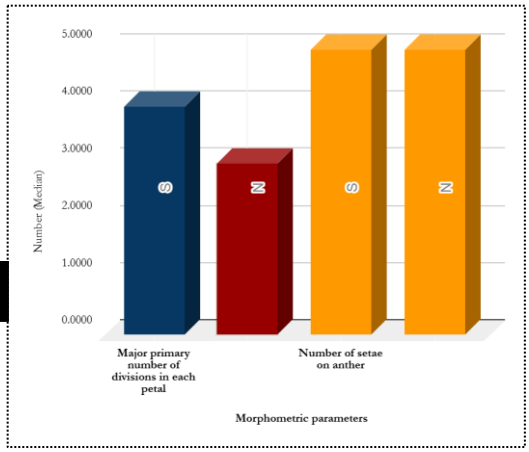

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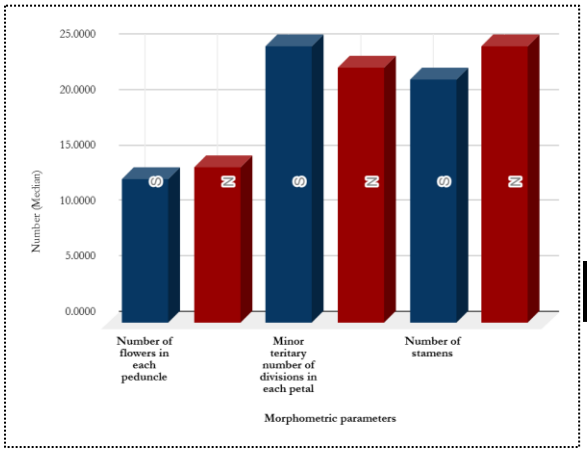
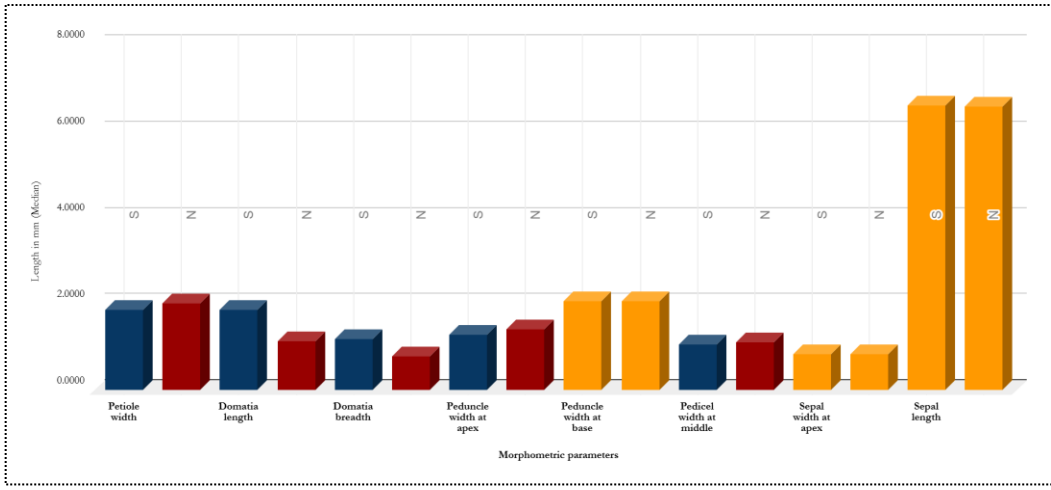


d

Plate 5.9: Comparison of morphometric quantitative parameters of *E. gadgilii* over the sky islands across the Palghat Gap within the study area: **a**. Mature leaf length, Lamina length, Lamina breadth at apex, Lamina breadth at the middle, Lamina breadth at the base, Petiole length and Midvein forks at the length., **b**. Distance between leaf teeth, Distance between vein pairs, Peduncle length, Length between each pedicel, Pedicel length and Floral length., **c**. Major primary number of divisions in each petal, Number of setae on anther apices., d. Number of flowers in each peduncle, Minor tertiary number of divisions in each petal and Number of stamens

Footnote: S = Population from the southern side, N = Populations from Northern side, blue and red colored bars are the parameters with significant level of variation. Yellow color: No significant level of variation across the Palghat gap.



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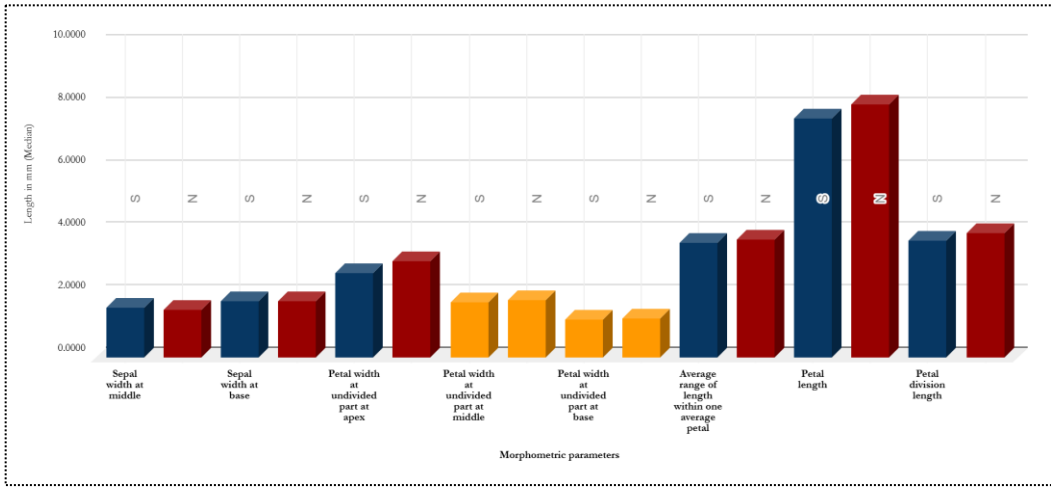

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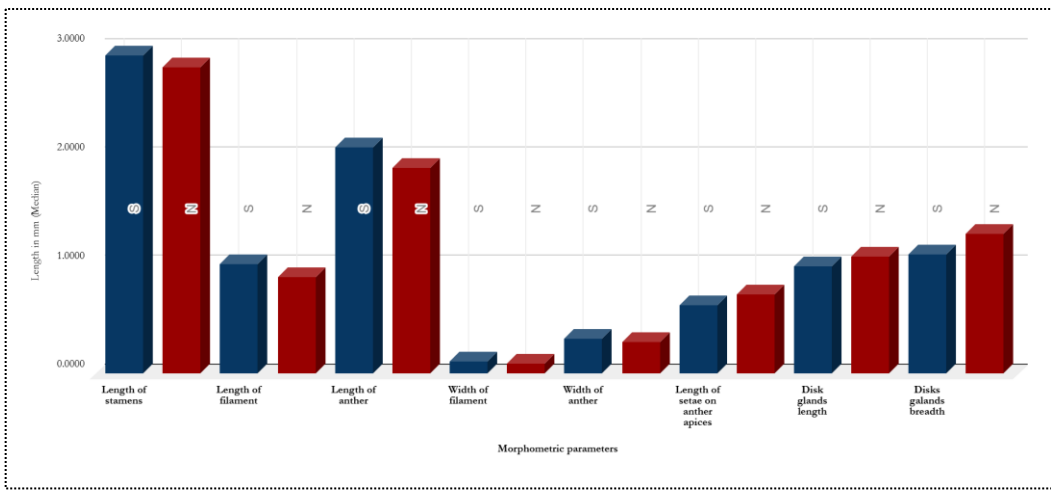

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Plate 5.10: Comparison of morphometric quantitative parameters of *E. gadgilii* over the sky islands across the Palghat Gap within the study area: **a**. Petiole width, Domatia length, Domatia breadth, Peduncle width at the apex, Peduncle width at base, Pedicel width at middle, Sepal width at apex and Sepal length., **b**. Sepal width at the middle, Sepal width at base, Petal width undivided part at apex, Petal width at the undivided part at the middle, Petal width at the undivided part at the base, Average range of length within one average petal, Petal length and Petal division Length., **c**. Length of Stamens, Length of filament, Length of the anther, Width of filament, Width of anther, Length of setae on anther apices, Disk glands length and Disk glands breadth

Footnote: S = Population from the southern side, N = Populations from Northern side, blue and red colored bars are the parameters with significant level of variation. Yellow color: No significant level of variation across the Palghat gap.

Those four parameters were distance between vein pairs, number of flowers in each peduncle, Major primary number of division in each petal and sepal width at base.

This different tiers of statistics and analysis clearly depicts that the major influential factor that affected intraspecific morphometric variability in the population of *E. gadgilii*, seems to be this geographical gap, other than topographic features like altitude. As 35 out of 42 quantitative parameters of *E. gadgilii* seems to show significant level of variation across the Palghat Gap.

The outcomes of this study underscored a marked and statistically significant level of variance in various morphometric traits. The study also discerns the impact of altitude on specific morphometric parameters within the populations of *E. gadgilii*. Through these findings the intricate interplay between population dynamics and ecological factors in shaping the morphological attributes of *E. gadgilii* within the sky islands of the Western Ghats was further enriched.

These findings underscored the significance of geographical factors in shaping the intraspecific morphological diversity of *Elaeocarpus gadgilii* populations. This study contributed valuable scientific insights to this field and enhanced our understanding of population dynamics and adaptation of the concerned species under study.

As per the analysis the parameters like Mature leaf length, Lamina length, Lamina Breadth at apex, Lamina breadth at middle, Lamina breadth at base, Petiole length, Petiole width, Leaf midvein forks at the length, Distance between vein pairs, Peduncle length, Peduncle width at apex, Number of flowers in each peduncle, Length between each pedicel, Pedicel length, Pedicel width at middle, Floral length, Sepal Width at middle, Sepal width at base, Petal width at undivided part at apex, Average range of length within one average petal, Petal length, Minor tertiary number of division in each petal, Petal division length, Number of stamens, Length of stamens, Length of filament, Length of setae on another apices, Length of disk glands length, breadth of disk glands were the morphological parameters that found to have higher values over populations of the sky islands on the northern side of Palghat Gap than the population on the southern side.

To effectively visualise and facilitate the comparison of morphometric variation between populations situated on the northern and southern sky islands, the median values of each quantitative measurement were employed. The observed morphometric parameter differences across the Palghat Gap were found to carry substantial significance. Consequently, the morphometric variances across the populations of the

Palghat Gap were represented graphically. In the graphical representation of this studied data, the variations are clearly depicted. Here, the designations are like, S (represented by the blue colour bar) pertains to the group of populations of *E. gadgilii* from the sky islands on the southern side of Palghat Gap, while N (depicted by the red colour bar) represents the group of the population from the northern side (Plate 5.9-5.10). The morphometric parameters demonstrated with no significant level of variation across the Palghat Gap were illustrated in yellow colour in the graph.

When assessing the significant variance among populations of *E. gadgilii*, including both northern and southern sky island populations, all 42 parameters displayed notable variation. However, upon specifically examining populations across the Palghat Gap, 35 out of the 42 parameters displayed a notable level of statistically significant variation. These findings yield valuable insights into the morphometric attributes and population dynamics of *Elaeocarpus gadgilii* within the surveyed regions. Noteworthy variations were observed at the population level in both vegetative and reproductive components of the species. The discernible variability in the reproductive attributes strongly implies that pollinators may have exerted a significant influence on these variations. Additionally, it is essential to acknowledge that other biotic and abiotic factors are also likely to contribute to the population-level morphometric variations evident in the species (Kudo 2006).

The variation is a step to adaptability, a means of requirement in natural selection. Geographical feature and morphological characters of organisms are closely connected to natural selection. Natural selection is the process by which organisms with better traits are adapted to the environment are more likely to survive and reproduce and thereby passing those favourable traits to their offspring. Organisms that are better adapted to the specific environmental conditions in a particular geographic location are more likely to survive and reproduce, leading to the development of unique sets of morphological characters in different populations. Morphological characters refer to the physical traits of an organism such as its body shape, size and coloration. These characteristics can also vary between populations in different geographic locations due to differences in selective pressures. Natural selection acts on these morphological characteristics, favouring those that increase its survival and reproductive success in a particular environment. Over time, these favourable traits become more common in the population, leading to the development of new species or subspecies (Endler 1977, Grant and Grant 2002). The pronounced variation observed over the

populations of *E. gadgilii* across the Palghat Gap underscored the dynamic adaptation of these populations to the distinct environments of the sky islands.

This study highlights the fact that the geographical gap, served as a demarcation between the sky islands, to be the most probable factor that would have significantly influenced the separation of these populations. The distinct adaptive trajectories and evolutionary processes undertaken by the populations on these sky islands may have caused the introduction of notable variations and are particularly evident over its populations across the Palghat Gap. As this species are inhabitants of sky islands like habitat, they respond to even small changes in ecological variables associated with the habitat. The perpetuation of such scenario raises the potential for the emergence of new species over time, potentially leading to the gradual loss of previous varieties.This phenomenon draws parallels to the classic illustration of Darwin's finches proposed by Darwin himself, exemplifying the mechanisms of evolution and divergence in response to environmental factors. Overall, the geographical variation and morphological characteristics of organisms are important indicators of how natural selection shapes the diversity of life on Earth. Darwin's concept of natural selection suggests that plant populations in different locations may exhibit morphological variation as a result of the differential survival and reproduction of individuals with advantageous traits in their respective environments. This helps us to understand how the morphological variation of plant populations in different locations can be attributed to the differential survival and reproduction of individuals with advantageous traits. This can lead to the development of new plant varieties or even the evolution of new species over time (Darwin 1896). Such variation is a pioneering step to speciation, which flourish biodiversity, but in adverse case, such changes can even lead to the disappearance of the ancestral one.

This observation over the study provides a visual representation of the historical configuration of the region. The major factor that found to separate the population of *E. gadgilii*, is the Palghat Gap. The presence of this geographical gap likely would have hindered the gene flow and interconnection between populations across Palghat Gap. Then after civilization in the Palghat Gap, movement of wild animals gradually stopped, thereby leading to no mark of secondary dispersal. This would have hindered the geneflow between sky islands across the gap. So, the gap distance and civilisation over the gap seems to be the most probable cause led to the emergence of two distinct groups of populations of *E. gadgilii* over the sky islands on the northern and southern

sides of the Palghat Gap. Although there is currently less variance exists between 6 populations out of 32 (15, 3, 12, 11, 29 and 28). This tenuous connection is likely to diminish over subsequent generations. This phenomenon will eventually culminate in the formation of two distinct population groups, over an extended timeline, which could even evolve into separate novel species.

Pollination and seed dispersal: -

Pollination and seed dispersal mechanism seems to have played a significant role accounting for the observed differences in populations of *E. gadgilii*. Since the species in question is new to scientific study, the precise mechanisms of pollination and seed dispersal remain poorly understood. But several literatures of the genus *Elaeocarpus* was available. It is, a genus consisting of thirty-three species in India, with 80% of them being unique to the Western Ghats, is primarily characterised by its leaf attributes. During the flowering season, the tree canopy becomes adorned with attractive white and red flowers, possessing floral features that entice pollinators. The diverse array of pollinating agents contributes to the development of various floral adaptations. Notably, the vibrant red sepals and delicate, fringed, pale white petals attract a range of pollinators, including honeybees, insects, and birds. Studies on *Elaeocarpus* have identified honeybees (*Apis dorsata* and *Apis cerana indica*), fly species namely *Phaenicia sericata*, moths, carrion flies, and regular flies as the primary visitors of this genus (Devy and Davidar 2003, Samy and Ramasubbu 2022). Studies on *E. blascoi* Weibel. showed that its flowering time typically initiates after a considerable time period and was found to be between 15- and 18-year's time period. Among these pollinators, *A. dorsata* was found to be the most efficient in transferring viable pollen grains from the anther to the stigma of the plant (Ramasubbu and Irudhyaraj 2016).

Frugivorous animals typically aid in the dispersal of seeds, but in the case of *E. gausnii*, both seed and fruit predators were identified. These predators included the Malabar giant squirrel (*Ratufa indica*), Nilgiri langur (*Semnopithecus johnii*), lion-tailed macaque (*Macaca silenus*), Bonnet macaque (*Macaca radiata*), Indian crested porcupine (*Hystrix indica*), and flying fox (*Pteropus giganteus*). The lion-tailed macaque was specifically observed as a significant forager of *E. munroi* in the Kakkachi wet evergreen forest of the Southern Western Ghats (Ganesh and Davidar 2005). *E. recurvatus* has several fruit predators such as the red-whiskered bulbul (*Pycnonotus jocosus*), green barbet (*Megalaima zeylanica*), Indian white-eye (*Zosterops pal-*

pebrosus), Malabar giant squirrel (*Ratufa indica*), and Bonnet macaque (*Macaca radiata*), which indicates that a considerable quantity of seeds would be damaged due to the predators breaking the hard seed coat and consuming the cotyledons. This foraging behaviour may cause a negative impact on natural seed storage, and seedling development, and ultimately decreases the species regeneration (Kasi and Ramasubbu 2021).

The consumption of fruits by frugivorous animals and the scatter-hoarding of nuts by granivorous animals can also contribute to the survival of seeds by reducing mortality near the parent tree, dispersing seeds to decrease competition among siblings, promoting genetic diversity among patches, and facilitating colonisation in new areas. *Elaeocarpus* fruits are consumed by various animals including the hornbill bill (*Anthracoceros malagricus* Gmelin), flying squirrel (*Belomys pearsoni* Gray, *Petaurista magnificus* Hodgson), bats (Rousettus sp., Scotophilus sp.), and monkeys (*Presbytis entellus* Dufresne, *P. pileatus* Blyth). Both frugivorous and granivorous mammals contribute to the secondary dispersal of its seeds. Deer species (*Cervus unicolour* Kerr., *Axis axis* brxleben, *Muntiacus muntiak* Zim.) also found to consume fallen ripe fruits on the forest floor and disperse the nuts as well. Viable nuts have also been found in the dung balls of elephants (*Elephas maximus* Linnaeus). Other wild animals such as buffalo (*Bubalus bubalis* Linnaeus), Mithun (*Bos frontalis* Linnaeus), and wild pig (*Sus scrofa* Blyth) have been observed near *Elaeocarpus* trees during the fruiting period (Bhuyan 2002). Additionally, rodents including *Vandeleuria oleracea* Bennet, *Rhizomus pruinosus* Blyth, *Mus musculus* Linnaeus, *Rattus rattus rufescens* Linnaeus, *R. rattus brunneusculus* Hodgson, *Micromys minutus* and *Micoromys erythrotis* Blyth, act as secondary dispersers (Khan *et al*., 2005) and these reduces the natural seed source.

As per field surveys *E. gadgilii* is rarely found in large numbers within a single location. The species already has seeds with a hard endocarp, may result in a prolonged germination period lasting several years. Many of its seeds discovered possessed this hard endocarp and were determined to be one or more years old. Interestingly, seedlings were not found in close proximity to the individual plants, and these trees were not clustered together, suggesting possible seed dispersal by animals. Since most *Elaeocarpus* fruits appear to be edible, it is plausible that seed dispersal occurs through animal consumption. During field visits, monkeys were also observed feeding fruits near the trees indicating the potential for them to contribute to seed dispersal.

The positioning of the nectar gland at the base of the anther serves two purposes: to attract pollinators towards the nectar and to trigger anther dehiscence. The floral structure of the species typically causes the flower to bend downward, with the stigma positioned in a way that encourages self-pollination. However, cross-pollination by pollinators was also observed, suggesting a preference for both self-pollination and cross-pollination. Overall, the *Elaeocarpus* genus appears to exhibit long periods of dormancy due to the hard endocarp, which impedes water absorption and hampers the regeneration of several *Elaeocarpus* species (Mathew 1999).

Based on the outcomes of the investigatory analysis focused on *Elaeocarpus gadgilii* populations, the species has been noted to display subtle morphological modifications as a responsive strategy to changing environmental circumstances, indicative of adaptive traits. The morphometric distinct variation was found between population *E. gadgilii* and was predominant between the populations separated by the gap. Significant disparities have been most prominently identified within the domain of foliar and floral components. Noteworthy distinctions manifest in the dimensions of leaves, wherein the northern population of *Elaeocarpus gadgilii* exhibits elongated and wider leaf structures, a departure from the corresponding attributes observed within populations situated on the southern side of the sky islands. The research conducted by Benavides Coode, Patterson and Garcia-Verdugo (Coode 1984, Patterson and Tanowitz 1989, Benavides *et al*., 2009, Garcia-Verdugo *et al*., 2010) collectively underscores the significance of environmental factors in shaping the morphological and physiological characteristics of plant populations. Their studies illustrated how geographic isolation and environmental conditions play a crucial role in influencing the divergence and heritability of these traits. Coode and Patterson (Coode 1984, Patterson and Tanowitz 1989) further stress the importance of these factors in the evolutionary process and adaptation of plant species. These findings highlight the intricate interplay between genetics and the environment in driving the diversity and adaptation of plant populations.

Since these populations of *Elaeocarpus gadgilii* are situated across sky islands spanning the geographic gap, it becomes an inevitable outcome for the distinctive features of the gap to exert an influence over its populations. In the context of the current study, the influence of gap features like gap distance, wind and associated environmental variables, upon the population inhabiting sky islands across the Palghat Gap has been conclusively demonstrated as significant, particularly in the case of *E.*

gadgilii population in sky islands across Palghat Gap. The significance of gap features on species in specialized habitats, like the sky islands surrounding the Palghat Gap, is notable. Howe and Fahey both stress the importance of gap size and shape in determining how much influence gaps have on tree species and understory plant communities, respectively (Howe 1990, Fahey and Puettmann 2008). This indicates that the specific characteristics of a gap, such as its dimensions and form, can directly affect the species in these habitats. Additionally, Graham and Socha highlighted the role of biomechanics in gap-crossing behaviours, particularly relevant in the context of sky islands (Graham and Socha 2020). Whereas Grant emphasized the impact of ecological change on diversification, a crucial factor in understanding how gap features affect species in these unique habitats (Grant 2003) .

However, it should be noted that the influence of these gap features on *E. gadgilii* does not necessarily imply that the same effects will be observed in all species within the sky islands surrounding the Palghat Gap. The changes induced by gap features will likely be reflected in species that have adaptability. Owing to the distinctive attributes of elevated terrain and insularity characterising sky islands, they exhibit heightened sensitivity to even minor environmental perturbations. Consequently, species dwelling within these specialised habitats are notably responsive even to subtle influences exerted by gap features upon their respective populations. This interplay, in essence, augments the species adaptive capacity and fosters an enhanced proliferation across its population. Several studies support the idea that species residing in specialized habitats, such as sky islands, exhibit increased adaptive capacity and proliferation. The unique evolutionary processes and heightened sensitivity to environmental changes in these habitats are emphasized by both Losos and Watling (Watling and Donnelly 2006, Losos and Ricklefs 2009). Lees and Peres delved into the connection between gap-crossing abilities and species persistence in fragmented landscapes, proposing that adaptability plays a crucial role in species occupancy (Lees and Peres 2009). Eloy de Amorim offers a specific illustration of rapid adaptive changes in lizards on newly created islands, illustrating the potential for species to swiftly adapt to environmental disturbances (Eloy de Amorim *et al*., 2017). Together, these studies highlight the significance of adaptability in species dwelling in specialized habitats and the potential for rapid adaptive changes in response to environmental disruptions.

In case of *E. gadgilii*, the chance of the species expanding its distribution is very high, as they can adapt to adverse environmental changes by introducing mor-

phometric variation at the population level across Palghat Gap is a proven fact. That is if a species can adapt, the chance for its existence is very high, but it relies on the adverse environmental gradient to which it is exposed. In chapter 4 the study dealt with the projection of highly probable habitat-suitable areas of the present species. As per that, it was found that the area that now exists will be unsuitable for its existence in 2100, so its existence in future is unsure. As per the present study, it is proved that the *E. gadgilii* can introduce variation at morphometric levels to cope with small changes in environmental variables. So, the chance of its disappearance is the least and the chance to expand its distribution is very high. But as they are mere predictions, we can't take a chance, as the tolerance level of the species to adapt to environmental changes is not known. As this species faces challenges like delayed germination, hard endocarp, frugivory caused seed damage, and long year of time it takes to mature, raises the chances of its disappearance. One more challenge faced by this species is that as per future ENM prediction depicted in Chapter 4, the present habitat will be least suitable for this *E. gadgilii* to exist. So, the conservation of the population of *E. gadgilii* under the present habitat is very essential, and ex-situ conservation is the most preferential method to conserve the populations of *E. gadgilii*.

The influence of gap features is substantiated at the morphological level as the variation analysis where specifically done across the 30 km wide Palghat Gap. One more thing that needs to put forward is that Palghat Gap features are one of the parameters that affect its population and induced variation. Upon juxtaposing the impacts of both gap features and altitude on *E. gadgilii* populations, it becomes evident that the influence exerted by gap features has outweighed that of altitude. This substantiates the fact that Palghat Gap features affect populations of *E, gadgilii* and gain more importance than other features like altitude. The effect of gap features on the plant species varies, which includes morphological variation, genetic variation or decline in population or extinction. So, the study justifies the fact that geographical factors play a crucial role in shaping intraspecific morphological variability between populations. In recent research Intraspecific variation received inadequate attention in conservation efforts despite its profound impact on ecological processes, species diversity, and ecological stability (Mimura *et al*., 2017). So, the present study raises the importance of intraspecific variability studies.

Human activities, like land use and climate change, further affect intraspecific variation. The study highlights the importance of monitoring intraspecific morpho-

metric variation and its ecological consequences. Additionally, it contributes valuable insights into the population dynamics and adaptation of *E. gadgilii* in the Western Ghats. It underscores the role of mountain gaps in shaping species distributions and genetic diversity, with the Palghat Gap acting as a major barrier. The study enriches our understanding of intraspecific variation and its ecological significance in the Western Ghats region.

This study significantly improves our comprehension of the morphological features and population dynamics of *Elaeocarpus gadgilii* within the sky islands of the Western Ghats. The study's outcomes hold significant scientific value and have direct implications for conservation initiatives, highlighting the crucial role of preserving the diverse and distinct traits present in various geographical areas. These variations play a vital role in the processes of speciation and biodiversity preservation, underscoring the urgency of conserving the wild varieties of this species.

5.4. Conclusions

The present chapter is focused on intraspecific variability in *E. gadgilii* populations present within and between the sky islands of the Western Ghats across the Palghat Gap.

As per the intraspecific variation analysis in *E, gadgilii,* the variation in majority of the quantitative and qualitative morphometric parameters of its populations within and between the sky islands across Palghat Gap are found to be statistically significant. Intraspecific variations are a means of local adaptation showing the potential of the species to survive in a heterogeneous environment. The variation was prominent be-tween its population inhabiting in the sky islands on the southern and northern flanks of Palghat Gap. The significant variation at the morphometric level of the species most probably appeared to be in response to the geographic gap features and sky Island's features. This shows that the species is flexible to undergo phenotypic plasticity to survive under the diverse environment of the sky islands.

This study thereby shows that this species capability to adapt to adverse environmental variants are probably very high. This depicts its potential to survive, exist and spread by surpassing natural selection. Even though its risk of loss varies, as each species tolerance level differs. So, the present Intraspecific morphometric variation study done over the populations of *Elaeocarpus gadgilii* showed that the Palghat Gap feature influenced the species of sky islands of Western Ghats across the Palghat Gap.

The findings extrapolated that certain species possess remarkable flexibility to pheotypic plasticity when exposed to environmental shifts and alterations in their habitat. This adaptive prowess allows them to modulate their physical characteristics in a way that reflects the fluctuations in their surrounding environment. The observed morphological variations depict the species capacity to not cope and surpass the challenges posed by environmental change by actively reflecting and responding to changes in their external environment. The strong relationship between the species and its habitat environment is discovered through such intra-specific morphometric variation studies.

CHAPTER 6:
CLIMATE VARIABLES OF SKY ISLANDS IN RELATION TO INTRASPECIFIC MORPHOMETRIC VARIATION OF *ELAEOCARPUS GADGILII* POPULATIONS

CHAPTER 6: - Climate Variables of Sky Islands in Relation to Intraspecific Morphometric Variation of *Elaeocarpus gadgilii* Populations

6.1. Introduction

The diversity and vulnerability of sky islands of the Western Ghats are acknowledged and examined in the context of their susceptibility to the impacts of climate change. These unique ecosystems face a range of risks due to climate change. The rising temperatures hold the potential to alter the vegetation zones situated on the mountains, consequently affecting the species that rely on these specific habitats. The implications of climate change have the potential to amplify these existing threats and may even lead to the extinction of certain species. Overall, the primary driving force behind changes in terrestrial ecosystems is the climate itself (Warshall 1995, IPCC 2022). The elevation related trait variations in plants are mainly influenced by the interaction of climate factors such as rainfall, temperature and dry season length. This dynamic interplay between elevation and climate conditions shape the characteristics of plant populations across different elevational levels. The distribution of rainfall, temperature, and dry periods dictates the types of plants that can thrive in the region, ultimately determining the overall makeup of the local vegetation. The combined insights underscore the intricate relationship between elevation, climate, and vegetation characteristics (Pascal 1982, Rixen *et al*., 2022). It is anticipated that there exists a high impact of climate change in elevated areas. This assertion underscores the concept that as altitude rises, the effects of climate change will become more pronounced. This phenomenon is likely due to the increased susceptibility of high-altitude ecosystems to alterations in temperature, patterns of precipitation, and various other influencing factors (McCarthey *et al*., 2001).

The fundamental catalyst for climate change is the escalation in CO_2 concentration, which results in high temperatures and subsequent modifications in diverse climatic elements. These impacted elements encompass atmospheric water vapour, tropospheric lapse rate, surface albedo (owing to shifts in ice, snow, and clouds), along biogeochemical cycling (Arora *et al*., 2020). Climate characteristics can be categorised into two main types: climate variables and bioclimatic variables. These serve as indicators of the environmental and physical attributes within specific geographical areas. Although they share certain similarities, distinct differences exist between these concepts. Climate variables predominantly encompass atmospheric attributes such as

temperature, precipitation, wind and atmospheric pressure. These factors are pivotal in comprehending the climatic dynamics of a particular region and are useful for modelling and forecasting long-term weather trends. The Climate is influenced by a combination of internal and external elements like the greenhouse effect and volcanic eruptions. So, to precisely predict the future course of global warming, comprehending the internal variability and its interplay with external factors are essential. This understanding is pivotal in assessing how much external forces will reshape the climate system (Shuman 2012, Trenberth and Fasullo 2013). In contrast, bioclimatic variables are more closely intertwined with the biological state of an area, encapsulating aspects like species distribution, organism growth, and survival. While these variables are often derived from climate variables, they undergo transformation or scaling to better capture their relevance to biological processes. Their focus is on assessing how climatic conditions influence living organisms, spanning both plant life and fauna. Bioclimatic variables offer insights into the enduring average or seasonal climatic conditions of a given location, facilitating a deeper understanding of species distribution, ecological shifts and projections about species reactions to climate alterations. Illustrations of bioclimatic variables encompass the length of the growing season, the annual mean temperature, annual precipitation, and temperature range. Climate variables predominantly address atmospheric attributes, whereas bioclimatic variables are intricately connected to a region's biological conditions. Bioclimatic variables frequently emerge from climate data, yet they are refined or converted to accurately reflect their significance in biological processes. That is the bioclimatic variables are the derived versions of climate variables (Guisan and Zimmermann 2000, Austin 2002, Wang *et al*., 2016, Fick and Hijmans 2017).

The effects of climate change on community structure and ecosystem operation hinge on the adaptive responses of individual organisms to climatic shifts, which manifest as changes in their phenological patterns. Phenology occupies a pivotal position in shaping the interplay between vegetation and the atmosphere, thereby influencing a spectrum of processes encompassing surface albedo, surface texture, canopy behaviour, water and energy dynamics, photosynthesis and CO_2 exchange and the emission of biogenic volatile organic compounds (BVOCs). Phenology, according to the International Biological Program (IBP), is about studying regular biological events and understanding what factors like both living and environmental, affect their timing.

It also explores the connections between different stages in the life cycles of various species, whether they're the same or different (Lieth 1974).

Overall climate change influences the geographical distribution of plant species, either through direct or indirect mechanisms. It is like the reduction in precipitation resulting from climate change decreased water availability in turn resulting in diminished vegetation. This decline in plant cover intensifies the reflection of sunlight (surface albedo) and decreases the emission of water into the atmosphere via plants (evapotranspiration). These alterations weaken atmospheric air circulation, exacerbating the decrease in precipitation within the impacted regions (Zeng *et al*., 1999). These intricate interconnections culminate the outcomes that reverberate throughout the broader climate system (Richardson *et al*., 2013).

In response to unpredictable climate changes, organisms are anticipated to undergo adaptive changes in their morphology or shift to more suitable locations. The observed morphological variations occur along climate gradients, enhancing the adaptive capacity of organisms. These changes can be either temporary, serving the purpose of local persistence or can manifest at the genetic level. The adaptive significance of these variations varies among different species (Peppe *et al*., 2011, Guerin *et al*., 2012).

Climatic conditions are characterised by their inherent unpredictability and substantial sway over biodiversity. Investigating the repercussions of climate on habitats, it becomes apparent that distinct species exhibit a spectrum of responses. While some species manifest adaptability, others undergo transient morphological alterations or confront the peril of extinction. Evaluating a species prospect necessitates the consideration of not only climate variables but also demographic factors and environmental circumstances. For instance, the introduction of an invasive species into a habitat amidst the backdrop of climate change escalates the jeopardy faced by indigenous species survival. A species susceptibility to climate-induced impacts hinges upon an array of interconnected elements. Hence, attributing a species endangerment solely to the impact of climate change does not inherently imply that it is the sole determinant responsible for the species vulnerability (Gidden *et al*., 2019).

So, to study the effect of climate variation, the climate data must be procured and is now available from multiple datasets, among which the CRU-TS dataset stands out. This dataset has been meticulously curated, regularly improved, and maintained with contributions from various funding sources, primarily the Natural Environment

Research Council (NERC) in the United Kingdom and the Department of Energy in the United States. The ongoing support for this dataset is currently extended by the UK National Centre for Atmospheric Science (NCAS), a collaborative institution established by NERC. The CRU-TS 4.06 dataset version (Harris *et al*., 2020), has climate data that spans from 1901 to 2021. The recently introduced interpolation algorithm remains consistent with version 4.03. Notably, the CRU-TS 4.06 dataset has been downscaled and was available within the framework of WorldClim 2.1 (Fick and Hijmans 2017).

The biodiversity-rich tropical rainforests are now facing a significant threat due to anthropogenic climate change. Despite acknowledging this challenge, our understanding on how tropical species might react and modulate their susceptibility to climate change remains constrained. One approach to gauging a species potential for adaptation across diverse climates involves scrutinising intraspecific diversity in traits relevant to climate response. The presence of such trait variation, coupled with its correlation with local climatic conditions, signifies the species ability to accommodate in diverse environments through phenotypic plasticity (Llewelyn *et al*., 2016).

The objective of the study included in the present chapter was to explore intraspecific variation in climate-relevant gradient traits within a rainforest, with the aim of shedding light on its adaptive capacity in the face of varying climatic conditions. Thereby, the present study analyses the climate variables of sky islands within the study area, in different time periods. The variability of climate data of sky islands across Palghat Gap was assessed and the effect of this variation over the sky island inhabiting *E. gadgilii* population was also tested. This study was done to demonstrate the effect of climate change over species inhabiting the sky islands.

6.2. Methodology

Climate data required for the study was sourced from WorldClim and were employed to assess climate conditions and fluctuations across the study area. These data were leveraged to explore the potential ramifications of climate change on populations of *E. gadgilii* found exclusively in sky island habitats. The climate data of locations of sky island from where the populations of *E. gadgilii* collected were considered for the analysis. Here the historical monthly climate data were accessed from the WorldClim framework, and there it was downscaled from the CRU-TS-4.06 dataset.

CRU-TS-4.06 is a creation of the Climatic Research Unit at the University of East Anglia (Fick and Hijmans 2017, Harris *et al*., 2020).

The three key historical monthly climate variables accessible for download from the WorldClim platform were the average minimum temperature (°C), average maximum temperature (°C), and total precipitation (mm). These historical monthly meteorological data were accessible in varying spatial resolutions, namely 2.5 minutes (~21 km² at the equator), 5 minutes (~85 km²), and 10 minutes (~340 km²) (Worldclim 2022).

Within the scope of this study, the 2.5-minute resolution was adopted for analysis, representing the highest available resolution within the WorldClim framework. The climate data procured was a GeoTiff (.tif) files containing weather data for each month throughout the year. The WorldClim website affords access to historical monthly weather data spanning from 1960 to 2021. For the specific objectives of this study, a targeted 12-year timeframe, spanning from 2010 to 2021 was selected. This time frame corresponds to the period during which field data collection was undertaken.

6.2.1. Climate data of sky islands across the Palghat Gap

In the present analysis, instead of conducting a broader analysis of climate patterns, the major focus of this study was to assess the climate of sky islands across the Palghat Gap within the study area. The data extraction procedure specific to each location from where *E. gadgilii* collected was performed using ArcMap 10.8, utilising the extraction-by-point tool from the suite of spatial analytical tools. By employing this approach, the retrieval of climate data values were made possible. Each climate variable's associated data values were systematically gathered and recorded.

The analytical approach adopted here utilised historical monthly weather data extracted from WorldClim, spanning multiple time intervals between 2010 and 2021. The primary aim of this research endeavour revolved around the in-depth examination of climate fluctuations specific to the designated study area encompassing sky islands across the Palghat Gap. To fulfil this goal, climate datasets corresponding to these distinct time periods were procured by retrieving information from the WorldClim repository, renowned for providing historical monthly weather data. This study centres its focus on three pivotal climate variables, average minimum temperature (°C), average maximum temperature (°C) and total precipitation (mm). Specifically, these climate parameters underwent meticulous analysis to discern substantial divergences in cli-

mate patterns existing over the sky islands situated on the northern and southern flanks of the Palghat Gap within the study area. To accomplish this objective, climate data spanning diverse time periods, as well as monthly climatic records for each year, were subjected to analysis in the ArcMap 10.8 platform. This facilitated the extraction of climate data values from specified geographical points. It is noteworthy that this analysis encompassed a selection of 32 specific locations. These locations were precisely chosen as they coincide with the sites from which populations of *Elaeocarpus gadgilii* were collected, forming the foundation for the earlier-mentioned studies.

The spatial analysis was executed within ArcMap, employing the "Extract values to points" tool, to derive climate variables specifically for the previously mentioned 32 locations. Subsequently, these climate data were exported as values to spread sheet and then subjected to further processing in IBM SPSS Version 22.

The statistical analysis was carried out using SPSS, to assess the significance of variance in each climate parameter at significance level of 0.05. Those parameters exhibiting a statistically significant level of variance were selected for subsequent analysis.

The statistical tests, namely the Kruskal-Wallis test and Mann-Whitney U test, were employed here to evaluate the significance of climate variance, at a predetermined significance level of 0.05. The analysis of variance was carried out in two distinct stages. The first set of analyses encompassed all 32 locations, probing into the level of variance within this larger dataset. Here the Kruskal-Wallis test was employed where significant level variance was assessed between each 32 locations. In the second stage of significant level of variance analysis, the Mann-Whitney U test was utilised to evaluate the variance of climate variables between sky islands on the northern and southern side of the Palghat Gap.

6.2.2. Climate factors in relation to the intraspecific morphometric variability of populations of *E. gadgilii.*

Here all the climate data extracted from 32 locations corresponds to the location from where population of *E. gadgilii* was collected. If there is a distinct variation in climate variables of sky islands across Palghat Gap, then the relationship between climate variations and the intraspecific morphometric variations of *E. gadgilii* was evaluated. Climate data pertinent to the specific locations from where the *E. gadgilii* species populations were sampled was extracted and subjected to spatial data analysis.

So as to investigate the potential significant impact of climate on the morphometric variation of *E. gadgilii*, statistical analysis was done.

Climate parameters exhibiting substantial significant variation were subsequently correlated with the morphometric parameters of the species under consideration. Spearman correlation test was conducted at significance levels of $P \leq 0.01$ and $P \leq 0.05$ to determine the associations between each variable and to establish the relation of climate with the species under concern. Thereby to explore the potential links between climate change and intraspecific variability in morphometric parameters of *E. gadgilii*.

6.3. Results and discussion

The focal objective of this chapter was centred around the climate data pertaining to the sky islands located on the northern and southern flanks of the Palghat Gap within the study area. This exploration seeks to establish a link between the climate data and the morphometric variations observed in populations of *E. gadgilii* from sky islands of the Western Ghats across the Palghat Gap.

6.3.1. Climate data of sky islands across the Palghat Gap

The Kruskal-Wallis test results done over the climate variable of 32 location were alike and the results were showing $\chi^2(31) = 31$, $P=0.499$, where the P value was ≥ 0.05, which shows that the level of variance was least significant. Therefore, Kruskal-Wallis test, proved that the significance of variance done at a significance level of 0.05 across all 32 locations, was found to be not statistically significant. This analysis within the sky islands establishes that the variation of climate variables among all locations with in the sky islands of the Western Ghats is deemed insignificant in the case of all three climate variables under consideration (Table 6.1 to 6.3). That is, comparing the climates variable of all the locations, the variability between locations was insignificant. Here the locations considered were from within sky islands and between sky islands and were considered all together as separate samples. This shows there are locations which have similar climate variables so that the variability was insignificant.

For the subsequent set of analysis, the climate data of locations were categorised into two distinct groups, the first group encompassing the locations situated on the sky islands on southern side of the Palghat Gap and the second group from the northern side of Palghat Gap. Then the climate variable data of the two group locations were compared, through IBM SPSS version 22 and the significance of the variance of the

Table 6.1. Kruskal Wallis test statistics analysis done on mean annual total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from 2010-2021, to analyse significant level of variation at 0.05.

Year	Chi-Square	df	Asymp. Sig.
2010	31	31	0.466
2011	31	31	0.466
2012	31	31	0.466
2013	31	31	0.466
2014	31	31	0.466
2015	31	31	0.466
2016	31	31	0.466
2017	31	31	0.466
2018	31	31	0.466
2019	31	31	0.466
2020	31	31	0.466
2021	31	31	0.466

Footnote: Kruskal–Wallis test on Annual Total Precipitation (2010- 2021)

Table 6.2. Kruskal Wallis test statistics analysis on mean annual minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from 2010-2021, to analyse significant level of variation at 0.05.

Year	Chi-Square	Df	Asymp. Sig.
2010	31	31	0.466
2011	31	31	0.466
2012	31	31	0.466
2013	31	31	0.466
2014	31	31	0.466
2015	31	31	0.466
2016	31	31	0.466
2017	31	31	0.466
2018	31	31	0.466
2019	31	31	0.466
2020	31	31	0.466
2021	31	31	0.466

Footnote: Kruskal–Wallis test on Annual TMIN (2010- 2021)

Table 6.3. Kruskal Wallis test statistics analysis on mean annual maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from 2010-2021, to analyse significant level of variation at 0.05.

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Year	Chi-Square	Df	Asymp. Sig.
2010	31	31	0.466
2011	31	31	0.466
2012	31	31	0.466
2013	31	31	0.466
2014	31	31	0.466
2015	31	31	0.466
2016	31	31	0.466
2017	31	31	0.466
2018	31	31	0.466
2019	31	31	0.466
2020	31	31	0.466
2021	31	31	0.466

Footnote: Kruskal–Wallis test on Annual TMAX (2010-2021)

Table 6.4. Mann-Whitney U test statistics analysis on mean annual total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from 2010-2021, to analyse significant level of variation at 0.05.

Year	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
2010	0	136	-5.01	0
2011	0	136	-4.824	0
2012	0	136	-4.824	0
2013	0	136	-5.01	0
2014	0	136	-5.01	0
2015	0	136	-5.01	0
2016	0	136	-5.01	0
2017	0	136	-5.01	0
2018	0	136	-5.01	0
2019	0	136	-4.911	0
2020	0	136	-5.01	0
2021	0	136	-5.01	0

Footnote: Mann–Whitney U test on Annual Total Precipitation (2010-2021)

Table 6.5. Mann-Whitney U test statistics analysis on mean annual minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from 2010-2021, to analyse significant level of variation at 0.05.

Year	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
2010	98	234	-1.191	0.233
2011	92	228	-1.409	0.159
2012	98	234	-1.177	0.239
2013	86	222	-1.645	0.1
2014	94	230	-1.331	0.183
2015	97	233	-1.234	0.217
2016	93	229	-1.387	0.165
2017	98	234	-1.177	0.239
2018	88	224	-1.569	0.117
2019	90	226	-1.491	0.136
2020	102	238	-1.018	0.309
2021	90	226	-1.491	0.136

Footnote: Mann–Whitney U test on Annual TMIN (2010-2021)

Table 6.6. Mann-Whitney U test statistics analysis on mean annual maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from 2010-2021, to analyse significant level of variation at 0.05.

Year	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
2010	86	222	-1.633	0.103
2011	82	218	-1.802	0.071
2012	124	260	-0.151	0.88
2013	82	218	-1.801	0.072
2014	82	218	-1.801	0.072
2015	82	218	-1.802	0.071
2016	82	218	-1.802	0.071
2017	82	218	-1.802	0.071
2018	111	247	-0.641	0.522

2019	102.5	238.5	-0.988	0.323
2020	82	218	-1.801	0.072
2021	82	218	-1.801	0.072

Footnote: Mann–Whitney U test on Annual TMAX (2010-2021)

Table 6.7. Mann–Whitney U test statistics analysis on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2010 to December 2010, to analyse significant level of variation at 0.05.

Year	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-10	32	168	-4.247	0
Feb-10	114	250	-0.627	0.53
Mar-10	114	250	-0.627	0.53
Apr-10	112	248	-0.886	0.376
May-10	112	248	-0.886	0.376
Jun-10	112	248	-0.887	0.375
Jul-10	125	261	-0.144	0.886
Aug-10	112	248	-0.887	0.375
Sep-10	51	187	-3.278	0.001
Oct-10	128	264	0	1
Nov-10	56	192	-3.188	0.001
Dec-10	93	229	-1.677	0.094

Footnote: Mann–Whitney U test on Maximum temperature (January 2010-December 2010)

Table 6.8. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2011 to December 2011, to analyse significant level of variation at 0.05.

	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-11	93	229	-1.677	0.094
Feb-11	114	250	-0.627	0.53
Mar-11	114	250	-0.627	0.53
Apr-11	46	182	-3.395	0.001
May-11	51	187	-3.278	0.001
Jun-11	112	248	-0.887	0.375
Jul-11	128	264	0	1
Aug-11	109	245	-0.859	0.391
Sep-11	51	187	-3.278	0.001
Oct-11	51	187	-3.278	0.001
Nov-11	56	192	-3.188	0.001
Dec-11	56	192	-3.188	0.001

Footnote: Mann–Whitney U test on Maximum temperature (January 2011-December 2011)

Table 6.9. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2012 to December 2012, to analyse significant level of variation at 0.05.

Year 2012	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-12	93	229	-1.677	0.094
Feb-12	128	264	0	1
Mar-12	114	250	-0.627	0.53

Apr-12	46	182	-3.395	0.001
May-12	112	248	-0.887	0.375
Jun-12	119	255	-0.471	0.638
Jul-12	49	185	-2.977	0.003
Aug-12	119	255	-0.471	0.638
Sep-12	112	248	-0.887	0.375
Oct-12	112	248	-0.887	0.375
Nov-12	128	264	0	1
Dec-12	128	264	0	1

Footnote: Mann–Whitney U test on Average Maximum temperature (January 2012-December 2012)

Table 6.10. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2013 to December 2013, to analyse significant level of variation at 0.05.

Year 2013	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-13	109	245	-0.859	0.391
Feb-13	128	264	0	1
Mar-13	114	250	-0.627	0.53
Apr-13	112	248	-0.887	0.375
May-13	112	248	-0.887	0.375
Jun-13	119	255	-0.471	0.638
Jul-13	119	255	-0.471	0.638
Aug-13	128	264	0	1
Sep-13	125	261	-0.144	0.886
Oct-13	119	255	-0.471	0.638
Nov-13	128	264	0	1
Dec-13	67	203	-2.654	0.008

Footnote: Mann–Whitney U test on Maximum temperature (January 2013-December 2013)

Table 6.11. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2014 to December 2014, to analyse significant level of variation at 0.05.

Year 2014	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-14	93	229	-1.677	0.094
Feb-14	114	250	-0.627	0.53
Mar-14	114	250	-0.627	0.53
Apr-14	46	182	-3.395	0.001
May-14	46	182	-3.395	0.001
Jun-14	51	187	-3.278	0.001
Jul-14	109	245	-0.859	0.391
Aug-14	119	255	-0.471	0.638
Sep-14	112	248	-0.887	0.375
Oct-14	128	264	0	1
Nov-14	109	245	-0.859	0.391
Dec-14	67	203	-2.654	0.008

Footnote: Mann–Whitney U test on Maximum temperature (January 2014-December 2014)

Table 6.12. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2015 to December 2015, to analyse significant level of variation at 0.05.

Year 2015	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-15	93	229	-1.677	0.094
Feb-15	114	250	-0.627	0.53
Mar-15	114	250	-0.627	0.53
Apr-15	112	248	-0.886	0.376
May-15	51	187	-3.278	0.001
Jun-15	112	248	-0.887	0.375
Jul-15	125	261	-0.144	0.886
Aug-15	51	187	-3.278	0.001
Sep-15	112	248	-0.887	0.375
Oct-15	109	245	-0.859	0.391
Nov-15	56	192	-3.188	0.001
Dec-15	93	229	-1.677	0.094

Footnote: Mann–Whitney U test on Maximum temperature (January 2015-December 2015)

Table 6.13. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2016 to December 2016, to analyse significant level of variation at 0.05.

Year 2016	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-16	128	264	0	1
Feb-16	114	250	-0.627	0.53
Mar-16	114	250	-0.627	0.53
Apr-16	51	187	-3.278	0.001
May-16	112	248	-0.887	0.375
Jun-16	51	187	-3.278	0.001
Jul-16	128	264	0	1
Aug-16	128	264	0	1
Sep-16	112	248	-0.887	0.375
Oct-16	51	187	-3.278	0.001
Nov-16	56	192	-3.188	0.001
Dec-16	128	264	0	1

Footnote: Mann–Whitney U test on Maximum temperature (January 2016-December 2016)

Table 6.14. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2017 to December 2017, to analyse significant level of variation at 0.05.

Year 2017	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-17	93	229	-1.677	0.094
Feb-17	114	250	-0.627	0.53
Mar-17	114	250	-0.627	0.53
Apr-17	112	248	-0.886	0.376
May-17	112	248	-0.887	0.375
Jun-17	112	248	-0.887	0.375

Jul-17	125	261	-0.144	0.886
Aug-17	125	261	-0.144	0.886
Sep-17	51	187	-3.278	0.001
Oct-17	51	187	-3.278	0.001
Nov-17	56	192	-3.188	0.001
Dec-17	128	264	0	1

Footnote: Mann–Whitney U test on Maximum temperature (January 2017-December 2017)

Table 6.15. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2018 to December 2018, to analyse significant level of variation at 0.05.

Year 2018	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-18	93	229	-1.677	0.094
Feb-18	128	264	0	1
Mar-18	114	250	-0.627	0.53
Apr-18	51	187	-3.278	0.001
May-18	114	250	-0.627	0.53
Jun-18	21	157	-4.033	0
Jul-18	128	264	0	1
Aug-18	119	255	-0.471	0.638
Sep-18	118	254	-0.521	0.602
Oct-18	119	255	-0.471	0.638
Nov-18	128	264	0	1
Dec-18	93	229	-1.677	0.094

Footnote: Mann–Whitney U test on Maximum temperature (January 2018-December 2018)

Table 6.16. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2019 to December 2019, to analyse significant level of variation at 0.05

Year 2019	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-19	93	229	-1.677	0.094
Feb-19	114	250	-0.627	0.53
Mar-19	51	187	-3.278	0.001
Apr-19	114	250	-0.627	0.53
May-19	125	261	-0.144	0.886
Jun-19	51	187	-3.278	0.001
Jul-19	109	245	-0.859	0.391
Aug-19	114	250	-0.627	0.53
Sep-19	51	187	-3.278	0.001
Oct-19	40.5	176.5	-3.564	0
Nov-19	109	245	-0.859	0.391
Dec-19	93	229	-1.677	0.094

Footnote: Mann–Whitney U test on Maximum temperature (January 2019-December 2019)

Table 6.17. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2020 to December 2020, to analyse significant level of variation at 0.05.

Year 2020	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-20	93	229	-1.677	0.094
Feb-20	114	250	-0.627	0.53
Mar-20	112	248	-0.887	0.375
Apr-20	46	182	-3.395	0.001
May-20	112	248	-0.886	0.376
Jun-20	119	255	-0.471	0.638
Jul-20	51	187	-3.278	0.001
Aug-20	114	250	-0.627	0.53
Sep-20	51	187	-3.278	0.001
Oct-20	109	245	-0.859	0.391
Nov-20	128	264	0	1
Dec-20	128	264	0	1

Footnote: Mann–Whitney U test on Maximum temperature (January 2020-December 2020)

Table 6.18. Mann–Whitney U test statistics on mean monthly maximum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2021 to December 2021, to analyse significant level of variation at 0.05.

Year 2021	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-21	109	245	-0.859	0.391
Feb-21	114	250	-0.627	0.53
Mar-21	51	187	-3.278	0.001
Apr-21	51	187	-3.278	0.001
May-21	114	250	-0.627	0.53
Jun-21	119	255	-0.471	0.638
Jul-21	128	264	0	1
Aug-21	114	250	-0.627	0.53
Sep-21	112	248	-0.887	0.375
Oct-21	109	245	-0.859	0.391
Nov-21	109	245	-0.859	0.391
Dec-21	128	264	0	1

Footnote: Mann–Whitney U test on Maximum temperature (January 2021-December 2021)

Table 6.19. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2010 to December 2010, to analyse significant level of variation at 0.05.

Year 2010	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-10	105	241	-1.714	0.086
Feb-10	105	241	-1.714	0.086
Mar-10	93	229	-1.677	0.094
Apr-10	56	192	-3.188	0.001
May-10	56	192	-3.188	0.001
Jun-10	120	256	-0.387	0.699
Jul-10	56	192	-3.188	0.001
Aug-10	56	192	-3.188	0.001
Sep-10	112	248	-1.438	0.151
Oct-10	67	203	-2.654	0.008

Nov-10	93	229	-1.677	0.094
Dec-10	83	219	-1.916	0.055

Footnote: Mann–Whitney U test on Average Minimum temperature (January 2010-December 2010)

Table 6.20. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2011 to December 2011, to analyse significant level of variation at 0.05.

Year 2011	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-11	77	213	-2.667	0.008
Feb-11	93	229	-1.677	0.094
Mar-11	93	229	-1.677	0.094
Apr-11	109	245	-0.859	0.391
May-11	128	264	0	1
Jun-11	120	256	-0.387	0.699
Jul-11	112	248	-1.438	0.151
Aug-11	128	264	0	1
Sep-11	128	264	0	1
Oct-11	56	192	-3.188	0.001
Nov-11	93	229	-1.677	0.094
Dec-11	105	241	-1.714	0.086

Footnote: Mann–Whitney U test on Average Minimum temperature (January 2011-December 2011)

Table 6.21. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2012 to December 2012, to analyse significant level of variation at 0.05.

Year 2012	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-12	77	213	-2.667	0.008
Feb-12	67	203	-2.654	0.008
Mar-12	67	203	-2.654	0.008
Apr-12	109	245	-0.859	0.391
May-12	56	192	-3.188	0.001
Jun-12	56	192	-3.188	0.001
Jul-12	119	255	-0.471	0.638
Aug-12	128	264	0	1
Sep-12	109	245	-0.859	0.391
Oct-12	56	192	-3.188	0.001
Nov-12	56	192	-3.188	0.001
Dec-12	77	213	-2.667	0.008

Footnote: Mann–Whitney U test on Average Minimum temperature (January 2012-December 2012)

Table 6.22. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2013 to December 2013, to analyse significant level of variation at 0. 05.

