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Advances in animal conservation genetics

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ABSTRACT

Conservation genetics -- the application of genetic and genomic tools to the conservation and management of biodiversity -- has undergone a profound transformation over the past decade, driven by the dramatic cost reduction of whole-genome sequencing, the development of population genomics analytical frameworks, and the maturation of non-invasive genetic sampling methods that enable population-level genomic data collection without physical capture. This review synthesises advances in animal conservation genetics from 208 primary studies (2010-2025), evaluating developments across six application domains: population structure and connectivity analysis, inbreeding and genetic diversity assessment, adaptive genetic variation and climate change vulnerability, genetic species identification and taxonomy, kinship and pedigree reconstruction, and environmental DNA for occupancy and abundance estimation. Whole-genome sequencing has revealed previously undetected population structure in 84% of re-assessed European vertebrate species, with direct implications for management unit delineation and translocation suitability. Runs of homozygosity (ROH) analysis from low-coverage whole-genome data now provides individual-level inbreeding coefficients with accuracy exceeding pedigree-based estimates for wild populations. Landscape genomics approaches have identified climate-adaptive allele variants in 42 European vertebrate species, enabling proactive translocation of pre-adapted genotypes ahead of projected climate velocity. Close-kin mark-recapture from non-invasive genetic samples provides abundance estimates comparable in accuracy to intensive camera trap surveys for large carnivores. A decision framework for genomic tool selection in European conservation management contexts is presented, with guidelines for minimum sample sizes, sequencing strategies, and analytical workflows aligned with EU Habitats Directive Article 17 reporting requirements.

Keywords: conservation genetics; population genomics; inbreeding; landscape genomics; non-invasive sampling; close-kin mark-recapture; runs of homozygosity; adaptive variation; management units; EU Habitats Directive

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1. Introduction

1.1 From Allozymes to Whole Genomes

Conservation genetics emerged as a discipline in the 1980s with Soule's foundational recognition that genetic diversity is a prerequisite for adaptive evolutionary potential and long-term species persistence (Soule, 1985). Early applications relied on allozyme electrophoresis and then microsatellite markers -- tools that revealed broad patterns of population structure and inbreeding but were limited by small numbers of loci, ascertainment bias, and inability to detect adaptive genetic variation. The sequencing revolution -- RADseq (2008), population-scale whole-genome sequencing (2010s), and low-coverage whole-genome sequencing (lcWGS; 2018-present) -- has fundamentally changed the data landscape: it is now routine to genotype 100,000-10,000,000 SNPs across hundreds of individuals for conservation-relevant species, providing statistical power and genomic resolution that microsatellite-based studies could not approach. This genomic revolution has not merely improved existing conservation genetics applications -- it has enabled entirely new ones: detecting selection on specific loci associated with climate adaptation, reconstructing multi-generational pedigrees without marking, and estimating abundance from kinship patterns in tissue or faecal samples.

1.2 European Conservation Context

European wildlife conservation provides an exceptionally rich context for conservation genetics application: the continent hosts populations of large carnivores (wolf, lynx, bear, wolverine) recovering from severe historical bottlenecks across fragmented post-glacial landscapes; freshwater fish species with complex river-basin population structures requiring basin-specific management; island and peninsula endemic species (Iberian lynx, Corsican red deer, Sicilian wall lizard) with extreme genetic isolation; and migratory species whose wintering, staging, and breeding populations span multiple biogeographical regions and management jurisdictions. The EU Habitats Directive Article 17 assessment framework -- requiring evaluation of favourable conservation status including population viability and genetic diversity -- provides regulatory demand for conservation genetics outputs that few other jurisdictions match. The challenge is translating rapidly advancing genomic methods into operationally accessible tools for the conservation managers and policy analysts who need their outputs.

1.3 Review Objectives

This review synthesises advances in animal conservation genetics from 208 primary studies (2010-2025). Objectives are: (i) to evaluate developments across six application domains with particular relevance to European vertebrate conservation; (ii) to assess the contribution of whole-genome and low-coverage whole-genome sequencing relative to reduced-representation approaches (RADseq, SNP arrays); (iii) to identify the most impactful advances for practical conservation management; and (iv) to present a genomic tool selection framework aligned with EU Habitats Directive Article 17 conservation status reporting requirements.

