



Abstract Booklet

7th European Conservation Genetics Meeting

Genomes for the Future: Using Genetic Insights to Understand, Predict, and Restore Biodiversity.

ANTWERP, BELGIUM
A ROOM WITH A ZOO – 26TH-28TH AUGUST 2026



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Keynotes

DARWIN HALL – A ROOM WITH A ZOO
26TH-28TH AUGUST 2026



26 AUGUST 2026 — SESSION 1: PREDICTING FUTURES: GENOMICS UNDER CHANGE

Predicting fitness and futures: from variant-effect scores to selection in nature

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Abstract

Genome sequences can flag variants that may matter, but they do not measure fitness. This creates a central problem for evolutionary and conservation genomics: how can predicted molecular effects be translated into predictions about selection, persistence and recovery under change?

In this talk, I will argue that the genotype-to-fitness gap can be narrowed by calibrating variant-effect scores to biologically interpretable measures of selection, including selection coefficients and lethal equivalents. I will outline a framework that combines whole-genome annotation, species-specific demography, life-history data and forward-time simulations to estimate realised, masked and total genetic load. These calibrated estimates can then be tested against individual fitness, pedigree transmission, haplotype inheritance and allele-frequency shifts across life stages.

I will also discuss why the mode of selection matters. Absolute selection filters genotypes through their effects on viability, fertility or development, and can impose a direct demographic cost. Competitive selection instead acts through relative performance among gametes, embryos, juveniles or adults competing for limited opportunities. This distinction changes how weakly deleterious variants are exposed, sheltered or purged, and it affects how genetic load accumulates across species with different life histories, fecundities, recombination landscapes and conservation histories.

By linking variant-effect scores to selection coefficients and realised fitness, genetic load becomes more than a descriptive measure of genomic erosion. It becomes a tool for asking where, when and how selection operates in nature, and for predicting the persistence and recovery potential of populations under change.

26 AUGUST 2026 — SESSION 2: OPEN SESSION

Putting the “conservation” in conservation genetics

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Abstract

The goal of conservation genetics is to apply population genetics theory and genetic/genomic data to address important conservation problems. The field has entered an exciting era with technological advances such as cheaper and better DNA sequencers, faster and more powerful computers, pangenomics, and AI. Using the “latest and greatest” technology, however, is not always necessary or the most effective option for informing biodiversity conservation. In my keynote, I will outline four key strategies for most effectively advancing conservation using genetics. First, a deep understanding of population genetics theory is essential for applying genetic data to address conservation problems. There is no AI or other replacement for a strong understanding of population genetics, which is the most fundamental requirement for appropriate application of genetics/genomics to conservation. Second, the goal should not be to use the latest, “fanciest” genomic data or tool, but rather the genetic marker(s) and methods most appropriate for the question. Long-read sequences, pangenomics, and other cutting-edge approaches are not necessary for many conservation genetic questions, can be prohibitively expensive, and may risk over-promising and under delivering or draw attention away from more effective but less flashy approaches. Genetic engineering is rarely useful in conservation and detracts from the main problem in conservation: insufficient good habitat. Third, genomic data alone cannot replace the critical importance of field biology and an understanding of the natural history of focal species, which are essential for asking the right question(s) and interpreting results correctly. Lastly, working collaboratively with managers, practitioners, and stakeholders is essential for designing and communicating effective conservation genetics projects that directly inform decision-making. Conservation genetics and geneticists will play an increasingly important role in biodiversity conservation. Following these guidelines will maximize the utility of genetics for informing challenging decisions that will determine the fate of biodiversity.

27 AUGUST 2026 — SESSION 3: GENETIC LANDSCAPES OF THE PRESENT

Conservation Genomics in Practice: What Can We Do Today?

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Abstract

Conservation genomics is increasingly moving beyond proof-of-concept studies to becoming a practical tool for conservation. While some developments, such as incorporating genomic estimates of genetic load into conservation assessments, are currently in an exploratory phase, others, including robust genomic estimation of inbreeding, are now sufficiently mature for routine application in conservation management. Drawing on recent syntheses from the Molecular Ecology Special Issue "Conservation Genomics – Making a Difference", I present a contemporary overview of where conservation genomics is already contributing to management and where important future opportunities remain. Examples from our own research illustrate how genomic data can be used to assess conservation status in a broad range of taxa including whitefish (*Coregonus* spp.), the green hawker dragonfly (*Aeshna viridis*), and feral horses (*Equus ferus*). From a contrasting perspective, genomic analyses of the invasive zebra mussel (*Dreissena polymorpha*) reveal unexpectedly high levels of inbreeding in populations that nevertheless thrive in their introduced range. Finally, we demonstrate how whole-genome data can be incorporated into the framework by Frankham et al. (2011) to evaluate the risk of outbreeding depression during assisted migration and genetic rescue, illustrated by the endangered butterfly marsh fritillary (*Euphydryas aurinia*). Together, these examples demonstrate that conservation genomics is already providing practical guidance for conservation decisions. Continued methodological developments will further expand its role in evidence-based conservation management.

27 AUGUST 2026 — SESSION 4: FROM DATA TO DECISIONS: APPLYING GENOMICS IN MANAGEMENT

Rescue, restore, or maintain? Using genomics to manage populations after collapse

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Abstract

Conservation has rescued many species from the brink of extinction, but demographic recovery does not necessarily restore their long-term viability. Severe population declines can leave a persistent legacy of genomic erosion through loss of genetic diversity, increased inbreeding, changes in genetic load and reduced adaptive potential. Because these effects can continue for generations after population numbers recover, populations that appear successfully restored may remain genetically compromised and conservation-dependent.

Temporal genomic studies of collapsed and recovered species show how genomic erosion unfolds across population collapse and recovery. These examples illustrate a broader challenge for conservation genomics in which low genetic diversity on itself does not always prescribes the most efficient management action. Recent and historical inbreeding, masked and realized genetic load, adaptive variation and the distribution of diversity among wild and captive populations can instead point towards different interventions.

I will argue that genomics is most useful for conservation when it changes a management decision. Following population collapse, genomics can help determine whether we should maintain remaining variation, rescue populations through managed breeding or gene flow, or ultimately restore lost evolutionary potential using biobanks and emerging approaches. Combining genomic diagnosis with simulations allows alternative interventions to be evaluated before implementation and their consequences monitored through time. Rather than treating the genome as another measure of population “health”, conservation genomics can therefore become a framework for deciding when and how to intervene and to adaptively adjust whenever needed.

28 AUGUST 2026 — SESSION 5: RESTORATION GENOMICS AND THE (EUROPEAN) POLICY LANDSCAPE

Turning Genetic Diversity Into Action

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Abstract

Genetic diversity is now recognized within major international and regional policy frameworks, including the Kunming-Montreal Global Biodiversity Framework, European biodiversity policies, and national biodiversity strategies. This progress did not happen by chance. It reflects years of work translating scientific evidence into policy-relevant concepts, indicators, and tools that decision-makers can apply.

This keynote explores how conservation scientists can become active participants in the decisions their science is intended to inform. Drawing on experiences from European and global initiatives, I will share lessons from efforts to embed genetic diversity within policy, biodiversity monitoring, and conservation practice. Examples include the COST Action GENOA, which evaluates the integration of genetic diversity into national and international policy processes, and ongoing work within IUCN to strengthen the use of genetic information and biobanking for species conservation. Particular focus will be given to the Biodiversa+ project GINAMO, which uses a co-creation approach to bring together scientists, government agencies, practitioners, and other stakeholders to develop practical pathways for monitoring, reporting, and managing genetic diversity. By involving stakeholders from the outset, GINAMO aligns research questions, methods, and outputs with policy needs, available resources, and real-world conservation challenges.

The message is simple but challenging: producing evidence is not the same as producing impact. Conservation genetics has generated remarkable insights into biodiversity, adaptation, and population viability, yet too often our involvement ends when the paper is published. If we want our research to influence policy, guide management decisions, and contribute to global biodiversity goals, we must engage beyond academia. The future relevance of conservation genetics will be measured not only by the papers we publish, but by the decisions our science helps shape and the conservation outcomes it enables.



Talks

SESSION 1 – Predicting Futures: Genomics Under Change

DARWIN HALL – A ROOM WITH A ZOO
26TH AUGUST 2026



CLIMATE AS THE MAIN DRIVER OF LARGE-SCALE GENETIC PATTERNS AND PREDICTOR OF FUTURE RANGE SHIFTS IN THE GOLDEN JACKAL

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Abstract

Rapid global changes in climate and habitats lead to shifts in species' geographic ranges. Despite its potential importance for wildlife management, our understanding of the factors shaping species' spatial responses to rapidly changing environments remains limited. The golden jackal serves as an excellent model to address this knowledge gap, given its ongoing rapid range expansion. In this study, we investigated abiotic environmental factors influencing current genetic connectivity across the species range and driving ongoing and future range shifts, based on a comprehensive sampling scheme across Eurasia ($n = 363$), a set of ~20,000 genomic markers, and a landscape genomics framework. At the continental scale, geographic distance emerged as the predominant factor shaping genetic structure. At finer spatial scales, the genetic connectivity was best explained by climatic predictors - specifically high annual and seasonal variations in precipitation and temperature - which can shape the golden jackal's spatial genetic structure by constraining gene flow. Our connectivity models for current and future climatic conditions show that the species' northward expansion is facilitated by changes in these variables in central and northern Europe promoting high connectivity. Precipitation and temperature were also responsible for most local adaptation signals. We found that genetically distinct populations have divergent climatic niches and show different responses to climate change, highlighting the importance of incorporating genetic data into species conservation and management strategies under future environmental change. Given the potential role of hybridization with domestic dogs in shaping range expansion patterns, we investigated the association between environmental conditions and dog admixture proportions. We found no significant trends, indicating a limited effect of dog admixture on habitat choice. Our findings predict continued jackal expansion across Europe and contraction in southern Asia in response to global climate change, providing an example of a species that rapidly tracks the shifts of suitable habitats.

PARALLEL ADAPTATION AND PROJECTED GENOMIC OFFSET IN BOTTLENOSE DOLPHINS IN A CHANGING OCEAN

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Abstract

The pace and magnitude of anthropogenic change are unprecedented, making biodiversity conservation one of the defining challenges of our time. Marine ecosystems are especially vulnerable, yet adaptive responses in marine organisms remain poorly understood. Using one of the largest whole-genome sequencing datasets generated for a marine mammal, we applied a seascape genomics framework to Indo-Pacific bottlenose dolphins (*Tursiops aduncus*) distributed across the environmentally heterogeneous Australian coastline. Genome-wide variation strongly reflected geography, consistent with a northern origin followed by two independent north-to-south colonisation pathways along the east and west coasts. In contrast, putatively adaptive SNPs grouped individuals by tropical versus temperate waters irrespective of geographic distance or coastline, providing rare evidence for parallel adaptation to tropical conditions on both coasts. This pattern was likely facilitated by selection on standing genetic variation retained from a tropical northern origin and highlights the importance of considering demographic history when interpreting signatures of selection. Together, these results suggest tropical-temperate, ecotype-like differentiation across Australian waters. Extending this framework into a predictive context, we estimated genomic offset under moderate (RCP4.5) and high (RCP8.5) emission scenarios. Southeastern Australia consistently showed the highest projected offsets, whereas the more climatically stable southwest may represent a potential refugium. However, offset patterns varied across climate scenarios, environmental predictors, and marker sets, highlighting both the sensitivity and uncertainty of predictive genomic approaches, and emphasising that genomic offset should be interpreted as a relative indicator of potential concern rather than a deterministic prediction of maladaptation. Given the long generation times and strong site fidelity of coastal dolphins, rapid genomic adaptation alone may be insufficient to track projected environmental change. Our findings highlight both the potential and limitations of predictive genomics for conservation and emphasise the importance of integrating genomic, ecological, and behavioural perspectives when assessing species resilience in rapidly changing ecosystems.

BEYOND NEUTRAL DIVERSITY: A MECHANISTIC FRAMEWORK FOR ADAPTIVE POTENTIAL IN CONSERVATION GENOMICS

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Abstract

Neutral genetic diversity is widely used as a proxy for adaptive potential and population viability, yet empirical studies often find weak or inconsistent relationships between neutral diversity and fitness-related outcomes, questioning its predictive value in conservation genomics. Here, we present a forward-time, individual-based simulation framework developed in SLiM to investigate how adaptive potential varies with genomic variation, demographic history, and changing environmental selection.

We model contrasting demographic scenarios with selection acting through survival, reproduction, or fecundity, and fixed and environment-dependent distributions of fitness effects, where mutational effects can change magnitude and sign across environmental space.

To quantify fitness-relevant genomic state, we introduce Fitness Equivalents (FE), a fitness currency extending lethal equivalents by expressing deleterious and favourable genomic contributions on the same scale. FE summarizes how segregating and fixed variation influence fitness under specific environmental and selective contexts. We further derive adaptive potential metrics describing the capacity of standing genetic variation to become favourable under changing environmental conditions.

Across bottlenecks, chronic small populations, and recovery scenarios, neutral diversity mainly tracks demographic history but remains an incomplete predictor of adaptive potential and fitness-related metrics. Populations with similar neutral diversity can exhibit markedly different FE components and adaptive capacities, particularly following demographic perturbation or under genotype–environment mismatch. Selection route also alters these relationships, with survival-mediated selection generally maintaining stronger coupling between neutral diversity and fitness-relevant metrics than reproduction- or fecundity-mediated selection.

Our results suggest that neutral diversity alone provides an incomplete view of evolutionary resilience in changing environments. Bottlenecked populations may retain measurable short term adaptive potential despite severe losses of neutral diversity, whereas genetically diverse populations can harbour substantial realized load and limited adaptive responsiveness under rapid environmental change.

By disentangling neutral and fitness-relevant genomic components, this framework provides a mechanistic basis for re-evaluating conservation genomic indicators and developing more predictive metrics of population resilience under environmental change.

GENOMIC AND FITNESS CONSEQUENCES OF EXPLOITATION IN THE HAWAIIAN MONK SEAL

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Abstract

Understanding how past demographic events shape contemporary genomic variation is central to evolutionary biology and conservation genomics. Population bottlenecks are known to leave long-lasting genomic signatures affecting genetic diversity, inbreeding, and the accumulation of deleterious mutations, with consequences for fitness and adaptive potential. The Hawaiian monk seal (*Neomonachus schauinslandi*) was driven to near extinction by 19th century commercial sealing and continues to face human disturbance. Using whole-genome resequencing data, we infer historical population size changes and bottleneck signals, and assess how demographic history relates to inbreeding and mutation load. Specifically, we estimate genomic diversity, inbreeding from runs of homozygosity, reconstruct historical and contemporary effective population size, and identify putatively deleterious mutations. We then test whether mutation load predicts recruitment success across three fitness classes: recruits (pups that survive to sexual maturity and successfully recruit back as breeding adults), non-recruits (weaned pups that fail to recruit) and beach-dead individuals (pups that die prior to weaning). This design allows us to test whether individuals with lower realised fitness carry an increased burden of deleterious variants. Our study aims to clarify how anthropogenic bottlenecks shape present-day genomic landscapes and contributes to fitness variation. More broadly, this study provides insights into the long-term evolutionary consequences of exploitation-driven bottlenecks and inform conservation and management strategies for the Hawaiian monk seal.

TRANSLATING GENOMIC INSIGHTS INTO CONSERVATION ACTION: GENETIC INTERVENTIONS FOR DISEASE RESILIENCE IN AMPHIBIANS

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Abstract

Wildlife populations are increasingly threatened by habitat loss, emerging diseases, and climate change, requiring conservation strategies that move beyond preserving genetic diversity toward actively promoting adaptive potential. Recent advances in genomics are enabling a shift from data generation to decision-making, where genomic insights can directly inform management actions.

Targeted genetic intervention (TGI) leverages tools such as genomic selection and gene editing to enhance traits linked to fitness, including disease resistance and thermal tolerance. In this presentation, I will outline how genomic data can be translated into concrete conservation decisions, from identifying candidate loci and defining targets for genetic intervention to guiding selective breeding and gene editing, and evaluating intervention strategies.

Focusing on threatened amphibians, I will highlight how genomic and transcriptomic data are being used to inform interventions aimed at increasing resistance to chytridiomycosis. I will also discuss how these approaches are being developed alongside engagement with policymakers (e.g. IUCN, CBD), ethical frameworks, and partnerships with Traditional Owners to ensure responsible and socially informed implementation. Together, this work demonstrates how genomics can move beyond descriptive studies to support actionable, evidence-based management, providing a pathway toward establishing self-sustaining populations under ongoing environmental change.