Year 2013	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)

Jan-13	67	203	-2.654	0.008
Feb-13	67	203	-2.654	0.008
Mar-13	109	245	-0.859	0.391
Apr-13	67	203	-2.654	0.008
May-13	67	203	-2.654	0.008
Jun-13	56	192	-3.188	0.001
Jul-13	119	255	-0.471	0.638
Aug-13	56	192	-3.188	0.001
Sep-13	56	192	-3.188	0.001
Oct-13	56	192	-3.188	0.001
Nov-13	56	192	-3.188	0.001
Dec-13	105	241	-1.714	0.086

Footnote: Mann–Whitney U test on Average Minimum temperature (January 2013-December 2013)

Table 6.23. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2014 to December 2014, to analyse significant level of variation at 0.05.

Year 2014	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-14	77	213	-2.667	0.008
Feb-14	83	219	-1.916	0.055
Mar-14	93	229	-1.677	0.094
Apr-14	109	245	-0.859	0.391
May-14	109	245	-0.859	0.391
Jun-14	121	257	-0.418	0.676
Jul-14	104	240	-1.438	0.151
Aug-14	128	264	0	1
Sep-14	119	255	-0.471	0.638
Oct-14	121	257	-0.418	0.676
Nov-14	105	241	-1.714	0.086
Dec-14	105	241	-1.714	0.086

Footnote: Mann–Whitney U test on Average Maximum temperature (January 2014-December 2014)

Table 6.24. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2015 to December 2015, to analyse significant level of variation at 0.05.

Year 2015	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-15	77	213	-2.667	0.008
Feb-15	93	229	-1.677	0.094
Mar-15	93	229	-1.677	0.094
Apr-15	67	203	-2.654	0.008
May-15	128	264	0	1
Jun-15	120	256	-0.387	0.699
Jul-15	56	192	-3.188	0.001
Aug-15	56	192	-3.188	0.001
Sep-15	56	192	-3.188	0.001
Oct-15	56	192	-3.188	0.001
Nov-15	93	229	-1.677	0.094
Dec-15	83	219	-1.916	0.055

Footnote: Mann–Whitney U test on Average Minimum temperature (January 2015-December 2015)

Table 6.25. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2016 to December 2016, to analyse significant level of variation at 0.05.

Year 2016	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-16	105	241	-1.714	0.086
Feb-16	93	229	-1.677	0.094
Mar-16	93	229	-1.677	0.094
Apr-16	121	257	-0.418	0.676
May-16	67	203	-2.654	0.008
Jun-16	128	264	0	1
Jul-16	128	264	0	1
Aug-16	56	192	-3.188	0.001
Sep-16	109	245	-0.859	0.391
Oct-16	112	248	-1.438	0.151
Nov-16	83	219	-1.916	0.055
Dec-16	77	213	-2.667	0.008

Footnote: Mann–Whitney U test on Average Minimum temperature (January 2016-December 2016)

Table 6. 26. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2017 to December 2017 to analyse significant level of variation at 0.05.

Year 2017	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-17	83	219	-1.916	0.055
Feb-17	83	219	-1.916	0.055
Mar-17	109	245	-0.859	0.391
Apr-17	56	192	-3.188	0.001
May-17	56	192	-3.188	0.001
Jun-17	120	256	-0.387	0.699
Jul-17	120	256	-0.387	0.699
Aug-17	24	160	-4.533	0
Sep-17	112	248	-1.438	0.151
Oct-17	56	192	-3.188	0.001
Nov-17	67	203	-2.654	0.008
Dec-17	77	213	-2.667	0.008

Footnote: Mann–Whitney U test on Minimum temperature (January 2017-December 2017)

Table 6.27. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2018 to December 2018, to analyse significant level of variation at 0.05.

Year 2018	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-18	77	213	-2.667	0.008

Feb-18	67	203	-2.654	0.008
Mar-18	109	245	-0.859	0.391
Apr-18	119	255	-0.471	0.638
May-18	56	192	-3.188	0.001
Jun-18	121	257	-0.418	0.676
Jul-18	128	264	0	1
Aug-18	128	264	0	1
Sep-18	56	192	-3.188	0.001
Oct-18	56	192	-3.188	0.001
Nov-18	56	192	-3.188	0.001
Dec-18	67	203	-2.654	0.008

Footnote: Mann–Whitney U test on Minimum temperature (January 2018-December 2018)

Table 6.28. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2019 to December 2019, to analyse significant level of variation at 0.05.

Year 2019	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-19	77	213	-2.667	0.008
Feb-19	105	241	-1.714	0.086
Mar-19	67	203	-2.654	0.008
Apr-19	56	192	-3.188	0.001
May-19	56	192	-3.188	0.001
Jun-19	121	257	-0.418	0.676
Jul-19	104	240	-1.438	0.151
Aug-19	119	255	-0.471	0.638
Sep-20	121	257	-0.418	0.676
Oct-19	112	248	-1.438	0.151
Nov-19	105	241	-1.714	0.086
Dec-19	83	219	-1.916	0.055

Footnote: Mann–Whitney U test on Minimum temperature (January 2019-December 2019)

Table 6.29. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2020 to December 2020, to analyse significant level of variation at 0.05.

Year 2020	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-20	77	213	-2.667	0.008
Feb-20	93	229	-1.677	0.094
Mar-20	56	192	-3.188	0.001
Apr-20	67	203	-2.654	0.008
May-20	56	192	-3.188	0.001
Jun-20	56	192	-3.188	0.001
Jul-20	56	192	-3.188	0.001
Aug-20	119	255	-0.471	0.638
Sep-20	56	192	-3.188	0.001
Oct-20	56	192	-3.188	0.001
Nov-20	56	192	-3.188	0.001
Dec-20	77	213	-2.667	0.008

Footnote: Mann–Whitney U test on Minimum temperature (January 2020-December 2020)

Table 6.30. Mann–Whitney U test statistics on mean monthly minimum temperature of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2021 to December 2021, to analyse significant level of variation at 0.05.

Year 2021	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-21	67	203	-2.654	0.008
Feb-21	83	219	-1.916	0.055
Mar-21	67	203	-2.654	0.008
Apr-21	119	255	-0.471	0.638
May-21	56	192	-3.188	0.001
Jun-21	56	192	-3.188	0.001
Jul-21	128	264	0	1
Aug-21	119	255	-0.471	0.638
Sep-21	109	245	-0.859	0.391
Oct-21	56	192	-3.188	0.001
Nov-21	105	241	-1.714	0.086
Dec-21	77	213	-2.667	0.008

Footnote: Mann–Whitney U test on Average Minimum temperature (January 2021-December 2021)

Table 6.31. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2010 to December 2010, to analyse significant level of variation at 0.05.

Year 2010	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-10	0	136	-5.014	0
Feb-10	0	136	-5.01	0
Mar-10	0	136	-5.047	0
Apr-10	0	136	-5.01	0
May-10	0	136	-5.01	0
Jun-10	0	136	-5.01	0
Jul-10	0	136	-5.01	0
Aug-10	0	136	-5.01	0
Sep-10	0	136	-5.01	0
Oct-10	0	136	-5.01	0
Nov-10	0	136	-5.01	0
Dec-10	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2010-December 2010)

Table 6.32. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2011 to December 2011, to analyse significant level of variation at 0.05.

Year 2011	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-11	0	136	-5.014	0
Feb-11	0	136	-5.182	0
Mar-11	0	136	-5.014	0
Apr-11	0	136	-5.01	0
May-11	0	136	-5.01	0
Jun-11	0	136	-5.01	0
Jul-11	0	136	-5.01	0

Aug-11	96	232	-1.253	0.21
Sep-11	0	136	-5.01	0
Oct-11	110	246	-0.705	0.481
Nov-11	0	136	-5.01	0
Dec-11	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2011-December 2011)

Table 6.33. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2012 to December 2012, to analyse significant level of variation at 0.05.

Year 2012	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-12	0	136	-5.014	0
Feb-12	0	136	-5.01	0
Mar-12	0	136	-5.01	0
Apr-12	0	136	-5.01	0
May-12	12	148	-4.541	0
Jun-12	0	136	-5.01	0
Jul-12	0	136	-5.01	0
Aug-12	110	246	-0.705	0.481
Sep-12	0	136	-5.01	0
Oct-12	0	136	-5.01	0
Nov-12	0	136	-5.01	0
Dec-12	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2012-December 2012)

Table 6.34. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2013 to December 2013, to analyse significant level of variation at 0.05.

Year 2013	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-13	0	136	-5.014	0
Feb-13	0	136	-5.071	0
Mar-13	0	136	-5.01	0
Apr-13	0	136	-5.182	0
May-13	110	246	-0.705	0.481
Jun-13	0	136	-5.01	0
Jul-13	0	136	-5.01	0
Aug-13	0	136	-5.01	0
Sep-13	96	232	-1.253	0.21
Oct-13	0	136	-5.01	0
Nov-13	0	136	-5.01	0
Dec-13	0	136	-5.071	0

Footnote: Mann–Whitney U test on Total precipitation (January 2013-December 2013)

Table 6.35. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2014 to December 2014, to analyse significant level of variation at 0.05.

Year 2014	Mann-Whitney U	Wilcoxon	Z	Asymp. Sig. (2-tailed)

		W		
Jan-14	0	136	-5.01	0
Feb-14	0	136	-5.249	0
Mar-14	0	136	-5.014	0
Apr-14	0	136	-5.01	0
May-14	0	136	-5.01	0
Jun-14	110	246	-0.705	0.481
Jul-14	0	136	-5.01	0
Aug-14	110	246	-0.705	0.481
Sep-14	110	246	-0.705	0.481
Oct-14	110	246	-0.705	0.481
Nov-14	0	136	-5.01	0
Dec-14	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2014-December 2014)

Table 6.36. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of Palghat Gap from January 2015 to December 2015, to analyse significant level of variation at 0.05

Year 2015	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-15	20	156	-4.228	0
Feb-15	0	136	-5.01	0
Mar-15	0	136	-5.01	0
Apr-15	0	136	-5.01	0
May-15	0	136	-5.01	0
Jun-15	0	136	-5.01	0
Jul-15	0	136	-5.01	0
Aug-15	0	136	-5.01	0
Sep-15	0	136	-5.01	0
Oct-15	0	136	-5.01	0
Nov-15	2	138	-4.932	0
Dec-15	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2015-December 2015)

Table 6.37. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2016 to December 2016, to analyse significant level of variation at 0.05.

Year 2016	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-16	3	139	-4.894	0
Feb-16	0	136	-5.249	0
Mar-16	0	136	-5.01	0
Apr-16	0	136	-5.01	0
May-16	0	136	-5.01	0
Jun-16	0	136	-5.01	0
Jul-16	110	246	-0.705	0.481
Aug-16	110	246	-0.705	0.481

Sep-16	0	136	-5.01	0
Oct-16	0	136	-5.01	0
Nov-16	0	136	-5.01	0
Dec-16	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2016-December 2016)

Table 6.38. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2017 to December 2017, to analyse significant level of variation at 0.05.

Year 2017	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-17	0	136	-5.01	0
Feb-17	0	136	-5.071	0
Mar-17	0	136	-5.014	0
Apr-17	0	136	-5.01	0
May-17	74	210	-2.114	0.035
Jun-17	0	136	-5.01	0
Jul-17	0	136	-5.01	0
Aug-17	0	136	-5.01	0
Sep-17	0	136	-5.01	0
Oct-17	8	128	-4.589	0
Nov-17	0	136	-5.043	0
Dec-17	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2017-December 2017)

Table 6.39. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2018 to December 2018, to analyse significant level of variation at 0.05.

Year 2018	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-18	0	136	-5.076	0
Feb-18	0	136	-5.01	0
Mar-18	0	136	-5.01	0
Apr-18	0	136	-5.01	0
May-18	0	136	-5.01	0
Jun-18	0	136	-5.01	0
Jul-18	0	136	-5.01	0
Aug-18	0	136	-5.01	0
Sep-18	0	136	-5.01	0
Oct-18	0	136	-5.01	0
Nov-18	0	136	-5.01	0
Dec-18	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2018-December 2018)

Table 6.40. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2019 to December 2019, to analyse significant level of variation at 0.05.

Year 2019	**Mann-Whitney U**	**Wilcoxon W**	**Z**	**Asymp. Sig. (2-tailed)**
Jan-19	0	136	-5.071	0
Feb-19	0	136	-5.071	0
Mar-19	0	136	-5.01	0
Apr-19	88	224	-2.085	0.037
May-19	110	246	-0.705	0.481
Jun-19	0	136	-5.01	0
Jul-19	0	136	-5.01	0
Aug-19	0	136	-5.01	0
Sep-19	0	136	-5.01	0
Oct-19	0	136	-5.01	0
Nov-19	0	136	-5.01	0
Dec-19	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2019-December 2019)

Table 6.41. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2020 to December 2020, to analyse significant level of variation at 0.05.

Year 2020	**Mann-Whitney U**	**Wilcoxon W**	**Z**	**Asymp. Sig. (2-tailed)**
Jan-20	0	136	-5.01	0
Feb-20	0	136	-5.071	0
Mar-20	0	136	-5.01	0
Apr-20	0	136	-5.01	0
May-20	0	136	-5.01	0
Jun-20	0	136	-5.01	0
Jul-20	0	136	-5.01	0
Aug-20	0	136	-5.01	0
Sep-20	0	136	-5.01	0
Oct-20	0	136	-5.01	0
Nov-20	0	136	-5.01	0
Dec-20	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2020-December 2020)

Table 6.42. Mann–Whitney U test statistics on mean monthly total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from January 2021-December 2021, to analyse significant level of variation at 0.05.

Year 2021	Mann-Whitney U	Wilcoxon W	Z	Asymp. Sig. (2-tailed)
Jan-21	0	136	-5.01	0
Feb-21	0	136	-5.01	0
Mar-21	0	136	-5.01	0
Apr-21	0	136	-5.01	0
May-21	0	136	-5.01	0
Jun-21	0	136	-5.01	0

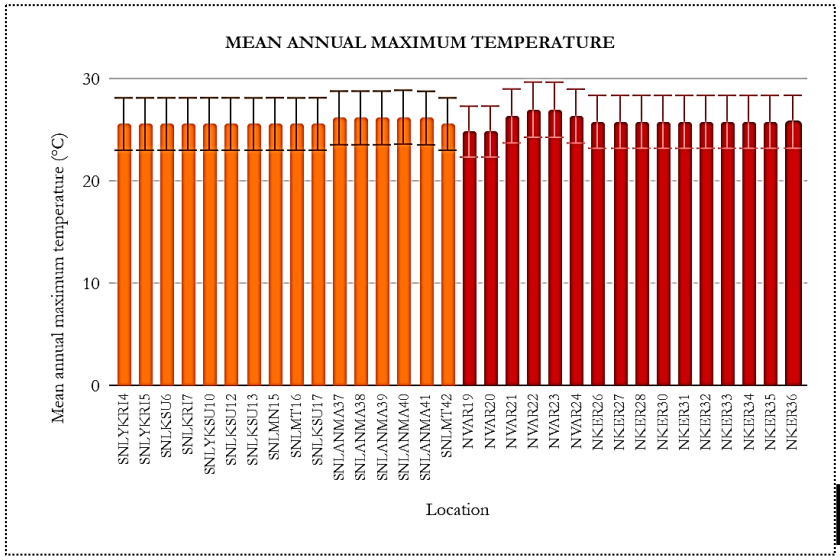
Jul-21	0	136	-5.01	0
Aug-21	0	136	-5.01	0
Sep-21	0	136	-5.01	0
Oct-21	110	246	-0.705	0.481
Nov-21	0	136	-5.01	0
Dec-21	0	136	-5.01	0

Footnote: Mann–Whitney U test on Total precipitation (January 2021-December 2021)

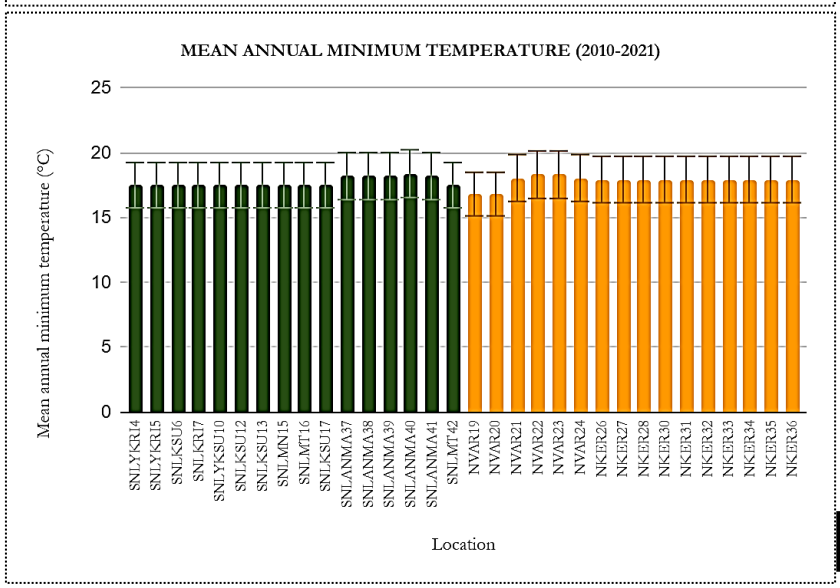
climate variables was assessed by the Mann-Whitney U test at the significance level of 0.05. Here the analysis was done over 12 years mean annual climate data (Table 6.4 – 6.6), and each year's monthly climate data (Table 6.7-6.42).

Here the climate variables were analysed specifically for comparing the climate of the sky islands of the Western Ghats on the southern and northern sides of the Palghat Gap. Where the level of variance was examined using the Mann-Whitney U test. According to the Mann-Whitney U test results, two variables annual maximum temperature and annual minimum temperature didn't show significant level variation across the Palghat Gap, as the P value was greater than 0.05 (Plate 6.1 a & b), (Table 6.5-6.30).The other climate variable, that is the total precipitation, including the annual total precipitation and monthly total precipitation, displayed a significant level of variation across the Palghat Gap at a significance level of 0.05. The test statistics revealed U = 0, W = 136, and a p-value of 0.000, where $P<0.05$ indicates a statistically significant level of variance over the sky islands across Palghat Gap (Table No: 6.4, 6.31 to 6.42). The significant level of variance of all three climate variables is depicted graphically (Plate 6.1), where only the climate variable precipitation (Plate 6.1c) showed a significant level of variance across the Palghat Gap.

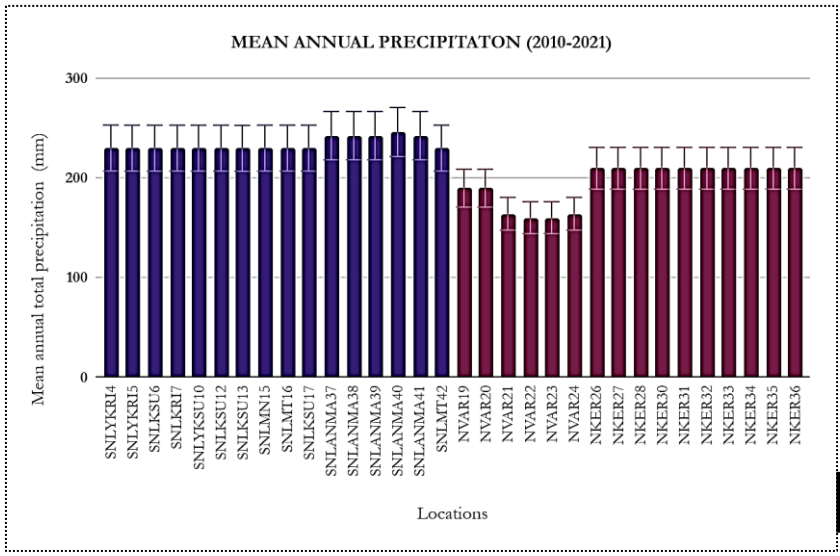
As per the climate data analysis over Annual and Monthly precipitation revealed that the precipitation received over the sky islands on the northern side was much less than that received over the sky islands on the southern sides. This result clearly goes along with the fact that the Western Ghats precipitation depends on the South-West monsoon, that is the southernmost side received more rainfall than the sky islands on the northern side (Pascal 1988). The Western Ghats receive substantial rainfall due to their unique position with respect to the low-level jet stream and the onset of the southwest monsoon. The observed patterns of rainfall in the northern and southern Western Ghats which peaks in low elevated areas and high inter-annual variability, are found to be influenced by various factors like orographic effects and local wind



a



b



c

Plate 6.1: Comparing the Mean annual climate data of sky islands of the Western Ghats across Palghat Gap within the study area, from 2010-2021: a. Annual average maximum temperature (2010-2021), b. Annual average minimum temperature (2010-2021), c. Annual total precipitation (2010-2021).

patterns. Monitoring these rainfall changes are essential for assessing regional climate variations and their potential impacts on the environment and society (Varikoden *et al*., 2019). The spatial distribution of monsoon rainfall in the Western Ghats was found to be influenced by its topography, therefore the study confirms that the orographic precipitation is primarily influenced by the topographic characteristics of mountain barrier's, including the steepness of the windward side slope and the altitude of the mountains. These findings indicate that areas with longer and broader cascaded topography, elevated summits and gradually increasing slopes experience greater enhancement in precipitation due to the orographic effect (Tawde and Singh 2015). The other two climate variables average maximum temperature (Table No: 6.6 and 6.7 to 6.18) (Plate 6.1 a) and average minimum temperature (Table No: 6.5 and 6.19 to 6.30) (Plate 6.1b), were found to be varied, but this variance was not significant across Palghat Gap as $P>0.05$.

The Western Ghats, renowned for its abundant biodiversity, which bears diverse range of plant formations are found to be influenced by factors like precipitation, topography, and geological history (Nayar 1996). This study reinforces the pivotal role of precipitation on the biodiversity of the Western Ghats. This region stands out for its distinct assemblage of species that are unique and indigenous to this specific geographic area (MacKinnon and MacKinnon 1986, Ramesh *et al*., 1991). This underscores the significance of climate variability in shaping species distribution and diversity. In light of this, the present study delved into the substantial annual and monthly precipitation variability across the geographical gap, revealing its noteworthy nature. This heightened the probability of Influence of precipitation over species in sky islands across the gap.

6.3.2. Climate factors in relation to the intraspecific morphometric variability of populations of *E. gadgilii.*

It's worth noting that among the climate variables of sky islands analysed the annual total precipitation data from the 32 locations of the sky islands of Western Ghats displayed a noteworthy level of variance. Therefore, the precipitation data was only subjected to correlation analysis with the 42 morphometric parameters of the corresponding *E. gadgilii* populations. Here, the spearman correlation analysis was conducted between the annual precipitation data from all 32 locations of sky islands and the 42 morphometric parameters of the *E. gadgilii* populations under study. The outcome of the Spearman correlation analysis revealed that there exists a significant as-

sociation between precipitation and intraspecific morphometric variation of *E. gadgilii*. Here in the correlation analysis, was done with mean annual total precipitation of 12 years from 2010-2021, instead of using monthly-wise climate data during correlation analysis, to get an overall result. The correlation analysis results were clearly depicted in Table 6.43. As per the analysis, there observed a significant negative correlation with some of the morphometric variables of *E. gadgilii*. That is mean annual precipitation of sky islands was found to have significant influence on the intraspecific morphometric variability of this sky island species.

Table 6.43. Spearman correlation of Morphometric parameters of *Elaeocarpus gadgilii* v/s mean annual total precipitation of sky islands of the Western Ghats on northern and southern side of the Palghat Gap from 2010-2021, to analyse significant level of correlation at 0.05 and 0.01.

Spearman Correlation			Average precipitation
Spearman's rho	Average precipitation	Correlation Coefficient	1.000
		Sig. (2-tailed)	
		N	32
	Mature leaf length	Correlation Coefficient	-.180
		Sig. (2-tailed)	.323
		N	32
	Lamina Length	Correlation Coefficient	-.303
		Sig. (2-tailed)	.091
		N	32
	Lamina Breadth at Apex	Correlation Coefficient	-.551**
		Sig. (2-tailed)	.001
		N	32
	Lamina Breadth at Middle	Correlation Coefficient	-.485**
		Sig. (2-tailed)	.005
		N	32
	Lamina Breadth at Base	Correlation Coefficient	-.691**
		Sig. (2-tailed)	.000
		N	32
	Petiole length	Correlation Coefficient	-.458**
		Sig. (2-tailed)	.008
		N	32
	Midvein fork at the length	Correlation Coefficient	-.231
		Sig. (2-tailed)	.203
		N	32
	Domatia length	Correlation Coefficient	.733**
		Sig. (2-tailed)	.000
		N	32
	Domatia breadth	Correlation Coefficient	.585**
		Sig. (2-tailed)	.000
		N	32
	Distance between leaf teeth	Correlation Coefficient	.088
		Sig. (2-tailed)	.634
		N	32
	Distance between vein pairs	Correlation Coefficient	-.017
		Sig. (2-tailed)	.928
		N	32
	Peduncle length	Correlation Coefficient	-.051
		Sig. (2-tailed)	.783
		N	32
	Peduncle width at apex	Correlation Coefficient	-.309

	Sig. (2-tailed)	.085
	N	32
Peduncle width at base	Correlation Coefficient	.103
	Sig. (2-tailed)	.575
	N	32
Number of flowers in each peduncle	Correlation Coefficient	.009
	Sig. (2-tailed)	.961
	N	32
Length between each pedicel	Correlation Coefficient	-.055
	Sig. (2-tailed)	.765
	N	32
Pedicel length	Correlation Coefficient	.160
	Sig. (2-tailed)	.382
	N	32
Pedicel width at middle	Correlation Coefficient	-.171
	Sig. (2-tailed)	.350
	N	32
Floral length	Correlation Coefficient	-.235
	Sig. (2-tailed)	.195
	N	32
Sepal width at apex	Correlation Coefficient	-.169
	Sig. (2-tailed)	.355
	N	32
Sepal length	Correlation Coefficient	-.065
	Sig. (2-tailed)	.726
	N	32
Sepal width at middle	Correlation Coefficient	-.079
	Sig. (2-tailed)	.669
	N	32
Sepal width at base	Correlation Coefficient	-.115
	Sig. (2-tailed)	.531
	N	32
Petal width at undivided part at apex	Correlation Coefficient	-.224
	Sig. (2-tailed)	.217
	N	32
Petal width at undivided part at middle	Correlation Coefficient	-.010
	Sig. (2-tailed)	.956
	N	32
Petal width at undivided part at base	Correlation Coefficient	.125
	Sig. (2-tailed)	.495
	N	32
Average range of length within one average petal	Correlation Coefficient	-.192
	Sig. (2-tailed)	.292
	N	32
Petal length	Correlation Coefficient	-.323
	Sig. (2-tailed)	.071
	N	32
Major primary number of divisions in each petal	Correlation Coefficient	-.031
	Sig. (2-tailed)	.866
	N	32
Minor tertiary number of divisions in each petal	Correlation Coefficient	.226
	Sig. (2-tailed)	.214
	N	32
Petiole width	Correlation Coefficient	-.336
	Sig. (2-tailed)	.060
	N	32
Petal division length	Correlation Coefficient	-.357*
	Sig. (2-tailed)	.045
	N	32
Number of stamens	Correlation Coefficient	-.382*

	Sig. (2-tailed)	.031
	N	32
Length of stamens	Correlation Coefficient	-.111
	Sig. (2-tailed)	.545
	N	32
Length of filament	Correlation Coefficient	.162
	Sig. (2-tailed)	.376
	N	32
Length of anther	Correlation Coefficient	-.010
	Sig. (2-tailed)	.959
	N	32
Width of filament	Correlation Coefficient	.311
	Sig. (2-tailed)	.084
	N	32
Width of anther	Correlation Coefficient	.004
	Sig. (2-tailed)	.984
	N	32
Number of setae on anther	Correlation Coefficient	.056
	Sig. (2-tailed)	.759
	N	32
Length of setae on anther apices	Correlation Coefficient	-.276
	Sig. (2-tailed)	.127
	N	32
Disk glands length	Correlation Coefficient	-.205
	Sig. (2-tailed)	.260
	N	32
Disks glands breadth	Correlation Coefficient	-.316
	Sig. (2-tailed)	.078
	N	32

**. Correlation is significant at the 0.01 level (2-tailed), *. Correlation is significant at the 0.05 level (2-tailed).

The mean annual precipitation exhibited a significant negative correlation with Lamina breadth at apex, Lamina breadth at middle, Lamina breadth, petiole length, Petal division length and Number of stamens. On the other hand, Domatia length and Domatia breadth displayed a positive correlation with annual total precipitation. These findings underscored influence of precipitation over the sky island species at morphometric level. Therefore, these findings uphold paramount importance in understanding the influence of climate variability on species distribution and diversity within the species of the Western Ghats. The observed significant correlations between annual total precipitation and intraspecific morphometric variability of *E. gadgilii* indicated the role of climate in influencing the characteristics of *Elaeocarpus gadgilii* populations. Such insights assume critical relevance for conservation endeavours, emphasising the necessity of incorporating climate fluctuations into the management and preservation strategies aimed at safeguarding biodiversity within this region.

The precipitation levels in the sky islands on the Southern side were observed to be significantly higher compared to those in the sky islands on the northern side of

Palghat Gap (Plate 6.1c). This discrepancy in precipitation is attributed to various interconnected environmental factors, including edaphic parameters, which in turn, contribute to population-level variations in species. As per the present study, among the three climate variables examined, the total precipitation was the one identified to be the primary driver of the observed intraspecific variation over populations of *E. gadgilii* on the sky islands of the Palghat Gap. That is total precipitation plays a significant role in the intraspecific morphological variability of *E. gadgilii*, but it is not the only factor that contributing to these variations. It is thereby important to understand that the environmental factors are multifaceted in nature and the impact of it on species varies. Therefore, this study hereby provides valuable insights into the ecological dynamics and its complexities on species distribution and adaptation within this unique geographical habitat the sky islands.

Investigating intraspecific variation in functional traits of the species was fundamental to understand species adaptability within its habitat. In order to assess the vulnerability of a widely distributed tree species to shifting environmental dynamics, it becomes imperative to quantify the phenotypic diversity of functional traits across diverse ecological levels. Moreover, the evaluation of the resilience of trait-environment relationships along spatial gradients and in response to annual shifts in weather conditions holds notable importance (Vasey *et al*., 2022). The present study discoveries yielded substantial insights into the realms of ecology and biodiversity conservation within the Western Ghats. Nevertheless, further investigations and continuous monitoring are imperative to attain a more profound comprehension of the intricate interplay linking climate, species dispersion and environmental transformations across temporal dimensions. Changes in climate, both over time and across different areas, are the main factors influencing the variability in plant environments. These climatic changes offer a framework for understanding the recorded variations in vegetation found in palaeoecological data. Climate variation happens at various scales, both in terms of time (temporal) and geographical extent (spatial) (Bartlein 1988).

Species with extensive geographical ranges often showcase heightened intraspecific variability. This variation leads to consistent shifts in phenotypes along environmental gradients, reflecting patterns observed in the broader community. Yet, the pace of intraspecific trait change is typically limited and is attributed to plasticity or adaptive adjustments within populations. This restraint impedes rapid adaptation to envi-

ronmental gradients, contrasting with faster interspecific changes due to community assembly dynamics. In essence, changes in intraspecific phenotypes follow gradient directions and occur more gradually compared to interspecific differences driven by community processes (Sides *et al*., 2014, Zhichao *et al*., 2022). The arrangement and diversity of presently studied taxa of the Western Ghats resulted from complex influences. Historical biogeographic events and past climatic conditions have intricately shaped the spatial distribution and diversity patterns of species in the region. This underscores the significant role of historical processes and climatic variations in shaping the present ecological and evolutionary characteristics of the Western Ghats taxa (Bose *et al*., 2018).

Preserving habitats with diverse small- and medium-scale environmental conditions is pivotal for maintaining substantial intraspecific diversity within local populations (Wellstein *et al*., 2013). In other words, safeguarding environments with varying ecological characteristics is crucial for sustaining meaningful genetic variation within species.

6.4. Conclusions

This chapter dealt with the impact of climate variables on species distribution and intraspecific variability within the sky islands of the Western Ghats. This study was done in association with representative species *E. gadgilii*, that accurately reflect the change in local environment. This allows to investigate the influence of the Palghat Gap features on the species from the sky islands of the Western Ghats in association with climate variability.

The findings demonstrate that climate variables, specifically total precipitation, played a substantial role in shaping intraspecific morphometric variability within *Elaeocarpus gadgilii* populations. This highlight the importance of climate-related factors in variability within this species and gives inference on the impact of climate on species specific adaptation and distribution in sky island separated by the geographical gap. There by the association of the climate with the geographic gap features and other ecological components like the vegetation of the sky islands was inferred. This study justifies the influence of the Palghat Gap on varying climatic conditions of sky islands of Western Ghats and intraspecific variation within biodiversity.

This climate variation has cascading effects on the biodiversity present within the region. For instance, the distribution and amount of precipitation across the Western Ghats are significantly influenced by the presence of the biogeographic gap. The

mechanism of the South-west monsoon leads to differing patterns of rainfall, with the southern Western Ghats receiving more rainfall compared to the northern Western Ghats. This difference in climate conditions is most probably due to the biogeographic gap, which was found to have caused to the establishment of diverse ecological niches and habitats within the Western Ghats. The concept of this study hereby underscores the interdependencies between geographical features, climate patterns and their impact on the biological makeup and diversity of the Western Ghats.

CHAPTER 7:
EDAPHIC FACTORS OF SKY ISLANDS IN RELATION TO INTRASPECIFIC MORPHOMETRIC VARIATION IN *ELAEOCARPUS GADGILII* POPULATIONS IN SKY ISLANDS ACROSS THE PALGHAT GAP

CHAPTER 7: - Edaphic Factors of Sky Islands in relation to Intraspecific Morphometric Variation in *Elaeocarpus gadgilii* Populations in Sky Islands across the Palghat Gap

7.1. Introduction

Plants necessitate a well-balanced supply of micro and macronutrients to achieve optimal growth and productivity. This principle aligns with Liebig's law, also known as the law of the minimum, states that the growth or yield of a system is limited by the nutrient or factor that is in the shortest supply. In other words, even if all other conditions are optimal, the lack of a single essential nutrient or factor will limit the overall productivity of the system. It's like saying a chain is only as strong as its weakest link. This concept is often applied in ecology, and various other fields to understand and improve the conditions for growth and productivity. Maintaining equilibrium among essential nutrients is crucial for effective plant thriving (White *et al*., 2012, Whitcomb *et al*., 2014). Alterations in environmental parameters, such as modifications in soil composition and climatic conditions, evoke noticeable responses in plants, like diverse array of changes in leaf traits. These traits include a spectrum of morphological features like colouration, texture, dimensions and more. The study of leaf morphology assumed to be an essential preliminary step in comprehending the mechanisms through which plants acclimate to shifts in their surroundings (Bussotti *et al*., 2000).

Temperature and precipitation are environment variants directly that influence nutrient transport processes. Elevated temperatures have the potential to enhance nutrient accessibility. However, rapid temperature increase coupled with soil desiccation might impede nutrient movement due to stomatal closure and restricted nutrient flux. The elevated temperatures promote loss of soil organic carbon via wind erosion. In contrast, precipitation can positively impact nutrient availability, by facilitating nutrient flow and absorption. Nonetheless, heightened soil displacement caused by increased precipitation can also result in nutrient leaching (Sun *et al*., 2008, Zougmore *et al*., 2009).

Soil, being an influential component, exerts its influence over all interconnected ecosystems either associated with or dependent upon it. Within the intricate web of an ecosystem, each constituent is interlinked. Edaphic attributes including soil colour,

organic carbon (OC), texture, pH, and electrical conductivity (EC), as well as macro and micronutrients, are the elements that characterise the soil ecosystem (Furtak and Galazka 2019).

The colour of soil plays a pivotal role as an indicative parameter for a multitude of soil attributes. In the context of soil analysis, traditional laboratory methodologies encompass several techniques for assessing soil colour, including pipette, elutriation, decantation and the Munsell colour chart. Soil colour serves as the identifier, offering insights into both its physical traits and chemical composition. The analysis of soil colour provides researchers with valuable perspectives across a spectrum of soil properties, thereby expediting the efficient acquisition of pertinent and substantial soil data (Srivastava *et al*., 2021).

Among the spectrum of techniques utilised for colour detection, the Munsell colour System, developed by artist Albert Henry Munsell, holds notable significance (Cochrane 2014). The Munsell colour system has established itself as a globally recognised standard for colour specification. This system is an extensively adopted method and carries substantial importance across diverse disciplines. Within the Munsell framework, colour is characterised by three primary components: hue, value, and chroma, denoted through an alphanumeric (Nickerson 1946). The matching of Munsell colours between two charts signifies a semblance in at least one variable (Cochrane 2014, Munsell Color 2022). As per various literature, the colour of the soil often found to exhibit a significant correlation with organic carbon (OC), whereas darker hues are indicative of higher OC content (Wills *et al*., 2007).

Soil colours vary significantly, displaying a diverse range of hues such as grey, black, white, red, brown, yellow, and green. Various colours observed in soils arise from a combination of different processes and environmental conditions that the soil undergoes, as well as the mineral composition and the presence of soil organic matter (SOM) in it. Among these factors, the content of organic matter plays a crucial role in determining soil colour. There has been a longstanding association between the darkness of soil colour and the quantity of organic matter present. Typically, darker soil colours are indicative of higher levels of decomposed organic matter, commonly referred to as humus. Humus, being composed of carbon-based polymers, absorbs a wide range of visible light wavelengths, resulting in soils with abundant organic matter appearing dark brown or nearly black in colour (Konen *et al*., 2003, Aitkenhead *et al*., 2013, Vodyanitskii and Savichev 2017).

Soil organic carbon (SOC) plays a crucial role in regulating soil moisture levels, facilitating nutrient uptake, and improving soil structure and fertility through processes such as cation exchange and mineralisation. Moreover, SOC acts as a significant reservoir of carbon dioxide, thereby mitigating the adverse impacts of climate change (Lal 2006, Yu *et al*., 2009). The presence of soil organic carbon is essential for maintaining optimal soil moisture, establishing a critical link between soil and climate dynamics. Decreased moisture levels in the soil can result in reduced transportation of water-soluble nutrients, prompting compensatory root growth as a mechanism to counteract nutrient deficiencies (Barber 1995, Lynch and Brown 2001).

The texture is another important factor that influences the water retention capacity and aeration of the soil and thereby determines how fertile the soil is. Texture analysis can be conducted by using traditional methods or digital soil mapping techniques. Traditional methods tend to be costly and involve heavy collection of a large number of soil samples. On the other hand, digital soil mapping outperforms traditional methods as they can predict soil type or properties by utilising available data such as climate information, land use, land cover and various other factors (Dharumarajan *et al*., 2017, Mahmoudabadi *et al*., 2017). Random forest and Gradient boosting are considered the most effective linear models for making prediction for such purposes (Hengl *et al*., 2017). Soil texture exhibits variation both horizontally and vertically, with differences observed across different depths and surface areas (Malone *et al*., 2009).

The pH of the soil is a crucial soil property that influences the mobility of metal elements within the soil and regulates nutrient availability to plants (Gondal *et al*., 2021, Kicinska *et al*., 2022). Another factor controlling the availability of macro-micro elements to plants is electrical conductivity (EC). Low EC levels can result in nutrient deficiencies and hinder plant growth and development, while high EC levels can impede nutrient uptake by elevating osmotic pressure and inducing salt stress (Nguyen *et al*., 2021). Salt stress caused by high salinity can accelerate leaf ageing, reduce chloroplast and chlorophyll levels (Javadi *et al*., 2020) and ultimately lead to plant mortality. High salinity stress poses challenges for nutrient and water absorption in plants due to decreased water potential in the soil, resulting in water scarcity within plants (Larbi *et al*., 2020).

Plants necessitate approximately 14 vital nutrients for their growth and development, with a specific emphasis on inorganic macronutrients. The 14 mineral nutri-

ents include six macronutrients namely nitrogen (N), phosphorus (P), potassium (K), calcium (Ca), magnesium (Mg), and sulphur (S) and eight micronutrients: boron (B), chlorine (Cl), copper (Cu), iron (Fe), manganese (Mn), molybdenum (Mo), nickel (Ni) and zinc (Zn) (Brady and Weil 2008). The accessibility of nutrients to plants can be influenced by multiple factors, including precipitation, wind, soil pH and soil composition. Under the limited nutrient availability, plants have the capability to modify their morphology in order to enhance nutrient absorption. The key nutrients that plants require are nitrogen (N), phosphorus (P), and potassium (K) commonly referred to as NPK and are called primary macronutrients. S, Ca and Mg are secondary macronutrients as their effect over yield limit was less than primary macronutrients (Van Maarschalkerweerd and Husted 2015, Bekele and Birhan 2021, Tewari *et al*., 2021).

The atmospheric nitrogen exists predominantly in a stable form (N_2), thereby it is less accessible to plants. However, nitrogen is an indispensable element for the growth and development of plants. In the soil, readily available forms of nitrogen include nitrate (NO_3^-) and ammonia (NH_4^+), with their abundance particularly notable in soils with lower pH levels. Plants uptake nitrogen in these forms to fulfil various essential functions, including the production of coenzymes, photosynthetic pigments, polyamines, secondary metabolites, macromolecules, organic metabolites and more. Insufficient nitrogen availability can manifest in observable symptoms such as purple discolouration on leaves, stems and petioles as well as compromised shoot branching, early flowering, and slender stems (Gruber *et al*., 2013, Xu *et al*., 2015).

Wetland ecosystems typically encompass soils containing organic phosphorus compounds that release nutrients at a gradual pace, especially in those soils enriched with iron and aluminium. Moreover, in soils with higher pH levels, the formation of phosphorus salts in conjunction with calcium (Ca) and magnesium (Mg) is an inevitable occurrence that cannot be avoided, thereby affecting its uptake (Reich *et al*., 1995, Niinemets *et al*., 2001).

The scarcity of phosphorus presents a notable agricultural challenge, primarily attributed to the considerable fixation and unavailability (approximately 90%) of soil phosphorus (P) for direct plant uptake. However, plants have the capacity to assimilate inorganic P in the form of $H_2PO_4^-$. To overcome the constrained accessibility of phosphorus, numerous plants form a mutually advantageous association called mycorrhizal symbiosis with fungi, wherein the fungi contribute approximately 80% of the

plant's phosphorus needs (Jansa *et al*., 2011). Phosphorus is a vital element crucial for DNA and cellular membrane formation and it significantly impacts the photosynthetic rate of plants. Insufficient phosphorus levels can lead to inhibited growth in young plants and manifest as dark green foliage, patches of tissue necrosis, weakened stems, chlorosis, and anthocyanosis (Carstensen *et al*. 2018, Muindi 2019, Lambers 2022).

Potassium (K^+) is a significant macronutrient and while its deficiency is not common, supplementing it can enhance plant growth. It plays a crucial role in activating essential enzymes that facilitate turgor pressure generation, enabling the movement of substances through the xylem and phloem. Inadequate potassium levels can lead to leaf edge discolouration, tip necrosis, weak and stunted stems, reduced internode length, and stomatal guard cell closure (Anschutz *et al*., 2014, Ueno *et al*., 2018, White *et al*., 2021).

Sulphur exists in both organic and inorganic forms, and it is recognised as the fourth vital macronutrient. Plants predominantly uptake sulphur in the form of sulphates (SO_4^{2-}) owing to their high mobility in the soil. Sulphates are rich in essential amino acids such as cysteine and methionine. Inadequate sulphur levels can lead to inhibited growth, leaf discolouration, and the synthesis of leuco-anthocyanin (Schnug and Haneklaus 2005, Zheng and Leustek 2017).

Calcium (Ca) is abundant in the Earth's solid surface, but it can become deficient due to leaching and weathering. Free calcium ions ($Ca2^+$) tend to form complexes with other elements, like phosphorus, reducing its availability. In plants, calcium plays various vital roles like providing structural support, acting as a secondary messenger, regulating stomatal function, offering protection against physical damage, participating in the formation of mitotic spindles and facilitating cellular signalling (Pathak *et al*., 2020). Insufficient calcium availability can lead to necrosis of leaf and root tips, as well as the death of young leaf meristematic tissue (Yu *et al*., 2018, Winkler and Knoche 2019).

Magnesium ions ($Mg2^+$) serve as essential cofactors in various enzymatic reactions, including nucleic acid synthesis, respiration, phloem transport and photosynthesis processes (Schmidt and Husted 2019). In plants, magnesium is typically absorbed in its ionic form and are involved in the synthesis of carotene, ascorbic acid, riboflavin, and oxygen production through water splitting in the electron transport chain. Furthermore, magnesium contributes to the tricarboxylic acid cycle, which aids in carbon dioxide assimilation during photosynthesis. Insufficient magnesium levels

can result in symptoms such as premature leaf shedding, leaf yellowing or whitening, the development of necrotic patches and chlorosis along the veins (Trankner *et al*., 2018).

Apart from the essential macronutrients, plants also require micronutrients for proper growth. One such micronutrient is manganese (Mn) and its availability in soil is influenced by several factors, including microbial activity, redox potential, soil pH, and porosity. In acidic soil with a dense texture, manganese is more readily available. Conversely, in dry, arid soil with a high lime and sand content and limited water availability, manganese becomes less accessible to plants (Pedas *et al*., 2005).

Recent scientific research has highlighted boron's vital role in various plant physiological processes, including cell elongation, nucleic acid synthesis, cell anatomy alterations, cell wall structure maintenance, indole acetic acid (IAA) metabolism and phenol metabolism. Compared to other essential plant nutrients, boron has high permeability, mainly absorbed in the form of boric acid. Inadequate boron availability can negatively impact plant growth and development, leading to structural abnormalities, root cap loss, halted root growth, undersized leaves with necrotic tips, and disturbances in cell structure and physiological functions (Dell and Huang 1997, Furlani *et al*., 2003).

Zinc plays a vital role in multiple enzymatic reactions, notably DNA polymerase activation. Additionally, it is essential for maintaining cellular membrane integrity, facilitating chlorophyll production, synthesising cytochromes, regulating gene expression, and supporting DNA replication. Zinc deficiency is indicated by reduced internode development, undersized leaves, leaf chlorosis and related symptoms. Soil pH significantly impacts zinc availability, as higher pH levels may lead to decreased zinc absorption through variations exist depending on the plant species (Wear 1956, Brown *et al*., 1993). Zinc availability is influenced by several other factors, including organic matter content, calcareousness, soil texture and the occurrence of waterlogging conditions (Rehman *et al*., 2012).

Iron plays a vital role as an enzyme component in the electron transport system and is involved in various biological processes such as nitrogen fixation, DNA synthesis, hormone production, metal balance, photosynthesis, chlorophyll synthesis, and mitochondrial respiration (George *et al*., 1997). In soil, iron is commonly present in its oxidized form, Fe^{3+}, which exhibits low solubility due to its sensitivity to pH and oxygen levels. For plant growth, a minimum concentration of approximately 10^{-8}

M iron is required (Guerinot and Yi 1994). To counter iron deficiency, plants employ mechanisms to enhance iron solubility by acidifying the soil through the action of H^+-ATPase (Zhang *et al*., 2019b). Prolonged iron deficiency leads to symptoms such as leaf vein chlorosis, leaf whitening, stunted growth, and chlorotic shoots (Lemanceau *et al*., 2009).

Copper exists in both divalent and monovalent forms in soil. The availability of copper in the soil is influenced by processes such as precipitation and dissolution, absorption and desorption, as well as oxidation. Insufficient copper levels in the soil can lead to symptoms like premature shedding of young leaves and the appearance of necrotic patches on dark-green foliage. Plants cultivated in acidic soil are more susceptible to copper toxicity (McBride 1994, Brunetto *et al*., 2016). The bioavailability of soil copper variation is based on the plant species and other soil properties. It is crucial to understand that a high concentration of soluble copper in the soil solution does not guarantee complete availability to plants, only a portion of it remains accessible. The copper complexes that roots can readily absorb are the key contributors to their availability (Gobran *et al*., 2000). That is, the availability of copper is determined by the plant species and soil properties.

Copper exhibits solubility in acidic soil. Root exudates released into the rhizosphere interact with copper, enhancing its availability to the plant (De Conti *et al*., 2016). Copper toxicity induces various morphological, anatomical, and biochemical responses, impacting photosynthetic activity, accumulation of mineral nutrients (both positively and negatively) and seed germination (Ambrosini *et al*., 2018, Trentin *et al*., 2022).

Plastocyanin is a copper-containing enzyme serving as a cofactor for diverse proteins. Its crucial functions include involvement in mitochondrial respiration, carbohydrate metabolism and the synthesis of phenolic compounds that defend against pathogens. Moreover, plastocyanin contributes to superoxide scavenging, cell wall remodelling and ethylene precipitation (Kumar *et al*., 2021).

In soil, the interconnection between its components is evident, where the presence or absence of one element can significantly affect the availability of others. For example, a low zinc environment coupled with high phosphorus content can lead to phosphorus accumulation in leaves, causing increased toxicity and a higher demand for zinc. Additionally, insufficient calcium concentration in the soil can restrict zinc accessibility, along with other essential elements like potassium, ammonium, iron,

and magnesium. Copper, nitrogen and other nutrients can also influence zinc availability. Providing a substantial amount of zinc can impact the availability of other elements, and vice versa. In situations where there is a high concentration of other nutrients, plants may face inadequate access to sufficient zinc supply. Blackman's principle of limiting factors emphasises the necessity of supplying multiple nutrients, including zinc, to support optimal plant growth (Chaudhry and Loneragan 1972, Webb and Loneragan 1988).

The soil with abundant nitrogen (N) content, elevate the availability of phosphorus (P) and manganese ions (Mn2+). Humid regions tend to be acidic soil, and which enhances the availability of iron (Fe), manganese (Mn) and zinc (Zn). In contrast, alkaline arid soils are rich in boron (B) (Masunaga and Fong 2018). Manganese is an essential element that acts as a catalyst in the oxygen-evolving complex of Photosystem II (PSII). Its absence can disrupt photosynthesis and affect the availability of other elements, such as phosphorus (Umena *et al*., 2011). Plants exhibit symptoms resembling interveinal chlorosis when there is a deficiency of manganese. These symptoms are usually evident in newly sprouting leaves, as older leaves cannot supply an adequate amount of manganese. In severe and persistent cases, necrotic patches develop between the leaf veins. Furthermore, manganese deficiency can increase root vulnerability to fungal infections due to its role in lignin polymerisation (Reuter and Robinson 1997). Apart from essential macronutrients, plant growth also necessitates other micronutrients like molybdenum, nickel and chlorine (Broyer *et al*., 1954, Rana *et al*., 2020). The accessibility of these nutrients varies with soil conditions and are influenced by factors such as pH, temperature, precipitation and overall climatic conditions (Hou *et al*., 2018).

Evaluating nutrient availability in the soil can be a time-consuming endeavour. Nonetheless, advancements in computer vision and image processing techniques have facilitated the analysis of soil colour, which offers valuable insights into the soil's chemical composition, texture, moisture retention, nutrient storage and erosion potential. Furthermore, soil texture plays a crucial role in influencing significant factors, such as organic matter dynamics, microbial populations, distribution of plant and animal species and soil aggregation (Adhikari and Hartemink 2016, Xue *et al*., 2018,).

Soil mapping is of utmost importance, not only for crop management, and disaster management in landslide-prone areas but also for effectively addressing soil ero-

sion. Soil erosion causes nutrient leaching and degradation, posing significant risks to soil health and overall productivity (Dharumarajan and Hegde 2022).

Numerous studies have explored the correlation between soil parameters and other environmental variables in relation to intraspecific morphometric variability (Sereneski-Lima *et al*., 2022, Sharma *et al*., 2022, Wang *et al*., 2022, Assaeede *et al*., 2023, Maillard *et al*., 2023, Rashid *et al*., 2023). However, there has been limited research exploring the relationship between leaf structure and soil nutrients. This highlights the importance of conducting studies in this area to better understand how soil nutrient variations can impact visible changes in plants. The present study aims to find out the variation in edaphic factors of sky islands across Palghat Gap, and to study its influence over the intraspecific variability of *E. gadgilii* in sky islands across Palghat Gap.

7.2. Methodology

Soil samples were systematically collected from 47 different locations within the study area. These collected samples underwent physical and chemical analyses. This analysis included a total of 19 distinct soil parameters such as pH, electrical conductivity (EC), organic carbon (OC), nitrogen (N), phosphorus (P), potassium (K), calcium (Ca), magnesium (Mg), sulphur (S), manganese (Mn), zinc (Zn), copper (Cu), boron (B), iron (Fe), clay percentage (Clay%), silt percentage (Silt%), sand percentage (Sand%), colour, and texture. The interrelationships among the soil parameters were examined using IBM SPSS Statistics 22. The soil samples collected from the sky islands of the Western Ghats situated on the southern and northern sides of the Palghat Gap, were subjected to soil analysis, where each test was triplicated. Triplicate result of edaphic parameters outcomes was recorded from each of the 47 samples. Among them the 32 locations were specifically gathered in conjunction with locations from where 32 populations of *Elaeocarpus gadgilii* was collected.

This was done to study the diversity of soil samples throughout the sky islands within the study area across the Palghat Gap and to examine the effect of edaphic diversity over the sky island inhabitants. To assess the statistical significance of variants in 19 soil parameters, the non-parametric statistical tests were done on 47 soil samples. The edaphic parameters considered for the study includes pH, electrical conductivity (EC), organic carbon (OC), nitrogen (N), phosphorus (P), potassium (K), calcium (Ca), magnesium (Mg), sulphur (S), manganese (Mn), zinc (Zn), copper (Cu), bo-

ron (B), iron (Fe), sand, silt, clay, colour, and texture. The Kruskal-Wallis test, the non-parametric test employed to determine the significance level of variation in each edaphic characteristic of the sky islands of Western Ghats across the Palghat Gap.

7.2.1. Collection of samples

Soil samples were collected from field sites by excavating at a depth of 10-15 cm, specifically targeting the A-horizon (Fonseca *et al*., 2006). The collected soil samples were placed in polythene bags and were shade dried. In the laboratory, the samples were spread out under shade to ensure complete drying. Organic debris, such as dry leaves and roots, were meticulously removed from the soil. Subsequently, the dried soil was passed through sieves of different sizes (2mm, 1mm, and 0.5mm) to achieve a uniform particle size of the soil samples. For the analysis purposes, 500 grams of soil sieved through a 1mm mesh, and 30 grams of soil sieved through a 0.5mm mesh were separately packed in airtight polythene bags and stored in a dry location for future use.

7.2.2. Soil colour

The Munsell colour Chart is a widely used method for soil colour determination, defining the soil colour with the Munsell colour System with hue, value, and chroma as key variables. Hue indicates the relationship to basic colours, while chroma denotes saturation and Value represents lightness. Each Munsell chart exhibits a consistent hue and visually equal colour increments from top to bottom, becoming lighter as the value increases. Chroma increases to the right and decreases to the left, represented horizontally, while value is depicted vertically on the left column. The Munsell colour system is a scientific approach to comprehend and reproduce colours in soil analysis (Cochrane 2014).

The Munsell book contains a collection of diagrams categorised into three scales: radial, vertical, and horizontal. For colour notation, the book employs two methods: 1) conventional colour names for general use and, 2) Munsell notation for statistical analysis. The Munsell notation analysis improved precision and comparability (Indow 1988). The Munsell notation is employed for precise colour specification, utilising distinct symbols for each of its three variables. The hue variable is denoted by symbols R (Red), YR (Yellow-Red) and Y (Yellow) with values ranging from 0 to 10, where 0 signifies absolute black and 10 signifies absolute white. The chroma variable ranges from 0 (neutral grey) to 20. Soils that are pure, grey, white, or black are

classified as achromatic. When there is no hue or chroma present, the letter N is used instead (Ferguson 2014).

The Munsell notation system utilises a system of comma-separated values to denote the chroma, hue and value of a colour. This notation can also be represented using decimal values, providing a high degree of precision. The process of identifying a colour using the Munsell system involved placing a sample behind the aperture in the Munsell chart and then comparing it to the colour chips on a hue card. The challenges associated with using this system include accurately determining the hue, distinguishing between different values and chroma, and identifying extremely dark and intense colours that are commonly found in moist soils (Munsell colour 1975).

