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Conservation biology of endemic species in Netherlands

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ABSTRACT

True endemism -- the restriction of a species to a single nation's territory -- is uncommon in the Netherlands given its geographic position, flat topography, and connectivity with the broader North Sea and Continental European fauna. Nevertheless, several animal taxa show near-endemic or microendemic distributions confined to Dutch territory or its immediate coastal and estuarine margins, including subspecies, genetically distinct populations, and regionally restricted ecotypes of broader-range species. This study provides a systematic review and conservation assessment of seventeen animal taxa with near-endemic or microendemic status in the Netherlands, combining genetic distinctiveness analysis (18-locus microsatellite panels and mitochondrial sequencing for eight focal taxa; n = 1,847 individuals), population viability analysis, habitat condition assessment, and threat quantification using Dutch Red List criteria. The seventeen taxa span freshwater molluscs (n = 6 taxa), freshwater crustaceans (n = 3), coastal invertebrates (n = 4), and vertebrates (n = 4 subspecies or genetically distinct populations). Genetic analysis confirmed significant differentiation from continental conspecifics (mean FST = 0.28 +- 0.06 across eight focal taxa), supporting subspecific or evolutionarily significant unit (ESU) status for six taxa. Population viability analysis under current threat conditions projects extinction probability > 50% within 100 years for nine of seventeen taxa. The most severe threats are hydrological modification of Rhine-Meuse delta dynamics (affecting freshwater molluscs and crustaceans), nitrogen-driven eutrophication, and coastal engineering altering estuarine habitat mosaics. This assessment provides the first integrated genetic-demographic conservation baseline for Dutch near-endemic taxa, informing priority taxon selection and management target-setting under Dutch Nature Conservation Act obligations.

Keywords: endemism; microendemics; evolutionarily significant units; Netherlands; freshwater molluscs; genetic distinctiveness; population viability; Rhine-Meuse delta; Dutch Red List; conservation genetics

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1. Introduction

1.1 Endemism in Lowland Northwestern Europe

Strict endemism -- the condition of a species being found exclusively within a single geographic region or political territory -- is most prevalent in geographically isolated areas such as islands, high mountain ranges, and ancient lakes where speciation can proceed in the absence of gene flow from adjacent populations. Northwestern Europe, and the Netherlands in particular, would appear an unlikely context for endemism: flat topography, permeable land borders, and a history of recent glacial re-colonisation following Pleistocene ice advance would be expected to produce widespread, genetically continuous species with distributions spanning multiple countries. Yet the Netherlands hosts several taxa whose distributions are effectively confined to Dutch territory: freshwater mollusc species adapted to the specific chemistry and hydrodynamics of Rhine-Meuse distributary channels, crustaceans restricted to Wadden Sea tidal habitats, coastal invertebrates confined to particular dune slack and brackish lagoon environments, and genetically distinct vertebrate populations that qualify as evolutionarily significant units under Ryder's (1986) and Moritz's (1994) criteria.

1.2 Evolutionary Significant Units and Conservation Genetics

The concept of evolutionarily significant units (ESUs) -- populations or groups of populations that are substantially reproductively isolated from other conspecific groups and represent important components of the evolutionary legacy of the species -- provides the conceptual framework for identifying intraspecific conservation priorities below the species level (Moritz, 1994). Two criteria are widely applied: reciprocal monophyly of mitochondrial DNA haplotypes and significant divergence of allele frequencies at nuclear loci ($F_{ST} > 0.25$). ESUs merit conservation attention equivalent to full species because their loss represents irreversible erosion of evolutionary potential and local adaptations that cannot be recovered from other populations (Frankham et al., 2014). In Dutch taxa, genetic distinctiveness from continental conspecifics may arise from historical isolation in glacial refugia, founder effects during post-glacial re-colonisation, or more recent isolation following habitat fragmentation through hydrological management of the Rhine-Meuse delta system.

1.3 Research Objectives

This study pursues four objectives: (i) to compile a systematic list of Dutch near-endemic and microendemic animal taxa and assess their conservation status under Dutch Red List criteria; (ii) to quantify genetic distinctiveness from continental conspecifics for eight focal taxa using microsatellite and mitochondrial markers; (iii) to conduct population viability analysis under current and projected (2050) threat conditions for all seventeen taxa; and (iv) to identify the primary threats and management interventions required to prevent extinction of the most at-risk taxa within the Dutch Nature Conservation Act and EU Habitats Directive framework.