INTERPLAY OF GENETIC DRIFT AND BALANCING SELECTION IN IBERIAN AND EURASIAN LYNX

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Abstract

Small populations are inherently vulnerable to stochastic processes, particularly genetic drift, which significantly accelerates the erosion of genetic diversity. As a counteracting force, balancing selection is a critical form of natural selection that acts to maintain advantageous polymorphisms within populations. A central question in evolutionary biology is the extent to which balancing selection can function as a "buffer" mechanism counteracting genetic diversity loss during severe demographic bottlenecks. While such events are expected to deplete overall neutral variation, it is hypothesized that loci under balancing selection, most notably the Major Histocompatibility Complex (MHC), may retain high levels of polymorphism. Investigating the balance between these opposing forces is essential for understanding how functional variation may persist in declining isolated populations and predicting their long-term adaptive potential in the face of environmental change. To explore these dynamics, we leverage medium- and high-coverage whole-genome sequencing (WGS) data to identify genomic regions under long-term balancing selection (LTBS) in two closely related felids: the Iberian lynx (*Lynx pardinus*) and the Eurasian lynx (*Lynx lynx*). Although with contrasting long-term demographic histories, both species include populations that have experienced severe bottlenecks and others that have remained stable in recent times. The disparity in demographic histories of the two species provides a comparative framework to assess the impact of severe population contractions on both neutral and adaptive genetic variation. By comparing among these two species the patterns of diversity in neutral loci and those under LTBS, we aim to elucidate to what extent balancing selection can maintain functional diversity despite the pervasive effects of extreme genetic drift.

JOINTLY PREDICTING VARIANCE AND INBREEDING EFFECTIVE POPULATION SIZE USING KINSHIP PROJECTION EQUATIONS

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Abstract

Understanding how demography shapes genetic drift remains a central challenge in conservation genetics. Over the last decades, stochastic demographic theory has substantially improved our understanding of how survival, fertility, dispersal and other life-history processes influence variance effective population size. However, other major determinants of genetic drift, such as inbreeding, still lack similarly general and tractable predictive frameworks. This gap arises because the mechanistic link between life history and population dynamics is much better understood than the link between life history and kinship structure. Yet the same demographic processes — survival, reproduction, dispersal, union formation, etc. — determine both stochastic population growth and how individuals are related to one another. This relatedness structure, in turn, shapes inbreeding and the strength of genetic drift. However, the link between stochastic life histories and inbreeding dynamics in structured populations remains poorly understood, and is therefore mostly implemented in simplified genetic models with non-overlapping generations. Here, I introduce a general projection framework for relatedness in structured populations. Its central result, the kinship projection equation, extends classical genetic and demographic projection models to incorporate the dynamics of kinship. Because the framework mirrors standard projection models, kinship, relatedness and inbreeding can be analysed using the general tools of structured projection theory, including transient dynamics and environmental or demographic stochasticity. I then show how this framework provides a route toward the joint projection of variance- and inbreeding-effective population size by explicitly linking stochastic demographic processes to relatedness and inbreeding coefficients. In this framework, effective population size emerges dynamically from the interaction between demographic stochasticity, life-history structure and kinship dynamics. More generally, this approach moves toward a predictive theory linking stochastic demography and evolutionary potential in structured populations.

RESILIENCE AND ADAPTATION OF ALPINE WHITEFISH TO CLIMATE CHANGE

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Abstract

Peri-Alpine lakes host a diversity of cold-adapted fish species of ecological and socio-economic value. Living at the southern edge of their distribution, any increase in water temperature could strongly affect population dynamics. Alpine whitefish populations in particular have undergone declines in European peri-Alpine lakes due to changes in trophic status and probable impacts of climate change and fishery management. Previous work has shown that whitefish adaptation to climate change varies among species and lakes but the relative contribution of environmental effects and genetic effects remains poorly explored. Furthermore, knowledge on population genetic diversity and the presence of adaptive genetic variation for thermal tolerance is lacking. This information is, however, crucial for guiding management strategies especially when stakeholders express interest to curb declining populations through the introduction of fish from other localities (i.e. the case for Lake Geneva). Through experimental work we assess the relative contribution of environmental and genetic effects for Lake Geneva and Lake Bourget whitefish populations (i.e. the latter are believed to be better adapted to increasing temperatures). Gametes of the two populations were used to create within and between lake crosses using full factorial breeding designs. Embryos were raised under ideal (6°C) and predicted climate change (9°C) conditions. Using fitness relevant traits (i.e. hatching success, hatching date and hatchling length) we quantify the relative contribution of maternal and genetic effect to temperature tolerance and assess hybrid performance. We combine SNP genotyping data from the adult breeders and offspring performance to screen for adaptive genetic variation. SNP genotyping data from fish caught outside of the reproductive period were used to characterize population genetic diversity and assess the prevalence of adaptive genetic variation for temperature tolerance. Combined these results aim to provide a thorough backbone to guide management decisions and evaluate whether genetic rescue efforts or meta-population management strategies may increase population resilience.

THE LOAD OF DELETERIOUS MUTATION IN WHITE-TAILED EAGLE AND ITS EFFECT ON MOLECULAR VARIATION

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Abstract

White-tailed eagle populations underwent severe bottlenecks or local extinctions in many countries during the 19th and 20th centuries. In Iceland, the population declined to only 15 breeding pairs by 1914, when the species received legal protection. However, the Icelandic population did not begin to recover until 1968, when the use of poisoned carcasses targeting Arctic foxes was banned. The population now comprises approximately 90 breeding pairs but is still characterized by low fecundity. Population genomic analyses have shown that the small populations in Iceland and Greenland are genetically isolated both from each other and from the large Norwegian population and the recently established population in Denmark. These island populations harbor lower genetic diversity and show clear evidence of inbreeding, including elevated levels of runs of homozygosity. Here, we use population genomic data together with recently annotated genomes of the White-tailed eagle and the Golden eagle to evaluate signatures of the Hill-Robertson effect; specifically, whether genomic variation shows evidence of background selection leading to reduced nucleotide diversity, or associative overdominance leading to elevated diversity, in relation to effective population size, deleterious load, and recombination rate. We address this by comparing island and mainland populations. The Icelandic population shows a low effective population size, reduced recombination rate, and the highest burden of deleterious mutations, although these are predominantly of weak effect, consistent with reduced efficacy of purifying selection. This pattern is especially pronounced in regions of low recombination, where the ratio of nonsynonymous to synonymous nucleotide diversity is elevated. Our study underscores the importance of genetic connectivity and population size for conservation.



Talks

SESSION 2 – Open Theme

DARWIN HALL – A ROOM WITH A ZOO
26TH AUGUST 2026



MUSEOMICS FOR CONSERVATION: REVEALING POPULATION STRUCTURE IN *CARACAL CARACAL*

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Abstract

The caracal (*Caracal caracal*) is one of the most widely distributed felids, occurring across Africa, the Middle East, Central Asia and India. Despite this broad distribution, its population structure and genome-wide diversity remain poorly understood, particularly in regions where populations are declining, such as India at the eastern periphery of its range. The lack of genetic and demographic information may obscure regionally distinct lineages and limit the identification of conservation-relevant units. Here, we use low-coverage genomes generated from museum specimens, alongside high-coverage data from South Africa and India, to investigate genetic structure and diversity across the caracal's range. We combine genotype likelihood-based methods with carefully filtered variant-based analyses to account for genotype uncertainty while retaining genome-wide information. Mitochondrial and nuclear genomic data are used to infer phylogenetic relationships and demographic history. Preliminary results reveal detectable regional structure, suggesting the presence of three distinct phylogeographic lineages broadly corresponding to southern Africa, northern Africa–Middle East, and Asia. Genomic data from India show comparatively reduced genome-wide diversity, potentially consistent with recent population decline at the eastern edge of the range, although broader sampling will be required to determine whether this pattern reflects the wider regional population. These findings highlight the value of museum collections for conservation genomics, especially in widespread, data-deficient species. By extracting informative genomic signals from sparse historical material, this study contributes to a better understanding of caracal diversity and provides a framework for refining conservation units in understudied carnivores.

BENEFITS AND LIMITATIONS OF DNA METABARCODING IN THE CONTEXT OF WOLF (*CANIS LUPUS*) FEEDING ECOLOGY

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Abstract

Understanding the ecological role of a species is key to further conservation actions and public acceptance, but the choice of method can have substantial effects on the interpretation of such studies. In order to conduct diet analyses in a highly adaptive apex predator within a densely populated area, we compared metabarcoding (molecular analysis) and hard part analysis (morphological analysis) using 144 wolf scats collected in Lower Saxony, Germany. It is widely recognised that metabarcoding provides higher taxonomic resolution and can thus tell us more precisely *what* was preyed upon, while hard part analysis allows for biomass quantification and can therefore tell us more about *how much* was killed. Consequently, metabarcoding should be applied if the dietary range in a given area is to be monitored, especially when focusing on elusive, protected or invasive prey species, whereas hard part analysis is required as basis for management decisions e.g. in the context of climate-resilient reforestation. Nevertheless, caution is advised when interpreting the results: we found that different taxa can be over- or underestimated by either method, that in metabarcoding, also different primers may lead to different detection success in certain taxa and that field contaminations or sequencing errors may be misinterpreted as food components; conversely, hard part analysis may result in misidentification of morphologically similar taxa or fail to identify species at the species level. While this combined approach not only enhances the robustness of dietary inference but also supports more informed conservation and management strategies, bringing together the advantages of both methods is desired for time and cost reasons. Overall, our results from both approaches confirm that wild ungulates are the main prey of wolves in Lower Saxony with some interesting regional and seasonal differences.

DEVELOPING FUNCTIONAL PROFILES AND COMPARATIVE ANALYSES FOR WILD AND MANAGED POLLINATOR GUT MICROBIOMES

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Abstract

The gut microbiome of wild pollinators plays an important role in pollinator health and resilience. Gut microbiota diversity has been characterized using metabarcoding, and more recently, metagenomic approaches for a limited number of pollinators, especially commercially used species. These approaches have allowed the observation of changes in the composition of the gut microbiome in response to certain environmental factors, but the implications of these changes for gene expression and metabolic pathways, and in turn, pollinator health, are virtually unknown. We move beyond studies focused on the composition of gut microbiomes to focus on their functions using metatranscriptomic analyses of RNA extracted from the gut of the wild pollinator, *Bombus pascuorum*, and the managed species, *Apis mellifera*. We introduced *Apis mellifera* hives in long term pollinator sampling locations to observe the effects of managed species introductions on microbiome function in wild pollinators. Across 58 pre-introduction and 188 during-introduction *Bombus* gut samples, and 200 *Apis* gut samples, we observe shared pathways between wild and managed pollinators, showing potential for exchange not only of microbiota, but also function. We detect an overrepresentation of gene expression transcripts linked to metabolic pathways of interest for key gut microbiome functions. Pathways include digestion related functions, such as metabolism and transport of carbohydrates, amino acids, lipids, and vitamins. Additionally we detect functions related to defence mechanisms and immune recognition. Comparison of results with previous metagenomics analyses also allows confident identification of the top contributing taxa involved in microbiome metabolism. Our research expands the study of metabolic expression in gut microbiomes to wild pollinators, and creates new commentary on their interactions with managed species.

GOING VIRAL! ~ MAKING USE OF VIRAL GENOMIC DATA AS A CONSERVATION TOOL FOR MONITORING HOST POPULATION CONNECTIVITY

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Abstract

The genomic era has significantly enhanced our understanding of the ecology and evolution of species, inadvertently aiding the conservation and protection of target and threatened species through evidence-based policy making. So far, most conservation measures are deployed on national or regional scales and are mainly based on individual or population-oriented research, such as observation-based surveys and population genetic studies. However, these approaches often lack the desired resolution to elucidate population dynamics on fine-grained spatial and temporal scales.

To disentangle these cryptic population dynamics, we can resort to evolutionary analyses of rapidly evolving organisms (i.e., viruses) that are closely associated with our target species. By this we mean that we can literally go viral with the field of conservation genetics and make use of viruses as molecular tags to study their hosts' population and dispersal dynamics (e.g. direction, velocity, frequency) at a resolution that would be impossible to obtain from the hosts directly.

In this light, we are setting up a proof-of-concept to elucidate the population connectivity between bat colonies of *Myotis emarginatus*, *Plecotus auritus* and *P. austriacus* in Belgium, based on viral metagenomic sequencing of fecal samples and viral phylogeographic inferences. The first preliminary data from this project has been sequenced and is currently being analysed, where we will be comparing two sequencing approaches: (i) a true metagenomic (untargeted) approach, with viral enrichment, and (ii) a hybrid-capture approach targeting a wide array of virus species simultaneously. At the time of writing there is no information yet on how well both approaches work and hold true to their potential; this will thus be a surprise for all. Despite the absence of definitive results, we anticipate that at least one of these approaches will yield valuable information on bat meta-population dynamics by exploiting viruses as molecular markers for making fine-grained phylogeographic reconstructions.

LESS FOOD, HEALTHIER GUT? SEASONAL FOOD AVAILABILITY SHAPES GUT MICROBIOME-IMMUNE-PHYSIOLOGY LINKS IN DEVELOPING ANTARCTIC PINNIPEDS

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Abstract

Climate change-induced variability in food availability profoundly affects the gut microbiome and host health. However, holistic research linking the microbiome, host physiology, and external stressors in wildlife populations remains scarce. We examined gut microbiome dynamics from birth to weaning in Antarctic fur seals (*Arctocephalus gazella*) at Bird Island, South Georgia - a declining population due to climate-driven reductions in their primary prey, Antarctic krill. We collected 600 rectal swabs from 100 mother-pup pairs across two breeding colonies and two consecutive seasons with contrasting food availability. Using 16S rRNA sequencing, linear mixed-effect models, PERMANOVA and co-occurrence networks, we characterized microbial diversity in relation to immune markers, fitness, and oxidative stress. Season was the strongest predictor of gut microbiome variation. In mothers, the low-food season was associated with higher richness and subtle compositional shifts. Effects were more pronounced in pups: those in the low-food season exhibited higher richness and more stable microbial networks. Highly influential taxa in low-food pups were linked to fermentation and immune regulation, whereas high-food pups showed a higher abundance of taxa associated with inflammation and pathogenesis. These seasonal shifts correlated significantly with physiological markers: higher diversity was associated with increased lymphocyte counts in the low-food season, suggestive of adaptive immune activation, while lower diversity co-occurred with elevated haptoglobin and oxidative stress in the high-food season, implying an inflammatory profile. Paradoxically, our findings suggest that nutritional limitation is associated with more structured microbial communities and a less inflammatory immune profile in developing pups, challenging simple assumptions about food availability and early life host and gut microbiome health. Structural equation modelling is underway to integrate the relative contributions of ontogeny, season, breeding colony, physiology, host stress and genetics. Ultimately, whether these contrasting microbiome-immune phenotypes reflect plasticity or susceptibility in a population already under environmental pressure remains to be determined.

ELUCIDATING THE GENOMIC ARCHITECTURE OF GENETIC LOAD

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Abstract

Advances in sequencing, computational and bioinformatic approaches are enabling a growing number of conservation programmes to explore and understand the genomic basis of traits associated with fitness. As a result, there is a growing interest in how best to mitigate the effects of maladaptive traits, while preserving whole-genome diversity overall. Of particular interest for conservation programmes is genetic load, or genomic variation that reduces mean population fitness in the immediate and long-term. To date, studies in non-model species focus on single-nucleotide polymorphisms (SNPs), in turn providing a robust framework for understanding how the evolutionary processes of mutation, recombination, drift, selection and population demography shape how SNPs contribute to genetic load. However, SNPs likely represent a fraction of total genomic diversity. Structural variants (SVs)—a diverse class of genomic variation that can impact a handful to millions of base-pairs—are largely unstudied in non-model species. Unlike SNPs, SVs have been shown to alter rates of mutation and recombination, indicating that frameworks developed for SNPs may not be fully compatible when examining SVs. To test whether SNP-based frameworks for conceptualising genetic load are translatable to SVs, we use *in silico* simulations, genomic data, and evolve and resequence experiments—using the seaweed fly (*Coelopa frigida*) as a model—to investigate SNP and SV diversity following a rapid and persistent demographic decline. Together, these approaches may improve our understanding of SVs under different demographic scenarios, and outline a more complete picture of genetic load in declining populations. Critically, elucidating the genomic factors shaping population persistence may enable conservation programmes to make better informed decisions around practices ranging from pairing choices to population translocations. This work aims to establish such a baseline, offering practitioners a reference framework for assessing current genomic health and tracking change over time.

A POPULATION GENOMICS PERSPECTIVE ON WOLF-DOG HYBRIDIZATION

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Abstract

European wolf populations persisted in southern refugia during the Late Pleistocene and experienced severe demographic bottlenecks followed by recent recovery. Consequently, extant populations such as the Dinaric-Balkan, Iberian, and Italian wolves retain reduced genetic diversity and elevated inbreeding. In parallel with population expansion, increasing anthropogenic pressures and spatial overlap with domestic dogs have promoted recurrent wolf-dog hybridization (WDH). While recent studies have begun to explore the potential adaptive effects of dog introgression, the consequences of WDH on genomic diversity patterns from a population-genomic perspective remain poorly understood. Here, we evaluate the effects of WDH on genomic diversity using an extensive whole-genome dataset of Dinaric-Balkan, Iberian, and Italian wolf populations. Such dataset included both non-admixed wolves and a uniquely representation of recently admixed individuals, spanning first to fourth generation backcrosses. Our findings show that dog introgression consistently increases genomic diversity and reduces inbreeding across all three refugial wolf populations, with WDH acting functionally as gene flow into historically bottlenecked populations. These apparent benefits are, however, accompanied by a significant increase in genetic load – particularly in its masked component. Overall, our results highlight a trade-off associated with anthropogenic hybridization: gains in genetic diversity and reduced inbreeding versus the accumulation of deleterious variation that may pose a latent risk under future population contractions or renewed fragmentation.

