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The Role of Biotechnology in Biodiversity Conservation and Ecological Restoration: A Review

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ABSTRACT

More recently, biotechnology is increasingly adopted alongside conventional approaches to biodiversity conservation and ecosystem restoration. In this study, we examined 60 articles published from year 1998-2024 by grouping the literature into six areas: conservation genomics and genetic rescue, environmental DNA (eDNA), biobanking and reproductive biotechnology, synthetic biology and genome editing, microbiome-based restoration and the governance of genetic data, risks and benefit sharing. The studies reviewed show that genomic approaches can provide information on genetic diversity, inbreeding, population structure, adaptation and whether interventions such as translocation or genetic rescue may be appropriate. eDNA has also expanded the options available for biodiversity monitoring because organisms can be detected from water, soil and air samples without necessarily being captured or directly observed. Studies on cryopreservation, assisted reproduction and stem-cell technologies further demonstrate ways of retaining genetic material that may be difficult to conserve through captive breeding alone. However, the evidence was less straightforward for genome editing and gene drives. Although these technologies may allow highly targeted interventions, the examined studies repeatedly raise questions about unintended ecological effects, reversibility, regulation and public acceptance. Microbiome-based approaches are also becoming promising, particularly where microbial communities influence establishment, stress tolerance or recovery, but their outcomes appear to depend strongly on the species and environmental conditions involved. Hence, the studies reviewed suggest that biotechnology should not be treated as a replacement for habitat protection or ecological restoration. Its value lies mainly in extending the range of tools available to conservation practitioners. Effective use will require appropriate sampling, reliable genetic and ecological data, field validation, long-term monitoring and careful consideration of risk, access to genetic information and benefit sharing.

INTRODUCTION

Biodiversity conservation increasingly relies on evidence across genetic, population, community and ecosystem levels. Genome-wide data improve estimates of inbreeding, connectivity, demographic history and adaptive variation in threatened populations (Allendorf *et al.*, 2010). They can also clarify conservation units by revealing meaningful genetic differences that smaller marker sets may miss (Funk *et al.*, 2012). However, genomic variation does not always translate directly into management action (Shafer *et al.*, 2015). High-quality reference genomes help identify structural variation, harmful alleles and population-specific patterns (Formenti *et al.*, 2022), which is increasingly important as habitat loss reduces within-species genetic diversity (Exposito-Alonso *et al.*, 2022). Environmental DNA has expanded biodiversity monitoring beyond direct observation or capture. Early studies showed that amphibian DNA in water could reliably indicate species presence (Ficetola *et al.*, 2008), while targeted eDNA assays detected rare aquatic species missed by conventional surveys (Jerde *et al.*, 2011). Seawater metabarcoding revealed diverse marine fish communities (Thomsen, Kielgast, Iversen, Møller, *et al.*, 2012) and freshwater studies supported monitoring

of endangered aquatic vertebrates (Thomsen, Kielgast, Iversen, Wiuf, *et al.*, 2012). Metabarcoding later expanded monitoring from single species to whole communities (Deiner *et al.*, 2017). Its reliability still depends on sampling, DNA transport and degradation, laboratory controls, marker choice and reference databases.

Biotechnology also supports biological preservation and direct intervention. Genome-resource banking allows long-term storage of sperm, oocytes, embryos, tissues, cells and DNA (Wildt, 2000), while in vitro culture and cryopreservation are especially valuable for plants unsuitable for conventional seed banking (Pence, 2013). White-rhinoceros embryos and embryonic stem cells have shown how assisted reproduction can preserve reproductive options when few founders remain (Hildebrandt *et al.*, 2018). Gene drives are more interventionist, as engineered inheritance systems can spread selected traits through wild populations (Esvelt *et al.*, 2014). Targeting the doublesex gene caused complete suppression of caged *Anopheles gambiae* populations (Kyrou *et al.*, 2018), highlighting both their potential and the need to assess resistance, unintended spread, ecological effects, reversibility, welfare and public approval.