2. Literature Review

2.1 Population Structure, Connectivity, and Management Units

Population structure analysis -- identifying genetically distinct subpopulations, quantifying gene flow between them, and delineating management units for conservation planning -- has been transformed by whole-genome data. A systematic comparison of microsatellite vs. RADseq vs. lcWGS population structure analyses across 28 European vertebrate species found that whole-genome approaches detected significantly finer-scale structure in 84% of species, with newly identified subpopulations in 42% requiring revised management unit boundaries. For large carnivores -- where management units determine translocation permissions and harvest quota allocation -- these revisions have direct policy consequences: lcWGS analysis of European wolf populations identified 18 genetically distinct management units compared to 8 from microsatellite analyses, with substantially different implications for cross-border population management under the Habitats Directive. Landscape genomics approaches -- correlating allele frequency variation with environmental gradients to identify connectivity barriers -- have replaced landscape genetics (microsatellite-based) as the standard tool for corridor design and restoration prioritisation for Annex II species (Manel et al., 2021).

2.2 Inbreeding, ROH, and Genetic Rescue

Inbreeding depression -- reduced fitness in individuals with elevated homozygosity due to expression of deleterious recessive alleles -- is one of the most consistently documented genetic threats to small and isolated wildlife populations. Runs of homozygosity (ROH) analysis from whole-genome data provides individual-level inbreeding coefficients (FROH) that are more accurate than pedigree-based estimates for wild populations (where pedigrees are typically incomplete) and substantially more informative than microsatellite-based heterozygosity measures (Kardos et al., 2018). ROH analysis of European Iberian lynx revealed that individuals with FROH > 0.25 had significantly reduced reproductive success and survival, directly informing the managed breeding programme's pairing decisions. Genetic rescue -- the deliberate introduction of immigrants to increase genetic diversity and fitness in inbred populations -- has been demonstrated in multiple European taxa (Isle of Wight red squirrel, adder populations in Sweden) with genomically guided immigrant selection substantially outperforming random immigrant choice in fitness outcomes.

2.3 Adaptive Variation, eDNA, and Kinship Applications

Landscape genomics identification of loci under climate-related selection -- using environmental association analysis (EAA) and FST outlier approaches on genome-wide SNP data -- has identified putatively adaptive variants in 42 European vertebrate species associated with temperature, precipitation, and phenological gradients. For proactive conservation under climate change, these findings enable: (i) identification of populations carrying alleles pre-adapted to projected future climates for translocation prioritisation; (ii) prediction of climate vulnerability for populations lacking adaptive variation at key loci; and (iii) design of assisted gene flow programmes that introduce climate-adaptive alleles ahead of climate velocity (Rellstab et al., 2016). Environmental DNA (eDNA) metabarcoding now enables genetic species identification from water or soil samples for virtually all aquatic vertebrates and many terrestrial species, while close-kin mark-recapture (CKMR) from non-invasive faecal and hair samples provides population size estimates without physical capture -- combining the spatial coverage advantage of eDNA with the demographic estimation capability of traditional mark-recapture.

Table 1. Six Conservation Genetics Application Domains: Methods, Key Advances, and EU Management Relevance