7.2.3. Soil texture

The soil texture, a fundamental physical characteristic, was determined by the distribution of particle sizes within the soil. The United States Department of Agriculture (USDA) has established twelve textural classes, defined by the USDA textural triangle, which serves as a standard for assessing soil texture and density. The relative proportions of three primary soil particle sizes, namely sand, silt and clay, are determined by measuring their settling rates in a liquid solution using a soil hydrometer, following standards such as ASTM-D422 and others. According to the specifications outlined by the USDA, particle size of sand particles was within the range of 2000-50μm, silt particles ranging from 50-2.0μm, and clay particles less than 2.0μm in size (Table 7.1). The percentages of clay and silt are plotted on the appropriate sides of the triangle. A line parallel to the sand axis is drawn for the clay percentage, and another line parallel to the clay axis is drawn for the silt percentage. The point of intersection between these two lines represents the textural group of the soil. The soil is classified into one of twelve textural classes based on the relative proportions of sand, silt, and clay (Shirazi and Boersma 1984, Gangwar and Baskar 2019). The hydrometer method, similar to the pipette method, utilises dispersion and sedimentation techniques to determine the weight of a soil sample. It is commonly used in routine particle size analysis and does not require high levels of precision. The process of sedimentation refers to the settling rates of scattered particles in water, governed by Stokes' law.

The hydrometer was used to measure the density of a soil suspension, and in practice, an average density is taken at the depth of the inserted hydrometer. This method is based on the fact that initially homogeneous and dispersed suspension settles, the density at a given depth decreases.

Table 7.1. Different types of texture classification based on concentration of sand, silt and clay based on USDA textural triangle (Moreno-Maroto and Alonso-Azcarate 2022)

Sl.No	Soil textural class name	Sand	Silt	Clay
1	Sand	85-100	0-15	0-10
2	Loamy sand	70-90	0-30	0-15
3	Sandy Loam	43-80	0-50	0-20
4	Loam	23-53	28-50	7-27
5	Silt Loam	0-50	50-88	0-27
6	Silt	0-20	80-100	0-12
7	Sandy Clay Loam	45-80	0-28	20-35
8	Silty Clay Loam	0-20	40-73	27-40
9	Clay loam	20-45	15-53	27-40
10	Sandy Clay	45-65	0-20	35-45
11	Silty clay	0-20	40-60	40-60
12	Clay	0-45	0-40	40-10

The rate of decrease in density is directly related to the settling velocities of the particles, which are in turn related to their size. The hydrometer reading indicates that after 4 minutes of sedimentation, particles larger than 0.02mm settle, while after 2 hours, only particles smaller than 0.002mm remain in the soil suspension (Bouyoucos 1962, Shirazi and Boersma 1984).

Procedure: -

To prepare the soil sample for analysis, either 50g of fine-textured soil or 100g of coarse-textured soil is taken and dried in an oven. The dried soil was then passed through a 2 mm sieve to remove large particles. In a beaker, the sieved soil is mixed with 50 ml of 6% H_2O_2 to oxidise organic materials. Then the beaker was covered with a watch glass and placed in a water bath until effervescence occurs. Once cooled, the liquid portion is transferred to a dispersion cup containing 400 ml of distilled water. To facilitate dispersion, 100 ml of calogen solution was added, and the mixture was stirred for 10 minutes using an electric stirrer. The resulted suspension was transferred to a small sedimentation cylinder, and distilled water was added to reach a total volume of 1 litre. The top of the cylinder was sealed, and vigorous agitation was performed in an inverted position for approximately 60 seconds. The cylinder was then placed on a flat surface and kept still for some time. After 4 minutes, the specific gravity of the suspension was measured using a hydrometer, ensuring that particles

larger than 0.02 mm have settled by inserting the hydrometer 10 seconds prior to the measurement. Care was taken in handling the hydrometer and are to be cleaned with distilled water after each use. The temperature of the suspension was also recorded. After the initial shaking, the suspension was allowed to settle for two hours. Another hydrometer reading was taken at the point where larger particles such as sand and silt, that is particle size greater than 0.002 mm was settled. Finally, the soil structure is classified based on the composition of sand, silt, and clay present and was determined using the USDA's textural triangle (Bouyoucos 1962).

7.2.4. Soil pH

The acidity or alkalinity of a soil-water suspension with a ratio of 1:2.5 is determined using a pH metre. The pH metre measures the activity of hydrogen ions in the soil-water system, providing information about the soil's acidity, neutrality, or alkalinity.

Reagents: -

- Buffer solutions were prepared with pH values of 4.0, 7.0, and 9.2 by dissolving buffer tablets obtained commercially in recently prepared distilled water. Ensured that the final volume of each solution is 100 ml. It is important to note that buffer solutions have limited stability and should be freshly prepared every few days.

Procedure: -

The soil pH measurement was conducted with a pH metre, where buffer solutions were used to calibrate a pH metre. To measure soil pH, soil samples were sieved through a 2mm sieve, then 10 grams of it was weighed out of it and placed in a 50- or 100-ml beaker, and 25 ml distilled water was added to it. Then the mixture was thoroughly stirred for 5 minutes and allowed to settle for 30 minutes. After stirring once more, the pH reading was obtained using a calibrated pH metre. The electrodes of the pH metre (glass and calomel or combined electrodes) were carefully immersed in the water suspension, and the pH value is measured on a logarithmic scale ranging from 0 to 14. The electrodes were slightly adjusted to remove any water film around them, and the reading was recorded once it was stabilised. The pH reading of the soil was classified as acidic if the pH was less than 7, neutral at pH 7, and basic if the pH above 7. The mixture was stirred again before taking additional pH readings using the pH metre (Sorenson 1909).

7.2.5. Electrical Conductivity (EC)

The electrical conductivity (EC) of a soil-water system serves as an indicator of the concentration of soluble salts and the salinity level in the soil. To measure the EC, a conductivity metre was employed, where the conductive properties of ions, particularly metals, in an electric current was utilised. An elevation in the concentration of soluble salts leads to a proportional increase in the EC value. The EC measurement holds significant importance in assessing plant growth. The soil sample was passed through a 0.2mm sieve, and 20g was weighed out from it, and was placed in a 100ml beaker. Subsequently, 40 ml of distilled water was added to, and the mixture was then left undisturbed for one hour. After settling, a clear supernatant was formed, and that transparent extract was utilised to measure the EC.

Reagents: -

- Potassium chloride solution: A small amount of analytical grade potassium chloride was subjected to drying in a hot air oven set at 600°C for a duration of 2 hours. After drying, 0.7456 grams of potassium chloride was weighed out for preparing the solution. This was then dissolved in 1 litre of freshly prepared distilled water. Subsequently, the electrical conductivity of the resulting solution was measured at a temperature of 25°C, yielding a value of 1.41 dS m^{-1}. Prepared to calibrate EC.

Procedure: -

The electrical conductivity (EC) of soil was determined from the clear supernatant liquid water suspension obtained from the suspension, which was previously used for measuring pH. Before conducting the EC measurement, it is important to calibrate the conductivity metre using a prepared 0.01N KCl solution and calculate the cell constant. Subsequently, the conductivity of the supernatant liquid can be determined using the calibrated metre (Suresh Kumar *et al*., 2010).

7.2.6. Estimation of Nitrogen

To assess the available nitrogen (N) content in soil, the distillation of the soil was done with an alkaline solution containing potassium permanganate, followed by the measurement of the released ammonia. This method was suggested as a soil test to determine the availability of nitrogen (Subbaiah and Asija 1956).

Reagents: -

- Solution of potassium permanganate ($KMnO_4$) with a concentration of 0.32% was prepared by dissolving 3.2 grams of high-purity $KMnO_4$ in distilled water,

followed by dilution to a final volume of one litre in a volumetric flask. The solution should be thoroughly mixed to ensure uniformity.

- The 2.5% solution of sodium hydroxide (NaOH) was prepared by dissolving 25 grams of NaOH flakes in distilled water and then adjusted the volume to one litre in a volumetric flask. The solution was thoroughly mixed to ensure homogeneity.
- 0.02N standard sulfuric acid
- The Combination indicator was created by dissolving 0.07 grams of methyl red and 0.1 grams of bromocresol in 100 millilitres of 95% ethanol.
- Solution of the boric acid as an indicator was prepared by dissolving 20 grams of pure boric acid (H_2BO_2) in approximately 700 millilitres of hot water. After cooling, the solution is then transferred to a one-litre volumetric flask containing 200 millilitres of ethanol and 20 millilitres of the mixed indicator solution. The contents of the flask were thoroughly mixed, and 0.05N NaOH was added incrementally until a reddish-purple colour was observed. The solution was then diluted with water to the final volume and mixed rigorously.

Procedure: -

5g of soil was taken in a Kjeldahl flask, and to it 0.25% NaOH and 0.324 $KMnO_4$ was added. The distillation process was carried out using a Lelplus Elite-Ex Vats Distillation unit. The end tube of the distillation unit was connected to a conical flask containing 20 ml of Boric acid mixed with the indicator. Upon distillation, the liberated ammonia causes the pink colour of the boric acid to turn green. Approximately 100 ml of distillate was collected within a 30-minute period. The contents were then titrated with 0.02N H_2SO_4 until the original pink colour was restored. A blank correction must be made for the final calculation.

The Kelplus Elite-EX Vats, a semi-automatic instrument commonly used for the determination of nitrogen levels using the Kjeldahl distillation method. In this particular version of the device, it was not necessary to adjust the sample volume after digestion, as the sample tube was directly connected to the distillation unit. This setup enables the capture of liberated ammonia automatically to the conical flask containing boric acid solution and mixed indicator. The trapped ammonia was subsequently titrated against a standard sulfuric acid solution. However, it was observed that the

conventional formula employed for interpreting the titration results resulted in the estimation of the nitrogen levels.

Calculation: -

$$\text{Total Nitrogen} = \frac{(\text{Titre Value} \times \text{Normality Of } H_2SO_4 \times 0.014 \times 1000000 \times 2.24 \text{kg/ha})}{\text{Weight of soil}}$$

$$\text{Normality of } H_2SO_4 = 0.0224 \text{ N}$$

7.2.7. Estimation of Phosphorus

In an acidic molybdate solution, orthophosphate ions form phosphomolybdate complexes which can be reduced by certain chemicals such as ascorbic acid and stannous chloride. This reduction results in a blue colour. The intensity of this colour can be affected by various factors including the concentration of P, the acidity of the solution, the presence of other elements such as arsenates and silicates, and chemicals that impact the oxidation-reduction conditions of the system. The methods used to extract this form of P can also vary depending on the pH level of the soil (Bray and Kurtz 1945).

Reagents: -

- 1N solution of Ammonium fluoride was prepared by mixing 37 grams of NH_4F with one litre of distilled water in a plastic container suitable for storage.
- 0.5N solution of diluted Hydrochloric acid (HCl) was prepared by diluting 20.2 ml of concentrated Sulphuric acid in 500 ml of distilled water.
- The Bray number one solution was prepared by mixing 460 ml of distilled water, 15 ml of 1N NH_4F, and 25 ml of 0.5N HCl in a glass container. This solution exhibits long-term stability and can be stored for a duration exceeding one year.
- Ammonium paramolybdate solution $[(NH_4)_6Mo_7O_{24}\cdot 4H_2O]$ (Reagent A) was prepared as follows: 12 grams of ammonium paramolybdate was dissolved in 250 millilitres of distilled water. Then a solution of 0.2908 grams of potassium antimony tartrate ($KSbO\cdot C_4H_4O_6$) in 100 millilitres of distilled water was prepared. These dissolved reagents were then mixed with 1 litre of 5N sulfuric acid (141 millilitres of concentrated H_2SO_4 diluted to 1 litre), followed by dilution to 2 litres using distilled water. The resulting solution was stored in a Pyrex glass container in a cool and dark area.

- Ascorbic acid solution (Reagent B) was prepared by dissolving 1.056 g of ascorbic acid in 200 ml of Reagent A. To prepare this solution as required and avoid storing it for more than 24 hours.

Procedure: -

Into a 100 mL conical flask, 50 mL of Bray No. 1 reagent and 5 g of soil was added. Thoroughly mix the contents by shaking the flask precisely for 5 minutes. Subsequently, its filtrate was made using Whatman No. 42 filter paper. If required, mitigate fluoride by mixing 5 mL of the extract with 7.5 mL of 0.8 M boric acid solution (prepared by dissolving 50 g of H_3BO_3 per litre). Finally, the quantity of phosphorus present in the extract was determined (Watanabe and Olsen 1965, Olsen *et al*., 1954).

Estimation by reduced molybdate blue colour method: -

5mL of the extract was measured out using a pipette and transferred to a 25mL volumetric flask. Dilute the contents to approximately 20 mL by adding an appropriate volume of solvent. 4 mL of reagent B was added to the flask and was thoroughly mixed by shaking. Then the liquid level was adjusted in the flask by adding distilled water until the desired volume was reached. After a 10-minute incubation period, the colour intensity of the solution was evaluated at a wavelength of 660nm using a spectrophotometer or colorimeter. The maximum colour intensity will be achieved within 10 minutes and the colour will remain stable for a duration of 24 hours. Measure the intensity of the blue colour and utilise the standard curve to determine the concentration of phosphorus present in the sample.

Calculation: -

$$\text{Available P (kg ha}^{-1}\text{ soil)} = \text{Available P (mg kg}^{-1}\text{ soil)} \times 2.24$$

7.2.8. Estimation of exchangeable Potassium

The term "available potassium (K)" commonly referred to the combined amount of exchangeable and water-soluble potassium. Exchangeable potassium is the primary constituent of available potassium, excepted in saline or saline-sodic soils. The determination of available potassium, also referred to as exchangeable potassium, was typically conducted using a neutral normal ammonium acetate soil extract, which also includes the determination of exchangeable calcium and magnesium. The extraction process involves shaking the soil and subsequently filtering or centrifuging the resulting solution. Potassium content is quantified using a flame photometer. In soils where there are considerable amounts of soluble potassium, calcium, and magnesium,

these cations are assessed in a saturation extract (Jackson 1958) and subtracted from the NH_4OAc extractable potassium, calcium, and magnesium to derive the respective exchangeable cation concentrations.

Exchangeable potassium in soils refers to the potassium content that can be replaced by cations in salt solutions. However, the extent of potassium exchangeability was influenced by the nature of the replacement solution utilised. In the context of assessing soil fertility, exchangeable potassium was precisely defined as the quantity of potassium extracted through neutral 1N ammonium acetate, with the exclusion of water-soluble potassium. The combined amount of exchangeable potassium and water-soluble potassium represents the available potassium pool in typical soils, as the contribution of water-soluble potassium was negligible and did not significantly impact the accuracy of the measurement. It is not advisable to eliminate water-soluble potassium prior to ammonium acetate extraction, as reducing the salt concentration in the soil solution enhances the adsorption of divalent cations present in the solution.

Reagents: -

- Neutral 1N ammonium acetate solution (CH_3COONH_4) as follows: 77.08 grams of ammonium acetate was dissolved in 1 litre of distilled water. If required, the pH of the solution was made to 7 by using acetic acid or ammonium hydroxide.
- Standard potassium (K) solution was dissolved 1.908 grams of dried analytical-grade potassium chloride (KCl) in distilled water to achieve a concentration of 1000 µg/ml. Adjust the volume to 1 litre.

Procedure: -

Five grams of soil sample was thoroughly mixed with 25 millilitres of 1N neutral ammonium acetate for a duration of 5 minutes to ensure homogenization. The resulted mixture was then filtered through a pre-weighed, dry Whatman No. 42 filter paper. A small volume of the initial filtrate, usually a few millilitres, was discarded. Employing suitable equipment and ensuring proper calibration, the potassium content of the extract was determined using flame photometry.

Calculation: -

$$\text{Available K (mg kg}^{-1}\text{ soil)} = \text{µg K mL}^{-1}\text{ of the aliquot x 5}$$

7.2.9. Estimation of Organic Carbon

In 1927, Schollenberger proposed the oxidation of soil organic matter through the application of a hot solution of potassium dichromate ($K_2Cr_2O_7$) and sulfuric acid (H_2SO_4) as a viable method (Schollenberger 1927). Following the reaction, the re-

maining dichromate ions ($Cr_2O_7^{2-}$) are quantified using a standard iron ammonium sulphate (Fe $(NH_4)_2SO_4.6H_2O$) solution, and the amount of dichromate reduced during the reaction with the soil was considered to be proportional to the amount of organic carbon present in the sample.

$$2\ Cr_2O_7^{2-} + 3\ C + 16\ H^+ = 4\ Cr^{3+} + 3\ CO_2 + 8\ H_2O$$

The suitability of O-phenanthroline as an indicator in $Cr_2O_7^{2-}$ titrations is supported by its ability to undergo complexation with Fe^{2+} and produce a noticeable colour change at a higher oxidation-reduction potential, as documented by Jackson in 1958. It is important to acknowledge that while the majority of active forms of organic carbon can be converted to CO_2 through dichromate procedures, methods employing heat of dilution or minimal heating may not completely oxidise all organic molecules present in the soil. Walkley and Black (1934) observed an approximate recovery rate of 76% for organic carbon using the heat dilution method. To address this issue, they proposed the utilisation of a correction factor of 1.32 to compensate for the unreacted portion of organic carbon.

Reagents: -

- 1N solution of potassium dichromate ($K_2Cr_2O_7$): 49.04 grams of reagent grade $K_2Cr_2O_7$, was dried at 105°C, and was dissolved in water. Then the solution was diluted to a final volume of 1000ml.
- Ferrous ammonium sulphate hexahydrate solution – 0.5N: 197g of reagent grade $Fe(NH_4)_2SO_4.6H_2O$ was dissolved in water, and to it 15 millilitres of concentrated sulfuric acid was added, then the mixture was cooled and then diluted it to a final volume of 1000ml. This reagent should be standardised daily by titrating it against 10 ml of 1N potassium dichromate.
- 0.025M solution of the O-phenanthroline-ferrous complex commonly known as Ferroin, was prepared by dissolving 14.85 grams of the o-phenanthroline monohydrate and 6.95 grams of ferrous sulphate heptahydrate ($FeSO_4 \cdot 7H_2O$) in water. Then the solution was diluted to a final volume of 1000 millilitres.
- Concentrated sulfuric acid (H_2SO_4) was used, in the presence of chloride in the soil, and Ag_2SO_4 is introduced to the acid at a concentration of 15g per litre.

Procedure: -

To prepare a soil sample for determining its chromium content, the soil was first grounded and sieved through a 0.5 mm mesh to remove large particles. It is important to use a mortar and pestle made of a material other than iron or steel. Next, 0.5

to 1 g of the sieved soil was added to a 500 ml wide-mouthed conical flask. The soil was evenly mixed by gently shaking the flask while adding 10 ml of 1N potassium dichromate solution. 20 ml of pure sulfuric acid was then added, and the flask was gently swirled for one minute. The mixture was then kept undisturbed for 30 minutes. 200 ml of water was then added to the flask, and then the solution was titrated with 0.5N ferrous ammonium sulphate using o-phenanthroline as an indicator. As the end-point reached, the solution changes colour from greenish to dark green, and then the ferrous ammonium sulphate was added dropwise until the colour changes sharply from blue to red. A blank was prepared by following the same procedure but omitting the soil to standardise the potassium dichromate (Walkley-Black Wet Digestion Method), (Walkley 1947).

Calculation: -

$$\text{Organic Carbon\%} = \frac{(\text{Blank-Titre Value}) \times (\text{Normality of FAS} \times 0.003 \times 100)}{\text{Weight of Soil}}$$

$$\text{Normality of FAS} = \frac{\text{(Volume of potassium dichromate)}}{\text{Blank Value (Titration Volume) 0.003: Constant}}$$

7.2.10. Estimation of Calcium and Magnesium

The available calcium and magnesium resources for plants consist of exchangeable and water-soluble forms, much like potassium. To extract these resources, a neutral normal ammonium acetate solution was utilised. In the absence of additional $CaCO_3$, it was noted that the cations Ca^{2+}, Mg^{2+}, Na^{+}, and K^{+} exhibit complete exchangeability with neutral normal ammonium acetate.

Reagents: -

- To prepare a neutral ammonium acetate solution, 77.08 grams of ammonium acetate was dissolved in one litre of distilled water. Adjusted the pH to 7 by adding acetic acid or ammonium hydroxide.

Procedure: -

Approximately 5 grams of air-dried soil was weighed out carefully after being sieved in a 2mm sieve and placed in a 150ml Erlenmeyer flask. Then, 25 ml of neutral ammonium acetate solution with a pH of 7 was added to the flask. Then the flask was shaken in a reciprocating shaker for 5 minutes. Then the mixture was filtered using Whatman no. 1 filter paper and ensured that the initial few millilitres of filtrate was discarded. For calcium analysis the sample solution was diluted.

Estimation of Calcium and Magnesium by Atomic Absorption Spectrophotometry

The use of atomic absorption spectroscopy (AAS) enabled the determination of calcium (Ca) and magnesium (Mg) concentrations in soil extracts. However, the presence of stable compounds formed between Ca and Mg ions and accompanying anions can introduce chemical interferences that reduce absorption efficiency. To overcome this interference, the addition of a releasing agent, such as strontium or lanthanum, can effectively eliminate it.

Calculation: -

$$\text{Available Ca/Mg (mg kg}^{-1}\text{ soil)} = \mu\text{g Ca/Mg mL}^{-1}\text{ of the aliquot x 5}$$

7.2.11. Estimation of Sulphur

Multiple methods have been suggested for extracting sulphur that is readily available to plants from the soil. These methods include the use of water, salt solutions (such as 0.15% $CaCl_2$), phosphate-containing solutions (such as 500 ppm P as $Ca(H_2PO_4)_2$ or KH_2PO_4), and acidic solutions (such as 0.5 N ammonium acetate plus 0.25 N acetic acid and Bray No. 1). In general, solutions containing phosphates are observed to extract a higher amount of sulphur from soils compared to water or salt solutions. This is attributed to the displacement of adsorbed sulphate by phosphate ions, as adsorbed sulphate is known to be easily accessible to plants.

Reagents: -

- 0.15% calcium chloride solution was prepared by dissolving 1.5 grams of calcium chloride dihydrate in 500ml of distilled water. The final volume was adjusted to 1 litre.
- Gum acacia-acetic acid solution was prepared by dissolving 0.25 grams of chemically pure gum acacia in hot water. Filter the solution using a Whatman No. 42 filter paper, then the filtrate was allowed to cool. Finally, the cooled filtrate was diluted and made up to a final volume of 100ml.
- Barium chloride: analytical grade barium chloride was finely grinded and passed through a 1-millimetre sieve.
- Concentrated standard sulphate solution was prepared by dissolving 0.5434 grams of oven-dried AR potassium sulphate in distilled water, and then the final volume was adjusted to 1 litre.

Procedure: -

In a 250-millilitre conical flask, 10g of dehydrated and purified soil was vigorously mixed with 50 millilitres of 0.15% calcium chloride solution for a duration of 30 minutes. Afterwards, the extract was separated using Whatman No. 42 filter paper and a turbidimetric technique was employed to quantify the concentration of sulphate (Tabatabai 1982).

Turbidimetric estimation of Sulphur: -

Using a micropipette, 10 millilitres of the soil extract was carefully dispensed into a 25ml of volumetric flask. Then 1g of barium chloride crystals was added to it and stir to aid in dissolution. Then 1 ml of 0.25% gum acacia solution was added to it, then the volume was adjusted to its final measurement using distilled water and was thoroughly mixed. After the solution becomes turbid the solution's absorbance was measured at 440 nanometres using a spectrophotometer (Massoumi and Cornfield 1963). Then the sulphur content was estimated.

Calculation: -

Amount of sulphur (mg kg^{-1} soil) = Concentration from the instrument x (25/10) x (50/10).

7.2.12. Estimation of Iron (Fe), Manganese (Mn), Zinc (Zn) and Copper (Cu).

The DTPA (Diethyl triamine Pentaacetic acid) soil test, was formulated by Lindsay and Norvell in 1978, exemplifies the derivation of a soil testing extractant based on theoretical principles. To maintain pH of 7.3, a 0.1M triethanolamine (TEA) solution was employed, along with 0.005M DTPA and 0.01 M calcium chloride dihydrate in the extraction solution. The DTPA extractant demonstrates optimal stability constants, allowing for the simultaneous extraction of four micronutrient cations (Fe, Mn, Cu, and Zn). The presence of soluble calcium ions and the buffered pH prevent the excessive dissolution of calcium carbonate, thus preventing the release of inaccessible micronutrients bound in this solid phase.

Reagents: -

- 0.1 N Hydrochloric acid (HCl): 8.1 ml of reagent-grade concentrated HCl was added to 900 mL of distilled water. Then the solution was mixed well and cooled to room temperature and was brought to the final volume of 1 litre.
- DTPA extractant: 1.967 g of DTPA, 14.92 g of TEA (Triethanolamine) and 1.47g of $CaCl_2.2H_2O$ was dissolved in 200 ml of distilled water. Then the solu-

tion was diluted to 900 mL and then the pH was adjusted to 7.3 ± 0.05 with 1:1 HCl. Then the solution was made to a final volume of 1 litre.

Estimation of Fe, Mn, Zn, and Cu in acid soils (pH < 6.5): -

20 ml of 0.1M hydrochloric acid was mixed with 2 grams of soil and was stirred for 5 minutes. Impurities were removed by filtering the mixture using Whatman No. 42 filter paper. Then the filtrate was collected and the concentrations of iron (Fe), manganese (Mn), zinc (Zn), and copper (Cu) was measured using atomic absorption spectrophotometer.

Calculation: -

Amount of micronutrient (mg kg^{-1} soil) = Concentration from the instrument x 10

Estimation of Fe, Mn, Zn, and Cu in near neutral to alkaline soils (pH > 6.5): -

2 grams of soil was agitated with 20 mL of 0.1 M hydrochloric acid for a duration of 5 minutes. Then the impurities were removed using Whatman No. 42 filter paper. The collected filtrate was subjected to analysis using an atomic absorption spectrophotometer to quantify the concentrations of iron (Fe), manganese (Mn), zinc (Zn), and copper (Cu).

Calculation

Amount of micronutrient (mg kg^{-1} soil) = Concentration from the instrument x (20/10).

7.2.13. Estimation of Boron (Hot-Water Soluble Boron)

Boron in the sample forms a coloured complex with Azomethine-H in an acidic medium. The complex is pink to reddish violet in colour.

Reagents: -

- Buffer solution: 250 g of ammonium acetate, 15 g of EDTA (disodium salt), and 125 mL of glacial acetic acid was mixed thoroughly in 400 ml of distilled water.
- Azomethine-H reagent: 0.45 g of azomethine-H was dissolved in 100 ml of 1% L-ascorbic acid solution. Then the solution was stored in a refrigerator in a polypropylene bottle. Fresh solution was prepared every week.
- Boron standard solution: 1.14 g of AR grade boric acid (H_3BO_3) was dissolved in distilled water and the solution was made to 1000 ml. Each ml of the solution contains 20µg of B. Then 0.5, 1, 2, 3, 4, 5, 10, 20, 30, 40 and 50 ml of this stock solution was diluted to 100 ml with distilled water to have solution concentrations of 0.1, 0.2, 0.4, 0.6, 0.8, 1.0, 2.0, 4.0, 6.0, 8.0, and 10 µg of B ml^{-1}, respectively.

- Activated charcoal.

Procedure: -

20g of air-dried soil was weighed out and placed in a boron-free flask of 250 ml, preferably made of quartz, and 40 mL of distilled water was added to the flask. Then boil the mixture on a hot plate for 5 minutes after adding 0.5 g of activated charcoal. Immediately filter the solution using Whatman No. 42 filter paper. Once the filtrate was cooled to ambient temperature, 1 ml portion of blank, diluted boron standard, or sample solution was transferred to a 10 mL polypropylene tube. Then 2 ml of buffer was added to it and mixed well. Then, 2 mL of azomethine-H reagent was added, and theses contents were thoroughly mixed and allowed to react for 30 minutes. Then the absorbance of the solution was measured at 420 nm on a spectrophotometer. To create a standard curve, solutions were prepared with B concentrations and the corresponding absorbance values were plotted on Y-axis (Gupta 1967).

Calculation: -

Amount of B in soil (mg kg^{-1} soil) = (Absorbance reading x (40/20))/ Slope from curve).

7.2.14. Analysis of edaphic parameters of sky islands

7.2.14.1. Soil colour in relation to Organic Carbon and micro-macro nutrients

The correlation analysis was conducted on 47 soil samples sourced from the sky islands of the Western Ghats across the Palghat Gap in relation to OC. Significant level of correlation between Munsell colour notation and OC were done with Spearman correlation coefficient analysis in SPSS. Then the soil colours intricate relation between other edaphic elements were also evaluated with spearman correlation.

7.2.14.2. Soil texture in relation to water retention

The SWCC (Soil Water Characteristic Curve) is greatly influenced by the inherent soil texture, making it an important aspect to consider. The Fractal analysis provides a valuable approach to study the relationship between physical properties and soil hydraulic parameters. In the context of the SWCC fractal model, it has been observed that the water retention capacity increases with higher clay content. The water retention capacity follows a specific pattern, where clay soil exhibits the highest water retention capacity, followed by silty clay, sandy clay, clay loam, silty clay loam, sandy clay loam, loam, silt loam, sandy loam, silt, loamy sand, and sandy soil (Miller *et al*., 2002). Understanding the role of soil texture through SWCC fractal analysis

enhances our comprehension of the physical properties and hydraulic behaviour of soil. This knowledge is vital for various applications, such as water management and environmental studies (Yang *et al*., 2023). There by all the soil samples water retention capacity was compared based on the clay %.

7.2.14.3. Interpolation of edaphic parameters over sky islands across Palghat Gap

The soil samples edaphic parameter results were subjected to interpolation, kringing and spatial mapping techniques using ArcGIS 10.8 software, contributing to the assessment of the expected probable concentration of edaphic components in the study area. The interpolation process involved estimating the values of various soil parameters, including pH, EC, OC, N, P, K, Ca, Mg, S, Mn, Zn, Cu, B, Fe, clay%, silt%, and sand% within the study area. By employing this mapping technique, the spatial distribution of these soil parameters were visualised and analysed, thereby enhancing our understanding of soil variations across the sky islands with in the study area.

7.2.14.4. Synergistic and antagonistic effects of edaphic parameters

Spearman correlation analysis was utilised to explore the associations and inter-relationships among these soil parameters and their ratios. The findings of this analysis will reveal if there is a significant correlation between edaphic element, encompassing both positive and negative relationships, with statistical significance determined by P-value at a level of significance $P \leq 0.01$ or $P \leq 0.05$.

7.2.14.5. Intricate relation between edaphic parameters and intraspecific morphometric variability of *Elaeocarpus gadgilii*

Effect of variation of edaphic parameters of sky islands across Palghat Gap over the intraspecific morphometric variability of *E. gadgilii* across Palghat Gap were tested. For that the spearman correlation analysis was done between the edaphic variables and morphometric quantitative variables of *E. gadgilii* populations of sky islands across Palghat Gap. Here the soil samples considered for the correlation were the samples collected from the vicinity of each population of *E. gadgilii*. The edaphic parameters of all 47 locations were not considered here, instead, the locations from where the *Elaeocarpus gadgilii* population was collected were considered. The present study employed Spearman correlation to analyse the interrelationship between soil parameter variability and their effects over the intraspecific morphometric variability of 32 populations of *E. gadgilii.*

7.3. Results and discussion

7.3.1. Collection of samples

Soil samples were collected, and shade dried and processed and stored airtight in polythene cover for analysis. The soil samples were analysed over 19 edaphic variables which include Hue variable, Hue Value, Value, Chroma, Texture, pH, EC, N, P, K, OC, Ca, Mg, S, Fe, Mn, Zn, Cu and B (Table 7.2 & 7.3).

7.3.2. Soil colour

In the present Investigation, the determination of soil colour was adhered to the guidelines set forth by the Munsell colour chart. The study encompassed examination of 47 distinct soil samples, and the three variables inherent to the Munsell colour system were identified and quantified. Subsequent analysis unveiled that there were 26 discrete soil colours within the 47 soil samples analysed and were classified based on their Munsell notations within the collected soil samples (Table 7.4). This conspicuous divergence in colouration underscored a substantial degree of heterogeneity manifesting among the sampled entities. Each unique sample manifested distinct and discernible attributes, particularly in terms of its inherent hue value, hue variable, value, and chroma as denoted by the Munsell notation. Noteworthy was the pronounced extent of colour variance, prominently observed between the soil samples obtained from the northern sky island, in stark contrast to those sourced from the southern region. The colour of the observed soil was found to be delicate shades of yellow to profound hues of brown. It warrants emphasis that isolated colour descriptors alone failed to provide the requisite precision for accurate correlation and differentiation among the samples under study.

However, the systematic integration of the Munsell notation emerged as a reliable, and specialised method to effectively surmount the limitations. The manifestation of soil colour, as delineated by the Munsell notation, exhibited a more controlled divergence in terms of the actual visual colours they represented. The colour of the soil samples varied in accordance with the Munsell notation while exhibiting less variation in terms of actual colours, which enable statistical correlation analysis of Munsell colour with the specific habitat from which each sample was collected. The hue notation represents the primary colours red, yellow, blue and purple. Chroma denotes the level of saturation or intensity of the colour, whereas value represents the degree of lightness or darkness (Munsell color 2022). As depicted in table 7.4, each soil sample has its own colour, as per the colours

Table 7.2. The soil parameters pH, EC, OC, N, P and K of 47 soil samples collected from sky islands of the Western Ghats across the Palghat gap within the study area.

Samples	Altitude	Lat-Long	Location	pH Mean±SD	EC Mean±SD	OC (%) Mean±SD	N(Kg/ha) Mean±SD	P(Kg/ha) Mean±SD	K(Kg/ha) Mean±SD
1	1297.0m	10°31' 55"N 76°43' 48"E	Karimala to Karasurimala	4.913 ± 0.00577	0.717 ± 0.001	4.12± 0.0248	421.4784 ± 0	15.258 ± 0.045	578.33 ± 0.5037
2	1285m	10°31' 52"N 76°43' 46"E	Karimala to Karasurimala	4.433 ± 0.00577	0.451 ± 0	2.88 ± 0.0149	632.2176 ± 0	30.64 ± 0.166	192.677 ± 0.053
3	1307.6m	10°31'55"N 76°43' 47"E	Karimala to Karasurimala	4.71 ± 0.01	0.427 ± 0.000577	2.504 ± 0.01488	702.464 ± 0	21.448 ± 0.049	390.88 ± 0
4	1267.4m	10°31'48.072"N 76°44' 17.934"E	Karimala to Karasurimala	4.223± 0.00577	1.7747 ± 0.000577	2.96664 ± 0	716.51328 ± 0	116.256 ± 0	333.797 ± 0.052797
5	1260.8m	10°31' 50.1492"N 76°44' 25.6704"E	Karimala to Karasurimala	4.423 ± 0.01528	0.353 ± 0.000577	2.66156 ± 0.0298	744.61184 ± 0	14.8848 ± 0	175.84 ± 0
6	1252.1m	11°12'18"N 76°42' 17"E	Varadimala	4.867 ± 0.011547	0.022 ± 0.000577	0.316 ± 0.0258	252.88704 ± 0	19.9509 ± 0.0065	269.995± 0.106
7	1295.2m	11°2' 15"N 76°42' 19"E	Varadimala	5.64 ± 0.01	0.215 ± 0.001	2.872 ± 2.564E-16	772.7104 ± 0	17.6811 ± 0.0065	780.677 ± 0.0528
8	1422.8m	11°2' 23"N 76°42' 54"E	Varadimala	5.18 ± 0.01	0.112 ± 0.000577	2.4512± 0.0149	505.77408 ± 0	19.843 ± 0.0065	323.68 ± 0
9	1419.7m	11°2' 33"N 76°42' 54"E	Varadimala	5.22 ± 0.01	0.083 ± 0.001	4.734 ± 0	547.922 ± 0	15.471 ± 0.0067	268.8 ± 0
10	1405.8m	11°2' 32"N 76°42' 44"E	Varadimala	5.367 ± 0.011547	0.242 ± 0.001	2.4196 ± 0.0149	758.66112 ± 0	18.94293 ± 0.0065	319.2373 ± 0.0528
11	1341.7m	11°2' 21"N 76°43' 44"E	Varadimala	5.6267± 0.00577	0.27267 ± 0.000577	2.104 ± 0	842.9568 ± 0	21.0411 ± 0.0065	403.2 ± 0
12	1318.3m	11°2' 22"N 76°44' 10"E	Varadimala	5.707 ± 0.00577	0.436 ± 0.001	1.315 ± 0.0149	772.7104 ± 0	15.363 ± 0.0065	166.88 ± 0
13	1364.8m	11°2' 27"N 76°43' 38"E	Varadimala	5.96 ± 0.01	0.1583 ± 0.000577	1.753 ± 0.0248	505.77408 ± 0	15.20587 ± 0.0065	469.28 ± 0
14	887.4m	10°58'25.86"N 76°38' 4.07"E	Keralamedu	4.973 ± 0.00577	0.051 ± 0	1.8936 ± 0.0258	435.52768 ± 0	8.4971 ± 0.00646	100.837 ± 0.0528
15	936.6m	10°58'26.26"N 76°38'43.48"E	Keralamedu	5.13 ± 0.01	0.053 ± 0.001	0.4208 ± 0.0149	463.62624 ± 0	8.7099 ± 0.0065	45.547 ± 0.528
16	904.6m	10°58'25.92"N 76°39'55.62"E	Keralamedu	5.97 ± 0.0115	0.2313 ± 0.000577	1.81996 ± 0.0149	547.92192 ± 0	111.0891 ± 0.0065	137.76 ± 0

Samples	Altitude	Lat-Long	Location	pH Mean±SD	EC Mean±SD	OC (%) Mean±SD	N(Kg/ha) Mean±SD	P(Kg/ha) Mean±SD	K(Kg/ha) Mean±SD
17	897.3m	10°58'27.54"N 76°38' 52.49"E	Keralamedu	4.93 ± 0.01	0.0273 ± 0.000577	0.19988 ± 0.0149	295.03488 ± 0	9.67307 ± 0.0065	21.357 ± 0.052798
18	906.9m	10°58'17.97"N 76°39' 19.58"E	Keralamedu	4.94 ± 0.00577	0.1173 ± 0.000577	0.5996 ± 0.02577	224.78848 ± 0	14.4368 ± 0	69.5147 ± 0.0528
19	954.8m	10°57'56.56"N 76°39' 59.79"E	Keralamedu	5.52 ± 0.01	0.0347± 0.000577	1.14668 ± 0.014877	323.13344 ± 0	7.4592 ± 0	319.2 ± 0
20	1011.6m	10°30'9.57"N 76°41' 31.34"E	Anamedu and Mattumala	5.06 ± 0.00577	0.2913 ± 0.000577	1.9988 ± 0.0149	660.31616 ± 0	15.4 ± 0	280 ± 0
21	1120.9m	10°29'54.78"N 76°41' 47.93"E	Anamedu and Mattumala	5.93 ± 0.01	0.1263 ± 0.000577	2.0163 ± 0.024796	435.52768 ± 0	23.13547 ± 0.0065	518.635 ± 0.052797
22	1226.3m	10°30'9.30"N 76°42' 13.51"E	Anamedu and Mattumala	5.67 ± 0.01	0.0983 ± 0.000577	2.0514 ± 0	421.4784 ± 0	30.7477 ± 0.0067	557.76 ± 0
23	1187.0m	10°30'4.71"N 76°42' 10.87"E	Anamedu and Mattumala	5.37 ± 0.0153	0.053 ± 0.000577	2.83689± 0.0049	337.18272 ± 0	27.05547 ± 0.00647	655.312 ± 0.091447
24	1145.4m	10°26'15"N 76°38' 48"E	Pothumala	5.13 ± 0.01	0.1073 ± 0.000577	3.61187 ± 0.0248	590.06976 ± 0	22.1872 ± 0	246.4 ± 1.6409E-14
25	1142.3m	10°26'16"N 76°38' 46"E	Pothumala	4.86 ± 0.01	0.11467 ± 0.000577	4.41139± 0.0049	604.11904 ± 0	35.4816 ± 0	144.48 ± 0
26	1219.4m	10°26' 5"N 76°38' 45"E	Pothumala	5.17 ± 0.01	0.2077 ± 0.000577	3.01924 ± 0.041	871.05536 ± 0	32.5770 ± 0.00646	474.88 ± 0
27	1117.4m	10°26'20"N 76°38' 51"E	Pothumala	5.2567 ± 0.01528	0.1527 ± 0.000577	4.5236 ± 0	632.2176 ± 0	32.2597 ± 0.0064	311.36 ± 0
28	1140.6m	10°30'41.993"N 76°42' 36.079"E	Sisilimala	5.117 ± 0.01528	0.0573 ± 0.000577	2.82287 ± 0.025	449.57696 ± 0	21.982± 0.0065	286.72 ± 0
29	1078.4m	10°33'27"N 76°44' 28"E	Valiyamanpara	5.2267 ± 0.01528	0.0663 ± 0.000577	2.104 ± 0.0372	533.87264 ± 0	64.176 ± 0	193.76 ± 0
30	1073.6m	10°33' 33"N 76°44' 51"E	Valiyamanpara	5.043 ± 0.00577	0.08167 ± 0.000577	1.5254 ± 0.0372	295.03488 ± 0	75.6373 ± 0.006	68.32 ± 0
31	1221.4m	10°33' 27"N 76°45' 24"E	Valiyamanpara	5.377± 0.01155	0.197 ± 0.001	2.752± 0.025	618.16832 ± 0	30.1616 ± 0	400.96 ± 0
32	1411.5m	10°31' 27.114"N 76°44' 18.037"E	Karasurimala	5.257 ± 0.01528	0.041 ± 0.0006	6.26 ± 0.074	660.31616 ± 0	30.782 ± 0.0065	240.8 ± 1.641E-14

Samples	Altitude	Lat-Long	Location	pH Mean±SD	EC Mean±SD	OC (%) Mean±SD	N(Kg/ha) Mean±SD	P(Kg/ha) Mean±SD	K(Kg/ha) Mean±SD
33	1346.6m	10°31' 53.033"N 76°44' 37.039"E	Karasurimala	5.66 ± 0.01155	0.065 ± 0.000577	3.945 ± 0	407.43 ± 0	93.023 ± 0.0065	208.32 ± 0
34	1355.4m	10°31' 53.033"N 76°44' 37.039"E	Karasurimala	5.227 ± 0.01528	0.043 ± 0.000577	2.893 ± 0.04	491.7248 ± 0	37.158 ± 0.0065	259.84 ± 0
35	1292.5m	10°31' 42.758"N 76°43' 11.310"E	Mattumala	5.37 ± 0.061	0.018 ± 0.000577	1.14 ± 0.025	210.7392 ± 0	27.7387 ± 0.00646	14.56 ± 0
36	1289.304 m	10°32' 20"N 76°42' 53"E	Minnampara	4.507 ± 0.0115	0.0187 ± 0.000577	1.5079 ± 0.025	238.83776 ± 0	26.06 ± 0.0681	151.2 ± 0
37	1302.41m	10°31' 54"N 76°43' 49"E	Karimala	5.24 ± 0.01	0.143 ± 0.0005773	3.945 ± 0	519.82336 ± 0	35.76 ± 0.00646	287.84 ± 0
38	1282.598 m	10°31'47"N 76°43' 52"E	Karasurimala	5.47 ± 0.061	0.1163 ± 0.000577	2.9719 ± 0.0372	463.62624 ± 0	22.811 ± 0.0065	197.12 ± 0
39	1312.469 m	10°31' 47.7402"N 76°43' 9.8322"E	Mattumala	5.207± 0.006	0.057 ± 0.000577	1.841 ± 0	716.51328 ± 0	21.299 ± 0.0065	408.8 ± 0
40	1270.102 m	10°31' 58"N 76°44' 33"E	Karasurimala	5.213± 0.0115	0.3337 ± 0.000577	1.7358 ± 0	730.56256 ± 0	28.653 ± 0.00646	428.96 ± 0
41	904.0368 m	10°58' 18.062"N 76°39' 19.687"E	Keralamedu	5.57 ± 0.02	0.113 ± 0.001	3.13605 ± 0	196.68992 ± 0	42.75 ± 0.065	217.28 ± 1.641E-14
42	895.5024 m	10°58' 6.154"N 76°39' 28.843"E	Keralamedu	5.973 ± 0.0208	0.573 ± 0.000577	2.45 ± 0	491.72 ± 0	26.48 ± 0	191.52 ± 0
43	900.9888 m	10°58' 24.997"N 76°38' 50.158"E	Keralamedu	6.31 ± 0.0265	0.2853 ± 0.000577	2.1 ± 0	224.788 ± 0	145.84 ± 0.0065	235.2 ± 0
44	901.2936 m	10°58' 16.288"N 76°39' 19.326"E	Keralamedu	5.857± 0.0208	0.4183 ± 0.000577	0.94 ± 0.01286	154.54 ± 0	16.52 ± 0	267.68 ± 0
45	957.072m	10°57' 54.639"N 76°39' 59.311"E	Keralamedu	6.37 ± 0.021	0.033 ± 0.000577	1.43622 ± 0.0129	435.53 ± 0	17.0053 ± 0.0065	656.357 ± 0.0528
46	900.3762 m	10°58' 23.377"N 76°38' 57.255"E	Keralamedu	5.89± 0.021	0.161 ± 0.001	2.86335 ± 0	463.64 ± 0	31.44 ± 0.0065	281.12 ± 0
47	897.636m	10°58' 10.388"N 76°39' 10.632"E	Keralamedu	7.577 ± 0.021	0.4117 ± 0.000577	3.7875 ± 0.0214	266.94 ± 0	25.3717 ± 0.0065	153.44 ± 0

Table 7.3. The soil parameters Ca, Mg, S, B, Cu, Fe, Mn and Zn of 47 soil samples collected from sky islands of the Western Ghats across the Palghat gap within the study area.

Sample	Lat-Long	Ca(ppm) Mean±SD	Mg(ppm) Mean±SD	S (ppm) Mean±SD	B (ppm) Mean±SD	Cu (ppm) Mean±SD	Fe(ppm) Mean±SD	Mn (ppm) Mean±SD	Zn (ppm) Mean±SD
1	10°31'55"N 76°43' 48"E	345.417 ± 0.0722	253.142 ± 0.00722	37.3058 ± 0.0029	0.4035 ± 0.00012	0.36 ± 0.00577	23.423 ± 0.00577	14.15 ± 0.00577	0.916 ± 0.035
2	10°31'51.7296"N' 76°43' 46.1352"E	134.375 ± 0	104.6375 ± 0	36.3625 ± 0	0.3885± 0.00012	0.853± 0.00577	21.343 ± 0.22811	18.59 ± 0.00577	1.47 ± 0.344
3	10°31'55.092"N 76°43' 47.7012"E	176.42 ± 0.0722	129.167± 0.014	35.03917 ± 0.0014	0.4113± 0.0001155	0.3033 ± 0.005774	51.263 ± 0.00577	15.477± 0.00577	1.058 ± 0.05023
4	10°31'48.072"N 76°44' 17.934"E	500.208 ± 0.0722	226.108 ± 0.00722	41.077 ± 0.00144	0.4183 ± 0.0001155	0.73 ± 0.00577	47.66 ± 0.01	53.75 ± 0	6.159 ± 0
5	10°31'50.1492"N 76°44' 25.6704"E	73.21 ± 0.0722	51.88 ± 0.0144	35.24 ± 0	0.362 ± 0.0001155	0.463 ± 0.00577	50.31 ± 0.00577	3.87 ± 0	0.658 ± 0
6	11°12'18"N 76°42' 17"E	646.458 ± 0.0722	83.146 ± 0.00722	35.228 ± 0.00144	0.3745 ± 0.0001155	2.03 ± 0.0577	20.33 ± 0.021	92.1 ± 0	0.7 ± 0
7	11°2'15"N 76°42' 19"E	172.792 ± 0.0722	494.9 ± 0	43.43 ± 0.0014	0.3856 ± 0.00019	1.4167 ± 0.00577	24.72 ± 0.01	115.75 ± 0	6.343 ± 0
8	11°2' 23"N 76°42' 54"E	227.2083 ± 0.0722	112.7708 ± 0.00722	33.8142 ± 0.0014	0.4095 ± 0.0001155	0.3 ± 0	32.22 ± 0.0153	47.5 ± 0	1.587 ± 0.0003
9	11°2' 33"N 76°42' 54"E	202.083 ± 0.0722	99.383 ± 0.014	36.247± 0.0014	0.3868 ± 0	0.69 ± 0.00577	26.46 ± 0.01155	63.5 ± 0	1.82 ± 0.000577
10	11°2' 32"N 76°42' 44"E	188.875 ± 0.125	190.8875 ± 0	40.897 ± 0.0014	0.3781 ± 0.000115	0.303 ± 0.00577	39.34 ± 0.1097	23.277± 0.00577	0.735 ± 0
11	11°2' 21"N 76°43' 44"E	326.417 ± 0.0722	148.0458 ± 0.00721	37.8042 ± 0.0014	0.3727 ± 0.000115	0.917± 0.00577	18.963 ± 0.0153	46.25 ± 0	1.593 ± 0.0005774
12	11°2' 22"N 76°44' 10"E	444.875 ± 0	219.45 ± 0	46.7342 ± 0.00144	0.3743 ± 0.0001155	0.653 ± 0.005774	91.4317 ± 0.0029	71.17 ± 0.0577	3.469± 0.0005774
13	11°2' 27"N 76°43' 38"E	61.33 ± 0.0722	266.2042 ± 0.014	37.21 ± 0.00144	0.36473± 0.0001155	0.49 ± 0.005774	12.117 ± 0.0153	106.75 ± 0	1.726 ± 0
14	10°58' 25.86"N 76°38' 4.07"E	35.375 ± 0	90.283 ± 0.00722	34.8892 ± 0.001	0.365± 0.0001155	1.157 ± 0.00577	22.273 ± 0.01155	52 ± 0	1.158 ± 0

Sample	Lat-Long	Ca(ppm) Mean±SD	Mg(ppm) Mean±SD	S (ppm) Mean±SD	B (ppm) Mean±SD	Cu (ppm) Mean±SD	Fe(ppm) Mean±SD	Mn (ppm) Mean±SD	Zn (ppm) Mean±SD
15	10°58' 26.26"N 76°38' 43.48"E	167. ± 0	38.571 ± 0.00722	41.1342 ± 0.0014	0.3527 ± 0.000115	1.153 ± 0.00577	23.957 ± 0.01155	15.1 ± 0	1.304 ± 0.0005774
16	10°58' 25.92"N 76°39' 55.62"E	188.875 ± 0.125	107.5125 ± 0	36.3142 ± 0.0014	0.3583 ± 0.0001155	0.487 ± 0.00577	9.207 ± 0.00577	35.247 ± 0.00577	2.085 ± 0
17	10°58' 27.54"N 76°38' 52.49"E	16.958 ± 0.0722	27.7292 ± 0.014	33.342 ± 0.0014	0.3427 ± 0.0001155	0.763 ± 0.00577	12.113 ± 0.00577	6.657 ± 0.00577	1.004 ± 0
18	10°58' 17.97"N 76°39' 19.58"E	65.875 ± 0	69.792 ± 0.014	36.9142 ± 0.0014	0.347 ± 0	0.71 ± 0	7.83 ± 0.01155	24.087 ± 0.00577	0.8987± 0.000577
19	10°57' 56.56"N 76°39' 59.79"E	122.75 ± 0	160.47 ± 0.0144	50.6392 ± 0.0014	0.3715 ± 0.0001155	1.453 ± 0.00577	20.11 ± 0.010	51.183 ± 0.00577	0.9137± 0.000577
20	10°30' 9.57"N 76°41' 31.34"E	168.458 ± 0.0722	218.025 ± 0	48.75 ± 0.0014	0.347± 0.00012	9.46 ± 0.01	15.87 ± 0.0153	51.92 ± 0	1.6253 ± 0.0005774
21	10°29' 54.78"N 76°41' 47.93"E	222.125 ± 0	228.48 ± 0.014	46.11 ± 0.0014	0.35747 ± 0.00012	1.257 ± 0.00577	23.21 ± 0	79.75 ± 0	2.376 ± 0
22	10°30' 9.30"N 76°42' 13.51"E	155.875 ± 0	193.483 ± 0.00722	48.297 ± 0.0014	0.4187 ± 0.00012	1.07 ± 0.0058	34.68 ± 0.01155	49.827 ± 0.00577	1.327± 0.00577
23	10°30' 4.71"N 76°42' 10.87"E	113.2917 ± 0.0722	135.2 ± 0	37.053 ± 0.0014	0.4283 ± 0.00012	1.05 ± 0.00577	34.35 ± 0.01	57.42 ± 0.0058	1.203 ± 0
24	10°26' 15"N 76°38' 48"E	176.375 ± 0.125	131.65 ± 0	35.642 ± 0.0014	0.44227 ± 0.00012	0.70 ± 0.00577	89.86 ± 0.00577	47.04 ± 0	1.222± 0.000577
25	10°26' 16"N 76°38' 46"E	93.33 ± 0.0722	74.9 ± 0	38.5142 ± 0.001	0.4353 ± 0.00012	0.413± 0.00577	80.02 ± 0.010	21.84 ± 0	2.33 ± 0.000577
26	10°26' 5"N 76°38' 45"E	288.875 ± 0	223.0083 ± 0.014	49.66 ± 0	0.415 ± 0	0.337 ± 0.006	72.52 ± 0.0153	60.46 ± 0	2.21 ± 0
27	10°26' 20"N 76°38' 51"E	227 ± 0	168.158 ± 0.00722	37.735 ± 0	0.4092 ± 0	0.5 ± 0	68.98 ± 0.01	60.06 ± 0	1.452 ± 0
28	10°30' 41.993"N 76°42' 36.079"E	45.17± 0.0722	92.65 ± 0	37.502 ± 0.0014	0.386 ± 0.00012	0.38 ± 0.01	42.27 ± 0.058	27.45 ± 0	0.493 ± 0
29	10°33' 27"N 76°44' 28"E	67.125 ± 0	40.542 ± 0.02	34.3675 ± 0	0.41 ± 0.00011	0.86 ± 0.00577	37.73± 0.05	42.95 ± 0	2.208 ± 0
30	10°33' 33"N 76°44' 51"E	49.625 ± 0	77.542 ± 0.014	38.0592 ± 0.0014	0.3695 ± 0.00012	1.8567 ± 0.006	4.847 ± 0.05	36.96 ± 0	1.833 ± 0

Sample	Lat-Long	Ca(ppm) Mean±SD	Mg(ppm) Mean±SD	S (ppm) Mean±SD	B (ppm) Mean±SD	Cu (ppm) Mean±SD	Fe(ppm) Mean±SD	Mn (ppm) Mean±SD	Zn (ppm) Mean±SD
31	10°33' 27"N 76°45' 24"E	259.58 ± 0.0722	173.896 ± 0.00722	41.1575 ± 0	0.361 ± 0.0001155	0.62 ± 0	70 ± 0	71 ± 0	1.074 ± 0
32	10°31' 27.114"N 76°44' 18.037"E	119.8 ± 0.0722	72.65 ± 0	39.6125 ± 0	0.3242 ± 0	0.283 ± 0.00577	22.67 ± 0.00577	21.54 ± 0	1.151 ± 0
33	10°31' 53.033"N 76°44' 37.039"E	119.25 ± 0	67.83± 0.00722	32.951± 0.0014	0.34 ± 0.0001155	0.527 ± 0.00577	26.6 ± 0	26.9 ± 0	1.4087 ± 0.000577
34	10°31' 53.033"N 76°44' 37.039"E	31.958 ± 0.0722	57.017± 0.014	28.38± 0.0014	0.331 ± 0.00012	1.71 ± 0	27.217± 0.006	20.257 ± 0.00577	1.015 ± 0
35	10°31' 42.758"N 76°43' 11.310"E	41.875 ± 0.22	0.7875 ± 0.022	28.2725 ± 0	0.4047 ± 0.00012	0.35 ± 0	39.157 ± 0.01155	0.62 ± 0	0.4377± 0.000577
36	10°32' 20"N 76°42' 53"E	133.875 ± 0	57.83 ± 0.00722	34.13 ± 0.001	0.32± 0.0001155	1.15 ± 0	49.39 ± 0	11.03 ± 0.01	1.92 ± 0.00577
37	10°31' 54"N 76°43' 49"E	463.33± 0.0722	391.821 ± 0.00722	30.8975 ± 0	0.339 ± 0	0.52 ± 0	26.95 ± 0.01	51.74 ± 0.01155	4.538 ± 0
38	10°31' 47"N 76°43' 52"E	283. ± 0	319.8875 ± 0	30.092 ± 0.0014	0.3445± 0.00012	1.44 ± 0.00577	38.61 ± 0.0577	18.94 ± 0	1.375 ± 0
39	10°31'47.7402"N 76°43' 9.8322"E	261.875 ± 0	7214.375 ± 0	30.76 ± 0.001	0.3957 ± 0.00012	0.92± 0.00577	16.53 ± 0	56.74 ± 0.006	3.81± 0.000577
40	10°31' 58"N 76°44' 33"E	129.75 ± 0	7401.875 ± 0	33.737 ± 0.0014	0.3552 ± 0.0002	0.48 ± 0	71.527 ± 0.0153	35.887 ± 0.00577	3.799 ± 0.000577
41	10°58'18.062"N 76°39' 19.687"E	364.458 ± 0.072	347.771 ± 0.00722	30.5783 ± 0.001	0.3343 ± 0.0001155	0.453 ± 0.00577	5.863 ± 0.00577	8.81 ± 0	2.186 ± 0
42	10°58' 6.154"N 76°39' 28.843"E	329.08± 0.0722	379.48 ± 0.00722	31.8683 ± 0.001	0.3173 ± 0.0001155	0.39 ± 0	13.32 ± 0.01155	47.32 ± 0	4.359± 0.000577
43	10°58'24.997"N 76°38' 50.158"E	199.375 ± 0	201.396 ± 0.00722	35.238 ± 0.00144	0.3343 ± 0.0001155	0.33 ± 0.00577	7.74 ± 0	5.73 ± 0.00577	2.132 ± 0.000577
44	10°58'16.288"N 76°39' 19.326"E	24.583 ± 0.0722	103.892 ± 0.014	28.0375 ± 0	0.31473 ± 0.0001155	1.12 ± 0	28.477 ± 0.0153	6.63 ± 0.01155	1.2253 ± 0.000577
45	10°57'54.639"N 76°39' 59.311"E	184.458 ± 0.0722	245.458 ± 0.00722	30.9258± 0.001	0.3224 ± 0.0002	0.713 ± 0.00577	5.87 ± 0.01	3.64± 0.00577	0.616 ± 0
46	10°58' 23.377"N 76°38' 57.255"E	257.71± 0.0722	209.771 ± 0.00722	34.2142 ± 0.0014	0.3272 ± 0	0.64 ± 0.00577	17.93 ± 0.00577	8.67 ± 0.005773	2.777 ± 0.000577
47	10°58'10.388"N 76°39' 10.632"E	726.583 ± 0.0722	289.6375 ± 0.0125	30.051 ± 0.0014	0.3138 ± 0	0.223 ± 0.00577	21.513 ± 0.00577	5.363 ± 0.00577	0.1953± 0.000577

Table 7.4. The soil parameters Munsell Notations, Colour, Hue Value, Hue Variable, Value and Chroma of 47 soil samples from sky islands of the Western Ghats across the Palghat Gap within the study area.