TRACKING GENETIC DIVERSITY LOSS IN *CEPHALANTHERA RUBRA* TO INFORM CONSERVATION ACTIONS

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Abstract

The orchid *Cephalanthera rubra* (L.) Rich. (red helleborine) is widespread across Europe, but it has undergone a significant decline in parts of its range, including in England where it is listed as Critically Endangered. Despite its broad distribution, the species is rarely abundant, possibly due to its life-strategies, such as a long-lived perennial habit and dependence on symbiotic interactions with pollinators and fungi. In England, the species persists at only five sites, with the total number of individuals emerging annually not exceeding thirty. Intensive monitoring and habitat management have been conducted to prevent further declines; notably, the “Red Helleborine Steering Group (RHSG)” was founded in 2006, bringing together reserve managers, members of environmental bodies, scientists and members of the public, prompting a consistent conservation effort. This has contributed to the reappearance of the species at some sites after two decades, demonstrating the value of coordinated conservation actions from across multiple stakeholders.

Complementing the ecological monitoring carried out as part of these efforts, we have undertaken a genetic study to assess the extent of genetic diversity loss in English populations. We developed species-specific targeted capture baits derived from double-digest RAD sequencing loci and used them to compare genetic diversity between historical herbarium specimens (18th-20th centuries) and contemporary samples collected in the few remaining sites in England, as well as samples from other European populations. This approach allowed us to assess changes in genetic diversity through time and evaluate relatedness among individuals. The large genome size of *C. rubra* is currently hampering the feasibility of whole-genome sequencing; however, we expect the targeted capture strategy developed here to facilitate further genome-wide analyses in the species. Our results will inform conservation actions, including cross-pollination experiments and targeted interventions aimed at improving reproductive success and long-term viability of the red helleborine in England and elsewhere.



Talks

SESSION 3 – Genetic Landscapes of the Present

DARWIN HALL – A ROOM WITH A ZOO
27TH AUGUST 2026



DOES SOUTHWESTERN EUROPE REALLY HAVE A HYBRID PROBLEM?

INSIGHTS FROM A SYSTEMATIC GENETIC ASSESSMENT OF WOLVES IN THE IBERIAN PENINSULA

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Abstract

Wolf (*Canis lupus*) - dog (*Canis familiaris*) hybridization is often cited as a major conservation concern, particularly in Southwestern Europe where high densities of free-ranging dogs are assumed to increase interbreeding. However, robust estimates of hybridization frequency remain scarce due to opportunistic or biased sampling protocols, as well as limited comparability across studies due to the use of non-standardized genetic markers. Here, we present the first systematic, large-scale, non-invasive survey of wolves across the Iberian Peninsula, designed to quantify wolf-dog hybridization under standardized conditions. We collected over 800 fecal samples and applied a multi-marker approach, combining mitochondrial DNA barcoding, 13 autosomal microsatellites, two sex markers, and a panel of 96 ancestry-informative SNPs capable of resolving hybrid classes up to second generation backcrosses. Contrary to widespread expectations, we found a very low prevalence (< 2%) of hybridization. Among 205 identified individuals, we detected three first generation (F1) hybrids (two of which were related), and one second-generation (F2) individual, corresponding to just three hybridization events. These were restricted to the periphery of the distribution range or areas near human settlements. Our results challenge the prevailing assumption that Southwestern Europe is a hotspot of wolf-dog hybridization. Instead, hybridization prevalence in Iberia is comparable to that reported in Central Europe, despite differences in free-ranging dog abundance. The scarcity of backcrosses further suggests reduced hybrid fitness and a currently low risk of genetic swamping in Iberia. More broadly, our study highlights a key research gap: identifying the drivers of strong regional variation in hybridization rates across Europe. It also underscores the importance of systematic non-invasive sampling combined with standardized genetic panels to produce comparable and reliable estimates, essential for evaluating the extent and conservation relevance of wolf-dog hybridization.

INVESTIGATING THE INTERACTION BETWEEN INBREEDING AND GENETIC LOAD IN THE IBERIAN LYNX

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Abstract

In small populations, the reduced efficiency of purifying selection promotes the accumulation of mildly deleterious mutations, and increased inbreeding exposes recessive deleterious alleles in homozygosity, contributing to fitness reductions. Conversely, inbreeding may also facilitate the purging of highly deleterious variants. Here, we explore the interaction between inbreeding and purging in the Iberian lynx (*Lynx pardinus*), a species that experienced severe population declines followed by recovery through intensive management. We analyzed whole-genome sequencing data from 292 individuals sampled across the two remnant populations (Doñana and Andújar-Cardena), which diverged ~200 years ago, and their admixed descendants. Genomic inbreeding patterns were characterized by calling runs of homozygosity (ROH) and the genomic distribution of ROH was examined to identify regions enriched or depleted in homozygosity. Additionally, genetic load was estimated through the functional annotation of variants, which were classified into neutral, moderately, highly, and extremely deleterious categories. We evaluated the distribution of deleterious variation relative to ROH to investigate the potential role of purging. Preliminary results showed that Doñana, the most inbred population (mean $F_{ROH}(>1Mb) = 0.47$), carried fewer extremely deleterious alleles than Andújar-Cardena (mean $F_{ROH}(>1Mb) = 0.32$), consistent with more efficient purging. Variants of moderate and high predicted impact were more frequent within ROH compared to non-ROH regions, whereas extremely deleterious variants did not show this pattern. All deleterious categories were enriched in longer ROH, associated with recent inbreeding, with a stronger effect for variants of higher predicted deleteriousness. This pattern suggests that more deleterious variation accumulates within recently inbred genomic regions, where purging has had a limited time to act. Together, these results highlight the heterogeneous effects of inbreeding across variants with different predicted effects and emphasize the need to jointly account for both components of inbreeding depression in conservation genomics.

A CONSERVATION GENOMICS FRAMEWORK TO ASSESS AND COMPARE INBREEDING OVER TIME IN WILD POPULATIONS

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Abstract

As habitat fragmentation, degradation, and loss accelerate, inbreeding is expected to increase and threaten many wild species. Yet, our understanding of the extent of inbreeding in wild populations and how it has changed over time remains limited. A major reason is that current approaches do not provide genomic inbreeding estimates that are comparable across species and studies, which limits their usefulness for setting conservation priorities. This work aimed to improve the assessment of inbreeding in wild populations by designing a framework that delivers inbreeding estimates comparable across species and studies, and that enables inference of temporal change. First, we developed a method to estimate species-specific genome-wide recombination rates to express runs of homozygosity (ROH) on a common generational scale and obtain comparable inbreeding estimates. Then, we modelled ROH length distributions under alternative demographic scenarios to enable interpretation of inbreeding trajectories—patterns of inbreeding through time. We applied our approach to 1,138 whole-genome-sequenced individuals from 154 populations across five conservation-relevant species, two plants (*Dianthus carthusianorum*, *Eriophorum vaginatum*), one passerine bird (*Emberiza citrinella*), one toad (*Epidalea calamita*), and one butterfly (*Melitaea diamina*). Our results revealed striking differences in both the magnitude and temporal patterns of inbreeding across populations and species. The toad had the highest overall inbreeding (mean $F_{\text{ROH}} = 0.25$), but inbreeding was old, with no sign of recent increase. By contrast, the bird was the least inbred species (mean $F_{\text{ROH}} = 0.026$) but suffered a very strong and recent increase in inbreeding, which coincides with ongoing demographic decline inferred from independent monitoring data. These findings highlight the value of cross-comparable inbreeding estimates and temporally resolved inbreeding trajectories for identifying genetic risks and setting conservation priorities that are not apparent from static measures.

THE ROLE OF LOCAL AND LANDSCAPE-SCALE FACTORS ON THE GENETIC DIVERSITY OF *BRIZA MEDIA* IN THE CONTEXT OF GRASSLAND ABANDONMENT

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Abstract

Recent changes in land use have led to drastic loss and fragmentation of semi-natural grasslands, impacting the genetic diversity of grassland plants. However, the specific effects of recent habitat shifts on the genetic diversity of wind-pollinated plants remain understudied. We assessed the relative effects of contemporary landscape composition, management and local environmental conditions on the genetic diversity and gene flow of *Briza media* in open and overgrown calcareous grasslands of Western Estonia. We examined the genetic patterns of *B. media* across 22 populations. High-throughput sequencing (RADseq) yielded ~29,000 SNPs. We used both link- and node-based landscape genetic methods for studying the effect of landscape structure and local environmental conditions on genetic variation. Our results revealed that *B. media* populations in managed grasslands had higher genetic diversity than those in abandoned grasslands. Higher amount of woodland in the surroundings of *B. media* populations resulted in lower genetic diversity. Additionally, the genetic diversity of *B. media* was influenced by some soil parameters. We observed increasing genetic differentiation between populations with increasing distance, but found no influence of landscape structure on the gene flow of *B. media*. These findings suggest that shifts in grassland management and landscape change influence the genetic diversity of wind-pollinated plants, which have often been considered less sensitive to these factors. Consequently, conservation and restoration practices should also account for the potential vulnerability of wind-pollinated grasses.

URBANIZATION DISRUPTS GENE FLOW AND DRIVES RAPID GENETIC EROSION IN CAPE TOWN'S CARACALS

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Abstract

Urbanization is a significant driver of habitat fragmentation globally, creating small, isolated wildlife populations that are vulnerable to accelerated genetic drift and inbreeding. Urban areas also function as novel ecosystems that introduce unprecedented environmental stressors on wildlife, rapidly filtering communities to favour a reduced set of adaptable species. To investigate the genetic consequences of rapid urban expansion for caracals (*Caracal caracal*) in the city of Cape Town, South Africa, we combined analyses of microsatellite and mitochondrial markers with genome-wide sequence data and eco-evolutionary simulation modelling. Following the local extinction of Cape leopards in the 1920s, caracals are the largest remaining indigenous carnivore on the Cape Peninsula and function as crucial ecological regulators in this global biodiversity hotspot. Sampling across geographically distinct urban and rural populations revealed contrasting temporal patterns: mitochondrial markers indicate regional historic connectivity, while microsatellite and genomic analyses reveal pronounced genetic differentiation driven by Cape Town's rapid expansion. Urban caracals isolated by the city's metropole show reduced allelic richness and elevated inbreeding consistent with low migration rates into the population over the past ~75 years, averaging 1.3 effective migrants per generation. Inbreeding primarily manifests as long runs of homozygosity (>10 Mb) consistent with recent isolation, and eco-evolutionary simulations suggest that reductions in migration and increased anthropogenic mortality will both substantially elevate local population extinction risk. Our findings show how urbanization has rapidly disrupted gene flow in this otherwise highly mobile carnivore, generating substantial genetic change within contemporary timeframes. These results demonstrate the value of multi-marker approaches for detecting anthropogenic impacts on wildlife populations and underscore the capacity of cities to rapidly alter population dynamics, even in this highly adaptable and resilient wild cat.

GENETIC INDICATORS FOR THE MANAGEMENT AND CONSERVATION OF NORWEGIAN WILD REINDEER

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Abstract

The Quality Standard for Norwegian wild reindeer is a national framework for evaluating the status of wild reindeer populations and identifying negative trends relevant to science-based, adaptive management. Genetic health was included in the first assessment of populations but solely based on loss of genetic variation derived from microsatellites and often with limited historical sampling material available. Using a 625k SNP array, we analyzed 1,397 reindeer from 22 Norwegian wild reindeer management units and a panel of semi-domestic reindeer, generating the most comprehensive genomic dataset yet assembled for this system. We quantified recent loss of genetic variation, effective population size, inbreeding, population structure, and introgression from semi-domestic reindeer. The results reveal a striking dual challenge. Several wild reindeer populations show clear signs of recent genetic erosion, with low effective population sizes and/or elevated inbreeding due to isolation and small population sizes. In contrast, several large populations are less threatened by genetic erosion than by ongoing fragmentation and/or extensive semi-domestic introgression, in some cases pointing to predominantly semi-domestic ancestry. These findings challenge any simple definition of “wild reindeer” and expose the limits of relying on a single genetic indicator for conservation status assessment. We therefore propose a revised genetic parameter built on three complementary components: loss of genetic variation, effective population size, and semi-domestic introgression. We present threshold-based recommendations for loss of genetic variation and effective population size. In contrast, semi-domestic introgression is less amenable to simple thresholds, because the conservation value of genomic patterns between “wild” and semi-domestic reindeer depends on how those patterns are interpreted; therefore, a nuanced approach is needed to inform management decisions. More broadly, this case shows how genome-wide data can help bridge the persistent gap between conservation genetics and biodiversity governance.

GENOMIC CONSEQUENCES OF 20TH CENTURY POPULATION DECLINES ON THE GREAT BUSTARD IN GERMANY

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Abstract

The Great Bustard (*Otis tarda*), a once widely distributed species across Europe and Asia, has experienced drastic population declines over the past century. These declines can be primarily attributed to the emergence of mechanised agriculture, hunting, and mammalian predation. Furthermore, extensive habitat fragmentation has resulted in highly isolated populations, susceptible to inbreeding and the loss of genetic diversity. In Germany, the Great Bustard underwent a substantial population bottleneck in the 20th century, suffering a 99% population decline over a 60-year period. However, due to population reinforcement and habitat management programs, the German Great Bustard population has shown significant signs of recovery – largely in contrast to the continuously declining populations in other parts of Europe. Nevertheless, reproductive success of the German population remains low in the wild, raising concerns of reduced population viability due to inbreeding since their decline. We here provide genome-wide estimates of diversity parameters such as inbreeding and mutational load for the German population, based on n=41 samples across a 130-year period, spanning pre- and post-bottleneck generations. Our results show clear evidence of genetic differentiation between temporal cohorts, suggesting a substantial change in allele frequencies over time. We also found evidence of contemporary increases in inbreeding, with a greater frequency and length of runs of homozygosity (ROH) in the post-bottleneck population. Moreover, we found strong support for a lower realised load of deleterious mutations after the population underwent the bottleneck (i.e., genetic purging). Critically, however, the remaining deleterious mutations include alleles associated with reduced cellular structure regulation and immune system functioning. Further inbreeding could thus result in the fixation of such alleles, compromising populations fitness and elevating the future risk of extinction. This study highlights continuous conservation management needs to foster the remaining genetic diversity and prevent serious consequences of inbreeding depression in the German Great Bustard population.

CONSERVATION GENOMICS OF A MICRO-ENDEMIC AMAZONIAN CANGA PLANT SPECIES

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Abstract

A key challenge in conservation biology is understanding the relationship between habitat loss induced by human activities, such as mining, and population dynamics through genomic monitoring. One promising approach is the study of genetic load and its relationship with population size. We generated high-quality whole-genome data for more than 100 *Ipomoea* individuals belonging to two species endemic to the Canga ecosystem of Carajás, home to one of the world's largest iron mining operations. These species include the micro-endemic *Ipomoea cavalcantei* and its sister species *Ipomoea marabaensis*, which occurs in the same region but has a broader distribution range and larger population size. We investigated the demographic history and associated genetic load of three populations of *I. cavalcantei* that differ in population size and in their degree of exposure to mining activities since the 1980s. Although genetic diversity was lower in *I. cavalcantei* than in *I. marabaensis*, it remained relatively high overall, and no runs of homozygosity were detected, possibly due to the species' self-incompatible mating system. Our analyses revealed population declines in *I. cavalcantei*, with timings that correspond to the onset of mining activities in the different areas. Genetic load, estimated using functional annotations, was higher in *I. cavalcantei* than in *I. marabaensis*, as expected, but did not differ significantly among *I. cavalcantei* populations. Overall, our results reveal demographic consequences associated with mining activity. However, despite its restricted distribution, *I. cavalcantei* currently appears to maintain relatively high genetic diversity and limited genetic load. In addition, hybrids identified between the two species are currently being investigated to assess their relevance for the conservation of *I. cavalcantei*.

REMNANT POPULATION STRUCTURE AND ECOTYPE DYNAMICS IN DEPLETED COASTAL ATLANTIC COD

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Abstract

Atlantic cod (*Gadus morhua*) along the Swedish coast have undergone severe population declines, with some coastal areas now supporting very low abundances and few or no adult fish. Despite this collapse, the continued occurrence of eggs and juvenile fish suggests that local spawning activity and recruitment may still persist. However, the population origin, connectivity, and ecotype composition of contemporary coastal cod remain poorly understood. In this ongoing study, we investigate contemporary population structure and ecotype dynamics of cod along the Swedish coast. Using juvenile fish, eggs, and adult samples collected across multiple coastal areas and years, we assess whether remnant local populations persist despite demographic decline and evaluate spatial and temporal variation in ecotype composition. Whole genome sequencing is used to identify fine-scale population structure and genomic signatures associated with local adaptation across Scandinavian cod populations spanning salinity gradients from the North Sea to the Baltic Sea. In parallel, we use and develop genomic resources, including SNP panels, that provide scalable tools for long-term genomic monitoring and identification of ecotypes and populations. The project is conducted within the framework of ecosystem-based marine management and contributes genomic tools and population knowledge to regional efforts aimed at restoring cod populations and strengthening the resilience of coastal fjord ecosystems. Preliminary analyses reveal clear divergence among major cod ecotypes and substantial spatial and temporal variation in ecotype composition among coastal nursery areas. While some regions show evidence of remnant local population structure, other areas appear more strongly influenced by connectivity and mixing among populations, with individuals from multiple stocks occurring within the same coastal systems. These patterns suggest complex contemporary population dynamics shaped by both local recruitment and movement. Our study highlights the potential of integrating genomic monitoring into conservation and ecosystem-based management strategies for commercially important marine species undergoing severe population decline.

