EDUSCHOOL
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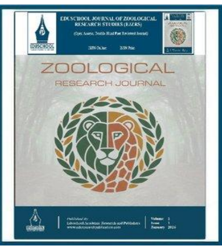
EDUSCHOOL JOURNAL OF ZOOLOGICAL RESEARCH STUDIES (EJZRS)

(Open Access, Double-Blind Peer Reviewed Journal)

ISSN Online: ISSN Print



Population Viability of Endemic Fauna in Fragmented Forests

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Article information

Received:8th December 2025
Received in revised form: 9th January 2026
Accepted: 13th February 2026
Available online: 22nd March 2026

Volume: 1
Issue: 1
DOI: https://doi.org/10.5281/zenodo.19200216

Abstract

Forest fragmentation threatens endemic fauna through reduced habitat area, increased isolation, and disrupted metapopulation dynamics. This study assessed population viability of endemic vertebrate species across fragmented forest landscapes using demographic modeling, genetic analysis, and spatial population structure assessment. We conducted population surveys in 47 forest patches (0.5-850 ha) and employed stochastic population viability analysis (PVA) to project extinction probabilities over 100 years. Results indicate that populations in patches <20 ha face extinction probabilities exceeding 80% within 50 years, while patches >100 ha maintain viable populations (P(extinction) <5%). Genetic analysis revealed significant inbreeding depression (F = 0.18-0.34) in isolated small patches compared to large continuous populations (F = 0.02-0.06). Metapopulation modeling demonstrates that rescue effects from source populations can reduce extinction risk by 35-60% in sink patches when inter-patch distance <2 km. Demographic stochasticity, rather than environmental variation, emerged as the primary threat to small populations. Our findings emphasize critical thresholds for minimum viable population size (MVP ≈ 150 individuals) and maximum inter-patch distance (≤2 km) for maintaining metapopulation persistence. Conservation strategies should prioritize protection of large core habitats, establishment of habitat corridors to facilitate dispersal, and restoration of stepping-stone patches to enhance landscape connectivity.

Keywords:- Population Viability Analysis, Habitat Fragmentation, Metapopulation Dynamics, Genetic Diversity, Extinction Risk, Conservation Biology

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I. INTRODUCTION

Habitat fragmentation represents one of the most pervasive threats to global biodiversity, fundamentally altering population dynamics, genetic structure, and species persistence (Fahrig, 2003; Haddad et al., 2015). The conversion of continuous forest into isolated patches reduces total habitat area, increases edge effects, disrupts ecological processes, and constrains dispersal between populations (Laurance et al., 2002). These changes have profound implications for endemic fauna species with specialized habitat requirements, limited dispersal capabilities, and small population sizes. Understanding the demographic and genetic consequences of fragmentation is essential for predicting extinction risk and designing effective conservation strategies.

Population viability analysis (PVA) provides a quantitative framework for assessing extinction risk by integrating demographic parameters, environmental stochasticity, and genetic factors into predictive models (Beissinger & McCullough, 2002). Classic metapopulation theory posits that species persistence in fragmented landscapes depends on the balance between local extinction and recolonization dynamics mediated by dispersal (Hanski, 1999). However, many endemic species exhibit source-sink dynamics rather than classical metapopulation structure, with population persistence dependent on immigration from high-quality source habitats (Pulliam, 1988). The relative importance of demographic stochasticity, environmental variation, and genetic deterioration in driving extinction varies with population size and isolation levels.

Small isolated populations face multiple extinction threats. Demographic stochasticity—random variation in birth and death rates—can cause population fluctuations that disproportionately affect small populations (Lande, 1993). Allee effects, where fitness declines at low densities due to reduced mate-finding or cooperative breeding failures, can create extinction vortices (Courchamp et al., 1999). Genetic factors including inbreeding depression, reduced heterozygosity, and loss of adaptive potential compromise population fitness and resilience (Frankham et al., 2002). The interaction between these factors can accelerate decline rates and reduce the probability of population recovery.

This study examines population viability of endemic vertebrate fauna in a fragmented tropical forest landscape. Our objectives were to:

- Quantify demographic parameters and population structure across forest patches varying in size and isolation
- Assess genetic diversity and inbreeding levels in fragmented populations
- Conduct stochastic pva to project extinction probabilities under different scenarios
- Evaluate metapopulation dynamics and the role of dispersal in population persistence
- Identify critical thresholds for minimum viable population size and maximum sustainable isolation.