Soil Samples	Lat-Long	Munsell Notation	Color	Hue Value	Hue Variable	Value	Chroma
1	10°31'55"N 76°43' 48"E	10R .2.5/2	Very dusky red	10	R	2.5	2
2	10°31'51.7296"N 76°43' 46.1352"E	5YR. 3/4	Dark reddish brown	5	YR	3	4
3	10°31' 55.092"N 76°43' 47.7012"E	7.5YR . 3/4	Dark brown	7.5	YR	3	4
4	10°31' 48.072"N 76°44' 17.934"E	7.5YR . 3/4	Dark brown	7.5	YR	3	4
5	10°31' 50.1492"N 76°44' 25.6704"E	5YR.3/4	Dark reddish brown	5	5YR	3	4
6	11°12'18"N 76°42' 17"E	7.5YR . 5/8	Strong brown	7.5	YR	5	8
7	11°2'15"N 76°42' 19"E	10YR. 3/2	Very dark geayish brown	10	10YR	3	2
8	11°2'23"N 76°42' 54"E	2.5Y. 3/2	Very dark greyish brown	2.5	Y	3	2
9	11°2'33"N 76°42' 54"E	10YR. 4/2	Dark greyish brown	10	YR	4	2
10	11°2'32"N 76°42' 44"E	10YR. 4/3	Dark brown	10	YR	4	3
11	11°2'21"N 76°43' 44"E	10YR. 4/1	Dark greay	10	YR	4	1
12	11°2'22"N 76°44' 10"E	10YR. 6/4	Light yellowish brown	10	YR	6	4
13	11°2'27"N 76°43' 38"E	2.5Y. 3/2	Very dark greyish brown	2.5	Y	3	2
14	10°58'25.86"N 76°38' 4.07"E	7.5YR. 5/6	Strong brown	7.5	YR	5	6
15	10°58'26.26"N 76°38' 43.48"E	5YR. 6/6	Reddish yellow	5	YR	6	6
16	10°58'25.92"N 76°39' 55.62"E	7.5YR. 5/6	Strong brown	7.5	YR	5	6
17	10°58'27.54"N 76°38' 52.49"E	7.5YR. 6/6	Reddish brown	7.5	YR	6	6
18	10°58'17.97"N 76°39' 19.58"E	10YR. 7/6	Yellow	10	YR	7	6
19	10°57'56.56"N 76°39' 59.79"E	7.5YR. 5/6	Strong brown	7.5	YR	5	6
20	10°30'9.57"N 76°41' 31.34"E	7.5YR. 4/4	Dark brown	7.5	YR	4	4
21	10°29'54.78"N 76°41' 47.93"E	10YR. 4/3	Dark brown	10	YR	4	3
22	10°30'9.30"N 76°42' 13.51"E	10YR. 3/3	Dark brown	10	YR	3	3
23	10°30'4.71"N 76°42' 10.87"E	10YR. 4/3	Dark brown	10	YR	4	3

Soil Samples	Lat-Long	Munsell Notation	Color	Hue Value	Hue Variable	Value	Chroma
24	10°26'15"N 76°38' 48"E	10YR. 4/4	Dark yellowish brown	10	YR	4	4
25	10°26'16"N 76°38' 46"E	10YR. 3/6	Dark yellowish brown	10	YR	3	6
26	10°26'5"N 76°38' 45"E	10YR. 3/4	Dark yellowish brown	10	YR	3	6
27	10°26'20"N 76°38' 51"E	10YR. 4/3	Dark brown	10	YR	4	3
28	10°30'41.993"N 76°42' 36.079"E	10YR. 4/4	Dark yellowish brown	10	YR	4	3
29	10°33'27"N 76°44' 28"E	10YR. 2/2	Very dark brown	10	YR	2	2
30	10°33'33"N 76°44' 51"E	10YR. 4/3	Dark brown	10	YR	4	3
31	10°33'27"N 76°45' 24"E	10YR. 4/3	Dark brown	10	10YR	4	3
32	10°31' 27.114"N 76°44' 18.037"E	10YR. 3/2	Very dark greyish brown	10	YR	3	2
33	10°31' 53.033"N 76°44' 37.039"E	10YR. 3/3	Dark brown	10	YR	3	3
34	10°31' 53.033"N 76°44' 37.039"E	10YR. 3/3	Dark brown	10	YR	3	3
35	10°31' 42.758"N 76°43' 11.310"E	10YR. 5/3	Brown	10	10YR	5	3
36	10°32' 20"N 76°42' 53"E	7.5YR. 4/6	Strong brown	7.5	YR	4	6
37	10°31' 54"N 76°43' 49"E	7.5YR. 3/2	Dark brown	7.5	YR	3	2
38	10°31' 47"N 76°43' 52"E	7.5YR. 3/4	Dark brown	7.5	YR	3	4
39	10°31' 47.7402"N 76°43' 9.8322"E	5YR. 3/2	Dark reddish brown	5	YR	3	2
40	10°31' 58"N 76°44' 33"E	1OYR. 3/3	Dark brown	10	YR	3	3
41	10°58' 18.062"N 76°39' 19.687"E	7.5YR. 4/6	Strong brown	7.5	YR	4	6
42	10°58' 6.154"N 76°39' 28.843"E	5YR. 3/4	Dark reddish brown	5	YR	3	4
43	10°58' 24.997"N 76°38' 50.158"E	5YR. 5/6	Yellowish red	5	YR	5	6
44	10°58' 16.288"N 76°39' 19.326"E	2.5YR. 4/6	Red	2.5	YR	4	6
45	10°57' 54.639"N 76°39' 59.311"E	7.5YR. 5/6	Strong brown	7.5	YR	5	6
46	10°58' 23.377"N 76°38' 57.255"E	5YR. ¾	Dark reddish brown	5	YR	3	4
47	10°58' 10.388"N 76°39' 10.632"E	10YR. 4/3	Dark brown	10	YR	4	3

they may be found to be the same. To make colour more precise and discrete, Munsell notation was considered for defining the colour of the sample. As per that the southern sides soil samples Munsell notations hue value ranged from 5-10, value ranged from 2.5-4, and chroma ranged from 2-6. The sky islands soil from northern side Munsell notations ranges were hue value 2.5-10, value 3-6, and chroma ranged from 1-6. Here as we compare northern and southern soil samples based on Munsell notation values, the maximum and minimum values of its the ranges vary.

Mean values of the Munsell notation components of the soil samples of sky islands across the Palghat Gap, showed distinct variations across the Palghat Gap. As per the analysis done over the soil sample colour, some soil sample even though they had similar colour, but they differed as per the Munsell notation component values. This visually presents the possible variability in the edaphic environment of sky islands across Palghat Gap in different aspects.

7.3.3. Soil texture

The soil texture is one of the important parameters of soil, which refers to the relative composition of sand, silt, and clay particles and was determined using the USDA textural classification system. Soil texture influences several parameters, including its ability to retain water and allow water to permeate. In 47 soil samples, the soil texture exhibited significant variation in texture (Table 7.5). Among these various textures, the predominant types of texture observed within the sky islands region were Sandy loam accounted for 55.32 % of the samples, Sandy clay loam was 34.04%, and Loamy sand 10.64% of the samples. Upon comparing the soil texture variations across the Palghat Gap, it is noteworthy that Loamy sand is relatively less common on both sides of the gap. That is 15.38 % of soil samples from southern side and 4.77% of soil samples from northern side were loamy sand. That is more % of soil samples were loamy sand over sky islands of Western Ghats on the southern side of Palghat Gap. In contrast, Sandy loam and Sandy clay loam exhibited higher and distinct distribution patterns over northern sky islands. Sandy loam is notably predominant in the southern sky islands with 61.54%, and over the northern side it was about 47.62%. Then the Sandy clay loam, which is more prominently found over the northern side with 47.62% and 23.08 % over southern sky islands. That is, in northern sky islands sandy clay loam and sandy loam were equally found (Table 7.5).

Table 7.5. Soil texture of 47 soil samples collected from sky islands of the Western Ghats on the northern and southern side of the Palghat Gap within the study area.

Samples	Clay (%)	Silt (%)	Sand (%)	Soil texture
1	26.16	4	69.84	Sandy clay loam
2	28.16	4	67.84	Sandy clay loam
3	26.16	4	69.84	Sandy clay loam
4	18.16	6	75.84	Sandy loam
5	30.16	4	65.84	Sandy clay loam
6	34.16	4	61.84	Sandy clay loam
7	14.16	6	79.84	Sandy loam
8	20.16	6	73.84	Sandy clay loam
9	16.16	6	77.84	Sandy loam
10	22.16	4	73.84	Sandy clay loam
11	14.16	2	83.84	Sandy loam
12	24.16	4	71.84	Sandy clay loam
13	12.16	4	83.84	Loamy sand
14	26.16	6	67.84	Sandy clay loam
15	24.16	8	67.84	Sandy clay loam
16	16.16	4	79.84	Sandy loam
17	20.16	8	71.84	Sandy clay loam
18	18.16	8	73.84	Sandy loam
19	30.16	4	65.84	Sandy clay loam
20	16.16	4	79.84	Sandy loam
21	14.16	6	79.84	Sandy loam
22	14.16	4	81.84	Sandy loam
23	26.16	2	71.84	Sandy loam
24	16.16	4	79.84	Sandy loam
25	16.16	6	77.84	sandy loam
26	14.16	2	83.84	Sandy loam
27	16.16	4	79.84	Sandy loam
28	26.16	6	67.84	Sandy clay loam
29	14.16	4	81.84	Sandy loam
30	14.16	2	83.84	Sandy loam
31	14.16	6	79.84	Sandy loam
32	14.16	6	79.84	Sandy loam
33	12.16	2	85.84	Loamy sand
34	16.16	6	77.84	Sandy loam
35	12.16	2	85.84	Loamy sand
36	18.16	8	73.84	Sandy loam
37	12.16	2	85.84	Loamy sand
38	16.16	4	79.84	Sandy loam
39	12.16	2	85.84	Loamy sand
40	20.16	6	73.84	Sandy clay loam
41	16.16	8	75.84	Sandy loam
42	18.16	2	79.84	Sandy loam
43	16.16	4	79.84	Sandy loam
44	28.16	10	61.84	Sandy clay loam
45	22.16	6	71.84	Sandy clay loam
46	16.16	4	79.84	Sandy loam
47	14.16	4	81.84	Sandy loam

7.3.4. Soil pH

The pH value of 47 soil samples ranged from 4.2 to 7.58. That is, it's not too basic and slightly acidic. Even though the variance of pH value between samples were minimum, but there was variance between samples within the sky islands across Palghat Gap. But the variation of soil pH across Palghat Gap appeared to be within a confined range. That is pH value of soil samples towards the southern side ranged from 4.2 to 5.93, and then towards the northern side the pH value ranged from 4.8 to 7.58. That is, by comparing the mean value of pH of soil samples across Palghat Gap, soil samples on the southern side are more acidic than the northern side (Table 7.2).

7.3.5. Electrical conductivity (EC)

EC of 47 soil samples from sky islands of Western Ghats across Palghat Gap were evaluated and analysed and found that the EC value of these samples ranged from 0.022 - 1.774. Higher EC values were found over the soil samples from sky islands on the southern side of Palghat Gap. All the samples were found to show different EC values, thereby defining that each sample was unique, but soil samples across Palghat Gap EC value range appear to be connected. That is the EC value of soil samples from the Southern side ranged from 0.043 to 1.774 and in the northern side the value ranged within 0.02 to 0.436. Higher EC content is over the southern side sky islands (Table 7.2).

7.3.6. Estimation of Nitrogen

Nitrogen content of the soil samples ranged from 295 to 871 kg/ha. The Nitrogen content variation between soil samples was there but the variation of nitrogen content between the sky islands across Palghat was not distinct. The soil N content on southern sky islands ranged from 295 to 871 kg/ha. But in northern sky islands it ranged from 154 to 842 kg/ha (Table 7.2).

7.3.7. Estimation of Phosphorus

The phosphorus content within the soil of the sky islands exhibited a range from 7.46 to 145 kg/ha. In the northern region of the Palghat Gap, the soil phosphorus content varied within a range from 7.46 to 145.836 kg/ha. In the southern sky islands, the phosphorus content ranged from 14.885 to 116.256 kg/ha. Higher concentration of phosphorus found over the soil samples over the northern sky islands samples (Table 7.2).

7.3.8. Estimation of exchangeable Potassium

The potassium (K) content of the individual soil samples exhibits significant variation ranging from 14.56 to 780 kg/ha. In the soil samples from the southern region of the sky islands, the potassium content within the soil ranged from 14.56 to 655 kg/ha. In the northern region of the sky islands, the potassium content ranged from 21.35 to 780 kg/ha. It is noteworthy that the variation in potassium content across the Palghat Gap region does not display a distinct pattern (Table 7.2).

7.3.9. Estimation of Organic Carbon

The percentage of organic carbon (OC%) content of each soil sample was assessed, and thereby revealed the distinct variations found between the soil samples collected from different locations of sky islands within the study area. In the southern sky islands, the OC % content ranged from 1.51 to 4.52 %, while in the northern sky islands, it ranged from 0.20 to 4.73% (Table 7.2).

7.3.10. Estimation of Calcium and Magnesium

The calcium (Ca) content within the soil samples from the sky islands under study exhibited a range spanning from 24 to 646 ppm, while the magnesium (Mg) content ranged from 0.79 to 7401 ppm. The variation in calcium content across the Palghat Gap exhibited less distinctiveness, but with higher concentrations observed in the northern sky islands. The variation in magnesium content across the Palghat Gap was notably pronounced, with elevated magnesium levels predominantly found in soil samples from the southern sky islands (Table 7.3).

7.3.11. Estimation of Sulphur

The sulphur content within the soil samples exhibits variability among individual samples, yet this variation does not display distinct patterns across the Palghat Gap. Specifically, the sulphur content ranges from 28 to 49 ppm in the southern sky islands and from 28 to 50 ppm in the northern sky islands (Table 7.3).

7.3.12. Estimation of Fe, Mn. Zn and Copper

The iron (Fe) content of soil samples collected from the southern sky Islands exhibited a range from 15.86 to 89.86 ppm, while in the northern sky islands, the Fe content ranged from 5.86 to 91.432 ppm. Moving on to manganese (Mn) content, in the soil sample from southern sky islands ranged from 0.62 to 79 ppm, whereas in the northern sky islands, the Mn content varied between 3.6333 to 115 ppm. Regarding zinc (Zn) levels, the southern sky islands exhibited a Zn content range of 0.66 to 6.16 ppm, while in the northern sky islands, Zn content ranged from 0.616 to 6.343 ppm.

Additionally, the copper (Cu) content of soil samples collected from the southern sky islands ranged from 0.34 to 9.46 ppm, while in the northern sky islands, the Cu content in the soil varied from 0.22 to 2.03 ppm. Notably, the Cu content was observed to be higher in the southern sky islands (Table 7.3).

7.3.13. Estimation of Boron

The boron (B) content within soil samples collected from the southern sky islands ranged from 0.322 to 0.454 ppm, while in the northern sky islands, where the B content varied between 0.314 to 0.41 ppm. Interestingly, there is no discernible difference found in boron content across the Palghat Gap (Table 7.3).

7.3.14. Analysis of edaphic parameters of sky islands: -

The significant level of variance was accessed through Kruskal-Wallis test. The Kruskal-Wallis test results revealed that all edaphic parameters (Table 7.6), had statistically significant differences at the significance level of 0.05. Significant variations were observed in all the considered soil parameters, as indicated by the analysis. The parameters with significant levels of variance were pH, EC, OC%, N (kg/ha), P (kg/ha), K (kg/ha), Ca (ppm), Mg (ppm), S (ppm), Mn (ppm), Zn (ppm), Cu (ppm), B (ppm), Fe (ppm), Clay%, Silt%, Sand%, colour, and Texture (Table 7.6). All these aforementioned parameters exhibited a significant level of variation at $P \leq 0.05$.

Table 7.6. Kruskal Wallis test statistics over soil parameters (pH, OC, N, P, K, Ca, Mg, S, B, Cu, Fe, Mn, Zn, Clay, Silt and Sand) of soil samples from sky islands of the Western Ghats across the Palghat Gap within the study area, to analyse significant correlations at 0.05.

Edaphic parameters	Chi-Square	df	Asymp. Sig.
pH	139.616	46	0
OC	139.79	46	0
N	140	46	0
P	139.947	46	0
K	139.985	46	0
Ca	139.959	46	0
Mg	139.97	46	0
S	139.964	46	0
B	139.954	46	0
Cu	139.888	46	0
Fe	139.945	46	0
Mn	139.981	46	0
Zn	139.155	46	0
Clay	140	46	0
Silt	140	46	0
Sand	140	46	0

This shows that each edaphic parameter played a significant role in making each location distinct with its own unique edaphic environment. This justifies that all these 19 edaphic parameters showed statistically significant variability between the samples from sky islands. This thereby demonstrates that the edaphic parameters also act as one of the factors with important role in isolating the habitat. Therefore, the species inhabiting in different location within the sky islands are found to be exposed to a different edaphic environment, thereby substantiating the fact that edaphic elements may also have been a cause for the intraspecific variability found in populations of *E. gadgilii*, as it provides the diversity in edaphic environment to evolve. Furthermore, the relationships among these parameters were analysed using a correlation matrix, applying Spearman's rho coefficient statistics. This method involves a two-tailed significance test with a default significance level of 0.05 (Tables 7.7 and 7.8). This analysis helps to identify antagonistic and synergistic effects among the soil parameters. The significant correlations between these edaphic parameters are subsequently discussed.

7.3.14.1. Soil colour in relation to Organic Carbon and micro-macro nutrients

Soil colour emerged as a pivotal determinant for the assessment of vital soil attributes encompassing organic content, mineral constituents and drainage capability. The hue of soil assumes significance as it offers insights into its inherent qualities. A darker soil colour signifies an augmented presence of organic substances, indicative of sluggish drainage properties. In contrast, a lighter soil colour points towards diminished organic content and heightened leaching propensity. Furthermore, the visual assessment of soil colour bestows valuable insights into its mineral composition. Notably, variations in red hues are chiefly attributable to the prevalence of iron minerals. The array of soil colours, including yellow, red, grey, black, or brown, are indicative of the underlying edaphic components within the soil matrix. The intricate interplay of biological and chemical processes within the soil ecosystem is effectively elucidated through the medium of soil colour. This influence of multifaceted interactions gives rise to the diverse spectrum of colours observed in soil. In summation, soil colour serves as an illuminating indicator, facilitating the comprehension of intricate soil dynamics (Schulze *et al*., 1993).

The results depicted in Table 7.7, revealed the outcomes of this rigorous examination unveiled robust and statistically significant correlations that underscored

Table 7.7. Spearman correlation of Edaphic parameters (Hue Value, Value, Chroma, pH, EC, OC and N) of 47 soil samples from sky islands of the Western Ghats across the Palghat Gap within the study area, to analyse significant correlations at 0.05 and 0.01.

			Hue Value	Value	Chroma	pH	EC	OC	N	Fe (ppm)	Mn (ppm)	Zn (ppm)
Spearman's rho	Hue Value	Correlation Coefficient	1	0.005	-.356*	0.008	-0.115	.316*	0.139	.374**	0.215	-0.135
		Sig. (2-tailed)		0.976	0.014	0.959	0.443	0.031	0.352	0.01	0.146	0.366
		N	47	47	47	47	47	47	47	47	47	47
	Value	Correlation Coefficient	0.005	1	.522**	0.127	-.315*	-.584**	-.401**	-0.277	-0.071	-.359*
		Sig. (2-tailed)	0.976		0	0.395	0.031	0	0.005	0.059	0.633	0.013
		N	47	47	47	47	47	47	47	47	47	47
	Chroma	Correlation Coefficient	-.356*	.522**	1	-0.148	-0.09	-.396**	-.350*	-0.122	-.303*	-0.142
		Sig. (2-tailed)	0.014	0		0.322	0.548	0.006	0.016	0.413	0.038	0.342
		N	47	47	47	47	47	47	47	47	47	47
	pH	Correlation Coefficient	0.008	0.127	-0.148	1	0.094	-0.033	-0.167	-.292*	0.021	0.13
		Sig. (2-tailed)	0.959	0.395	0.322		0.53	0.828	0.261	0.046	0.891	0.383
		N	47	47	47	47	47	47	47	47	47	47
	EC	Correlation Coefficient	-0.115	-.315*	-0.09	0.094	1	0.248	.433**	0.129	0.034	.322*
		Sig. (2-tailed)	0.443	0.031	0.548	0.53		0.093	0.002	0.386	0.819	0.027
		N	47	47	47	47	47	47	47	47	47	47
	OC	Correlation Coefficient	.316*	-.584**	-.396**	-0.033	0.248	1	.318*	.301*	0.057	0.156
		Sig. (2-tailed)	0.031	0	0.006	0.828	0.093		0.029	0.04	0.704	0.295
		N	47	47	47	47	47	47	47	47	47	47
	N	Correlation Coefficient	0.139	-.401**	-.350*	-0.167	.433**	.318*	1	.426**	.399**	.361*
		Sig. (2-tailed)	0.352	0.005	0.016	0.261	0.002	0.029		0.003	0.005	0.013
		N	47	47	47	47	47	47	47	47	47	47
	P (kg/ha)	Correlation Coefficient	0.211	-.353*	-0.097	0.146	0.071	.436**	0.009	0.098	-0.06	.406**
		Sig. (2-tailed)	0.155	0.015	0.515	0.326	0.634	0.002	0.95	0.514	0.689	0.005
		N	47	47	47	47	47	47	47	47	47	47
	K (kg/ha)	Correlation Coefficient	0.115	-.380**	-.418**	0.199	0.192	0.207	.333*	0.13	.439**	0.143
		Sig. (2-tailed)	0.442	0.008	0.003	0.179	0.196	0.163	0.022	0.385	0.002	0.339
		N	47	47	47	47	47	47	47	47	47	47
	Ca (ppm)	Correlation Coefficient	-0.053	-0.112	-0.081	0.204	.418**	.316*	0.253	0.008	0.25	.328*
		Sig. (2-tailed)	0.722	0.455	0.586	0.168	0.003	0.031	0.086	0.959	0.09	0.024
		N	47	47	47	47	47	47	47	47	47	47

		Hue Value	Value	Chroma	pH	EC	OC	N	Fe (ppm)	Mn (ppm)	Zn (ppm)
Mg (ppm)	Correlation Coefficient	-0.092	-0.276	-0.213	.427**	.495**	0.218	0.259	-0.098	.314*	.457**
	Sig. (2-tailed)	0.538	0.061	0.15	0.003	0	0.141	0.079	0.512	0.032	0.001
	N	47	47	47	47	47	47	47	47	47	47
S (ppm)	Correlation Coefficient	.320*	0.087	-0.039	-0.127	0.174	0.015	.413**	0.166	.521**	0.122
	Sig. (2-tailed)	0.028	0.56	0.795	0.395	0.243	0.919	0.004	0.265	0	0.414
	N	47	47	47	47	47	47	47	47	47	47
B (ppm)	Correlation Coefficient	.311*	-0.214	-0.238	-.410**	0.023	0.18	.381**	.482**	.430**	0.055
	Sig. (2-tailed)	0.033	0.148	0.108	0.004	0.88	0.225	0.008	0.001	0.003	0.716
	N	47	47	47	47	47	47	47	47	47	47
Cu (ppm)	Correlation Coefficient	-0.062	0.208	0.169	-0.115	-.324*	-.391**	-0.16	-0.206	.298*	0.095
	Sig. (2-tailed)	0.677	0.161	0.256	0.44	0.026	0.007	0.283	0.164	0.042	0.526
	N	47	47	47	47	47	47	47	47	47	47
Fe (ppm)	Correlation Coefficient	.374**	-0.277	-0.122	-.292*	0.129	.301*	.426**	1	0.151	0.007
	Sig. (2-tailed)	0.01	0.059	0.413	0.046	0.386	0.04	0.003		0.309	0.963
	N	47	47	47	47	47	47	47	47	47	47
Mn (ppm)	Correlation Coefficient	0.215	-0.071	-.303*	0.021	0.034	0.057	.399**	0.151	1	.412**
	Sig. (2-tailed)	0.146	0.633	0.038	0.891	0.819	0.704	0.005	0.309		0.004
	N	47	47	47	47	47	47	47	47	47	47
Zn (ppm)	Correlation Coefficient	-0.135	-.359*	-0.142	0.13	.322*	0.156	.361*	0.007	.412**	1
	Sig. (2-tailed)	0.366	0.013	0.342	0.383	0.027	0.295	0.013	0.963	0.004	
	N	47	47	47	47	47	47	47	47	47	47
Clay (%)	Correlation Coefficient	-.308*	0.271	.510**	-.382**	0.1	-0.274	-0.107	0.089	-0.21	-.376**
	Sig. (2-tailed)	0.035	0.065	0	0.008	0.505	0.063	0.476	0.554	0.157	0.009
	N	47	47	47	47	47	47	47	47	47	47
Silt (%)	Correlation Coefficient	-0.093	0.245	.314*	-0.182	-0.155	-0.16	-0.198	0.018	-0.189	-0.111
	Sig. (2-tailed)	0.534	0.097	0.032	0.22	0.299	0.283	0.183	0.904	0.204	0.458
	N	47	47	47	47	47	47	47	47	47	47
Sand (%)	Correlation Coefficient	0.271	-.301*	-.496**	.395**	-0.004	0.278	0.144	-0.09	0.204	.401**
	Sig. (2-tailed)	0.065	0.039	0	0.006	0.976	0.058	0.336	0.548	0.169	0.005
	N	47	47	47	47	47	47	47	47	47	47

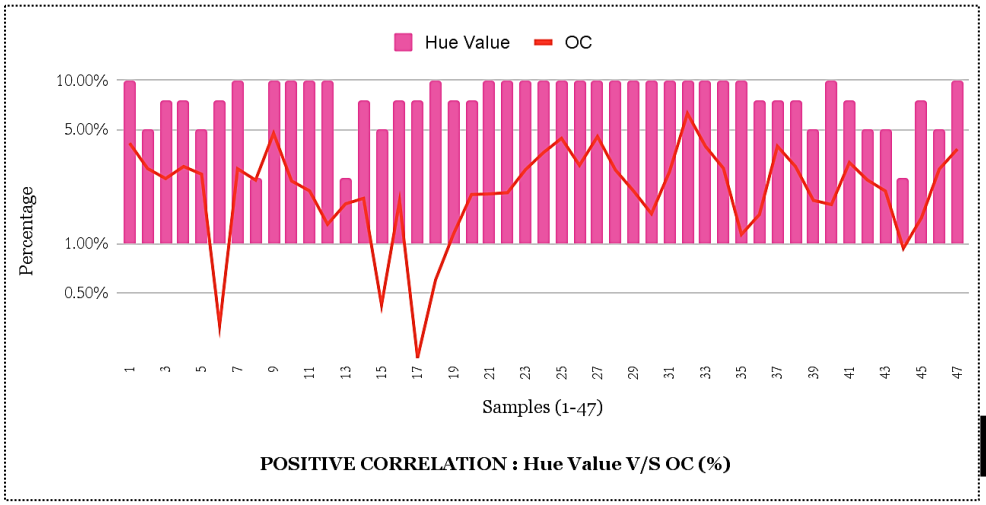
****. Correlation is significant at the 0.01 level (2-tailed), *. Correlation is significant at the 0.05 level (2-tailed).**

Table 7.8. Spearman correlation of Edaphic parameters (P, K, Ca, Mg, S, B, Cu, Clay, Silt, and Sand) of 47 soil samples from sky islands of the Western Ghats across the Palghat Gap within the study area, to analyse significant correlations at 0.05 and 0.01.

			P (kg/ha)	K (kg/ha)	Ca (ppm)	Mg (ppm)	S (ppm)	B (ppm)	Cu (ppm)	Clay (%)	Silt (%)	Sand (%)
Spearman's rho	Hue Value	Correlation Coefficient	0.211	0.115	-0.053	-0.092	.320*	.311*	-0.062	-.308*	-0.093	0.271
		Sig. (2-tailed)	0.155	0.442	0.722	0.538	0.028	0.033	0.677	0.035	0.534	0.065
		N	47	47	47	47	47	47	47	47	47	47
	Value	Correlation Coefficient	-.353*	-.380**	-0.112	-0.276	0.087	-0.214	0.208	0.271	0.245	-.301*
		Sig. (2-tailed)	0.015	0.008	0.455	0.061	0.56	0.148	0.161	0.065	0.097	0.039
		N	47	47	47	47	47	47	47	47	47	47
	Chroma	Correlation Coefficient	-0.097	-.418**	-0.081	-0.213	-0.039	-0.238	0.169	.510**	.314*	-.496**
		Sig. (2-tail	0.515	0.003	0.586	0.15	0.795	0.108	0.256	0	0.032	0
		N	47	47	47	47	47	47	47	47	47	47
	pH	Correlation Coefficient	0.146	0.199	0.204	.427**	-0.127	-.410**	-0.115	-.382**	-0.182	.395**
		Sig. (2-tailed)	0.326	0.179	0.168	0.003	0.395	0.004	0.44	0.008	0.22	0.006
		N	47	47	47	47	47	47	47	47	47	47
	EC	Correlation Coefficient	0.071	0.192	.418**	.495**	0.174	0.023	-.324*	0.1	-0.155	-0.004
		Sig. (2-tailed)	0.634	0.196	0.003	0	0.243	0.88	0.026	0.505	0.299	0.976
		N	47	47	47	47	47	47	47	47	47	47
	OC	Correlation Coefficient	.436**	0.207	.316*	0.218	0.015	0.18	-.391**	-0.274	-0.16	0.278
		Sig. (2-tailed)	0.002	0.163	0.031	0.141	0.919	0.225	0.007	0.063	0.283	0.058
		N	47	47	47	47	47	47	47	47	47	47
	N	Correlation Coefficient	0.009	.333*	0.253	0.259	.413**	.381**	-0.16	-0.107	-0.198	0.144
		Sig. (2-tailed)	0.95	0.022	0.086	0.079	0.004	0.008	0.283	0.476	0.183	0.336
		N	47	47	47	47	47	47	47	47	47	47
	P (kg/ha)	Correlation Coefficient	1	-0.035	0.158	0.055	-0.13	0.027	-0.208	-.472**	-0.266	.519**
		Sig. (2-tailed)		0.813	0.289	0.715	0.385	0.857	0.161	0.001	0.071	0
		N	47	47	47	47	47	47	47	47	47	47
	K (kg/ha)	Correlation Coefficient	-0.035	1	.310*	.600**	.288*	.294*	-0.002	-0.076	-0.129	0.074
		Sig. (2-tailed)	0.813		0.034	0	0.05	0.045	0.988	0.61	0.388	0.621
		N	47	47	47	47	47	47	47	47	47	47
	Ca (ppm)	Correlation Coefficient	0.158	.310*	1	.643**	0.068	0.017	-0.202	-0.112	-0.259	0.185
		Sig. (2-tailed)	0.289	0.034		0	0.648	0.907	0.174	0.453	0.078	0.212
		N	47	47	47	47	47	47	47	47	47	47

		P (kg/ha)	K (kg/ha)	Ca (ppm)	Mg (ppm)	S (ppm)	B (ppm)	Cu (ppm)	Clay (%)	Silt (%)	Sand (%)	
Mg (ppm)	Correlation Coefficient	0.055	.600**	.643**	1	0.043	-0.067	-0.115	-0.204	-0.216	0.259	
	Sig. (2-tailed)	0.715	0	0		0.776	0.653	0.44	0.169	0.145	0.078	
	N	47	47	47	47	47	47	47	47	47	47	
S (ppm)	Correlation Coefficient	-0.13	.288*	0.068	0.043	1	.431**	0.132	0.03	-0.017	-0.05	
	Sig. (2-tailed)	0.385	0.05	0.648	0.776		0.003	0.375	0.839	0.91	0.739	
	N	47	47	47	47	47	47	47	47	47	47	
B (ppm)	Correlation Coefficient	0.027	.294*	0.017	-0.067	.431**	1	-0.048	0.038	-0.271	0.009	
	Sig. (2-tailed)	0.857	0.045	0.907	0.653	0.003		0.749	0.8	0.066	0.951	
	N	47	47	47	47	47	47	47	47	47	47	
Cu (ppm)	Correlation Coefficient	-0.208	-0.002	-0.202	-0.115	0.132	-0.048	1	0.09	0.111	-0.125	
	Sig. (2-tailed)	0.161	0.988	0.174	0.44	0.375	0.749		0.547	0.458	0.403	
	N	47	47	47	47	47	47	47	47	47	47	
Fe (ppm)	Correlation Coefficient	0.098	0.13	0.008	-0.098	0.166	.482**	-0.206	0.089	0.018	-0.09	
	Sig. (2-tailed)	0.514	0.385	0.959	0.512	0.265	0.001	0.164	0.554	0.904	0.548	
	N	47	47	47	47	47	47	47	47	47	47	
Mn (ppm)	Correlation Coefficient	-0.06	.439**	0.25	.314*	.521**	.430**	.298*	-0.21	-0.189	0.204	
	Sig. (2-tailed)	0.689	0.002	0.09	0.032	0	0.003	0.042	0.157	0.204	0.169	
	N	47	47	47	47	47	47	47	47	47	47	
Zn (ppm)	Correlation Coefficient	.406**	0.143	.328*	.457**	0.122	0.055	0.095	-.376**	-0.111	.401**	
	Sig. (2-tailed)	0.005	0.339	0.024	0.001	0.414	0.716	0.526	0.009	0.458	0.005	
	N	47	47	47	47	47	47	47	47	47	47	
Clay (%)	Correlation Coefficient	-.472**	-0.076	-0.112	-0.204	0.03	0.038	0.09	1	.328*	-.961**	
	Sig. (2-tailed)	0.001	0.61	0.453	0.169	0.839	0.8	0.547		0.024	0	
	N	47	47	47	47	47	47	47	47	47	47	
Silt (%)	Correlation Coefficient	-0.266	-0.129	-0.259	-0.216	-0.017	-0.271	0.111	.328*	1	-.530**	
	Sig. (2-tailed)	0.071	0.388	0.078	0.145	0.91	0.066	0.458	0.024		0	
	N	47	47	47	47	47	47	47	47	47	47	
Sand (%)	Correlation Coefficient	.519**	0.074	0.185	0.259	-0.05	0.009	-0.125	-.961**	-.530**	1	
	Sig. (2-tailed)	0	0.621	0.212	0.078	0.739	0.951	0.403	0	0		
	N	47	47	47	47	47	47	47	47	47	47	

****. Correlation is significant at the 0.01 level (2-tailed), *. Correlation is significant at the 0.05 level (2-tailed).**



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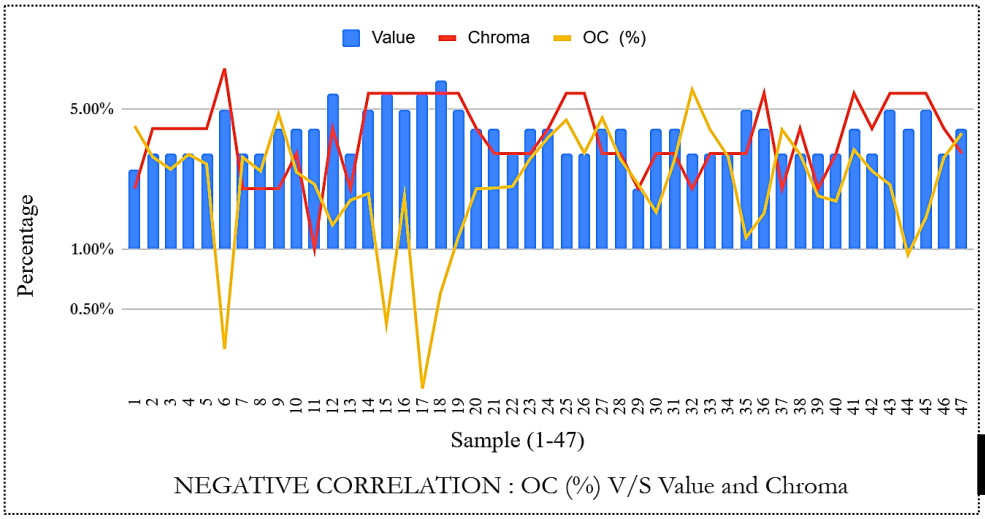

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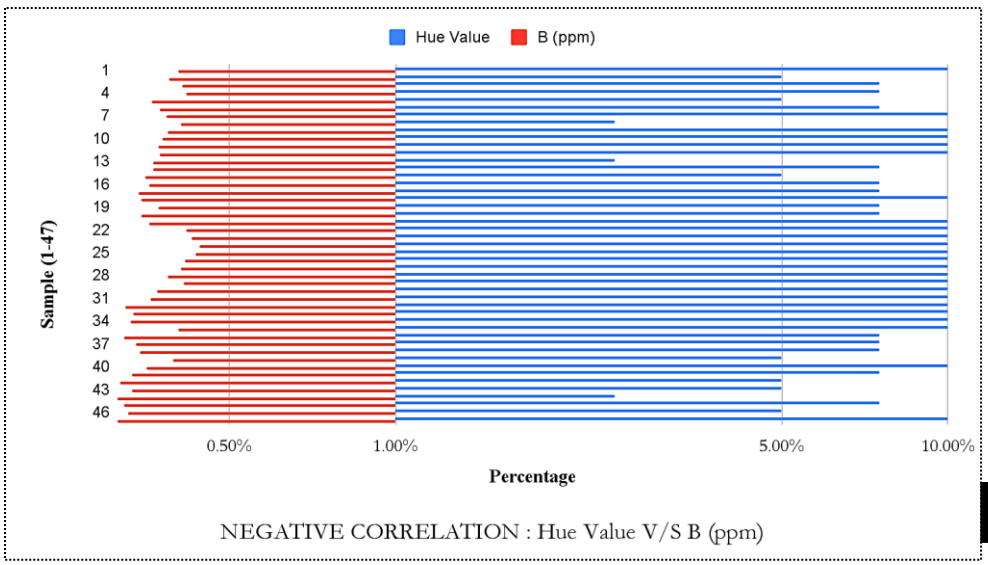
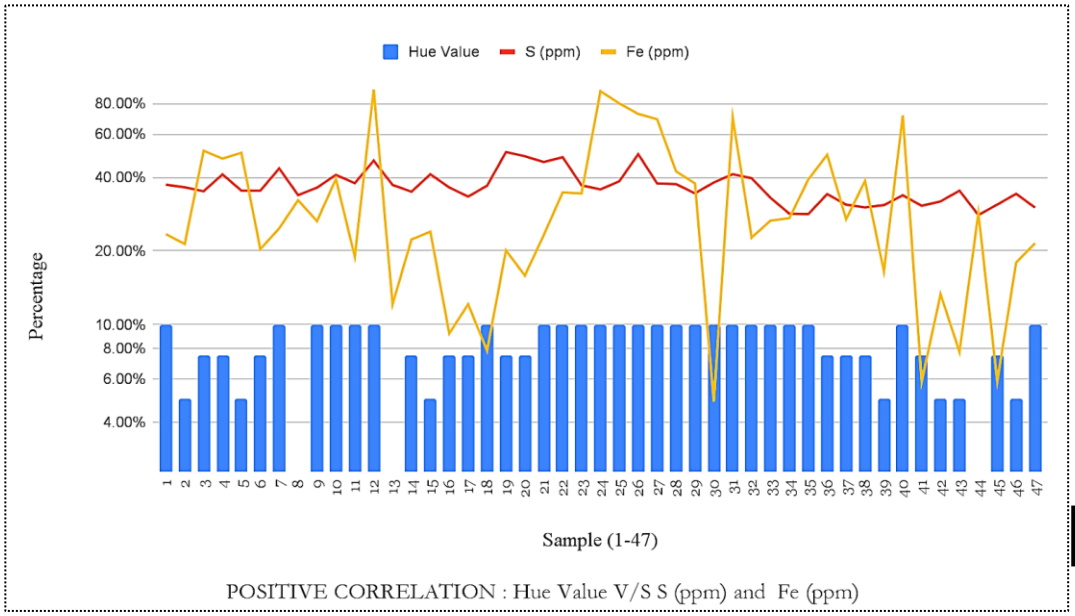


c

Plate 7.1: Correlation analysis done over edaphic parameters of 47 soil samples of sky islands of the Western Ghats across the Palghat Gap within the study area: a. Correlation of Munsell Hue Value v/s OC, b. Correlation of Munsell Chroma and Value v/s OC (%), c. Correlation of Munsell Hue value v/s B.



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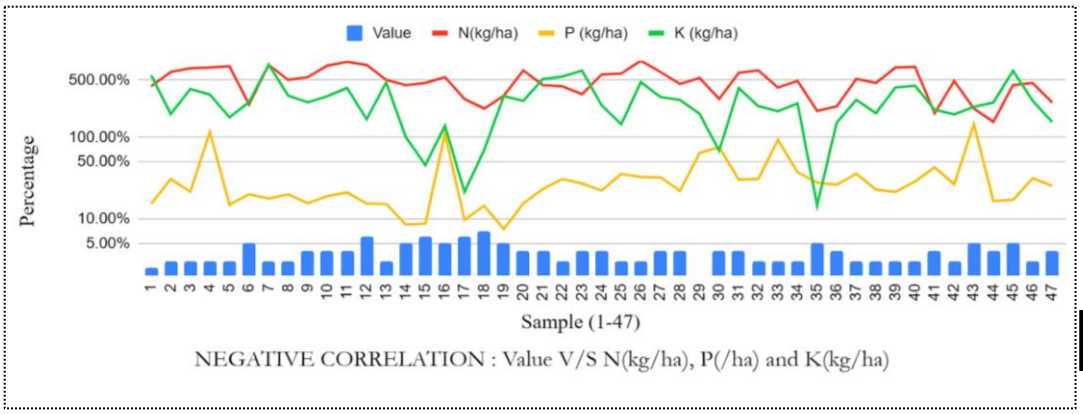

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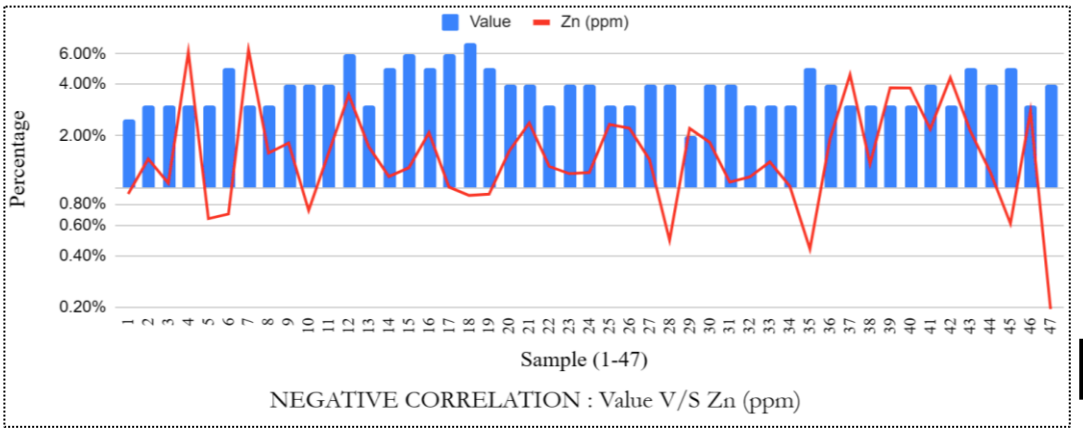

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Plate 7.2: Correlation analysis done over edaphic parameters of 47 soil samples of sky islands of the Western Ghats across the Palghat Gap within the study area: a. Correlation of Munsell Hue value v/s S and Fe, b. Correlation of Munsell Value v/s N, P and K, c. Correlation of Munsell Value v/s Zn.

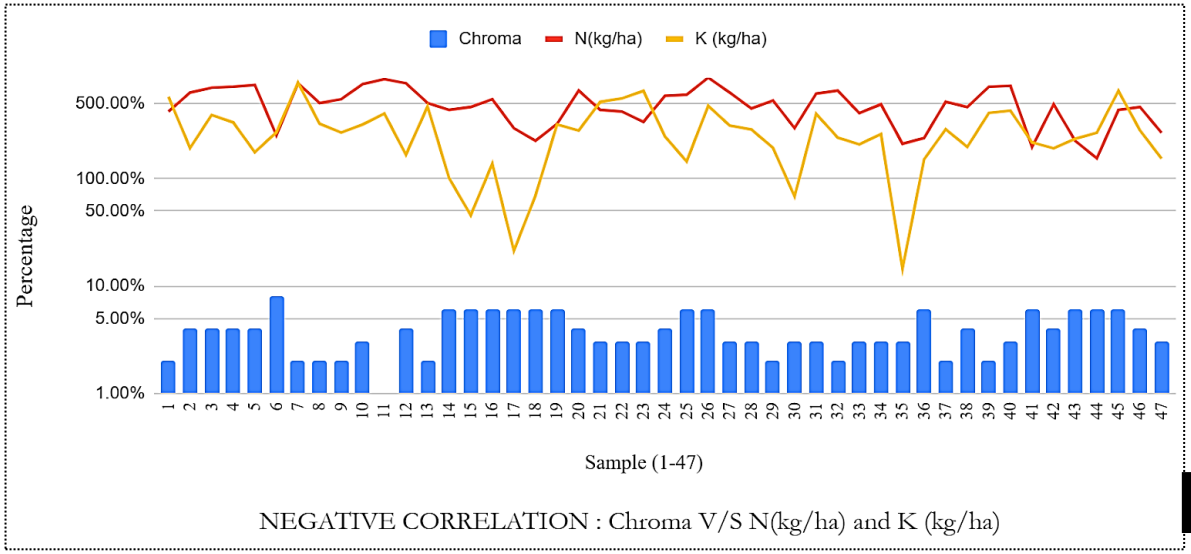


Plate 7.3: Correlation analysis done over edaphic parameters of 47 soil samples of sky islands of the Western Ghats across the Palghat Gap within the study area: a. Correlation of Munsell Chroma v/s N and K, b. Correlation of Munsell chroma v/s Mn.

the relationship between colour attributes and the organic carbon content. The relationship between three Munsell colour system variables and organic carbon (OC) was examined through Spearman correlation analysis (Table 7.7). The results revealed that a significant correlation exist between colour and OC. Specifically, OC showed a positive correlation with Hue (r (45) = 0.316*, p = 0.031) (Plate 7.1a), while exhibiting negative correlations with Value (r (45) = -0.584**, p = 0.000) and Chroma (r (45) = -0.396**, p = 0.006) (Plate 7.1b). Darker soil colour indicates higher organic matter content and reduced drainage rate, whereas lighter soil colour suggests lower organic content and increased leaching. The capacity of soil to support plant growth and biological activity relies on its morphological, physical, and chemical properties, which are affected by soil organic carbon content (Sims and Haby 1971, Steinhardt & Franzmeier 1979, Ahukaemere *et al*., 2013).

As per the present correlation analysis, one of the Munsell notation variables that have the highest significant correlation with OC was value (r (45) = -0.584**, p = 0.000), with P value 0.00. Therefore, while considering colour in relation to the determination of OC (organic carbon), the order of significance should be considered, with Value being the most important, followed by Chroma, and then Hue. This order is based on the P-value, which is a statistical measure indicating the level of significance of a relationship. A lower p-value suggests a more significant relationship between the variables being studied. Therefore, in this context, the Value component of colour has the highest impact on determining the OC content, followed by Chroma and then Hue. Understanding the importance of each unit of Munsell notation increases the essentiality for enhancing the precision of nutrient prediction based on soil colour correlations. These discernible relationships serve to underscore the connections between colour attributes and the organic carbon composition inherent to the soil samples. The spearman correlation analysis clearly depicted the intricate connections between colour attributes and various mineral nutrients. The outcomes of this analysis distinctly elucidated that Hue exhibited significant positive correlations with crucial elements such as boron (B) (Plate 7.1c), sulphur (S), and iron (Fe) (Plate 7.2a), accentuating the nuanced interdependencies between these attributes. The parameter of Munsell notation the Value displayed discernible negative correlations with fundamental mineral nutrients including nitrogen (N), phosphorus (P), potassium (K) (Plate 7.2b), and zinc (Zn) (Plate 7.2c). Additionally, Chroma displayed significant negative correlations with nitrogen (N), potassium (K) (Plate 7.3a), and manganese (Mn) (Plate

7.3b). The present study correlated the hue, value, and chroma of the Munsell notation with organic carbon (OC) and various mineral nutrients. Thereby highlighting the significance of each unit of Munsell notation in predicting OC, and mineral nutrients like S, B, Fe, N, P, and Mn, through its significant correlation with Hue, Value and Chroma. These perceptive findings offer insights into the intricate web of associations that exist between colour attributes and the diverse array of mineral nutrients present within the soil ecosystem. Such associations of Munsell colour notations with organic carbon and various mineral nutrients hold great significance. This eases the identification and prediction of mineral nutrient content in the soil with respect to the colour of each soil sample. These findings hold great significance for improving the prediction accuracy of mineral nutrients and OC of soil samples by using its significant correlation with Munsell notation of soil colour. The study had implications for practical applications, enabling more efficient nutrient management based on visual colour assessments. So, the study over the sky islands of Western Ghat on the northern and southern sides of Palghat Gap underscored the significance of soil colour as an indicator of organic content, and mineral composition.

The significance of soil colour in the sky islands of Western Ghat as an indicator of both organic content and mineral composition and the importance of spatial soil property maps for nutrient management are emphasized by Verma in his study (Verma *et al*., 2018). Subramanyam (Subramanyam and Nayar 1974) further supports this perspective by discussing the impact of seasonal rainfall on vegetation and the occurrence of red soils, laterites, black soils, and humid soils in the region. Huyssteen (Van Huyssteen *et al*., 1997) delves into the exploration of the relationship between subsoil colour and wetness levels, examining the role of soil colour in reflecting the soil water regime. Lastly, El-Baz (El-Baz *et al*., 2008) offers a preliminary analysis of colour variations in sand deposits in the Western Desert of Egypt, potentially applicable to the study of soil colour in the Western Ghats.

The fertility of soil relies on its organic matter content, influenced by drainage, texture and climate. Well-drained soils with various textures have different organic matter levels, influenced by factors like porosity and clay content. Soils with similar textures and good drainage tend to reach an optimal organic matter content that is challenging to exceed. Organic matter decomposition supplies vital nutrients for crops, leading to the adoption of cultural practices to preserve it. Soils of a specific texture may have varying organic matter levels, enabling the classification of soil fer-

tility based on organic matter content (Hester 1939). The specific colour observed in soil is influenced by the colour of its different components, especially in soils with seasonally high-water tables, which often display redoximorphic colours due to features like iron (Fe) depletions and concentrations in silicate or other primary structural minerals, like the colour of soil is influenced by the amount of iron oxides present (Qian *et al*., 1993, Rabenhorst and Parikh 2000). Thereby such results may have implications for practical applications in several fields, enabling more efficient nutrient management based on visual colour assessments.

7.3.14.2 Soil Texture in relation to water retention

The soil-water characteristics curve (SWCC) plays a crucial role in understanding the behaviour of soil-water interactions. Soil texture is a fundamental factor in this regard as it influences water drainage and the formation of air pockets within the soil. Texture, determined by the relative proportions of clay, silt and sand, has a direct impact on the hydraulic and mechanical properties of soil (Zhou *et al*., 2014).

In the current study, a total of 47 soil samples were analysed to determine their texture, as per the study the samples fell into three categories, and were namely sandy loam, loamy sand and sandy clay loam (Moreno-Maroto *et al*., 2022). The texture classification was based on the proportions of clay, silt and sand present in the samples. The concentrations of sand, silt and clay exhibited significant correlations with various soil parameters. These findings highlight the importance of soil texture in understanding and predicting other soil properties and behaviours, and all the results are depicted in table 7.7 - 7.8. Among the three types of texture, sandy clay loam was prominent and had a maximum water retention capacity than the other two types as per the SWCC fractal model. As per the SWCC fractal model, as the clay% increases, the water retention capacity of soil increases. Here in the 47 samples, the soil sample with the highest clay% was for S6, and the one with the least water retention capacity was for samples 13, 33, 35, 37, and 39th. So indirectly the texture water retention capacity depends on clay % in it. As per the present samples there were 3 textures, and of that sandy clay loam has higher water retention capacity.

As per spearman correlation Clay (%) found to be negatively correlated with Hue ($r(45) = -0.308^{*}$, $p = 0.035$), pH ($r(45) = -0.382^{**}$, $p = 0.008$), P ($r(45) = -0.472^{**}$, $p = 0.001$) and Zn ($r(45) = -0.376^{**}$, $p = 0.009$). Clay (%) was positively correlated with Chroma ($r(45) = 0.510^{**}$, $p = 0.000$). Silt (%) positively correlated with Chroma ($r(45) = 0.314^{*}$, $P = 0.032$). Sand (%) negatively correlated with Chro-

ma (r (45) = -0.496*, p = 0.000), Sand (%) positively correlated with pH (r(45) = 0.395**, p = 0.006), P (r(45) = 0.519**, p = 0.000), Zn (r(45) = 0.401**, p = 0.005), (** P<0.01, *P<0.05- Level of significance) (Table 7.7 - 7.8).

The significance of soil texture in influencing water availability, nutrient content, root development, aeration, soil biological processes, and susceptibility to erosion is paramount (Santos *et al*., 2022, Watcharamul *et al*., 2022, Huntley 2023c). Coarse-textured sandy soils excel in drainage capacity yet might struggle to retain adequate moisture for optimal plant growth (Watcharamul *et al*., 2022). Soils with a fine-textured clay composition possess heightened water-holding capabilities, but they often encounter challenges related to inadequate drainage and waterlogging issues (Huntley 2023a). The significance of soil texture's impact on various factors remains consistent across multiple studies (Santos *et al*., 2022, Watcharamul *et al*., 2022, Huntley 2023b).