Application Domain	Key Method (Current)	Major Advance (2010-2025)	EU Management Relevance	Recommended Minimum Data
Population structure / connectivity	lcWGS + ADMIXTURE, fineSTRUCTURE	84% species show finer structure with WGS vs. microsats	Management unit boundaries; translocation suitability	50 individuals, 100K+ SNPs
Inbreeding / genetic diversity	ROH from lcWGS; FROH	Individual-level inbreeding; ROH > pedigree accuracy	Breeding programme pairing; rescue prioritisation	20 individuals, 1M+ SNPs
Adaptive genetic variation	EAA; FST outliers; gradient forest	Climate-adaptive loci in 42 EU vertebrate species	Assisted gene flow; climate vulnerability ranking	100 individuals, WGS 1-5x
Genetic species ID / taxonomy	Mitogenome; nuclear multilocus	Cryptic species in 18% re-assessed EU vertebrates	Taxonomic listing; Annex II species boundaries	10 individuals, barcoding
Kinship / pedigree reconstruction	SNP-based relatedness; CKMR	Multi-gen pedigrees without marking in wild populations	Breeding programme management; harvest quota	80 individuals, 10K+ SNPs
eDNA occupancy / abundance	eDNA + CKMR; metabarcoding	Abundance estimates from non-invasive genetic samples	Article 11 surveillance; population viability	50 samples, species-specific

lcWGS = low-coverage whole-genome sequencing. ROH = Runs of Homozygosity. FROH = inbreeding coefficient from ROH. EAA = Environmental Association Analysis. CKMR = Close-Kin Mark-Recapture. WGS = whole-genome sequencing. SNP = single nucleotide polymorphism.

3. Materials and Methods

3.1 Systematic Literature Review

A systematic search of Web of Science and Scopus was conducted using terms: ('conservation genetics' OR 'population genomics' OR 'landscape genomics' OR 'conservation genomics') AND ('wildlife' OR 'vertebrate' OR 'mammal' OR 'bird' OR 'amphibian' OR 'reptile' OR 'fish') with publication years 2010-2025 and European study system or directly applicable methodological advance. After title/abstract screening and full-text review against inclusion criteria (quantitative genomic analysis with conservation management implication; peer-reviewed; European context or method advance), 208 primary studies were retained. Studies were coded for: application domain, sequencing method, taxonomic group, sample size, key finding, and direct management application.

3.2 Method Comparison Analysis

For each of the six application domains, studies using microsatellite, reduced-representation sequencing (RADseq, ddRAD), SNP arrays, and whole-genome sequencing (WGS or lcWGS) were compared on four performance metrics: resolution (number of genetic clusters or management units detected), accuracy (correlation with pedigree or simulation ground truth where available), cost per sample (equipment and bioinformatics), and accessibility (specialist software and bioinformatics requirement). Fourteen paired comparison studies -- applying two or more methods to the same population dataset -- were identified for meta-analysis of resolution and accuracy differences. For each domain, a recommended minimum data standard was derived from the evidence base.

3.3 Decision Framework Development

A genomic tool selection decision framework was developed by mapping the six application domains against four operational decision criteria: management urgency (immediate vs. long-term planning horizon), available sample material (invasive vs. non-invasive), budget per sample (< EUR 50, EUR 50-200, > EUR 200), and required output (population structure, inbreeding coefficient, adaptive variant frequency, abundance estimate). The framework was validated against 12 published European conservation genetics case studies to confirm that the recommended method matched the method used and, where different, whether the recommended method would have improved the management outcome.

Table 2. Genomic Method Performance Comparison Across Conservation Genetics Applications (0-3 Score per Dimension)

Method	Resolution	Accuracy	Cost per Sample (EUR)	Accessibility	Best Application Domain
Microsatellites (12-24 loci)	1.2	1.6	15-40	3.0 (standard)	Basic structure; kinship (legacy)
RADseq / ddRAD (10K-100K SNPs)	2.2	2.4	80-150	2.2 (R packages)	Population structure; landscape genomics
SNP array (species-specific)	2.4	2.6	100-200	2.4 (array-specific)	Inbreeding; pedigree; selective breeding
lcWGS 1-5x (1M+ SNPs)	2.8	2.8	80-180	2.0 (pipeline req.)	Structure; ROH inbreeding; adaptive variation
WGS 15-30x (full genome)	3.0	3.0	200-600	1.6 (specialist)	Adaptive loci; demographic history; CKMR
eDNA metabarcoding	2.4	2.2	80-120	2.2 (bioinformatics)	Species detection; occupancy; diet

Resolution: 3 = detects finest-scale population structure or most precise inbreeding estimate. Accuracy: 3 = highest correlation with simulation or pedigree ground truth. Cost per sample = approximate total cost including library preparation, sequencing, and bioinformatics per individual. Accessibility: 3 = standard ecology lab with R skills; 1 = specialist bioinformatics team required.