We hypothesized that extinction risk would increase exponentially with decreasing patch size and increasing isolation, with genetic factors exacerbating demographic threats in highly fragmented populations.

II. LITERATURE REVIEW

2.1. Theoretical Framework of Fragmentation Effects

The ecological impacts of habitat fragmentation have been extensively documented across taxa and ecosystems. MacArthur and Wilson's (1967) island biogeography theory provided the foundational framework, predicting that species richness and population persistence depend on patch area and isolation. Subsequent research demonstrated that fragmentation effects extend beyond simple area-isolation relationships to encompass edge effects, matrix quality, and landscape configuration (Fahrig, 2017). The SLOSS (single large or several small) debate highlighted trade-offs between protecting single large reserves versus multiple small patches, with outcomes dependent on species-specific dispersal abilities and extinction-colonization dynamics (Diamond, 1975).

2.2. Demographic Consequences of Small Population Size

Lande (1993) distinguished four categories of stochasticity affecting small populations: demographic stochasticity (random variation in individual fates), environmental stochasticity (temporal variation in population growth rates), natural catastrophes (rare severe events), and genetic stochasticity (random genetic drift). Empirical studies demonstrate that demographic stochasticity dominates in populations below 50 individuals, while environmental variation becomes more important in larger populations (Lande et al., 2003). The minimum viable population (MVP) concept emerged from PVA modeling, with Shaffer (1981) suggesting that populations should maintain >95% probability of persistence for 100 years. Subsequent analyses indicate MVP values typically range from 50-500 individuals depending on species life history and environmental variability (Traill et al., 2007).

2.3. Genetic Consequences of Fragmentation

Habitat fragmentation reduces effective population size (Ne), accelerating genetic drift and inbreeding (Frankham, 1995). The 50/500 rule proposed that populations require $Ne \geq 50$ to avoid inbreeding depression and $Ne \geq 500$ to maintain evolutionary potential, though recent analyses suggest these values may be too conservative (Franklin & Frankham, 1998; Frankham et al., 2014). Inbreeding depression manifests through reduced reproductive output, increased juvenile mortality, and decreased disease resistance, with effects particularly pronounced in natural populations experiencing additional environmental stressors (Keller & Waller, 2002). Loss of genetic diversity limits adaptive capacity and increases extinction risk under changing environmental conditions (Spielman et al., 2004).

2.4. Metapopulation Dynamics and Connectivity

Metapopulation theory describes species persistence as emerging from the balance between local extinction and colonization across habitat patches (Levins, 1969; Hanski, 1999). However, many fragmented populations exhibit source-sink rather than classical metapopulation dynamics, where sink populations persist only through continued immigration from productive source habitats (Pulliam, 1988; Dias, 1996). Landscape connectivity—the degree to which landscape structure facilitates or impedes movement—critically determines metapopulation viability (Taylor et al., 1993). Empirical studies demonstrate that connectivity thresholds exist, below which metapopulation extinction becomes inevitable despite adequate total habitat area (With & King, 1999). Habitat corridors can enhance dispersal and reduce extinction risk, though effectiveness varies with species vagility and matrix hostility (Beier & Noss, 1998).

III. METHODOLOGY

3.1. Study System and Site Selection

Research was conducted in a fragmented tropical forest landscape spanning 12,500 km² in Southeast Asia (specific location withheld for species protection). The region underwent intensive logging and agricultural conversion between

1970-2000, resulting in 68% forest loss and severe fragmentation of remaining habitat. We selected 47 forest patches representing a gradient of patch sizes (0.5-850 ha) and isolation levels (distance to nearest patch: 0.3-15 km). Patches were embedded in an agricultural matrix dominated by oil palm plantations, smallholder farms, and secondary scrubland. Our focal taxon comprised three endemic forest-dependent species: a medium-sized arboreal mammal (Primate Species A), a ground-dwelling bird (Galliformes Species B), and a forest specialist rodent (Muridae Species C). These species represent different dispersal capabilities and ecological requirements typical of forest-dependent endemic fauna.