The influence of soil texture encompasses diverse aspects. Root growth, for instance, is intricately impacted, as sandy soils foster the development of more profound root systems, thereby enhancing water and nutrient accessibility. In contrast, clayey soils may hinder root penetration and the availability of resources (Techer and Berthier 2023). Another critical facet is the imperative role of soil aeration in root respiration. Sandy soils excel in facilitating oxygen exchange, thereby fostering robust root development and mitigating root stress and susceptibility to diseases (Wang *et al*., 2023a). Additionally, the sway of soil texture extends to the domain of microbial activity, nutrient cycling, and the decomposition of organic matter. These processes collectively exert a profound influence on soil health and the availability of nutrients (Islam *et al*., 2022). This knowledge underscores the importance of comprehending soil texture for informed decision-making and sustainable land management practices. Several studies reported that understanding the correlation between edaphic parameters has the potential impact on determining soil fertility, water retention and agricultural productivity (Muhammad *et al*., 2008, Troeh and Thompson 2005). That is if one edaphic parameter gets affected, its impact will be shown over by the interconnected edaphic components. Such interconnectedness gives insights into predictions in modelling techniques and it will give an important impact in biodiversity conservation. This collective understanding underscores the significance of comprehending soil texture's farreaching implications in ecological studies.

7.3.14.3. Interpolation of edaphic parameters over sky islands across Palghat Gap

The assessment of spatial variability in soil properties was essential for evaluating the efficacy of measures implemented to address diverse land surface processes. Through interpolation technique, we can predict the percentage of occurrence of each edaphic parameters on overall study area with the knowledge of edaphic parameters of few soil samples. This technique found to play a crucial role in formulating accurate land management strategies. Spatial interpolation maps can serve as an effective tool for identifying areas of land degradation within the study area. Geostatistical analysis using the Ordinary Kriging (OK) approach was deemed the most suitable model for mapping the spatial variability of soil parameters (Rasool *et al*., 2020). Such geospatial variability maps can serve as an effective tool for site-specific nutrient management (George *et al*., 2021). Soil parameter variability was utilised to differentiate the soil samples collected from the sky islands on the northern and southern sides of the Palghat Gap.

The interpolation mapping of the 19 soil parameters in this study provided insights into the probable expected concentration levels of edaphic components and its spatial variations all over the sky islands of Western Ghats within the study area across the Palghat Gap. The resultant spatial map from interpolation mapping are depicted in Plate 7.4-7.6. As per the interpolated map, the edaphic parameters that spatially exhibited distinct variations in expected probable concentration levels over sky islands across Palghat Gap were pH, EC, OC, B, Fe, N and Cu, Clay %, Silt % and Sand %. Here in different habitats, the composition of soil and the availability of micronutrients may vary. If a particular micronutrient is scarce in a certain habitat, it becomes the limiting factor for plant growth in that environment, even though the macronutrients are abundantly present there. So as per Liebig's Law of the Minimum and the differences in micronutrients within habitats, it emphasizes that the availability of the scarcest resource (micronutrient) will limit the overall growth and productivity (Agren *et al*., 2012).

These findings emphasised the role of these soil parameters in delineating soil habitat of sky islands of the Western Ghats across the Palghat Gap as two separate habitats. Thereby the variability in edaphic environment depicted valuable insights on soil nutrient dynamics and its influence over the differential distribution of vegetation patterns within the study area. Monitoring these changes over the edaphic gradients,

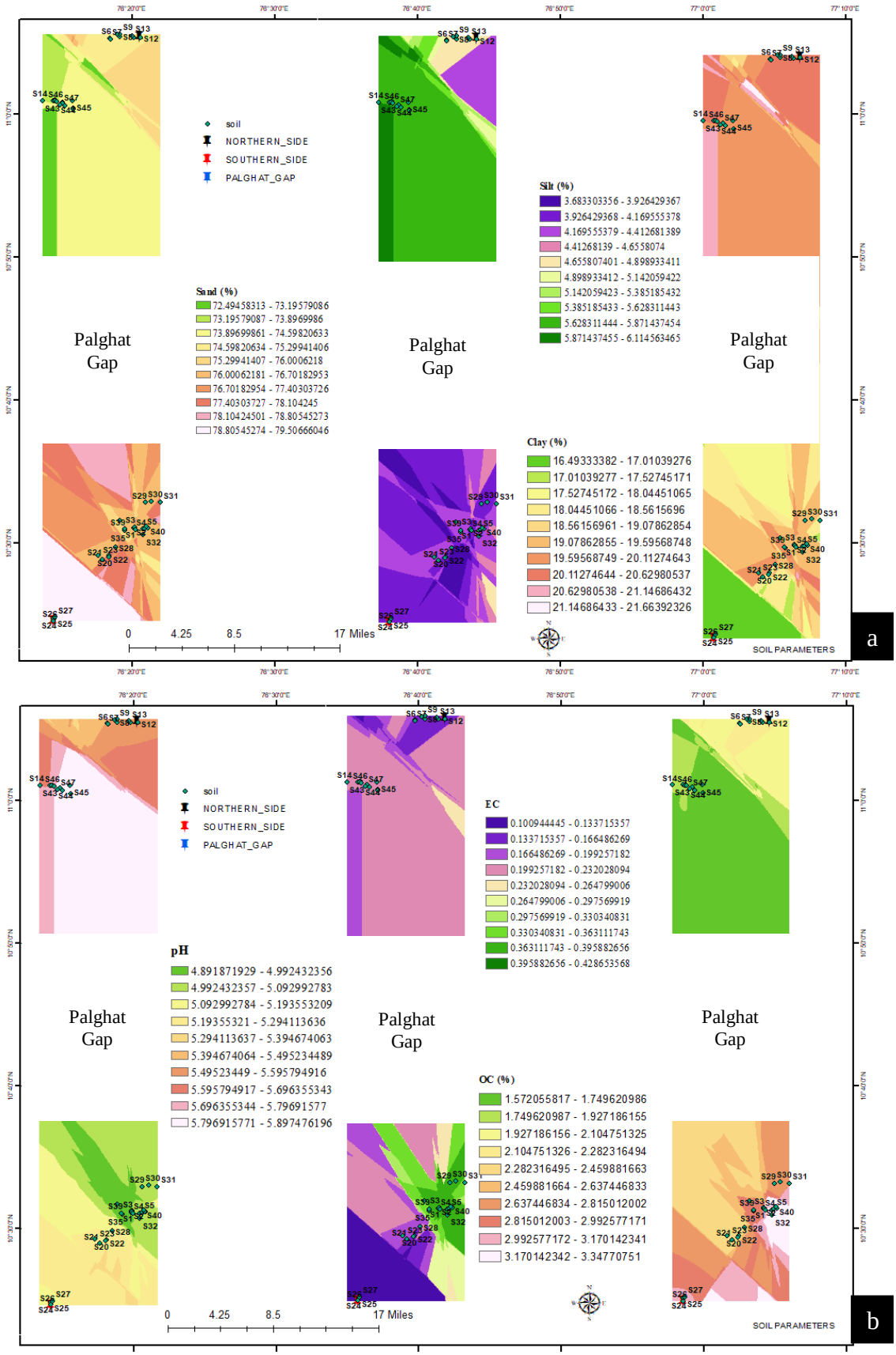


Plate 7.4. Interpolation spatial mapping on edaphic parameters over the sky islands of the Western Ghats across the Palghat Gap within the study area: a. Interpolation on Sand, silt and clay, b. Interpolation of pH, OC, and EC.

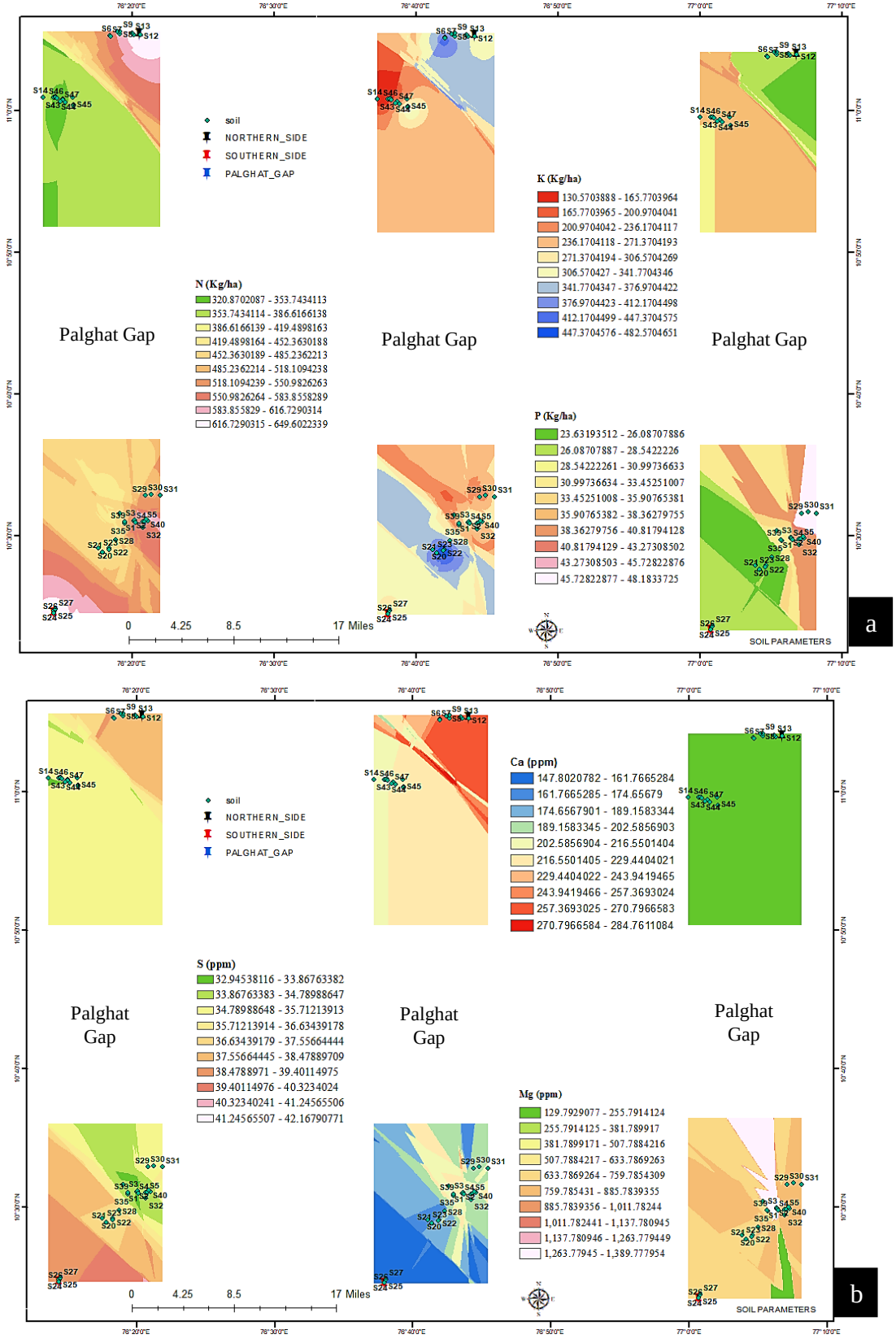


Plate 7.5. Interpolation spatial mapping on edaphic parameters over the sky islands of the Western Ghats across the Palghat Gap within the study area: a. Interpolation on N, K and P, b. Interpolation on S, Ca, and Mg.

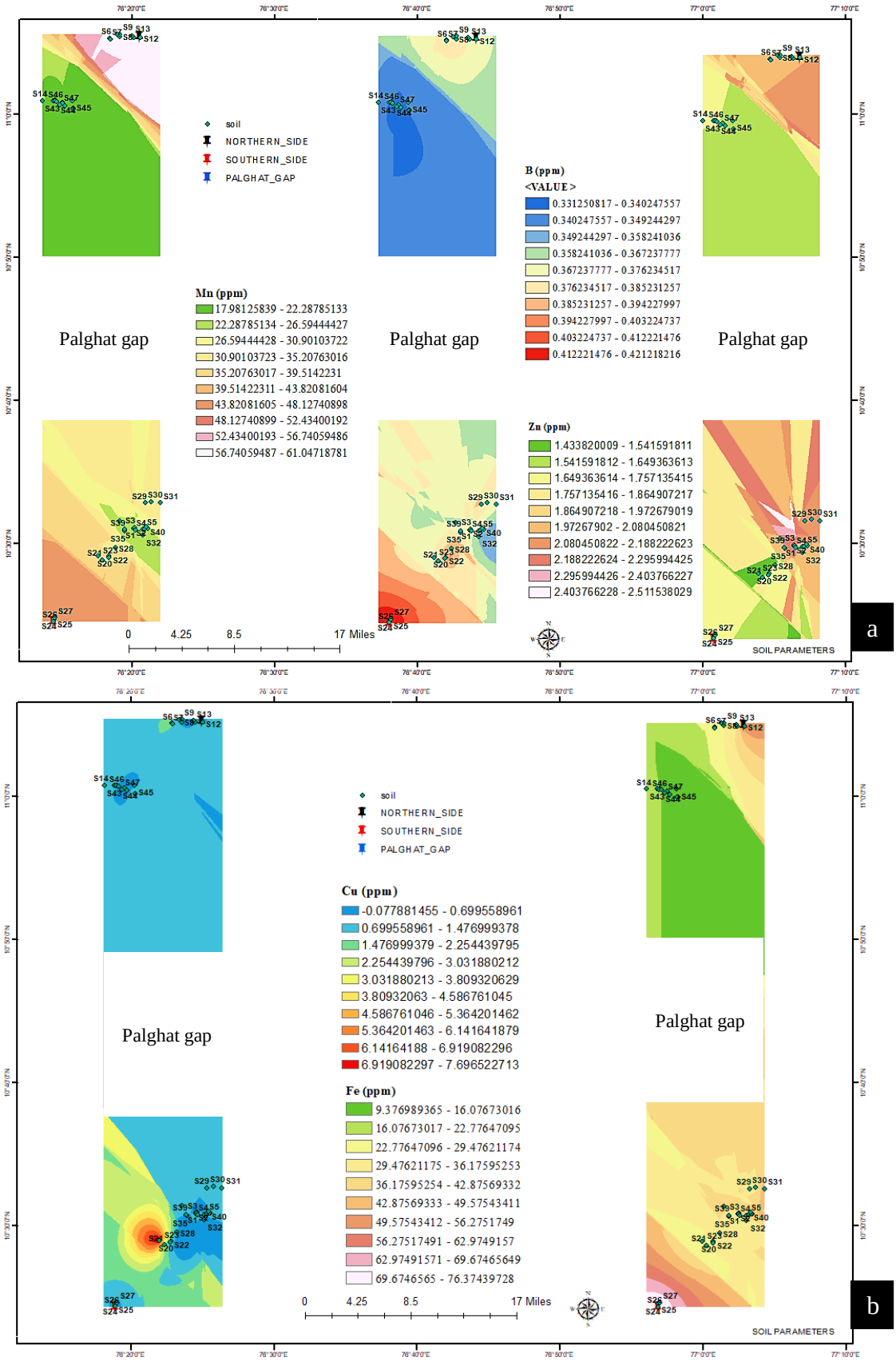


Plate 7.6: Interpolation spatial mapping on edaphic parameters over the sky islands of the Western Ghats across the Palghat Gap within the study area: a. Interpolation on Mn, B, and Zn, b. Interpolation on Cu and Fe.

helps in identifying areas that are at risk of nutrient desertification and in understanding the factors contributing to it and thereby implementing effective measures to mitigate and manage desertification in arid and semiarid grasslands globally. This concept thereby highlights the critical role of soil as an indicator of environmental health and provides valuable information for land management and conservation efforts in these vulnerable regions (Schlesinger *et al*., 1996, Younas *et al*., 2023).

The relationship between soil and each plant species is noteworthy, as it is influenced by several habitat conditions, ecological requirements, and tolerance levels (Mousaei Sanjerehei *et al*., 2013). Therefore, the interpolation over the study area helped in understanding the edaphic parameters to compare the habitat separated by the geographical gap like Palghat Gap.

7.3.14.4. Synergistic and antagonistic effects of edaphic Parameters

The Availability of nutrients from the soil was influenced by various factors including soil pH, texture and temperature. Moreover, there exist a complex interrelations and interactions between these nutrients, characterised by both synergistic and antagonistic relationships (Rietra *et al*., 2017). In several studies, it is reported that potassium (K) in the soil found to have positively influenced the uptake of essential elements such as phosphorus (P), magnesium (Mg), iron (Fe), manganese (Mn), and zinc (Zn) (Neshev and Manolov 2015). Similarly, the presence of copper (Cu) and boron (B) can enhance nitrogen (N) uptake, while the presence of molybdenum (Mo) can improve the uptake of both nitrogen and phosphorus. Adequate sulphur (S) levels contribute to increased uptake of manganese and zinc, whereas sufficient manganese promotes copper uptake. Even the soil alkalinity can impact nutrient availability. In alkaline soils, calcium (Ca) concentrations tend to increase while potassium availability decreases. As plants grow, the concentration of calcium decreases while potassium increases. Furthermore, excessive nitrogen supply can negatively affect the uptake of phosphorus, potassium, iron, manganese, zinc, and copper, as well as most secondary micronutrients (Bojtor *et al*., 2022). Excessive phosphorus, on the other hand, can reduce the uptake of cationic micronutrients such as iron, manganese, zinc and copper. Excessive potassium can decrease magnesium uptake, while excessive calcium can hinder iron uptake. Moreover, excessive iron levels can lead to reduced zinc uptake, and excessive zinc levels can impede manganese uptake. Understanding these intricate relationships between nutrients was crucial for maintaining optimal nutrient bal-

ance in the soil and promoting healthy plant growth. Hence, there exists interdependence among soil parameters, wherein alterations in one element can trigger modifications in multiple others, ultimately impacting vegetation (Malvi 2011, Mousavi *et al*., 2013, Bhatla *et al*., 2018, Akila 2023, Jayara *et al*., 2023, Long and Peng 2023).

Previous research has proved the significance of interrelationships among soil parameters in facilitating optimal plant development. This underscores the importance of thoroughly understanding the correlation between various micro and macronutrients, further emphasising their individual and collective importance. In this chapter, the correlation between each soil parameter with particular emphasis on the edaphic parameters that exhibited a notable gradient of variation across the northern and southern sky island habitats of the Western Ghats in the vicinity of the Palghat Gap was done. Spearman correlation analysis was utilised to explore the statistically significant associations and interrelationships among these soil parameters and their ratios. The findings of this analysis revealed the presence of significant correlations, encompassing both positive and negative relationships, at a level of significance $P < 0.01$ or $P < 0.05$.

The current investigation unveiled significant associations between micro-macronutrients, and their ratios (Table 7.7 - 7.8). For instance, iron (Fe) exhibited significant correlations with Munsell notation variables, pH, boron (B), organic carbon (OC), and nitrogen (N). Similarly, manganese (Mn) showed strong correlations with Munsell notation, zinc (Zn), potassium (K), magnesium (Mg), sulphur (S), boron (B), copper (Cu), and N. Zinc demonstrated significant correlations with Munsell notation, electrical conductivity (EC), Manganese (Mn), phosphorus (P), calcium (Ca), Mg, and nitrogen (N), Phosphorus exhibited the highest and significant correlation with Munsell notation, Zn and OC. Potassium displayed its greatest correlation with Munsell notation, Mn, Ca, Mg, B, S and N. Calcium had the maximum and significant correlation with EC, OC, K, Mg and Zn. Magnesium showed strong correlations with pH, EC, K, Mn, Zn and Ca. Sulphur demonstrated its highest correlation with Munsell notation, N, K, B and Mn. Likewise. Boron had the maximum correlation with Munsell notation, pH, N, K, S, Fe and Mn. Copper showed the highest correlations with EC, Mn, and OC. pH was strongly related to Fe, Mg, and B. EC was found to be correlated with N, Ca, Mg, Cu, and Zn. while OC exhibited high correlations with Munsell notation, Fe, P, Ca, Cu, and N. Lastly, N showed a maximum correlation ($P = 0.00$) with Munsell notation, EC, K, OC, S, B and Fe (Table 7.7 - 7.8). This reveals that

each edaphic component is related to one or the other component of the soil. So, in the present study area, one of the major factors that may have caused isolation of this habitat seems to be the parameters that has gradient variation in concentration across the gap. Most of the edaphic parameters are interconnected with significant correlation, and this raises the importance of each edaphic parameter in isolating each habitat by providing unique edaphic environment.

7.3.14.5 Intricate relation between edaphic parameters and intraspecific morphometric variability of *Elaeocarpus gadgilii*

This section of the study examines the impact of gap features on species that serve as indicators of environmental changes. It investigates the relationship between the intraspecific morphometric variability of *E. gadgilii* and the edaphic parameters of sky islands across the Palghat Gap. As per the analysis, the micro and macronutrients and their ratios were found to be interconnected. But the intraspecific morphometric variability of *E. gadgilii* of the Western Ghats sky islands across the Palghat Gap is not dependent solely on the soil parameters of the habitat. Edaphic parameters are just one of the environmental variables influenced by biogeographical features that directly or indirectly affect the populations of *E. gadgilii*. So, this chapter has its own significance in analysing the hypothesis of the present study.

Here the Spearman correlation test results revealed that, with the exception of Hue values of Munsell notation and Sand%, all other parameters displayed significant correlations with at least one of the morphometric variables of *Elaeocarpus gadgilii* populations (Table 7.9 -7.10). This indicates that the intra-specific morphometric variability of *E, gadgilii* are significantly related with the physical and chemical parameters of soil. The correlation between all soil parameters and morphometric parameters were examined at the significance levels of 0.01 and 0.05. Among these correlations, a remarkable finding was that the presence of a strong negative correlation ($r(31) = -.604^{**}$, $p = .000$) between Fe content and Lamina breadth at the base, at the P value < 0.01 level of significance. Fe, which is one of the soil parameter showing a significant gradient over the sky islands across the Palghat Gap and displayed higher concentrations on the Southern side. Fe plays a crucial role in the electron transport chain and serves as a component of vital enzymes. It is also essential for photosynthesis and chlorophyll synthesis. Higher Fe concentration was observed on the southern side than on the northern side of the sky islands.

Table No: 7.9. Spearman correlation between Edaphic parameters (Hue, Value, Chroma, pH, EC, OC, N, P, K, and Ca) of 32 soil samples from sky islands of the Western Ghats across the Palghat Gap and Morphological parameters of 32 populations of *Elaeocarpus gadgilii*, to analyse significant correlations at 0.05 and 0.01.

			Hue	Value	Chroma	pH	EC	OC (%)	N (kg/ha)	P (kg/ha)	K (kg/ha)	Ca (ppm)
Spearman's rho	Mature Leaf length	Correlation Coefficient	0.041	0.217	0.223	0.228	0.179	-0.11	-0.195	0.114	-0.019	0.145
		Sig. (2-tailed)	0.819	0.224	0.212	0.202	0.32	0.542	0.278	0.526	0.918	0.421
		N	32	32	32	32	32	32	32	32	32	32
	Lamina length	Correlation Coefficient	-0.195	0.223	.395*	0.13	0.196	-0.216	-0.121	0.016	0.017	0.103
		Sig. (2-tailed)	0.276	0.211	0.023	0.469	0.275	0.228	0.504	0.927	0.925	0.569
		N	32	32	32	32	32	32	32	32	32	32
	Lamina Breadth at Apex	Correlation Coefficient	-0.145	.457**	.488**	0.236	-0.055	-0.266	-.499**	-0.038	-0.11	0.123
		Sig. (2-tailed)	0.422	0.008	0.004	0.186	0.762	0.134	0.003	0.832	0.541	0.494
		N	32	32	32	32	32	32	32	32	32	32
	Lamina Breadth at Middle	Correlation Coefficient	-0.1	0.316	.392*	0.296	0.082	-0.197	-0.287	0.017	0.181	0.174
		Sig. (2-tailed)	0.581	0.073	0.024	0.094	0.652	0.271	0.105	0.925	0.314	0.333
		N	32	32	32	32	32	32	32	32	32	32
	Lamina Breadth at Base	Correlation Coefficient	-0.194	.422*	.346*	0.314	0.058	-0.203	-0.297	-0.252	0.073	0.203
		Sig. (2-tailed)	0.279	0.014	0.049	0.075	0.747	0.257	0.093	0.157	0.688	0.257
		N	32	32	32	32	32	32	32	32	32	32
	Petiole length	Correlation Coefficient	-0.159	0.316	.358*	0.15	0.176	-0.071	-0.046	-0.117	-0.167	0
		Sig. (2-tailed)	0.377	0.073	0.041	0.406	0.328	0.693	0.8	0.517	0.354	0.999
		N	32	32	32	32	32	32	32	32	32	32
	Petiole width	Correlation Coefficient	-0.003	0.255	0.232	0.165	0.23	-0.202	-0.166	-0.001	-0.059	0.054
		Sig. (2-tailed)	0.986	0.153	0.194	0.359	0.197	0.259	0.355	0.998	0.746	0.767
		N	32	32	32	32	32	32	32	32	32	32

		Hue	Value	Chroma	pH	EC	OC (%)	N (kg/ha)	P (kg/ha)	K (kg/ha)	Ca (ppm)
Midvein fork at the length	Correlation Coefficient	-0.104	0.065	0.03	-0.066	0.189	-0.094	0.089	-0.225	0.204	0.337
	Sig. (2-tailed)	0.563	0.719	0.869	0.714	0.293	0.604	0.621	0.207	0.255	0.055
	N	32	32	32	32	32	32	32	32	32	32
Domatia length	Correlation Coefficient	0.322	-0.327	-0.158	-.411*	0.011	0.18	0.089	.362*	-0.01	-0.278
	Sig. (2-tailed)	0.068	0.063	0.379	0.017	0.951	0.316	0.624	0.038	0.958	0.118
	N	32	32	32	32	32	32	32	32	32	32
Domatia breadth	Correlation Coefficient	0.335	-0.296	-0.12	-0.312	-0.015	0.197	0.046	0.323	0.02	-0.207
	Sig. (2-tailed)	0.056	0.094	0.507	0.077	0.932	0.272	0.799	0.067	0.91	0.247
	N	32	32	32	32	32	32	32	32	32	32
Distance between leaf teeth	Correlation Coefficient	-0.268	-0.065	0.268	-0.096	.451**	-0.022	0.013	0.168	0.067	.449**
	Sig. (2-tailed)	0.132	0.718	0.131	0.595	0.008	0.903	0.944	0.349	0.71	0.009
	N	32	32	32	32	32	32	32	32	32	32
Distance between vein pairs	Correlation Coefficient	-0.063	0.188	0.245	-0.04	0.298	-0.312	0.069	-0.075	0.184	0.091
	Sig. (2-tailed)	0.728	0.295	0.17	0.825	0.093	0.077	0.703	0.677	0.305	0.615
	N	32	32	32	32	32	32	32	32	32	32
Peduncle length	Correlation Coefficient	0.126	0.076	0.021	-0.165	0.193	-0.105	0.316	-0.049	0.115	0.231
	Sig. (2-tailed)	0.485	0.675	0.908	0.359	0.282	0.562	0.073	0.787	0.525	0.197
	N	32	32	32	32	32	32	32	32	32	32
Peduncle width at apex	Correlation Coefficient	-0.299	0.029	0.207	0.159	0.1	-0.11	-0.011	-0.256	-0.048	-0.168
	Sig. (2-tailed)	0.091	0.873	0.248	0.378	0.581	0.543	0.953	0.151	0.792	0.349
	N	32	32	32	32	32	32	32	32	32	32

		Hue	Value	Chroma	pH	EC	OC (%)	N (kg/ha)	P (kg/ha)	K (kg/ha)	Ca (ppm)
Peduncle width at base	Correlation Coefficient	-0.163	-0.113	-0.025	-0.281	0.192	0.022	0.286	-0.094	0.086	0.17
	Sig. (2-tailed)	0.365	0.53	0.89	0.113	0.285	0.901	0.107	0.601	0.632	0.343
	N	32	32	32	32	32	32	32	32	32	32
Number of flowers in each peduncle	Correlation Coefficient	0.212	-0.073	-0.183	-0.105	0.043	0.039	0.262	0.212	-0.028	0.064
	Sig. (2-tailed)	0.236	0.686	0.309	0.559	0.811	0.831	0.141	0.235	0.879	0.722
	N	32	32	32	32	32	32	32	32	32	32
Length between each pedicel	Correlation Coefficient	-0.254	0.071	0.194	-0.334	0.333	-0.209	0.319	-.388*	-0.014	0.037
	Sig. (2-tailed)	0.154	0.696	0.28	0.058	0.058	0.244	0.07	0.026	0.939	0.838
	N	32	32	32	32	32	32	32	32	32	32
Pedicel length	Correlation Coefficient	0.198	-0.003	0.105	0.02	-.396*	-0.019	-0.196	.399*	-0.02	-0.218
	Sig. (2-tail8ed)	0.271	0.986	0.562	0.914	0.022	0.916	0.274	0.021	0.913	0.224
	N	32	32	32	32	32	32	32	32	32	32
Pedicel width at middle	Correlation Coefficient	-0.038	0.046	-0.002	0.189	0.176	-0.002	0.093	-0.113	.440*	0.252
	Sig. (2-tailed)	0.834	0.798	0.992	0.292	0.327	0.99	0.606	0.532	0.01	0.157
	N	32	32	32	32	32	32	32	32	32	32
Floral length	Correlation Coefficient	-0.031	0.285	.408*	-0.039	-0.064	-0.245	-0.071	-0.037	0.089	0.031
	Sig. (2-tailed)	0.862	0.107	0.018	0.827	0.724	0.17	0.694	0.837	0.621	0.863
	N	32	32	32	32	32	32	32	32	32	32
Sepal width at apex	Correlation Coefficient	-0.096	0.143	-0.055	0.038	-0.181	-0.075	0.075	-0.068	0.141	0.111
	Sig. (2-tailed)	0.596	0.426	0.762	0.835	0.315	0.678	0.678	0.705	0.434	0.539
	N	32	32	32	32	32	32	32	32	32	32

			Hue	Value	Chroma	pH	EC	OC (%)	N (kg/ha)	P (kg/ha)	K (kg/ha)	Ca (ppm)
	Sepal length	Correlation Coefficient	0.02	0.235	.419*	-0.1	-0.14	-0.204	-0.225	-0.109	0.154	0.008
		Sig. (2-tailed)	0.912	0.188	0.015	0.579	0.437	0.254	0.207	0.545	0.393	0.963
		N	32	32	32	32	32	32	32	32	32	32
	Sepal width at middle	Correlation Coefficient	0.241	0.212	-0.003	-0.027	-0.288	-0.143	-0.008	-0.084	0.298	0.007
		Sig. (2-tailed)	0.177	0.235	0.987	0.884	0.104	0.427	0.964	0.642	0.093	0.968
		N	32	32	32	32	32	32	32	32	32	32
	Sepal width at base	Correlation Coefficient	0.048	0.228	0.082	0.051	-0.341	-0.152	-0.056	-0.143	0.242	0.064
		Sig. (2-tailed)	0.792	0.201	0.651	0.777	0.052	0.397	0.757	0.426	0.175	0.723
		N	32	32	32	32	32	32	32	32	32	32
	Petal width at undivided part at apex	Correlation Coefficient	-0.051	0.138	0.001	0.106	-0.053	-0.189	0.239	-0.211	0.32	0.083
		Sig. (2-tailed)	0.78	0.443	0.997	0.558	0.771	0.292	0.18	0.239	0.07	0.645
		N	32	32	32	32	32	32	32	32	32	32
	Petal width at undivided part at middle	Correlation Coefficient	0.19	0.148	0.047	-0.069	-0.115	0.077	0.123	0.035	0.162	0.165
		Sig. (2-tailed)	0.289	0.41	0.793	0.703	0.525	0.668	0.495	0.845	0.367	0.359
		N	32	32	32	32	32	32	32	32	32	32
	Petal width at undivided part at base	Correlation Coefficient	0.051	-0.143	-0.264	-0.101	-0.09	0.099	.370*	-0.039	0.286	-0.056
		Sig. (2-tailed)	0.778	0.428	0.138	0.575	0.62	0.585	0.034	0.828	0.107	0.758
		N	32	32	32	32	32	32	32	32	32	32
	Average range of length within one average petal	Correlation Coefficient	0.207	0.152	0.015	0.058	-0.314	-0.002	-0.106	-0.007	0.317	0.099
		Sig. (2-tailed)	0.248	0.397	0.934	0.751	0.075	0.99	0.558	0.971	0.072	0.585
		N	32	32	32	32	32	32	32	32	32	32

			Hue	Value	Chroma	pH	EC	OC (%)	N (kg/ha)	P (kg/ha)	K (kg/ha)	Ca (ppm)
	Petal length	Correlation Coefficient	-0.052	0.319	0.076	0.027	-0.041	-0.111	0.04	-0.192	0.289	0.277
		Sig. (2-tailed)	0.773	0.071	0.674	0.881	0.822	0.538	0.827	0.285	0.103	0.119
		N	32	32	32	32	32	32	32	32	32	32
	Major primary number of divisions in each petal	Correlation Coefficient	0.034	-0.083	-0.032	0.048	0.218	0.022	0.015	0.045	0.064	0.19
		Sig. (2-tailed)	0.849	0.647	0.859	0.792	0.222	0.905	0.934	0.802	0.722	0.289
		N	32	32	32	32	32	32	32	32	32	32
	Minor teritary number of divisions in each petal	Correlation Coefficient	0.103	-0.14	-0.194	-0.239	-0.037	0.195	0.148	-0.115	0.055	0.062
		Sig. (2-tailed)	0.57	0.436	0.28	0.18	0.836	0.276	0.412	0.525	0.761	0.73
		N	32	32	32	32	32	32	32	32	32	32
	Petal division length	Correlation Coefficient	-0.051	.441*	0.163	-0.05	-0.047	-.385*	-0.057	-0.32	-0.019	-0.012
		Sig. (2-tailed)	0.779	0.01	0.366	0.781	0.795	0.027	0.752	0.069	0.916	0.949
		N	32	32	32	32	32	32	32	32	32	32
	Number of stamens	Correlation Coefficient	-0.119	-0.023	0.187	0.137	-0.013	-0.089	-0.209	-0.138	-0.177	-0.121
		Sig. (2-tailed)	0.51	0.898	0.299	0.448	0.944	0.623	0.243	0.445	0.324	0.503
		N	32	32	32	32	32	32	32	32	32	32
	Length of stamens	Correlation Coefficient	-0.108	0.165	0.006	0.135	0.006	-0.147	0.126	-0.019	.468**	0.08
		Sig. (2-tailed)	0.549	0.359	0.975	0.455	0.973	0.413	0.484	0.915	0.006	0.657
		N	32	32	32	32	32	32	32	32	32	32
Spearman's rho	Length of filament	Correlation Coefficient	-0.034	-0.036	0.057	-0.083	0.111	-0.075	0.075	0.175	0.281	0.114
		Sig. (2-tailed)	0.851	0.843	0.752	0.647	0.539	0.679	0.678	0.329	0.114	0.529
		N	32	32	32	32	32	32	32	32	32	32

		Hue	Value	Chroma	pH	EC	OC (%)	N (kg/ha)	P (kg/ha)	K (kg/ha)	Ca (ppm)
Length of anther	Correlation Coefficient	-0.002	0.049	-0.12	0.214	-0.019	0.08	0.198	0.16	.461**	0.195
	Sig. (2-tailed)	0.993	0.785	0.507	0.232	0.916	0.659	0.269	0.374	0.007	0.277
	N	32	32	32	32	32	32	32	32	32	32
Width of filament	Correlation Coefficient	0.13	-0.041	-0.151	-0.107	-0.331	0.076	0.057	0.011	0.241	-0.017
	Sig. (2-tailed)	0.472	0.821	0.4	0.554	0.06	0.672	0.754	0.952	0.177	0.925
	N	32	32	32	32	32	32	32	32	32	32
Width of anther	Correlation Coefficient	-0.056	0.188	0.142	-0.141	-.454**	-0.189	-0.144	-0.222	0.166	-0.095
	Sig. (2-tailed)	0.757	0.294	0.431	0.434	0.008	0.291	0.423	0.215	0.355	0.598
	N	32	32	32	32	32	32	32	32	32	32
Number of setae on anther	Correlation Coefficient	-0.211	0.094	0.234	-0.304	0.142	-0.153	0.047	-0.06	-0.072	0.236
	Sig. (2-tailed)	0.239	0.603	0.191	0.086	0.431	0.394	0.797	0.739	0.69	0.187
	N	32	32	32	32	32	32	32	32	32	32
Length of setae on anther apices	Correlation Coefficient	-0.081	0.334	0.165	0.061	0.027	-0.177	-0.168	-0.117	-0.012	-0.087
	Sig. (2-tailed)	0.656	0.057	0.359	0.735	0.881	0.324	0.349	0.517	0.948	0.631
	N	32	32	32	32	32	32	32	32	32	32
Disk glands length	Correlation Coefficient	0.104	0.15	0.022	0.249	-0.001	-0.246	-0.026	-.364*	0.339	0.06
	Sig. (2-tailed)	0.564	0.403	0.904	0.162	0.997	0.168	0.887	0.037	0.054	0.738
	N	32	32	32	32	32	32	32	32	32	32
Disks galands breadth	Correlation Coefficient	-0.147	0.328	0.33	-0.033	-0.082	-0.263	-0.012	-0.212	0.121	0.224
	Sig. (2-tailed)	0.416	0.063	0.061	0.855	0.651	0.14	0.945	0.237	0.502	0.21
	N	32	32	32	32	32	32	32	32	32	32

****. Correlation is significant at the 0.01 level (2-tailed), *. Correlation is significant at the 0.05 level (2-tailed).**

Table No: 7.10. Spearman correlation between Edaphic parameters (Mg, S, B, Cu, Fe, Mn, Zn, Clay, Silt and Sand) of 32 soil samples from sky islands of the Western Ghats across the Palghat Gap and Morphological parameters of 32 populations of Elaeocarpus gadgilii, to analyse significant correlations 0.05 and 0.01.

			Mg (ppm)	S (ppm)	B (ppm)	Cu (ppm)	Fe (ppm)	Mn (ppm)	Zn (ppm)	Clay (%)	Silt (%)	Sand (%)
Spearman's rho	Mature Leaf length	Correlation Coefficient	-0.043	0.321	0.115	0.059	-0.04	0.002	0.071	-0.06	0.14	0.022
		Sig. (2-tailed)	0.812	0.069	0.525	0.743	0.824	0.993	0.693	0.74	0.439	0.902
		N	32	32	32	32	32	32	32	32	32	32
	Lamina length	Correlation Coefficient	0.059	0.243	-0.001	0.051	-0.185	-0.101	0.045	0.151	0.14	-0.126
		Sig. (2-tailed)	0.743	0.173	0.997	0.779	0.302	0.575	0.802	0.401	0.437	0.485
		N	32	32	32	32	32	32	32	32	32	32
	Lamina Breadth at Apex	Correlation Coefficient	-0.029	0.038	-0.166	0.072	-.484**	-0.061	-0.104	0.202	-0.037	-0.15
		Sig. (2-tailed)	0.872	0.836	0.355	0.692	0.004	0.736	0.566	0.259	0.838	0.406
		N	32	32	32	32	32	32	32	32	32	32
	Lamina Breadth at Middle	Correlation Coefficient	0.182	0.187	-0.069	0.141	-.471**	0.058	0.011	0.152	0.188	-0.158
		Sig. (2-tailed)	0.311	0.297	0.702	0.434	0.006	0.747	0.951	0.397	0.294	0.379
		N	32	32	32	32	32	32	32	32	32	32
	Lamina Breadth at Base	Correlation Coefficient	0.145	0.019	-0.053	-0.051	-.604**	-0.064	-0.148	0.247	-0.043	-0.205
		Sig. (2-tailed)	0.422	0.915	0.772	0.776	0	0.722	0.413	0.165	0.813	0.252
		N	32	32	32	32	32	32	32	32	32	32
	Petiole length	Correlation Coefficient	-0.148	0.184	-0.295	-0.073	-0.187	-0.289	-0.166	.374*	0.067	-0.306
		Sig. (2-tailed)	0.41	0.306	0.096	0.687	0.298	0.103	0.357	0.032	0.713	0.083
		N	32	32	32	32	32	32	32	32	32	32
	Petiole width	Correlation Coefficient	0.086	0.171	0.136	-0.217	-0.058	-0.151	0.061	0.124	0.209	-0.1
		Sig. (2-tailed)	0.632	0.342	0.45	0.226	0.75	0.403	0.738	0.491	0.242	0.581
		N	32	32	32	32	32	32	32	32	32	32

			Mg (ppm)	S (ppm)	B (ppm)	Cu (ppm)	Fe (ppm)	Mn (ppm)	Zn (ppm)	Clay (%)	Silt (%)	Sand (%)
Spearman's rho	Midvein fork at the length	Correlation Coefficient	.347*	-0.019	0.196	0.026	-0.297	0.201	0.017	0.145	-0.018	-0.143
		Sig. (2-tailed)	0.048	0.917	0.275	0.885	0.093	0.262	0.923	0.422	0.922	0.427
		N	32	32	32	32	32	32	32	32	32	32
	Domatia length	Correlation Coefficient	-0.162	-0.031	0.13	0.065	.446**	-0.002	0.084	-0.135	0.034	0.074
		Sig. (2-tailed)	0.369	0.865	0.471	0.718	0.009	0.991	0.642	0.455	0.853	0.681
		N	32	32	32	32	32	32	32	32	32	32
	Domatia breadth	Correlation Coefficient	-0.065	-0.089	0.007	0.036	0.338	-0.044	0.015	-0.104	0.031	0.046
		Sig. (2-tailed)	0.721	0.624	0.97	0.84	0.054	0.807	0.936	0.566	0.862	0.8
		N	33	33	33	33	33	33	33	33	33	33
	Distance between leaf teeth	Correlation Coefficient	.468**	-0.046	-0.136	-0.116	0.047	-0.132	0.238	0.169	0.002	-0.085
		Sig. (2-tailed)	0.006	0.8	0.451	0.522	0.794	0.465	0.182	0.347	0.991	0.64
		N	32	32	32	32	32	32	32	32	32	32
	Distance between vein pairs	Correlation Coefficient	0.122	.389*	0.315	0.227	0	0.113	0.03	0.179	0.018	-0.114
		Sig. (2-tailed)	0.498	0.025	0.074	0.204	1	0.53	0.869	0.32	0.921	0.527
		N	32	32	32	32	32	32	32	32	32	32
	Peduncle length	Correlation Coefficient	0.114	0.228	0.067	0.195	-0.011	0.15	0.208	0.028	0.239	0.005
		Sig. (2-tailed)	0.529	0.203	0.713	0.277	0.95	0.405	0.246	0.877	0.181	.978=
		N	32	32	32	32	32	32	32	32	32	32
	Peduncle width at apex	Correlation Coefficient	0.168	0.093	-0.055	-0.015	-0.202	0.007	0.179	0.081	0.167	-0.081
		Sig. (2-tailed)	0.35	0.606	0.763	0.933	0.258	0.969	0.318	0.656	0.353	0.656
		N	32	32	32	32	32	32	32	32	32	32

			Mg (ppm)	S (ppm)	B (ppm)	Cu (ppm)	Fe (ppm)	Mn (ppm)	Zn (ppm)	Clay (%)	Silt (%)	Sand (%)
Spearman's rho	Peduncle width at base	Correlation Coefficient		0.179	0.252	0.081	0.042	0.332	0.164	0.086	-0.033	-0.053
		Sig. (2-tailed)	0.907	0.32	0.157	0.655	0.818	0.059	0.363	0.636	0.854	0.768
		N	32	32	32	32	32	32	32	32	32	32
	Number of flowers in each peduncle	Correlation Coefficient	0.071	-0.108	-0.13	-0.104	-0.002	-0.126	0.119	-0.163	0.27	0.134
		Sig. (2-tailed)	0.696	0.548	0.471	0.565	0.991	0.483	0.509	0.363	0.128	0.457
		N	32	32	32	32	32	32	32	32	32	32
	Length between each pedicel	Correlation Coefficient	0.015	0.251	0.205	0.127	0.067	0.235	0.091	.377*	0.024	-0.311
		Sig. (2-tailed)	0.934	0.158	0.253	0.48	0.712	0.188	0.616	0.03	0.893	0.078
		N	32	32	32	32	32	32	32	32	32	32
	Pedicel length	Correlation Coefficient	-0.246	0.078	0.068	0.158	0.16	-0.041	0.084	-0.28	0.257	0.164
		Sig. (2-tailed)	0.167	0.667	0.708	0.379	0.374	0.821	0.643	0.115	0.149	0.363
		N	32	32	32	32	32	32	32	32	32	32
	Pedicel width at middle	Correlation Coefficient	0.295	.397*	.426*	0.318	-0.144	.514**	0.172	0.041	-0.118	-0.002
		Sig. (2-tailed)	0.096	0.022	0.014	0.072	0.425	0.002	0.339	0.819	0.513	0.993
		N	32	32	32	32	32	32	32	32	32	32
	Floral length	Correlation Coefficient	0.023	0.3	0.061	0.251	-0.06	-0.001	0.046	0.219	.449**	-0.234
		Sig. (2-tailed)	0.898	0.09	0.737	0.16	0.741	0.996	0.798	0.22	0.009	0.191
		N	32	32	32	32	32	32	32	32	32	32
	Sepal width at apex	Correlation Coefficient	0.156	-0.104	0.202	0.235	-0.114	0.246	0.158	-0.126	0.156	0.07
		Sig. (2-tailed)	0.387	0.564	0.26	0.187	0.527	0.168	0.38	0.484	0.387	0.7
		N	32	32	32	32	32	32	32	32	32	32

		Mg (ppm)	S (ppm)	B (ppm)	Cu (ppm)	Fe (ppm)	Mn (ppm)	Zn (ppm)	Clay (%)	Silt (%)	Sand (%)
Sepal length	Correlation Coefficient	-0.033	0.296	0.164	0.284	-0.096	0.024	-0.075	0.194	0.245	-0.238
	Sig. (2-tailed)	0.853	0.094	0.362	0.109	0.595	0.894	0.68	0.28	0.17	0.182
	N	32	32	32	32	32	32	32	32	32	32
Sepal width at middle	Correlation Coefficient	0.064	0.199	.392*	.412*	-0.032	.387*	0.094	-0.091	0.242	0.006
	Sig. (2-tailed)	0.725	0.267	0.024	0.017	0.86	0.026	0.601	0.613	0.174	0.973
	N	32	32	32	32	32	32	32	32	32	32
Sepal width at base	Correlation Coefficient	0.024	0.101	0.3	.406*	-0.011	0.239	-0.032	-0.006	0.074	-0.033
	Sig. (2-tailed)	0.896	0.575	0.09	0.019	0.953	0.181	0.858	0.975	0.684	0.854
	N	32	32	32	32	32	32	32	32	32	32
Petal width at undivided part at apex	Correlation Coefficient	0.093	0.205	0.001	0.321	-0.188	0.317	0.183	0.082	0.099	-0.074
	Sig. (2-tailed)	0.607	0.253	0.997	0.069	0.296	0.072	0.308	0.649	0.582	0.682
	N	32	32	32	32	32	32	32	32	32	32
Petal width at undivided part at middle	Correlation Coefficient	-0.063	0.157	-0.161	0.296	-0.075	0.187	0.135	0.094	0.331	-0.169
	Sig. (2-tailed)	0.726	0.384	0.369	0.094	0.679	0.298	0.452	0.604	0.06	0.346
	N	32	32	32	32	32	32	32	32	32	32
Petal width at undivided part at base	Correlation Coefficient	0.025	0.067	0.074	0.13	0.107	0.22	0.041	0.029	0.111	-0.089
	Sig. (2-tailed)	0.889	0.711	0.684	0.469	0.555	0.218	0.821	0.873	0.538	0.621
	N	32	32	32	32	32	32	32	32	32	32
Average range of length within one average petal	Correlation Coefficient	0.113	-0.008	0.088	0.089	-0.106	0.176	-0.096	0.086	0.076	-0.123
	Sig. (2-tailed)	0.529	0.964	0.627	0.622	0.556	0.329	0.597	0.634	0.673	0.495
	N	32	32	32	32	32	32	32	32	32	32

			Mg (ppm)	S (ppm)	B (ppm)	Cu (ppm)	Fe (ppm)	Mn (ppm)	Zn (ppm)	Clay (%)	Silt (%)	Sand (%)
	Petal length	Correlation Coefficient	0.12	0.249	0.194	0.119	-.350*	0.218	-0.014	0.072	0.175	-0.11
		Sig. (2-tailed)	0.505	0.163	0.279	0.508	0.046	0.222	0.938	0.691	0.33	0.542
		N	32	32	32	32	32	32	32	32	32	32
	Major primary number of divisions in each petal	Correlation Coefficient	0.303	-0.228	0.099	-0.285	0.119	-0.169	0.002	0.083	-0.124	0.012
		Sig. (2-tailed)	0.086	0.203	0.585	0.108	0.509	0.347	0.991	0.646	0.49	0.946
		N	32	32	32	32	32	32	32	32	32	32
	Minor tertiary number of divisions in each petal	Correlation Coefficient	-0.014	0.073	.369*	0.175	0.126	0.139	0.176	-0.141	0.07	0.061
		Sig. (2-tailed)	0.941	0.687	0.035	0.329	0.485	0.439	0.328	0.435	0.7	0.737
		N	32	32	32	32	32	32	32	32	32	32
	Petal division length	Correlation Coefficient	-0.084	0.15	-0.116	0.01	-.375*	-0.042	-0.099	0.092	0.293	-0.116
		Sig. (2-tailed)	0.642	0.405	0.52	0.954	0.032	0.815	0.582	0.612	0.098	0.522
		N	32	32	32	32	32	32	32	32	32	32
	Number of stamens	Correlation Coefficient	0.127	-0.241	-0.261	-0.206	-0.287	-0.315	-0.287	0.08	0.072	-0.066
		Sig. (2-tailed)	0.482	0.176	0.143	0.25	0.105	0.074	0.106	0.658	0.689	0.715
		N	32	32	32	32	32	32	32	32	32	32
Spearman's rho	Length of stamens	Correlation Coefficient	0.171	.409*	.383*	0.179	-0.119	.412*	0.211	-0.074	-0.109	0.058
		Sig. (2-tailed)	0.341	0.018	0.028	0.318	0.51	0.017	0.239	0.684	0.547	0.748
		N	32	32	32	32	32	32	32	32	32	32
	Length of filament	Correlation Coefficient	0.331	0.168	0.24	0.118	0.145	.366*	.412*	0.005	0.065	0.01
		Sig. (2-tailed)	0.06	0.35	0.178	0.515	0.42	0.036	0.017	0.978	0.718	0.957
		N	32	32	32	32	32	32	32	32	32	32

		Mg (ppm)	S (ppm)	B (ppm)	Cu (ppm)	Fe (ppm)	Mn (ppm)	Zn (ppm)	Clay (%)	Silt (%)	Sand (%)
Length of anther	Correlation Coefficient	0.288	0.194	0.276	0.242	-0.054	.364*	0.26	-0.216	-0.22	0.223
	Sig. (2-tailed)	0.104	0.278	0.121	0.174	0.765	0.038	0.144	0.227	0.219	0.212
	N	32	32	32	32	32	32	32	32	32	32
Width of filament	Correlation Coefficient	-0.03	-0.044	.364*	0.272	0.227	0.265	-0.095	-0.126	-.347*	0.112
	Sig. (2-tailed)	0.871	0.806	0.037	0.126	0.203	0.136	0.599	0.484	0.048	0.536
	N	32	32	32	32	32	32	32	32	32	32
Width of anther	Correlation Coefficient	-0.038	0.041	0.203	.426*	-0.085	0.195	-0.222	0.064	0.09	-0.175
	Sig. (2-tailed)	0.833	0.819	0.256	0.013	0.64	0.276	0.214	0.724	0.617	0.331
	N	32	32	32	32	32	32	32	32	32	32
Number of setae on anther	Correlation Coefficient	0.085	0.002	0.162	0.153	-0.049	0.101	0.148	0.113	-0.134	-0.014
	Sig. (2-tailed)	0.638	0.992	0.367	0.395	0.786	0.576	0.411	0.53	0.459	0.939
	N	32	32	32	32	32	32	32	32	32	32
Length of setae on anther apices	Correlation Coefficient	-0.078	0.001	0.081	-0.282	-0.057	-0.26	-0.121	0.169	0.173	-0.154
	Sig. (2-tailed)	0.667	0.994	0.655	0.112	0.752	0.144	0.502	0.347	0.335	0.391
	N	32	32	32	32	32	32	32	32	32	32
Disk glands length	Correlation Coefficient	0.181	0.297	0.253	0.153	-0.188	0.111	-0.152	0.062	0.053	-0.057
	Sig. (2-tailed)	0.314	0.094	0.155	0.394	0.294	0.537	0.4	0.734	0.77	0.751
	N	32	32	32	32	32	32	32	32	32	32
Disks glands breadth	Correlation Coefficient	0.141	0.235	0.181	0.264	-0.181	0.098	0.046	0.162	0.311	-0.173
	Sig. (2-tailed)	0.435	0.187	0.313	0.138	0.314	0.588	0.798	0.367	0.078	0.334
	N	32	32	32	32	32	32	32	32	32	32

**. Correlation is significant at the 0.01 level (2-tailed), *. Correlation is significant at the 0.05 level (2-tailed).

Considering this information in conjunction with the findings presented in Chapter 5, it revealed that the measure of several morphological variables of *E. gadgilii* was greater for populations collected from the sky islands on northern sides of the Palghat Gap. The negative correlation between iron levels and lamina breadth is evident, as higher iron concentrations are associated with reduced lamina length. Chapter 5 results indicate that most vegetative quantitative parameters of *E. gadgilii* populations, including lamina length, tend to be smaller in its populations from the sky islands on the southern side. That is *E. gadgilii* populations from the northern sky islands populations showed more plant growth. In such a way all other edaphic parameters were correlated with at least with one of the morphometric variables of *E. gadgilii*. This study thereby depicts the fact that edaphic parameters are one of the feature that drives the intraspecific morphometric variability in *E. gadgilii*. This also showcases the significance of edaphic elements in shaping the population of the sky island species. The Palghat Gap, which separates the sky islands, is the major factor that separated this habitat, so its influence over the edaphic ecological characteristics of sky islands of the Western Ghats surrounding the gap is inevitable. This in turn shows the high probability of it to indirectly effect the populations of *E. gadgilii* and induce the intraspecific morphometric variability in *E. gadgilii*.

Hulshof (Hulshof and Spasojevic 2020) further reinforces this idea by illustrating how edaphic variation plays a crucial role in shaping plant diversity and affecting community assembly processes. Mills (Mills *et al*., 2004) and Putra (Putra *et al*., 2018) contribute additional insights, with the former examining the conservation significance of island populations and the latter delving into the genetic differentiation of a tropical seagrass species, both of which are influenced by soil-related factors. These studies collectively stress the significance of considering edaphic elements when comprehending and safeguarding the population dynamics of *E. gadgilii*.

This interlink not remains within edaphic parameters and *E. gadgilii* population but also connected to climate factors. As per climate data analysis done in chapter 6, the precipitation is the one major factor that is found to have negative correlation with most morphometric variables of *E. gadgilii*, which includes lamina breadth too. In the present study, among all the ecological parameters the gap is the one of the factor found to have a greater influence over populations of *E. gadgilii*. Because the factors like climate and edaphic parameters found to have statistically significant correlation with only few of the morphometric parameters of *E. gadgilii*, but the gap's corre-

lation was with majority of its morphometric parameters. So, the prominent factor that separates the population of *E. gadgilii* to northern and southern side populations is obviously the Palghat Gap.

In the case of climate, the precipitation is lower in northern sky islands, the lamina breadth of *E. gadgilii* of population of northern sky islands also smaller, and where the precipitation is negatively correlated with lamina breadth. Then the edaphic elements like iron having negative relation with lamina breadth and Fe content is lower over sky islands soil samples from northern side, this goes with the above fact.

