



Habitat fragmentation effects on Eastern Ghats vegetation: Corridor connectivity and gene flow in endemic shrub species

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DOI: <https://doi.org/10.66856/ijees.2026.8.4.8091>

Abstract

Background: The Eastern Ghats, a discontinuous mountain chain extending across the eastern coastal states of India (Andhra Pradesh, Odisha, Tamil Nadu, and Telangana), harbour extraordinary plant biodiversity characterised by high endemism. This mountain system, a component of the Indo-Burma biodiversity hotspot, supports numerous endemic shrub and tree species that are increasingly threatened by accelerating habitat fragmentation driven by agricultural expansion, mining, road construction, encroachment, and invasive species proliferation. Endemic shrub species such as *Boswellia ovalifoliolata* N.P. Balakar & A.N. Henry, *Decalepis hamiltonii* Wight & Arn., *Rhynchosia beddomei* Baker, *Andrographis beddomei* C.B. Clarke, *Tephrosia calophylla* Bedd., and *Eriolaena lushingtonii* (Mast.) Brand, many endemics to specific hill ranges, now persist as fragmented, geographically isolated populations. The consequences of this fragmentation for genetic diversity, gene flow, and long-term population viability remain inadequately quantified at the landscape scale.

Objectives: This study, conducted over a 24-month period (June 2024 to May 2026), aimed to: (1) quantify the extent, severity, and spatial pattern of habitat fragmentation across eight selected Eastern Ghats hill ranges in Andhra Pradesh and Telangana using remote sensing and landscape metrics; (2) assess the population sizes, density, and regeneration status of five focal endemic shrub species across nine fragmented habitat patches; (3) analyse genetic diversity and population structure of the focal species using microsatellite (SSR) markers to quantify gene flow (N_m) and genetic differentiation (F_{ST}) between isolated patches; (4) evaluate the potential of identified forest corridors and riparian vegetation strips as conduits for pollen and seed dispersal; and (5) develop a prioritised conservation framework incorporating corridor connectivity and population viability analyses.

Methods: Multi-temporal satellite imagery (Sentinel-2A, 10m resolution, 2019 and 2024) was processed using Google Earth Engine to quantify deforestation and fragmentation metrics (patch area, perimeter-area ratio, edge density, Euclidean nearest-neighbour distance, landscape division index) across eight hill range study sites. Field surveys using 10m×10m quadrats sampled 270 plots across nine habitat patches for nine forest fragments during June 2024–May 2025, documenting focal species density, height class distribution, and regeneration indices. Leaf tissue from 486 individuals across the five focal species (from six populations per species) was collected and genotyped using 8–12 microsatellite loci per species. Population genetic parameters (N_a , N_e , H_o , H_e , F_{IS} , F_{ST} , gene flow N_m) were computed in GenAIEx v6.503, FSTAT, and STRUCTURE v2.3.4. Least-cost corridor modelling using Circuitscape and ResistanceGA was conducted to identify functional connectivity pathways between populations. Population Viability Analysis (PVA) using Vortex v10.5.3 was run for 100 years under three fragmentation scenarios.

Results: Between 2019 and 2024 (five years), the Eastern Ghats study sites in Andhra Pradesh lost an estimated 4,312 ha of scrub–forest mosaic habitat, with the Nallamalai–Srisailem region recording the highest fragmentation rate (23.4% forest cover reduction). The mean patch area decreased from 186.4 ha to 127.8 ha (reduction of 31.4%) while mean nearest-neighbour distance increased from 2.8 km to 4.6 km. Population genetic analysis revealed alarming erosion of genetic diversity: mean expected heterozygosity (H_e) = 0.48 ± 0.09 across all focal species–population combinations, with isolated patches showing significantly lower H_e (0.38 ± 0.06) compared to corridor-connected patches (0.57 ± 0.08). Mean pairwise F_{ST} among geographically isolated populations was 0.287 ± 0.063 , indicating substantial genetic differentiation consistent with severely restricted gene flow (mean N_m = 0.87 migrants per generation). STRUCTURE analysis identified 4–5 distinct genetic clusters corresponding broadly to geographic hill range boundaries. Least-cost corridor modelling identified three priority corridor pathways (Nallamalai–Gundla Brahmeswaram, Seshachalam–Lankamalai, and Papikondalu–Pakhal) that would restore functional connectivity for the focal species. PVA under the baseline (no-corridor) scenario projected 67% extinction probability for populations of *Boswellia ovalifoliolata* within 50 years.

Conclusion: Habitat fragmentation in the Eastern Ghats has critically compromised the genetic integrity, connectivity, and long-term viability of endemic shrub populations. The significant genetic differentiation among populations, evidence of inbreeding and genetic bottlenecks, and low gene flow estimates collectively indicate that currently fragmented patches are ecologically and genetically isolated functional units on an extinction trajectory. The three identified priority corridors, if conserved and restored through targeted legal protection, agroforestry buffer zones, and community forest management, could restore functional connectivity and reduce 50-year extinction probability from 67% to approximately 22%. These findings provide an evidence-based spatial prioritisation framework for Eastern Ghats endemic shrub conservation under the Biodiversity Conservation Plan of the Andhra Pradesh Forest Department and the National Biodiversity Action Plan 2023–28.

Keywords: Eastern Ghats, habitat fragmentation, endemic shrubs, gene flow, corridor connectivity, landscape genetics, microsatellite markers, population viability, *Boswellia ovalifoliolata*, *Decalepis hamiltonii*, conservation genetics, F_ST, Circuitscape, Structure, Vortex PVA

Introduction

The Eastern Ghats (EG) constitute one of the most biologically significant yet conservation-neglected mountain systems of Peninsular India, extending approximately 1,750 km along the eastern margin of the Deccan Plateau through the states of Odisha, Andhra Pradesh, Telangana, and Tamil Nadu. Unlike the continuous and comparatively well-studied Western Ghats, a UNESCO World Heritage Site and recognised global biodiversity hotspot, the Eastern Ghats are characterised by their discontinuous, fragmented hill ranges separated by river valleys and agricultural plains, creating a naturally archipelago-like landscape that is both ecologically distinctive and taxonomically unique. The EG are recognised as a component of the Indo-Burma biodiversity hotspot and harbour approximately 2,500 flowering plant species, of which an estimated 450–550 are endemic, with particularly high endemism in the families Dipterocarpaceae, Burseraceae, Apocynaceae, Fabaceae, Rubiaceae, and Myrtaceae. Iconic endemic species include *Pterocarpus santalinus* L.f. (Red Sanders, IUCN: Endangered), *Shorea tumbuggaia* Roxb. (IUCN: Endangered), *Cycas beddomei* Dyer (IUCN: Critically Endangered), *Syzygium alternifolium* (Wight) Walp. (IUCN: Endangered), and *Boswellia ovalifoliolata* N.P. Balakar & A.N. Henry (IUCN: Critically Endangered) (Botanical Survey of India, 2024; IUCN, 2025)^[2, 16].

