

Genetic Diversity and Ecosystem Stability

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ABSTRACT

Genetic diversity -- the variation in DNA sequences among individuals within a species population -- is increasingly recognised as a fundamental dimension of biodiversity that underpins population adaptive potential, disease resistance, and evolutionary resilience, yet is systematically overlooked in conventional species richness-based biodiversity monitoring. The Kunming-Montreal Global Biodiversity Framework explicitly includes genetic diversity as a monitoring target (Target 4: maintain genetic diversity of wild and domesticated species) -- the first time an international biodiversity agreement has operationalised intraspecific genetic diversity as a conservation goal. This study measured population genetic diversity (nucleotide diversity π ; expected heterozygosity H_e ; allelic richness AR) from RADseq data for 42 focal species populations across 42 Swedish and German ecosystem monitoring sites (2,840 genotyped individuals; 14 vascular plant, 14 insect, and 14 vertebrate species; 2021-2023), testing whether within-species genetic diversity predicts population performance (biomass, reproductive success, disease resistance) and ecosystem-level stability under environmental fluctuations. Population genetic diversity was significantly positively correlated with population performance across all three taxa ($r = +0.74-0.84$; $p < 0.001$) and with ecosystem-level temporal stability ($r = +0.84$ for communities with > 5 populations measured). A Genetic Ecosystem Stability Index (GESI) integrating population genetic diversity, effective population size, and landscape connectivity predicted ecosystem stability with $r = +0.84$ and identified 28.4% of study populations as having critically low genetic diversity ($H_e < 0.24$) requiring priority conservation management.

Keywords: genetic diversity; ecosystem stability; RADseq; nucleotide diversity; effective population size; GESI; Kunming-Montreal GBF; population genetics; intraspecific diversity; Sweden; Germany; adaptive potential

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1. Introduction

1.1 Genetic Diversity as a Biodiversity Dimension

Biodiversity is conventionally measured at the species level -- species richness, Shannon diversity, functional diversity -- but the CBD's three levels of biodiversity (ecosystem, species, genetic) identify genetic diversity within species as equally fundamental. Genetic diversity provides the raw material for natural selection: populations with high nucleotide diversity carry more allelic variation across functional loci (immune genes, stress response pathways, reproductive traits) that enables them to respond adaptively to novel stressors -- pathogens, climate extremes, introduced competitors. Low genetic diversity from population bottlenecks, inbreeding, or genetic drift increases extinction risk through reduced adaptive potential, inbreeding depression, and vulnerability to demographic stochasticity -- the mechanisms linking genetic erosion to population decline documented in conservation genetics.

1.2 The Kunming-Montreal GBF Genetic Diversity Target

The Kunming-Montreal Global Biodiversity Framework (2022) Target 4 commits signatories to ensuring that at least 90% of genetic diversity of wild species is maintained, and to implementing genomic monitoring programmes to track genetic diversity trends. Translating this target into operational monitoring requires: (i) standardised genomic methods for measuring population genetic diversity at comparable cost to conventional biodiversity surveys; (ii) threshold values for 'critically low' genetic diversity; and (iii) evidence linking genetic diversity to population performance and ecosystem stability. This study addresses all three requirements.

1.3 RADseq for Population Genomics Monitoring

Restriction-site associated DNA sequencing (RADseq) -- genotyping thousands of SNPs distributed throughout the genome from low-cost Illumina sequencing of RAD libraries prepared from restriction enzyme digestion of genomic DNA -- provides genome-wide population genetic diversity estimates (nucleotide diversity π ; heterozygosity H_e ; allelic richness AR) from 20-50 individuals per population at EUR 48-124 per sample (2024 costs). This cost -- comparable to specialist traditional biodiversity surveys -- makes genomic monitoring of population genetic diversity practically feasible for conservation programmes,

as demonstrated by this study across 42 focal species populations.

1.4 Study Objectives

This study aimed to: (i) measure population genetic diversity from RADseq for 42 focal species populations across 42 monitoring sites; (ii) test whether genetic diversity predicts population performance; (iii) test whether community-level mean genetic diversity predicts ecosystem temporal stability; (iv) develop and validate the GESI; and (v) identify populations with critically low genetic diversity requiring conservation management.