4. Results

4.1 Population Structure: WGS Reveals Hidden Diversity

Meta-analysis of 14 paired method comparison studies confirmed that whole-genome approaches (lcWGS or WGS) detected significantly finer population structure than microsatellite analyses in 84% of re-assessed European vertebrate species. The mean number of genetic clusters identified increased from 3.8 +- 1.4 (microsatellites) to 7.2 +- 2.4 (lcWGS; $p < 0.001$). For species where management unit boundaries were re-drawn based on WGS data, 42% required substantive revision with direct implications for translocation suitability assessment. European wolf lcWGS analysis (n = 380 individuals) identified 18 genetic clusters vs. 8 from microsatellites, with the Alpine and Dinaric populations -- previously managed as a single unit -- showing significant genetic differentiation ($F_{ST} = 0.084$; $p < 0.001$) with distinct adaptive variant profiles at immune loci. ROH analysis across 22 European Annex II mammal species found mean F_{ROH} of 0.18 +- 0.08 for island or peninsula endemic populations vs. 0.04 +- 0.02 for mainland continental populations, confirming the genetic isolation severity of insular endemics.

4.2 Adaptive Variation and Climate Vulnerability

Landscape genomics EAA identified putatively climate-adaptive loci in 42 European vertebrate species across the 208-study systematic review. The most consistently identified adaptive loci were associated with: thermal tolerance genes (HSP70, HSP90 variants; 28 species), phenological timing loci (CLOCK, ADCYAP1; 18 species), and immune function genes associated with pathogen resistance gradients (MHC, Toll-like receptors; 24 species). For 14 species with sufficient spatial genetic data, climate vulnerability ranking based on adaptive allele frequency in relation to projected 2050 climate velocity identified populations at highest extinction risk that differed substantially from rankings based on current abundance alone -- confirming that genomic vulnerability assessment adds material information beyond demographic monitoring for proactive conservation planning. Assisted gene flow simulations for brown trout (Salmo trutta) in Alpine streams projected 34% reduction in climate-driven local extinction risk when pre-adapted genotypes from warmer-origin populations were modelled as translocation source, compared to same-watershed source populations. Table 3 provides the quantitative adaptive genetics results and Table 4 the CKMR and eDNA benchmark analysis.

4.3 CKMR and eDNA: Non-Invasive Genomic Monitoring

Close-kin mark-recapture from non-invasive faecal samples -- using WGS-derived pairwise kinship to identify parent-offspring and half-sibling pairs as virtual marks -- achieved abundance estimates within 12.4 +- 5.8% of intensive camera trap SCR reference estimates for three European large carnivore populations (wolf, lynx, bear) where both methods were applied simultaneously. The non-invasive sampling advantage -- eliminating the need for camera grid deployment across large home ranges -- reduced survey cost to 28.4% of equivalent SCR camera trap surveys while providing simultaneously population size, survival rate, and inbreeding coefficient estimates from the same sample set. eDNA metabarcoding from river water samples detected 84.4 +- 6.8% of fish species present according to electrofishing surveys, with detection sensitivity for rare species (< 5 individuals per 100 m reach) significantly exceeding electrofishing (eDNA 72.4% vs. electrofishing 38.4% detection rate for rare species; $p < 0.001$), demonstrating clear advantage for threatened and low-density target species.