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In ecological restoration, biotechnology can influence species interactions and ecosystem processes. Whole-soil inoculation can redirect plant communities toward target ecosystems (Wubs *et al.*, 2016), while mycorrhizal fungal diversity can affect plant diversity, productivity and stability (van der Heijden *et al.*, 1998). In corals, beneficial microbial consortia have increased resistance to bleaching stress (Rosado *et al.*, 2019) and heat-evolved algal symbionts have improved bleaching tolerance (Buerger *et al.*, 2020). Modelling suggests assisted evolution is most valuable when combined with demographic restoration and sustained deployment at meaningful ecological scales (DeFilippo *et al.*, 2022). Hence, this review shows that biotechnology can strengthen conservation and restoration when paired with ecological integrity, transparent risk assessment, equitable benefit sharing and long-term population viability.

MATERIALS AND METHODS

This study uses a structured integrative review because the evidence comes from several fields, including conservation genetics, genomics, molecular monitoring, reproductive biology, synthetic biology, restoration science and

biodiversity governance. Studies were identified through theme-based searches, citation tracking and an updated search focused on research published from 2020 onward. Articles were included if they were peer-reviewed, had a valid DOI and directly contributed to biodiversity assessment, genetic-resource preservation, biological intervention, ecological restoration or governance. Studies focused only on production biotechnology were excluded. The final review included 60 DOI-verified articles published between 1998 and 2024, with 23 published from 2020 to 2024. Each study was coded by biological scale, technology, conservation objective, evidence type, outcome, uncertainty and governance relevance. Studies were grouped into six themes: conservation genomics (13), environmental DNA (12), biobanking and reproductive biotechnology (8), synthetic biology and genome editing (10), microbiome-based restoration (10) and governance and benefit sharing (7). The review also compared measurement versus intervention, ex situ versus in situ conservation, laboratory versus field performance and technical capability versus legitimacy. A qualitative synthesis was used because the studies differed too widely for statistical meta-analysis.

Table 1: Thematic coverage and analytical construction of the review corpus

Theme	n	Evidence emphasized	Synthesis question
Conservation genomics and genetic rescue	13	Population genomics, rescue outcomes, genomic erosion	How does genomic evidence change diagnosis, founder choice and monitoring?
Environmental DNA and molecular biomonitoring	12	Target assays, metabarcoding, aquatic and terrestrial sampling	When does a molecular detection support a spatial or population inference?
Biobanking and reproductive biotechnology	8	Embryos, cells, gametes, tissue culture, cryostorage	Which biological options can be retained and later returned to conservation practice?
Synthetic biology and genome editing	10	Gene drives, inheritance bias, targeted editing	What evidence and containment are required as intervention intensity rises?
Microbiomes and ecological restoration	10	Soil inocula, mycorrhizae, coral symbionts, assisted evolution	Can manipulated interactions persist and improve population or ecosystem function?
Governance, equity and benefit sharing	7	Digital sequence information, open data, access and benefit sharing	How can data access, authority, risk and benefits be allocated legitimately?

Note. One dominant theme was assigned to each article for counting; cross-theme citations were retained during synthesis

RESULTS AND DISCUSSION

Conservation Genomics and Genetic Rescue

Conservation genomics provides detailed insight into population structure, demographic history, relatedness and adaptive variation. Genome-wide markers have improved estimates of connectivity and the identification of management units, but genetic differences alone do not determine what conservation action should be taken (Allendorf *et al.*, 2010; Funk *et al.*, 2012; Shafer *et al.*, 2015). Genomic data is most useful when linked to

clear decisions, such as selecting founders, identifying inbreeding, defining important lineages or assessing adaptive capacity under environmental change (Breed *et al.*, 2019; Formenti *et al.*, 2022; Hoffmann *et al.*, 2015). Genetic rescue shows how genomic evidence can guide intervention. Florida panther introgression was linked to demographic and phenotypic recovery, while broader evidence suggests that gene flow often improves fitness in small, inbred populations (Frankham, 2015; Johnson *et al.*, 2010). Similarly, the Isle Royale wolf genome revealed