The other connection was found between precipitation and edaphic elements was a clay percentage correlation with precipitation. According to Chapter 6, the precipitation received over the sky islands on the northern side is less than that received by the southern side. This corresponds to the fact that the clay percentage content in northern sky island samples is higher. According to SWCC fractal analysis, the relationship between clay percentage and water retention capacity is a well-established fact. Since the northern sky islands receive low precipitation, which goes with its soil samples higher clay content. Thereby the northern sky islands soil samples have high water retention capacity. Therefore, each element in a habitat changes with respect to the changes in other habitat components to maintain balance in ecosystem functioning within the habitat.

Biogeographic gaps in mountain systems shape species spatial distributions and the intraspecific morphometric variability of populations of *E. gadgilii*. Therefore, the Palghat Gap was found to be the significant barrier for taxonomic groups, among the other gaps like the Shencottah Gap and Goa Gap. The divergence occurred long after gap formation, thereby suggesting that other factors like ecology and biogeography may have also played a role in species distributions. This study illuminates the multifaceted relationship between mountain gaps, species distributions, and intraspecific variability of sky island species.

Future research should delve into the intricate mechanisms that drive species distributions and genetic differentiation in mountain systems, encompassing both spatial and temporal dimensions (Biswas and Praveen Karanth 2021). The observed variations in floristic diversity, morphometric characteristics at the population level, climate variability and soil gradients of sky islands across the Palghat Gap in this study highlighted the significant influence of these gap features on the isolated sky islands habitats in the Western Ghats. The variations in soil samples can be attributed to cli-

mate-related factors, such as temperature and precipitation changes, which in turn would have affected soil pedogenesis and lead to alterations in the soil composition. These findings provide evidence of the crucial role played by edaphic parameters in the development and growth of the studied plant species, and it is not limited to one specific edaphic parameter, as all soil parameters contribute equally to the plant's growth. Hence, substantial changes in edaphic parameters have a noteworthy impact. Variations in soil-related parameters significantly influence the distribution of various taxa (Jenny 1941, Wooten 1986).

Spatial interpolation involves estimating values at unmeasured locations based on the values observed at nearby locations. By creating such maps, researchers and land managers can gain insights into the distribution and severity of land degradation across the study area. These maps provide a visual representation of the spatial patterns of land degradation, allowing for the identification of specific locations or "spots" that exhibit signs of degradation. By analysing the patterns and trends depicted in the maps, researchers can pinpoint areas where land degradation is more or less prevalent or severe. This information is crucial for understanding the extent of land degradation and for implementing targeted interventions and conservation efforts to address the underlying causes and prevent further degradation (Karastogianni *et al*., 2017, Singha and Swain 2022).

In previous studies, various investigations have been conducted to assess soil properties and species diversity across diverse rangeland conditions. The outcomes of these studies revealed noteworthy disparages in species diversity between rangelands characterised by favourable and unfavourable conditions. Furthermore, an observed trend indicated heightened levels of soil organic matter within rangelands exhibiting positive conditions. The influence of human activities emerged as a pivotal determinant in both rangeland degradation and the subsequent reduction of species diversity (Eghdami *et al*., 2019). So, variability in the soil properties across these specific ecosystems can be used as a useful metric to understand the extent and severity of desertification processes occurring in these regions. Desertification refers to the degradation of once-productive lands into desert-like conditions, and monitoring shifts in soil properties can provide crucial insights into the progression of this phenomenon. By analysing and comparing soil properties such as texture, nutrient content, organic matter, and water retention, researchers and land managers can gain a deeper understanding of the health and resilience of arid and semiarid grasslands and devise effective

strategies to combat desertification and promote sustainable land management practices (Schlesinger *et al*., 1996). Thereby conservation of biodiversity regions can also be made possible. Therefore, the importance of the edaphic element and its variance caused by the geographic gap separation has proved to have a role in intraspecific morphometric variability shown by species of *E. gadgilii* in the sky islands across the gap.

7.5. Conclusions

This section of the study focused on finding the interdependencies of edaphic components with other ecological components. For that majority of the edaphic parameters of sky islands samples were analysed. Then they were compared with other eco-logical components like geographical features and the associated vegetation. Especially the association of edaphic parameters with representative sky island species *E. gadgilii* was analysed.

A notable discovery from the study was the gradation found in edaphic parameters of sky islands across the Palghat Gap. This edaphic gradient may have led to the differentiation between sky islands. Furthermore, each edaphic parameter displayed a correlation with each other and was also found to be correlated with more than one quantitative morphometric variable of *E. gadgilii*. This substantiated the significant role of edaphic factors in driving species diversity and intraspecific variability in *E. gadgilii.*

These findings highlight the significant role of the Palghat Gap in shaping the ecological characteristics of the surrounding sky islands in the Western Ghats. Acting as a major barrier, the Palghat Gap creates a distinct separation between these habitats, leading to notable edaphic diversity along the north-south axis. The study provides substantial evidence of the critical role edaphic parameters play in plant development and growth. Variations in soil composition and population samples across the sky islands further support the impact of these parameters. This research illustrates the connections between gap features, soil composition, and plant population responses to environmental factors, underscoring the importance of edaphic parameters in this ecological context. It offers valuable insights into the relationship between tropical environmental diversity, plant specialization, and the enhancement of tropical floral diversity.

CHAPTER 8:

ASSESSING INTRASPECIFIC GENETIC VARIATION OF *ELAEOCARPUS GADGILII* IN SKY ISLANDS OF THE WESTERN GHATS

8.1. Introduction

Each species plays a crucial role in the formation and organisation of a community. The presence of multiple species within the same community was largely influenced by their respective ecological niches. A species niche encompasses its specific requirements, such as its preferred habitat, resources, and interactions with other species. For a species to endure over time, it is imperative for individual members to possess a high level of viability (Mougi and Nishimura 2005). Consequently, the environment and habitat act as filters, allowing only those species that are well-suited and adapted to the prevailing conditions to persist within the community. Unsuitable species are effectively sieved out by these environmental factors. The coexistence of species within a community relies on their ability to tolerate and interact with one another. While some species can coexist harmoniously, others engage in competitive interactions for limited resources, reinforcing the principle of survival of the fittest, as proposed by Darwin. Through this process, species that possess advantageous traits and adaptations have a higher chance of survival and reproductive success, leading to the continuation of their genetic lineages over time (Gupta *et al*., 2021).

Interspecific interactions, which occur between different species within a community, play a pivotal role in driving evolutionary changes and promoting the formation of new species (CaraDonna *et al*., 2021). These interactions can take various forms, including competition, predation, mutualism and symbiosis. Such interactions exert selective pressures on species, influencing their morphology, behaviour, and genetic composition (Huntley 2023b). Over time, this process of natural selection and adaptation lead to the divergence of populations and the emergence of distinct species through a phenomenon known as speciation. Even with continuous gene flow, the presence of diversifying selection at a small number of genetic loci can suffice for the establishment and persistence of taxonomically well-defined species (Schluter 2009, Chapman *et al*., 2013). In the field of phylogeography, scientists investigate the relationship between geographical attributes and the genetic variation observed among species (Edwards *et al*., 2022). This discipline seeks to understand how historical processes, such as geographic barriers and dispersal patterns, have shaped the genetic diversity and population structure of species (Wellenreuther *et al*., 2011). By

studying the genetic variation across different geographical regions, researchers can gain insights into the evolutionary history, migration patterns, and adaptive responses of organisms to their changing environments (Young 2003). Phylogeography provides valuable information for conservation efforts, species management, and understanding the intricate connections between geography and genetic evolution (Avise 2000)

Phylogeographic techniques have been increasingly used to study the genetic diversity of temperate plant species in relation to these climatic fluctuations. This approach is particularly popular in Europe, North America, the Japanese Archipelago, and Taiwan. Species had to adapt to changing conditions, including temperature, precipitation and habitat availability. Research on the genetic makeup of temperate plants provides valuable insights into their responses to past climate changes and their current distribution and genetic diversity. Alterations in the climate and subsequent environmental transformations have facilitated the division of ranges, occurrence of vicariance events, and isolation of populations, thereby creating favourable conditions for the occurrence of allopatric speciation (Avise 1995, 2000).

Angiosperms have distinct evolutionary histories and demographic fluctuations. By analysing the genetic variation through sequencing techniques and fingerprint markers, researchers gain insights into the historical and geographical factors that have shaped the genetic diversity within and among populations of plants. This information is invaluable for understanding patterns of migration, adaptation, and divergence, as well as the processes that have influenced the distribution and evolution of plant species. By combining different types of data, researchers can create more and accurate phylogeographic reconstructions, shedding light on the evolutionary processes and historical events that have influenced the genetic makeup of plant species (Qiu *et al*., 2011).

The primary reaction of plant species to environmental changes often involves the fragmentation of their ranges and the subsequent isolation of populations. This response is particularly evident in the recurring occurrence of multiple localised refugia. The process of habitat fragmentation resulting from environmental change leads to population divergence within the same species (Wang *et al*., 2023b). When habitat faces environmental changes, such as shifts in climate or land use, plant populations separate from one another, either by physical barriers or through the loss of suitable habitats. This fragmentation of their ranges often results in isolated pockets of populations, referred to as refugia. These refugia act as localised havens where plant species

can persist and adapt to altered environmental conditions (Inogwabini 2020). The process of habitat fragmentation and the subsequent isolation of populations can have profound effects on the genetic makeup and evolutionary trajectory of plant species. When populations become isolated, they experience reduced gene flow and are subjected to different selection pressures in their respective habitats. These factors can lead to genetic divergence between populations, then they accumulate distinct genetic variations and adapt in response to their local environments (Salmona *et al*., 2023).

The phenomenon of range fragmentation and population isolation is a widespread pattern observed in numerous plant species facing environmental change. It highlights the importance of understanding the dynamics of habitat fragmentation and its consequences for population genetics and species evolution (Jacquemyn *et al*., 2012). By studying these processes, scientists can gain insights into the mechanisms driving population divergence and the potential impacts on the long-term survival and adaptation of plant species in rapidly changing environments (Ewers and Didham 2006). In the realm of co-evolution and species interaction, there has been a growing recognition of the significance of local adaptation and spatially variable selection. It has become increasingly evident that the interactions between species can differ across diverse landscapes, leading to variations in the traits exhibited by these species. This geographical variation in species traits reflects the interplay between organisms and their associated environments (Kraaijeveld and Godfray 1999, Thompson and Cunningham 2002). Numerous studies were held to explore such phenomena at the phenotypic level. However, a limited number of such investigations delved into the genetic aspects of these phenomena (Hoeksema and Forde 2008).

Variations in geography can result in significant differences observed among populations. When populations are geographically separated, they can experience different environmental conditions, such as differences in climate, topography, or available resources. These environmental variations can drive changes in the genetic makeup and traits of populations over time, leading to higher-level variation across different populations. In other words, geographical factors act as a driving force that shapes the characteristics and diversity of populations in different regions (Storz 2005, Stinchcombe and Hoekstra 2008).

The Galapagos Islands also found to exhibit a notable variation in small populations, which was primarily maintained by limited migration between the islands (Grant and Grant 1992). The geographical characteristics of the islands, including re-

stricted seed dispersal and insect pollinators, contribute to reduced gene flow within and between populations. These limitations have significant implications for the genetic and demographic aspects of small populations, with even minor effects exerting a substantial impact on metapopulations. The impact of these geographical factors is less pronounced in populations that undergo self-pollination. The study of molecular variation in isolated plant populations provides insights into the genetic dynamics and evolutionary processes operating within these populations (Schaal and Leverich 1996).

The detectability of genotypic variation through nuclear polymorphism is relatively limited. It is generally expected that if a phenotypic change is observed in plants, the underlying variation should first emerge at the molecular level. However, identifying and understanding the precise location and mechanisms of these molecular variations can be a challenging task, especially when phenotypes are influenced by complex genetic control. In simpler terms, when there are changes in the physical characteristics of plants, it is assumed that there are corresponding changes at the molecular level in their genes. However, pinpointing the specific genetic changes and understanding how they contribute to the observed traits can be difficult, especially when traits are influenced by multiple genes and complex genetic interactions (Kelly 2006). The precise mechanisms by which environmental changes influence nucleotide diversity at the gene level are not yet fully understood. It is important to note that local adaptation does not solely rely on the introduction of new mutations or alleles through migration (Moeller and Tiffin 2008).

The integration of molecular information with ecological, demographic, behavioural, and physiological data yields valuable insights. The advancements in molecular techniques have enhanced the ability to identify individuals and understand population structures with higher resolution (Haig 1998). DNA barcoding is a valuable tool for species identification in plants, it has limitations when it comes to address questions related to population-level analyses. DNA barcoding typically focuses on a specific region of the genome, such as the chloroplast or mitochondrial DNA, which provides information on species identity. However, to understand patterns and processes within populations, more genetic data, such as microsatellites or whole-genome sequencing, are required. These additional molecular markers can capture the genetic diversity and structure within populations, allowing for a deeper exploration of evolutionary and ecological dynamics at the population level. While DNA barcoding was

useful for species-level identification, but it was not sufficient for addressing population-level questions, necessitating the use of more molecular approaches (Moritz and Cicero 2004, Chase *et al*., 2005). The phenotypic variations observed among populations reflect the local adaptation of species and are sustained through the process of natural selection.

In scientific studies, the sequencing of chloroplast DNA, is a widely used technique for examining genetic variation in flowering plants (angiosperms). In gymnosperms, researchers commonly analyse cpDNA (chloroplast DNA) or mitochondrial DNA. Additional genetic data for analysis can be obtained from nuclear DNA fingerprint markers like AFLPs (Amplified Fragment Length Polymorphisms) or ISSRs (Inter Simple Sequence Repeats). Less frequently, researchers utilised nuclear microsatellites or DNA sequence variation at nuclear loci. These molecular approaches complement and expand upon existing knowledge derived from paleo-ecological and geological data (Qiu *et al*., 2011). Mitochondrial DNA has been utilised as a valuable source of data for distinguishing variations within and between populations. However, the interpretation of such data is contentious due to the fact that mitochondrial DNA is exclusively inherited from the maternal lineage (Moritz 1994, Avise 1995)

The nuclear internal transcribed spacer (ITS) region and the plastid trnH-psbA intergenic spacer have been identified as DNA regions suitable for barcoding techniques in flowering plants. The ITS region is the one widely used in plant phylogenetic studies at the species level due to its high levels of divergence between different species. On the other hand, the trnH-psbA spacer, despite being relatively short (around 450 base pairs), exhibits the highest variability among plastid regions in flowering plants and can be successfully amplified across a wide range of land plants. These two regions offer valuable molecular markers for plant barcoding, enabling accurate species identification and facilitating research on the evolutionary relationships and biodiversity of flowering plants (Kress *et al*., 2005). The four major chloroplast genes with high variability and identification ability were matK, rbcL, rpoC1 and psbA-trnH. These genes thereby provide reliable and accurate identification of plant species, aiding in taxonomy, biodiversity assessments, and conservation efforts. The presence of extensive variation within these genes allows for the differentiation and discrimination of plant species, contributing to our understanding of their evolutionary relationships and ecological interactions. The utilisation of these chloroplast genes as molecular markers enhance our ability to accurately identify and classify plant spe-

cies, facilitating research and conservation efforts in the field of plant biology (Kress *et al*., 2005, Kress *et al*., 2007, Lahaye *et al*., 2008). Inter transcribed spacer is the nuclear gene used for variability analysis of angiosperms. However, this gene variability depends on species too (Sass *et al*., 2007).

Here the species considered for the genetic variation analysis was *E. gadgilii*. This genus found to be challenging while extracting DNA. The mucilaginous nature while grinding and the chemical compounds in the plants interfere with DNA extraction. Most of the species of Family Elaeocarpaceae found to have high phenol content and several other chemical components and were a major hindrance in DNA extraction (Coode 2004, Hardainiyan *et al*., 2015b, Mariani *et al*., 2021). This chapter focused on analysing the intraspecific genetic variation within populations of *E. gadgilii* found on sky islands across the Palghat Gap, aiming to understand how the features of the gap influence the species at the genetic level.

8.2. Methodology

The species selected for the study was *Elaeocarpus gadgilii* A.M. Maya, V. Suresh & K.M. P. Kumar, a novel species described from the southern Western Ghats (Manoharan *et al*., 2021a). It was chosen as the subject of this study at the genetic level, as it fulfils all the criteria of species selection. The selection of this taxon was based on its fulfillment of several key criteria. These include its status as a newly identified endemic species from the southern Western Ghats, the economic and medicinal importance of the Elaeocarpus genus, and findings from numerous pharmacological studies showing various secondary metabolites in different plant parts. Furthermore, significant morphometric variation in *Elaeocarpus gadgilii* populations in sky islands of the Western Ghats across the Palghat Gap was a crucial factor in its selection. The intraspecific morphological variability of this species is detailed in Chapter 5.

8.2.1. Selection of gene

DNA barcode gap is a metric used to assess the genetic dissimilarity between DNA sequences utilised as barcodes for species identification. The genetic diversity within a DNA barcode should exhibit distinct and non-overlapping patterns of genetic divergence between samples taken from within a species (intraspecific) and those from different species (interspecific). As the number of closely related species rises, there is a notable rise in the overlap of genetic variation, particularly in the absence of clear genetic differences or barcode gaps (Moritz and Cicero 2004, Meyer and Paulay

2005). The divergence measures are obtained through sequence alignment and pairwise comparison algorithms. The genetic distance is typically determined by quantifying the number or percentage of nucleotide differences between DNA barcode sequences. A smaller distance value signifies a closer genetic relationship, indicating that the sequences likely belong to the same species. Conversely, a larger distance value suggests greater genetic divergence, potentially indicating differences at the species level (Chen *et al*., 2010, Kress and Erickson 2007).

To calculate the genetic distance, the interspecific and intraspecific diversity of all available genes within the selected genus in the NCBI database was used to substantiate the above results. Subsequently, the interspecific and intraspecific diversity indices were computed through the Kimura-2-distance parameter in MegaX11.0.10 (Kumar *et al*., 2018). These calculations allowed for the determination of barcode gap distances between species and within species. Genes exhibiting higher intraspecific diversity indices were identified as the ones more prone to variation within species at the population level. So, for that the reference gene sequence for the analysis are made available from NCBI. All the genes available at NCBI under the genus were considered for the gene selection process. Among them matK, rbcL, and psbA-trnH available from NCBI over this genus *Elaeocarpus* were downscaled in fasta format and were considered as the reference genes for analysing Barcode Gap distance. The reference gene sequences for each gene of this genus were analysed using MegaX 11.0.10 to assess interspecific and intraspecific divergence. The evolutionary distances were calculated using the Kimura 2-distance parameter in MegaX. The gene that exhibited the greatest barcode gap distance was chosen as the primary focus of this study.

8.2.2. Gene sequencing

DNA extraction was carried out on the leaf tissue of *E. gadgilii*. Leaf samples were obtained from all populations of *E. gadgilii* residing in the sky islands of Western Ghats on the southern and northern sides of the Palghat Gap. The collected leaf samples underwent a thorough cleaning process. Subsequently, a portion of the leaf samples were subjected to deep-freezing at a temperature of -20°C for preservation, while others were dried using herbarium techniques or desiccated with the aid of silica gel before being sealed in polyethene bags (Chase and Hills 1991, Taylor and Swann 1994).

DNA extraction: -

Both fresh and dried leaf samples were utilised for DNA extraction. Nevertheless, the extraction of DNA from the leaf of *Elaeocarpus gadgilii* presented numerous difficulties. Several extraction techniques were employed, such as CTAB, SDS, Doyle and Doyle, Himedia Kit, Primordia Kit, Phenol: chloroform: isoamyl alcohol extraction, and several modified CTAB procedures sourced from previously published papers (Doyle and Doyle 1987, Doyle and Doyle 1990, Zhou *et al*., 1996, Porebski *et al*., 1997, Huang and Sun 2000, Xin and Chen 2012, Arruda *et al*., 2017, Rishi *et al*., 2021). Despite these various attempts, achieving a successful DNA extract from leaves of *Elaeocarpus gadgilii* remained challenging. None of the above-mentioned protocols gave the desired levels of purity and quantity of DNA, except the general CTAB method. But the DNA concentration obtained through this CTAB method was below 50ng/µl with very low purity. Therefore, this general conventional CTAB protocol for DNA extraction from the leaf was modified specifically for the species *E. gadgilii*. To accomplish this, a series of 42 trials were conducted, testing six significant modifications. The selection of each step was based on a thorough comparison of nanodrop and gel electrophoresis outcomes. Here a conventional modification was applied to the standard CTAB DNA extraction procedure to establish a precise and optimised method capable of extracting DNA suitable for PCR. Each step of the CTAB method was meticulously adjusted until the final protocol was devised, leveraging the insights gained from the comparative analysis. Each step given below was the modifications tried over the standard procedure of CTAB. The modifications were done step-by-step, but some failed and few were successful. The modifications considered here in each step of CTAB were as follows:

1. 0.012g PVP was added during grinding leaf samples without liquid nitrogen.
2. 70-80µl β-Mercaptoethanol was added to the grounded mixture and incubated at 45°C 15 min. Just after incubation add tri-unsaturated phenol.
3. Added 3M Sodium acetate $(1/10)^{th}$ volume of isopropanol) at the step where isopropanol was added.
4. Adding not-chilled Isopropanol at room temperature
5. Changing incubation temperature and time to 60 -65°C for 15 min to 48 min.
6. The proportion of the weight of the leaf was changed from 0. 2 g to 1g of the leaf with the amount of CTAB.

After several trials and errors, a modified protocol was developed. The modified protocol was successful, in extracting DNA in good quality and quantity from fresh, dried, and freeze-dried leaf samples of *E. gadgilii*. But the steps in protocol differed depending on the leaf sample either fresh, dried or deep frozen. It is noteworthy that the protocol employed for dried samples differed from that used for fresh and freeze-dried samples, underscoring the necessity to further adapt the existing CTAB method to meet the specific requirements of the species under investigation.

Reagents and chemicals used: -

CTAB powder, Tris HCl, Nacl, EDTA, Chloroform, Isoamyl alcohol, Distilled water, Ethanol, PVP, IPP, TBE Buffer, Dnase free water, Agar molecular grade, Ethidium bromide, 100 kb ladder and 1000 bp ladder.

Buffer for DNA extraction: -

1 gram of CTAB powder was weighed and dissolved in 5 mL of distilled water. To this solution, 5 mL of Tris HCl, 2 mL of 0.5 M EDTA, and 14 mL of 5 M NaCl were added. The total volume was adjusted to 50 mL with distilled water. Prior to preparing the CTAB buffer, the pH of Tris HCl and 0.5 M EDTA was adjusted to 8 to deactivate DNAse enzymes. The CTAB buffer was modified step-by-step, and each modification's impact on DNA extraction efficiency was assessed using a nanodrop (Thermo Fisher Scientific Nanodrop One) and electrophoresis.

Modified conventional CTAB protocol for DNA extraction from dry leaf samples of *E. gadgilii*: -

1. The dry leaf sample was sterilised with 70% alcohol and then 0.16g of it was weighed out.
2. The leaf was ground with 0.02g spatula of PVP and 2100µl CTAB buffer in frozen mortar and pestle. Ground in a way that the mixture was not vicious, as it would cause difficulties to get the good DNA. The ground mixture was then transferred to the eppendorf tube.
3. The extract was incubated at 65°C for 48 minutes.
4. Subsequently, the extract was allowed to cool to room temperature.
5. Following cooling, the extract underwent centrifugation at 10,000 rpm for 10 minutes at ambient temperature.
6. Then the supernatant was transferred to the next vial and centrifuged at 4°C for 5 min at 10,000 rpm.
7. Took the supernatant into a new vial and discarded the precipitate.

8. To the supernatant an equal volume of Chloroform: Isoamyl alcohol (CI) (24:1) mixture was added. Then by inverting the tube several times the mixture was gently mixed and centrifuged at 4°C for 5 min 10,000 rpm.
9. Then the supernatant was taken out carefully into the next vial. To supernatant an equal volume of CI (24:1) mix was added and was mixed by inverting the tube gently several times and was centrifuged for 5 min at 10,000 rpm in 4°C. After centrifugation the supernatant was take out and continued this 9th step until the supernatant was clear.
10. Then the clear supernatant was taken out to new vial and centrifuged for 5 min in 10,000 rpm to precipitate out any remaining debris.
11. After carefully transferring the supernatant into a new vial and discarding the precipitate, IPP was added at room temperature in an amount three times the volume of the supernatant to facilitate further processing. The mixture was then kept overnight at -20°C.
12. The mixture was centrifuged for 10 minutes at 12,000 rpm in a cooled centrifuge. Subsequently, the supernatant was removed, and the pellet was stored at room temperature.
13. 200 µl of 70% ethanol was added to the pellet (700 µl ethanol: 300µl Nuclease free water) and was centrifuged for 5 min at 12000 rpm at 4 °C, and the supernatant was discarded. The step was repeated until a salt precipitate in the white form was removed from the pellet.
14. Ethanol wash was done for minimum 1 to maximum 4 times.
15. Then the ethanol was discarded and the eppendorf tube with pellet was kept open in laminar airflow for the pellet to dry.
16. After the ethanol evaporated out, 100 µl of nuclease-free water was added to the pellet and then the tube was tapped slightly to dissolve DNA and was then kept at 4 °C for 30 mins.
17. After ensuring the pellet was dissolved, the DNA extract was preserved at -20 °C.

Modified CTAB Protocol for DNA Extraction from Deep Frozen or Fresh Leaf Sample: -

The aforementioned procedure underwent minor adjustments for extracting DNA from fresh or deep-frozen leaf samples. Initially, the leaf sample was sterilised

using 70% ethanol. Subsequently, 0.36 grams of leaf material was weighed out and ground with PVP (polyvinylpyrrolidone) and 2500µl of CTAB buffer in a frozen mortar and pestle. For mature leaves, approximately 0.091g of PVP was used, while 0.012g of PVP was employed for young leaves. Care was taken during the grinding process to prevent the extract from becoming viscous. Following this, the mixture was incubated at 60-65 degrees Celsius for 45 minutes. The subsequent steps in the aforementioned protocols were followed, starting from the 4th to the 10th step. Then in the 11^{th} step, the IPP was added at room temperature, then kept at ˉ4 °C for about 2-3 hours, next centrifuged for 15minutes 12000rpm and then followed the 13^{th} step to the last step as in the modified protocol for dry leaf sample.

Quantitative and qualitative analysis of extracted DNA: -

Qualitative and quantitative analysis of extracted DNA was done with the nanodrop. The modified protocol's effectiveness was evaluated first by measuring absorbance using a nanodrop (Thermo Fisher Scientific Nanodrop One) and then by running gel electrophoresis with a 1 Kb DNA ladder. Subsequently, the quality of PCR amplicons was assessed using gel electrophoresis with a 1000 bp ladder.

The quality and quantity of DNA are estimated based on absorbance at 260, 230 and 280 nm. The purity of DNA was estimated based on the absorbance ratio at 260/280nm value. If the ratio falls in between 1.8 to 2.0 value means the quality of DNA is good. If the nanodrop absorbance ratio at 260/230 nm was 2. indicated absence of polysaccharide contamination in the DNA sample. Absorbance at 280 nm shows the concentration of DNA in the extract. Finally, the quality of DNA was confirmed by running the extract on a 0.8% agarose gel in electrophoresis at 25 mV for approximately 30 minutes.

All PCR extracts were sent to different laboratories for sequencing. Amplification and sequencing were done with primers of the selected gene. Amplification was carried out in a PCR reaction mixture volume of 10 µl containing 5 µl Takara - EmeraldAmp GT PCR master mix, 1 µl forward primer, 1 µl reverse primer, 0.1 µl template DNA, and the volume was made up to 10 µl with nuclease-free water (2.9 µl). The PCR products were fractionated on a 2.0% agarose gel using 0.5 X TBE buffer containing 15 µl ethidium bromide. They were visualised under UV light and photographed using a UV gel documentation system. The DNA was amplified using the specified primers, and the quality of the amplicon was assessed through gel electro-

phoresis. Then the amplicon was purified by a commercial column-based purification kit (Invitrogen, USA). Sequencing was performed with forward and reverse primer in the ABI 3730 XL cycle sequencer. Each gene was sequenced separately, following the specific conditions mentioned earlier. The sequencing results were obtained in ab1 file and fasta format, containing both the forward and reverse sequences. Subsequently, sequencing was conducted on DNA extracts from all 32 populations of *Elaeocarpus gadgilii* specifically targeting the chosen genes. The obtained sequences were subsequently analysed, edited, and aligned using the Geneious software (Trial version). The forward and reverse sequences of each sample were aligned in the geneious trial version, and the consensus sequence of each sample was created.

The intraspecific divergence among populations of *E. gadgilii* within and between sky islands across the Palghat Gap was evaluated using Mega X 11.0.10 (Kimura 1980). The Kimura 2-parameter method was employed to calculate evolutionary distances, measured as the number of base substitutions per site (Kumar et al., 2018). To assess the diversity within and between populations of *Elaeocarpus gadgilii*, gene sequences from 32 populations were aligned and formatted into a .fasta file using Geneious software. These sequences were then imported into MegaX, where they were categorized into two groups: sequences from populations located on the southern side, and those from the northern side of the study area. The evolutionary distances calculated were utilized to analyse genetic variations within populations across the sky islands and between the sky islands across the Palghat Gap.

8.2.3. Intraspecific phylogenetic relationships

To broaden the scope of the study, five additional outgroup sequences were incorporated alongside the 32 selected gene sequences of *Elaeocarpus gadgilii* populations. These outgroup sequences were selected from species belonging to the *Elaeocarpus* and *Sloanea* genera of the Elaeocarpaceae family. The selected gene sequences of *Sloanea* species and *Elaeocarpus* species were obtained from the NCBI database and were utilised as outgroups. The trial version of Geneious software was employed to align these five outgroup sequences with the selected gene sequences from the 32 populations of *Elaeocarpus gadgilii*. Subsequently, the aligned sequences ends were trimmed, resulted in an aligned 37 sequences (32 from *Elaeocarpus gadgilii* populations and 4 sequences from outgroups). This alignment was saved as a fasta file and served as the input for the construction of the phylogenetic tree.

To understand the intraspecific divergence between populations, phylogenetic hierarchical tree construction methods were employed. To minimize errors in evolutionary predictions, more than two phylogenetic tree construction methods were utilized to explore intraspecific divergence between populations. The methods considered include Neighbour-joining (Saitou and Nei, 1987), Maximum Likelihood (ML), and Bayesian tree inference methods. These are widely utilised techniques in phylogenetic analysis for the construction of evolutionary trees. Neighbour-joining is a rapid distance-based method assuming a consistent rate of evolution. On the other hand, Maximum Likelihood and Bayesian tree inference are probabilistic methods that considered more as intricate evolutionary models. ML involves intensive computational processing, while Bayesian methods yield a posterior distribution of trees.

In addition to the Neighbour-Joining (NJ) method, we also utilized the Minimum Evolution method, providing an alternative perspective in phylogenetic analysis. This approach, rooted in distance-based principles, aims to construct evolutionary trees by identifying the tree that requires the fewest evolutionary changes to accurately represent observed sequence data. The Minimum Evolution method strives to find a tree consistent with available data while minimizing the necessary evolutionary steps, assuming adherence to the principle of minimum evolution. While efficient and suitable for larger datasets, it may not fully account for more intricate evolutionary processes, such as variations in rates at specific sites or the presence of ancestral sequences (Rzhetsky and Nei 1992). All these methods were applied to the same sequence data to ensure a comprehensive analysis with minimized errors.

The Neighbour-Joining method (Saitou and Nei 1987, Brodal *et al*., 2003).) was employed in this study to deduce evolutionary history. This method constructs phylogenetic trees based on evolutionary distance data, identifying pairs of operational taxonomic units (OTUs) that minimize total branch length at each stage of clustering. Starting with a starlike tree, both branch lengths and the topology of a parsimonious tree are efficiently obtained. The approach involves conducting 10,000 bootstrapping iterations, where the percentage of replicate trees showing taxa clustering together is indicated adjacent to the branches (Felsenstein 1985). The tree is proportionally presented, with branch lengths expressed in the same units as the evolutionary distances used for phylogenetic inference. The Kimura 2-parameter method (Kimura 1980) computed evolutionary distances as the number of base substitutions per site. The analysis included 37 nucleotide sequences, and ambiguous positions were elimi-

nated. The final dataset comprised 470 positions, and all analyses were performed using MEGA X (Kumar *et al*., 2018).

The Bayesian approach is another method in phylogenetics study and has experienced increasing popularity over the last twenty years (Lartillot Nicolas 2020). Where the advanced software tools, enabled the implementation of sophisticated models for molecular sequence evolution, facilitating the exploration of significant inquiries in evolutionary biology (Nascimento *et al*., 2017, Dos Reis and Yang 2019, Hassler *et al*., 2023). Here the Bayesian phylogenetic tree was constructed using several software tools, namely Beauti v1.10.4, BEAST v1.10.4, BEAGLE.v3.1.0, Tree Annotator v1.10.4, and FigTree v1.4.4. The substitution model employed in this analysis was the HKY (Hasegawa-Kishino-Yano) model, which accounts for biases in nucleotide substitutions, including different transition and transversion rates. The Coalescent Constant size model was chosen as the tree prior, assuming a constant effective population size over time. This model aligns with populations or species characterised by stable population sizes and is commonly applied in phylogenetic investigations (Hasegawa *et al*., 1985).

The field of phylogenetics offers various methodologies for estimating unknown population parameters, and one alternative is the maximum-likelihood method. Unlike traditional approaches requiring the computation of expected values such as averages and variances, the maximum-likelihood method utilizes the likelihood function to estimate parameters. This study delves into the principles of maximum likelihood, discussing the variance and efficiency of estimators while considering factors like information content and potential minimum variance bounds. Likelihood intervals, similar to confidence intervals in sample-based inference, are introduced. The method is extended to handle scenarios involving simultaneous determination of relationships between multiple parameters and to encompass likelihood regions as generalizations of likelihood intervals (Murthy 1973, Zabarankin and Uryasev 2013, Sirca 2016, Suchard *et al*., 2018). In this study, the maximum-likelihood method employs the Kimura 2-parameter model (Kimura 1980). The heuristic search is initiated by generating initial trees through the Neighbour-Joining method applied to a pairwise distance matrix estimated using the Maximum Composite Likelihood (MCL) approach. The resulting tree is presented proportionally, with branch lengths indicated in the number of substitutions per site (displayed next to the branches). The dataset

comprises a total of 470 positions, and all evolutionary analyses were conducted using MEGA X (Kumar *et al*., 2018).

The Minimum Evolution method (Rzhetsky and Nei 1992) was employed in this study to deduce the evolutionary history. The optimal tree was created with a bootstrap value of 10,000, and bootstrap values are indicated next to the branches (Felsenstein 1985). The tree is drawn to scale, with branch lengths presented in the same units as the evolutionary distances used for inferring the phylogenetic tree. Evolutionary distances were computed using the Kimura 2-parameter method (Kimura 1980) and are expressed as the number of base substitutions per site (Kumar *et al*., 2018). For the construction of the Minimum Evolution (ME) tree, the Close-Neighbour-Interchange (CNI) algorithm (Nei and Kumar 2000) was employed with a search level of 1. In this method the initial tree was generated using the Neighbour-joining algorithm (Saitou and Nei 1987). Thus, this analysis elucidates the genetic diversity and evolutionary relationships among populations of *E. gadgilii* from the sky islands across the Palghat Gap.

8.3. Results and discussion

The leaf samples of *E. gadgilii* were processed for extracting DNA, and pure DNA was extracted out through the modified CTAB extraction method. Then the gene specific for the study was selected.

8.3.1. Selection of gene

The four genes namely matK, rbcL, rpoc1, and psbA-trnH, found to have significant high variation and identification ability, other than all other plastid genes, mitochondrial genes and nuclear genes (Plate 8.1) (Kress *et al*., 2005, 2007, Lahaye *et al*., 2008, Roslim *et al*., 2016a). Among these chloroplast genes, coding genes such as matK and rbcL, seems to have lower variability at the population level compared to the psbA-trnH region.

To validate the selection of gene, the barcode gap distance analysis was done over the three genes. Then the barcode gap distance of these reference genes of this genus was examined by graphically plotting the intraspecific and interspecific divergence. Plate 8.2. a. displays the number of base substitutions per site between matK sequences. The analysis was conducted using the Kimura 2-parameter model (Kimura, 1980), incorporating a total of 13 nucleotide sequences. Codon positions considered in the analysis were 1st, 2nd, 3rd and noncoding sites. Ambiguous positions

were eliminated for each sequence pair using pairwise deletion. The final dataset contained 638 positions.

The same approach was applied for the barcode distance analysis of the rbcL gene (Plate 8.2b), illustrating the number of base substitutions per site among rbcL sequences.

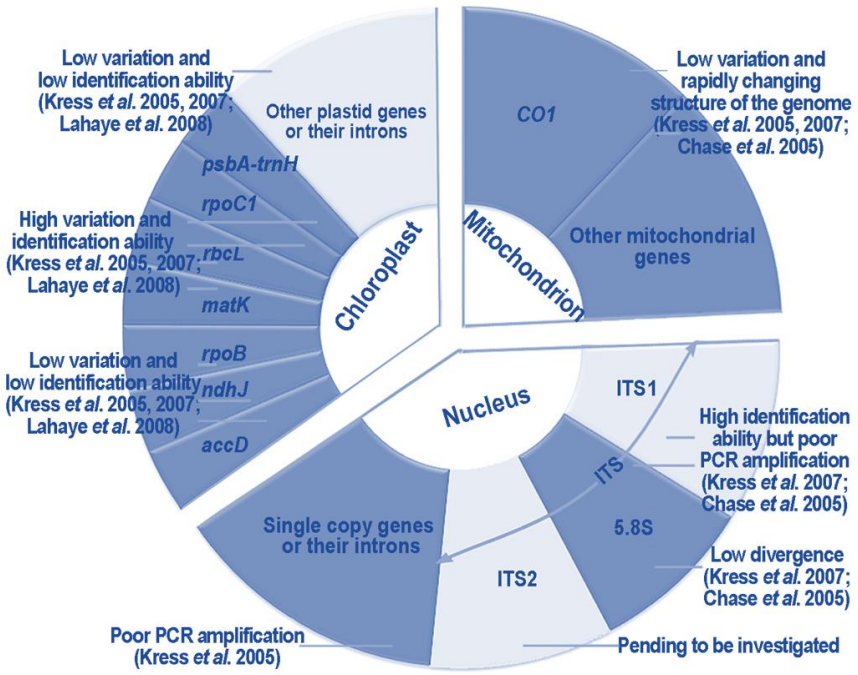


Plate 8.1. Candidate barcodes for plant genomes consist of genes from three different genomes (Chen *et al*., 2010).

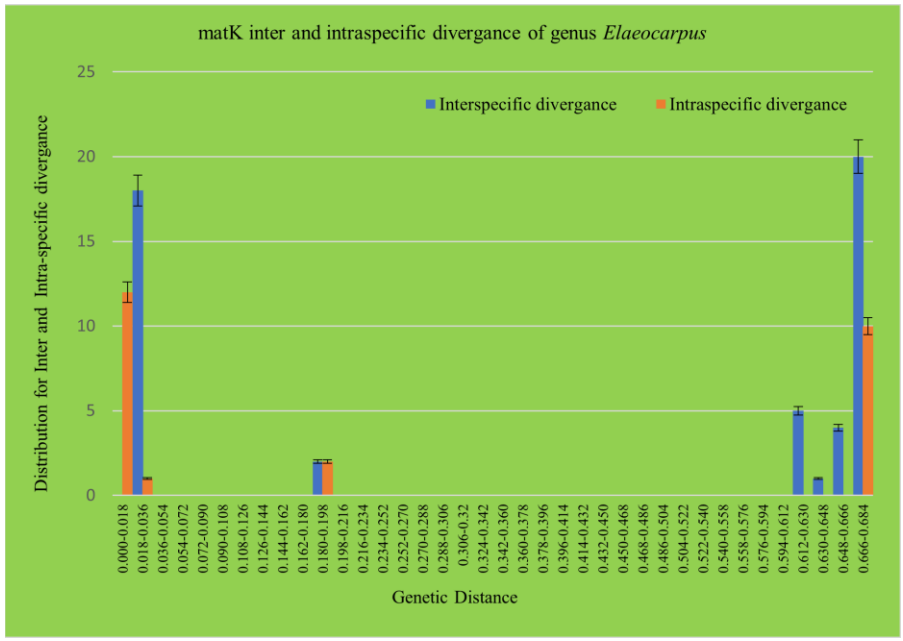
Table 8.1: Inter and Intraspecific divergence of three genes (matK, rbcL and psbA-trnH) of *Elaeocarpus* genus sourced from NCBI.

SL.No	Elaeocarpus	Genes	Intraspecific divergence	Intraspecific divergance
1	*Elaeocarpus* angustifolius Blume	matK	0.01	*E. austoyunnannensis*-0.204 *E. chinensis*-0.657
		rbCL	0.00	*E. amplifolius*-0.00552 *E. austroyunnannensis*-0.01059
		psbA-trnH	0.00	*E. floribundus*-0.0227 *E. mastersii*-0.0130 *E. stipularis*-0.0243
2	*Elaeocarpus austroyunnanensis* Hu	matK	0.33	*E. angustifolius*- 0.204 *E. chinensis*-0.496

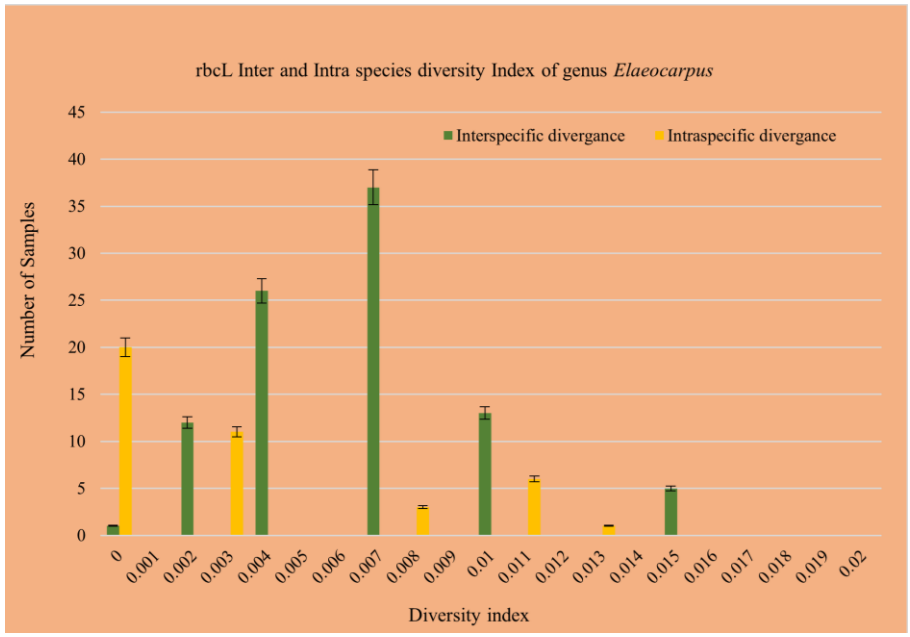
		rbCL	0.01	*E. amplifolius*-0.00660 *E. angustifolius*-0.01059
3	*Elaeocarpus chinensis* (Gardner & Champ.) Hook.f. ex Benth.	matK	0.12	*E. angustifolius*-0.657 *E. austoyunnannensis*-0.496
4	*Elaeocarpus amplifolius* Schltr.	rbCL	0.00	*E. angustifolius*-0.00552 *E. austroyunnanensis*-0.00660
5	*Elaeocarpus floribundus* Blume	psbA-trnH	0.02	*E. angustifolius*-0.0227 *E. mastersii*-0.0240 *E. stipularis*-0.0141
6	*Elaeocarpus stipularis* Blume	psbA-trnH	0.00	*E. angustifolius*-0.0243 *E. floribundus*-0.0141 *E. mastersii*-0.0281
7	*Elaeocarpus mastersii* King	psbA-trnH	0.000	*E. angustifolius*-0.0130 *E. floribundus*-0.240

This analysis involved 17 nucleotide sequences, resulting in a final dataset of 377 positions. The barcode distance analysis for the psbA-trnH gene sequence was depicted in Plate 8.2c. The Kimura 2-parameter model was applied to analyse the number of base substitutions per site between a set of 13 nucleotide sequences of psbA-trnH, with ambiguous positions removed. The final dataset for psbA-trnH consisted of 462 positions. The evolutionary analyses were carried out using MEGA X (Kumar *et al*., 2018). The results indicated that intraspecific divergence was found over the three genes, at least over one species of this genus. However, only the noncoding psbA-trnH intergenic spacer exhibited a barcode gap distance with minimal overlap (Plate 8.2) (Table 8.1). Consequently, based on the available literature data and barcode distance analysis, the psbA-trnH gene was found to have higher variability, thereby it was chosen for further investigation.

The psbA-trnH region corresponds to a distinct DNA sequence widely utilised as a DNA barcode in the identification of plant species. The psbA-trnH intergenic spacer is a DNA segment found within the chloroplast genome of plants, situated between the psbA and trnH genes. This DNA region displays noteworthy variability across different plant species, making it a valuable tool for distinguishing and classifying plant species. The psbA-trnH sequence serves as a common DNA barcode for plant identification, located between the psbA and trnH genes within the chloroplast genome of plants. It exhibits substantial variation among diverse plant species, thus facilitating accurate differentiation and identification of plant species at population level.



a



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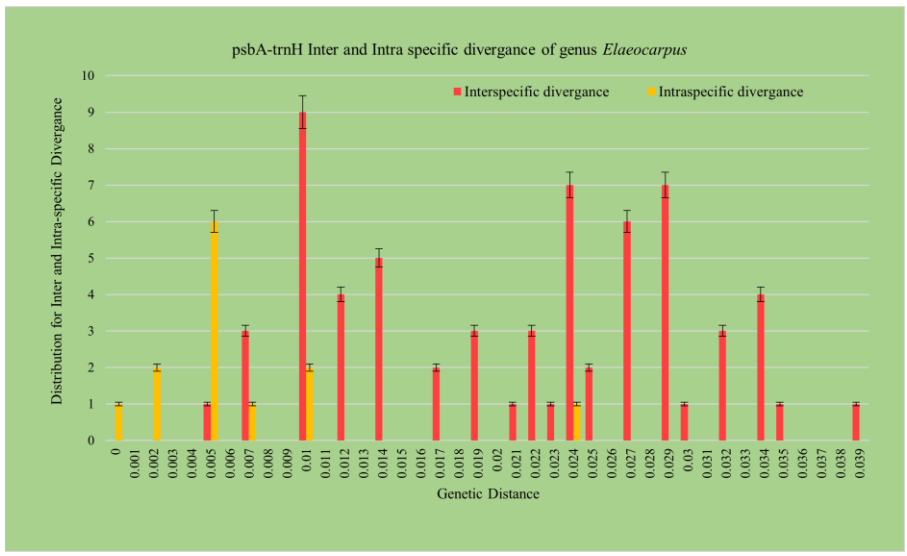

c

Plate 8.2: Selection of high variability gene of *Elaeocarpus* genus, by Barcode gap distance analysis: a. matK, b. rbcL, c. psbA-trnH.

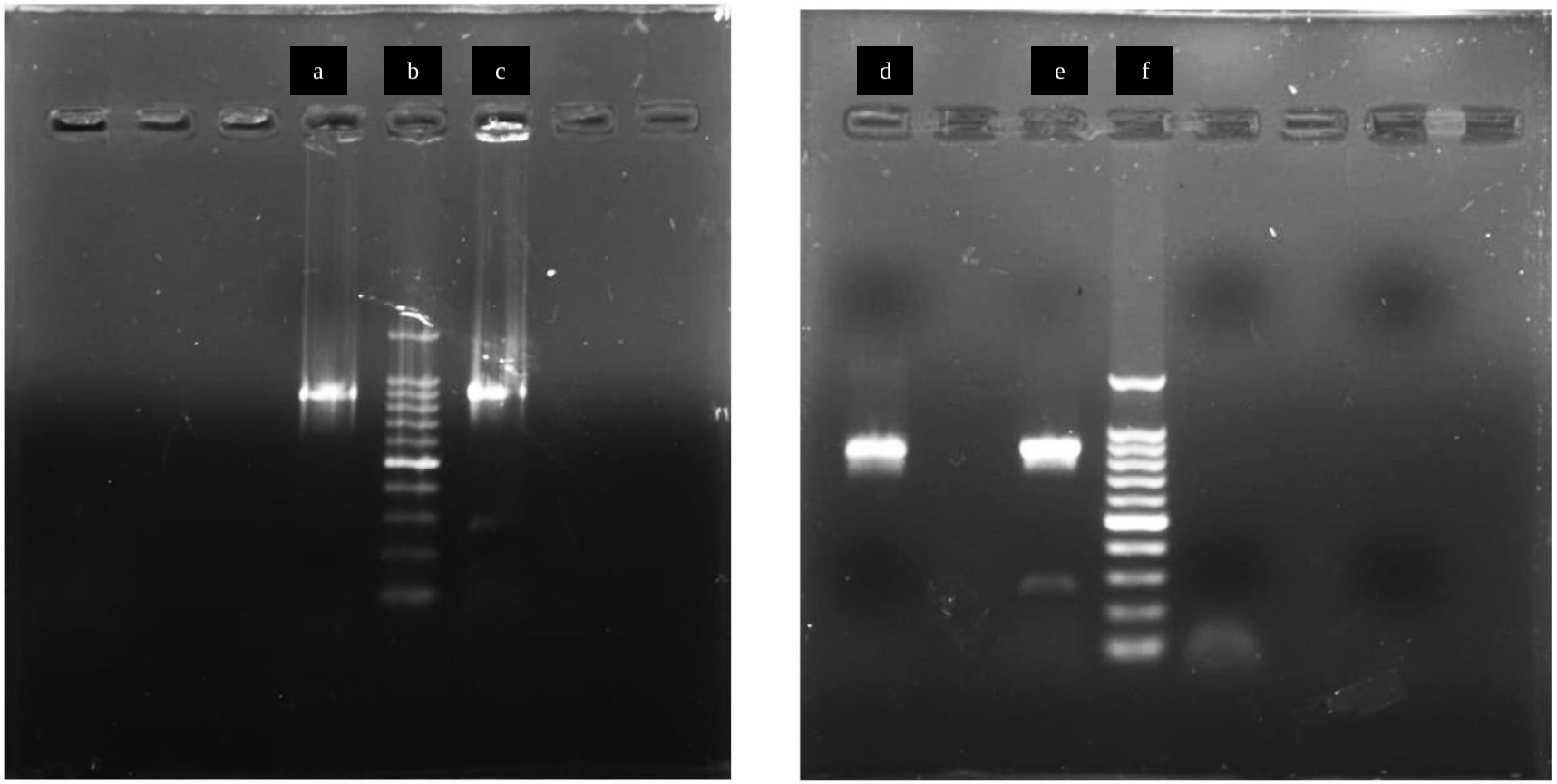

Plate 8.3: Gel Electrophoresis of PCR product from psbA-trnH Gene amplification on *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P. Kumar: a. DNA extraction was done over dry leaf sample, b. 1000bp ladder, c. DNA extract from dried leaf sample, d. DNA extract from fresh leaf sample, e. DNA extract from fresh leaf sample, f. 1000bp ladder.

8.3.2. Gene sequencing

The DNA extraction protocol modified and designed specifically for dry, fresh, and deep-frozen leaf samples of *E. gadgilii* was cost-effective and efficient in obtaining high-quality DNA. The quantity and quality of the extracted DNA were confirmed through electrophoresis and nanodrop tests. For the fresh sample, the DNA quantity obtained was approximately 1066ng/µl with a high level of purity. The deep-frozen sample yielded a DNA quantity of 613ng/µl, while from the dry sample 300ng/µl was obtained and both were of high quality. The absorbance ratios of DNA at 260/280 nm fell within the range of 1.6 to 1.85, indicating low protein contamination and a higher likelihood of obtaining optimal PCR products. Additionally, the absorbance at 260/230 nm ranged from 1.8 to 2.0, further supporting the minimal protein contamination. Gel electrophoresis analysis indicated satisfactory DNA quality for the DNA extracted from dry, fresh, and deep-frozen leaf samples (Plate 8.3).

These findings demonstrate the promising nature of the modified DNA extraction protocol, which proves to be both cost-effective and highly efficient. The extracted DNA was subsequently stored in a deep freezer and sent to laboratories for DNA sequencing. The gene that was selected for the present study was psbA-trnH. To amplify the psbA-trnH gene region, the following primers were utilised: forward primer: 5' GTTATGCATGAACGTAATGCTC 3', and reverse primer: 5' CGCGCATGGTGGATTCACAATC 3'. The resulted amplicon size was 512 base pairs (Srirama *et al*., 2010). PCR was performed using a 10 µl reaction mixture. The mixture comprised 5 µl of Takara-EmeraldAmp GT PCR Master Mix, 1 µl of forward primer, 1 µl of reverse primer, 0.1 µl of template DNA, and the remaining volume (2.9 µl) was adjusted with nuclease-free water. The PCR process involved 35 cycles, starting with an initial denaturation step at 95°C for 3 minutes, followed by denaturation at 95°C for 15 seconds, annealing at 50°C for 30 seconds, extension at 72°C for 1 minute, and a final extension step at 72°C for 5 minutes.

Consensus sequences of psbA-trnH gene from all 32 populations were aligned, and this alignment was further processed within the geneious platform. Specifically, the alignment included 32 sequences, and a detailed examination of it, showed that four nucleotide positions differed between the psbA-trnH sequences of populations from the southern and northern sky islands (Plate 8.4). The genetic distance between the populations of *E. gadgilii* across Palghat Gap, was evaluated with Megax. As per the analysis the genetic distance between the populations of *E. gadgilii* within the sky

Plate 8.4: Gene sequence alignment on psbA-trnH gene sequence of 32 populations of *Elaeocarpus gadgilii* A. M. Maya, V. Suresh & K. M. P. Kumar. in Geneious 4.8.

Footnote: Populations of *E.gadgilii* from the Northern side of Sky islands: -Varadimala (NVAR19, NVAR20, NVAR21, NVAR22, NVAR23, NVAR24), Keralmedu (NKER26, NKER27, NKER28, NKER30, NKER31, NKER32, NKER33, NKER34, NKER35, NKER36). Southern side Sky Islands populations of *E.gadgilii* :-Karimala (SNKRI4, SNLKRI5, SNLKRI7), Karasurimala (SNLKSU6, SNLKSU10, SNLKSU12, SNLKSU13, SNLKSU17), Minnampara (SNLMN15), Mattumala (SNLMT16, SNLMT42), Anamala (SNLANMA37, SNLANMA38, SNLANMA39, SNLANMA40, SNLANMA41).

islands of both northern and southern sky islands was 0.000. However, there was a genetic divergence of 0.00833 between the populations from sky islands on southern and northern sides of the Palghat Gap, with a diversity coefficient of differentiation of 1 (Kumar *et al*., 2018).

8.3.3. Intraspecific phylogenetic relationships

The phylogenetic tree generated by these four methods clearly depicts the relation of the populations of *Elaeocarpus gadgilii*. The analysis involved the utilisation of four distinct phylogenetic tree methods, comprising two distance-based methods and two probability-based methods. Each method possesses its own advantages and limitations. Despite their differences, all the employed phylogenetic tree methods yielded consistent inferences. Specifically, these results revealed that the populations of *Elaeocarpus gadgilii* from the southern and northern sky islands have diverged and are grouped into two distinct subclades within a major clade. An interesting observation is that all species within the *Elaeocarpus* genus form a single major clade, were distinctly separated from the clade where *Sloanea* is located. Furthermore, among the *Elaeocarpus* genus, one species, *Elaeocarpus dubius*, was consistently placed at a significant distance from the populations of *Elaeocarpus gadgilii* in all generated trees. These findings are consistent across all employed tree inference methods, which included both distance-based and probability-based approaches. This convergence of results enhances the confidence and reliability of the inferred outcome.

Among the four phylogenetic trees, one of that is neighbour joining method, which clearly demarcated the genetic variation between population of *E. gadgilii* across the Palghat Gap (Plate 8.5). This method is a distance-based method, where evolutionary distance between each clade is separately mentioned over the phylogenetic tree. Here as per the analysis each population within sky islands on same side of Palghat Gap are found to be in a single clade. The populations of *E. gadgilii* across Palghat Gap are separated as two separate sub clades with 100% reliability. These two sub clades of *E. gadgilii* population are placed within in a major clade, separating from other lineages connected to other species of *Elaeocarpus*. Among the group of species connected outside, the species that distantly placed from the clade with populations of *E. gadgilii*, was *Sloanea* species with 100% reliability. From other *Elaeocarpus* genus, *E. gadgilii* is placed in separate clade with 99.67% bootstrap measure and the one from which it was distantly placed was *E. dubius* with 99.86% reliability.