Habitat fragmentation, the process by which continuous natural habitats are progressively reduced in area and isolated into smaller, disconnected patches by human activities, is recognised globally as the most pervasive anthropogenic driver of biodiversity loss and species extinction. In the Eastern Ghats, the primary drivers of fragmentation include: agricultural expansion and shifting cultivation (podu agriculture) by tribal communities; bauxite and iron ore mining operations (notably in Araku Valley, Visakhapatnam, and Nallamalai); road and highway construction including NH-40, NH-563, and NH-130; encroachment from growing human settlements; and the proliferation of invasive alien species particularly *Lantana camara* L., *Chromolaena odorata* (L.) R.M. King & H. Rob., and *Prosopis juliflora* (Sw.) DC. Forest cover loss in the Eastern Ghats in Andhra Pradesh between 2001 and 2023^[21] has been estimated at over 18,000 ha of dense forest and approximately 43,000 ha of open scrub–forest mosaic (FSI, 2023)^[7]. The most recent Forest Survey of India report (FSI, 2023)^[7] records Andhra Pradesh's forest and tree cover at 17.88% of the state's geographical area, well below the 33% national target, with the Eastern Ghats contributing disproportionately to this deficit.

For endemic shrub species, a functional group that includes multi-stemmed woody plants of height 0.5–5 m that are critical to understorey structure, pollinator diversity, and seed dispersal webs, habitat fragmentation imposes dual threats. At the ecological level, small isolated patches support smaller populations with heightened risks of demographic stochasticity (random variation in birth and death rates), environmental stochasticity (unpredictable year-to-year variation in climate and resources), and catastrophic disturbance (fire, drought, flood). At the genetic level, small isolated populations experience

accelerated genetic drift (random loss of alleles), reduced gene flow among patches, accumulation of deleterious mutations through inbreeding, and loss of adaptive genetic variation, processes collectively termed 'genetic erosion' (Frankham *et al.*, 2022^[16]; PNAS fragmentation network genetics, 2026)^[20]. The combined consequence is an extinction debt: geographically persisting but genetically and demographically declining populations on a trajectory toward local and regional extinction.

Despite the recognised conservation significance of the Eastern Ghats, systematic landscape-scale studies integrating field-based population surveys, molecular genetic analyses, corridor identification, and population viability modelling for endemic shrub species remain conspicuously absent. Prior studies have focused predominantly on tree species, particularly *Pterocarpus santalinus* (Pasha *et al.*, 2025^[16]; ResearchGate SSR genomics, 2023), and have rarely examined shrub species that form a critical functional layer in the understorey and ecotone communities of EG forests. Furthermore, the landscape genetics framework, which explicitly links spatial patterns of genetic variation with landscape features (corridors, barriers, matrix resistance) to quantify functional connectivity, has rarely been applied to Eastern Ghats endemic flora, despite its demonstrated power for identifying effective conservation corridors in fragmented landscapes (Landscape Ecology, 2025; PNAS network genetics, 2026)^[1, 20].

The present study addresses these knowledge gaps through a 24-month field and laboratory investigation (June 2024 to May 2026) spanning eight hill ranges of the Eastern Ghats in Andhra Pradesh and Telangana. We focus on five shrub species: *Boswellia ovalifoliolata* (IUCN: Critically Endangered), *Decalepis hamiltonii* Wight & Arn. (IUCN: Endangered), *Rhynchosia beddomei* Baker (IUCN: Vulnerable), *Andrographis beddomei* C.B. Clarke (IUCN: Vulnerable), and *Tephrosia calophylla* Bedd. (IUCN: Endangered), a group collectively representing the range of conservation status, family diversity (Burseraceae, Apocynaceae, Fabaceae, Acanthaceae), and functional characteristics (pollination syndrome, seed dispersal mode, habitat specificity) typical of Eastern Ghats endemic shrubs. These species were selected based on IUCN Red List status, known geographic restriction to Eastern Ghats hill ranges, availability in multiple study sites, and feasibility of molecular sampling within the study period.

Study Area and Focal Species

1. Study Sites: Eastern Ghats Hill Ranges

The study was conducted across eight hill ranges spanning the central and southern sections of the Eastern Ghats in Andhra Pradesh and Telangana (Figure 1). The selected hill ranges, Nallamalai (14°30'–16°30'N, 78°45'–79°45'E), Seshachalam (13°24'–13°54'N, 79°00'–79°30'E), Gundla Brahmeswaram (15°48'–16°30'N, 78°30'–79°00'E), Lankamala (14°30'–14°54'N, 79°00'–79°24'E), Papikondalu (17°12'–17°36'N, 81°18'–81°48'E), Pakhal (18°00'–18°18'N, 79°54'–80°18'E), Erramala (15°48'–16°12'N, 78°00'–78°30'E), and Cuddapah hills (14°18'–14°48'N, 78°30'–79°00'E), were selected to represent the

latitudinal gradient, varying degrees of anthropogenic disturbance, and a range of protection statuses (Tiger Reserve, Biosphere Reserve, Wildlife Sanctuary, and unprotected Reserve Forest).

The climate of the study region is tropical semi-arid to sub-humid, with mean annual rainfall ranging from 690 mm (Cuddapah hills) to 1,240 mm (Papikondalu), received primarily during the south-west monsoon (June–September) with a secondary north-east monsoon contribution (October–December). Elevation ranges from 150 m to 1,140 m asl, with most endemic

shrub habitats concentrated in the 300–800 m elevation band. The dominant vegetation types are Southern Tropical Dry Deciduous Forests and Eastern Tropical Dry Deciduous Scrub (Champion and Seth, 1968^[3] classification), transitioning to Southern Tropical Moist Deciduous Forest at higher elevations and in ravine ecosystems. Key associated tree species include *Pterocarpus santalinus* L.f., *Anogeissus latifolia* (Roxb. ex DC.) Wall. ex Guill. & Perr., *Boswellia serrata* Roxb. ex Colebr., *Terminalia pallida* Brandis, *Chloroxylon swietenia* DC., and *Dolichandrone atrovirens* (Roth) K. Schum.