severe inbreeding and damaging variation that census size alone could not show (Robinson *et al.*, 2019). Habitat loss can further reduce genetic diversity and even recovering populations may retain lasting genomic damage (Exposito-Alonso *et al.*, 2022; Jackson *et al.*, 2022). Current guidance therefore supports maintaining relevant genetic diversity while considering local adaptation, demographic history, disease risk and monitoring capacity (Hohenlohe *et al.*, 2021; Ralls *et al.*, 2020). Thus, it can be said that genome data can reveal harmful genetic variation, but results depend on data quality and sampling. Regular monitoring is needed to track long-term risks. Genetic rescue works best when combined with demographic data, habitat suitability and post-release monitoring

Environmental DNA and Molecular Biomonitoring

Environmental DNA (eDNA) uses DNA released into water, soil, air and other materials to detect biodiversity without directly observing organisms. Early studies showed that rare amphibians, invasive species, endangered freshwater species and marine fish could be identified using water samples (Ficetola *et al.*, 2008; Jerde *et al.*, 2011; Thomsen *et al.*, 2012; Thomsen *et al.*, 2012). Metabarcoding later expanded this approach from single species to whole communities (Deiner *et al.*, 2017). However, DNA can travel through rivers, increasing survey coverage while making exact location estimates more difficult (Deiner *et al.*, 2016). Recent studies have detected mammals, arthropods and vertebrates using river water, flowers and airborne samples (Clare *et al.*, 2022; Sales *et al.*, 2020; Thomsen & Sigsgaard, 2019). Different sample types also vary in species detection and contamination risk (van der Heyde *et al.*, 2020). Laboratory methods, including filtration, extraction and replication, strongly influence detection success (Stoeckle *et al.*, 2022). False positives, false negatives, DNA persistence and incomplete reference databases remain key limitations (Bohmann *et al.*, 2014). Reliable eDNA monitoring therefore requires strong sampling design, controls, replication, confirmatory surveys and updated reference databases.

Biobanking, Cryopreservation and Reproductive Biotechnology

Biobanking preserves biological material even when an organism or population is at risk of disappearing. Genome-resource banks store sperm, oocytes, embryos, tissues, cell lines and DNA, while plant conservation uses seeds, embryos, shoot tips and tissue cultures depending on species needs (Comizzoli, 2015; Li & Pritchard,

2009; Pence, 2013; Wildt, 2000). The white-rhinoceros program demonstrated embryo production and stem-cell development for species with very few remaining founders (Hildebrandt *et al.*, 2018). Induced pluripotent stem cells also provide renewable cellular material, although they do not guarantee successful gamete production or viable offspring (Friedrich Ben-Nun *et al.*, 2011). Effective biobanks depend on accurate records, verified identity, viability, contamination control, standardized metadata and secure storage. Reproductive biotechnology can preserve lineages and move genes without transporting animals. However, extinction-reversal pathways involve many difficult stages, from sample collection to embryo development and population integration (Saragusty *et al.*, 2016). Fertility preservation and sperm cryopreservation are also highly species-specific (Burger *et al.*, 2023; Comizzoli, 2015). These technologies complement rather than replace habitat protection and ecological recovery (Breed *et al.*, 2019; Exposito-Alonso *et al.*, 2022). Ethical concerns also include ownership, future use, access and benefit sharing across jurisdictions (Brink & van Hintum, 2022; Scholz *et al.*, 2022).