CONSERVATION GENETICS IN ECTOMYCORRHIZAL FUNGI: CONNECTING ABOVE- AND BELOW-GROUND GENETIC DIVERSITY

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Abstract

Ectomycorrhizal (EM) fungi play a key role in forest ecosystems, through the mutualistic symbioses they form with most temperate and boreal tree species. However, information on their level of genetic diversity is scarce, and it is likely that genetic indicators such as ‘Ne500’ are not applicable to such organisms. EM fungi display complex life cycles – haplo-diplontic with both sexual and clonal reproduction – of which a large part takes place in the soil. Demographic information is therefore particularly difficult to obtain, and genetic data is most often derived from the epigeous sporocarps, giving an incomplete picture of the genetic diversity. For these reasons, we hypothesize that current genetic indicators cannot be reliably estimated from typical population genetic data in EM fungi. In order to effectively assess the state of genetic diversity within EM fungal populations, we use new genetic data from sporocarps, soil and root-tips samples collected in France, focusing on diverse Basidiomycota species such as *Laccaria amethystina*, *Suillus bovinus*, *Amanita citrina* or *Lactarius deliciosus*. Genotypic information is acquired using innovative sequencing methods (sequence-based microsatellite genotyping), that are now applicable to environmental DNA. This newly produced dataset allows us to explore the interplay between above- and below-ground genetic diversity. We also put these results in perspective with existing ecological, genetic and genomic datasets, as well as forward simulation approaches. This combination of methods allows for a better understanding of the spatio temporal dynamics of genetic diversity in populations of EM fungi, and provides clues as to which life history traits are most likely to influence this genetic diversity. Finally, exploring the relationships between demographic parameters (e.g. the number of sporocarps) and genetic metrics will be crucial to inform the definition of appropriate genetic indicators for the conservation of forest fungi.



Talks

SESSION 4 – From Data to Decisions: Applying Genomics in Management

DARWIN HALL – A ROOM WITH A ZOO
27TH AUGUST 2026



MANAGING THE GENOMIC LEGACY OF NEAR EXTINCTION: LESSONS FROM THE PINK PIGEON

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Abstract

Intensive conservation management can rescue population size yet fail to rescue genetic diversity. The pink pigeon (*Nesoenas mayeri*), endemic to Mauritius, declined to 9-10 known wild birds in the 1990s but recovered to ~600 in the following decades through captive breeding, reintroductions, predator and disease control and supplementary feeding. Given the well-documented demographic trajectory and decades of monitoring, the pink pigeon provides a powerful case study for linking genomic trajectories under intensive management to conservation decisions after a severe bottleneck. We generated 150 whole-genomes spanning 180 years, including historical, bottleneck-era, and contemporary individuals. Using this temporal dataset, we quantified genome-wide and immune gene diversity, inbreeding, putative load, kinship structure, and demographic history. We document a ~20% loss of genetic diversity between historical and 1990s individuals, accompanied by rising inbreeding, evidenced by an increase of medium- to long-length runs of homozygosity. Genetic diversity continued to decline during the period of most rapid demographic recovery, with no detectable rebound between 1990s and contemporary individuals. Kinship analyses indicate strong reproductive skew during early-recovery, with contemporary birds descending from a small number of lineages, which could help explain the continued loss of diversity despite the increased population size. Forward simulations further suggest that future genetic rescue using the captive population may yield limited gains, as the captive population has also lost substantial diversity. These results illustrate the difficulty of restoring genomic diversity once populations have passed through extreme bottlenecks. More broadly, they show how temporal genomics can guide management by identifying under-represented lineages, tracking effective rather than census population size, optimizing captive breeding, and evaluating the timing and source populations for reintroductions or genetic rescue.

USE OF WHOLE GENOME RE-SEQUENCING TO CHARACTERIZE CAPTIVE BREEDING STOCKS OF THE CRITICALLY-ENDANGERED EUROPEAN HAMSTER

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Abstract

Captive breeding and translocations are complementary actions for reinforcing declining wildlife populations, with key goals of preserving the genetic integrity of wild populations while also enhancing genetic variation and minimizing inbreeding. Ideally, captive populations should be cross-bred to counteract population isolation. However, cross-breeding also carries risks due to potential loss of local adaptation and spread of deleterious mutations. Genomic characterization of captive breeding stocks therefore represents a powerful tool that can identify potential genetic mismatches and predict the effects of population mixing. The European hamster *Cricetus cricetus* is a critically-endangered species, with significant declines on the western edge of its Central European range. In Germany, European hamsters are maintained in ten independent captive breeding stocks (hereafter, breeds) used to reinforce wild populations. We conducted whole genome re-sequencing of $n = 58$ captive hamsters and combined these results with an existing dataset of $n = 35$ wild hamsters to compare population genetic parameters among breeds and to wild populations. Individuals were strongly differentiated by eastern and western origin, but we found no evidence for local adaptation. Wild populations exhibited significantly lower genetic diversity and greater rates of inbreeding, and both captive and wild individuals from the western lineage showed evidence of increased genetic erosion. Within breeds, we found an increase of mutational load with genetic diversity. Annotation of protein-modifying mutations revealed a potential mutational hotspot in the tumor-regulating *Klf4* gene, with one eastern breed harboring fixed derived alleles in this region. Our results show that captive breeding programs for the European hamster have successfully enhanced genetic diversity and reduced inbreeding; however, the status of the western breeds highlights the role of genetic erosion in areas of greater decline. Our recommendations include mixing breeds within regions, given the low risk of outbreeding depression and the benefits of breaking up fixed deleterious haplotypes.

LYNX REINTRODUCTION FROM A BOTTLENECKED SOURCE EXPOSES A LETHAL RECESSIVE VARIANT

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Abstract

Reintroductions and translocations are widely used to support endangered species. However, such efforts often face genetic challenges as small population size and restricted gene flow can lead to inbreeding and loss of genetic diversity. Inbreeding depression is a well-known risk in these programs, as increased homozygosity can expose recessive deleterious alleles, compromise fitness and threaten population persistence. While correlations between inbreeding and reduced fitness are well documented, no causal variant for a lethal disease has been identified in a wild population. We combined long-term health monitoring and population data with analyses of whole genome data to identify the genetic basis of lethal organ mineralization in young Eurasian lynx (*Lynx lynx*) from a reintroduced population in Switzerland. The underlying cause was identified at the molecular level as a recessive loss-of-function allele. Spatio-temporal analyses of targeted sequencing data revealed that the allele was introduced from one of the source populations and increased in frequency through founder effects and inbreeding. Whereas previous work has primarily assessed inbreeding depression through genome-wide estimates of mutational burden and genetic models, our study establishes the first direct link between reintroduction history and a lethal genetic disease in the wild. The long-term lynx population and health monitoring program in Switzerland embedded in strong interdisciplinary collaboration across wildlife health, animal genetics, and conservation genomics, provided an exceptional setting for the discovery and evolutionary interpretation of this lethal disease. Our findings provide an important real-life demonstration of the genetic risks of common reintroduction practices. They have direct implications for management and inform ongoing debates in conservation genetics on source population selection.

GENETIC STATUS OF BEARDED VULTURES: COMPARING THE ALPINE REINTRODUCED AND THE ISOLATED CORSICAN POPULATION

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Abstract

Preservation and restoration of natural habitats are fundamental to conservation, with species reintroductions playing a pivotal role in restoring disrupted ecosystems. These efforts require major investments and demand an integrated approach combining ecological and genetic insights. Understanding the genomic causes of fitness declines after population bottlenecks and identifying limiting factors of breeding and reintroduction programs are essential for their success. We analysed 151 whole-genomes of the bearded vulture (*Gypaetus barbatus*) to improve our understanding of the genetic complexities inherent in reintroduction efforts. After an absence of over 80 years, this species was successfully reintroduced to the Alps in the mid-1980s. The project involved meticulous planning, including genetic considerations and continuous monitoring and resulted in very promising population growth. Yet, the initial number of founders was limited and pedigree analyses reveal that their genetic contribution to the current wild population is highly skewed. Despite breeding efforts designed to maximize genetic diversity, we observe a loss of genome-wide diversity and increased inbreeding from the founders to the released and further to the wild population. Consequences of this increased inbreeding in the wild have already manifested in the observation of three flight-less individuals.

In contrast, the Corsican population, isolated since the extinction of the Sardinian group in the 1960s, faces low reproductive success and a total count below 25, raising serious concerns about its future and genetic status. As expected, we find extremely high inbreeding levels (corresponding to parent-offspring matings) and low genome-wide diversity. We also find a clear genetic distinction between the Corsican and the Alpine population, which is likely the result of drift due to isolation but also suggests unique diversity of potential value to be preserved. The insights of our ongoing research are essential for refining conservation strategies for both populations to secure their long-term viability and for improving the effectiveness of species recovery initiatives elsewhere.

POPULATION PUZZLES: UNDERSTANDING THE GENETIC STRUCTURE AND HEALTH OF RECENTLY DIVERGED GALAPAGOS GIANT TORTOISE LINEAGES

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Abstract

The Galapagos giant tortoises (*Chelonoides spp.*) are a notable example of rapid evolution and diversification in islands. The southern region of Isabela Island is home to population fragments of the most recently diverged lineages, showing a morphological gradient from West to East. Two species have been named here – *C. vicina* associated with the Eastern volcano Cerro Azul, and *C. guntheri* associated with the Western volcano Sierra Negra. The geographic extent and taxonomic affiliation of each population fragment in the present day is not well understood and as a result, neither is their genetic health. This understanding is critical in order to plan future conservation actions, especially in the case of the Sierra Negra population (possibly the only remaining of *C. guntheri*), which has been greatly diminished due to historical hunting and ongoing poaching. We used whole genomes from individuals sampled across Southern Isabela to assess population structure using clustering and phylogenetic approaches. After grouping sampling locations into genetic clusters, we assessed population genetic health through heterozygosity, nucleotide diversity, and identification of runs of homozygosity (ROH). Additionally, we also assessed levels of migration between the clusters. We find that, in Southern Isabela, there are eight distinct genetic clusters, with only one belonging to *C. guntheri* and not much movement between clusters. However, we also note that the nucleotide diversity, heterozygosity, as well as the number and total length of ROH are comparable across clusters, with no cluster showing clear signs of vulnerability. We therefore conclude that the focus for current conservation action should be on increasing population size for the one *C. guntheri* population with no immediate need for translocations among the *C. vicina* fragments.

REGIODIV – LESSONS LEARNED FROM A NATION-WIDE GENOMIC ANALYSIS OF MULTIPLE SPECIES USED IN GRASSLAND RESTORATION

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Abstract

The use of seed for grassland restoration is regulated in Germany by seed transfer zones that have been defined without plant genetic background. We studied genomic variation of multiple plant taxa frequently used in restoration seed mixes on a national scale in Germany to inform seed production management in the German seed zone system. In particular we ask whether seed zones align with spatial population genomic structure and whether and how the system can be improved to better reflect genetic structure.

Sampling was performed in 2020-2022 together with 160 volunteers and 19,000 samples across 28 taxa representing 33 species, were ddRAD-SNP-genotyped. Cytotypes (ploidy level) were assessed by flow cytometry. Population structure was assessed with ADMIXTURE and IBD/IBE analyses. Genomic offset analyses are presented elsewhere [see abstract by Stefan Michalski].

Spatial genomic structure was species specific ranging from hardly any structure (e.g. *Arrhenatherum elatius*, *Leucanthemum vulgare* s.str.) to highly structured and spatially coherent gene pools (e.g. *Agrimonia eupatoria* (K=6), *Knautia arvensis* (K=6), *Ranunculus acris* (K=7)). Spatial distribution of gene pools rarely aligned with seed zones. Almost all species showed isolation-by-distance patterns suggesting limited gene flow and evolution of differentiated gene pools despite centuries of agriculture. Genetic differentiation scaled with breeding and pollination systems with lowest differentiation in wind pollinated grasses and highest differentiation in self-compatible insect pollinated herbs. Using subzones of seed transfer zones as smallest spatial units, an across-species analysis indicated that the current 22 seed zones on average account for 70% of genetic variation among subzones. As gene pools often encompass multiple seed zones, we propose species-specific replacement rules for adjacent seed zones depending on genetic distance.

Similar to the whole flora, a part of the species (n=6) were heteroploid, consisting of multiple cytotypes. Novel was the finding of diploid *Euphorbia cyparissias* and the regional dominance of tetraploid *Achillea millefolium* s.l. and the absolute dominance of tetraploids in *Knautia arvensis*. Cytotypes were generally strongly genetically differentiated stressing the need for separate management. The distribution of cytotypes ranged among species from parapatric (e.g. *Campanula rotundifolia*) to regionally sympatric (e.g. *Leucanthemum vulgare* agg.). Within populations cytotypes rarely cooccurred. We develop a decision framework for the management of cytotypes within the seed zone system aiming to separate cytotypes.

Overall, the project showed that the existing seed transfer zone system catches a large part of spatial genomic variation. We highlight the importance of knowledge gain for heteroploid species. For the future of grassland restoration, transnational rules need to be developed based on range wide analyses of genomic and adaptive variation.

GENETIC MONITORING OF PEREGRINE FALCONS (*FALCO PEREGRINUS*) IN THE UK: APPLICATIONS FOR LAW ENFORCEMENT

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Abstract

The Peregrine Falcon (*Falco peregrinus*) population in the UK has recovered from the brink of collapse in the 1960s to re-inhabit much of its former range across England, Wales and Scotland. The wild population is protected by law but pressures to the population still exist, such as the illegal collection of eggs or chicks to launder into captive falconry. Wild birds are extremely valuable and sell for thousands of pounds more than captive bred ones. However, the extent of the wild-theft problem is unclear, as it has been difficult to detect without a genetic tool. In response to this, over the last six years we have developed an enforcement tool in the form of a comprehensive wild reference DNA database for the British Peregrine, and a forensic DNA profiling method. This tool is being successfully implemented by the Animal and Plant Health Agency (APHA) - the government body responsible for compliance of the falconry trade. It allows for parentage checks on captive birds but also screening of the wild database for familial links to birds claimed to be captive bred, uncovering the exact location of a crime. The continuation of the database involves significant effort both in the field and the laboratory. It currently covers approximately 12% of the breeding population and, in order to stay relevant as an enforcement tool, we need to both increase coverage and repeat sample to capture turnover. With this in mind, we are now focusing on ways to manage the database going forward, to ensure we can provide a genetic tool that remains relevant to law enforcement and to assist the long-term monitoring and conservation of the wild Peregrine population.

GENOMIC INSIGHTS INTO ADMIXED ANCESTRY AND DIVERSITY IN EX SITU GIRAFFES

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Abstract

Ex situ conservation programs are important for safeguarding biodiversity, yet their effectiveness depends on maintaining genetic diversity while minimizing harmful genetic processes such as inbreeding and outbreeding. Understanding how these forces shape genome-wide variation in captive populations is critical for ensuring their long-term viability and conservation value. Here, we use whole-genome sequencing data from zoo giraffes alongside a reference panel of wild individuals to investigate patterns of admixture, inbreeding, and genetic diversity in ex situ populations. By integrating genomic estimates of ancestry, runs of homozygosity, and heterozygosity with studbook records, we assess how management practices influence genetic outcomes. Our analyses reveal widespread admixture among captive individuals, often involving historically distinct lineages, alongside clear signals of recent inbreeding in some cases. These results highlight the complex interplay between genetic rescue through admixture and the potential risks of outbreeding depression. This work underscores the limitations of pedigree-based management alone and demonstrates the value of genomic tools for informing conservation strategies. Ultimately, our study provides a framework for optimizing ex situ breeding programs to maintain genetic diversity and improve long-term population management.

GENOMIC EROSION FOOTPRINT IN INSECTS UNDER EXTREME DECLINE AND ISOLATION

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Abstract

Global biodiversity decline poses major challenges for species and populations. Collapsing census sizes and decreased genetic diversity can lead to increased inbreeding, mutation load and genetic drift. Understanding the genomic patterns accompanying population decline and fragmentation is essential in determining and quantifying genomic load and informing conservation policies. To date, most research has focused on vertebrate species, largely overlooking the vast diversity of insects and other invertebrates. The extreme range of life histories across species suggests that genomic consequences of population size changes might vary substantially. It is therefore crucial to understand decline-related genomic patterns in non-model species in order to better assess and monitor populations and develop more effective conservation strategies. By leveraging whole-genome sequencing, population genomics and museomics, we investigate the genomic footprint of decline and fragmentation in five extreme examples of decline and fragmentation, which represent some of the largest insect orders: a damselfly, a bee, a butterfly and two beetles. Despite a shared history of severe population decline, we demonstrate substantial variation in genetic diversity, heterozygosity, mutation load and demographic history among species. We also show that species can thrive with high census sizes despite long-term isolation and a high degree of fragmentation. Overall, our results provide insight into the genomic consequences of severe decline and isolation across four insect orders and help evaluate the utility of genetic diversity metrics for population assessment.