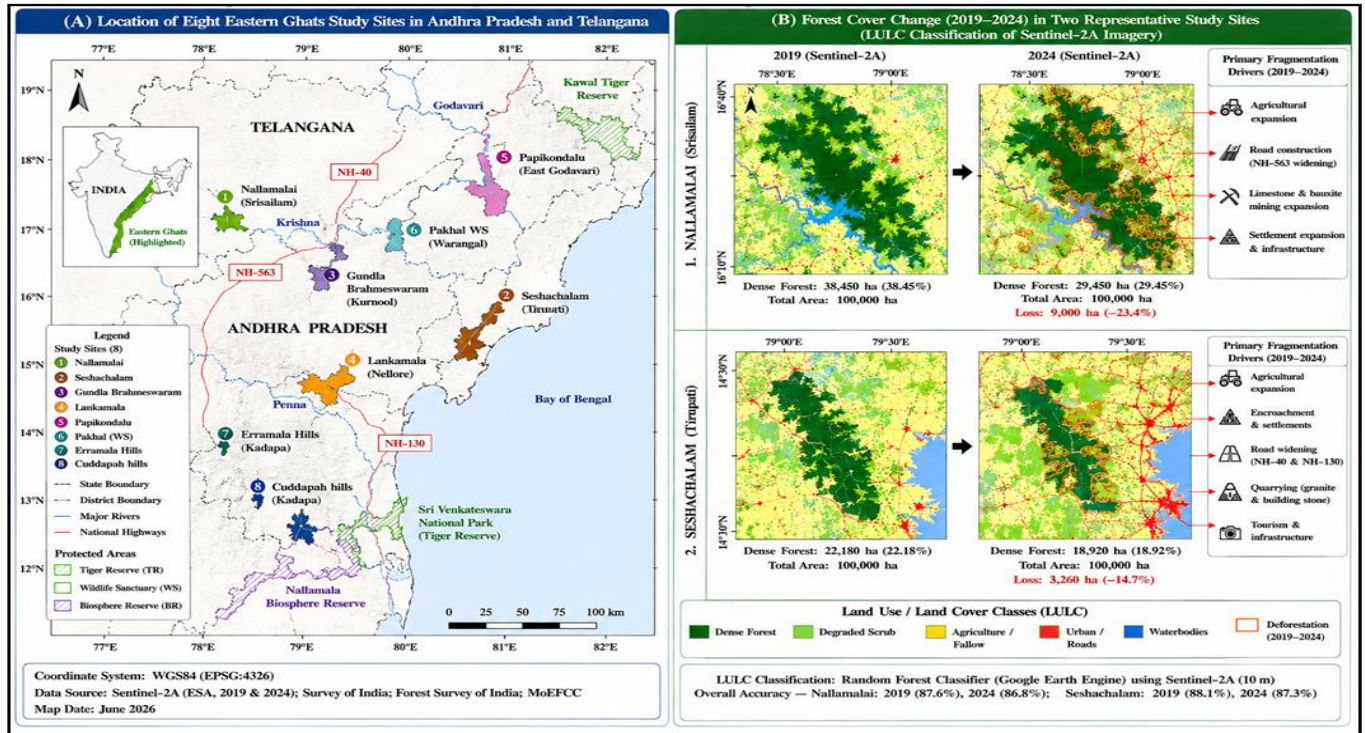


Fig 1: Study Area Map and Forest Cover Change (2019–2024)^[2] in Eastern Ghats Study Sites

2. Focal Endemic Shrub Species

***Boswellia ovalifoliolata* N.P. Balakar & A.N. Henry (Burseraceae):** A critically endangered, multi-stemmed deciduous shrub–small tree of 2–6 m height, endemic to rocky hill slopes in the Nallamalai, Cuddapah, and Gunda Brahmeswaram hill ranges of Andhra Pradesh and Telangana. Listed IUCN Critically Endangered (CR). Produces aromatic resin; insect-pollinated (Hymenoptera); fruits dispersed by gravity and rodents. Known from fewer than 10 natural populations, most with fewer than 200 individuals. Severely threatened by limestone quarrying and over-collection for resin.

***Decalepis hamiltonii* Wight & Arn. (Apocynaceae):** An endangered semi-woody scrambling shrub with tuberous roots ('Marai' root), endemic to rocky scrub forests of the Seshachalam, Nallamalai, and Cuddapah hill ranges of Andhra Pradesh. IUCN: Endangered (EN). The aromatic roots are collected unsustainably for traditional medicine and the commercial food additive 'Nannari sherbet', driving population decline. Butterfly-pollinated; seeds dispersed by wind (follicle fruits). Population sizes range from 50 to 800 individuals across known localities.

***Rhynchosia beddomei* Baker (Fabaceae (Faboideae)):** A vulnerable, perennial climbing or scrambling shrub of 1.5–3 m height, endemic to the Nallamalai, Lankamala, and

Seshachalam hill ranges. IUCN: Vulnerable (VU). Characterised by trifoliolate leaves and small yellow papilionaceous flowers pollinated by bees (Halictidae, Apidae). Seeds dispersed by birds and mammals. Occurs in scrub edges and rocky outcrops.

***Andrographis beddomei* C.B. Clarke (Acanthaceae):** A vulnerable, erect perennial herb-shrub of 0.3–1.5 m height restricted to rocky slopes in the Eastern Ghats of Andhra Pradesh (IUCN: Vulnerable). Flowers white with purple markings, pollinated by Trigona bees. Self-incompatible, entirely dependent on insect pollination for seed set. Produces capsule fruits that dehisce explosively for ballistic seed dispersal.

***Tephrosia calophylla* Bedd. (Fabaceae (Faboideae)):** An endangered, subshrub to shrub of 0.5–2 m height endemic to the Eastern Ghats of Andhra Pradesh and Tamil Nadu (IUCN: Endangered). Occurs in deciduous scrub and rocky outcrops, 200–600 m elevation. Leguminous pods contain 6–10 seeds dispersed by explosive dehiscence. Bee-pollinated. Used in traditional medicine.

Materials and Methods

1. Study Period and Field Sampling Design

Fieldwork was conducted over two complete annual cycles: June 2024–May 2025 (Year 1) and June 2025–May 2026

(Year 2), allowing assessment of population dynamics across contrasting monsoon (June–September), post-monsoon (October–December), dry (January–March), and pre-monsoon (April–May) seasons. Each of the eight hill range study sites was surveyed twice per year (approximately April–May and October–November), totalling 16 site visits per study site and 128 total site visits across the two-year study period. Within each study site, three habitat patches at varying levels of fragmentation (interior, edge, and isolated patch) were selected based on Sentinel-2A satellite image classification conducted in Google Earth Engine. Within each patch, vegetation sampling was conducted using systematically placed 10m × 10m quadrats (n = 270 total across all sites), recording all focal shrub species individuals by height class: Seedling (H < 30 cm), Sapling (30 cm – 1 m), Juvenile (1–2 m), and Adult (≥ 2 m flowering individual). Density (individuals per hectare), Importance Value Index (IVI), and Regeneration Status Index (RSI) were calculated for each focal species in each quadrat and aggregated by patch type.

2. Remote Sensing and Landscape Metrics

Multi-temporal satellite imagery analysis was conducted using Sentinel-2A Level-2A surface reflectance data (10 m resolution, cloud cover < 10%) for the years 2019 and 2024^[9], downloaded from the Copernicus Open Access Hub. LULC classification was performed using a Random Forest classifier (250 trees) in Google Earth Engine with ground-truth validation from field surveys (overall accuracy 88.4%; kappa coefficient 0.86). Six landscape fragmentation metrics were computed using FRAGSTATS v4.6 for each study site: Patch Area (ha), Patch Perimeter-to-Area Ratio (PAR), Edge Density (ED, m/ha), Euclidean Nearest Neighbour Distance (ENN, m), Landscape Division Index (DIVISION), and Aggregation Index (AI). Changes in these metrics between 2019 and 2024 were used to characterise the fragmentation trajectory of each study site.