Synthetic Biology, Genome Editing and Assisted Evolution

Synthetic biology moves conservation beyond selecting existing genetic variation toward deliberately directing biological change. Potential uses include invasive-species control, disease resistance, restoration of lost functions and targeted genetic rescue, although technical feasibility does not always mean ecological suitability (Piaggio *et al.*, 2017; Redford *et al.*, 2014). Gene-drive studies have demonstrated biased inheritance and population suppression in laboratory organisms, including systems targeting female reproduction and the doublesex gene (Esvelt *et al.*, 2014; Gantz & Bier, 2015; Hammond *et al.*, 2016; Kyrou *et al.*, 2018). Risk assessment is essential because gene drives may spread beyond intended ecological or political boundaries (Noble *et al.*, 2018). Similar inheritance-bias systems have also been demonstrated in mammals, though effectiveness and welfare concerns vary greatly among species (Grunwald *et al.*, 2019). Improved mosquito gene drives further highlight challenges such as resistant alleles, fitness costs and the need for controlled validation (Carballar-Lejarazú *et al.*, 2020). In plants, genome editing may support disease resistance, reproductive rescue and recovery of threatened genotypes, but delivery, off-target effects and public acceptance remain barriers (Yin *et al.*, 2024). Safe application therefore requires staged testing, ecological

Table 2: Biotechnology intervention matrix for conservation decision-making

Platform	Biological scale	Conservation function	Principal limitation	Source
Population genomics	Genome to population	Diagnose structure, inbreeding, adaptive variation & founder representation	Inference depends on sampling, reference quality, annotation & decision context	(Formenti <i>et al.</i> , 2022; Funk <i>et al.</i> , 2012; Hohenlohe <i>et al.</i> , 2021; Robinson <i>et al.</i> , 2019)

Environmental DNA	Organism to community	Detect rare taxa & monitor assemblages without physical capture	Transport, degradation, inhibition, contamination & reference bias	(Bohmann <i>et al.</i> , 2014; Deiner <i>et al.</i> , 2016; Ficetola <i>et al.</i> , 2008; Stoeckle <i>et al.</i> , 2022)
Cryobanking & assisted reproduction	Cell to population	Preserve gametes, embryos, tissues & lineages for future use	Species-specific protocols & uncertain route from storage to viable populations	(Burger <i>et al.</i> , 2023; Comizzoli, 2015; Hildebrandt <i>et al.</i> , 2018; Wildt, 2000)
Genome editing & gene drive	Gene to population	Alter targeted traits or inheritance for rescue, disease control or suppression	Spread, resistance, off-target effects, reversibility & transboundary legitimacy	(Esvelt <i>et al.</i> , 2014; Kyrou <i>et al.</i> , 2018; Noble <i>et al.</i> , 2018; Yin <i>et al.</i> , 2024)
Microbiome & symbiont management	Holobiont to ecosystem	Improve establishment, stress tolerance, succession or ecological function	Context-dependent persistence, dispersal & community-level effects	(Doering <i>et al.</i> , 2021; Rosado <i>et al.</i> , 2019; Santoro <i>et al.</i> , 2021; Wubs <i>et al.</i> , 2016)

modelling, reversibility planning, independent review and community approval (Esvelt *et al.*, 2014; Noble *et al.*, 2018; Piaggio *et al.*, 2017; Scholz *et al.*, 2022).

Microbiome Engineering and Ecological Restoration

Restoration biotechnology acts on ecological relationships as well as focal organisms. Whole-soil inoculation can redirect succession toward target communities and mycorrhizal diversity can increase plant diversity, ecosystem productivity and stability (van der Heijden *et al.*, 1998; Wubs *et al.*, 2016). Coastal-sage restoration experiments show that arbuscular mycorrhizal inoculation can alter native plant establishment, but outcome varies with inoculum origin, host identity, soil condition and competition (Aprahamian *et al.*, 2016). Soil microbial communities may lead or follow vegetation change, creating a causal identification problem for restoration design (Harris, 2009). The practical unit is a plant-soil-microbe system: culture success in a greenhouse offers limited evidence if introduced organisms fail to persist, disperse inappropriately, or interact negatively with resident communities. Coral research provides a second model of assisted ecological adaptation. Assisted-evolution frameworks combine selective breeding, symbiont manipulation, acclimatization and managed gene flow to increase thermal tolerance (van Oppen *et al.*, 2015). Beneficial-microorganism consortia have reduced bleaching-related effects in experimental settings, while microbiome manipulation has produced metabolic and genetic restructuring associated with heat-stress survival (Rosado *et al.*, 2019; Santoro *et al.*, 2021). Heat-evolved algal symbionts increased bleaching tolerance and tissue-homogenate transplantation altered coral microbiomes under controlled treatment (Burger *et al.*, 2020; Doering *et al.*, 2021). Population models indicate that assisted evolution and demographic restoration can interact, with intervention value depending on deployment scale,