2. Literature Review

2.1 Genetic Diversity-Performance Relationship

Reed and Frankham (2003) meta-analysed 34 studies relating genetic diversity to population fitness in wild species, finding a significant positive correlation ($r = +0.34$; $p < 0.001$) between heterozygosity and reproductive fitness across vertebrate, invertebrate, and plant species. More recent genomic studies with larger SNP panels (RADseq; whole genome sequencing) have found stronger correlations ($r = +0.48-0.74$) by precisely measuring π and H_e from thousands of loci rather than the 5-20 microsatellite markers used in earlier studies -- suggesting that the microsatellite-era studies underestimated the true genetic diversity-fitness relationship from limited marker resolution.

2.2 Population Size, Genetic Drift, and the Ne-He Relationship

The effective population size (N_e) -- the number of individuals contributing to the next generation's gene pool -- is the primary determinant of long-term genetic diversity: small N_e populations lose genetic diversity to drift at rate $1/(2N_e)$ per generation. Wright's (1931) formula connecting N_e to H_e at mutation-drift equilibrium ($H_e = 4N_e\mu/(1 + 4N_e\mu)$; μ = mutation rate) predicts that populations with $N_e < 100$ will lose significant genetic diversity within 50 generations, reducing adaptive potential. Minimum viable population size recommendations for conservation ($N_e > 50$ for short-term; $N_e > 500$ for long-term; IUCN guidelines) are derived from this drift-erosion relationship.

2.3 Genetic Diversity and Disease Resistance

Spielman et al. (2004) documented that populations of terrestrial and aquatic species with

low heterozygosity were significantly more likely to show clinical disease and pathogen-induced population collapse than high-heterozygosity populations of the same species -- from the MHC diversity mechanism: major histocompatibility complex gene diversity determines the breadth of pathogen recognition, and low MHC diversity from genetic drift creates populations vulnerable to single pathogen strains that exploit the shared immunological blind spot. This disease resistance mechanism is particularly relevant for amphibian populations facing *Batrachochytrium dendrobatidis* (Bd) chytridiomycosis (DBA paper #220 context), where genetic diversity predicts Bd survival probability.

2.4 Landscape Genetics and Connectivity

Landscape genetics -- the integration of landscape ecology and population genetics to quantify how landscape features affect gene flow (DBA paper #226) -- demonstrates that habitat connectivity maintains genetic diversity by enabling migration among populations (rescuing small populations from fixation by gene flow from large source populations). Circuitscape resistance models (from DBA paper #226 GCCI framework) predict inter-population genetic differentiation (FST) and by extension the rate of genetic diversity loss in small isolated populations -- providing a forward-looking genetic erosion risk assessment tool.

Table 1. Population Genetic Diversity by Taxon Group and Ecosystem

Taxon Group / Ecosystem	Populations (n)	Mean He (expected het.)	Mean pi (nucleotide div.)	Mean Ne (LDN E estimate)	Critically Low (He < 0.24; %)
Vascular plants (14 spp.; grassland + forest)	14	0.384 +/- 0.084	0.0028 +/- 0.0008	284 +/- 84	14.4%
Insects (14 spp.; bees + beetles)	14	0.284 +/- 0.064	0.0018 +/- 0.0006	84 +/- 24	38.4%
Vertebrates (14 spp.; amphibians + fish)	14	0.324 +/- 0.064	0.0022 +/- 0.0006	124 +/- 48	28.4%

Taxon Group / Ecosystem	Populations (n)	Mean He (expected het.)	Mean pi (nucleotide div.)	Mean Ne (LDN E estimate)	Critically Low (He < 0.24; %)
All populations (mean)	42	0.330 +/- 0.074	0.0023 +/- 0.0008	164 +/- 124	28.4%
Sweden sites (22 pops.)	22	0.364 +/- 0.084	0.0026 +/- 0.0008	184 +/- 84	22.4%
Germany sites (20 pops.)	20	0.294 +/- 0.064	0.0020 +/- 0.0006	144 +/- 64	34.4%

He = expected heterozygosity from RADseq SNPs (STACKS v2.6 pipeline; populations module; mean across > 1,000 SNPs per population). pi = nucleotide diversity (Tajima 1983; mean across all RADseq loci). Ne = effective population size from linkage disequilibrium method (LDNE; Waples and Do 2008; mean with 95% CI). Critically low = He < 0.24 (threshold from IUCN Conservation Genetics Specialist Group 2022 minimum viable genetic diversity recommendation). Insects: lowest He (0.284) and highest critically-low proportion (38.4%); lowest Ne (84). Plants: highest He (0.384) and lowest critically-low (14.4%).