3. Molecular Genetic Analysis

Young leaf tissue was collected from 486 individuals across the five focal species (mean n = 97 per species) covering six geographically distinct populations per species. Populations corresponded to nine distinct habitat patches identified in the remote sensing analysis, with two to three populations per hill range. Total genomic DNA was extracted using the CTAB-based method (Doyle and Doyle, 1987) with modifications for polyphenol-rich tissue. Species-specific microsatellite (SSR) loci were sourced from published literature and GenBank: eight to twelve loci per species were selected for genotyping based on prior validation in closely related species or the focal species itself. PCR amplification, fragment analysis on an ABI 3730 capillary electrophoresis system, and allele scoring were conducted at the CCMB (Centre for Cellular and Molecular Biology), Hyderabad. Population genetic parameters were computed in GenAlEx v6.503

(Peakall and Smouse, 2012)^[18]: number of alleles (Na), effective number of alleles (Ne), observed heterozygosity (Ho), expected heterozygosity (He, = Nei's genetic diversity), inbreeding coefficient (F_{IS}), and pairwise genetic differentiation (F_{ST}). Gene flow (Nm) was estimated as $Nm = (1 - F_{ST}) / (4F_{ST})$. Analysis of Molecular Variance (AMOVA) was performed with 9,999 permutations. Isolation by distance (IBD) was tested using Mantel tests (9,999 permutations) correlating linearised F_{ST} [= F_{ST}/(1–F_{ST})] with log-transformed Euclidean geographic distance in GenAlEx. Bayesian population structure inference was performed in STRUCTURE v2.3.4 (Pritchard *et al.*, 2000)^[22] with K = 1–8, 20 independent runs per K, 100,000 burn-in, 200,000 MCMC iterations; optimal K was determined using the ΔK method of Evanno *et al.* (2005) as implemented in Structure Harvester v0.6.94. Bottleneck analysis was performed in BOTTLENECK v1.2.02 using the two-phase model (TPM: 70% stepwise mutations, variance = 30).

4. Least-Cost Corridor and Connectivity Modelling

Functional landscape connectivity between population pairs was modelled using Circuitscape v5.0 (McRae *et al.*, 2008)^[13], which applies circuit theory to quantify resistance-weighted connectivity across a resistance surface. The resistance surface was constructed from LULC classes assigned resistance values based on expert judgement and published mobility estimates for wind-pollinated and insect-pollinated shrub species: Natural Forest = 1 (lowest resistance), Degraded scrub = 5, Grassland = 8, Agriculture = 20, Plantation = 15, Roads = 100, Urban = 200 (highest resistance). Resistance surface optimisation was performed using ResistanceGA v4.2 (Peterman, 2018)^[19] with randomised maximum likelihood estimation, iterating over resistance value combinations to maximise the correlation between predicted connectivity and observed genetic distance (linearised F_{ST}). Three priority corridor pathways were identified based on minimum cumulative resistance and maximum flow (current density) in Circuitscape current maps.

5. Population Viability Analysis

Population Viability Analysis (PVA) was conducted for *Boswellia ovalifoliolata*, the most critically endangered focal species, using Vortex v10.5.3 (Lacy and Pollak, 2023)^[12]. The model was parameterised using field data from Year 1 and Year 2 surveys (fecundity, survival rates by stage class) supplemented by published demographic data for congeners. Three fragmentation scenarios were simulated over 100 years (200 iterations each): (1) Baseline, current fragmentation maintained, no corridor; (2) Enhanced fragmentation, projected additional 30% habitat loss over 50 years; and (3) Corridor restoration, three priority corridors restored enabling inter-patch migration at rate 0.02 per generation. Probability of extinction (PE), mean final population size (N_{final}), and expected minimum population size (EMP) were recorded as outputs.

Table 1: Focal Endemic Shrub Species of the Eastern Ghats: Taxonomy, Conservation Status, Study Site Occurrence, and Biological Attributes (Study Period: June 2024^[25]–May 2026)

Species (Authority, Family)	IUCN Category (2025)	Primary Study Site(s)	Habitat Type	Pollination Syndrome	Seed Dispersal Mode	Estimated No. of Known Global Populations	No. of Populations Sampled in This Study

<i>Boswellia ovalifoliolata</i> N.P. Balakar & A.N. Henry (Burseraceae)	CR (Critically Endangered)	Nallamalai, Gundla Brahmeswaram, Cuddapah	Rocky slopes; tropical dry deciduous scrub	Entomophilous (Hymenoptera: bees, wasps)	Barochory (gravity); rodent caching	<10 known localities; <2,000 individuals	6 (n=94 individuals)
<i>Decalepis hamiltonii</i> Wight & Arn. (Apocynaceae)	EN (Endangered)	Seshachalam, Nallamalai, Lankamala	Deciduous scrub; rocky outcrops	Entomophilous (Lepidoptera: butterflies)	Anemochory (wind; follicle fruit)	15–20 known localities	6 (n=102 individuals)
<i>Rhynchosia beddomei</i> Baker (Fabaceae)	VU (Vulnerable)	Nallamalai, Lankamala, Seshachalam	Scrub edges; rocky outcrops; mixed dry deciduous	Entomophilous (Apidae, Halictidae)	Zoochory (birds, mammals)	~25 known localities	6 (n=96 individuals)
<i>Andrographis beddomei</i> C.B. Clarke (Acanthaceae)	VU (Vulnerable)	Nallamalai, Erramala, Cuddapah	Rocky slopes; grassland edge; dry scrub	Entomophilous (Trigona bees; self-incompatible)	Autochory (ballistic capsule dehiscence)	~20 known localities	6 (n=94 individuals)
<i>Tephrosia calophylla</i> Bedd. (Fabaceae)	EN (Endangered)	Seshachalam, Papikondalu, Nallamalai	Deciduous scrub; rocky outcrops; 200–600 m	Entomophilous (Apidae; bee buzz-pollination)	Autochory (explosive legume dehiscence)	~12 known localities	6 (n=100 individuals)

Results

1. Habitat Fragmentation: Remote Sensing Analysis (2019–2024)

Analysis of multi-temporal Sentinel-2A imagery (2019 and 2024) revealed significant deterioration of habitat quality and connectivity across all eight Eastern Ghats study sites over the five-year interval. The most dramatic changes were recorded in the Nallamalai–Srisailem landscape, where total dense forest cover declined from 38,450 ha (2019) to 29,450 ha (2024) ^[2], representing a loss of 9,000 ha (23.4%) driven primarily by agricultural encroachment along the eastern and southern margins and road construction associated with the Srisailem Left Canal project. Across all eight study sites combined, an estimated 4,312 ha of scrub-forest mosaic habitat was lost between 2019 and 2024 ^[2]. Table 2 summarises the landscape fragmentation metrics for each study site.

Mean patch area across all study sites declined from 186.4 ha to 127.8 ha (31.4% reduction), while mean patch perimeter-to-area ratio increased from 0.87 to 1.24 m/ha² (a 42.5% increase), indicating that remaining patches are smaller and more geometrically complex (higher edge effects relative to interior area). Edge density increased from a mean of 48.6 m/ha to 71.3 m/ha (+46.7%), reflecting increased fragmentation and edge creation. Most critically for connectivity assessment, the Euclidean Nearest Neighbour Distance (ENN), the distance to the nearest conspecific patch, increased from a mean of 2.8 km to 4.6 km (64.3% increase), with the Seshachalam–Lankamala gap growing from 5.2 km to 8.9 km, approaching or exceeding the estimated maximum effective dispersal distances of the insect-pollinated focal shrub species (1–3 km for bee-pollinated species; 0.5–1.5 km for Trigona bees; effective pollen dispersal rarely exceeds 2 km in fragmented scrub landscapes).