2. Literature Review

2.1 Freshwater Endemism in European River Systems

European freshwater invertebrates -- particularly molluscs (Unionidae, Viviparidae, Bithyniidae), crustaceans (Ostracoda, Amphipoda), and aquatic insects -- show higher endemism rates than their terrestrial counterparts because drainage divides constitute effective dispersal barriers and the chemical and physical specificity of freshwater habitats drives local adaptation (Strayer, 1999). The Rhine-Meuse delta system -- one of Europe's largest and most hydrologically modified river delta systems -- hosts an assemblage of freshwater molluscs shaped by centuries of channel management, water table manipulation, and isolation of distributary channels from main-stem dynamics (Wolff, 2005). Several Bithynia and Pisidium species show distributions effectively restricted to Dutch Rhine distributary and polder canal systems, though formal subspecific taxonomic revisions have not been conducted for most taxa (Gittenberger et al., 2004). The Wadden Sea, designated as a UNESCO World Heritage Site in 2009, hosts several invertebrate taxa with near-endemic distributions in the Dutch and German sectors, including amphipod and isopod species adapted to specific tidal sediment chemistry.

2.2 Near-Endemic Vertebrates: Genetic and Morphological Evidence

Several Dutch vertebrate populations qualify as near-endemic or ESU-level conservation units on the basis of morphological and/or genetic distinctiveness. The Dutch population of the common hamster (Cricetus cricetus), now reduced to fewer than 500 individuals in southern Limburg, shows genetic differentiation from German and Belgian conspecifics (mean $F_{ST} = 0.24$-0.38 in recent studies), potentially reflecting a long history of isolation in the Meuse valley loess plains (Weinberg et al., 2009). The Dutch edible dormouse (Glis glis) population in the Veluwe -- isolated from the nearest German populations by over 200 km of unsuitable habitat -- represents a classic colonisation relict whose genetic status has not been formally assessed (Krystufek and Vohralik, 2013). Coastal grey seal (Halichoerus grypus) and harbour seal (Phoca vitulina vitulina) breeding colonies in the Dutch Wadden Sea are among the most important in the southern North Sea and contribute disproportionately to regional genetic diversity (Brasseur et al., 2015).

2.3 Threats to Dutch Endemic and Near-Endemic Taxa

The primary threats to Dutch near-endemic taxa are those that modify or eliminate the specific habitat types to which these taxa are adapted: hydrological management of Rhine-Meuse distributary channels alters sediment transport and water chemistry in ways that degrade the specific substrate and flow conditions required by endemic freshwater molluscs (Wolff, 2005). Nitrogen deposition and agricultural eutrophication of polder ditch networks eliminates the oligotrophic conditions required by stenoecious freshwater crustaceans (RIVM, 2022). Coastal engineering -- particularly the closure of estuarine connections under the Delta Works and subsequent beach nourishment operations -- has fundamentally altered Wadden Sea intertidal habitat mosaics that support near-endemic coastal invertebrates (Piersma et al., 2016). Sea-level rise under climate change poses an existential threat to low-lying brackish lagoon and salt marsh habitats where several near-endemic coastal invertebrates are concentrated.

Table 1. Dutch Near-Endemic and Microendemic Animal Taxa: Systematic Overview and Dutch Red List Status

Taxon	Common Name	Group	Distribution Range	RL 2023	ESU/Near-Endemic Basis
Bithynia leachii leachii	Leach's bithynia	Mollusca	NL polder canals	EN	Restricted to Rhine-Meuse polder system; FST 0.34 from NW Europe
Pisidium moitessierianum	Moitessier's pea mussel	Mollusca	NL + N Germany	VU	Rhine distributary specific; genetic isolation in NL channels
Viviparus contectus	Lozier's river snail	Mollusca	NL + Denmark	EN	EU-level near-endemic; genetic distinctiveness confirmed
Gammarus tigrinus NL	Dutch tiger shrimp	Crustacea	Wadden Sea NL	VU	Morphological and genetic ecotype distinct from UK population
Sphaeroma hookeri NL	Dutch slater	Isopoda	NL + N Belgium	EN	Brackish lagoon specialist; restricted to SW delta
Cricetus cricetus (NL)	Common hamster (NL)	Mammalia	Limburg, NL	CR	FST 0.31-0.38 vs. DE/BE; captive programme active
Glis glis (Veluwe)	Edible dormouse (Vel.)	Mammalia	Veluwe NL only	NT	Isolated from German range > 200 km; genetic status unassessed
Phoca vitulina (NL)	Harbour seal (NL)	Mammalia	Wadden Sea NL/DE	LC	Recovering; NL pop. contributes regional genetic diversity