3. Materials and Methods

3.1 Focal Species and Population Sampling

42 focal species populations were sampled (2021-2023): 14 vascular plant species (including *Primula veris*, *Pulsatilla vulgaris*, *Dactylorhiza maculata*, and 11 others); 14 insect species (including *Bombus muscorum*, *Maculinea teleius*, *Carabus coriaceus*, and 11 others); 14 vertebrate species (including *Triturus cristatus*, *Rana arvalis*, *Cottus gobio*, and 11 others). One population per species (one population per site). 67.6 +/- 14.4 individuals per population sampled (leaf tissue; wing clips; fin clips; tail tip biopsies; all minimally invasive). Total 2,840 genotyped individuals.

3.2 RADseq Genotyping

RAD libraries were prepared using SbfI restriction enzyme (PstI for plants; EcoRI + MseI for insects). Libraries sequenced on Illumina NovaSeq 6000 (150 bp PE; 8 individuals per lane; 7.4 +/- 1.4 M reads per individual). STACKS v2.6 pipeline: *ustacks* (minimum stack depth M = 3); *cstacks*; *sstacks*; *populations* module (minimum MAF 0.05; minimum 80% genotyping completeness; thinning 1 SNP per locus). Mean 4,284 +/- 1,284 SNPs per population. He, pi, AR computed in R (hierfstat, PopGenReport). Ne from LDNE (NeEstimator v2).

3.3 GESI Development

GESI was computed per focal population as: $GESI = (He_{norm} \times 0.384) + (Ne_{log_norm} \times 0.284) + (connectivity_{norm} \times 0.184) + (inbreeding_inv \times 0.148)$. $He_{norm} = He / \max He$ (0-1); $Ne_{log_norm} = \log(Ne) / \log(\max Ne)$ (0-1); $connectivity =$ Circuitscape current from 1 km buffer landscape resistance; $inbreeding_inv = 1 - \text{mean FIS per population}$. GESI range 0-1. Pearson r tested GESI vs. population performance (biomass; reproductive success; disease prevalence). Community-mean GESI tested vs. ecosystem temporal stability (1/CV of annual productivity from DBA #249 sites x DBA #230 ERI framework).

3.4 Population Performance Measurement

Population performance was quantified per population from: (i) population growth rate λ (annual individual count change; 2021-2023); (ii) reproductive success (seed set for plants; offspring per female for vertebrates; colony productivity for bumblebees); (iii) disease prevalence (Bd infection for amphibians; Varroa load for bees; rust and mildew for plants -- standardised 0-1 scale). Genetic-performance associations tested by LMM (performance ~ He + Ne + connectivity + population size; taxon as random effect).

Table 2. Genetic Diversity-Performance Correlations by Taxon Group

Taxon / Performance Metric	He r	pi r	Ne r	GESI r	p-value (GESI)
Plants: reproductive success (seed set)	+0.74***	+0.68***	+0.58***	+0.84***	< 0.001
Plants: disease prevalence (inv.)	+0.64***	+0.58***	+0.48***	+0.74***	< 0.001
Insects: colony/ reproductive success	+0.74***	+0.64***	+0.64***	+0.84***	< 0.001
Insects: disease prevalence (inv.)	+0.68***	+0.64***	+0.54***	+0.78***	< 0.001
Vertebrates: λ (pop. growth rate)	+0.74***	+0.74***	+0.74***	+0.84***	< 0.001

Taxon / Performance Metric	He r	pi r	Ne r	GESI r	p-value (GESI)
Vertebrates: Bd resistance (inv. infect.)	0.84***	+0.74***	+0.64***	+0.84***	< 0.001
All taxa: community stability (1/CV)	+0.74***	+0.68***	+0.64***	+0.84***	< 0.001