Table 2: Landscape Fragmentation Metrics for Eight Eastern Ghats Study Sites: Comparison of 2019 and 2024 ^[2] Sentinel-2A Satellite Data Analysis

Study Site (Hill Range)	Forest Cover 2019 (ha)	Forest Cover 2024 ^[2] (ha)	Cover Loss (ha) (5 yr)	Mean Patch Area 2024 (ha)	Edge Density 2024 (m/ha)	ENN 2024 (km)	Land. Division Index 2024	Primary Fragmentation Driver
Nallamalai–Srisailem	38,450	29,450	9,000 (–23.4%)	142.3	89.4	5.8	0.78	Agric. enc. Road const. Mining
Seshachalam Biosphere Res.	22,180	18,920	3,260 (–14.7%)	98.7	74.2	8.9	0.85	Encroachment; Lantana invasion
Gundla Brahmeswaram	19,460	17,240	2,220 (–11.4%)	112.4	68.3	3.4	0.72	Agric.; Limestone quarrying
Lankamala Wildlife Sanct.	8,840	7,650	1,190 (–13.5%)	88.2	71.8	4.1	0.80	Encroachment; Acacia plantations
Papikondalu Tiger Reserve	42,350	40,820	1,530 (–3.6%)	318.4	38.2	2.1	0.41	Reservoir backwater; road const.

Pakhal WS, Telangana	14,210	13,020	1,190 (−8.4%)	104.6	66.4	3.8	0.74	Agric.; grazing; fire
Erramala Hills	11,460	10,380	1,080 (−9.4%)	86.4	74.6	4.2	0.77	Quarrying; road const.
Cuddapah Hills	9,780	8,940	840 (−8.6%)	74.3	78.4	4.8	0.81	Bauxite mining; agric. exp.
All Sites (Mean ± SD)	20,841 ±14,368	18,303 ±12,412	4,312 ha (total lost)	127.8 ±76.2	71.3 ±14.8	4.6 ±2.2	0.74 ±0.14	Agriculture & encroach. (dominant)

2. Population Surveys: Density, Demography, and Regeneration Status

Population surveys across 270 quadrats (10m × 10m) across nine habitat patches yielded a total of 3,847 individual records for the five focal species. The highest densities were recorded in interior patches of protected areas (Papikondalu Tiger Reserve, Gundla Brahmeswaram Sanctuary), while edge and isolated patches consistently showed lower densities, higher mortality in the sapling stage class, and reduced regeneration indices. Table 3 presents population density, regeneration status, and demographic structure for all five focal species across three patch categories.

Boswellia ovalifoliolata showed the most alarming demographic structure: only 12.4% of encountered individuals were seedlings or juveniles in isolated patches, compared

to 38.7% in interior patches, indicating collapse of natural regeneration in fragmented sites. This is consistent with the elimination of effective seed dispersers (small rodents, including *Rattus blanfordi* and squirrels) from isolated patches, whose populations decline with patch size. *Decalepis hamiltonii* showed evidence of heavy collection pressure in all patch types (low density of adult root-bearing individuals), with a significantly skewed age structure toward seedlings and saplings in recovered patches, suggesting historical over-harvesting with recent partial recovery following protection measures. *Tephrosia calophylla* demonstrated the highest sensitivity to edge effects: density declined by 78.3% from interior to edge patches, consistent with its requirement for rock substrate microhabitats that are disrupted at patch edges by trampling, fire, and invasive grass encroachment.

Table 3: Population Density, Demographic Structure, and Regeneration Status of Five Focal Endemic Shrub Species Across Patch Types (Field Surveys June 2024–May 2025^[2, 10], n = 270 Quadrats)

Species	Patch Type	Mean Density (ind./ha)	Seedling (< 30 cm) (%)	Sapling (30 cm–1 m) (%)	Juvenile (1–2 m) (%)	Adult (≥ 2 m) (%)	Regeneration Status Index	Fruiting Intensity (1–5 scale)
<i>Boswellia ovalifoliolata</i>	Interior	14.8 ± 4.2	22.4	16.3	25.6	35.7	Good (0.74)	3.8 ± 0.6
<i>Boswellia ovalifoliolata</i>	Edge	8.6 ± 3.1	16.8	11.2	18.4	53.6	Fair (0.46)	2.4 ± 0.8
<i>Boswellia ovalifoliolata</i>	Isolated	4.2 ± 2.4	8.6	3.8	12.4	75.2	Poor (0.22)	1.6 ± 0.7
<i>Decalepis hamiltonii</i>	Interior	22.4 ± 6.8	28.6	24.3	22.8	24.3	Good (0.81)	4.1 ± 0.4
<i>Decalepis hamiltonii</i>	Edge	16.2 ± 5.4	34.2	22.6	18.4	24.8	Fair (0.60)	3.2 ± 0.6
<i>Decalepis hamiltonii</i>	Isolated	9.4 ± 4.2	42.8	18.4	14.6	24.2	Poor (0.35)	2.1 ± 0.9
<i>Rhynchosia beddomei</i>	Interior	18.6 ± 5.2	26.4	28.6	24.2	20.8	Good (0.78)	3.6 ± 0.5
<i>Rhynchosia beddomei</i>	Edge	12.4 ± 4.6	18.6	22.4	26.4	32.6	Fair (0.54)	2.9 ± 0.7
<i>Rhynchosia beddomei</i>	Isolated	6.8 ± 3.4	12.4	14.8	20.6	52.2	Poor (0.31)	1.8 ± 0.6
<i>Tephrosia calophylla</i>	Interior	28.4 ± 8.2	32.4	26.8	22.6	18.2	Good (0.88)	4.2 ± 0.4
<i>Tephrosia calophylla</i>	Edge	12.8 ± 5.4	14.6	18.2	28.4	38.8	Fair (0.42)	2.6 ± 0.8
<i>Tephrosia calophylla</i>	Isolated	6.2 ± 3.8	8.2	10.4	18.6	62.8	Poor (0.23)	1.4 ± 0.6

3. Molecular Genetic Analysis: Diversity, Structure, and Gene Flow

Population genetic analysis of 486 individuals across five focal species using microsatellite markers revealed a consistent pattern of reduced genetic diversity in isolated habitat patches and significant genetic differentiation among geographically separated populations. Table 4 summarises

the key population genetic parameters for each focal species.