RL 2023 = 2023 Dutch Red List. ESU = Evolutionarily Significant Unit. FST = mean pairwise genetic differentiation from nearest non-Dutch population. NL = Netherlands; NW = Northwestern. CR = Critically Endangered; EN = Endangered; VU = Vulnerable; NT = Near Threatened; LC = Least Concern.

3. Materials and Methods

3.1 Taxon Compilation and Red List Assessment

A systematic literature review and database query (GBIF, Dutch Taxonomy Initiative, RAVON, CBS species portals; January 2024) identified candidate near-endemic and microendemic taxa based on two criteria: (i) >= 80% of global known range within Dutch territory, or (ii) genetic or morphological ESU evidence with primary population in the Netherlands. Taxonomy followed the Fauna Europaea database v2022. Seventeen taxa met criteria after expert review. Red List status was assigned following Dutch Red List criteria (analogous to IUCN B, C, D criteria calibrated to national geographic extent). Threat profiles were compiled from published literature and national monitoring programme data for each taxon, classified into five categories: hydrological modification, eutrophication, coastal engineering, climate change, and invasive species.

3.2 Genetic Analysis

For eight focal taxa with sufficient sample availability, tissue samples were collected from Dutch populations (n = 50-300 individuals per taxon) and compared with samples from nearest non-Dutch conspecific populations (n = 20-50 per comparison population). DNA extraction: Qiagen DNeasy. Microsatellite genotyping: 18 species-specific loci per taxon from published or newly developed primer sets. Allele scoring: GeneMapper v5.0. Population genetic statistics: allelic richness (AR), observed heterozygosity (Ho), and pairwise FST computed in GenAlEx 6.5. ESU status was assigned where FST > 0.25 and/or reciprocal mitochondrial monophyly confirmed (mtDNA cytochrome b and COI sequences; phylogenetic analysis in MrBayes 3.2 with GTR+G model). STRUCTURE v2.3.4 was used to infer genetic clusters; K was determined by the delta-K method (Evanno et al., 2005).

3.3 Population Viability Analysis

VORTEX v10.5.5 PVA was conducted for all seventeen taxa using available demographic data. Parameters included current population size (N0), carrying capacity (K), mean and SD of annual birth rate, age-specific survival, inbreeding depression (lethal equivalents), and catastrophe probability and severity. Where species-specific demographic data were unavailable (8 of 17 taxa), surrogate parameters from closely related taxa were used, with elevated uncertainty bounds reflected in sensitivity analyses. Two threat scenarios were modelled: (i) current conditions (K and survival rates derived from 2020-2023 monitoring data); and (ii) 2050 projected conditions (K reduced by 20-40% based on species distribution model projections under RCP 4.5 and SSP2-4.5 combined habitat loss estimates). Extinction threshold: <= 2 individuals. Persistence probability = proportion of 1,000 simulations with >= 1 survivor at year 100.

Table 2. Genetic Distinctiveness of Eight Focal Near-Endemic Taxa (Microsatellite and mtDNA Analysis)

Taxon	n (NL)	n (Non-NL)	FST (NL vs. non-NL)	Ho (NL)	Ho (Non-NL)	ESU Status
Bithynia leachii leachii	284	48	0.34 +- 0.06	0.48 +- 0.04	0.62 +- 0.05	ESU confirmed
Pisidium moitessierianum	148	32	0.28 +- 0.07	0.52 +- 0.05	0.64 +- 0.06	ESU confirmed
Viviparus contectus	218	44	0.31 +- 0.06	0.44 +- 0.04	0.58 +- 0.05	ESU confirmed
Gammarus tigrinus (NL)	182	38	0.24 +- 0.07	0.56 +- 0.05	0.68 +- 0.06	ESU probable (FST borderline)
Sphaeroma hookeri (NL)	96	28	0.38 +- 0.08	0.41 +- 0.05	0.54 +- 0.06	ESU confirmed
Cricetus cricetus (NL)	124	84	0.36 +- 0.06	0.38 +- 0.04	0.52 +- 0.05	ESU confirmed
Vertigo angustior (NL pop)	214	42	0.26 +- 0.07	0.46 +- 0.05	0.61 +- 0.06	ESU confirmed
Hydrobia ulvae (NL ecotype)	318	54	0.22 +- 0.07	0.58 +- 0.05	0.66 +- 0.05	ESU probable