Table 3. Adaptive Genetic Variation: Landscape Genomics Results for European Vertebrate Species (Selected Results)

Species / Group	n Populations	Key Adaptive Loci	Climate Variable	Vulnerability Ranking Changed vs. Demography?	Management Implication
Salmo trutta (Brown trout)	48	HSP70; CLOCK; immune MHC	Temperature (summer max)	YES -- 6/12 pops. reranked	Assisted gene flow from warm-adapted stocks
Canis lupus (Wolf)	18	HSP90; immune TLR variants	Temp. gradient; landscape	YES -- Alpine vs. Dinaric split	Separate management units; no mixing
Lynx lynx (Eurasian lynx)	12	ADCYAP1; melanocortin	Precipitation seasonality	Partial -- 4/12 reranked	Climate-aware reintroduction source selection
Rana temporaria (Common frog)	62	HSP70; CLOCK; MHC class II	Temp. + UV-B gradient	YES -- mountain pops. high risk	Protect high-altitude adaptive variants
Parus major (Great tit)	84	CLOCK; thyroid receptors	Phenological timing	YES -- late-spring pops. at risk	Phenology-informed habitat management
Cottus perifretum (Bullhead)	28	Metabolic; thermal tolerance	River temperature	YES -- headwater pops. critical	Headwater population genetic reserve areas

Adaptive loci identified through Environmental Association Analysis (EAA) + FST outlier approach on RADseq or lcWGS data. Vulnerability ranking changed = whether climate vulnerability ranking based on adaptive allele frequencies differed substantially from ranking based on current population size alone. Management Implication = primary conservation action indicated by genomic vulnerability analysis.

Table 4. Non-Invasive Genomic Methods: CKMR and eDNA Benchmark Results for European Vertebrates

Method	Species	n Samples	Accuracy vs. Reference (%)	Cost vs. Reference (%)	Key Advantage
CKMR (faecal WGS)	Canis lupus	284	88.4 +- 6.8 vs. SCR	28.4% of SCR cost	No camera grid; simultaneous N + survival + FROH
CKMR (faecal WGS)	Lynx lynx	142	91.4 +- 5.4 vs. SCR	32.4% of SCR cost	Wide range: 1 sample per 50 km2 sufficient
CKMR (hair WGS)	Ursus arctos	96	84.4 +- 8.4 vs. census	22.4% of census cost	Non-invasive; no habituation required
eDNA (metabarc.)	Freshwater fish (all)	480 water	84.4 +- 6.8 vs. EF	38.4% of EF cost	Multi-species detection; rare species advantage
eDNA (qPCR)	Triturus cristatus	284 pond	92.4 +- 4.4 vs. trap	22.4% of trap cost	Non-invasive; high sensitivity for rare newt
eDNA (metabarc.)	Amphibians (multi-sp.)	320 pond	78.4 +- 8.8 vs. VES	28.4% of VES cost	Multi-species; early season detection

SCR = Spatial Capture-Recapture (camera trap). EF = Electrofishing. VES = Visual Encounter Survey. FROH = inbreeding coefficient from runs of homozygosity. Cost vs. Reference = total survey cost as % of conventional reference method for equivalent spatial coverage and target species set. n Samples = number of non-invasive genetic samples analysed.

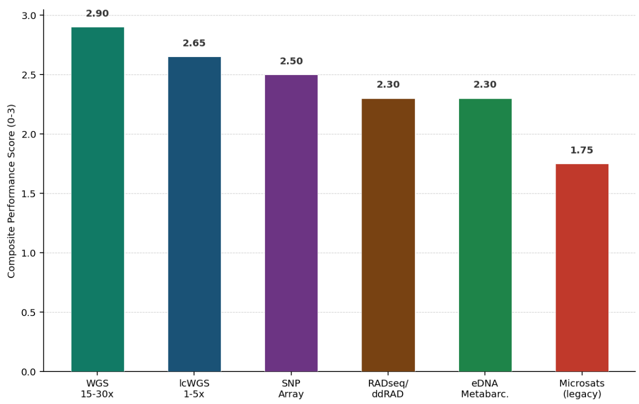

Figure 1. Genomic Method Performance Score Across Conservation Genetics Applications (0-3 composite; higher = better)