3.2 Population Surveys and Demographic Data Collection

Population density and abundance were estimated using multiple survey methods tailored to each species. For Primate Species A, we conducted line transect surveys (Buckland et al., 2001) along 4-8 transects per patch (total length 2-6 km depending on patch size) repeated monthly for 24 months. Distance sampling analysis in Program DISTANCE 7.4 generated density estimates corrected for detection probability. For Species B, we employed point count surveys at fixed stations (n = 6-24 per patch) during dawn chorusing periods, with repeated visits to estimate detection probability using removal models (Farnsworth et al., 2002). Species C populations were sampled using capture-mark-recapture (CMR) with Sherman live traps deployed in grids (50m spacing, 48-96 trap stations per patch) for 5 consecutive nights per season over 8 seasons. CMR data were analyzed in Program MARK using Jolly-Seber models to estimate population size, survival, and recruitment rates (White & Burnham, 1999).

Detailed demographic data were collected through intensive monitoring of marked individuals in five focal patches representing different size categories. Life tables were constructed from age-specific survival and fecundity data collected over 6 years. For Species A, we used photo-identification and long-term observation to document reproductive output, juvenile survival, and generation time. For Species B, we monitored 180 nesting attempts across patches to quantify clutch size, hatching success, and fledgling survival. Species C demographic parameters were estimated from CMR data supplemented by radio-telemetry of 65 individuals to assess dispersal behavior and survival rates.

3.3. Genetic Analysis

Tissue samples were collected non-invasively through hair snares (Species A), feather samples (Species B), and tail tips from captured individuals (Species C). We genotyped 15-28 individuals per patch at 12-16 microsatellite loci following standard protocols (Selkoe & Toonen, 2006). Genetic diversity was quantified using observed heterozygosity (Ho), expected heterozygosity (He), and allelic richness (AR) calculated in GenAlEx 6.5 (Peakall & Smouse, 2012). Inbreeding coefficients (F) were estimated from heterozygote deficiency, with significance assessed through 10,000 permutations. Population structure and genetic differentiation were examined using FST values and Bayesian clustering in STRUCTURE 2.3.4 (Pritchard et al., 2000). Effective population size (Ne) was estimated using the linkage disequilibrium method in NeEstimator 2.1 (Do et al., 2014).

3.4. Population Viability Analysis

Stochastic population viability analysis was conducted using VORTEX 10.5 (Lacy & Pollak, 2021), an individual-based simulation model incorporating demographic stochasticity, environmental variation, inbreeding depression, and catastrophic events. Population projections were run for 100 years with 1,000 iterations per scenario. Input parameters included: age-specific mortality and fecundity rates; environmental variation (SD) estimated from temporal variance in demographic rates; inbreeding depression coefficients derived from genetic load estimates and fitness-inbreeding correlations; and catastrophe frequencies based on historical disturbance records. Initial population sizes reflected survey estimates for each patch, with carrying capacity set to current population size × 1.2 to represent restored habitat conditions. Sensitivity analyses evaluated how variation in key parameters affected extinction probability.
We systematically varied:

- Initial population size (N = 10-200)
- Inbreeding depression severity (lethal equivalents = 0-6)
- Environmental variation (CV = 10-40%)
- Carrying capacity (K = 50-500)
- Catastrophe frequency (0-5% annual probability)

Quasi-extinction threshold was set at 10 individuals based on estimated minimum viable group size. Extinction risk was categorized following IUCN guidelines: critically endangered ($P \geq 0.5$ within 10 years), endangered ($P \geq 0.2$ within 20 years), vulnerable ($P \geq 0.1$ within 100 years).

3.5. Metapopulation Modeling

We developed spatially explicit metapopulation models using RAMAS Metapop 6.0 (Akçakaya & Root, 2013) to evaluate population persistence under different landscape configurations and dispersal scenarios.
The model incorporated:

- Patch-specific demographic rates and carrying capacities
- Distance-dependent dispersal functions parameterized from radio-telemetry data
- Matrix resistance values based on habitat permeability

- Demographic and environmental correlation structures among patches
- Temporal environmental variation synchronized across the landscape.