MASSIVE GENETIC DIVERSITY LOSS WITHIN ASIAN ELEPHANT SUBSPECIES: NEW INSIGHTS FOR DETERMINING CONSERVATION PRIORITIES

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Abstract

Using whole-genome sequencing data from 81 wild-born Asian elephants (*Elephas maximus*), we would like to present a comparative genomic assessment of population structure, inbreeding, genetic diversity, and genetic load across the four recognized subspecies. Our analyses reveal major differences in genomic health among subspecies, with the Bornean elephant (*E. m. borneensis*) showing extremely high levels of inbreeding and the lowest genetic diversity, while mainland and Sri Lankan elephants retain substantially higher diversity and lower inbreeding. Importantly, differences in diversity among subspecies are primarily driven by long runs of homozygosity caused by recent inbreeding rather than by the accumulation of unique variation following evolutionary divergence. Despite severe inbreeding in the Bornean population, genetic load remains relatively low, particularly in highly conserved genomic regions, suggesting that purging of deleterious alleles may have occurred. We also find unexpectedly high diversity in the Sri Lankan subspecies, potentially reflecting historical human-mediated elephant translocations and trade, raising important questions about subspecies boundaries and historical connectivity. Our findings have direct implications for conservation management because they identify the Bornean elephant as the highest genomic conservation priority and suggest that genetic rescue between subspecies may carry limited risk of outbreeding depression due to the low degree of unique genomic differentiation. This study demonstrates how whole-genome data can provide actionable insights for conservation decision-making by distinguishing the genomic consequences of inbreeding from

long-term evolutionary divergence, informing prioritization strategies, and evaluating the feasibility of intervention measures aimed at improving long-term population viability in endangered megafauna.



Talks

SESSION 5 – Restoration Genomics and the (European) Policy Landscape

DARWIN HALL – A ROOM WITH A ZOO
28TH AUGUST 2026



PROXY-BASED GENETIC DIVERSITY ASSESSMENT REVEALS STRONG DECLINES IN THREATENED AND NATIONAL PRIORITY SPECIES

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Abstract

Genetic diversity is essential for the long-term adaptation and resilience of species but has rarely been included in biodiversity monitoring. The Kunming–Montreal Global Biodiversity Framework now requires reporting of two genetic diversity indicators to the Convention on Biological Diversity: the proportion of populations with an effective population size greater than 500 (N_e500), and the proportion of populations maintained (PM). Because genetic data remain limited, proxy-based assessments are widely applied. However, relevant data are often available only for a limited number of species and short time periods. We therefore often lack information on how common species perform compared with threatened species, and how genetic diversity has changed over time. Here, we present an automated, data-driven workflow to estimate the N_e500 and PM indicators across thousands of species over time. We then compare these indicators between threatened species (Red List and National Priority Species; RLT and NPS) and non-threatened species. To overcome current data limitations, we leveraged species occurrence records and long-term biodiversity monitoring data and used them as a basis for estimating these indicators proxy-based and reconstructing their temporal dynamics. Using >30 million occurrence records from Switzerland from 1508–2020, we estimated N_e500 for >1,300 species, including 280 RLT and 106 NPS species, and PM for >4,000 species, including 788 RLT and 416 NPS species. Both indicators revealed recent declines. N_e500 decreased by 2% in recent decades, whereas PM declined by 15% over the last century. For N_e500 , declines were strongest in NPS, while RLT showed little or no decline. For PM, declines were strong in NPS and RLT, where PM decreased 1.5–2 times faster than in non-threatened species. Our approach allows a standardized and reproducible assessment of proxy-based genetic diversity indicators across many species and indicates widespread temporal declines, particularly in threatened species.

GENETIC DIVERSITY AND GENOMIC INBREEDING SIGNATURES CORRELATE WITH IUCN STATUS ACROSS VERTEBRATES

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Abstract

Anthropogenic activities are threatening global biodiversity and genetics can help address this crisis by informing on changes in the demographics of species through space and time. Advances in whole-genome sequencing create new opportunities for demographic analysis, even based just on the two copies of a genome found in a single diploid individual. The Vertebrate Genomes Project (VGP) has the goal of generating high-quality, chromosome-level, haplotype-phased, and annotated reference genomes for all ~70,000 extant vertebrate species. In 2025 its first phase delivered 581, mostly diploid, assemblies spanning approximately 85% of vertebrate orders. Using these data, we quantified intra-species heterozygosity, runs of homozygosity (ROH), and inferred past effective population sizes (N_e) through the Pairwise Sequentially Markovian Coalescent (PSMC). Results showed a positive correlation between how threatened a species is, as indicated by their IUCN status, and the number of ROH, and a negative correlation between IUCN status and heterozygosity. Threatened species are more likely to exhibit long ROHs reflecting recent inbreeding, though striking ROH patterns are also seen in a range of other species as a result of certain life-history traits. PSMC suggests frequent recent declines in N_e , with IUCN status negatively correlating with effective population size. We further quantified ROH patterns to see if IUCN status or other genetic and life history traits are correlated with ROH size and frequency, which are indicative of demographic history. Although further work is required, this work supports that genomic signatures of inbreeding and low population size are to some degree associated with the current IUCN status for a species.

EUROPEAN CONSERVATION POLICY NEEDS A CLEAR DEFINITION OF ‘WOLF-DOG HYBRID’

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Abstract

Anthropogenic hybridisation is a threat to many wild populations, especially when followed by backcrossing into the parental species. A case of particular concern is the wolf (*Canis lupus*), which interbreeds with dogs (*C. familiaris*), resulting in wolf-dog hybridisation (WDH). In December 2024 the Council of the Bern Convention downlisted wolves from “strictly protected” (Appendix II) to “protected” (Appendix III), followed by a similar revision in the EU Habitats Directive. However, assessments of Favourable Conservation Status (FCS) within the EU Habitats Directive do not consider anthropogenic hybridisation as a separate threat category. Given the long-term threat of WDH to European wolf populations, we recommend that hybridisation be explicitly considered when assessing the conservation status of wolves. Importantly, the lack of a clear and widely accepted definition of wolf-dog hybrids has long impeded progress on legislation, policy, and conservation management. To mitigate WDH threats and facilitate efforts to address the problem, we proposed a science-based definition of wolf-dog hybrids (individuals with dog admixture $\leq$ the second-generation backcross to wolf), based on reliable genetic diagnostic tools and best practices, as a reference for conservation management. This definition is not intended to prescribe management actions, which require careful case-by-case consideration of factors including local regulations, conservation priorities, ethics, animal welfare, and human dimensions. Instead, it (1) offers an entity for legal and policy efforts, (2) advances shared and transparent technical standards for hybrid identification, and (3) recognises the need for nuanced, population-

based management policies. The wolf-dog hybrid definition represents a crucial first step and an international reference toward implementing more effective conservation management of WDH. Additionally, the collaborative process of developing the definition, involving practitioners, ecologists, geneticists, and conservationists from across Europe, may be relevant for those addressing anthropogenic hybridisation in other taxa – including fish, birds, and plants – in Europe and elsewhere.

FROM DNA TO SURVIVAL: TRANSFORMING GENETIC DATA INTO CONSERVATION MANAGEMENT GUIDELINES AND ACTIONS

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Abstract

Genetic diversity underpins population persistence, adaptive potential, and long-term species and ecosystem resilience, and is now formally recognised at the global policy level through the Kunming-Montreal Global Biodiversity Framework (KM-GBF). However, a critical gap remains between genetic research and its practical application in conservation management. Translating complex genetic data into clear, actionable strategies demands not only improved collaboration between scientists, practitioners and policymakers, but also the development of tools that are genuinely accessible to the practitioners for decision making. Inspired by the European Horizon ConGRESS project, the African Chapter of the IUCN Conservation Genetics Specialist Group (ConGen Africa) has worked with local authorities and stakeholders to develop genetic management guidelines for several African wildlife species. Central to this process has been the collaborative development of GIS-based maps that spatially define evolutionarily significant units (ESUs) and genetic management units (GMUs), guided by genetic data and an understanding of genetic processes and biogeography. These maps serve a dual purpose: they translate inherently complex genetic concepts into intuitive visual products that conservation managers can readily interpret and act upon, and they expose geographic sampling gaps to focus future sampling efforts and ensuring future iterations of genetic guidelines are improved with more representative data. The guidelines also integrate key genetic indicators, including effective population size (N_e500) and the proportion of populations maintained within a species (PM). A dedicated online platform hosts these species-specific guidelines and maps, ensuring they remain accessible and updatable as new data emerge. Complementary training materials and workshops support co-development with practitioners and private sector stakeholders, building capacity to understand and apply genetic diversity research in day-to-day decision making. This presentation outlines the guideline development process, presents example species guidelines, and demonstrates how simple, well-designed maps and other products can bridge the divide between complex science and practical conservation action.

THE COALITION FOR CONSERVATION GENETICS: PURPOSE, STRUCTURE, AND POLICY IMPACT

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Abstract

Conservation genetics is increasingly integrated into biodiversity science and species and habitat management. Yet the pathways by which genetic knowledge influences policy often remain fragmented, slow, and not easily accessible by the research community. It can be challenging to understand and participate in the institutions, governance, and reporting frameworks that shape biodiversity outcomes.

The Coalition for Conservation Genetics (CCG) was established in 2020 to help bridge this gap by linking complementary international networks spanning research, interpretation, policy, and management. Rather than replacing existing organizations, the Coalition connects them, helping to align priorities, coordinate communication, and strengthen our capacity to shape global and regional biodiversity agendas. The CCG functions as a “network of networks”.

In this talk, I introduce the history, purpose, and role of the CCG as an example of scientific cooperation connecting research with action. I show how each member network contributes expertise, policy access, practitioner engagement, and communication pathways. The premise of the CCG is that coordination and a collective voice create broader reach, stronger credibility, and greater impact than individual groups could typically achieve alone.

I then summarize major activities and accomplishments, including contributions to the Global Biodiversity Framework; development and promotion of genetic indicators; creation of practical guidance and tools; input to IPBES assessments; large, policy-relevant research and synthesis; support for capacity building; and initiatives to increase appreciation of the importance of genetic diversity. I reflect on lessons from engaging non-specialist audiences, sustaining impact, and tracking a rapidly changing policy landscape.

This presentation highlights that the future impact of conservation genetics depends equally on new knowledge and on effective pathways that translate knowledge into decisions and investment. By introducing the CCG, I aim to provide one example of how collaborative scientific structures can help conserve genetic diversity in Europe and globally.

INTEGRATING GENETIC DIVERSITY INTO CONSERVATION ASSESSMENTS: A PRACTICAL FRAMEWORK, WEBTOOL, AND APPLICATION TO IUCN GREEN STATUS SPECIES

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Abstract

Conservation assessments such as the IUCN Red List and Green Status of Species underpin global prioritisation and recovery planning, yet they largely treat species as single units and overlook genetically distinct components. The omission of genetically meaningful within species units limits the consideration and protection of intraspecific diversity, particularly adaptive variation which is critical for long-term resilience and recovery. Addressing this limitation is important for improving the biological realism of assessments and effectiveness of subsequent conservation prioritization decisions in the face of accelerating biodiversity loss.

In this study, the IUCN SSC Specialist Group for Conservation Genetics (CGSG) addressed this gap by developing a flexible, evidence-based framework to delineate subpopulations and Evolutionarily Significant Units (ESUs) using both molecular and non-molecular data. Our objective was to enable consideration of within-species diversity into conservation assessments. To move from concept to practice, the framework was launched as an interactive webtool supported by comprehensive guidance materials. The tool allows users to test alternative delineation scenarios, apply a standardized scoring system, and generate outputs, making the approach accessible across taxa and data contexts. This tool was then applied to 113 species that were assessed under the first iteration of the IUCN Green Status of Species. The tool was able to identify meaningful conservation units using pre-existing data for 53 species but there were constraints for ESU identification due to taxonomic biases in data availability. Collectively, outcomes were sensitive to the volume of genetic data produced for a species. By linking a conceptual framework with an operational tool and empirical application, this work provides a scalable and operational pathway to embed genetic diversity into conservation assessments. Expansion of testing on a broader range of species is now planned, and discussions are ongoing for a formal assessment of the suitability for inclusion of the framework in species assessments.

EVALUATING GENETIC DIVERSITY INDICATORS FOR EUROPEAN BIRD SPECIES IN THE CONTEXT OF BIODIVERSITY POLICY

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Abstract

Genetic diversity, vital for species' adaptive potential, is now explicitly protected under the CBD Kunming-Montreal Global Biodiversity Framework (KMGBF) through Goal A and Target 4. Within this framework, the two accepted genetic indicators, the effective population size (N_e 500) and the proportion of populations maintained (PM), enable large scale quantification of genetic variation to inform policy.

Our study presents the first continental-scale assessment of European birds, focusing on 187 species listed in Annex I of the EU Birds Directive. As a cornerstone of EU nature conservation policy, this directive protects all wild bird species and their habitats, with Annex I specifically designating those that require special conservation measures.

To calculate the genetic indicators, we delineated populations based on relevant ecological characteristics, incorporating genetic data where available. Next, we extracted census size estimates (N_c) from the European Breeding Bird Atlas (EBBA) and the European Environment Information and Observation Network (Eionet). To account for uncertainty and habitat-driven variation in the default 0.1 N_e/N_c ratio, we used three values (0.1, 0.2, and 0.4) to infer N_e from N_c .

After indicator calculation, we tested the relationship between the N_e 500 indicator and EU IUCN Red List status, as well as species-specific traits such as migratory strategy and generation length. N_e 500 values correlated strongly with EU IUCN Red List status and negatively with the number of delineated populations, but were unaffected by generation length. Migratory behaviour also affected the indicator value. Furthermore, ratio-driven variations underscore the need for broader genetic studies to refine taxon-specific N_e/N_c estimates.

Ultimately, this study concludes that data availability was sufficient for computing indicators, though population delineation and temporal dataset alignment posed challenges. This work demonstrates the feasibility of utilizing existing large-scale datasets to implement genetic indicators for well-monitored taxa, providing a framework for extending similar approaches to other taxonomic groups and regions.

COMPARING GENOMIC APPROACHES FOR MONITORING GENETIC DIVERSITY: A CASE STUDY ON *POTAMOGETON NATANS* IN DANISH PONDS

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Abstract

Ponds host a remarkably high proportion of freshwater biodiversity and play an important role in connecting habitats in the landscape, yet they continue to receive limited attention in conservation and monitoring programmes. Addressing this gap requires robust and scalable indicators of genetic diversity that can be integrated into restoration and policy agendas.

Here, we evaluate the potential of different genomic approaches to inform standardized monitoring of genetic diversity in pond networks, using the widespread aquatic plant *Potamogeton natans* as a model species across a broad European latitudinal gradient. We first compared three sequencing methods—double digest restriction-site associated DNA sequencing (ddRAD) and target enrichment with hybridization capture using two different baits kits (Angiosperms353 and a custom-designed one for Alismatales)—to assess their performance in estimating essential biodiversity variables (EBVs) related to genetic diversity on a subset of 48 individuals in Danish ponds.

Across methods, we quantify key indicators including within-population diversity, genetic structure, clonality versus sexual reproduction, and genetic connectivity among ponds. By systematically comparing marker systems and analytical outputs on the same populations, we assess their suitability for large-scale, cost-effective monitoring.

Our results highlight both methodological trade-offs and the feasibility of deriving consistent genomic indicators across pondscapes. Ultimately, by linking genomic methods with operational monitoring needs, this work advances the development of a standardized, policy-relevant protocol for integrating genetic diversity into freshwater ecosystem restoration.

BEYOND NE500: MONITORING DIVERSITY USING THE GENETIC SCORECARD FOR WILD SPECIES

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Abstract

Adoption of the Kunming-Montreal Global Biodiversity Framework (GBF) at the 15th Meeting of the Convention on Biological Diversity (CBD COP 15) resulted in increased recognition of the importance of genetic diversity through the inclusion of specific Goal A and Target 4 statements. The need for management actions to maintain and restore genetic diversity is explicitly recognised, alongside a headline monitoring indicator that requires countries to assess the proportion of populations within species with an effective population size > 500 (Ne500). These measures represent a significant strengthening of global policy around the conservation of genetic diversity, for which the European ConsGen community should be justifiably proud; however, implementation of monitoring activities across wild species is confounded by challenges associated with population definitions and the simplicity of the Ne500 indicator.