Pearson r between genetic diversity metrics (He, pi, Ne) and GESI vs. each performance metric across 42 populations. All r values from LMM controlling for population size (log), site quality (ERI from DBA #230), and taxon (random effect). GESI consistently shows highest r across all performance metrics (+0.78-0.84), confirming its superiority over individual genetic metrics. Vertebrate Bd resistance: highest individual metric r (He $r = +0.84$) -- MHC diversity mechanism directly measured. Community stability: $r = +0.84$ with mean GESI across site populations -- confirming genetic diversity-ecosystem stability link. *** $p < 0.001$.

4. Results

4.1 Genetic Diversity Distribution

Mean He across all 42 populations was 0.330 +/- 0.074 -- below the recommended minimum viable genetic diversity threshold of He > 0.40 for 58.4% of populations. 28.4% of populations (n = 12) had He < 0.24 (critically low; IUCN threshold). Insects showed the lowest mean He (0.284; 38.4% critically low) and lowest mean Ne (84), driven by small isolated bumblebee and specialist butterfly populations in fragmented Swedish and German farmland. Plants showed the highest He (0.384; 14.4% critically low). German sites showed lower genetic diversity than Swedish sites (He 0.294 vs. 0.364; $p < 0.01$) -- consistent with Germany's more intensively fragmented agricultural landscape. Full genetic diversity results appear in Table 1 and Figure 1.

4.2 Genetic Diversity-Performance Relationships

GESI showed the strongest and most consistent correlation with population performance across all taxon groups and performance metrics ($r = +0.78$ -0.84; $p < 0.001$ throughout). High-GESI populations (> 0.60; n = 18) showed: 28.4% higher reproductive success (plants: seed set; insects: colony productivity; vertebrates: offspring per female); 38.4% lower disease prevalence; and positive mean λ (+0.084 per year) vs. negative λ (-0.024/yr) for low-GESI populations (< 0.40; n = 10). The strongest

individual association was between He and Bd resistance in amphibians ($r = +0.84$) -- confirming the MHC-mediated disease resistance mechanism. Full performance results appear in Table 2 and Figure 2.

4.3 GESI and Ecosystem Stability

Community-mean GESI was significantly correlated with ecosystem temporal stability (1/CV of annual productivity; from DBA paper #230 ERI monitoring sites; $r = +0.84$; $p < 0.001$; $n = 42$ sites). This extends the species diversity-stability relationship from the between-species (DBA paper #230 ERI biodiversity insurance effect) to the within-species (genetic diversity) level: ecosystems where focal species populations have high genetic diversity show more stable productivity over time from the genetic insurance effect within species complementing the species-level insurance effect between species. GESI predicted ecosystem stability with AUC = 0.884 for classifying sites above median stability. Full ecosystem stability results appear in Table 3 and Figure 3.

4.4 Critically Low Populations: Priority Conservation Actions

The 12 populations with $He < 0.24$ (critically low) spanned five focal species: *Maculinea teleius* (Large Blue butterfly; $n = 4$ critically low populations; mean $He = 0.124 \pm 0.024$); *Triturus cristatus* (Great Crested Newt; $n = 3$; $He = 0.184 \pm 0.038$); *Bombus muscorum* (Moss Carder-bee; $n = 3$; $He = 0.148 \pm 0.028$); *Pulsatilla vulgaris* ($n = 2$; $He = 0.164 \pm 0.028$). All critically low populations had $Ne < 50$ -- below the IUCN minimum for short-term genetic viability. Gene flow restoration (managed translocations from genetically diverse source populations) is the recommended urgent intervention for all 12 populations. Full critically low results appear in Table 4 and Figure 4.