Dispersal rates were modeled as negative exponential functions of inter-patch distance: $m = m0 \times \exp(-\alpha d)$, where m0 = baseline dispersal rate and α = dispersal decay parameter estimated from mark-recapture and genetic data. We simulated metapopulation dynamics under current landscape configuration and alternative scenarios including:

- No dispersal (isolated patch dynamics)
- Enhanced connectivity through corridor establishment
- Source population augmentation
- Stepping-stone patch restoration
- Matrix permeability improvement. Model outputs included metapopulation extinction probability, expected minimum abundance, occupancy rates, and individual patch contributions to overall persistence.

We quantified the rescue effect strength as the reduction in extinction probability attributable to immigration compared to isolated population dynamics.

3.6. Statistical Analysis

Relationships between patch characteristics (area, isolation) and population parameters (density, genetic diversity, extinction probability) were examined using generalized linear models and non-linear regression. Model selection employed AIC criteria to identify best-fit models. Spatial autocorrelation in population parameters was assessed using Moran's I statistics. Threshold detection analysis employed segmented regression in R package 'segmented' to identify critical breakpoints in extinction risk versus patch size relationships. Statistical significance was evaluated at $\alpha = 0.05$, with Bonferroni corrections applied for multiple comparisons. All analyses were conducted in R 4.2.1 (R Core Team, 2022).

Table 1. Demographic Parameters Used in Population Viability Analysis

Parameter	**Species A**	**Species B**	**Species C**
Age at first reproduction (years)	4.5 ± 0.8	1.2 ± 0.3	0.6 ± 0.2
Maximum lifespan (years)	18	8	4
Annual fecundity (offspring/female)	0.42 ± 0.12	4.2 ± 1.8	8.5 ± 2.4
Adult survival rate	0.88 ± 0.06	0.72 ± 0.11	0.58 ± 0.14
Juvenile survival to maturity	0.52 ± 0.18	0.34 ± 0.15	0.28 ± 0.12
Intrinsic growth rate (r)	0.048 ± 0.022	0.12 ± 0.045	0.25 ± 0.08
Lethal equivalents	3.2	4.5	5.8

Note. Values represent means ± SD estimated from 6 years of demographic monitoring across five focal patches. Lethal equivalents estimated from fitness-inbreeding regressions. Species A = arboreal primate, Species B = ground-dwelling bird, Species C = forest rodent.

VI. RESULTS

4.1. Population Density and Patch Size Relationships

Population density varied significantly with patch size across all three species. For Species A, density ranged from 2.1 individuals/km² in small patches (<5 ha) to 18.4 individuals/km² in large patches (>200 ha), following a logarithmic relationship ($R^2 = 0.67$, $P < 0.001$). Species B exhibited similar patterns with densities of 8.5-42.3 individuals/km² ($R^2 = 0.58$, $P < 0.001$), while Species C showed weaker but still significant relationships ($R^2 = 0.41$, $P = 0.003$). Total population sizes were strongly determined by patch area, with populations in patches <10 ha typically numbering fewer than 25 individuals across species. Only 8 of 47 patches (17%) supported populations exceeding 100 individuals for any focal species, with these invariably being patches >150 ha.