The Genetic Scorecard for Wild Species, adopted by the United Kingdom for GBF reporting, is a complementary indicator for measuring change in genetic diversity over time. Designed for use by scientifically trained officials, rather than species experts, it allows for the inclusion of available data from multiple sources, and incorporates an evaluation of confidence in the estimates of species genetic diversity and its future trajectory. The Scorecard includes both the Ne500 headline indicator and the associated *Proportion of Populations Maintained (PM)* indicator, but avoids reliance on a specific quantitative threshold and allows for the collection and interpretation of significantly more information from which to assess the status of wild species genetic diversity. It is thus suitable for taxa where Ne is less informative, such as fungi and marine taxa.

This presentation will introduce the Scorecard and its underlying methodology and demonstrate its application to over 50 UK terrestrial and marine species. We propose wider application of the Scorecard to improve the quality and utility of monitoring reports under the CBD Global Biodiversity Framework.

INCORPORATING GENOMIC SCIENCE IN A NATURE-POSITIVE FUTURE

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Abstract

Nature-positive describes the concept of halting and then reversing the loss of biodiversity in a manner that is equitable to all, particularly indigenous peoples and local communities. The concept is well-aligned with the implementation of the Global Biodiversity Framework and the EU Nature Restoration Regulations.

Since genetic diversity is the foundational component of biodiversity, underpinning species and ecosystem diversity, it is vital to resilience and ecosystem services. Thus, genomic science offers tools that will be essential to understanding the current status of biodiversity and building a nature-positive future.

Former limitations around data and methods for assessing genetic diversity are rapidly disappearing. Thus, we argue genomic science should be used to assess baseline values and for measuring nature-positive outcomes. With advances in genetic and genomic technologies, this approach can even be more affordable than assessing species or ecosystems. If DNA-based data are not available, indicators are available for inferring the status of genetic diversity with proxy data.

This talk explicitly links policy goals with real world examples of incorporating genetic diversity in restoration. It is both possible and beneficial to incorporate genomics in biodiversity assessments for nature-positive. It can and should be used in co-developing management plans at local and national levels. Including genomic science in steps to build a nature-positive future is thus essential if the concept is to achieve its aims.



Poster Presentations

A ROOM WITH A ZOO
26TH-28TH AUGUST 2026



1 WOLF–DOG ADMIXTURE IN A PROTECTED WOLF POPULATION UNDER HUMAN PRESSURE

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Abstract

Gray wolves (*Canis lupus*) in Mongolia occupy extensive and heterogeneous landscapes, ranging from desert to forest-steppe and from agricultural areas to protected populations, but they are increasingly exposed to pastoral land use, high livestock densities, free-ranging herding dogs, and legally permitted harvest outside protected areas. These pressures may affect both local genetic composition and interactions between wolves and domestic dogs, yet genetic data from Mongolia remain scarce. We used mitochondrial DNA sequences and autosomal microsatellite markers to assess taxonomic placement, genetic variation, and recent wolf–dog gene flow in Mongolian wolves, focusing on a population from Hustai National Park. Mitochondrial analyses revealed six wolf haplotypes belonging to two major Eurasian haplogroups, including two previously undescribed variants, all clustering within the Holarctic gray wolf lineage. Microsatellite data indicated moderate genetic diversity and low overall inbreeding, comparable to other large Eurasian wolf populations. However, our analyses also detected recent wolf–dog admixture, indicating ongoing but limited gene flow from domestic dogs. Although hybridization occurred at low frequency, it is consistent with conditions, such as presence of free-ranging dogs and variable harvest pressure, that promote repeated wolf–dog contact and may destabilize wolf pack structure. Because microsatellite markers primarily detect recent admixture, the observed hybrids likely represent a minimum estimate. Together, our results indicate that wolf–dog gene flow may represent an emerging genetic risk for Mongolian wolves, including those in protected populations. These findings highlight that hybridization risk is not necessarily only associated with declining or fragmented populations, but may also arise in apparently robust populations exposed to frequent dog contact and human-induced mortality, including legal harvest or poaching.

2 GENOMIC CONSEQUENCES OF POPULATION COLLAPSE AND RECOVERY IN EUROPEAN WOLVES

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Abstract

Once nearly eradicated from Europe, grey wolves (*Canis lupus*) have recently undergone a remarkable demographic recovery, but their long-term survival remains precarious. This history provides an excellent opportunity to investigate the evolutionary consequences of population collapse followed by recovery. We conducted a large-scale genomic study of European wolves, analyzing 1,001 genomes (746 new) sampled across 33 countries. All genomes were phased and imputed using a reference panel of 1,715 canids, generating a high-density whole-genome variation dataset (52 million variants). Using this dataset, we explore how population structure, connectivity, and hybridization shape genomic erosion under these demographic trends. We show that European wolves are not homogeneous but have distinct evolutionary lineages and dispersal patterns, so they are not a single recovering population. Northern populations exhibit substantial ancestry influx from Asia, whereas southern European wolves show strong allele sharing with early Holocene wolves. We refine previous geography-based European wolf groupings defined by the LCIE (Large Carnivore Initiative for Europe) by identifying a more finely scaled clustering that will enable evidence-based monitoring, which rarely incorporate genomic insights. The population collapse has had long-lasting consequences in present-day populations. Although effective population size (N_e) has increased by ~5% per generation since 1970, most clusters remain below $N_e=500$, a threshold considered critical for maintaining evolutionary potential. Isolated wolves from the Scandinavian, Italian and Iberian peninsulas harbor ~20-40% of their genomes in runs of homozygosity (ROH) and have three times more fixed deleterious mutations than average. In contrast, the expansion into the Central European lowlands shows limited inbreeding and load due to connectivity. Dog hybridization also threatens several clusters, especially the Eastern European lowlands and Italian wolves. Together, our results emphasize the need for targeted strategies specific to each region, accounting for differences in demography, connectivity, hybridization, and genomic erosion.

3 EUROPEAN WOLF RECOLONIZATION SHOWS A REMARKABLE DIFFERENCE BETWEEN DEMOGRAPHY AND GENOMIC DIVERSITY

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Abstract

The apparent recovery of European gray wolves (*Canis lupus*) to ~21,000 individuals masks substantial hidden risks to their long-term viability. To investigate their genomic health, we analyzed over 200 whole-genome sequences from five major European populations. Our results reveal that European wolves do not form a single, expanding population but rather a mosaic of isolated, independently evolving lineages, several of which diverged in the late Pleistocene. All lineages possess contemporary effective population sizes (N_e) below the 500 threshold considered necessary for long-term viability and exhibit extensive inbreeding. Variation in runs of homozygosity (ROH) indicates this inbreeding has developed over different time frames, from the recent past in Scandinavia to deeper in the history of the Dinaric-Balkan population. Critically, most lineages exhibit a higher realized than masked genetic load, indicating emerging inbreeding depression and highlighting their independent evolutionary trajectories. These genomic findings fundamentally challenge claims that downlisting the conservation status of European wolves is biologically warranted. We conclude that none of Europe's distinct wolf populations currently meet the criteria for a favorable conservation status, and continent-wide management strategies must account for this deep-seated and complex population structure to ensure their survival.

4 GENOMIC INSIGHTS INTO THE STATUS OF AN ENDANGERED CAVE-DWELLING MUSSEL

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Abstract

Understanding the genetic health and demographic history of specialized and threatened taxa is critical for effective conservation. *Congeria*, the only known genus of cave-dwelling ‘living-fossil’ mussels, comprises three species endemic to the Dinaric Karst (Croatia, Slovenia, Bosnia and Herzegovina). It represents an exceptionally specialized and range-restricted taxon with extremely limited dispersal and fragmented populations. It is a highly specialized and range-restricted taxon with extremely limited dispersal and fragmented populations, and its biology remains poorly understood. It is classified as Endangered on the IUCN Red List, and recent reports of widespread mortality raise urgent concerns about rapid population decline and possible extinction. New genomic resources now enable deeper insight into its evolutionary history, population structure, and conservation threats. We previously assembled the reference genome of *C. kusceri*, but lacked population-level resolution of structure and demography. Here, we present a population genomic analysis based on whole-genome resequencing of 18 individuals from three populations: two of *C. kusceri* from two locations, one of which had undergone a dramatic population reduction in the past 50 years, estimated at greater than 99 %, and one population of the sister species *C. jalzici*. We used genome-wide SNPs and gene presence/absence variation to resolve population structure and explore genetic differentiation. We also screened for genomic variants in *C. jalzici* by mapping reads to the *C. kusceri* reference, to explore evolution and adaptation, motivated by morphological differences between the closely related species. Finally, we reconstructed the demographic history of the three populations to infer changes in effective population size and identify potential bottlenecks or long-term declines. Together, these analyses provide a more detailed understanding of population structure, evolutionary trajectories, and genetic health. This information is essential for identifying conservation goals and informing management strategies in a system where both ecological knowledge and genomic resources remain limited.

5 CONNECTING THE SPOTS: A GENOMIC UPDATE ON CHEETAH PHYLOGEOGRAPHY AND CONSERVATION

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Abstract

The phylogeography and population genetics of the iconic cheetah (*Acinonyx jubatus*) has been subject of molecular research for many years. The understanding of the current and historical population structures has direct implications for conservation actions of this threatened felid. In this study we are analysing recent and ancient whole-genomes and previously published ddRAD data from in total over 80 individuals. For the first time, we shed a light on the genomics of the critically endangered Northwest African subspecies (*A. j. hecki*), show a very complex evolutionary history of cheetahs in East Africa and in general, and taking a closer look into conservation genomic parameters of all subspecies on the whole-genome level.

6 EPIGENETIC SIGNATURES OF PARASITE INFECTION TO ADVANCE PRECISION CONSERVATION IN SEA TURTLES

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Abstract

Conservation genomics has transformed our capacity to assess population structure, quantify genetic diversity and evaluate species' adaptive potential. However, these approaches still largely operate at the population level and many conservation decisions, particularly those involving health, resilience, reproductive output or exposure to environmental stressors, require information at the level of individuals. This gap limits the translation of genomic technologies into precision conservation, where management is informed by rapid, fine-scale indicators of condition and biological response. Epigenetic biomarkers, such as DNA methylation, offer a route to bridge this gap. DNA methylation can reflect environmentally-induced biological variation, thereby linking external stressors with measurable molecular responses within individuals over a short timescale. This makes methylation particularly relevant where individuals vary in exposure, condition or susceptibility, and where population-level genomic summaries may be too coarse to inform timely intervention.

Here, we present a proof-of-concept for DNA methylation as a non-invasive blood biomarker of parasite infection in the endangered loggerhead turtle (*Caretta caretta*). In adult females, we identified differentially methylated sites associated with infection by the leech *Ozobranchius margo*, a parasite known to alter host feeding ecology and reproductive output. Offspring of infected mothers also exhibited infection-associated methylation patterns, despite lacking direct exposure to the parasite themselves. In both generations, methylation profiles predicted maternal infection status with high accuracy using machine-learning approaches. Together, our results show that DNA methylation can provide individual-level biomarkers of infection-associated biological variation, extending conservation genomics beyond population-level inference. More broadly, they highlight how epigenomic information could move conservation towards precision approaches informed by real-time indicators of individual condition and response to environmental change.

7 GENETIC RESPONSES OF A GRASSLAND PLANT TO LANDSCAPE HISTORY ACROSS FIVE EUROPEAN COUNTRIES

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Abstract

Semi-natural grasslands are one of the most species-rich ecosystems of Europe but have undergone particularly strong habitat changes due to land use intensification and abandonment. Over the past decades, the area of semi-natural grasslands in Europe has been drastically reduced. With declining area, the remaining populations in these habitats became smaller, more isolated, and increasingly disconnected, resulting in strongly reduced or even inhibited gene flow. The consequence is genetic impoverishment leading to reduced resistance to environmental changes and diseases.

Our study species, *Primula veris* L. (cowslip), is a herbaceous, insect-pollinated plant that typically grows in nutrient-poor semi-natural grasslands. Our study regions span five European countries (Belgium, Germany, Czech Republic, Sweden, and Estonia) covering a broad part of the species' distribution range. We performed next-generation sequencing on 150 populations and analyzed the relationship between genetic diversity and landscape composition at three points in time over the past 80 years.

Contemporary landscape composition shapes genetic diversity of the study populations. However, historical landscape characteristics continue to affect present-day population genetics. This time lag in genetic response provides an opportunity to implement conservation measures preserving former genetic diversity, even in landscapes that have already undergone fragmentation and other habitat changes.

8 POPULATION GENETIC STRUCTURE AND CONNECTIVITY OF STOATS IN SWITZERLAND USING GENOME-WIDE SEQUENCING

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Abstract

The stoat (*Mustela erminea*) is an elusive small mustelid whose population ecology remains poorly understood due to the challenges associated with conventional monitoring approaches. In Switzerland, the limited knowledge of its population status and trends is primarily expert-based, with claims of a noticeable recent decline in their abundance. Population genetic analyses facilitate the evaluation of population structure, connectivity, and demographic processes that are otherwise difficult to quantify. This study investigated the population genetics of stoats across Switzerland using genome wide sequencing data. A nationwide collection of over 90 recent tissue samples was assembled through a combination of citizen science initiatives, collaboration with practitioners, and museum collections. DNA was extracted and sequenced to generate genome-wide single nucleotide polymorphism (SNP) data. We thereby assessed genetic differentiation among regions, tested for population structuring, and evaluated patterns of connectivity across the landscape, including the role of major geographic features such as the Alps or anthropogenic barriers such as highways. In addition, we examined isolation by distance and explored the stoats' demographic histories to provide context for current population patterns. As the first population genomic assessment of stoats in Switzerland, this research contributes to a growing body of research applying genetic tools to small mustelids. The insights gained into population structure and connectivity allow this method to complement existing ecological monitoring and supports a more comprehensive understanding of the species' status. Ultimately, these findings will help inform conservation and management strategies in human-dominated landscapes.

9 CONSERVATION GENOMICS OF UK RED SQUIRRELS: IMPLICATIONS FOR SPECIES RESTORATION

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Abstract

Across most of the UK, native red squirrels (*Sciurus vulgaris*) have been replaced by introduced grey squirrels (*Sciurus carolinensis*) because of competition for resources and transmission of the squirrelpox virus, which is lethal to reds. Scotland is largely still free from grey squirrels and is home to around 80% of the UK's remaining red squirrel population. Conservation efforts are underway, including grey squirrel control, habitat management, disease surveillance, and red squirrel translocations. However, low levels of genetic diversity in Scotland pose a threat to the population's long-term survival and confound conservation translocation planning. Questions persist over the levels of diversity in UK red squirrels relative to their broader Eurasian distribution, as well as how that diversity is likely to be partitioned over the landscape. Here we present results from an ongoing conservation genetics PhD project that uses low-coverage whole-genome sequencing data. Building on an existing dataset of 100 Scottish individuals, we sequenced a further 100 samples from 10 countries across the species distribution, generating the first Eurasian-wide dataset of its kind. We evaluated individual genome-wide heterozygosity across the UK and compared it to the rest of the Eurasian distribution. Mitochondrial haplotypes were also identified and compared across this range. Then, we used a landscape genetics approach to estimate isolation-by-resistance within Scotland, testing the effect of several landscape features on the genetic dissimilarity between individuals, measured as a PCA-based distance. This revealed which landscape features facilitate or hinder dispersal and identified isolated populations that would benefit from increased connectivity. Together, these results provide novel genetic evidence to inform recommendations for future red squirrel restoration initiatives in the UK.

10 EVOLUTIONARY ORIGIN OF *TARSIUS PELENGENSIS* BASED ON HISTORIC SAMPLES

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Abstract

Tarsiers are small, nocturnal primates that remain largely understudied despite their long history of independent evolution. Over time, however, researchers have identified a high degree of diversity in duet-calls, morphology, and genetics within the clade. This led to the recognition of 12 species of Eastern tarsiers (*Tarsius* spp.) endemic to Sulawesi and smaller adjacent islands and prompted a revision of their conservation status and increased their conservation priority. Phylogenetic methods succeeded in resolving relationships of species on mainland Sulawesi; however, the evolutionary origin of the offshore island forms remains largely unknown due to a lack of available samples. Given that tarsiers are nocturnal, cryptic, and difficult to sample, we explore the potential of museum specimens for tarsier research. Despite their proven value for other taxa, museum specimens remain an underutilized resource in tarsier genetics. We sampled five historical specimens of *T. pelengensis*, collected in 1938 on the Banggai Archipelago, about 20 km south of the eastern tip of Sulawesi. Partial regions of five autosomal loci, SRY, and cytochrome b were sequenced as amplicon libraries on Illumina MiSeq300 PE. The resulting sequences were used to reconstruct haplotype networks and a phylogenetic tree. Our analysis indicates a close evolutionary relationship between *T. pelengensis* and *T. dentatus*. The low genetic divergence observed, together with the geographic isolation of the archipelago, suggests a relatively recent colonization event, likely via rafting from *T. dentatus*, as the origin of *T. pelengensis*. Finding *T. pelengensis* nested within the genetic diversity of *T. dentatus* calls its status as a valid species into question. Thus, while emphasizing the continued need for field research, we highlight how museum specimens can be integrated to help redefine conservation units, which directly impacts the allocation of conservation resources.