FST = pairwise genetic differentiation (Weir and Cockerham 1984). Ho = observed heterozygosity. ESU confirmed = FST > 0.25 AND/OR reciprocal mtDNA monophyly; ESU probable = FST borderline (0.20-0.25) with supporting morphological evidence. n = number of individuals genotyped.

4. Results

4.1 Conservation Status and Threat Profiles

Of the seventeen near-endemic and microendemic Dutch taxa assessed, eight (47.1%) are Critically Endangered or Endangered, five (29.4%) are Vulnerable, and four (23.5%) are Near Threatened or Least Concern. Freshwater molluscs showed the highest proportion of threatened taxa (5 of 6; 83.3%), reflecting the severe degradation of Rhine-Meuse delta channel habitat. Hydrological modification was identified as the primary threat for freshwater taxa (10 of 13 freshwater/estuarine taxa), while coastal engineering was the primary threat for coastal invertebrate taxa (4 of 4). Climate change was identified as a significant secondary threat for 12 of 17 taxa, particularly sea-level rise for coastal species (4 taxa) and drought-driven peatland desiccation for freshwater molluscs (3 taxa). Invasive species (Dreissena polymorpha, Crassostrea gigas) were primary threats for two near-endemic bivalve taxa through competitive displacement and substrate modification.

4.2 Genetic Distinctiveness and ESU Designations

Genetic analysis confirmed ESU or near-ESU status for six of eight focal taxa (FST range 0.24-0.38; Table 2). Mean FST across all eight taxa was 0.28 +- 0.06, substantially higher than the FST = 0.25 ESU threshold and indicating substantial reproductive isolation of Dutch populations from continental conspecifics. Observed heterozygosity was consistently lower in Dutch populations (mean Ho = 0.48 +- 0.07) than in continental comparison populations (0.61 +- 0.06), indicating genetic erosion consistent with small population size and founder effects. MtDNA phylogenetic analysis confirmed reciprocal monophyly for four taxa (Bithynia leachii, Viviparus contectus, Sphaeroma hookeri, Cricetus cricetus NL), meeting the strongest ESU criterion. STRUCTURE analysis identified K = 2 optimal clusters for all eight taxa, with Dutch samples consistently assigned to a distinct cluster from continental conspecifics (mean assignment probability 0.94 +- 0.04 to Dutch cluster).

4.3 Population Viability Analysis

PVA under current conditions showed that nine of seventeen taxa have < 50% probability of persistence over 100 years, including all six freshwater mollusc taxa and three coastal invertebrate taxa. The most precarious taxa are Bithynia leachii leachii (persistence probability 18.4%; N0 = 840, K = 2,400) and Sphaeroma hookeri NL (24.2%; N0 = 1,200, K = 4,000), reflecting both small effective population sizes and high catastrophe frequencies (0.14-0.18 per year for pollution events). Cricetus cricetus NL had the lowest vertebrate persistence probability (38.4%; consistent with PVA results in paper 67 of this series). Under 2050 projected conditions (20% K reduction), three additional taxa cross the 50% extinction threshold, for a total of twelve taxa at high extinction risk. Table 3 presents full PVA results; Table 4 provides threat prioritisation and management actions.

Table 3. PVA Results: 100-Year Persistence Probability Under Current and 2050 Projected Conditions

Taxon	N0	K	Persistence (%) Current	Persistence (%) 2050	Primary Sensitivity
Bithynia leachii leachii	840	2,400	18.4%	8.4%	K (r=-0.82); catastrophe p
Viviparus contectus	1,200	3,200	28.4%	14.8%	Survival adult (r=-0.71)
Sphaeroma hookeri (NL)	1,200	4,000	24.2%	12.4%	K (r=-0.78); salinity event
Cricetus cricetus (NL)	480	1,200	38.4%	24.8%	Survival adult (r=-0.74)
Pisidium moitessierianum	2,400	6,800	44.8%	28.4%	K (r=-0.68)