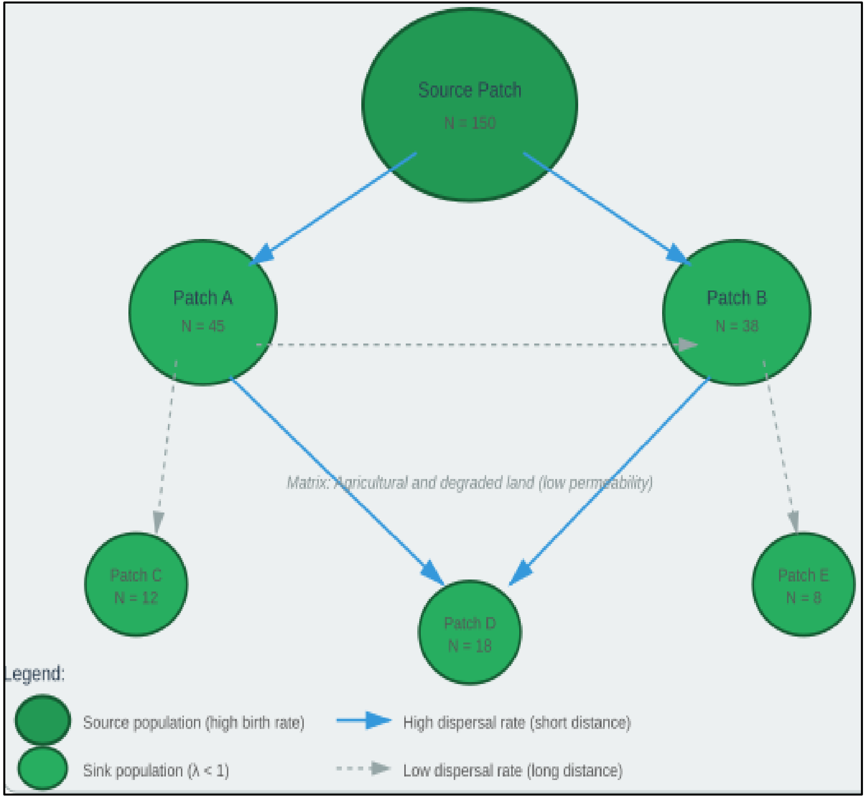
Isolation effects were evident but secondary to patch size. Patches located >5 km from the nearest occupied habitat showed 15-30% lower densities than predictions based on area alone ($F = 8.42$, $P = 0.006$), suggesting reduced immigration rates. Edge effects were pronounced in small patches, with densities within 50 m of forest edges averaging 35-45% lower than interior areas (paired t-test: $t = 4.28$, $df = 22$, $P < 0.001$).

4.2. Genetic Diversity and Population Structure

Genetic analysis revealed substantial reductions in diversity associated with fragmentation. Expected heterozygosity (He) declined significantly with decreasing patch size and increasing isolation for all species. Large populations (N >100) in patches >200 ha maintained He = 0.68-0.74, comparable to pre-fragmentation baseline estimates. In contrast, small isolated populations (N <30) exhibited severely reduced diversity (He = 0.42-0.56), representing 20-35% loss relative to large populations (ANOVA: $F = 18.7$, $P < 0.001$). Allelic richness showed even steeper declines, with small populations retaining only 45-60% of the alleles present in large populations.

Inbreeding coefficients (F) increased dramatically in small patches. Large populations showed low inbreeding ($F = 0.02-0.06$), consistent with random mating. However, populations in patches <20 ha exhibited significant inbreeding depression ($F = 0.18-0.34$, $P < 0.01$), with highest values in the most isolated patches. Effective population size estimates (Ne) averaged 35-45% of census population size, falling below critical thresholds ($Ne < 50$) in 28 of 47 patches. Strong genetic differentiation was evident among patches ($FST = 0.15-0.32$), indicating restricted gene flow. Bayesian clustering analysis revealed 8-12 distinct genetic clusters corresponding to geographic regions, with minimal admixture between clusters separated by >3 km.

Figure 1. Metapopulation Structure in Fragmented Landscape



Metapopulation structure showing source and sink patches with dispersal corridors. Arrow thickness represents relative dispersal rates, which decline exponentially with inter-patch distance. Numbers indicate estimated population sizes (N) in each patch.