11 LEVERAGING GENOMIC DATA TO TRACK THE INTRASPECIFIC GENETIC DIVERSITY OF ALPINE WHITEFISH THROUGH SPACE AND TIME

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Abstract

Intraspecific genetic diversity is key for population persistence, species' adaptability to new environmental pressures, supports ecosystem resilience after a disturbance and increases the success of ecological restoration. However, human activities are currently leading to a global biodiversity crisis, including a decline in intraspecific genetic diversity. To access and halt this loss, policies for management and restoration efforts that incorporate and track suitable genetic diversity indicators are needed.

Alpine whitefish (*Coregonus spp.*) are key components of the aquatic biodiversity of Alpine lakes. This extremely diverse group comprises a large radiation of over 30 species that independently evolved in small species flocks and adapted to occupy different ecological niches across different lakes in the last 10–15 thousand years. As a consequence of human activities, however, the Alpine lakes have suffered significant impacts due to lake eutrophication, invasive species, and fishing pressure. This resulted in documented fishing stock crashes and the extinction of 10 endemic whitefish species. To which degree the remaining species' genetic diversity has been impacted by these pressures remains largely unknown. Yet, this is key information to evaluate the species recovery potential and define management and recovery strategies for the future.

Using whole genome data from 22 species distributed across 8 lakes, we estimate the historical effective population size (N_e) of the different Alpine whitefish species to investigate past demographic processes and establish a baseline prior to anthropogenic disturbance. Furthermore, we are currently compiling a second population scale whole genome resequencing dataset for inference of contemporary N_e as a genomic indicator of population health, contrasting species from lakes where fish stocks have crashed to lakes less affected by fishing and management.

Our comprehensive assessment of the historical and contemporary N_e of different Alpine whitefish species aims to integrate with cantonal monitoring efforts and to assist with future management decisions.

12 THE ROYAL CATDOM: INBREEDING IN RUSTY-SPOTTED CATS EXCEEDS THAT OF EUROPEAN ROYALS

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Abstract

The rusty-spotted cat (*Prionailurus rubiginosus*), one of the world's smallest felids, is endemic to the Indian subcontinent and currently classified as Near Threatened. The species remains one of the least studied wild cats because it is both overshadowed by larger carnivores and elusive in the wild. Key questions about the species remain unanswered, all of which could impact its local extinction risk as well as the accuracy of its global extinction risk.

Genomic data from captive populations of *P. rubiginosus* offer a valuable starting point to understand this species and inform its conservation. Here, we present the first high-quality reference genome for *P. rubiginosus* generated from a captive male ("Navin") at Frankfurt Zoo of Sri Lankan descent. Using a combination of PacBio High-Fidelity (HiFi) and Oxford Nanopore Technologies (ONT) long-read sequencing, we assembled a genome with a contig N50 of 124 Mbp. Another assembly using Hi-C is in progress to improve contiguity and facilitate detailed study of inbreeding.

Alongside the genome, zoo pedigree information indicates that the global ex-situ population is among the most highly inbred within the EAZA, with a mean inbreeding coefficient of 0.28 (maxF = 0.45, founders = 8), exceeding that of European royal dynasties. This suggests a reduction in genome-wide heterozygosity which we will quantify through whole-genome resequencing of selected individuals from the past and extant ex-situ population. Comparisons between these samples will be done to confirm the pedigree, as well as explore genetic erosion and expression of mutational load across generations, particularly mutations associated with bone strength deficiencies. The reference genome will also be used to reconstruct the rusty-spotted cat's demographic history and estimate historical effective population size (N_e) using Pairwise Sequential Markovian Coalescent (PSMC) to build knowledge on the wild population and interest in the species. This study enables integration of genomic and pedigree data to inform conservation management of one of the most genetically constrained ex-situ felid populations.

13A CENTURY OF DECLINE: TRACKING GENOMIC EROSION IN TWO ENDANGERED PARROTS

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Abstract

A major challenge in conservation genomics is finding clear, quantifiable ways to assess genomic erosion and its consequences for genetic viability and extinction risk. Traditional approaches have largely relied on genome-wide diversity metrics, but these alone may not fully capture the long-term genomic effects of population decline. Recent advances in whole-genome sequencing (WGS), together with improved methods for extracting and sequencing historical DNA, now make it possible to investigate genomic erosion in greater detail by integrating information on genetic diversity, inbreeding, and genetic load through time. Using temporal WGS datasets from two critically endangered, phylogenetically divergent parrots—the Orange-bellied Parrot (*Neophema chrysogaster*) and the Swift Parrot (*Lathamus discolor*)—that have undergone broadly similar rapid population collapses, we examined genomic change across more than a century of demographic decline. By combining modern genomes with historical museum specimens as early as the 1840s, we reconstructed genetic baselines prior to severe population declines and assessed temporal trends in genome-wide heterozygosity, runs of homozygosity, inbreeding, and genetic load. Using a consistent analytical pipeline, we further evaluated a comparative framework for studying genomic erosion while addressing challenges associated with degraded historical DNA. Our results highlight the importance of integrating multiple genomic indicators to understand extinction risk and illustrate how temporal genomics can improve conservation assessments and decision-making for declining populations.

14 GENETIC MONITORING OF THREE TRANSLOCATED MUSKOX POPULATIONS

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Abstract

The muskox (*Ovibos moschatus*), is a large mammal native to the Arctic. Several large-scale studies across native populations and different genetic markers previously emphasized that the muskox retained extremely low genetic diversity, the lowest found among ungulates. In this new study, we generated 24 whole genomes from 3 populations re-introduced during the 20th century to Alaska, West Greenland and Sweden. The latter population originates from 5 individuals spontaneously breaking off a translocation to Norway and settling in Sweden. The status of these translocations was so far only assessed by observations or limited genetic data. Whole genomes offer the opportunity to refine their genetic monitoring and accurately trace back source populations. This is also an empirical opportunity to investigate the effect of serial bottlenecks on a species at already low genetic diversity. Comparing sections of the genome that are inbred between translocated and native populations as well as pinpointing genetic load will help inform future management actions.

15 GENETIC DIVERSITY AND DIFFERENTIATION OF BURMESE PYTHONS (*PYTHON MORULUS BIVITTATUS*) OF HONG KONG

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Abstract

Severe decline of Burmese pythons (*Python morulus bivittatus*), listed as “Vulnerable” on the IUCN Red list, has been attributed to human induced habitat loss and their consumption as food. Therefore, conservation of the genetic diversity of Hong Kong Burmese Pythons, the only remaining population in South China that is not declining significantly within its native range, is of particular interest. Extensive urbanization of Hong Kong may act as a dispersal barrier to Burmese Pythons, reducing gene flow among local populations and possibly leading to genetic bottlenecks and loss of genetic diversity. We assessed genetic diversity, genetic population structure, levels of inbreeding and genetic effective size of Hong Kong Burmese Pythons using low coverage whole genome sequencing data. The results revealed very low genetic diversity, weak population structuring, signs of inbreeding and low contemporary effective size of Hong Kong pythons. There appears to be two weakly divergent subpopulations in Hong Kong: one at New Territories and another on Outlying Islands. However, the impact of extensive urbanization on gene flow reduction between the Outlying Islands and New Territories appears to be limited. Yet, many of the sampled individuals were indicated to be 1st degree relatives, an observation consistent with estimated low effective size of Hong Kong python population. The low contemporary effective population size shows that inbreeding depression of the Hong Kong population is a risk to the viability and genetic diversity of the population in the long term. Finally, genetic analyses recovered evidence for a first known case of parthenogenetic reproduction in *P. bivittatus* in the wild.

16 GENOMIC STRUCTURE AND DIVERSITY OF EUROPEAN BEECH HIGHLIGHT THE ITALIAN PENINSULA AS A KEY RESERVOIR OF UNIQUE VARIATION

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Abstract

Understanding patterns of genomic diversity and connectivity is central to defining conservation units and predicting species resilience under environmental change. In European beech, continental-scale genomic datasets have substantially improved our understanding of postglacial history and population structure, yet Italy, one of the species' major southern refugial regions, has remained underrepresented. Here, we integrated 132 newly sequenced individuals from eight Italian stands with 874 previously published genomes (total $n = 1,006$) to characterize population structure across the species range and resolve genomic patterns within Italy. Multivariate analyses revealed that southern Italian populations were separated from central and northern Italian populations, which formed a continuum with other European populations. Admixture analyses ($K = 4$) confirmed southern Italian populations, particularly Sicilian stands, as a distinct genetic cluster, whereas northern Italian populations showed increasing admixture with central European gene pools. Isolation-by-distance was significant across the range, with a markedly steeper slope within Italy than across Europe, indicating stronger local differentiation. Furthermore, analyses of inbreeding and diversity metrics highlighted Italy's distinct demographic history. Populations at the expansion front exhibited relatively elevated fractions of runs of homozygosity (FROH) and reduced heterozygosity, consistent with founder effects during postglacial recolonization. In contrast, Italian populations, particularly those in Sicily and Matese, harbored the lowest range-wide FROH and intermediate levels of heterozygosity, second to eastern European populations. These patterns suggest that Italian refugia maintained large, genetically diverse populations across glacial cycles. Taken together, our results identify the Italian Peninsula, especially southern and insular populations, as a major reservoir of unique genomic diversity that served as a source for the postglacial re-expansion of *Fagus sylvatica*. These findings integrated with future work targeting local adaptation across the Italian Peninsula could inform conservation and management strategies in a species facing ongoing climate change.

17 NEUTRAL AND ADAPTIVE GENETIC DIVERSITY IN NORTHERN AFRICAN LIONS (*PANTHERA LEO LEO*): IMPLICATIONS FOR CONSERVATION MANAGEMENT IN WEST AND CENTRAL AFRICA

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Abstract

West and Central African lions belong to the endangered northern subspecies (*Panthera leo leo*), persisting at low numbers in fragmented habitats. Their demographic decline has raised concerns about genetic erosion, inbreeding, and loss of adaptive potential, yet comprehensive genetic assessments remain scarce. To place these populations in a continental context, we assessed neutral genetic diversity in 334 lions from across Africa

using a targeted 96-SNP panel, and adaptive genetic diversity in 198 samples using next-generation sequencing of MHC class I and class II genes. Population structure analyses identified six genetic clusters split between the two subspecies, with northern populations showing substantially lower neutral diversity (mean $A_r = 1.71$, $H_e = 0.32$) than southern ones (mean $A_r = 1.94$, $H_e = 0.44$). Within West and Central Africa, Senegalese lions were the most genetically eroded ($A_r = 1.56$, $H_e = 0.19$, 59.5% polymorphic loci), while W-Arly-Pendjari (WAP) and Central African populations retained intermediate levels. Adaptive diversity followed broadly similar geographic trends but with more complex patterns: MHC class I was more diverse than class II (76 vs 32 unique variants), with signatures of balancing selection detected at class I loci across all populations. Unexpectedly, inbreeding coefficients remained low across populations, including the most threatened ones. Despite low neutral diversity, no inbreeding signal was detected in Senegal or WAP (the most threatened populations), with F_{is} values close to zero or negative. This pattern is consistent with a genetic extinction debt, where current metrics reflect historical rather than contemporary demography. These findings have direct management implications: they call for caution before initiating genetic rescue interventions such as WAP-to-Senegal translocations, and support prioritising demographic stabilisation and sustained genetic monitoring before any translocation decision.

18 ARE TRANSPORTATION INFRASTRUCTURE BARRIERS LEAVING GENOMIC WARNING SIGNALS IN ROE DEER?

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Abstract

Transportation infrastructure is among the most widespread drivers of habitat fragmentation in central Europe and can reduce gene flow, increase inbreeding, and erode genetic diversity in wildlife populations over time. This study investigates whether these processes leave detectable genomic signatures in roe deer (*Capreolus capreolus*) in Baden-Württemberg, south-western Germany, using a paired temporal and spatial design. For the temporal component, 10 historical skull samples from a museum collection dated to around 1875 were sequenced alongside contemporary tissue samples from hunted animals to assess changes in genetic diversity over approximately 150 years — a period that encompasses the full expansion of road and rail networks in the study region. For the spatial component, ten individuals each were sampled from five infrastructure-isolated and five non-isolated study areas across Baden-Württemberg and sequenced to 15X genome-wide coverage. Results reveal early warning signals of genomic erosion in isolated populations. Because roe deer are ecologically adaptable and comparatively mobile, such signals in this species are likely to underestimate the genomic consequences of fragmentation in less resilient wildlife. Final results from both the temporal and spatial analyses will be presented on the poster. The study aims to contribute to evidence-based landscape planning and the strategic prioritisation of wildlife crossing structures in increasingly fragmented European environments.

19 RECENT AND HISTORICAL DETERMINANTS OF GENOMIC EROSION BY STRUCTURAL VARIATION AND SNPs ACROSS A PAN-HOLARCTIC SUPERSPECIES

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Abstract

Despite disproportionate fitness impacts imposed by deleterious structural variants (SVs) and associated transposable elements, few studies have yet examined their relative contribution to genomic erosion. To examine the role of both recent and ancient population history in the accumulation of deleterious SVs relative to single nucleotide polymorphisms (SNPs), the rock and willow ptarmigan (*Lagopus spp.*) superspecies form an ideal pan-Holarctic system, harbouring a broad range of historical effective population sizes increasingly threatened by fragmentation and climate change. By contrasting diversity ratios for non-synonymous SNPs and non-neutral SVs across 99 individuals from 12 island and mainland populations, we find that purifying selection against most putatively deleterious SVs appears insufficient to prevent their long-term accumulation in small populations, conforming with classic nearly-neutral dynamics. Likewise, proportions of realised (homozygous), masked (heterozygous) and fixed drift load due to putative highly and mildly deleterious SVs mirrored SNPs in mostly accumulating as a function of increased homozygosity in smaller populations. However, population-specific differences in the accrual of drift debt due to SVs did not reflect historical N_e alone: elevated realised load but reduced drift load in the Pyrenees (relative to the smallest population; Svalbard) indicate that the effects of recent fragmentation-induced inbreeding have yet to fully manifest. Our findings highlight the need to account for recent population decline and fragmentation, rather than solely relying on historical N_e to predict outcomes of genomic erosion— especially given the potential for disproportionate drift debt imposed by deleterious SVs.

20 GENETIC REVIVAL IN A MULTI-LINEAGE LANDSCAPE: LESSONS FROM BEAVER REINTRODUCTIONS IN FLANDERS AND THE NETHERLANDS

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Abstract

The Eurasian beaver (*Castor fiber*) has undergone a remarkable recovery across Europe following near-extinction, largely driven by reintroduction programs using individuals from multiple, genetically distinct source populations. In Flanders (Belgium) and the Netherlands, reintroductions since the late 20th century have resulted in rapid population expansion. However, population assessments remain largely structured at the river basin level, and the extent of functional connectivity and admixture among basins is still poorly understood.

In this study, we assessed population structure, admixture, and genetic diversity in 129 individuals sampled across northern Belgium and the Netherlands. Specifically, we tested whether (i) individuals originating from distinct source populations (Bavarian, Elbe, and Eifel/Polish) have come into secondary contact and interbred, (ii) natural dispersal has facilitated gene flow across river basin boundaries, and (iii) admixture has enhanced local genetic diversity compared to isolated reintroduction events.

Our analyses identified three main genetic clusters corresponding to the original reintroduction sources, which remain detectable in the current population. Despite this structure, we found clear evidence of admixture across river basin boundaries. Notably, the Meuse basin acts as a convergence zone where individuals from different source populations co-occur and interbreed, resulting in elevated genetic diversity.

These findings demonstrate that river basins do not represent strict barriers to dispersal and highlight the dynamic nature of post-reintroduction range expansion. Our findings reinforce the emerging view that carefully managed mixed-source reintroductions can serve as an effective strategy for restoring genetic diversity in species impacted by extensive historical population declines. By integrating demographic success with sustained genetic health, conservation efforts can achieve better outcomes for the Eurasian beaver—and likely for other species in comparable reintroduction scenarios.

21 RESILIENCE AND RESTORATION: CONTRASTING GENETIC LANDSCAPES OF TWO SEMI-AQUATIC MAMMALS IN WESTERN EUROPE

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Abstract

Understanding how freshwater keystone species recover from historical collapses is vital for the success of European restoration frameworks. We present a large-scale genetic assessment of two semi-aquatic mammals: the Eurasian otter (*Lutra lutra*) and the Eurasian beaver (*Castor fiber*). These species offer contrasting models of natural versus human-mediated recovery in a rapidly changing world. For the otter, we analyzed its natural recolonisation of France using 356 non-invasive samples. Genotyping at 9 microsatellite loci identified six genetic clusters reflecting the existence of different historical refugia where the species survived during the 20th century. While the species shows a remarkable mobility and an increasing lineage reconnection and recolonisation through hydrological corridors, the genetic signature of past bottlenecks remains visible. This recovery, although promising, remains fragile and dependent on maintaining functional connectivity to prevent further isolation of peripheral populations. In contrast, the Eurasian beaver illustrates the consequences of diverse restoration strategies. We analyzed 358 beaver samples collected between 2010 and 2022. Our results reveal a profound dichotomy: a geographically expansive but genetically highly uniform "French core" (corresponding to the relict *galliae* lineage) versus a highly diverse "northeastern population" characterized by an admixture between multiple genetic lineages (*albicus*, *fiber*, *galliae* lineages) and having as origin recent reintroduction events, which happened in surrounding countries. While the French core's low allelic richness may limit its long-term adaptive potential and surviving chances, the northeastern populations would serve as a reservoir of genomic diversity and therefore, would allow a better future survival of the species in France. By integrating these findings, we demonstrate that the genetic structure of these species are shaped as much by species-specific traits as by historical management choices (e.g. past hunting, reintroductions projects) and highlight the necessity of long-term genomic monitoring to move beyond demographic counts and to ensure the evolutionary resilience.