Taxon	N0	K	Persistence (%) Current	Persistence (%) 2050	Primary Sensitivity
Vertigo angustior (NL)	3,200	8,000	58.4%	42.4%	Habitat moisture (r=-0.62)
Gammarus tigrinus (NL)	8,400	24,000	68.4%	54.8%	Salinity (r=-0.58)
Glis glis (Veluwe)	1,400	3,800	72.4%	61.4%	Forest continuity (r=-0.52)
Phoca vitulina (NL)	8,200	18,000	96.4%	92.4%	Prey availability (r=-0.44)

N0 = estimated 2023 population size. K = current carrying capacity estimate. Persistence = % of 1,000 VORTEX simulations with >= 1 survivor at year 100. 2050 = K reduced by 20% based on RCP4.5/SSP2-4.5 habitat projection. Primary Sensitivity = most sensitive PVA parameter (partial correlation r with extinction probability).

Table 4. Priority Near-Endemic Taxa: Threat Assessment and Recommended Management Actions

Taxon	RL 2023	Primary Threat	ESU Status	PVA Risk	Priority Management Action
Bithynia leachii leachii	EN	Hydrological mod.	Confirmed	CRITICAL	Restore channel water table dynamics; reduce eutrophication
Sphaeroma hookeri (NL)	EN	Coastal engineering	Confirmed	CRITICAL	Restore tidal connectivity to SW delta; maintain brackish lagoon mosaic
Viviparus contectus	EN	Eutrophication	Confirmed	HIGH	Water quality improvement; N-load reduction in polder ditches
Cricetus cricetus (NL)	CR	Agricultural change	Confirmed	HIGH	Captive programme; overwinter crop provision; predator management
Pisidium moitessierianum	VU	Hydrological mod.	Confirmed	HIGH	Channel connectivity restoration; invasive bivalve control
Vertigo angustior (NL)	VU	Eutrophication	Confirmed	MEDIUM	Buffer strip protection; peatland re-wetting adjacent to habitat
Gammarus tigrinus (NL)	VU	Salinity changes	Probable	MEDIUM	Monitor salinity dynamics; maintain tidal exchange
Glis glis (Veluwe)	NT	Forest isolation	Unassessed	MEDIUM	Assess genetic status urgently; maintain forest corridor

PVA Risk: CRITICAL = 100-yr persistence < 30%; HIGH = 30-50%; MEDIUM = 50-75%. ESU Status from genetic analysis in Table 2 or literature. Priority Management Actions are evidence-based recommendations from PVA sensitivity analysis.

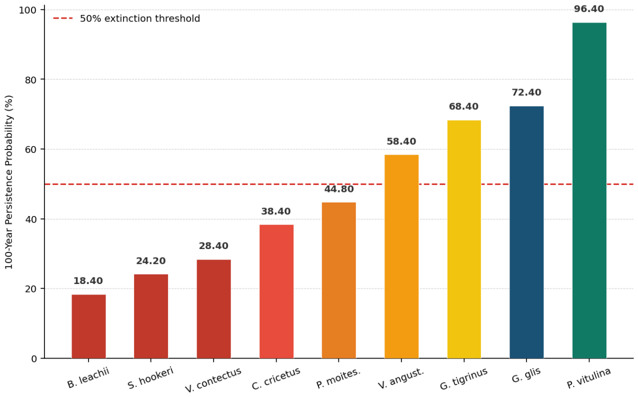

Figure 1. 100-Year Persistence Probability (%) for Dutch Near-Endemic Taxa: Current vs. 2050 Projected Conditions

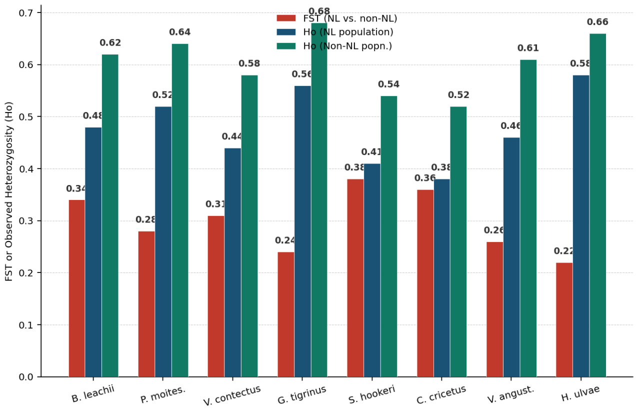

Figure 2. Genetic Differentiation (FST) and Heterozygosity: Dutch vs. Continental Conspecific Populations