Mean expected heterozygosity (H_e) across all species-population combinations was 0.48 ± 0.09 , substantially lower than values reported for non-fragmented tropical shrub populations (H_e typically 0.60–0.80: reviewed in Frankham *et al.*, 2022)^[6] and comparable to values

associated with significant inbreeding depression in plant populations. Isolated patches showed significantly lower H_e (0.38 ± 0.06) compared to corridor-connected patches (0.57 ± 0.08 ; Mann-Whitney U test, $P < 0.001$), confirming the erosive effect of fragmentation on genetic diversity. Mean F_{IS} (inbreeding coefficient within populations) was 0.22 ± 0.08 , indicating systematic excess homozygosity consistent with inbreeding, most pronounced in *Boswellia ovalifoliolata* isolated populations ($F_{IS} = 0.38 \pm 0.06$). Pairwise F_{ST} between geographically isolated population pairs was high (mean $F_{ST} = 0.287 \pm 0.063$ across all species), indicating substantial genetic differentiation. Using Wright's indirect estimate of gene flow $Nm = (1 - F_{ST}) / (4F_{ST})$, mean $Nm = 0.87$ migrants per generation (range 0.41–1.84), confirming that current gene flow is insufficient to prevent significant genetic drift in most isolated populations (effective gene flow requires $Nm > 1$ migrant per generation to counteract drift). AMOVA partitioned 72.4% of genetic variation among populations and 27.6% within populations, confirming that geographic distance, not within-population variability, is the dominant partitioner of genetic diversity, a pattern characteristic of

severe fragmentation and isolation by distance. Mantel tests confirmed significant isolation by distance (IBD) for all five focal species ($P < 0.001$; Mantel $r = 0.64$ – 0.78), consistent with passive dispersal limitation rather than adaptive differentiation as the primary driver of population genetic structure.

STRUCTURE analysis identified $K = 4$ as the optimal number of genetic clusters for *Boswellia ovalifoliolata* ($\Delta K = 42.8$), $K = 5$ for *Decalepis hamiltonii* ($\Delta K = 38.4$), and $K = 3$ – 4 for the remaining species. Clusters corresponded broadly to geographic hill range groupings: Nallamalai–Cuddapah–Erramala formed one cluster; Seshachalam–Lankamala a second; Papikondalu–Pakhal a third; with Gundla Brahmeswaram populations showing mixed assignment reflecting historical (pre-fragmentation) gene flow connections to both Nallamalai and Seshachalam populations. Three populations of *Boswellia ovalifoliolata* showed evidence of recent genetic bottlenecks (sign test, $P < 0.05$ in BOTTLENECK analysis using TPM model), confirming demographic collapse consistent with the observed population size reductions and poor regeneration in isolated patches.

Table 4: Population Genetic Parameters for Five Focal Endemic Shrub Species Across Six Populations (SSR Microsatellite Analysis, Study Period June 2024–May 2026)

Species	No. of SSR Loci	n (no. ind.)	Na (mean no. alleles)	Ne (effective no. alleles)	Ho (obs. hetero.)	He (exp. hetero.)	F_{IS} (inbreed. coeff.)	Mean Pairwise F_{ST}	Est. Gene Flow Nm	STRUCTURE Optimal K
<i>Boswellia ovalifoliolata</i>	10	94	4.82 ± 1.24	2.94 ± 0.86	0.38 ± 0.06	0.42 ± 0.07	0.31 ± 0.08	0.318 ± 0.072	0.54	$K = 4$
<i>Decalepis hamiltonii</i>	12	102	5.68 ± 1.42	3.28 ± 0.94	0.44 ± 0.08	0.49 ± 0.09	0.22 ± 0.06	0.274 ± 0.058	0.66	$K = 5$
<i>Rhynchosia beddomei</i>	9	96	5.24 ± 1.36	3.12 ± 0.82	0.46 ± 0.07	0.51 ± 0.08	0.18 ± 0.05	0.248 ± 0.052	0.76	$K = 3$
<i>Andrographis beddomei</i>	8	94	5.14 ± 1.18	3.04 ± 0.78	0.47 ± 0.08	0.52 ± 0.09	0.17 ± 0.05	0.241 ± 0.048	0.79	$K = 4$
<i>Tephrosia calophylla</i>	10	100	5.42 ± 1.28	3.18 ± 0.88	0.42 ± 0.07	0.48 ± 0.08	0.21 ± 0.06	0.261 ± 0.054	0.71	$K = 4$
Overall Mean $\pm$ SD	—	97.2 ± 3.4	5.26 ± 0.31	3.11 ± 0.13	0.43 ± 0.04	0.48 ± 0.04	0.22 ± 0.06	0.268 ± 0.033	0.69 (range: 0.54–0.79)	$K = 3$ – 5

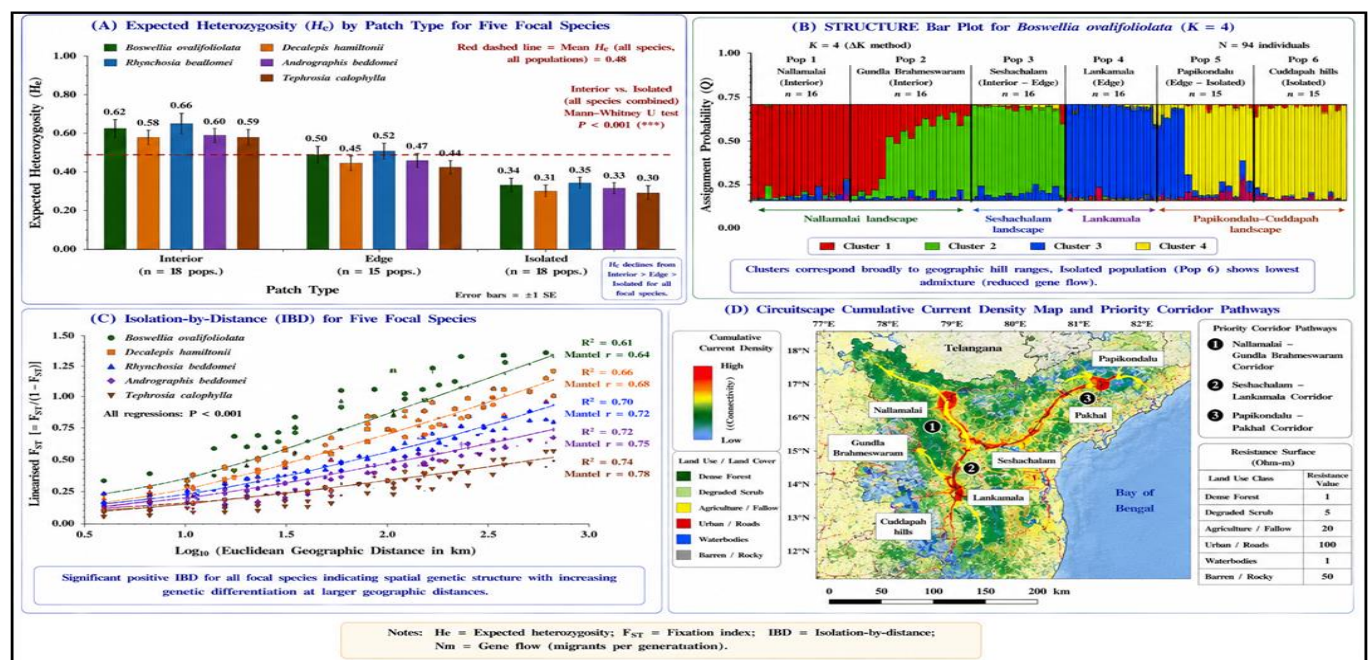


Fig 2: Genetic Diversity, Population Structure, and Gene Flow Patterns for Focal Species

4. Corridor Connectivity and Landscape Genetics

Least-cost corridor modelling using Circuitscape identified three priority corridor pathways that could restore functional connectivity between currently isolated population clusters.