heritability, survival and continuing climate pressure (DeFilippo *et al.*, 2022).

Governance, Equity and Risk

Conservation biotechnology relies on genetic samples and digital sequence information that often cross institutional and national borders. Open databases support species identification, genome construction, assay design and comparative research, but existing benefit-sharing rules were largely designed for physical genetic resources (Scholz *et al.*, 2022; Sherman & Henry, 2021). In plant genebanks, different definitions of digital sequence information can affect reporting duties, costs and data exchange (Brink & van Hintum, 2022). Marine genetic-resource research also shows that sequence data can complicate legal jurisdiction, especially beyond national boundaries (Lawson & Rourke, 2020). Governance must therefore balance open science with Indigenous rights, community interests, national sovereignty and unequal research capacity. Recent proposals favor multilateral benefit-sharing because tracing every sequence use can be difficult and may limit research access (Klunker & Richter, 2022; Scholz *et al.*, 2022).

New approaches increasingly connect benefit sharing to use and value creation, while recent biodiversity negotiations have made digital sequence information a central policy issue (Halewood *et al.*, 2023; Scholz *et al.*, 2023). Governance must also address ecological risk, animal welfare, data quality, cybersecurity and consent. Gene drives require cross-border consultation, while biobanks need clear rules on ownership and future reproductive use (Esvelt *et al.*, 2014; Hildebrandt *et al.*, 2018; Noble *et al.*, 2018). eDNA may also reveal sensitive species locations or human genetic material, creating privacy and anti-poaching concerns (Clare *et al.*, 2022; Deiner *et al.*, 2017).

Discussion

Table 3: Decision framework for biotechnology-supported ecological restoration

Restoration problem	Biotechnology option	Outcome signal	Safeguard or control	Source
Uncertain species presence or recolonization	Targeted eDNA or metabarcoding	Validated detection, occupancy, or community change	Field blanks, replication, detection models, confirmatory survey	Deiner <i>et al.</i> , 2017; Stoeckle <i>et al.</i> , 2022; Thomsen <i>et al.</i> , 2012; van der Heyde <i>et al.</i> , 2020
Low genetic diversity or inbreeding	Genomic assessment & managed gene flow	Fitness, recruitment, retained diversity, & adaptive representation	Demographic model, disease screening, post-release genomic monitoring	Exposito-Alonso <i>et al.</i> , 2022; Frankham, 2015; Johnson <i>et al.</i> , 2010; Ralls <i>et al.</i> , 2020
Loss of irreplaceable germplasm	Cryobanking, cell culture, or assisted reproduction	Viability, developmental competence, & contribution to a managed population	Provenance records, redundant storage, welfare review, recovery pathway	Burger <i>et al.</i> , 2023; Friedrich Ben-Nun <i>et al.</i> , 2011; Hildebrandt <i>et al.</i> , 2018; Pence, 2013
Poor plant establishment or altered soil function	Native soil or mycorrhizal inoculation	Establishment, diversity, soil function, & multiseason persistence	Local-source controls, pathogen screening, community tracking	Aprahamian <i>et al.</i> , 2016; Harris, 2009; van der Heijden <i>et al.</i> , 1998; Wubs <i>et al.</i> , 2016
Thermal stress in coral restoration	Symbiont evolution, probiotics, or microbiome transfer	Survival, bleaching response, reproduction, & field persistence	Reciprocal controls, dispersal monitoring, ecological interaction tests	Buerger <i>et al.</i> , 2020; DeFilippo <i>et al.</i> , 2022; Rosado <i>et al.</i> , 2019; van Oppen <i>et al.</i> , 2015
Cross-border sequence use or environmental release	Data-sharing or intervention governance	Documented consent, access, benefit flow, compliance, & monitoring	Decision authority, liability, stopping rules, multilateral benefit mechanism	Klünker & Richter, 2022; Lawson & Rourke, 2020; Scholz <i>et al.</i> , 2022; Scholz <i>et al.</i> , 2023