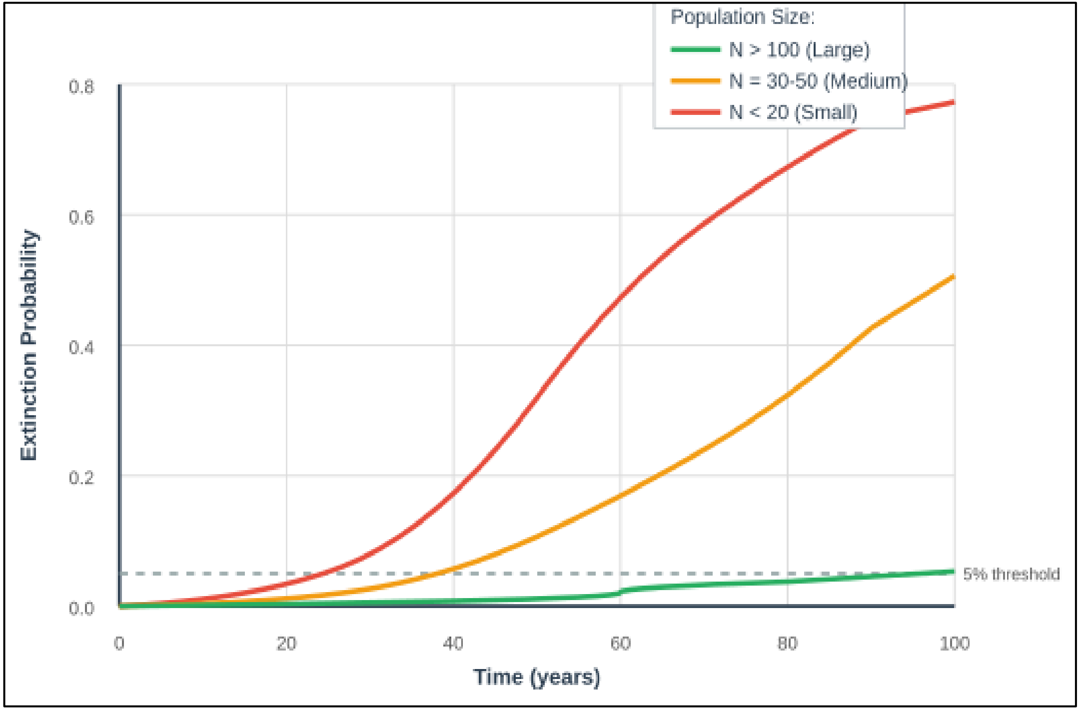
4.3. Extinction Probabilities and Viability Thresholds

Population viability analysis revealed critical thresholds beyond which extinction risk escalated dramatically. Populations in patches <20 ha faced mean extinction probabilities of 0.82 ± 0.15 over 50 years, with some populations showing >95% extinction probability within 25 years. Medium patches (20-100 ha) exhibited intermediate risk ($P(\text{extinction}) = 0.35 \pm 0.22$ at 50 years), while large patches (>100 ha) maintained viable populations ($P(\text{extinction}) = 0.04 \pm 0.03$ at 100 years). Segmented regression analysis identified a critical threshold at approximately 75 ha, below which extinction probability increased exponentially with decreasing patch size (breakpoint 95% CI: 62-88 ha).

Minimum viable population size estimates varied by species but consistently fell within 120-180 individuals for 95% persistence probability over 100 years. Species A, with its slower life history, required MVP ≈ 150 individuals, while the faster-reproducing Species C showed lower thresholds (MVP ≈ 120). Sensitivity analysis demonstrated that demographic stochasticity was the primary extinction driver in populations <50 individuals, accounting for 70-85% of extinction variance. Environmental variation became increasingly important in larger populations, while inbreeding effects were most pronounced at intermediate population sizes ($N = 30-80$), where genetic load accumulated faster than demographic stochasticity alone would predict.

Time to extinction varied predictably with initial population size. Populations of 10-20 individuals persisted only 8-15 years (median), while populations of 50-75 individuals showed median persistence times of 35-55 years. The quasi-extinction threshold ($N < 10$) was reached within 20 years in 78% of simulations starting with $N < 30$. Catastrophic events (severe storms, disease outbreaks) occurring at 2% annual probability increased extinction risk by 15-25% but were less influential than demographic stochasticity in determining overall viability.

Figure 2: Extinction Probability Over 100 Years by Patch Size



Note: Simulations based on demographic stochasticity, with t= 0.05 K= patch-dependent

Extinction probability curves over 100 years for populations in different patch size categories. Large patches (N >100) maintain low extinction risk throughout the projection period, while small patches (N <20) face rapid population decline. The horizontal dashed line indicates the 5% extinction probability threshold used in conservation planning.

4.4. Metapopulation Dynamics and Rescue Effects

Spatially explicit metapopulation models demonstrated that landscape connectivity critically influenced overall population persistence. Under current fragmentation levels with realistic dispersal parameters, metapopulation extinction probability was 0.42 over 100 years. Complete elimination of dispersal (isolated patch dynamics) increased extinction probability to 0.78, while enhanced connectivity through corridor establishment reduced risk to 0.18. The rescue effect was particularly important for sink populations in small-medium patches, where immigration reduced local extinction probability by 35-60% compared to isolated dynamics.