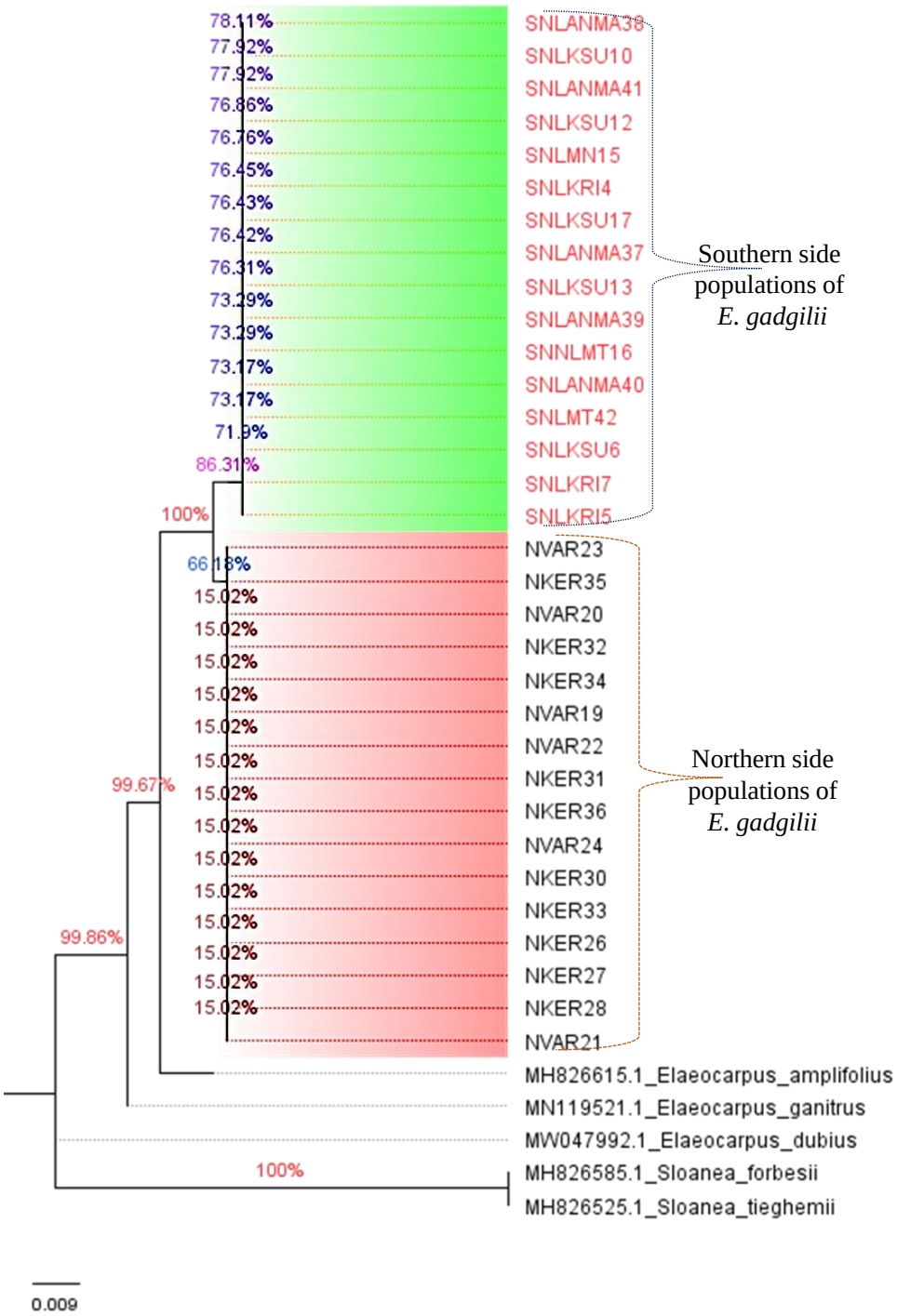

Plate 8.5: Molecular Phylogenetic tree constructed by Neighbour joining method, over 32 populations of *Elaeocarpus gadgilii*, based on psbA-trnH and the outgroup species includes *Sloanea species* and other *Elaeocarpus* species of Elaeocarpaceae family.

Footnote: Populations of *E.gadgilii* from the Northern side of Sky islands: -Varadimala (NVAR19, NVAR20, NVAR21, NVAR22, NVAR23, NVAR24), Keralmedu (NKER26, NKER27, NKER28, NKER30, NKER31, NKER32, NKER33, NKER34, NKER35, NKER36). Southern side Sky Islands populations of *E.gadgilii* :- Karimala (SNKRI4, SNLKRI5, SNLKRI7), Karasurimala (SNLKSU6, SNLKSU10, SNLKSU12, SNLKSU13, SNLKSU17), Minnampara (SNLMN15), Mattumala (SNLMT16, SNLMT42), Anamala (SNLANMA37, SNLANMA38, SNLANMA39, SNLANMA40, SNLANMA41). Outgroups:- MH826615.1 *Elaeocarpus amplifolius*, MW047992.1 *Elaeocarpus dubius*, MN119521.1 *Elaeocarpus ganitrus*, MH826585.1 *Sloanea forbesii*, MH826525.1 *Sloanea tieghemi*).

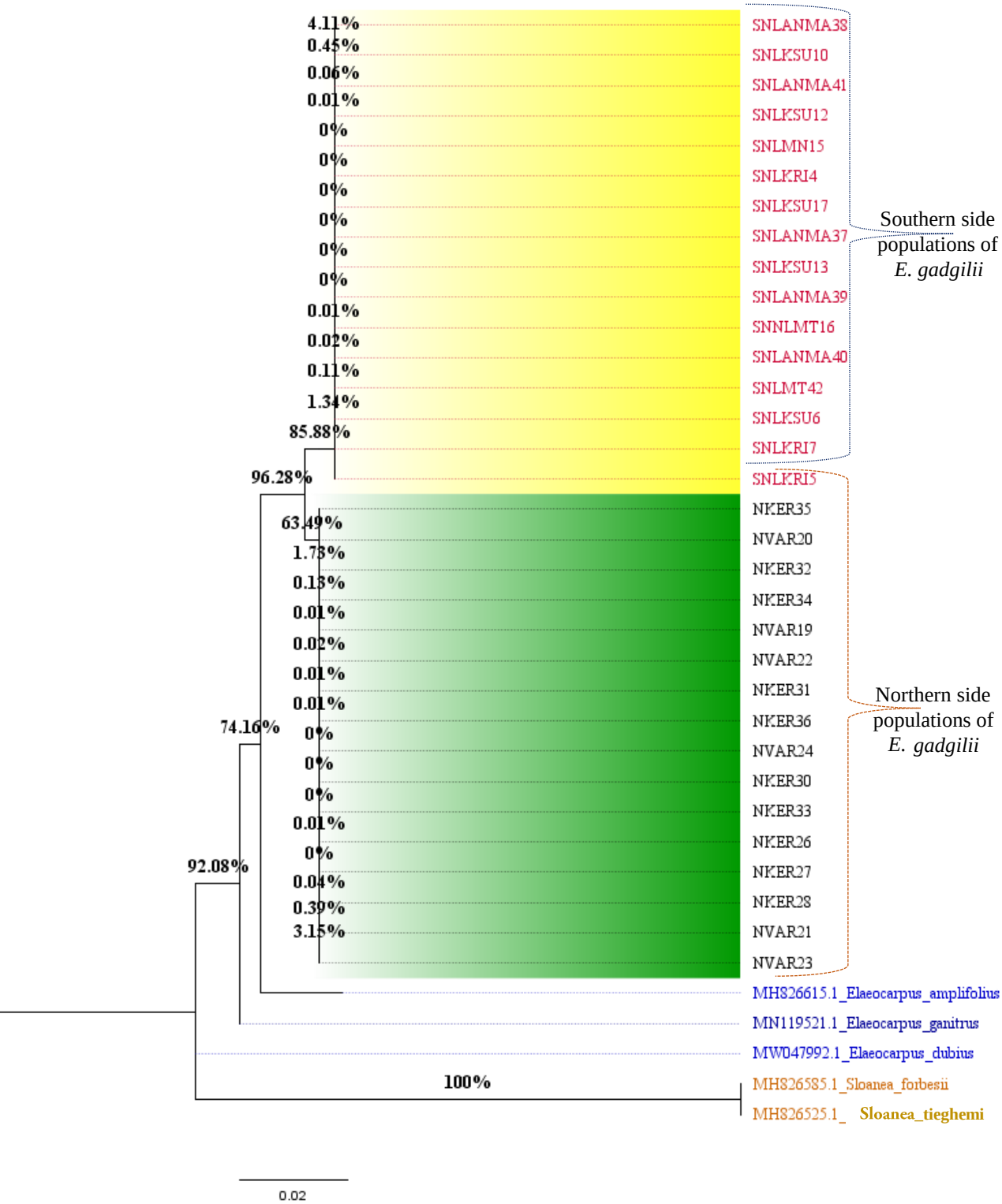

Plate 8.6: Molecular Phylogenetic tree constructed by Maximum Likelihood method, over 32 populations of *Elaeocarpus gadgilii*, based on psbA-trnH and the outgroup species includes *Sloanea species* and other *Elaeocarpus* species of Elaeocarpaceae family.

Footnote: Populations of *E.gadgilii* from the Northern side of Sky islands: -Varadimala (NVAR19, NVAR20, NVAR21, NVAR22, NVAR23, NVAR24), Keralmedu (NKER26, NKER27, NKER28, NKER30, NKER31, NKER32, NKER33, NKER34, NKER35, NKER36). Southern side Sky Islands populations of *E gadgilii* : Karimala (SNKRI4, SNLKRI5, SNLKRI7), Karasurimala (SNLKSU6, SNLKSU10, SNLKSU12, SNLKSU13, SNLKSU17), Minnampara (SNLMN15), Mattumala (SNLMT16, SNLMT42), Anamala (SNLANMA37, SNLANMA38, SNLANMA39, SNLANMA40, SNLANMA41) Outgroups:- MH826615.1 *Elaeocarpus amplifolius*, MW047992 1 *Elaeocarpus dubius*, MN119521.1 *Elaeocarpus ganitrus*, MH826585.1 *Sloanea forbesii*, MH826525.1 *Sloanea tieghemi*).

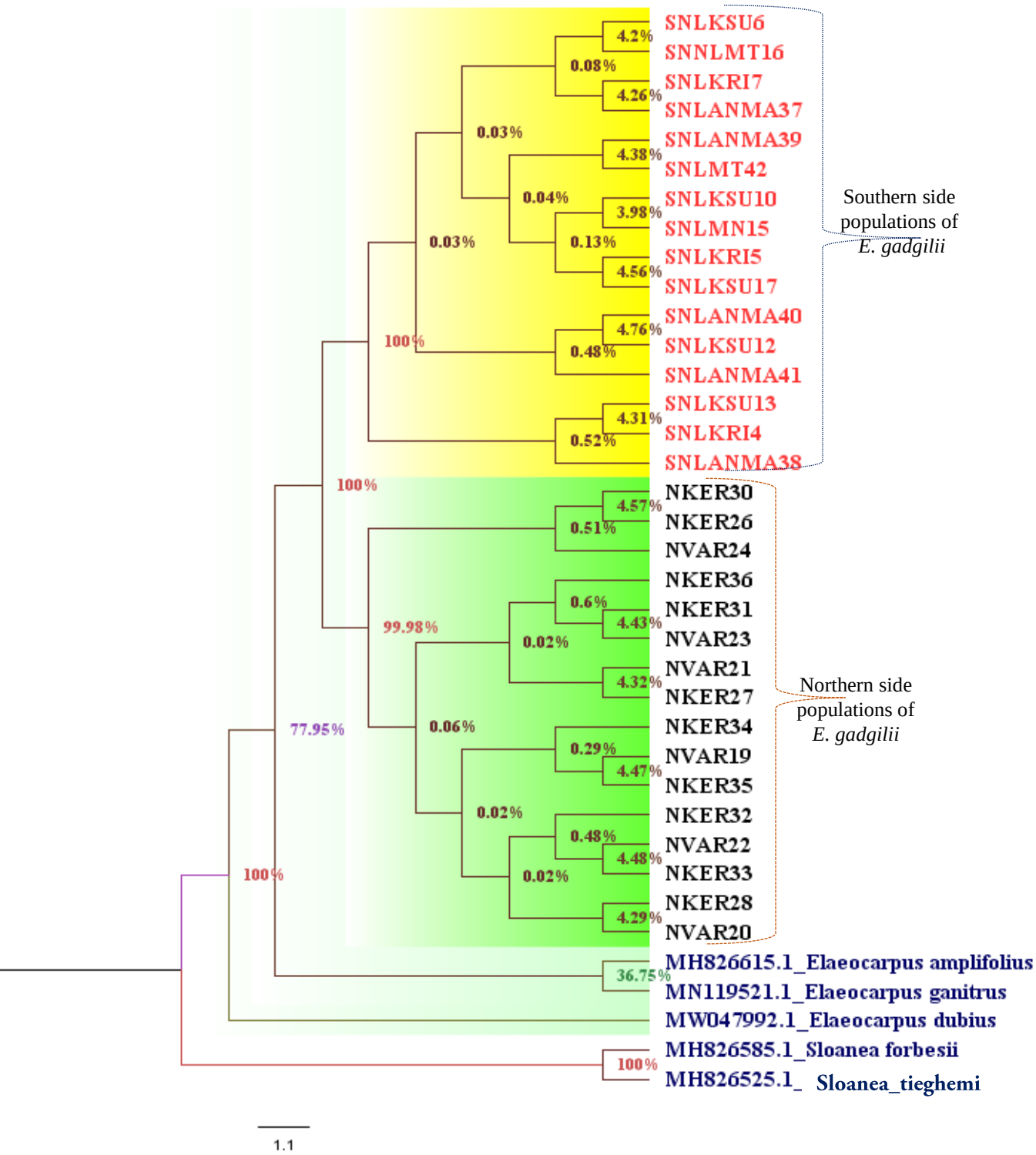

Plate. 8.7: Molecular Phylogenetic tree constructed by Bayesian tree method, over 32 populations of *Elaeocarpus gadgilii*, based on psbA-trnH and the outgroup species includes *Sloanea species* and other *Elaeocarpus* species of Elaeocarpaceae family.

Footnote: Populations of *E.gadgilii* from the Northern side of Sky islands: -Varadimala (NVAR19, NVAR20, NVAR21, NVAR22, NVAR23, NVAR24), Keralmedu (NKER26, NKER27, NKER28, NKER30, NKER31, NKER32, NKER33, NKER34, NKER35, NKER36). Southern side Sky Islands populations of *E.gadgilii* :- Karimala (SNKRI4, SNLKRI5, SNLKRI7), Karasurimala (SNLKSU6, SNLKSU10, SNLKSU12, SNLKSU13, SNLKSU17), Minnampara (SNLMN15), Mattumala (SNLMT16, SNLMT42), Anamala (SNLANMA37, SNLANMA38, SNLANMA39, SNLANMA40, SNLANMA41). Outgroups: - MH826615.1 *Elaeocarpus amplifolius*, MW047992.1 *Elaeocarpus dubius*, MN119521.1 *Elaeocarpus ganitrus*, MH826585.1 *Sloanea forbesii*, MH826525.1 *Sloanea tieghemi*).

The divergence between the population with the sky islands were 71 to 86% reliability in the clade within southern side populations, in the clade within northern population the divergence reliability was between 15 to 66%.

The next tree generated as per the Maximum likelihood (ML) method showed that, the population of *E. gadgilii* within the sky islands on the same side of the Palghat Gap was identified as a single clade, as like as the way it placed in aforementioned tree (Plate 8.6). That is the populations of *E. gadgilii* on either side of the Palghat Gap formed two distinct sub-clades, with 96.28% reliability. These sub-clades are part of a larger clade, distinct from other lineages linked to different *Elaeocarpus* species. Notably, among the species outside this clade, *Sloanea* was the species from which it was distantly placed with 100% reliability. One difference that was found in the tree created through ML was that the evolutionary distance between some of the populations within the sky islands were negligible. As in the case of the neighbour joining tree there found to exist a minimum divergence between the populations within the sky islands.

Then the Bayesian method, a probabilistic method where it clearly depicted the evolutionary relations between populations within and between the sky islands across Palghat Gap (Plate 8.7). In the tree it was observed that each population within the sky islands on the same side of the Palghat Gap belongs to a single clade. However, the populations of *E. gadgilii* on either side of the Palghat Gap are distinct, that is in two separate sub-clades with 100% reliability in their divergence. These two sub-clades of the *E. gadgilii* population are grouped together in a major clade, distinct from other lineages associated with different *Elaeocarpus* species. Notably, *Sloanea* species was placed distantly in the outer clade, away from other Elaeocarpus species with 100% reliability. The divergence of the population *E. gadgilii* into two distinct clades, one comprising populations from the northern sky islands and the other from the southern side, was depicted with 100% reliability in the phylogenetic tree. The difference observed in this tree, compared to the aforementioned tree, lies in its clear demarcation of evolutionary distances within and between populations on the sky islands. It clearly portrays maximum divergence between populations within the sky islands, indicating a high likelihood of populations evolving distinct variants. This increasing divergence between populations within the sky islands reveals significant evolutionary potential.

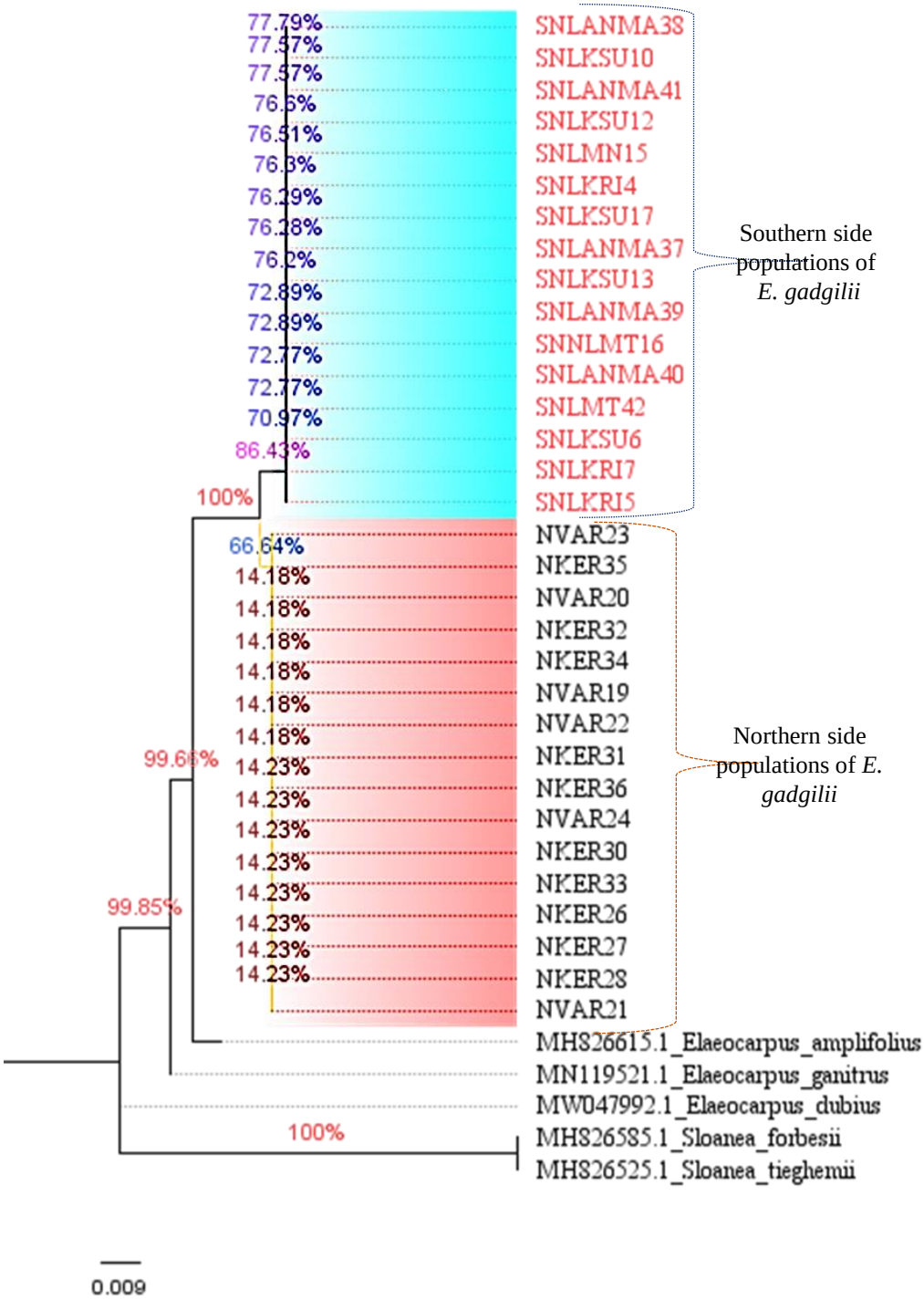

Plate 8.8: Molecular Phylogenetic tree constructed by Minimum Evolution method, over 32 populations of *Elaeocarpus gadgilii*, based on psbA-trnH and the outgroup species includes *Sloanea species* and other *Elaeocarpus* species of Elaeocarpaceae family.

Footnote: Populations of *E.gadgilii* from the Northern side of Sky islands: -Varadimala (NVAR19, NVAR20, NVAR21, NVAR22, NVAR23, NVAR24), Keralmedu (NKER26, NKER27, NKER28, NKER30, NKER31, NKER32, NKER33, NKER34, NKER35, NKER36). Southern side Sky Islands populations of *E.gadgilii* :-Karimala (SNKRI4, SNLKRI5, SNLKRI7), Karasurimala (SNLKSU6, SNLKSU10, SNLKSU12, SNLKSU13, SNLKSU17), Minnampara (SNLMN15), Mattumala (SNLMT16, SNLMT42), Anamala (SNLANMA37, SNLANMA38, SNLANMA39, SNLANMA40, SNLANMA41). Outgroups:- MH826615.1 *Elaeocarpus amplifolius*, MW047992.1 *Elaeocarpus dubius*, MN119521.1 *Elaeocarpus ganitrus*, MH826585.1 *Sloanea forbesii*, MH826525.1 *Sloanea tieghemi*).

The tree generated from Minimum Evolution is depicted in plate 8.8, were each population of *E. gadgilii* within sky islands on the same side of Palghat Gap belongs to a single clade. However, the populations of *E. gadgilii* on either side of Palghat Gap are divided into two separate subclades with 100% reliability. These two subclades of *E. gadgilii* are a part of a larger clade, distinct from other lineages associated with different *Elaeocarpus* species. Among the species of Elaeocarpaceae, *Solanea* species was placed with 100% reliability in the outer clade, marking it as the most distant from others. The major advantage of this tree is its ability to capture minute differences, clearly depicting maximum divergence between populations within the sky islands, which is greater than that observed in the Bayesian tree.

According to the four phylogenetic trees, the populations of *Elaeocarpus gadgilii*, consisting of 16 populations from the southern sky islands and 16 populations from the northern sky islands, were observed to be placed in separate subclades with high bootstrap %, indicating the reliability of the divergence between the two groups of populations of *E. gadgilii* across Palghat Gap. However, it is notable that the divergence within populations of *E. gadgilii* within the sky islands is relatively low compared to the divergence observed between the populations across the Palghat Gap. Among all the tree the Minimum Evolution (ME) tree was advantageous in accurately representing the relationships between species at the population level within the sky islands, particularly when dealing with minor divergences. Based on the phylogenetic trees and the levels of inter- and intraspecific divergence among the populations of *Elaeocarpus gadgilii*, it can be inferred that the geographical features of the Palghat Gap found to have directly or indirectly influenced the genetic-level characteristics of the *Elaeocarpus gadgilii* populations, particularly with regards to the psbA-trnH gene.

Hence, the aforementioned results provide substantial evidence supporting the hypothesis that the Palghat Gap, the geographical barrier in the Western Ghats, that separates the sky islands of the Western Ghats, played a crucial role in shaping the populations of *E. gadgilii* at the molecular level. Gaps or wide valleys in mountain systems are of significant interest to biogeographers and evolutionary biologists as they play a crucial role in shaping species distributions and genetic diversity within and between species (Biswas and Praveen Karanth 2021). The physical features of the gap, including its gap distance found to have the ability to influence various parameters such as precipitation and wind patterns, subsequently affecting the edaphic prop-

erties of the sky islands. Differences in climate–distribution relationships among broad taxonomic groups might be linked to variations in relevant ecological traits, although the specific ecological traits that play a crucial role are not yet fully understood (Kharouba *et al*., 2013). Therefore, these distinct features of the Palghat Gap found to be responsible for the separation of sky islands in the Western Ghats, and this demonstrates that these have a significant impact on the genetic composition, particularly concerning the psbA-trnH gene located in the non-coding region of the chloroplast of *Elaeocarpus gadgilii* populations. The significance of comprehending the speciation processes in the studied species is underscored by the influence of the Palghat Gap feature. This clearly substantiate a fact that biogeographic gap would play a crucial role in driving speciation, particularly in the case of adaptable plant species like *Elaeocarpus gadgilii.* The influence of the gap feature reflects the environmental changes occurring within the region. However, in unfavourable circumstances, the species may face the risk of extinction, leading to the loss of its gene pool. Such an outcome would represent a substantial loss of overall biodiversity. Therefore, it is crucial to recognise that these gap features have a direct impact on the biodiversity of sky islands. Moreover, the influence of the gap features on the population is in turn influenced by the unique characteristics of these special habitats, the sky islands.

The focus of the present study was on understanding the impact of the Palghat Gap on the genetic composition of *E. gadgilii* populations, particularly regarding the psbA-trnH gene located in the chloroplast's non-coding region. This emphasises the significance of comprehending speciation processes, especially in adaptable plant species, and the potential consequences of biodiversity loss due to an unfavourable environment. The psbA-trnH intergenic spacer region has been widely employed in numerous DNA barcoding studies. Nevertheless, there is a notable absence of a thorough assessment, including rigorous sequence preprocessing and statistical testing, regarding the effectiveness of psbA-trnH and its combinations as DNA barcodes. Based on investigations across various taxonomic groups, the psbA-trnH combination demonstrates superior or comparable performance compared to other combinations (Pang *et al*., 2012).

Geographical obstacles, encompassing factors like habitat type, drainage system, and physical barriers, exert a notable influence on genetic divergence within populations (Reusch *et al*., 2001). These barriers give rise to phenomena such as isolation by distance (IBD) and isolation by environment (IBE), which are further shaped

by non-random dispersal and morphological adaptation (Weber *et al*., 2017). The interplay of these elements can lead to widespread genomic differentiation, with a substantial portion of this divergence attributed to isolation by adaptation (IBA) (Safran *et al*., 2016). The geographical features of the Palghat Gap seem to have influenced the molecular-level characteristics of *E. gadgilii* populations, especially with regards to the psbA-trnH gene. Therefore, the Palghat Gap, as a geographical barrier found to play a crucial role in shaping populations of *E. gadgilii* at the molecular level.

Mountain gaps, characterised as wide valleys within mountain systems, they are important due to their influence on species distributions and genetic diversity at both inter- and intraspecific levels. The impact of geographical gaps on genetic diversity is an intricate and multifaceted process, which emphasizes the substantial barrier effect of these gaps on diverse taxonomic groups, indicating genetic divergences persisting long after their formation. This suggests that factors extending beyond geology, such as ecology and life-history traits, may contribute to this process (Biswas and Praveen Karanth). Similarly, Liu (Liu *et al*., 2019) and Crisp and Cook (Crisp and Cook 2007) highlight the role of geographical barriers in fostering population divergence and speciation, with the latter presenting evidence of multiple simultaneous ancient divergences across a barrier. These findings are further substantiated by Lessios (Lessios 1981), who explores the molecular and morphological differentiation among sea urchins separated by the Isthmus of Panama, a geographical barrier that has endured for a specified period. Collectively, these studies underscore the intricate interplay between geographical gaps, genetic diversity, and speciation. The pivotal role of mountain gaps in shaping species distributions and genetic diversity in the Western Ghats was underscored by the present research.

8.4. Conclusions

The present chapter presents the important perception of the interlink between the gap features and sky island species genetic makeup. The role played by Palghat Gap, in shaping the distributional range of *Elaeocarpus gadgilii* and its genetic makeup, and speciation, is thereby elucidated through the study. The intraspecific genetic variability analysis on *E. gadgilii* within the sky islands of Western Ghats across the Palghat Gap allowed the understanding of the influence of the Palghat Gap features over its genetics. As per the analysis the population of *E. gadgilii* from the sky islands on the on northern and southern side of Palghat Gap exhibited distinct genetic divergence. The genetic divergence between its populations within the sky islands

was found to be negligible, but between the sky islands, there was higher genetic divergence. This study thereby justified that the Palghat Gap through geographical isolation separated the populations of *E. gadgilii*, and the chance of this to get evolved to a new variety or even to a new species is highly probable. Therefore, the probable chance of speciation to happen over the sky island is high due to impact of the Palghat Gap and its other features on it. The in-depth knowledge on the study enumerates the key routes that have historically facilitated gene flow across these gaps, thereby enabling more effective preservation of the genetic pool of *E. gadgilii* populations.

This study thereby unveils the interconnection between geographic barriers, ecological niches, adaptive processes, and intraspecific variability that have collectively moulded the genetic structure of species inhabiting in the sky islands of the Western Ghats. This broadens the field of knowledge on evolutionary biology and the mechanisms driving speciation and genetic diversification in sky islands.

CHAPTER 9: GENERAL DISCUSSION

Sky island complexes are notable for their high species diversity, endemism, climatic variation, and unique biogeographical features, providing greater evolutionary differentiation potential compared to other inland terrains (Warshall 1995). These ecosystems, acting as diversity sources, are characterized by distinct vegetation, microclimates, and ecological processes, particularly in the Shola ecosystem (Robin and Nandini 2012). At high elevations, these habitats shrink in spatial extent with increasing altitude, and the size of a habitat is crucial for supporting biodiversity and species abundance (Anderson *et al*., 2012). Highland regions enhance biodiversity in neighboring lowlands by promoting speciation and species dispersal in response to climate changes (Rull 2005). Sky islands, with their long-term isolation and climatic variability since the Pleistocene, serve as ideal natural laboratories for studying climate change impacts (Love *et al*., 2023b). Alpine floras relate to higher elevated mountainous regions, specifically referring to the vegetation occurring above the tree line. Challenging conditions, such as low temperatures characterise these high-altitude environments. Alpine floras displayed idiosyncrasy in their composition, with a limited number of dominant plant families. These plant families evolved specific adaptations that facilitate their successful establishment and flexibility to face harsh environmental conditions, particularly the low temperatures predominant in alpine habitats (Qian *et al*., 2021).

The Western Ghats are mountains formed through river erosion of a dissected plateau (Bagyaraj *et al*., 2011). These isolated sky island chains as are on the north-to-south axis are more prone to climatic variation, thereby having a high evolutionary differentiation potential. A major valley within this mountain chain is the Palghat Gap (Warshall 1995). The climate variation along mountain ranges on the North-South axis promotes evolutionary processes and differentiation (Larsen 2013). Several studies substantiated the influence of the biogeographical gap, especially the Palghat Gap over intraspecific and interspecific variability of several taxa namely *Kingidodendron pinnatum, Indirana beddomi, Indirana semiplanata,* loin-tailed macaque and Asian elephants. Several studies already mentioned that the Palghat Gap serves as a significant barrier for multiple taxonomic groups, with Shencottah and Goa Gaps showing comparatively lesser effects. These observed patterns align with the dimensions of the gaps, with the Palghat Gap being the deepest and widest among them (Robin *et al*.,

2010). However, studies on sky islands of the Western Ghats and the influence of the Palghat Gap over it are comparatively fewer.

The genetic composition of species residing in these sky islands has been impacted by complex topographical variations, climatic conditions, and diverse habitats. Species in these regions display unique and individual-specific responses, leading to alterations in their distributions and adaptations to specific environmental conditions. The genetic structures of species in the sky islands have been moulded by the interaction of complex topography, climate, and varied habitats (He and Jiang 2014). Sky island species have a limited threshold of tolerance, making them highly susceptible to significant alterations in the ecosystem induced by minor alterations in climatic conditions, soil composition, or any abiotic and biotic components. Even slight modifications in these factors can trigger substantial variation within the species composition (Fazalova *et al*., 2010, Liu *et al*., 2012).

Globally several studies have taken place over the sky islands to study their ecological and evolutionary responses to long-term isolation and glacial cycles. These studies included all the kingdoms of life such as mammals, reptiles, amphibians, invertebrates, and plants (Love *et al*., 2023b). Among such studies, only 8% of the studies showed connectivity between populations inhabiting different sky islands, of that the majority of the studies were over mobile species or the non-mobile sky island species which had a connecting agent (Tusiime *et al*., 2020). Then about 67% of the studies on sky islands showed that the major cause for the isolation of sky island habitat was isolation by distance or isolation by environment (Love *et al*., 2023b). Many other studies on sky islands reported that habitat contraction of sky islands was the major cause of their isolation. The habitat's initial contraction is influenced by natural climate shifts but is now being prolonged and made worse by the ongoing impact of human activities on the climate (Deng *et al*., 2020). Some studies also showed that the adverse climate change caused a reduction in genetic diversity and adaptation ability of sky island species, and later became a threat to its existence. The study on the genetic differentiation of White-bellied Shortwing bird species (*Brachypteryx major*), across sky islands of the Western Ghats showed that the geophysical barriers caused the population difference under the unpredictable climate change (Robin *et al*., 2010). The studies over the sky islands of Western Ghats and especially the studies on its isolation mechanism was found to be limited.

The present study done here was on the sky islands of Western Ghats in the vicinity of Palghat Gap, which significantly put forward the crucial significance of evaluating species composition and conservation status within these isolated habitats. The presence of species, whether unique to specific sky islands or shared between the sky islands across the Palghat Gap, underlines the influential role of localised factors in shaping species distribution dynamics. Ecologically, sky islands denote the isolated and elevated habitats, which are strategically positioned atop mountain peaks and ridges (Hayward 2022). The present study thus deepens our knowledge on these remarkable ecosystems of the Western Ghats, highlighting the need for meticulous assessment and devising conservation efforts to safeguard their distinctiveness. The preliminary floristic survey analysis displayed the distinctive features of these sky islands, such as significant levels of endemism, constrained land extents and complex conservation challenges. The above-mentioned features of this habit strongly suggest that these islands hold a vital position within worldwide initiatives for biodiversity preservation. The term endemic taxa are the organisms exclusively restricted to a specific geographical area. These geographical zones are characterised by a substantial prevalence of endemic species that inherently hold profound conservation implications, as their irreplaceable nature gives them a foremost focal point in the hierarchy of conservation priorities (Kier *et al*., 2009). The notable count of endemic species unveiled through this investigation serves as proof of the remarkable biodiversity of the sky islands. The Palghat Gap induced geographical isolation is assumed to have a pivotal impact in promoting the processes of speciation and neo-endemism within these ecosystems (Zhang *et al*., 2019a). The fragmentation of the Western Ghats continuity facilitated the emergence of discrete species groups within each individual sky island. The study especially focuses on tree species, thereby this study offers a crucial explanation of the complex evolutionary mechanisms that act within these ecological niches. Trees were a significant indicator of ecosystem vitality and dynamics, making this focus particularly informative and insightful.

The floristic survey analysis done over sky islands of the Western Ghats is detailed in chapter 3 and depicts the differential floristic diversity of sky islands across the Palghat Gap. Sky islands of the Western Ghats on the southern side of the Palghat Gap were more diverse than the sky islands on the northern side. The species that showed common occurrence over the sky islands across the Palghat Gap was minimal, and unique species were high. The endemic status of this habitat was profoundly

high. These justified the effect of the gap features like its gap distance has a direct influence on the floristic divergence of sky islands across the Palghat Gap. These observations outlined the discernible and divergent pattern of species diversity over the expanse of the sky islands across the Palghat Gap. Here the sky islands on the southern Western Ghats appeared to be richer in biodiversity than the northern side sky islands and were substantiated by other studies referred in chapter 2. As per those studies in the Western Ghats, the southernmost region (SWG) was the one that exhibited elevated diversity with a larger proportion of unique species, when compared to the central and northern parts (NWG). Some of the earlier studies have connected these patterns to ecological factors, but the understanding of speciation and biogeography in the Western Ghats remains limited (Aravind and Gururaja., 2011).

As per the present study, the differentiation observed between the sky islands across the Palghat Gap highlights the necessity of considering their unique ecological traits, the potential implications of climate change and other factors of these habitats. The sky islands vulnerability causes the frequent manifestation of distinctive environmental conditions like diverse climates and habitat features and later this drives speciation. So, in this study, other ecological parameters were included. The divergence in climate and edaphic environment of sky islands across the Palghat Gap are elaborated in chapters 6 and 7. This study even substantiated the fact that these habitats are the cradles of evolution, as these habitats bore a greater number of unique species and the influence of the Palghat Gap that isolated it geographically and promoted speciation in it. These specialised habitats serve as vital points for the emergence of diverse and distinctive life forms, yet their complex attributes make them highly susceptible to environmental changes (Fordham and Brook 2010). The importance of these habitats arises due to their isolated evolutionary histories, relatively small population sizes and the vulnerability of the species inhabiting these islands to withstand minor disturbances, and these are making these habitats more prone to catastrophic consequences (Harter *et al*., 2015). That's why the sky islands are called the best natural experimental set-up for studying the impacts of such gap features.

As per the preliminary floristic observation over the sky islands across the Palghat Gap, the gap features seem to have even influenced the phenology of a few species. Currently, there is a lack of extensive studies on the phenology of those species. Even with this limited study on phenology, those observed differences in the flowering time shown in some tree species across the sky islands substantiated the

potential influence of seasonal variations induced by the major gap that separated their populations. This thereby promotes the process of reproductive isolation and speciation in these habitats but is primarily dependent on the divergent natural selection operating in distinct niches or environments (Rundle and Schluter 2004).

The present study on the sky islands of Western Ghats showed that some species were under vulnerable, endangered, and nearly threatened categories. So, the risk of extinction of such species from this habitat points out the importance of introducing conservation measures over such habitat. However, a cautionary consideration arose from the fact that 65 % of species documented during the survey were under the "Not Evaluated" category of conservation status. This denotes that there exists a lack of assessment regarding the vulnerability or conservation status of most species in the sky Islands. This thereby highlights the need for further scrutiny and conservation initiatives over these habitats. Viewing the habitat through general sky island systems theories highlighted its complexity as an interlinked system. The conservation status of such habitats displayed, not only the status of its individual components but also their interactions with each other and with the environment. Evaluating the conservation status involves assessing the interdependent structure, composition, and functions of the habitat. This approach was to assess habitat as a vital component of management plans for protected areas (Maciejewski *et al*., 2016). Therefore, conservation status analysis is crucial for these habitats to increase awareness and prevent further loss of their species. So, efforts should be made to assess and monitor these unevaluated species over these habitats to efficiently devise conservation strategies and prevent potential losses. This raises the importance of modelling approach, as a pioneering step to conserve biodiversity. Thereby prediction over the risk in the existence of several species can be made. In the present study, the ensemble modelling was applied over three representative sky islands species. The spatial distribution of the three sky island species in past and future periods was evaluated and is detailed in Chapter 4. This analysis contributes to our understanding of the unique ecological processes and factors influencing species diversity of sky islands across the Palghat Gap.

The precise origin of the Palghat Gap remains a topic of discussion. It is estimated to have emerged approximately 500 million years ago, predating the reported divergence timeframe of the majority of species in the Western Ghats (Soman *et al*., 1990). Hence, it can be inferred that species shared among the various sky islands across the Palghat Gap might have originated when the Western Ghats was assumed

to be a continuous landmass before the gap appeared. Conversely, species unique to specific sky islands might have emerged after the establishment of this geographic divide, especially after civilization.

From a distributional perspective, an interesting observation was made from the study on the limited presence of the monotypic genus *Kendrickia walkeri* from the Melastomataceae family. This species was found in the Anamudi region of the Anamalais in south India and Adam's Peak in Ceylon. Both Anamudi and Adam's Peak represent the highest peaks in their respective regions, suggesting a potential connection between these two areas. This finding over the study on *Kendrickia* provided supportive evidence for the hypothesis that Ceylon and South India were once geographically connected, and this taxon would have served as a shared element within the floras of the mountainous regions of both South India and Ceylon. Additionally, it is crucial to note that this taxon has not been recorded from lower elevations within the Western Ghats (Subramanyam and Nayar 1974).

So, distribution analysis through modelling is an important perspective of analysis to predict the future and past connections of the species. Bioclimate envelope modelling employs a simplified approach by considering climatic variables as the primary determinants of species distribution. Bioclimate envelope modelling approach, which is rooted in ecological niche theory. This approach is centred around the fundamental ecological niche concept introduced by Hutchinson (Hutchinson 1957), which defines the range of environmental conditions in which a species can survive and thrive. Hutchinson's idea postulates that a species ecological characteristics are encompassed within a theoretical space defined by various environmental factors. The climatic subset of the fundamental ecological niche is often referred to as the "climatic niche". Bioclimatic models primarily focus on climate variables to predict and understand species distributions. Unlike broader ecological models, bioclimatic models do not incorporate non-climatic factors like soil type or land cover in their analyses. Additionally, similar to Hutchinson's definition of the fundamental ecological niche, the concept of a bioclimate envelope excludes the impact of biotic factors (Austin *et al*., 1990, Leibold 1995).

Here, in the present study, the habitat suitability of selected three sky island species of Western Ghats across the Palghat Gap was assessed through bioclimate modelling. The ensemble forecast output of *Elaeocarpus gadgilli, Phoebe wightii and E. munroi* was done on the R platform and depicted their habitat suitable areas from

the past (1970-2100) to the future (2021-2100). The four SSPs are four projected future bioclimate data in the least GHG to Very high GHG. So, all possible predictions of each species were made possible. As per the analysis, the important fact put forward was that the southern Western Ghats will become the least probable habitat suitable area for all the species in future. The high probable habitat suitable area of each species appears to be affected, but the least negative effect was observed over the projection as per SSP126 and high loss of high probable habitat suitable area as per SSP585 conditions. As per the present climate scenario and the global warming effect, the most probably expected scenario is SSP 585 rather than SSP 126. So even though these sky island habitats are conserved from human interference by protecting their habitat as reserve forests, the factor that mainly affects the species under concern seems to be the future climate rather than direct human interference. An adverse climate condition is expected in a high GHG emission scenario. As day-by-day, GHG is increasing, the chance of loss of southern Western Ghats diversity and desertification of the SWG is not too far. So as per the prediction done on the concerned species in future, compared to SWG, the CWG and NWG seem to be a more probable habitat suitable area for these species. The gap is the main factor that is found to separate SWG from other CWG and NWG. So, the gap effect is also exemplified here in the study. Even though the modelling was done only over three representative species of sky islands, it reflects the faith of the whole biodiversity of the sky island habitats of the Western Ghats.

The rising concern about the influence of climate change on biodiversity is the cause for applying bioclimatic models to predict potential range shifts of species in response to projected future climate scenarios. The impact of climate scenarios of past years is detailed in chapter 6, where the precipitation was found to be the major factor that isolated these habitats. Here SSP future climate data-based predictions were done, to study the impact of climate and external factors like GHG on the distribution of the species. These studies highlighted the importance of considering both edaphic and climatic factors in ENMs. Moreover, the significance of edaphic factors in influencing species distribution is exemplified in the case of African mahogany (Hall 2004). Ensemble forecasting has nowadays become a valuable tool, as it provides more robust and dependable predictions, thereby minimising the risk of errors and offering enhanced guidance for conservation planning (Araujo and New 2007). The conservation strategies with the application of modelling techniques are significant steps in ensur-

ing the future security of these species and preserving the biodiversity of the southern Western Ghats (Sony *et al*., 2018).

The significance of bioclimatic models in enhancing the perception of potential future consequences is high. These models stand out as a vital method in indicating the potential scope and general trends of species response to evolving environmental conditions (Pearson and Dawson 2003). While bioclimatic models give valuable initial assumptions, they must not be regarded as a precise imitation of future species distributions. Instead, they should be accepted as tools that provide potential impacts of ecological change.

In small, fragmented areas, the eminence of the edge effect is evident. The edge effect describes the ecological alterations occurring along the boundaries of an ecosystem. Due to the absence of a substantial interior or core habitat in these fragmented areas, they are at a heightened risk of undergoing a total disappearance or loss of biodiversity. This increased vulnerability is a consequence of the fragmented area's raised exposure to external influences and disturbances, including invasive species, modified microclimates, and heightened rates of edge-associated ecological processes (Bunyan *et al*., 2012, Lienert 2004). As the expanse of shola forests in the southern Western Ghats of India decreases, there is a concurrent reduction in the presence of rare species and those inhabiting the ecotone. Smaller shola forests demonstrate a diminished representation of these unique and specialised species in comparison to larger shola forests (Mohandass and Davidar 2010).

The modelling approach can help to identify appropriate habitat areas and facilitate the prioritisation of conservation efforts for the species found over such specialised habitats, as detailed in chapter 4. The importance of conserving these species within their natural habitats cannot be emphasised enough, because of the decreasing suitability of their habitats and the growing threat of collection from unsuitable areas. Preserving these species within their highly probable habitat suitable area is essential for sustaining their populations and safeguarding the distinct biodiversity of the Western Ghats. By considering modelling concepts in the study, we acquired a deep understanding of the risks and challenges faced by these species (Iverson *et al*., 2011). This understanding is vital for making the best conservation choices and formulating efficient management approaches.

BIOMOD2 is an SDM package that combines diverse models for each species, this facilitated the identification of the most precise model through evaluation tech-

niques and expert knowledge. This enhances the accuracy of species distribution predictions compared to the use of a single modelling technique for multiple species (Thuiller *et al*., 2016). Species distribution models (SDMs) played a vital role in mapping and monitoring the distributions of plants under the growing awareness of environmental changes. Initially, these were utilised for resource inventory and conservation mapping. Now SDMs have evolved with advancements in statistics and digital data. They provide improved predictions on species distributions, thereby serving as valuable decision-making tools for various applications, including climate change studies and the identification of protected areas (Cayuela *et al*., 2009, Miller 2010).

Understanding the impact of gaps on plant communities is a complex matter, as the level of influence depends on gap size and the surrounding vegetation (Fahey *et al*., 2008). Here in the present study, all major ecological components were considered to define the ecological diversity in sky islands, and are depicted in detail in chapters 3, 4, 5, 6 and 7. The study reflected that the effect of the gap feature is not only confined to its floristic diversity but also to the species population level. The first level of visible response a plant would show is at its morphological level and is revealed in chapter 5. Through this study, the interdependencies between all the ecological components of sky islands are verified, but the extent to which each ecological component affects the species in it varies. Among the ecological components, one of them is edaphic factors, which also play a role in regulating plant diversity (Hulshof *et al*., 2020). However, there is a notable concern about the reliability of data regarding plant occurrence and diversity. Biases and uncertainties are prevalent across taxonomic, geographical, and temporal dimensions (Meyer *et al*., 2016). The situation is further complicated using different diversity indices and observation scales, leading to diverse conclusions about ecological diversity (Yue *et al*., 2005).

The intraspecific variability is a reflectance of plants to environmental change, and in this study, this analysis was done over one of the representative sky island species *E. gadgilii*. The intraspecific morphometric variation analysis done on 32 populations of *E. gadgilii* from the sky islands across the Palghat Gap was depicted in chapter 5, which demonstrated the effect of gap features on its population level. Notably, some morphometric variables exhibited significant positive and negative correlations with altitude, highlighting the visible impact of altitude on species morphology**.** Most of the morphometric variables of its population showed statistically significant divergence across the Palghat Gap, thereby separating the populations into two groups be-

tween the sky islands across the Palghat Gap. However, a minority of the group of its populations did show relatedness with some of the morphometric variables. That is among the 32 populations 2 from the northern side and four from the southern side showed relatedness and the analytical findings on that suggested a potential association preceding their adaptation to environmental fluctuations, referring to a plausible ancestral linkage uniting them. As time passes, this relatedness may evolve and gradually diverge from nearby populations that currently co-occur. This shows that in between the sky island across Palghat Gap there existed a continuity in distribution, and after the civilisation in the Palghat Gap trespassing of wild animals has become merely impossible, which may have hindered gene flow. Therefore, continuous exposure to different environmental variants in between sky island habitats over extended periods would eventually cause severe loss of interconnection between populations over successive generations. This could later drive to speciation.

This study provides a vital perception of the interlink between population dynamics, ecological factors, and adaptation of *Elaeocarpus gadgilii* in the sky islands of the Western Ghats the Palghat Gap. Here *E. gadgilii* showed a statistically significant level of variation between its population across the Palghat Gap, where 35 out of 42 significant morphometric parameters were found to have a significant level of variation. Further investigation revealed a small but distinct variance between populations from sky islands on the northern and southern sides, underscoring the role of Palghat Gap factors in shaping all the 35 quantitative morphometric parameters of the species. This morphometric variation was interlinked with other important ecology of the sky islands of the Western Ghats and was detailed in chapter 6 and 7. Here natural selection is found to have played a vital role in altering the morphological characters of the species. Organisms that better adapt to their specific environments are more likely to survive and reproduce, leading to the development of unique sets of morphological traits in different populations. Phenotypic selection bears biological significance solely when it leads to evolutionary changes (Cleveland and Soleri 2007). This study goes with Darwin's concept of natural selection, suggesting that morphological variations in plant populations may have resulted from the differential survival and reproduction of individuals with the selection of favourable traits in their respective environments. Distinct phenotypes exhibit varying rates of survival and reproductive success in diverse environmental conditions (Lewontin 1970). The morphological variations between geographically separated populations are believed to impact not only

the functional aspects but also show statistically significant correlations with other environmental parameters. These correlations may have led to the establishment of generalisations known as ecogeographic rules (Gibson *et al*.,1984).

The physical features of the Palghat Gap, including gap distance, were found to influence various parameters such as precipitation, wind patterns, and edaphic properties of the sky island. The climatological normal rainfall pattern during the Southwest Monsoon Seasons (SWMS) in the southern region of the Indian peninsula exhibits a distinct rainfall gap in the vicinity of Palghat Gap. This gap in rainfall is attributed to the divergence resulting from Bernoulli's effect (Dutta *et al*., 2006). The distinct features of these gaps are responsible for the separation of sky islands in the Western Ghats, significantly impacting the genetic divergence in populations of *E. gadgilii* and are depicted in chapter 5.

The populations of *E. gadgilii* from the sky islands across the Palghat Gap were found to have higher values of divergence. However, the genetic distance of its population within the sky island populations was extremely low, suggesting a high degree of genetic similarity. That is the genetic diversity study on *E. gadgilii* hereby proved that not only at the morphological level but also at the genetic level the populations of *E. gadgilii* diverged into two distinct groups of populations across Palghat Gap, one on the southern side and the other on the northern side of Palghat Gap. This phylogenetic intraspecific analysis of *E. gadgilii* offers insights into the genetic divergence between the populations, shedding light on their evolutionary history and relationships. Thereby suggesting that the geographical features of the Palghat Gap, which separates the populations, have played a role in shaping the genetic divergence patterns. This inference highlights the potential impact of geographical barriers on the genetic makeup of populations and the importance of considering ecological and environmental factors in evolutionary studies.

The intraspecific variation, a significant aspect of biodiversity, has not received adequate attention from governmental and non-governmental organisations, particularly in the context of the conservation of plants and wild species management. These phenotypic and genetic variations within and between populations can extremely influence ecological and evolutionary processes, including responses to environmental changes, maintenance of species diversity, and ecological stability and resilience (Mimura *et al*., 2017). The impacts on intraspecific variation could have vital implications for ecological processes and ecosystem services, while re-

searchers have long recognised that variation among species influences the surrounding environment. Recent evidence highlights the ecological importance of variation within species. These intraspecific effects interact with the effects of species replacement or removal. They lead to changes in abundance (or biomass), rates of ecological processes, and alterations in community composition, resulting in both direct and indirect ecological responses. Notably, intraspecific effects are often comparable to and in some cases even stronger than species effects. Species effects generally play a larger role in direct ecological responses. Intraspecific effects become especially prominent when indirect interactions lead to changes in community composition (Des Roches 2017).

One of the major ecological components that poses a risk to plants is the climate, as it alters the availability of light, water, and nutrients, thereby impacting the process of photosynthesis. Consequently, plants need to make adaptations to cope with these challenging circumstances (Tikkanen and Aro 2012, Schottler and Toth 2014). The temperature conditions at higher elevations are relatively low compared to lower elevations. This temperature variation is likely a key influencing factor in the distribution pattern, as closely related species may not be able to tolerate the colder winter conditions prevalent at lower elevations. Consequently, the presence of warmer winter temperatures at higher elevations would restrict the occurrence of certain species that are better suited to colder conditions (Wiens *et al*., 2019).

The current study employed a statistical analysis of historical monthly weather data of the sky islands of the Western Ghats on the northern and southern sides of the Palghat Gap, as depicted in chapter 6. This analysis unveiled that there existed a statistically significant variation in precipitation received between the sky islands across the Palghat Gap. However, the remaining climate variables, i.e., maximum temperature and minimum temperature, did not exhibit significant variability. Consequently, the sky islands across the Palghat Gap are diversified based on their precipitation levels. This revealed that through the means of isolation by the environment and the features of the sky island habitat, its inhabitants were isolated. This isolation nature was one of the factors that may have isolated populations of *E. gadgilii* and with significant implications in its intraspecific morphometric variability.

This present study's finding is consistent with established literature emphasising the significance of precipitation on vegetation. Notably, the higher rainfall experienced by the southern Western Ghats contributes to the greater biodiversity in the

southern sky islands of Western Ghats than northern sky islands (Joseph *et al*., 2012). This observation lines up with the established dependence of the Western Ghats on the southwest monsoon, leading to enhanced rainfall in the southernmost regions of the Western Ghats. The interconnectedness between vegetation and precipitation is a well-known fact. Rito emphasised in his study the crucial role of precipitation as an environmental filter (Rito *et al*., 2017) and its strong impact on the distribution of water-demanding plant species. However, the response of plant communities to precipitation varies, as indicated by Sandel (Sandel *et al*., 2010), different plant communities show diverse trait responses to precipitation. The influence of precipitation on shaping the species at the population level was proved to be true by correlating intraspecific morphological variation of variables of the *E. gadgilii* with precipitation data. This unveiled the important findings about how climate variability affects the distribution, diversity, and physical characteristics of *E. gadgilii*, which thereby reflects the influence of climate variables on the sky island vegetation. We still need more research to understand the complex relationships between climate, species distribution, and other ecological changes over time. Increased climate instability leads to population decreases, extinctions, and more pronounced ecotones. Greater diversity provides only a limited relief for this. Rising environmental volatility has significant ecological effects, emphasising the need for further exploration and understanding of the consequences of unbalanced negative anomalies (Malanson 2018). Species were the central focus of global change and conservation biology-based investigations. But species are not homogenous entities; they comprise diverse populations, some of which exhibit local adaptations with varying degrees of plasticity. Population differences and limited movement can predict how species will change their habitat due to climate change. This forecasting method is more useful than assuming the species to adapt consistently across their entire range. Unfortunately, data at the population level are often lacking for many species, highlighting the need to identify general patterns of population differentiation to bridge this knowledge gap. Therefore, it is important to integrate modelling and theoretical research on intraspecific phenotypic variation. Such integration is crucial for gaining a better understanding of the implications of population differentiation on species' responses to environmental changes (Valladares *et al*., 2014).

Ecological factors, life-history traits, and historical biogeography could better explain the distributions of taxa (Biswas and Praveen Karanth 2021). Diverse mor-

phological traits of plants can serve as valuable indicators for the necessity for conservation purposes, as they exhibit significant variations in response to various environmental conditions. Morphological plasticity allows for accurate and straightforward monitoring of species-specific growth responses under different environmental influences. The considerable variability in these traits makes them effective indicators for assessing the growth conditions of studied populations, closely associated with land use and conservation management efforts (Muckschel and Otte 2003).