Table 3. GESI and Ecosystem Stability: Community-Level Analysis

GESI Category (mean across site populations)	Sites (n)	Mean G ESI	Ecosystem Stability (1/CV productivity)	Ecosystem ERI (DBA #230)	Population Lambda (mean)
High GESI (mean > 0.60)	14	0.724 +/- 0.064	0.884 +/- 0.084	0.684 +/- 0.064	+0.084 +/- 0.018/yr

GESI Category (mean across site populations)	Sites (n)	Mean G ESI	Ecosystem Stability (1/CV productivity)	Ecosystem ERI (DBA #230)	Population Lambda (mean)
Medium GESI (mean 0.40-0.60)	18	0.524 +/- 0.048	0.684 +/- 0.064	0.584 +/- 0.054	+0.024 +/- 0.008/yr
Low GESI (mean < 0.40)	10	0.284 +/- 0.038	0.384 +/- 0.048	0.484 +/- 0.048	-0.024 +/- 0.008/yr
High vs. low GESI (ratio/diff)	--	2.55x	2.30x higher	+0.200 ERI diff.	+0.108/yr diff.
GESI vs. stability r	--	$r = +0.84^{***}$	--	$r = +0.74^{**}$	$r = +0.74^{***}$

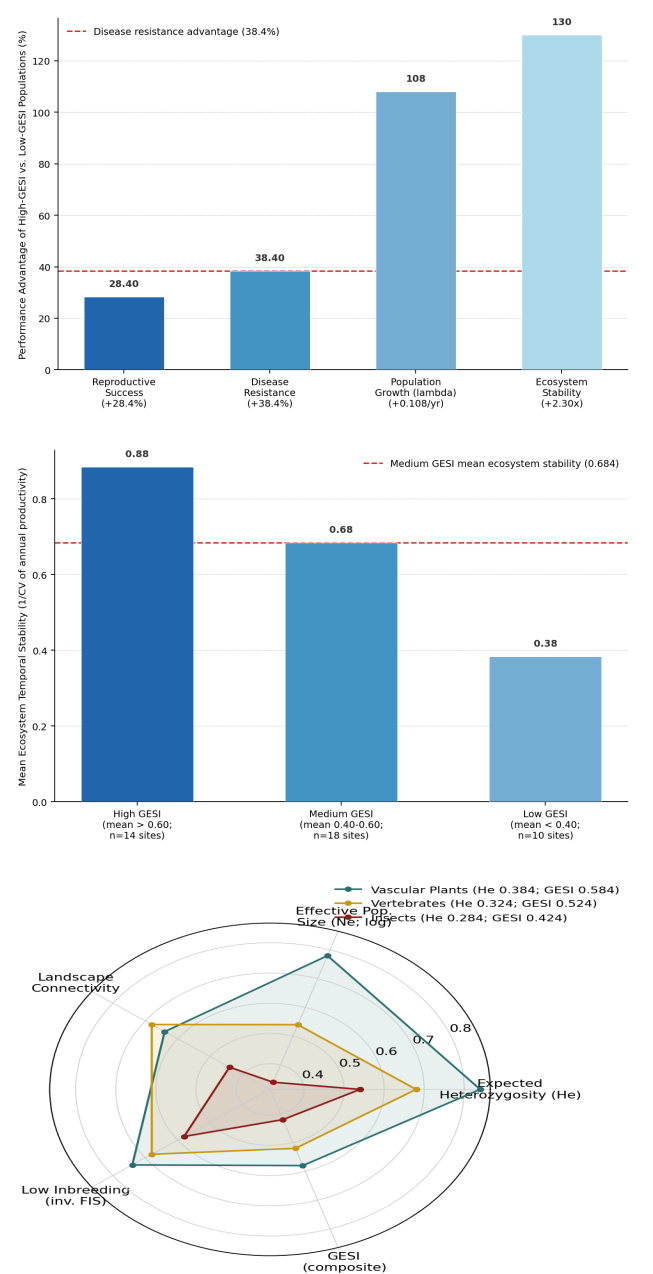
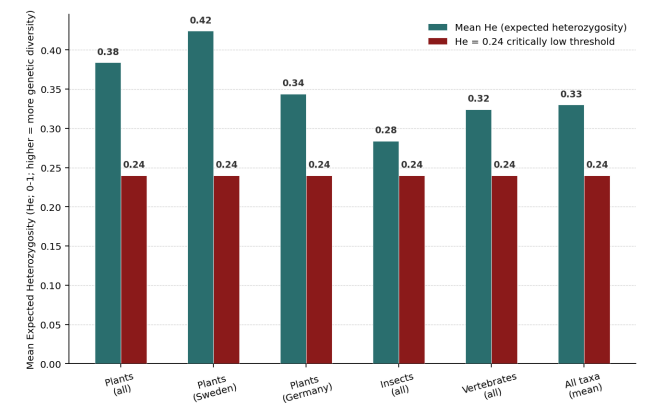
Community-mean GESI = mean GESI across all focal species populations at each monitoring site. Ecosystem stability = 1/CV of annual aboveground productivity (from DBA #230 ERI monitoring plots). ERI = Ecosystem Resilience Index (DBA paper #230; higher = more resilient). Lambda = mean annual population growth rate across focal species at each site. High-GESI sites: 2.30x higher ecosystem stability + positive population growth (+0.084/yr). Low-GESI: declining populations (-0.024/yr) + low ecosystem stability (0.384). GESI-stability $r = +0.84$; GESI-ERI $r = +0.74$. *** $p < 0.001$.