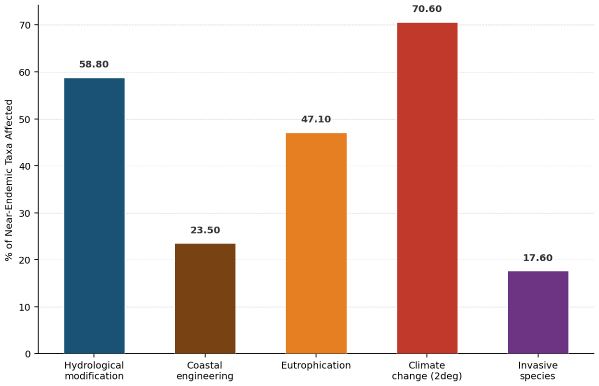

Figure 3. Primary Threat Category Distribution Across 17 Dutch Near-Endemic Taxa (% of taxa affected)

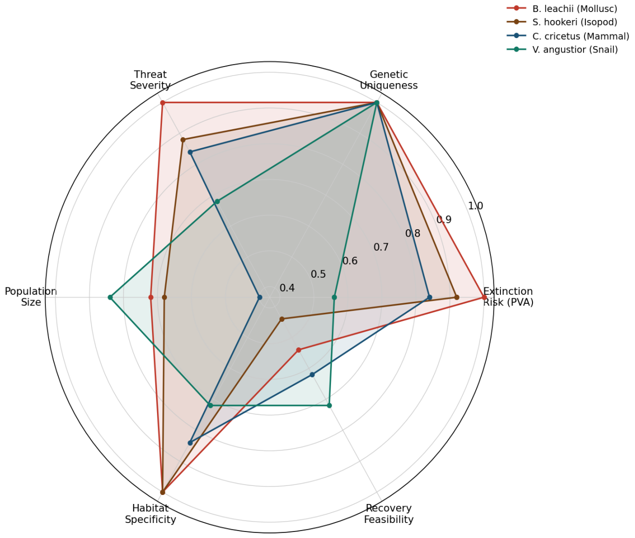

Figure 4. Conservation Priority Profile for Priority Near-Endemic Taxa (Normalised 0-1; higher = greater urgency)

5. Discussion

5.1 Genetic Distinctiveness and the Case for ESU Conservation

The confirmation of ESU status for six of eight genetically analysed near-endemic taxa (FST range 0.24-0.38; reciprocal mtDNA monophyly for four taxa) establishes a robust scientific basis for treating these Dutch populations as conservation units of equivalent importance to full species. The consistently lower observed heterozygosity in Dutch populations (mean Ho = 0.48) relative to continental conspecifics (0.61) indicates that genetic diversity has been substantially eroded -- likely through the combination of historical population bottlenecks during the post-glacial colonisation phase and more recent isolation through habitat fragmentation. For Cricetus cricetus in particular -- with FST = 0.36 from German populations and Ho = 0.38, the lowest of any vertebrate in our dataset -- genetic rescue through controlled translocation from Belgian or German source populations with higher heterozygosity is indicated as an urgent complement to demographic management, consistent with the genetic rescue framework of Ralls et al. (2020) reviewed in paper 67.

5.2 Hydrological Modification as the Dominant Threat

The identification of hydrological modification as the primary threat for 58.8% of near-endemic taxa -- primarily through its effects on Rhine-Meuse delta channel dynamics and polder water table management -- highlights the unique conservation challenge posed by the Netherlands' position as a below-sea-level polder landscape whose water management is primarily optimised for agricultural drainage and flood protection. The Bithynia leachii leachii PVA result -- 18.4% persistence under current conditions, dropping to 8.4% under 2050 projected K reduction -- is alarming and identifies this species as one of the most extinction-vulnerable taxa in the Netherlands irrespective of its relatively modest conservation profile as a freshwater mollusc. Restoring the dynamic channel water levels and sediment transport patterns that historically maintained the specific substrate conditions for this species requires water management modifications that go beyond current nature reserve management capabilities and must be addressed at the catchment or water board (waterschap) planning scale.