The gap features like gap distance and the changes it induced over wind, precipitation, and temperature may have induced changes in the soil formation and its composition that have collectively altered the populations under investigation. The plant responses in terms of morphometric parameters are influenced by both biotic and abiotic factors of the ecosystem. In this study, the role of edaphic parameters in shaping populations across the Palghat Gap was included in chapter 7. This study on the sky islands across Palghat Gap even focused on the interrelation between soil parameters and morphometric (physical measurement) characteristics of the species *E. gadgilii*. The study explored the relationships between soil characteristics, nutrient content, and plant morphology, aiming to understand how environmental factors like edaphic elements influenced the distribution and health of this plant species. The study unveiled the relation between soil parameters and morphometric characteristics of *Elaeocarpus gadgilii* across the Palghat Gap. As per the investigation done on edaphic factors of sky islands across Palghat Gap, the concentration of most edaphic factors was found to be higher in the soil samples from sky islands on the southern side. Some of the factors like clay % and silt % were higher over the northern side sky islands samples, and few didn't show any variants. The distinct concentration gradients observed in soil parameters have separated these sky islands based on their soil composition. These variations will have implications on plant nutrient dynamics and distribution patterns, potentially influencing vegetation growth and ecosystem dynamics. The geographical features of the Palghat Gap are the major factor that separates the sky islands geographically, so the influence of Palghat Gap features over soil composition is inevitable. This gap features and other associated ecological features most probably have caused the edaphic gradient displayed by sky islands soil samples. The soil composition of each ecosystem influences its vegetation. So, the existing soil gradient between the sky islands would pose challenges to the plants inhabiting this habitat. This promotes intraspecific variability in the species. The variability

in soil elements was found to significantly influence the intraspecific variability of *E. gadgilii*, as illustrated in Chapter 7. Additionally, a statistically significant correlation was observed between soil parameters and intraspecific variability in morphometric characteristics of *E. gadgilii*. It thereby highlights the importance of soil factors in shaping the population of this species in the sky islands. The variation in the climate conditions also played a crucial role in shaping soil formation and composition, which was found to have in turn affected these plant's characteristics. The study also introduced the importance of spatial interpolation maps to identify and visualise areas of land degradation within the study region. Thereby emphasising the importance of utilising spatial interpolation maps in the study of land degradation, providing valuable information for sustainable land use planning, resource management, and conservation strategies (Rasool *et al*., 2020).

Overall, the study provides an overview of a scientific study investigating the relationships between climate, soil parameters, floristic diversity and plant morphology, in a specific geographical region. Understanding these complex relationships aids in devising, managing, and implementing efficient strategies to restore the desertified or desertifying ecosystem. (Mousaei Sanjerehei *et al*., 2013).

Distinct plant species exhibit varying effects on different soil parameters, emphasising the intricate interplay between vegetation and soil properties (Chahouki 2014). The investigation in the Sanib Taftan Watershed in Iran underscored the influence of both soil and topographic features on plant distribution. In the above study topographic variables such as slope and altitude, were found to exert a more substantial influence on plant distribution than soil-related factors in the studied area (Ebrahimi *et al*., 2015).

The present study on sky islands depicted that these habitats are not only geographically separated by the Palghat Gap but also by environmental factors. This study has justified the impact of this gap across various fields, including floristic diversity (chapter 3), intraspecific variability of sky island species at morphometric levels (chapter 5) and genetic levels (chapter 8), the spatial distribution of species (chapter 4), the concentration gradient of the edaphic environment (chapter 7), and precipitation patterns (chapter 6). Thus, the study demonstrates that the Palghat Gap is the most significant valley in the Western Ghats and has influenced the isolated sky island habitats nearby. Within the study, the impact of climate, edaphic components, altitude, and features of the Palghat Gap on the intraspecific morphometric variability

of *E. gadgilii* indicates statistically significant correlations with morphometric variables (chapters 3, 4, 5, 6, and 7). The distance of the Palghat Gap and geographical separation also showed significant correlations with the majority of *E. gadgilii*'s morphometric variables. While other ecological components are correlated with morphometric variables, only a few exhibited significant correlations. Comparing the climate and edaphic parameters of sky islands with the features of the Palghat Gap, it was evident that the Palghat Gap features had the most significant and predominant impact on the population of *E. gadgilii*.

These findings contributed to a deeper understanding of the evolutionary dynamics of this species, underscoring the significance of employing various analytical approaches to enhance the robustness of scientific conclusions. This study shows how different environmental factors, like soil composition, landscape features, and climate conditions in sky islands, are interconnected. These factors play a crucial role in shaping the biological diversity and genetic makeup of species in sky islands. This recognition of interconnectedness is critical in ecological and evolutionary studies, as it highlights how changes in one aspect of the environment can have cascading effects on the entire ecosystem.

Gaps or wide valleys in mountain systems have captured the attention of biogeographers and evolutionary biologists due to their significant influence on species distributions and genetic diversity, both between different species (interspecific) and within the same species (intraspecific). The Western Ghats, a mountain range running parallel to India's west coast, serves as a biodiversity hotspot with remarkably high endemism in the Indian Subcontinent. Within this hill range, among the three large valleys or gaps, the Palghat Gap is found as a major obstacle. The present study is a major justification for that. These observations align with the fact that the Palghat Gap is the deepest and widest. Remarkably, all the divergences across these gaps occurred long after their formation, negating the possibility of geology-mediated vicariance as the cause for these patterns. These findings shed light on the role of these mountain gaps in shaping the ecological community, species distributions, and morphological and genetic divergence, and provided valuable insights into biogeographical and evolutionary processes in the Western Ghats (Biswas and Praveen Karanth 2021).

The influence of the Palghat Gap in adaptable plant species like *E. gadgilii* is displayed through its intraspecific variability. This variability between populations in turn reflected the environmental changes occurring within the region. However, in

unfavourable circumstances, species may face the risk of extinction, leading to the loss of their gene pool and it will be a substantial loss to overall biodiversity and is substantiated by ecological niche model forecasting. Understanding the impact of gap features is crucial in preserving the biodiversity of the sky islands. Restoration ecology often disregards the simultaneous investigation of species-level and gene-level biodiversity, despite the critical importance of high genetic diversity for the long-term success of restoration efforts. Landscape-scale dispersal plays a vital role in vegetation recovery and the preservation of species and genetic diversity after restoration. In fragmented landscapes, disruptions in seed and genetic material dispersal frequently lead to the failure of spontaneous recovery, and prevent the establishment and maintenance of genetically diverse populations. It is crucial to address these challenges for effective restoration strategies and the sustainable conservation of biodiversity (Aavik and Helm 2018). Importantly, all observed genetic divergences across these gaps occurred long after their formation, ruling out geology-mediated vicariance as the driving factor (Biswas and Praveen Karanth 2021). Hypotheses concerning ancient processes cannot be directly tested through observation or manipulative experiments. Nevertheless, their outcomes, as reflected in present patterns, can potentially be observed and examined using an inductive approach, allowing for testing. In some cases, ecological factors, life-history traits, and historical biogeography of the taxa offer a more suitable explanation for their current distributions. Instead, for certain groups, ecological factors, life-history traits, and historical biogeography of the taxa provide a better explanation for their distributions (Cabrero-Sanudo 2012).

Where the pioneering step in biodiversity conservation is modelling, and incorporating spatially explicit soil data into environmental models allows for more accurate predictions and helps in understanding the interactions between soil, water, and air components in various ecosystems (George *et al*., 2021). The occurrence of ecological speciation is significantly influenced by the action of selection on existing genetic variation within a population (Schluter 2009). To avert additional declines in these species, it is essential to implement efficient conservation measures, like the replanting of the sapling in its habitat besides conserving the habitat, as this species is already under conserved area. The next alternative is to introduce ex-situ strategies. The combined application of these approaches can increase the likelihood of species survival and serve as a safety net against habitat loss or other threats (Phartyal *et al*., 2002).

The current study used an interdisciplinary approach to examine various aspects of the ecosystem in the sky islands of the Western Ghats. It explored elements such as floristic diversity, future spatial distribution, intraspecific morphometric and genetic variability of selected taxa unique to sky islands, and the edaphic and climate data across the Palghat Gap. The study posits that the Palghat Gap is not solely responsible for the separation of the Western Ghats; rather, it has impacted each defining component of the sky islands. The isolation of habitat components resulted from factors like isolation by distance, isolation by environment and habitat contraction. Climate, influenced by high greenhouse gas (GHG) emissions, is identified as a key factor affecting the spatial distribution of the studied species. Sustained habitat contraction initiated by past natural factors like warming and reduced glaciation, are now prolonged by human activities impacting the climate. The study underscored the risk to biodiversity in the southern Western Ghats sky islands due to the current environmental scenario, projected climate changes and expected high GHG emissions. Consequently, the impact is predicted to significantly affect the southern Western Ghats, renowned for its biodiversity, making it less suitable for the majority of species. Preserving biodiversity in the Western Ghats is crucial. A common question arises is whether the areas that are already designated as reserve forests need extra conservation efforts or not. The straightforward answer is that it is better to implement conservation measures beyond the Western Ghats, particularly in society, to reduce greenhouse gas emissions. This is essential as these emissions have been found to harm the biodiversity of the Western Ghats. In summary, tackling elevated greenhouse gas emissions through wider societal initiatives is key to safeguarding the biodiversity of the Western Ghats. The study suggests that developing conservation strategies using ensemble forecasting, enhances the capacity to protect these species and their habitats proactively before the disappearance of sky island habitats, ensuring the conservation of these ecosystems.

CHAPTER 10: SUMMARY

This study highlights the ecological importance and conservation necessity on the sky islands of Western Ghats. The study substantiated the necessity of effective conservation measures to mitigate the challenges posed by climate change, geographical gap and to preserve endemic species. The findings of the study add to our understanding of ecological vital regions, by highlighting the importance of considering geographical factors in biodiversity research and conservation planning.

The floristic diversity observed between sky islands of Western Ghats across the Palghat Gap was analysed through floristic survey analysis conducted on the region. Then further studies were done on the species which were considered representative sky islands species. Three representative sky islands species were chosen based on several confined criteria. Among the criteria, the vital ones are their presence on sky islands on both the northern and southern sides of the Palghat Gap and their ability to reflect environmental variations. Ensemble modelling research done over these species revealed that there is a concerned spatial reduction in suitable habitat areas for *Phoebe wightii* and *Elaeocarpus munroi* from past to future scenarios. However, *Elaeocarpus gadgilii* is expected to have a spatial expansion in its suitable habitat areas, but now the species is found in an area which is facing threats, and this area is found to be an unsuitable habitat area in future as per forecasted projections. So, urgent conservation measures are inevitable over these habitats especially over the representative sky island species, by considering both in-situ and ex-situ strategies. This ensemble forecasting proved to be a valuable tool in predicting suitable spatial areas for the species under concern. This study underscores the remarkable relevance of preserving these species within their natural habitats and the pioneering role of modelling techniques in the Western Ghats biodiversity conservation.

Then in one of the representative species of sky islands *Elaeocarpus gadgilii*, remarkable intraspecific morphometric variability was observed. Intraspecific variability is a means of local adaptation to the diverse sky islands of the Western Ghats across the Palghat Gap. Here the geographic factors of the Palghat Gap emerged out to be as a pivotal determinant that shaped the species morphological characteristics through natural selection, leading to selective traits in different locales. These findings offer invaluable insights into population structure and adaptive strategies in diverse sky islands, contributing significantly to our scientific understanding of speciation and

adaptation in these unique habitats. Extended the investigation to intraspecific genetic diversity analysis on *Elaeocarpus gadgilii* populations from the sky islands revealed a significant divergence between its population on the southern and northern sky islands across the Palghat Gap. This highlighted the influence of the Palghat Gap's geographic features in shaping both the morphological and genetic diversity of species inhabiting in the sky islands of the Western Ghats. The size of the gap aligns with its influence on genetic diversity, indicating that ecological and historical factors are the driving forces for this variability

The impact of climate on the populations of *E. gadgilii* was explored, which unveiled notable significant correlation between precipitation and morphometric variables of *E. gadgilii.* It thereby substantiated the role of climate in shaping its population. A higher level of precipitation was observed in the southern sky islands, compared to the northern side, and this was attributed to other interconnected environmental factors. The total precipitation appeared to be one of the principal drivers of the observed gradient in the sky islands across the Palghat Gap and this was found to exert a substantial influence on the species inhabiting it. These findings hold profound implications for biodiversity conservation efforts in the region, highlighting the multifaceted nature of environmental factors in driving species variations.

Then the edaphic environment of the sky islands was investigated, and this revealed the significant role of edaphic parameters in intraspecific morphological variation within *Elaeocarpus gadgilii* Noteworthy correlations were found between soil parameters and sky islands species morphometric traits, which substantiated the vitality of specific soil attributes in its distribution and intraspecific variability of sky island species. Variations in macro and micronutrient content between sky islands habitats across the Palghat Gap were found to have potential implications for its desertification and conservation endeavours. This study underscored the pivotal role of soil in environmental health and its far-reaching impact on plant species, further highlighting the interdependence of edaphic components in modelling and biodiversity conservation.

The influence of the biogeographical gaps is not the sole contributor to the observed changes in the study area. The study area itself holds significance as a source of speciation and a centre for the evolutionary process. These unique habitats are isolated from other lowland ecosystems due to elevation and geographical gaps, this highlights the relationship between the distance of the geographical gap and its influence on genetic diversity in its inhabitants within the study area. This supports the no-

tion that ecological and historical factors play a vital role in the intraspecific morphological and genetic diversity of sky island species across gaps, and the sky island effect also contributes to it significantly. The study also pinpoints the fact that all ecological components of a habitat are interconnected. Each component has its importance, and one can't take up the role of another. In the absence of one of the elements in the ecosystem, the effect will be reflected over others.

This study generalised the isolation characteristics of sky islands of the Western Ghats, particularly those on the southern and northern flanks of the Palghat Gap, and the role of this gap. It highlights the vulnerability of the habitat and its biodiversity. Present and future climates are affected by global warming and the challenges it poses to the Western Ghats biodiversity are adverse. As per the study, it is anticipated that the effect would be heavier especially over the southern Western Ghats, as it is anticipated that the precipitation and favourable climate conditions of the southern side would shift to the northern side. The present study enumerated that the Palghat Gap isolated the sky islands of western Ghats not only geographically by geographical distance but also by environment and habitat contraction. So southern Western Ghats more probably can overcome the challenges posed by global warming. So, to safeguard southern Western Ghats efficient conservation strategies are to be devised. The conservation efforts should extend beyond Western Ghats boundaries by introducing strategies very much different from the traditional reserve forest conservation measures, to protect its biodiversity efficiently. As the major threat for the southern Western Ghats is the uncontrollable climate, which is adversely altered by the greenhouse gas effect. The major cause for it is human activities, and then geographical gaps like the Palghat Gap which hinders the gene flow.

The aspect of this study extends beyond the confines of academic research, reverberating through conservation practice and policy formulation. Introducing this newfound understanding, enables the sky islands biodiversity to cope with challenges posed by global warming, thereby ensuring the long-term viability of this unique ecosystem of the Western Ghats region.

CHAPTER 11: RECOMMENDATIONS

The present study explored the floristic diversity of sky islands of Western Ghats within the study area across the Palghat Gap. Evaluated the spatial distribution of selected taxa all over the Western Ghats with the aid of ENM. Foreseeing the spatial distribution of the sky island species enabled us to anticipate the risk of its existence and the expected high probable habitat suitable areas in future. Then intraspecific variability studies were done over the selected taxa, coupled with the investigation of climate and edaphic parameters of sky islands. The recommendations suggested for future studies over this field of study area hereby presented are:

1. Intraspecific anatomical variability in sky island species: investigating on intraspecific trait variability in sky island species at the anatomical level provides an in-depth and significant perception of the influence of environmental factors on the anatomical diversity within a species and thereby finding the impact of anatomical trait variability in ecological and evolutionary dynamics.
2. Sky islands edaphic data in modelling: an extensive study on significant edaphic components of the sky island ecosystem, deepens the understanding of the edaphic diversity of the sky islands of the Western Ghats, and its contribution to biodiversity. Introducing these detailed and precise edaphic data into modelling will improve the accuracy of modelling prediction. This thereby aids in the efficient management of such habitat.
3. Intraspecific variability in secondary metabolites in sky island species: The variation observed in secondary metabolites of a species inhabiting sky islands is concerned with the composition and concentration of secondary metabolites. Secondary metabolites are organic compounds not directly involved in the primary functions of growth and development. Instead, these metabolites play a vital role in ecological interactions, like defence against herbivores, attracting pollinators etc. Studying the vicariance in these secondary metabolites within a species helps to understand the influence of environmental factors of sky island habitats in the quality and quantity of secondary metabolites.
4. Long-term Monitoring: For an effective understanding of the distribution pattern of the species, continuous and long-term monitoring studies are necessary. Long-term monitoring tracks changes in the species distribution and abun-

dance over time, especially in response to climate and environmental variations. This will help to understand the impacts of ongoing climate change on distribution patterns.

5. Incorporate advanced molecular Techniques in sky island species exploration and analysis: To get an in-depth understanding of the intraspecific genetic diversity of sky island species, advanced molecular techniques and detailed whole chloroplast, mitochondrial and microsatellite DNA sequencing are to be done. This can provide vital information on the genetic basis in population connectivity, gene flow, and genetic structure of species populations within and between sky islands.
6. Study community interactions in sky species: Investigating coexistence in sky island species is necessary to avoid the coextinction of relevant species. Studying community interactions within the sky islands ecological communities will give a notion of factors influencing species coexistence. Community interactions include mutualistic relationships, predation, and competition.
7. Collaboration with local communities: Sharing the devised and effective conservation strategies and implementing and monitoring them through local communities increases the effectiveness of conservation measures. Involving local knowledge and participation in it can improve the effectiveness and acceptance of conservation efforts.
8. Restoration and conservation of sky island species: Investigate the potential of sky islands for habitat restoration and introduce effective ecological restoration techniques in degraded sky island habitats to enhance biodiversity conservation and ecosystem resilience.

Considering these recommendations in future studies will raise the importance of these habitats and enable them to effectively restore and conserve both the habitat and its diversity efficiently.

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Eugenia pokkudanii (Myrtaceae): a new species from Sky Islands of Nelliyampathy, Kerala, India

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Abstract

Eugenia pokkudanii, a new species of Myrtaceae from high ranges of the Western Ghats, Palakkad District, Kerala is described and illustrated here. The species shows similarities with *Eugenia discifera* and *Eugenia indica* but is distinct from them by the shape, size and indumentum of leaves, petioles, pedicels, calyces, petals and bracteoles. Detailed description, distribution and conservation notes are provided with photographs and illustration.

Keywords: Keshavanpara, Pothumala, Asia, Myrteae, taxonomy

Introduction

The genus *Eugenia* Linnaeus (1753: 470) has about 1100 species distributed in Africa, North to South America, Malaysia and Southeast Asia (IPNI 2019, WCSP 2020). It has 25 species and 2 varieties in India, of which 21 are endemic to Western Ghats (Shareef & Kumar 2020).

During a floristic survey in Nelliyampathy forests, the authors came across an interesting specimen of *Eugenia* from two locations including Keshavanpara and Pothumala hills of Nelliyampathy forest. On critical studies with relevant literature (Linnaeus 1753, Bentham & Hooker 1865, Duthie 1878–9, Gamble 1919, Vajravelu 1990, Mohanan & Sivadasan 2002, Sasidharan 2002, Govaerts *et al.* 2008, Wilson 2009, Sasidharan 2013, Kumar *et al.* 2014, Byng *et al*. 2015, Shareef & Kumar 2020) and consultation with the type specimens housed at different herbaria (K, P, BM, KFRI, CALI and MH; acronyms follow Thiers 2021), it turned out to be a species new to science, which is described and illustrated here.

Taxonomy

Eugenia pokkudanii A.M. Maya, K.M. Prabhukumar & V. Suresh, *sp. nov.* Figures 1–3.

Diagnosis:—*Eugenia pokkudanii* shows morphological similarities with *E. discifera* Gamble (1918: 239), but differs mainly by lateral nerves 6–8 pairs (versus 10–15 pairs in *E. discifera*), petioles 2–5 mm long (vs. 6–10 mm long), flowers 0.7–1 cm across (vs. up to 2 cm across), pedicels 0.3–0.56 cm long (vs. 0.5–0.9 cm long), bracteoles oblong (vs. lanceolate), calyx tubes 0.9–1.5 mm long (vs. 2–3 mm long), calyx lobes 1.6–2.5 mm wide (vs. 4–5 mm wide) and petals broadly elliptic (vs. orbicular). It is also similar to *Eugenia indica* (Wight 1842: 523) Chithra (1983: 153), but differs from it by its blades with 6–8 pairs of lateral veins (versus 5–6 pairs in *E. indica*), petioles 2–5 mm long (vs.

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3–8 mm long), bracteoles oblong (vs. linear), calyx tubes 0.9–1.5 mm long (vs. 4–6 mm long), calyx lobes 1.6–2.5 mm wide (vs. ca. 5 mm wide) and petals broadly elliptic (vs. orbicular). See also Table 1.

TABLE 1. Morphological comparison of *Eugenia pokkudanii* with *E. discifera* and *E. indica*.

Characters	***Eugenia pokkudanii***	***E. discifera***	***E. indica***
Leaves	elliptic	obovate or elliptic-ovate	elliptic-obovate or oblanceolate
Lateral vein nerves	6–8 pairs	10–15 pairs	5–6 pairs
Petioles	2–5 mm long	6–10 mm long	3–8 mm long
Flower at anthesis (diameter)	0.7–1 cm across	ca.2 cm across	ca.1 cm across
Bracteoles	oblong	lanceolate	linear
Bracteoles length	1.6–1.9 mm long	ca. 2 mm long	ca.3 mm long
Calyx tube length	0.9–1.5 mm long	2–3 mm long	4–6 mm long
Calyx lobe width	1.6–2.5 mm across	4–5 mm across	ca. 5 mm across
Calyx lobes indumentum	Rusty brown long hairs on the abaxial side and floccose white pubescent on adaxial side.	tomentose without, glabrous within	Fulvous tomentose, glabrous within
Petals	broadly elliptic	orbicular	orbicular
Seeds	1-2	1-2	many

Type:—INDIA. Kerala, Palakkad District, Nelliyampathy, Keshavanpara, 1002 m, 10°32’26.79” N, 76°40’49.23”E, 23 March 2019, *A.M. Maya, K.M. Prabhukumar & Suresh V. GVCP-SV122* (holotype MH!, isotype CALI!).

Description:—Large shrubs to small trees, 2–4 m height; profusely branched; branches terete, rusty brown appressed, sparsely pubescent; branchlets terete, greenish brown, rusty brown appressed pubescent; internodes 1.5–2.2 cm long. Leaves coriaceous, petiolate; lamina elliptic, 1.5–6.3 × 0.5–2.5 cm, base cuneate to attenuate, margins entire slightly revolute, apex obtuse to rounded, adaxially green glabrous and abaxially silvery whitish green, sparsely rusty brown puberulent at middle and apex, brown appressed puberulent at leaf base, midvein not conspicuous; lateral veins 6–8 pairs; Petiole 2mm–5mm long, slender, terete, green, rusty brown appressed tomentose. Inflorescences solitary or few-flowered, axillary or lateral. Flowers at anthesis 0.8–1.3 cm long × 0.7–1 cm in diameter, white, pedicellate; pedicels 3–5.6 × 0.3–0.9 mm, slender, terete, green, floccose rusty hairy; bracteoles 2, 1.6–1.9 × 0.4–0.5 mm, oblong, rounded at apex, green, floccose brown pubescent abaxially, white–brown appressed pubescent adaxially; hypanthium campanulate; calyx tube 0.9–1.5 × 1.5–1.7 mm, green, floccose brown pubescent; calyx lobes 4, 1.6–1.8 × 1.6–2.5 mm, orbicular to suborbicular, margin ciliate, rusty brown long hairs on abaxial side, floccose white pubescent adaxially; petals 4, broadly elliptic, 3–6 × 3.6–6.2 mm, margins entire, recurved at apex, pellucid, glabrous, white suffused with brown and purple stripes on abaxial side at tip. Androecium apostemonous; stamens extrorse, dithecous, numerous; staminal disk 3.2–4.6 mm in diameter, broad, fulvous white pubescent; filaments terete, 4.5–7 mm long, slender, white, gland-dotted, glabrous; anthers 2-celled, oblong, 0.6–0.7 × 0.55–0.6 mm, dorsifixed, yellowish brown and gland-dotted. Ovary 1.5–1.6 mm in diameter; style thick, 0.6–1.7 × 0.2–0.3 mm, gland-dotted; stigma entire; locules 2; ovules 2 in each locule, ovoid, 0.01–0.02 mm in diameter; placentation axillary. Fruits berries, ellipsoid, 0.9–1.3 × 0.5–0.9 cm, green when young and reddish orange when ripe, glabrous, crowned by the persistent calyx. Seeds 1–2.

Phenology:—February to April.

Etymology:—The species is named in honor of the late Mr. Kallen Pokkudan (1937–2015), an environmental activist from the state of Kerala, India, in recognition of his efforts for the protection and proliferation of the mangrove forests in Kerala.

Ecology:—The new species is known only from the type locality and grows as a small tree between 900 to 1000 m elev.

Paratypes:—INDIA. Kerala, Palakkad District, Nelliyampathy, Pothumala, 13 March 2019, *A.M. Maya & Suresh V. GVCP-SV113* (MH!). Pothumala, 20 February 2020, *A.M. Maya & Suresh V. GVCP-SV269* (CALI!). Keshavanpara, 21 February 2020, *A.M. Maya & Suresh V. GVCP-SV270* (KFRI!).

FIGURE 1. A. general aspect; B. Flower; C. Fruit & twigs with glaucous surface: D. Habit; E. Adaxial side of leaf; F. Abaxial side of leaf; G. Leaf apex, adaxial side; H. Brown indumentum at the abaxial side of leaf base. (Photos: K.M. Prabhukumar based on *A.M. Maya, K.M. Prabhukumar & Suresh V. GVCP-SV122.*)

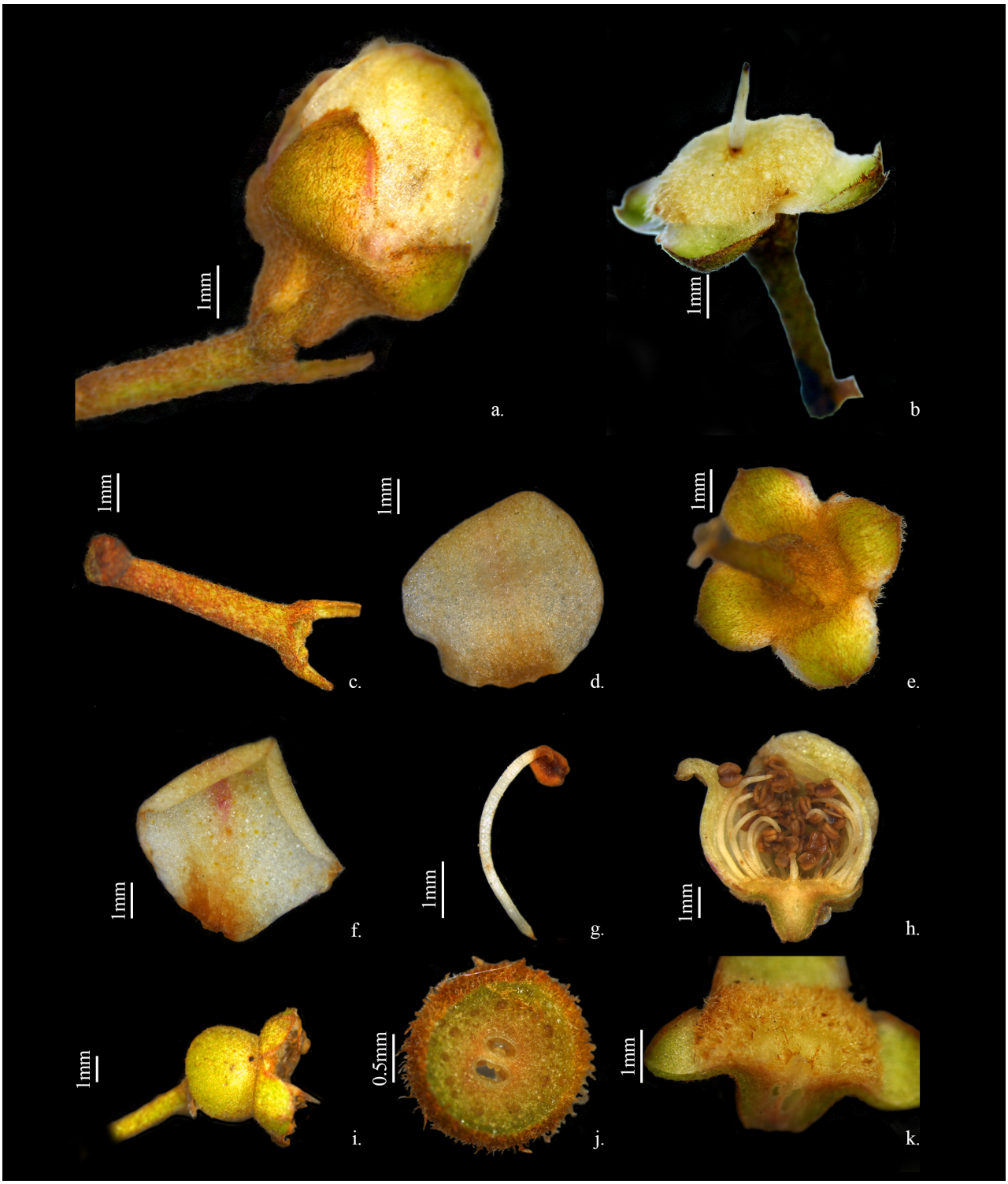

FIGURE 2. A. Flower bud; B. Staminal disk; C. Pedicel with two bracteoles; D. Petal, adaxial side; E. Calyx lobes; F. Petal, abaxial side; G. Stamen; H. Longitudinal section of flower bud; I. Young fruit with persistent calyx lobes; J. Transversal section of ovary; K. Longitudinal section of opened flower without petals. (Photos: A.M. Maya based on *A.M. Maya & Suresh V. GVCP-SV113*.)

Distribution and Habitat:—Semi-evergreen patches of Keshavanpara and Pothumala hills of Nelliyampathy forest, Western Ghats, Palakkad, Kerala, India.

Conservation status:—*Eugenia pokkudanii* is known only from the type locality. The extent of occurrence (EOO) of the species is estimated to be less than 1 km^2 and the area of occupancy (AOO) less than 50 m^2. Since the only extant locality is a tourist destination, it is possible to infer a reduction in the past of the potential habitat of the species. For this reason, the species can be categorized as Critically Endangered (CR) based on criteria B1 + B2 (a + bii + iii) (IUCN 2019).

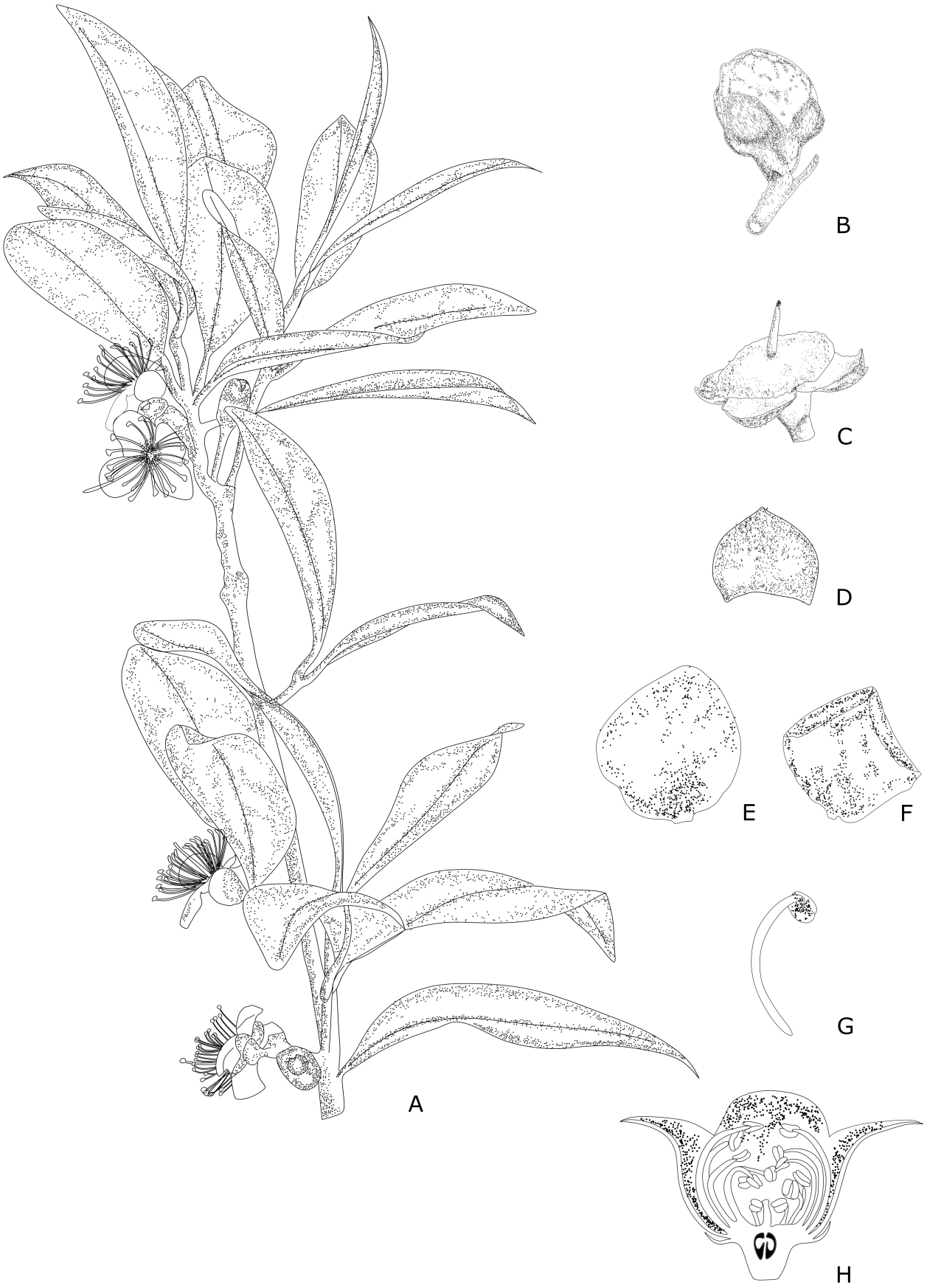

FIGURE 3. A. Habit; B.Flower bud; C. Staminal disk; D. Calyx lobe; E. Petal, adaxial side; F. Petal, abaxial side; G. Stamen; H. Longidtudinal section of flower. (Illustration by Suresh V. based on *A.M. Maya & Suresh V. GVCP-SV113*.)

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Elaeocarpus gadgilii (Elaeocarpaceae), a new species from Western Ghats (India)

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Abstract

Elaeocarpus gadgilii, a new species of *Elaeocarpus* (Elaeocarpaceae) from the southern part of Western Ghats (India) is described. Detailed description, distribution, phenology and photographs are provided. The differences between the new species and the similar *E. variabilis* Zmarzty and *E. serratus* L. are also discussed.

Keywords: Endemic flora, Kerala, Oxalidales, Palakkad, Taxonomy

Introduction

Elaeocarpus Burm. ex Linnaeus (1753: 515) is the largest genus of Elaeocarpaceae, represented by 488 species worldwide (POWO 2020). This Old-World genus is distributed in the subtropics from Asia and Pacific Islands to Australia and Madagascar (Coode 2004). The members of *Elaeocarpus* are mostly large to medium sized trees, found in evergreen forests of high elevations. Several species are characteristics of secondary forests, roadsides, or seems to be restricted to riversides (Zmarzty 2001). This genus is characterized by simple or 1-foliolate leaves, fragrant flowers, in axillary or lateral racemes, numerous stamens, sepals 4–5, petals 4–5; leaves changing colour from light green to dark green, turning then to yellow to red and to brown before shedding (Seetha 2008). In India, the genus is represented by 29 taxa, mainly occurring in southern and north eastern India, with a few species in Andaman and Nicobar Islands (Meitei & Khuraijam 2019, Zmarzty 2001). Zmarzty (2001) recorded 11 taxa (9 species and 2 varieties) from southern India and Sri Lanka which include 4 taxonomic novelties i.e., *E. hedyosmus* Zmarzty (2001: 423), *E. taprobanicus* Zmarzty (2001: 427), *E. variabilis* Zmarzty (2001: 429), and *E. serratus* L. (1753: 515) var. *weibelii* Zmarzty (2001: 437). Recently Meitei & Khuraijam (2019) reported 18 species from North East India. So far 12 species of *Elaeocarpus* were reported from Western Ghats (Peninsular India) and 6 among them are endemic. During an exploration of Nelliyampathy forests (Palakkad, District of Kerala), the authors collected some specimens of a taxon resembling *E. variabilis* Zmarzty (2001: 429) and also showing some similarity with *E. serratus* L. (1753: 515), but with remarkable uniqueness, described here.

Material and methods

Pertinent literature about *Elaeocarpus*, floras of India and relevant protologues (Hooker 1874, Gamble 1915, Manilal 1988, Vajravelu 1990, Murthi 1993, Sivarajan & Philip Mathew 1997, Zmarzty 2001, Mohanan & Sivadasan 2002,

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Daniel 2005, Sasidharan 2013, Meiti & Khuraijam 2019) were consulted. Types and other herbarium specimens at BM, BR, CAL, CALI, CMPR, E, K, KFRI, MH (herbarium codes according to Thiers 2020) were critically examined.

Results

On comparing the collected specimen with literature and relevant herbarium specimens, it is confirmed that the collected taxon belongs to *Elaeocarpaceae* sect. *Elaeocarpus* on account of the following features: 5 valvate sepals, 5 valvate petals, numerous stamens inserted on a cushion-like disk, anthers linear with terminal pores, ovary sessile, 3-celled with 2 ovules in each cell. However, it does not match with any known species of *Elaeocarpus* though there were some similarities with *E. serratus* and *E. variabilis*. Hence the specimens under consideration were confirmed to be a species of *Elaeocarpus* hitherto unknown to science.

A comparison of the new species with *E. variabilis*, *E. serratus* var. *serratus* and *E. serratus* var. *weibelii* is given in Table 1.

TABLE 1. Morphological comparison of *Elaeocarpus gadgilii sp. nov.* with *E. variabilis, E. serratus* var. *serratus* and *E. serratus* var. *weibelii*.

Characters	*E. variabilis*	*E. serratus* var. *serratus*	*E. serratus* var. *weibelii*	*E. gadgilii*
Leaf Texture	chartaceous	chartaceous	chartaceous	coriaceous
Leaf teeth distance	3–10 mm	2–10 mm	5–15 mm	3–17 mm
Main and mid veins on adaxial surface	not conspicuous	not conspicuous	not conspicuous	conspicuous
Main vein Pairs	4–8	4–7	6–9	3–5
Sepal colour	pinkish to reddish brown	greenish white	greenish white	pink to reddish
Petal Size	4.5–7.7 mm long	5–9.5 mm long	7.8 mm long	6–9 mm long
Disk lobes	fused, orbicular with reniform base	free, orbicular to broadly ovate with truncate base	free, broadly ovate with reniform base	free, ovate disk lobes with round or truncate base
Setae	absent	outer tooth with very short setae	outer tooth with very short setae	outer tooth with very long, shining setae
Style	1–3 mm long	2–4.5 mm	1.3–1.6 mm	1.6–4.4 mm long
Fruit	2.1–3.1 cm long, ellipsoid, ovoid, base round or cuneate	2.1–3.9 cm long, ellipsoid, base round or cuneate	1.5–1.7 cm long, globose, base reniform	3–5 cm long, ellipsoid, base round or cuneate
Stones over endocarp	ellipsoid to broadly obovoid	oblong, ellipsoid or obovoid	broadly ellipsoid to round,	ovoid

Taxonomic treatment

Elaeocarpus gadgilii A.M.Maya, V.Suresh & K.M.P.Kumar *sp. nov.* (Figs. 1, 2)

Diagnosis:—the new taxon differs from *E. serratus* and *E. variabilis* by the coriaceous leaves with conspicuous venation on adaxial surface, the outer tooth of anthers with very long shining setae, and the wider fruits.

FIGURE 1. *Elaeocarpus gadgilii sp. nov.* A. Habit; B. Flowering twigs; C. Fruiting twig (immature); D. Fruiting twig. (Photos: A.M. Maya & A.J. Robi).

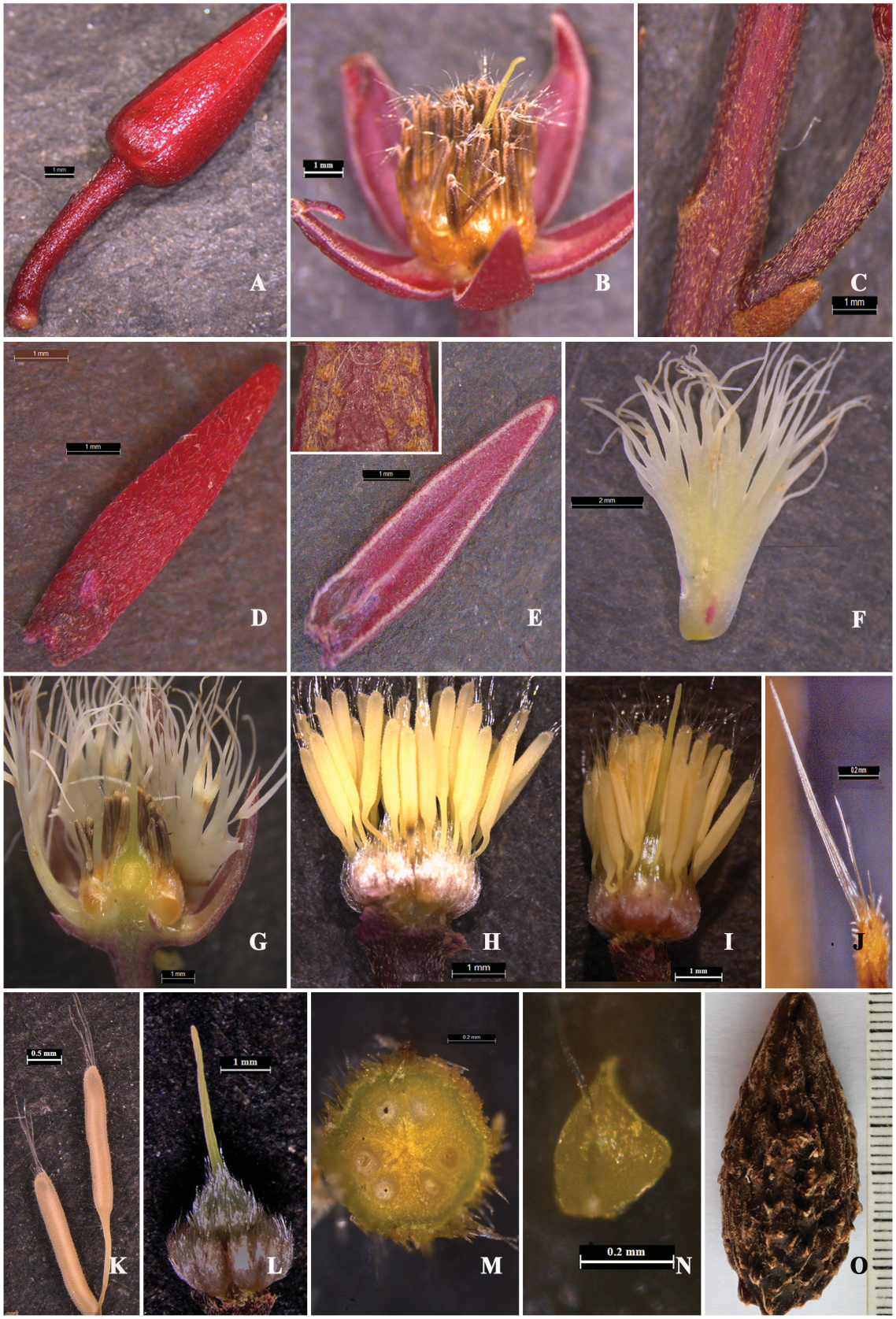

FIGURE 2. *Elaeocarpus gadgilii sp. nov.* A. Bud; B. Opened flower without petals; C. Bract at the base of pedicel; D. Outer surface of sepal; E. Inner surface of sepal (inset: magnification of the hairs on the abaxial surface of sepal); F. Petal; G. Flower L.S; H & I. Disk lobes, with numerous stamens inserted between disk lobes and ovary; J. Long shining setae on the apex of the outer anther tooth; K. Stamens; L. Gynoecium with the free disk lobes surrounding the base of ovary; M. Ovary (cross section); N. Ovule; O. Fruit without mesocarp and epicarp (Photos: A. M. Maya).

Description:—Trees, generally ≥ 12 m (up to 20 m high), with cylindrical trunk; stem grayish-green, with scattered adpressed, white hairs throughout. Branchlets slender, terete, felted, lenticellate. Leaves 1-foliate, alternately arranged and slightly crowded towards the branchlet apices; petiolate, petiole slender, terete, 13–30 × 1.2–2.4 mm, greenish to reddish, sparsely pubescent, with a pair of pegs at the apex. Lamina elliptic to broadly elliptic, 5–10 × 3.3–5.2 cm, thick, coriaceous; base cuneate, obtuse; apex acute or obtuse, shortly acuminate or emarginate; margin revolute, remotely crenate-serrulate; leaf teeth 3–17 mm long; main veins in 3–5 pairs, mid-vein and main veins conspicuous on adaxial side, more prominent on abaxial side, densely adpressed to semi spreading light brown hairs over mid vein and main veins on abaxial side, main vein forks at 8–19mm from mid vein. Domatia at the angle between the mid-vein and the main veins, covered with sparse adpressed brown hairs. Inflorescence axillary or lateral racemes, 8–28 flowered. Peduncles are slender, sub-terete, 35–82 × 1.2–2.1 mm, overtopping or condensed on twig tip, moderately to densely covered by adpressed brown hairs. Flower buds ovoid, with apex acute. Flowers pedicellate, pedicel slender, terete, 3.5–7 × 0.7–1.5 mm, pinkish to reddish-brown, densely covered in light brown hairs; bracts caducous, 2–2.2 mm long, lanceolate, brownish, floccose tomentose on outer surface. Sepals 5, free, 4–8.3 mm long, reddish-brown, lanceolate, with acute apex, base truncate, persistent after petals fall. Outer surface of sepals verrucose, densely covered by short, adpressed brown hairs, Inner surface of sepals margin and midvein are densely covered with adpressed white hairs with light brown tinge at its base. Petals 5, free, obovate, 6–9 × 1.2–4 mm, with 25–37 divisions, each divisions 2.2–4.7mm long with round apex, white colored with pinkish strips at the base of outer surface, both outer and inner surface with sparse white adpressed hairs in lower half and margin with few hairs. Disk lobes 1.0–1.05 × 2–3.5 mm, ovate, with rounded or truncate base, surrounding the ovary and partially covering its base, yellow to pink, densely covered with long, adpressed white hairs; hairs ½ times longer than disk remnants. Stamens 25–38; filaments straight, sometimes slightly curved to sigmoid (sigmoid ones more often in the outer ring of stamens), 0.05–1.70 × 0.04–0.17 mm; anthers 0.65–3.24 × 0.2–0.4 mm, basifixed, moderately hairy during anthesis, with the outer tooth longer than the inner, both with rounded apex, outer tooth apex having 3–6 long setae; setae 0.15–1.88 mm long, up to ½– ¾ times longer than anthers. Ovary 1.2–3 mm long and 0.9–1 mm in diameter, greenish, felted with long, adpressed white hairs, ½ times longer than ovary; locules three, each locule with 2 inversely comma-shaped ovules, fertile locule one, with only one functional ovule developing into 1 functional seed; style 1.6–4.4 × 0.14–0.4 mm. Fruits ellipsoid, 30–50 × 15–25 mm, with apex round and shortly acuminate, base acute to round, surface smooth or slightly knobby, greenish to reddish, with white small spots or patches, sparsely pubescent; mesocarp creamy white, suffused with reddish towards the inner side; endocarp 0.3–0.4 cm, surface with ovoid stone like hard projections and sparse, short, light brown, adpressed hairs. Seeds elliptic, round in cross section.

Type:—INDIA. Kerala: Palakkad District, Nelliyampathy, Mattumala, 10°31’41.34”N, 76°31’41.34’’E, 21 September 2018, *A. M. Maya GVCP-SV0025* (Holotype: MH; Isotypes: CALI, CMPR, KFRI).

Paratypes:**—**INDIA. Kerala: Palakkad District, Mannarkad, Varadimala, 22 October 2011, *K. A. Anilkumar 4133* (CMPR!), *Ibidem*, 21 September 2019, *A. M. Maya GVCP-SV183* (MH), Siruvani, s.d., 900 m, *D. B. Deb 28393* (MH!), Kearalamedu, 20 November 2019, *A M. Maya GVCP-SV266* (MH), Attumudi, 20 September 2012, *K. A. Anilkumar 4489* (CMPR!), Nelliyampathy, 26 August 2014, *K. M. Prabhukumar 07800* (CMPR!), Karasurimala, 19 October 2019, *A. M. Maya GVCP-SV232* (MH), Mattumala, 19 October 2019, *A. M. Maya GVCP-SV256* (MH). Ernakulam District, Mappilappara, 800 m, 26 September 2015, *K. M. Prabhukumar 08548* (CMPR!). Wayanad District, Chandanamthode, 18 November 1982, *N. Sasidharan 2608* (KFRI!). Thiruvananthapuram District, Agasthyamala Biosphere Reserve, Athirumala, 23 October 2003, 800m, *P. S. Udayan, Satheesh George, K. V. Thushar, N. K. Janarthanam 2013* (CMPR!). Kanyakumari District, Muthukayal, 1329 m, 9 November 2019*, K. A. Sujana* & *R. G. Vadhyan 147098* (MH).

Phenology:—Flowering in September–November; fruiting in November–January.

Etymology:—The species is named in honor of Sri. Madhav Dhananjaya Gadgil, an Indian ecologist and head of the Western Ghats Ecology Expert Panel (WGEEP), in recognition of his immense efforts towards conservation of Western Ghats.

Distribution:—Southern Western Ghats, Kerala and Tamil Nadu, India, apparently endemic to Southern Western Ghats, India.

Habitat:—Evergreen forests, at 800–1500 m a.s.l.

Identification key to *Elaeocarpus gadgilii sp. nov.* and its allied taxa

1. Apex of the outer tooth of anther without setae; disk with fused lobes ..... *E. variabilis*
– Apex of the outer tooth of anther with long setae about ½–¾ times as long as anther; disk with free lobes 2
2. Leaf coriaceous, margin crenate-serrulate; calyx red; fruit 3–5 cm long..... *E. gadgilii*

– Leaf chartaceous, margin serrate; calyx green; fruit 1.5–3.9 cm long 3
3. Fruit ellipsoid; seeds narrowly elliptic; fertile locule 1 ..... *E. serratus* var. *serratus*
– Fruit globose; seeds ovoid; fertile locules 2–3 ..... *E. serratus* var. *weibelii*

Additional specimens examined

Elaeocarpus variabilis:—INDIA. Tamil Nadu: Thirunelveli District, 6 March 1979, *V. S. Ramachandran 62096* (MH; barcode MH00181959). Dindigul District, Kodaikanal, Palini, 28 December 1914, *s.c.* (MH00181901), s.l., 23 August 1913, *s.c. 9175* (MH), s. l., 8 July 1970, 2100 m, *s.c. 34538* (MH), Palani hills, s.d., *s.c. s.n,* (MH; barcode MH00181900), Sirumalai, 23 August 1918, *s.c. 9175* (MH; barcode MH00181904). Coimbatore District, Udumanparai, Annamalai, s.d., *s.c. 5717* (MH; barcode MH00181893), 10 May 1903, *s.c. 5828* (MH; barcode MH00181895), *s.c. 5866* (MH; barcode MH00181888), Between Poonachi and Monica, Annamalai, 1 June 1903, *s.c. 6024* (MH; barcode MH00181887, MH00181884, MH00181885, MH00181887). Madurai, Prunharai, Pulney, 21 July 1920, *s.c. 16603* (MH; barcode MH00181902). Nilgiri District, Naduvattom, 11 May 2019, *P. S. Udayan 03531* (CMPR), Penstock, Manjur, 24 April 2001, *P. S. Udayan 06017* (CMPR), Naduvattom to Cinchona, 9 April 1968, 1200 m, *M. Mohanan and J. V. Sudhakaran 121361* (MH; barcode MH00181914), Ithalar, 8 July 1970, 2100 m, *J. L. Ellis 34538* (MH; barcode MH00181918), Kalhatti, 27 August 1970, 1900 m, *B. D. Sharma 35801* (MH; barcode MH00181923), Kateryroad, 6 September 1970, 1550 m, *B. D. Sharma 36052* (MH; barcode MH00181924), Rock wood Reserve Forest, 5 August 1975, 1000m, *E. Vajravelu 46543* (MH; barcode MH001928), s.d., 600 ft., *s.c. 6732* (MH; barcode MH00181933), 28 July 1957, 1700 m, *K. M. Sebastine 4067* (MH; barcode MH00181945), Kotagiri, Ooty Road, 8 March 1969, 1900 m, *DB Deb 31506* (MH; barcodes MH00181949, MH00181950), Thia shola to Dodaikumbai, 20 June 1970, 1800 m, *B. N. Shetty 34339* (MH, barcode MH00181951), Nadugani way to powerhouse, 18 October 1972, 700 m, *J. L. Ellis 43226* (MH, barcode MH181996), Samiyarmalai, Ayyamkali Forest, 23 June, 1974, 1000 m, *E. Vajravelu 44926* (MH; barcode MH00181919), Keradamattom, Kodanad, 19 July 1970, 2200m, *E. Vajravelu 34925* (MH; barcode MH00181921). Madras District, upper Tiger shola, 25 March 1957, 1750 m, *s.c. 2661* (MH; barcode MH00181943). Kerala: Kottayam District, Peeramede, 26 September 1964, 1000 m, *K Vivekananthan 21410* (MH, barcode MH00181970), 27 June 1968, 1025 m, *D. B. Deb 30442* (MH, barcode MH00181971). Kottayam District, Thenmala estate, 19 April 1964, 1700 m, *K. M. Sebastine 18325* (MH, barcode MH00181980), Lower Vagavarai to Devicolam, 25 April 1966, *B. V. Shetty 27364* (MH, barcode MH00181953). Malappuram District, Nellumbur, 17 October 1920, *s.c. 6669* (MH, barcode MH00181969). Idukki District, Uppupara, 26 June 1972, 1150 m, *B. D. Sharma 42010* (MH, barcode MH00181968), Vallakadavu, 15 May 1981, 50 m, *M. C. Nair 70220* (MH, barcode MH00181976). Cannore, Chandanathode, 29 April 1975, 840 m, *V. S. Ramachandran 61648* (MH; MH00181956), s.l., 17 August 1929, *R. B. Sharma 6733* (MH; barcode MH00181978).

Elaeocarpus serratus* var. *serratus:—INDIA. Kerala: Kannur District, Aralam, 23 February 2008, *P. S. Udayan, Satheesan George, A. K. Pradeep, N. K. Janardhanan & K Satheesh 04745* (CMPR). Thrissur District, Sholayar, Poorugalla, 12 March 1981, *N. G. Nair 1532* (KFRI), Peechi, Chakkapara, 10 March 1986, 400 m, *N. Sasidharan 3793* (KFRI), Poringalkuth, 14 August 1984, 650 m, *N. Sasidharan 3314* (KFRI), Vellanimala, 11 March 1986, 300 m, *N. Sasidharan 3807* (KFRI). Palakkad District, Attapadi, Chanthampotti, 11 March 1985, 500 m, *N. Sasidharan 3602* (KFRI). Tamil Nadu: Plappally, s.d., *s.c. s.n.*; 537 (MH), s.l., 29 February 1983, *s.c. 77106* (MH), Kilaviyur, 21 February 1983, *s.c. 77106* (MH).

Elaeocarpus serratus* var. *weibelii:—INDIA. Kerala: Thrissur District, Poruningalla, Sholayur, 12 March 1981, *s.c. 1532* (KFRI).

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