Biotechnology supports conservation through monitoring, preservation and direct intervention. Population genomics can reveal inbreeding, demographic history, population structure and adaptive variation (Hohenlohe *et al.*, 2021), while reference genomes improve the detection of important genomic differences in threatened species (Formenti *et al.*, 2022). Environmental DNA can detect difficult-to-observe species without capture (Ficetola *et al.*, 2008), although metabarcoding is generally more reliable for estimating species richness than abundance (Deiner *et al.*, 2017). Assisted reproduction has shown strong preservation potential through white-rhinoceros blastocysts and embryonic stem-cell lines (Hildebrandt *et al.*, 2018). Gene drives have also achieved complete suppression of caged *Anopheles gambiae* populations (Kyrrou *et al.*, 2018), while genome editing may improve resistance to pests, pathogens and climate stress in threatened plants (Yin *et al.*, 2024).

However, technical success does not always lead to population or ecosystem recovery. Pink pigeon populations increased while genetic diversity continued to decline (Jackson *et al.*, 2022) and habitat loss may already have reduced genetic diversity in many species by more than 10% (Exposito-Alonso *et al.*, 2022). eDNA

performance also varies among sample types (van der Heyde *et al.*, 2020) and conventional surveys may still be needed to confirm results (Sales *et al.*, 2020). Coral microbiome transplantation can reduce short-term bleaching, but long-term field effects remain uncertain (Doering *et al.*, 2021). Heat-adapted symbionts can improve bleaching tolerance (Buerger *et al.*, 2020), although modelling suggests assisted evolution requires sustained deployment and may offer limited protection under severe climate change (DeFilippo *et al.*, 2022).

Technology should therefore match a clearly defined conservation problem. Genetic rescue generally supports maintaining useful genetic diversity rather than avoiding gene flow because of broad outbreeding concerns (Ralls *et al.*, 2020). eDNA is valuable for mapping distributions but is stronger when supported by conventional surveys (Sales *et al.*, 2020). Cryopreservation also requires species-specific testing (Burger *et al.*, 2023), while soil inoculation depends strongly on inoculum origin (Wubs *et al.*, 2016). Governance remains equally important because digital sequence rules can create challenges for genebanks and open-data systems (Brink & van Hintum, 2022; Klünker & Richter, 2022). New approaches aim to separate benefit sharing from direct limits on sequence access (Halewood

et al., 2023), although how benefits should be measured and managed remains unresolved (Scholz *et al.*, 2023).

CONCLUSION

Biotechnology can make biodiversity more visible, preserve threatened biological material and expand the range of ecological restoration actions. Its conservation value emerges from a defined problem, an appropriate biological scale, a validated chain from molecular result to field outcome and governance that allocates risk and benefit openly. Genomics, environmental DNA, biobanking, reproductive tools, genome editing and microbiome management are not substitutes for habitat protection or demographic recovery. They are complementary instruments whose value varies with ecological context and institutional capacity. The strongest programs combine molecular precision with field ecology, long-term monitoring, transparent decision rules and equitable access to data and benefits. Such integration keeps technological novelty subordinate to the central objective: maintaining evolutionary potential, viable populations, ecological interactions and resilient ecosystems.

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