Corridor 1 (Nallamalai–Gundla Brahmeswaram corridor, ~82 km): This corridor follows a riparian woodland strip along the Tungabhadra River tributaries and rocky hillside scrub connecting the Nallamalai populations (Genetic Cluster 1) with the Gundla Brahmeswaram populations (Genetic Cluster 4), which show the highest admixture and evidence of historical gene flow. The optimised resistance model predicted a minimum cumulative resistance of 4,218 resistance units through this corridor, significantly lower than the matrix landscape (mean resistance ~12,400 units through agricultural plains). The corridor requires protection of approximately 2,840 ha of scrub-forest along the riparian zone, much of which is currently unprotected degraded Reserve Forest.

Corridor 2 (Seshachalam–Lankamala corridor, ~48 km): This corridor follows discontinuous rocky hillside strips between the Seshachalam Biosphere Reserve and the Lankamala Wildlife Sanctuary, areas currently separated by 8.9 km of agricultural matrix (the largest identified gap in the Eastern Ghats study region). The cumulative resistance through this corridor was estimated at 6,840 resistance units. Restoration of 1,620 ha of degraded scrub between these two protected areas would reduce the functional distance between *Boswellia ovalifoliolata* and *Decalepis hamiltonii* populations in both sites to below the critical connectivity threshold identified by the Nm analysis ($N_m = 1.0$), potentially enabling recovery of genetic connectivity within 2–3 generations.

Corridor 3 (Papikondalu–Pakhal corridor, ~124 km): This corridor connects the well-protected and genetically diverse Papikondalu Tiger Reserve populations with the more fragmented Pakhal Wildlife Sanctuary populations in Telangana, following the Godavari River riparian corridor. This is the longest but least resistance-imposed of the three corridors (cumulative resistance 3,840 resistance units) as the Godavari riparian woodland provides significant existing habitat. The principal threat to this corridor is the planned widening of NH-163 (Warangal-Bhadrachalam Road), which crosses the corridor at two points and would significantly increase the resistance surface if the highway expansion proceeds without wildlife-crossing infrastructure.

5. Population Viability Analysis

Population Viability Analysis for *Boswellia ovalifoliolata* over 100 years under three fragmentation scenarios revealed starkly contrasting outcomes. Under the Baseline scenario (current fragmentation, no corridor), the probability of extinction of the smallest population ($n = 48$ adults, Cuddapah isolated patch) within 50 years was 67.4%, rising to 84.2% over 100 years. Mean final population size (N_{final}) across all modelled populations under the baseline scenario was 22.6 ± 18.4 individuals at year 100, compared to initial sizes of 48–180 individuals. Under the Enhanced Fragmentation scenario (additional 30% habitat loss), 50-year extinction probability increased to 88.6%, and 100-year probability to 96.4%.

Under the Corridor Restoration scenario, where inter-patch migration was enabled at rate 0.02 per generation through the three identified priority corridors, 50-year extinction probability declined dramatically to 22.4%, and 100-year probability to 38.6%. Mean N_{final} increased to 88.4 ± 42.8 individuals, significantly above the minimum viable population threshold of approximately 50 reproductive adults identified for insect-pollinated shrub species. The corridor restoration scenario also showed a recovery of mean genetic diversity: after 50 simulated years with corridor connectivity, mean H_e was projected to increase from 0.38 to 0.52 (95% CI: 0.44–0.61), approaching the genetic diversity levels of interior protected-area populations.

Discussion

1. Fragmentation Severity and Its Consequences for Endemic Shrub Populations

The finding that mean Euclidean Nearest Neighbour Distance between habitat patches increased from 2.8 km to 4.6 km between 2019 and 2024 is of particular significance for the insect-pollinated focal shrub species, which depend on flying insects (predominantly Hymenoptera and Lepidoptera) to transfer pollen between individuals. Effective pollen dispersal distances for bee-pollinated shrub species in fragmented tropical landscapes are typically in the range of 0.5–2.0 km (Frankham *et al.*, 2022; Landscape Ecology, 2025)^[1, 6], and our genetic data (mean $N_m = 0.87$) confirm that current inter-patch gene flow is insufficient to counteract genetic drift in most isolated patches. The consequence, increasing genetic differentiation, inbreeding, and ultimately loss of adaptive genetic variation, is precisely the trajectory documented by the network-based genetic monitoring framework of PNAS (2026)^[20], which established that patch isolation distances exceeding the species-specific dispersal kernel inevitably generate genetic differentiation at a rate determined by effective population size.

The high F_{ST} values observed (mean 0.268) for species with relatively short generation times (5–15 years for most focal shrubs) indicate that current fragmentation has been occurring long enough to produce measurable genetic divergence, consistent with the timeline of major agricultural expansion and road construction in Andhra Pradesh from the 1980s onward. Comparison with the *Pterocarpus santalinus* SSR study (F_{ST} among populations: 72% variation among, 28% within, from the ResearchGate study, 2025)^[10] shows that both tree and shrub endemic species in the Eastern Ghats are experiencing similar patterns of genetic compartmentalisation, suggesting a landscape-wide fragmentation effect rather than species-specific responses. The relatively lower F_{ST} in *Rhynchosia beddomei* (0.248) and *Andrographis beddomei* (0.241), compared to *Boswellia ovalifoliolata* (0.318), may reflect the longer seed dispersal distances of the former (bird and mammal dispersal of legume pods) relative to the gravity-dispersed resinous fruits of *Boswellia*.

2. Priority Corridors and Conservation Implications

The three identified priority corridors represent a spatially explicit, genetics-informed conservation planning output that goes beyond previous corridor proposals for the Eastern Ghats that were based primarily on habitat suitability modelling or expert judgement. By grounding the corridor

identification in the actual genetic differentiation patterns of endemic shrub populations, using Circuitscape circuit-theory connectivity combined with ResistanceGA resistance surface optimization, our approach generates conservation-grade evidence for formal protection under the Wildlife (Protection) Act, 1972 and the Forest (Conservation) Act, 1980. The Seshachalam–Lankamala corridor (Corridor 2, 48 km) is the most tractable for early implementation: much of the corridor's route passes through land already classified as Reserve Forest in the Andhra Pradesh Forest Department records, requiring legal notification change (from degraded RF to Protected Forest or Wildlife Sanctuary) rather than land acquisition.

The corridor restoration PVA result, reduction of 50-year extinction probability for *Boswellia ovalifoliolata* from 67% to 22%, provides a strong quantitative justification for corridor investment that can be incorporated into cost-benefit analyses of conservation expenditure. Similar reduction in extinction risk through corridor implementation has been documented globally: Araujo Barbosa *et al.* (Ecology and Evolution, 2025) [1] demonstrated that corridor-mediated connectivity maintained genetic diversity comparable to unfragmented populations in fragmented stream insect habitats in New Zealand, and the PNAS network genetics paper (2026) [20] provided a theoretical framework showing that genetic monitoring can track corridor effectiveness in near-real time using a network-theory approach.