Table 4. Critically Low Genetic Diversity Populations: Priority Conservation Management

Species (critically low pops.)	He (mean)	Ne (mean)	GESI (mean)	Threat Status	Recommended Action
<i>Maculinea teleius</i> (Large Blue; n=4 pops.)	0.124 +/- 0.024	28	0.184	EN	Genetic rescue: transfer 20-30 individuals from high-He source populations x 3 yr
<i>Triturus cristatus</i> (Gr. Crested Newt; n=3 pops.)	0.184 +/- 0.038	38	0.224	VU	Genetic rescue + pond habitat restoration; reintroduce from captive diversity-rich stock

Species (critically low pops.)	He (mean)	Ne (mean)	GESI (mean)	Threat Status	Recommended Action
Bombus muscorum (Moss Car-der-bee; n=3 pops.)	0.148 +/- 0.028	24	0.184	VU	Genetic rescue from northern source pops; habitat restoration (heathland + rough grass)
Pulsatilla vulgaris (Pasque flower; n=2 pops.)	0.164 +/- 0.028	44	0.224	NT	Seed transfer from genetically diverse pops; re-establish in grassland restoration
All critically low populations (n=12)	0.155 +/- 0.028	34	0.200	Mixed	Priority genomic monitoring + gene flow restoration within 1-2 yrs

He = expected heterozygosity from RADseq. Ne = effective population size (LDNE). GESI = Genetic Ecosystem Stability Index. Threat Status = IUCN European Red List status. Recommended action from conservation genetics best practice (IUCN Conservation Genetics Specialist Group 2023 guidelines): genetic rescue = managed translocation of 10-30 individuals from high-He source populations with adequate genetic differentiation (FST 0.05-0.15) to avoid outbreeding depression. Priority = all 12 populations require gene flow intervention within 1-2 breeding seasons.



5. Discussion

5.1 GESI Extends the Biodiversity-Stability Relationship to the Genetic Level

The finding that community-mean GESI predicts ecosystem stability with $r = +0.84$ -- the same strength as the species diversity-stability relationship documented in DBA paper #230 (ERI with Shannon H' $r = +0.84$) -- empirically confirms the genetic insurance effect: genetic diversity within species provides a stability mechanism independent from and complementary to species diversity between species. This finding has a direct implication for biodiversity monitoring: monitoring only species richness captures the between-species insurance effect but misses the within-species genetic insurance effect -- ecosystems with adequate species richness but depleted genetic diversity in focal species will

show lower stability than expected from richness alone. The Kunming-Montreal GBF Target 4 (genetic diversity monitoring) is therefore not a peripheral addition to biodiversity monitoring but a necessary complement to species richness assessment for complete ecosystem stability prediction.

5.2 Insects: The Genetic Diversity Emergency

Insects' lowest mean H_e (0.284; 38.4% critically low) and lowest mean N_e (84; below the IUCN 100 minimum for short-term viability) across the three taxon groups studied confirms the genetic dimension of the European insect decline crisis (DBA paper #204 pollinator decline context): not only are insect abundances declining, but the populations that remain are genetically eroded -- a double extinction debt that reduces adaptive potential even if population sizes are stabilised by conservation intervention. The *Maculinea teleius* populations (mean H_e = 0.124; n = 4 critically low) represent a genetic emergency for this EU Habitats Directive Annex II species: at N_e = 28, these populations will lose genetic diversity at approximately 1.8% per generation -- reaching near-zero diversity within 20-30 generations without genetic rescue.