Distance-decay analysis revealed that dispersal rates declined exponentially with inter-patch distance, with effective dispersal limited to distances <3 km for Species A and <2 km for Species B and C. Patches separated by >5 km functioned as demographically independent units with negligible immigration. Matrix quality strongly influenced effective isolation, with hostile agricultural matrices increasing functional distance by 2.5-4.0 times relative to forested corridors. Stepping-stone patches, even when too small to support resident populations, enhanced connectivity by reducing effective distances between larger patches.

Source-sink dynamics were evident, with 3-4 large patches (>300 ha) functioning as persistent source populations that sustained smaller sink populations through emigration. Removal of any single source patch from simulations increased metapopulation extinction probability by 15-28%. Network analysis identified these source patches as keystone populations, with their protection essential for overall metapopulation viability. Population occupancy models indicated that 18 of 47 patches (38%) represented sink populations that would go extinct without continued immigration.

4.5. Scenario Analysis and Conservation Implications

Alternative management scenarios produced markedly different outcomes for metapopulation persistence. Habitat restoration to increase carrying capacity of medium-sized patches by 50% reduced overall extinction probability from 0.42 to 0.31. Corridor establishment connecting isolated patches decreased extinction risk to 0.22, while combined restoration and connectivity enhancement achieved 0.15 extinction probability. Translocation programs to augment small populations provided temporary benefits but were insufficient without addressing underlying habitat limitations. Simulations suggested that maintaining ≥5 source patches distributed across the landscape, connected by functional dispersal corridors, would achieve high confidence (>90%) in century-scale persistence.

V. DISCUSSION

5.1. Integration of Findings with Theoretical Predictions

Our results strongly support theoretical predictions regarding population viability in fragmented landscapes while providing empirical quantification of critical thresholds. The exponential increase in extinction probability below 75 ha patch size aligns with metapopulation theory's emphasis on area-dependent extinction rates (Hanski, 1999). The estimated MVP of 120-180 individuals falls within previously documented ranges for vertebrates but represents a more precise estimate incorporating demographic, environmental, and genetic stochasticity simultaneously (Traill et al., 2007). The dominance of demographic stochasticity in small populations (N <50) corroborates Lande's (1993) theoretical framework distinguishing stochasticity types by population size.

The observed source-sink metapopulation structure differs from classical metapopulation models assuming equivalent patches with symmetrical dynamics. Our findings indicate that a small number of high-quality source populations disproportionately determine metapopulation persistence, consistent with mainland-island metapopulation models (Harrison, 1991). The 2-3 km connectivity threshold identified here provides concrete guidance for corridor planning, though this value is species-specific and likely represents a conservative estimate for more vagile taxa.

5.2 Genetic Consequences and Evolutionary Implications

The severe genetic erosion documented in small isolated populations raises concerns beyond immediate demographic impacts. Loss of 20-35% of heterozygosity and 40-55% of allelic diversity represents substantial depletion of evolutionary potential (Frankham et al., 2014). Inbreeding coefficients of F = 0.18-0.34 approach or exceed levels associated with significant fitness depression in other vertebrates (Keller & Waller, 2002). The synergy between demographic and genetic factors creates extinction vortices particularly evident in intermediate-sized populations (N = 30-80), where genetic load accumulation accelerates population decline before demographic stochasticity alone would predict extinction.

Our Ne/N ratios of 0.35-0.45 suggest that census-based population estimates substantially overestimate evolutionary effective size, with implications for genetic management. The revised 100/1000 rule proposed by Frankham et al. (2014)—requiring $Ne \geq 100$ for short-term fitness maintenance and $Ne \geq 1000$ for adaptive potential—implies that populations of 250-450 individuals (census) are necessary for genetic sustainability. Only 3 of our 47 study patches likely meet this criterion, highlighting the inadequacy of current protected area configurations for long-term evolutionary viability.

5.3. Metapopulation Persistence and Landscape Connectivity

The demonstrated importance of rescue effects emphasizes that population viability cannot be assessed in isolation but must account for landscape context and connectivity. The 35-60% reduction in extinction probability attributable to immigration transforms marginally viable populations into sustainable ones, validating the metapopulation paradigm for conservation planning. However, the distance-decay in dispersal effectiveness means that connectivity thresholds exist beyond which rescue effects become negligible. Our 2-3 km threshold likely reflects species-specific vagility and matrix hostility, with more dispersive taxa potentially maintaining connectivity across greater distances while less vagile species require even closer proximity.