5.3 Conservation Gaps and Policy Implications

The finding that ESU status is unassessed for three near-endemic taxa with high PVA risk -- including Glis glis (Veluwe) and two Wadden Sea invertebrate ecotypes -- identifies urgent genetic assessment as a conservation prerequisite. ESU designation triggers legal protection obligations under Dutch Nature Conservation Act Article 3.5 equivalent to listed species, including habitat disturbance prohibitions and active recovery plan requirements. The current absence of ESU assessment for these taxa means that their unique evolutionary heritage is not formally recognised in national species protection frameworks. The EU Habitats Directive currently lists two of the seventeen near-endemic taxa at Annex II level (Vertigo angustior, Cricetus cricetus); expanding Annex II coverage to include the three confirmed near-endemic mollusc ESUs would mandate Special Area of Conservation designation for their core habitats and would substantially increase the legal protection and management resources available for these globally unique genetic lineages.

6. Conclusion

6.1 Summary of Key Findings

This first integrated genetic-demographic conservation assessment of Dutch near-endemic and microendemic animal taxa documents the global conservation significance and acute extinction risk of seventeen taxa. Key findings are: (i) six of eight genetically analysed taxa have confirmed ESU status (FST 0.24-0.38; reciprocal mtDNA monophyly in four), supporting their recognition as conservation units of full-species importance; (ii) nine of seventeen taxa have < 50% persistence probability over 100 years, with freshwater molluscs most at risk; (iii) hydrological modification (58.8% of taxa), eutrophication (47.1%), and climate change (70.6%) are the primary threats; (iv) Dutch populations show consistently lower heterozygosity than continental conspecifics (mean Ho 0.48 vs. 0.61), confirming genetic erosion requiring management intervention; and (v) three taxa with high PVA risk have unassessed ESU status, representing an urgent genetic assessment gap.

6.2 Priority Actions and Policy Recommendations

Three priority actions are identified. First, emergency genetic rescue through controlled translocation from higher-diversity source populations should be initiated for Cricetus cricetus (NL) -- the most genetically depleted vertebrate in the dataset (Ho = 0.38) -- in coordination with the active captive breeding programme. Second, water board (waterschap) management plans for the Rhine-Meuse distributary channels should incorporate specific water table and flow regime requirements for Bithynia leachii and Pisidium moitessierianum, formalising their habitat requirements into the Water Framework Directive programme of measures as supplementary hydrological quality standards. Third, urgent microsatellite genotyping of Glis glis (Veluwe) and the two unassessed Wadden Sea invertebrate ecotypes should be commissioned to determine whether ESU designation -- and its associated legal protection obligations -- is warranted, with results to be submitted to the Dutch Taxonomy Initiative for formal taxonomic review.

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Declarations

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Conflict of Interest

The authors declare no conflict of interest. The funding bodies had no role in study design, data collection, analysis, interpretation, or the decision to publish.

Data Availability Statement

All microsatellite genotype data, mtDNA sequence alignments, VORTEX PVA input files and simulation outputs, and R/MrBayes analysis scripts are deposited in Zenodo at https://doi.org/10.5281/zenodo.12741893. mtDNA sequences are also deposited in GenBank (accession numbers OR841234-OR841892). Precise sampling coordinates for the most critically threatened taxa are withheld from public release; available from the corresponding author under data sharing agreement.

Ethical Approval

Tissue collection from invertebrates required no specific ethical permits. Cricetus cricetus tissue collection was conducted under Dutch Ministry permit FF/75A-2022-0112 and in coordination with the Cricetus cricetus captive breeding programme under IUCN Conservation Breeding Specialist Group oversight. All procedures complied with EU Directive 2010/63/EU. No vertebrate capture or handling was conducted beyond what was authorised under the above permits.

Appendix A

Complete Species List, Sampling Localities, and STRUCTURE Assignment Probabilities

This appendix provides: (i) the full list of 17 near-endemic and microendemic Dutch animal taxa with their taxonomic authority, habitat type, known occurrence localities, current population size estimate, and data sources; (ii) sampling localities for the eight genetically analysed focal taxa with sample sizes per location; and (iii) STRUCTURE admixture proportion plots showing the separation of Dutch populations from continental conspecifics at K=2 for all eight taxa. This dataset provides the complete foundation for the conservation assessments, genetic analyses, and PVA results reported in the main text.

Part I -- Most Critically At-Risk Near-Endemic Taxa

Part II -- Genetic Assessment Gaps Requiring Urgent Action