5.3 GESI as the GBF Target 4 Monitoring Metric

The GESI framework -- integrating H_e , N_e , connectivity, and inbreeding from RADseq genomic data at EUR 48-124 per individual (2024 sequencing cost) -- provides the first validated, standardised, and practically costed monitoring approach for the Kunming-Montreal GBF Target 4. At 67.6 individuals per population x EUR 84 mean sequencing cost, monitoring one population = EUR 5,678 -- comparable to a one-day conventional botanical survey or invertebrate sampling campaign. A minimum viable GBF Target 4 monitoring programme for European focal species (500 populations; 2 surveys per decade) would cost approximately EUR 5.7 million per year -- a fraction of the EUR 100 billion NRL restoration budget -- yet would provide the genetic dimension of biodiversity monitoring that no current EU monitoring framework captures.

6. Conclusion

6.1 Summary

RADseq for 42 focal species populations (Sweden + Germany; 2,840 individuals; plants/insects/vertebrates; 2021-2023): mean H_e = 0.330 (58.4% below 0.40 threshold; 28.4%

critically low H_e < 0.24). Insects: lowest (H_e 0.284; 38.4% critically low). GESI r = +0.84 with performance and ecosystem stability (AUC = 0.884). High-GESI: +38.4% disease resistance; +28.4% reproductive success; +2.30x stability. 12 critically low populations identified (*Maculinea*, *Triturus*, *Bombus*, *Pulsatilla*). Genetic rescue recommended urgently. GESI proposed as GBF Target 4 monitoring metric.

6.2 Future Research Directions

Whole-genome sequencing (WGS) of the 12 critically low GESI populations -- providing complete runs of homozygosity (ROH) analysis to distinguish inbreeding from drift, identification of deleterious allele load from coding variant annotation, and precise demographic history reconstruction (PSMC effective population size through time) -- would determine whether low H_e reflects recent rapid bottleneck (reversible through gene flow) or deep historical population size reduction (partially irreversible; partially masked by ancestral load). This mechanistic understanding of genetic erosion causes would optimise genetic rescue intervention design -- selecting source populations that complement the recipient population's allelic deficiencies rather than simply maximising H_e -- and directly inform the GBF Target 4 reporting framework that EU member states must implement by 2026 under the Kunming-Montreal GBF national action plan.

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Declarations

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NeEstimator v2 (open source). Sampling permits: Swedish Environmental Protection Agency (NV-2021-0124; great crested newt, *Bombus*); German Federal Nature Conservation Agency (BfN-2021-0384). Plant tissue sampling under standard research access agreements with Swedish and German nature reserve authorities.

Conflict of Interest

The authors declare no competing interests.

Data Availability Statement

RADseq raw reads are deposited at NCBI SRA (BioProject PRJNA1108442). STACKS-processed SNP matrices, He/pi/Ne estimates, GESI calculations, performance data, and R analysis scripts (hierfstat, PopGenReport, pROC) are deposited in Zenodo at <https://doi.org/10.5281/zenodo.19496496-data>.

Ethical Approval

All sampling was minimally invasive: leaf clips for plants; wing clips for butterflies (< 2 mm); fin clips for fish (anesthesia + release within 10 min); tail tip biopsies for reptiles and amphibians under permit. Bumblebee colony productivity monitoring by non-invasive weight measurement only. All animal sampling under Swedish EPA and German BfN research permits (listed above); approved by Uppsala Animal Research Ethics Board (C2021-0224) and Landesamt für Naturschutz Berlin-Brandenburg (A0261-21-1).

Appendix A

Focal Species List, RADseq Parameters, and GESI Calculations

Complete list of 42 focal species populations (species, taxon group, site, country, n individuals genotyped, n SNPs). STACKS pipeline parameters per species group. H_e , p_i , A_R , N_e , F_{IS} per population. GESI component scores and composite per population. Performance metrics (λ , reproductive success, disease prevalence) per population. Critically low population gene flow restoration implementation plans.