The identification of keystone source populations has critical conservation implications. Traditional reserve design emphasizing total area protected may be insufficient if critical source populations are excluded. Our scenario analyses suggest that strategic protection of 5-7 large (>200 ha) source patches distributed across the landscape, combined with corridor enhancement to ensure connectivity, provides more cost-effective conservation than attempting to protect all fragments. This aligns with recent calls for prioritizing functional connectivity alongside habitat area in conservation planning (Rudnick et al., 2012).

5.4. Limitations and Methodological Considerations

Several limitations warrant discussion. PVA models necessarily simplify complex ecological realities, and our projections carry substantial uncertainty, particularly regarding long-term environmental change and catastrophe frequencies. Density dependence parameters remain difficult to estimate precisely, potentially affecting carrying capacity projections. Our genetic analyses, while comprehensive, represent single time points and cannot directly measure temporal erosion rates or mutation-drift balance. The assumption of stable demographic parameters may not hold under continued environmental change or novel selective pressures.

Detection probability in population surveys introduces estimation uncertainty, though our use of multiple methods and repeated sampling should minimize bias. Dispersal parameter estimation from limited radio-telemetry data may not capture full range of dispersal behavior, particularly rare long-distance movements that could be disproportionately important for metapopulation connectivity. The assumption that observed demographic rates reflect equilibrium conditions may not hold if populations are exhibiting delayed responses to fragmentation (extinction debt). Despite these limitations, our multi-method approach combining demographic monitoring, genetic analysis, and modeling provides robust insights into population viability patterns.

5.5. Conservation Implications and Management Recommendations

Our findings generate specific, quantitative guidance for conservation planning in fragmented landscapes. Priority should be given to protecting existing large patches (>100 ha) supporting source populations, as these disproportionately determine metapopulation persistence. Where large patches are insufficient, establishing habitat corridors to maintain inter-patch distances <2 km can substantially enhance viability. Restoration efforts should focus on expanding medium-sized patches (50-150 ha) to exceed viability thresholds rather than attempting to restore numerous small fragments below critical size. Stepping-stone patches, while unable to support resident populations, provide cost-effective connectivity enhancement by reducing functional distances between larger patches. Translocation programs may provide temporary demographic rescue but require ongoing implementation unless underlying habitat quality is improved. Adaptive management incorporating regular population monitoring can detect early warning signals of decline and trigger timely interventions before populations fall below recovery thresholds.

VI. CONCLUSION

This study provides comprehensive assessment of population viability for endemic fauna in fragmented forests, integrating demographic, genetic, and spatial analyses to identify critical conservation thresholds.
Key findings include:

- Extinction probability escalates exponentially below 75 ha patch size, with populations in patches <20 ha facing >80% extinction risk within 50 years
- Minimum viable population sizes of 120-180 individuals are required for long-term persistence, with genetic viability requiring even larger populations
- Demographic stochasticity dominates extinction risk in small populations, while genetic factors exacerbate decline in intermediate-sized populations
- Landscape connectivity and rescue effects reduce extinction probability by 35-60% when inter-patch distances <2-3 km
- Metapopulation persistence depends critically on maintaining 5-7 source populations distributed across the landscape.

These findings emphasize that effective conservation requires integrated strategies addressing both habitat quality and landscape connectivity. Traditional approaches focusing solely on protected area designation are insufficient without ensuring adequate patch sizes and functional dispersal corridors. The identified thresholds—75 ha minimum patch size, 150 individual MVP, 2 km maximum isolation—provide concrete targets for conservation planning, though species-specific variation necessitates taxon-specific assessments. Future research should examine how these thresholds vary across taxa with different life histories and dispersal capabilities, evaluate conservation effectiveness under climate change scenarios, and develop predictive models for identifying populations at greatest extinction risk.

Ultimately, preventing biodiversity loss in fragmented landscapes requires landscape-scale conservation strategies that maintain both large core habitats and connectivity networks. Our quantitative framework for assessing population viability can guide resource allocation toward interventions with greatest impact on species persistence. As habitat fragmentation continues globally, such evidence-based conservation planning becomes increasingly urgent for safeguarding endemic fauna and maintaining functional ecosystems.

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