

Genome Science at the Forefront of Biodiversity's Greatest Challenges: *GBE* Virtual Collection on Conservation Genomics

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It is critical to conserve the Earth's biodiversity given the high rates of species loss (Ceballos et al. 2015; Saban and Wiens 2025) and drastic population-level declines (Finn et al. 2023). These losses have prompted repeated warnings from scientists and practitioners, urgently alerting policymakers and the public to the need for immediate action. Implementing successful conservation strategies requires practitioners to factor in not only a species' ecological context, but also its life-history traits, demographic history, and adaptive potential. To reconstruct a comprehensive picture, conservation efforts are increasingly reliant on genome-scaled information to describe patterns of gene flow (i.e. migration), species boundaries, and genetic diversity.

It is now easier than ever to generate high-resolution data on non-model organisms to tackle pressing conservation challenges (Theissinger et al. 2023). However, generating vast amounts of sequencing data also poses challenges, particularly in their analysis and in how to share them to benefit the local communities that are directly impacted by conservation policy. To signal our commitment to advancing this field, *Genome Biology and Evolution* has launched a virtual collection on **conservation genomics**, featuring standout, open-access science published in our journal at the intersection of conservation biology, genome science, and evolutionary biology, and we invite additional contributions in this area.

Harnessing genomic data to its full potential requires high-quality, annotated reference genome sequences. These act as the backbone from which detailed insights can be gleaned. *GBE* is proud to provide a "Genome Resources" section as a platform for publishing genome assemblies to accelerate conservation research across

the tree of life. A particularly interesting example is that of Hill et al. (2025), who used long, high-accuracy PacBio HiFi reads to assemble the genome of the wood-decaying fungus *Somion occarium*, a species with economic potential that is endangered by the loss of old-growth forests. Their efforts yielded a telomere-to-telomere, chromosome-level assembly that the authors used to investigate carbohydrate-active enzyme (CAZyme) genes, crucial for fungal-driven wood decay. This genome assembly is among several produced under the European Reference Genome Atlas (ERGA) initiative (Mc Cartney et al. 2024); ERGA and other transnational genome consortia are cataloging the diversity of life and generating extraordinary resources for the research community.

Assembling high-quality reference genomes is just the first step toward leveraging sequencing data to generate biological insight. Quantifying levels of genetic diversity in natural populations—traditionally considered a proxy of a population's adaptive potential—is a major focus of those working in this field. Endangered species, such as the Papua New Guinea endemic Queen Alexandra's birdwing butterfly (*Ornithoptera alexandrae*), often display low genetic diversity. Reboud et al. (2023) sequenced genomes of *O. alexandrae* and found very low genome-wide levels of observed heterozygosity (used here as a measure of genetic diversity): approximately 0.08%, compared with a set of 38 continental European species, which frequently had heterozygosity values above 1%. Estimated demographic trajectories indicated low long-term effective population sizes, suggesting the species has persisted as an endemic for a long time. The authors leverage these insights to propose the establishment of specific

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protection areas and support a dedicated rearing program to preserve this emblematic species, the largest butterfly in the world.

Insights from measures of neutral genetic diversity paint only part of the picture—understanding how functional genetic diversity mediates adaptation can provide crucial insights for conservation. Some articles in this virtual collection explore the new frontier of adaptation genomics. In one of these articles, Dussex et al. (2025) investigated extreme cold adaptation in the insular Svalbard reindeer (*Rangifer tarandus platyrhynchos*). The authors compared the genomes of reindeer subspecies to identify signatures of positive selection in Svalbard reindeer genomes overlapping genes associated with energy physiology, thermoregulation, or hair growth. These are relevant phenotypes for extreme cold adaptation, illustrating how functional genomics captures adaptive evolution in action. Tracking variants of adaptive significance is critical for conservation efforts, as the Svalbard reindeer is an island endemic that is recovering after centuries of overharvesting and now faces the emerging threat of climate change (Le Moullec et al. 2019).

Understanding the past to inform the future is crucial for evidence-based conservation. Thus, reconstructing a species' demographic history is another key objective in conservation genomics. In a recent study, Lo et al. (2025) examined the reticulate evolutionary history of four recently diverged extant species of balaenid whales: phylogenomic analyses revealed discordant topologies, while follow-up introgression analyses supported historical gene flow between species. To connect introgression to their broader demographic history, Lo et al. (2025) reconstructed past effective population sizes using coalescence rate estimation approaches, which revealed asymmetric migration between species throughout the Pleistocene.

In another article featured in this virtual collection, Atağ et al. (2024) highlight how failing to account for past processes can lead to an uneasy relationship between population genomics and conservation practices. These authors investigated population structure and diversity in endangered mouflon subspecies (*Ovis gmelini*) and found a low correlation between a lineage's genetic diversity and its conservation status. Since genetic diversity measures tend to capture past processes rather than current population trends (the basis of most conservation assessments), this study is a strong argument for the critical importance of integrating past and present processes to determine conservation status.

Research articles and genome resources in our virtual collection are complemented by a selection of "Reviews" that highlight the power of integrative

approaches in this field. Shinzato and Yoshioka (2024) summarized how genome data from stony corals (Scleractinia) can support coral restoration efforts by shedding light on patterns of genetic variation in these ecosystem engineers, as well as the molecular underpinnings of their relationships with algal symbionts. In a different direction, Brenman-Suttner and Zayed (2026) review how technical developments in phylogenomics, transcriptomics, museomics, and environmental DNA applied to bee biology can generate insights to inform conservation of global pollinators.

As we publish GBE's newest virtual collection, we invite researchers and practitioners from across the world to submit their latest research on conservation genomics to our journal. As a not-for-profit journal affiliated with the Society for Molecular Biology and Evolution (SMBE), publishing in a society journal has the added benefit of returning a portion of revenue generated back to the community; a specific example is the organization by the SMBE of several symposia focused on topics relevant to conservation genomics at its 2026 annual meeting in Copenhagen. As life faces its biggest challenge in millions of years, GBE and the broader SMBE community join global efforts to advance biodiversity science.

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