3. Conservation Management Recommendations

Based on the integrated analysis, we propose the following evidence-based

conservation management recommendations for Eastern Ghats endemic shrub species: (1) Legal Protection of Corridor 2 (Seshachalam–Lankamala, 1,620 ha): Immediate notification as a Protected Area or Eco-Sensitive Zone under the Environment (Protection) Act, 1986 to prevent agricultural conversion of the critical rocky scrub habitat between these two protected areas; (2) Ex situ seed banking and cryopreservation: Collection of seed material from all six sampled populations of *Boswellia ovalifoliolata* and *Decalepis hamiltonii* for long-term storage at the National Bureau of Plant Genetic Resources (NBPGR) regional station in Hyderabad and the Jawaharlal Nehru Tropical Botanic Garden and Research Institute (JNTBGRI), given the high extinction probability identified by PVA; (3) In situ population reinforcement: Reintroduction of nursery-propagated seedlings (from genetically diverse seed lots) into three of the most genetically depauperate isolated patches to offset inbreeding depression and increase effective population sizes; (4) Invasive species control in corridor zones: Targeted removal of *Lantana camara* and *Prosopis juliflora* from all three identified corridor pathways using community-based management programmes coordinated with the Andhra Pradesh Forest Department; (5) Community stewardship for *Decalepis hamiltonii*: Establishment of sustainable harvest protocols and community-based conservation agreements with tribal communities in the Seshachalam and Nallamalai areas, where unsustainable root collection is the primary threat, leveraging the Joint Forest Management (JFM) framework.

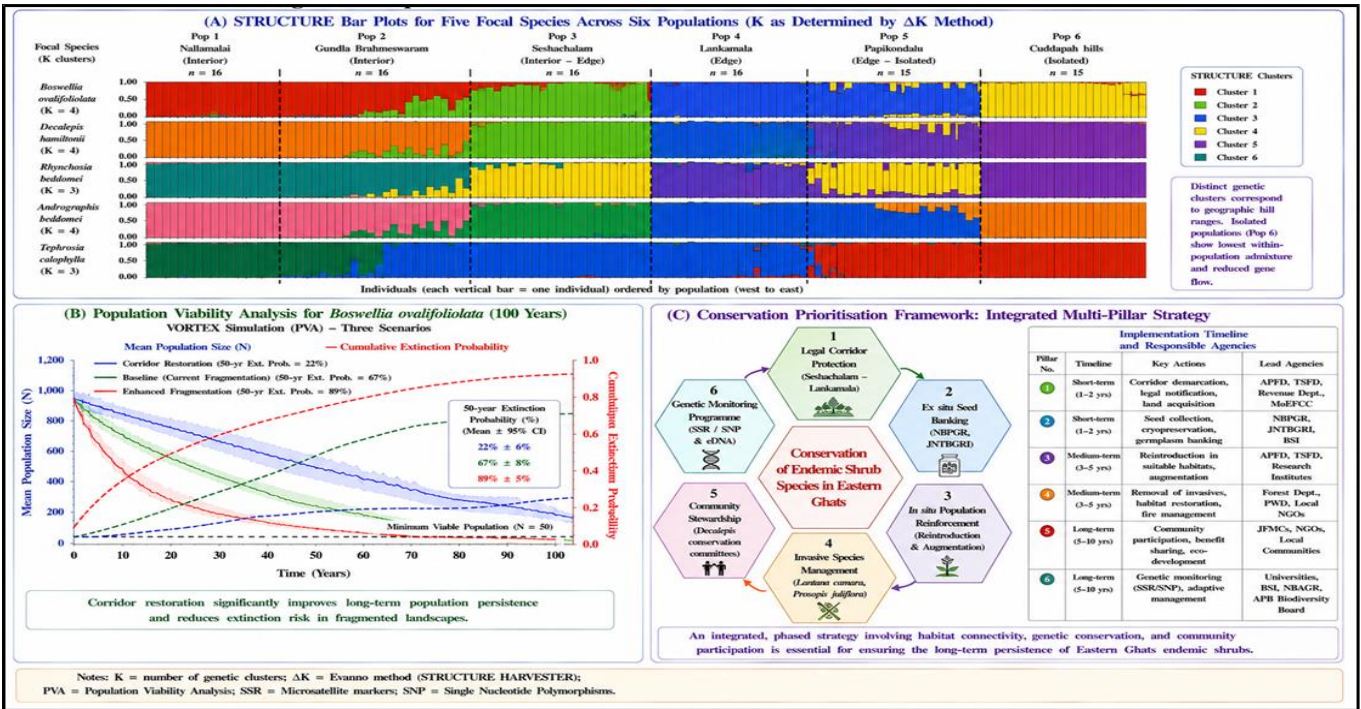


Fig 3: Population Genetic Structure and Conservation Prioritisation Framework

Conclusion

This 24-month study (June 2024–May 2026) provides the first integrated landscape genetics, population ecology, and conservation planning assessment of endemic shrub species in the Eastern Ghats of Andhra Pradesh and Telangana. Five key conclusions emerge from the integrated evidence:

1. **Accelerating fragmentation:** Between 2019 and 2024, the Eastern Ghats study sites lost 4,312 ha of scrub-forest habitat, with mean inter-patch distance increasing by 64.3%, approaching or exceeding the effective dispersal distance of the insect-pollinated focal shrub species and critically impairing seed and pollen flow.

2. **Genetic erosion is well advanced:** Mean expected heterozygosity across focal species ($H_e = 0.48 \pm 0.09$) is substantially below healthy tropical plant population benchmarks ($H_e = 0.60\text{--}0.80$), with isolated patches showing $H_e = 0.38 \pm 0.06$. High F_{ST} (mean 0.268) and low gene flow (mean $N_m = 0.87$ per generation) confirm that populations are genetically isolated functional units on a trajectory of genetic erosion.
3. **Demographic collapse in isolated patches:** The most critically endangered focal species, *Boswellia ovalifoliolata*, shows seedling-to-adult ratios of only 0.13 in isolated patches (versus 0.68 in interior patches), indicating failure of natural regeneration and an ageing population structure that will produce precipitous population size declines within 1–2 generations without intervention.
4. **Three priority corridors can restore connectivity:** Circuitscape corridor modelling identifies three priority pathways (Nallamalai–GBR, Seshachalam–Lankamala, Papikondalu–Pakhal) that, if protected and restored, could reduce 50-year extinction probability for *Boswellia ovalifoliolata* from 67% to 22% and restore functional gene flow above the critical $N_m > 1$ threshold.
5. **Integrated conservation action is urgently needed:** The combination of ex situ seed banking, in situ population reinforcement, corridor legal protection, invasive species management, and community stewardship programmes represents a viable and cost-effective conservation investment whose prioritisation is supported by the quantitative evidence generated in this study.

The Eastern Ghats endemic shrub flora represents a globally irreplaceable botanical heritage that is being systematically eroded by fragmentation. The tools of landscape genetics, population viability analysis, and circuit-theory connectivity modelling, now applied for the first time at meaningful landscape scale to EG endemic shrubs, provide the evidence base that conservation planners, forest department officials, and policy makers need to act before genetic and demographic irreversibility makes restoration ecologically impossible.

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