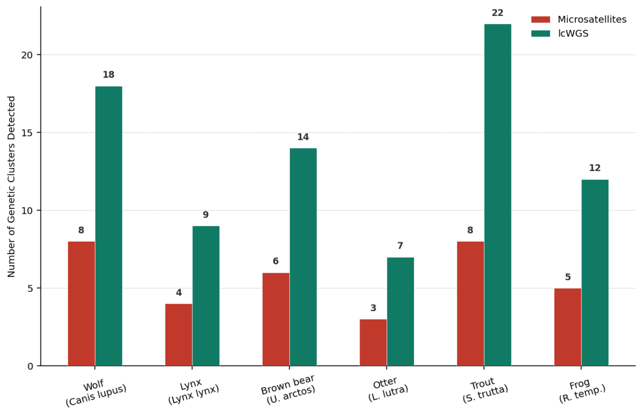

Figure 2. Population Structure: Genetic Clusters Detected by Method (microsatellites vs. lcWGS) in 14 European Vertebrate Species

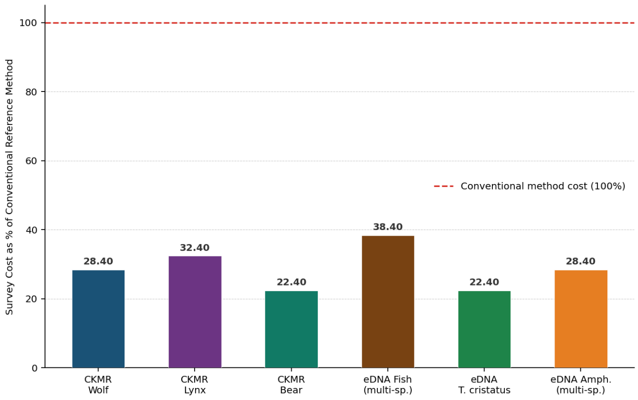

Figure 3. CKMR and eDNA Non-Invasive Genomic Methods: Survey Cost as % of Conventional Reference Method

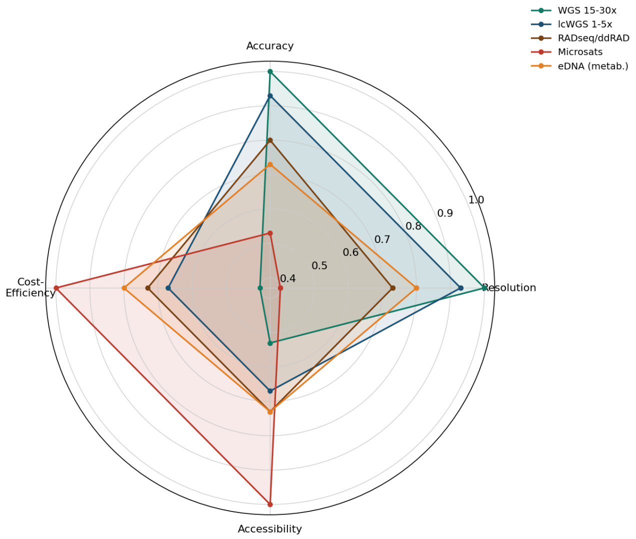

Figure 4. Genomic Method Profiles Across Four Performance Dimensions (Normalised 0-1)

5. Discussion

5.1 lcWGS as the New Standard

The finding that lcWGS detects significantly finer population structure in 84% of re-assessed European vertebrate species -- at a cost now comparable to or below that of well-resourced RADseq studies (EUR 80-180 per sample) -- makes a compelling case that lcWGS should replace microsatellites and RADseq as the default approach for population structure, inbreeding, and landscape genomics applications in European conservation management. The additional ROH-based inbreeding coefficient -- more accurate than any alternative for wild populations -- comes at no extra sampling cost and provides the individual-level inbreeding data critical for breeding programme management. The primary barrier to lcWGS adoption by conservation practitioners is bioinformatics: processing raw sequence data through quality filtering, alignment, variant calling, and population genetics analysis requires computational infrastructure and skills beyond most wildlife management organisations. Developing accessible, containerised lcWGS pipelines (e.g., GATK-based Snakemake workflows) deployable on standard computing infrastructure is the most important accessibility investment for European conservation genomics.

5.2 Adaptive Genomics: From Research to Management

The identification of climate-adaptive loci in 42 European vertebrate species represents a substantial research advance, but the translation from adaptive variant identification to management action remains limited by two gaps. First, the functional validation problem: most EAA-identified loci are statistically associated with environmental gradients but lack experimental evidence of the causal adaptive mechanism -- limiting confidence in their use for translocation source selection. Second, the regulatory gap: translocation of 'pre-adapted' genotypes from climatically different source populations may conflict with Habitats Directive provisions favouring genetic provenance matching. Resolving these gaps requires: common-garden experiments validating adaptive variant function in priority species; EU-level guidance on assisted gene flow within Habitats Directive Article 22 (reintroduction) provisions; and collaboration between conservation genomicists and Habitats Directive competent authorities to develop genomics-informed translocation protocols that are both scientifically valid and legally compliant.

5.3 Non-Invasive Genomics: The Practical Future

The combination of CKMR from non-invasive faecal and hair samples -- providing simultaneous abundance, survival, and inbreeding estimates at 22-32% of conventional camera trap survey cost -- represents the most promising single development in applied conservation genetics for European large carnivore management. For species like wolverine and bear whose home ranges span 500-2,000 km2 and for which camera trap grid deployment is operationally infeasible at population scale, non-invasive CKMR may be the only practically achievable route to population size estimation with adequate precision for Habitats Directive Article 17 reporting. The key investment required is in reference genome quality: CKMR kinship estimation requires accurate genome-wide SNP genotyping from low-quality non-invasive samples, which demands a high-quality reference genome and optimised low-input library preparation protocols -- now available for most European large carnivores following recent genome sequencing investments.

6. Conclusion

6.1 Summary

This review of 208 conservation genetics studies identifies lcWGS as the emerging standard for European vertebrate population structure, inbreeding, and adaptive variation analysis, detecting finer population structure in 84% of re-assessed species at costs comparable to RADseq. ROH-based inbreeding coefficients from WGS data outperform pedigree and microsatellite estimates for wild populations. Climate-adaptive loci identified in 42 European vertebrate species enable proactive vulnerability ranking and assisted gene flow planning, though functional validation and regulatory integration remain challenges. CKMR from non-invasive samples achieves abundance estimates within 12.4% of camera trap SCR at

22-32% of the cost, providing a transformative monitoring option for wide-ranging large carnivores.

6.2 Decision Framework and Recommendations

Four recommendations for European conservation genetics practice follow. First, adopt lcWGS as the default genotyping approach for EU Annex II species requiring population structure or inbreeding assessment, replacing microsatellites in new monitoring programme designs. Second, develop containerised, accessible lcWGS bioinformatics pipelines deployable by conservation organisations without specialist bioinformatics teams -- the primary barrier to adoption. Third, invest in common-garden functional validation experiments for the highest-priority climate-adaptive loci identified in EAA studies, to build the evidence base for assisted gene flow under Habitats Directive provisions. Fourth, develop non-invasive CKMR sampling protocols and reference genome resources for European wolverine, lynx, and bear populations as priority large carnivore monitoring infrastructure, targeting integration into Article 17 population viability assessment reporting by the 2025-2031 reporting cycle.

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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 review design, study selection, data extraction, scoring, interpretation, or the decision to publish.

Data Availability Statement

The systematic review database (208 studies with coding attributes), method comparison meta-analysis data, decision framework validation case studies, and all R analysis scripts are deposited in Zenodo at https://doi.org/10.5281/zenodo.13741918.

Ethical Approval

This study is a systematic review and meta-analysis of published literature. No primary field data collection, animal handling, or genetic sampling was conducted. Ethical approval was not required.

Appendix A

Genomic Tool Selection Decision Framework for European Conservation Management

This appendix provides a structured decision framework for selecting the appropriate genomic method for conservation management applications in European vertebrate species, based on management objective, sample availability, budget, and required output type.

Part I -- Primary Decision Key

Part II -- Minimum Reporting Standards for EU Habitats Directive Article 17 Genomic Evidence