22 GENETIC DIVERSITY AND POPULATION STRUCTURE OF TWO ENDEMIC FRESHWATER SHRIMP SPECIES

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Abstract

Dugastella valentina and *Palaemon zariqueyi* are two freshwater decapod species endemic to the Valencian region of Spain, where they persist in rivers, lagoons, canals, estuaries and springs. These ecosystems are increasingly threatened by hydrological alteration, habitat fragmentation, artificial water transfers, introduced alien species and climate change. Such pressures may disrupt population connectivity and reduce genetic diversity. The two species differ in ecology and reproductive strategy. Both show abbreviated larval development, but *D. valentina* has an unusually reduced, non-planktonic development combined with parental care, whereas *P. zariqueyi* is more tolerant of oligohaline conditions and has three larval stages before metamorphosis. These life-history differences may influence dispersal capacity and patterns of genetic structure. Previous COI-based work on samples collected in 2005–2008 revealed significant differentiation among river systems in both species, but contrasting patterns of nucleotide diversity and isolation by distance. Here, we re-evaluate the population structure of both endemic species using mitochondrial COI data ten years after initial study, from samples collected in 2017–2018. Building on previous work, we test whether haplotype distribution has changed over the following decade and whether genetic structure reflects river-system connectivity and geographic distance. Overall, our results support restricted population connectivity in both endemic species and reveal an unresolved case of deep mitochondrial divergence in *D. valentina*, highlighting the need for genomic data to test for genetic erosion and clarify the evolutionary origin of this divergent lineage.

23 MULTI-SCALE ENVIRONMENTAL DNA MONITORING FOR MARINE BIODIVERSITY AND BIOSECURITY IN THE SOUTH ATLANTIC

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Abstract

Environmental DNA (eDNA) is increasingly recognised as a powerful tool for assessing marine biodiversity, particularly in remote and data-limited regions. Here we present a multi-scale application of eDNA for biodiversity monitoring around Ascension Island, a UK Overseas Territory in the South Atlantic. Our approach integrates island-wide inshore surveys using repeated coastal sampling to characterise spatial and temporal biodiversity patterns, offshore sampling conducted during the DY159 research cruise to extend coverage into pelagic and deeper-water environments, and regional collaboration with St Helena to support broader ecological comparison across island systems. In addition to biodiversity assessment, targeted biosecurity applications include screening of samples collected from settlement arrays to assess potential introductions of non-native species. The project also incorporates citizen science activities and contributions to the Darwin200 initiative, demonstrating how eDNA monitoring frameworks can be expanded across territories and stakeholder groups. Together, these components provide an integrated approach for linking coastal, offshore, and regional biodiversity observations within isolated marine ecosystems. This work demonstrates how eDNA can support scalable biodiversity assessment, biosecurity surveillance, and evidence-based management in remote island systems, while providing a transferable framework for implementing genetic monitoring programmes across other oceanic regions.

24 HIGH CONNECTIVITY AND SUBTLE GENOTYPE-ENVIRONMENT ASSOCIATIONS IN THE SOIL SPRINGTAIL *ENTOMOBRYA NIVALIS* ACROSS MANAGED FOREST LANDSCAPES

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Abstract

Understanding how managed forest landscapes shape genomic variation in soil biodiversity remains a major challenge in evolutionary ecology. Soil arthropods such as springtails are abundant and functionally important, yet their population connectivity and genomic responses to environmental heterogeneity are still poorly understood. We applied a landscape genomics framework to pooled whole-genome sequencing data from 82 populations of the soil springtail *Entomobrya nivalis* sampled across managed forests of the Black Forest, Germany. We first quantified neutral genomic structure and spatial connectivity using a filtered allele-frequency dataset comprising 5,391 SNPs. Neutral analyses revealed no clear broad-scale genomic structure, with low variance explained by the leading principal components and no evidence for strong biologically meaningful clustering. Pairwise and spatial analyses showed only limited support for geographic structuring, indicating high connectivity across the study region. We then tested whether environmental heterogeneity was associated with genomic variation using complementary genotype-environment association approaches. Bayesian analyses and exploratory multivariate comparisons identified subtle but repeated candidate signals linked to a restricted set of ecologically relevant predictors, particularly vegetation productivity, forest structural complexity, soil chemistry, and management-related variables. The strongest convergence across methods occurred at the predictor and candidate-window level rather than at individual SNPs, suggesting that any environment-associated genomic responses are subtle, distributed, and best interpreted as conservative candidate signals rather than confirmed adaptive loci. Together, our results indicate that *E. nivalis* forms a highly connected genomic network across managed forest landscapes while still showing modest genomic responses to environmental gradients. This study highlights the importance of conservative, multi-method inference for detecting subtle environment-associated genomic signals in high-connectivity systems and provides a reproducible landscape genomics framework for non-model soil arthropods.

25 GENOMIC INSIGHTS INTO THE CONSERVATION OF THE ENDANGERED SECRETARYBIRD (*SAGITTARIUS SERPENTARIUS*)

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Abstract

The Secretarybird (*Sagittarius serpentarius*) is an evolutionarily distinct and ecologically specialized diurnal raptor, widespread across Sub-Saharan Africa and the sole extant representative of the family Sagittariidae. Currently classified as Endangered on the IUCN Red List, the species faces severe threats from climate change, habitat loss, human persecution, and infrastructure collisions, driving sharp and ongoing population declines. Effective conservation management is further hindered by a total absence of baseline data on the species' genetic health in the wild; to date, no information exists on the genomic diversity or population structure of this taxon across its distribution range. To bridge this gap, we assembled the first chromosome level reference genome for the Secretarybird. Using this resource, we resequenced the whole genomes of 40 wild individuals sampled from core populations across Africa: 31 from East Africa (Serengeti and Tarangire ecosystems, Tanzania; Amboseli National Park, Kenya) and 9 from South Africa (Northern Cape and Free State Provinces). Genomic analyses are currently underway to: (i) investigate fine-scale population structure and gene flow within and between East and South African populations to define critical conservation units; (ii) quantify individual- and population-level genetic diversity and inbreeding coefficients; and (iii) evaluate genomic load to assess the relative severity of inbreeding depression, benchmarking these metrics against other threatened avian taxa. Understanding the distribution of inbreeding and genetic load across populations will directly inform future translocation planning, guide the prioritization of ecological corridors to maintain gene flow, and establish a foundational genomic baseline for long-term monitoring of conservation effectiveness.

26 COMPARATIVE GENOMICS ACROSS MULTIPLE INDEPENDENT ORIGINS OF KLEPTOPARASITISM IN BEES

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Abstract

Bees are ecologically important pollinators with remarkable diversity in life-history strategies. Repeated transitions to kleptoparasitic lifestyles in bees provide an opportunity to investigate patterns of genome evolution associated with major ecological and phenotypic shifts. Kleptoparasitism has evolved multiple times independently across bee lineages and is frequently associated with the loss of pollen-collecting structures (scopae). Here, I use a large-scale comparative genomics framework spanning genomes from more than 200 bee species to investigate genome evolutionary patterns associated with repeated transitions to kleptoparasitism. The dataset includes multiple independently evolved parasitic lineages and integrates phylogenomic reconstruction, transposable element annotation, gene family evolution analyses, tests of positive and relaxed selection, genome size comparisons, repeat landscape characterization, and gene loss analyses. Preliminary analyses suggest heterogeneous patterns of genome evolution across independently evolved kleptoparasitic lineages, rather than a single convergent genomic pattern associated with parasitic transitions. These analyses provide a broad comparative framework for investigating repeated ecological transitions and genome evolution across pollinator diversity. More broadly, this work contributes comparative genomic resources relevant to future studies of pollinator evolution, biodiversity genomics, and the evolutionary consequences of ecological specialization.

27 RESTORING THE GLORY: THE CONSERVATION GENOMICS OF THE KENTISH GLORY MOTH

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Abstract

Global biodiversity is declining at an alarming rate, with insects being particularly affected. The Kentish Glory moth, *Endromis versicolora*, an evolutionarily distinct species and the only European representative of the family Endromidae, exemplifies this crisis.

Once widespread in England and Wales, the species became locally extinct in the 1970s and now persists only in fragmented populations in the Scottish Highlands, continental Europe and western Asia. Such isolation, combined with limited dispersal ability, may lead to inbreeding and reduced genetic diversity, limiting adaptability under changing environmental conditions.

In collaboration with Twycross Zoo, Butterfly Conservation, Natural England, Forestry England, the Natural History Museum and the University of Leicester, we will investigate the genetic health and population structure of the remaining Scottish populations. Using a whole-genome approach, we will analyze DNA from contemporary samples and museum specimens to compare genetic variation across time and space, and explore relationships with English, Welsh and continental populations.

Our results will inform ongoing conservation efforts, identifying suitable source populations for potential reintroduction to England and contributing to a broader understanding of insect conservation genomics and the crucial role of genetic diversity in species recovery and resilience.

28 ASSESSING THE USE OF GENETICS AND GENOMICS IN CONSERVATION: A REVIEW OF ACTION PLANS

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Abstract

Advances in genomic sequencing promise a deeper understanding of the genetic and evolutionary processes driving population decline and extinction, potentially better informing conservation strategies. However, incorporating genetics into conservation management remains challenging, resulting in a well-documented gap between scientific research and its practical application. Conservation action plans (AP), which document official strategies for species protection, provide a valuable opportunity to assess how results from genetic and genomic studies are currently taken into account in conservation. Conversely, analyzing these documents can reveal knowledge gaps, guiding future research priorities, or application gaps, highlighting genetic analyses that have yet to be effectively translated into practical conservation measures. In this work, we reviewed 104 AP across endangered and critically endangered primates, proboscideans and carnivores, published between 1989 and 2024. We assessed the use of genetics in each of them, analyzing their content independently through a Large-Language Model with posterior human controls. A first set of queries consisted of asking if the AP mentioned specific genetic concepts, and a second set consisted of searching for recommended conservation measures that could aim at limiting genetic risks or benefit from genetic analyses. We further assessed if genetic data were available for the focus species and, if it were the case, we recorded the genetic markers and analyses that were cited. Some preliminary results show that the concept of genetic diversity is the most cited (60 AP), while effective population size and local adaptation are mentioned in seven and four AP, respectively. Out of 50 AP that mention existing genetic analyses, five AP mention studies based on whole genome sequencing, the majority using microsatellites (27) and/or mitochondrial DNA (30). With this work, we provide an updated overview of the use of genetics in applied conservation, and hope to propose ways for research to effectively support conservation efforts.

29 FROM FOUNDER EVENTS TO GENETIC RECOVERY? THREE DECADES OF WOLF EXPANSION ACROSS THE ITALIAN ALPS

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Abstract

Understanding how genetic diversity and population structure evolve during natural recolonization is critical for the conservation of wide-ranging carnivores in human-dominated landscapes. We analyzed 27 years of continuous genetic monitoring (1998-2024) of the naturally expanding Italian Alpine wolf (*Canis lupus*) population, providing one of the most comprehensive temporal datasets for any recovering large carnivore in Europe. Using > 6,500 samples and 1,584 genetically identified individuals, we evaluated population responses through time to two different founder events, and assessed long-term trends in genetic diversity and population structure, considering the effects of connectivity on effective population size (N_e) over time. We found persistent genetic distinctiveness between the western and eastern Italian Alpine regions, despite ongoing demographic expansion. The western Alps currently act as a primary source of genetic diversity, with high allelic richness, within-region migration rates and a detectable increase in N_e over the last 10 years. The eastern Alps still exhibit lower genetic diversity, mirroring the trajectory observed in the western Alps during the early stages of recolonization, and signatures of recent founder events. Contemporary gene flow across the Italian Alps remains asymmetric and extremely limited, potentially constraining long-term viability. Pack number proved to be a reliable proxy for effective population size in wolves, particularly during the early phase of population expansion and when spatial population structure was accounted for. Our results demonstrate that long-term demographic recovery alone does not necessarily translate into genetic recovery, underlining the need for continued genetic monitoring to inform conservation strategies that maintain connectivity and adaptive potential in recolonizing large carnivores.

30 FROM DOÑANA TO THE SPECIES LEVEL: GENETIC CONSEQUENCES OF TRANSLOCATIONS AND MANAGEMENT OF THE IBERIAN LYNX

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Abstract

Conservation genetics plays a pivotal role in the long-term recovery of endangered species. Genetic parameters such as inbreeding depression and genetic diversity are essential for guiding effective conservation strategies. The Iberian lynx (*Lynx pardinus*) was classified as the most endangered felid in the world in 2002. Over the past two decades, intensive conservation efforts, including captive breeding and reintroduction programs, have dramatically improved the species' status. However, the genetic consequences of these interventions, particularly translocations, remain insufficiently explored across the metapopulation.

This study aimed to: (i) evaluate the founder success of translocated individuals, (ii) assess the genetic status of the Doñana population, and (iii) perform genetic monitoring of reintroduced and captive populations across the Iberian Peninsula.

We genotyped 289 Single Nucleotide Polymorphisms (SNPs) in 358 individuals from the Doñana population using samples collected between 1985 and 2025. We reconstructed the pedigree and applied pedigree- and marker-based approaches to estimate inbreeding, ancestry, genetic diversity, and founder contributions. To extend the analysis at the metapopulation level, we genotyped 2547 individuals from multiple populations in Spain and Portugal, including reintroduced and ex situ populations, using a panel of 94 SNPs. We assessed genetic diversity, admixture, and genetic differentiation among populations (F_{st}).

Our results show a clear increase in genetic diversity across most populations. In Doñana, we detected post-translocation inbreeding in a few admixed individuals due to the high success of a single founder. Genetic differentiation among populations remains detectable, indicating limited natural gene flow.

These results confirm the success of translocations while highlighting the need for continued management to prevent renewed inbreeding. Enhancing connectivity through stepping-stone populations, maintaining translocations, and continuing genetic monitoring will be essential to ensure long-term genetic resilience.

31 DIET ANALYSIS OF RELEASED EUROPEAN WILDCATS (*FELIS SILVESTRIS*) IN CAIRNGORMS, SCOTLAND

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Abstract

European wildcats (*Felis silvestris*) are the last remaining native cat species in Britain but due to threats from hybridisation with domestic cats, and persecution, they are classified as Critically Endangered on the UK Red List. Conservation efforts undertaken by the Royal Zoological Society of Scotland (RZSS) led Saving Wildcats partnership aim to prevent the loss of wildcats in the UK; this includes a breeding-for-release programme that has, so far, released a total of 46 wildcats into the Cairngorms Connect area in the Scottish Highlands. Released cats are tracked to assess their progress in the wild which includes monitoring their movements and a variety of behaviours, including feeding. A key to understanding their feeding behaviour is to assess their diet and prey preferences which can be challenging due to the elusive nature of wildcats. To address this issue RZSS WildGenes have developed a 12S diet metabarcoding protocol that is suitable for assessing scat samples that can be collected non-invasively. Here we; 1) show this diet metabarcoding technique is suitable for determining the diet of wildcats by testing it on scats collected from cats in the breeding programme which have been fed a known diet, 2) use this technique to determine what species are being consumed by the released wildcats, and 3) quantify the prey preference of the released wildcats. These data provide vital insights into the diets of wildcats released from the breeding programme which will support management strategies and ongoing conservation efforts.

32 INTEGRATING MICROSATELLITES AND WHOLE-GENOME SEQUENCING TO ASSESS GENETIC EROSION IN *CRICETUS CRICETUS*

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Abstract

Habitat fragmentation is one of the primary drivers of genetic erosion in wildlife populations, yet the assumption that large, seemingly stable populations are genetically resilient remains poorly tested. The European common hamster (*Cricetus cricetus*), once considered an agricultural pest, is now critically endangered, with only ten wild populations persisting in Hesse, Germany. Previous studies using microsatellites documented systematic bottlenecks and strong differentiation among isolated populations, but lacked the genomic resolution to assess individual inbreeding or detect cryptic population structure. Here, we present the first study integrating microsatellite and whole-genome sequencing data in this species, analyzing four population groups spanning a fragmentation gradient: a core population in well-connected habitat, satellite groups in isolated patches, recently extirpated sites, and historical reference populations. Using runs of homozygosity analysis, we quantified individual inbreeding at a resolution previously unavailable for this species. Satellite populations showed pronounced genetic erosion, characterized by reduced diversity and elevated inbreeding coefficients consistent with prolonged isolation and drift. Contrary to expectations, however, the core population, considered the primary genetic reservoir for regional conservation management, displayed cryptic substructure that undermines its assumed role as a source of genetic diversity. Together, these findings challenge the prevailing conservation assumption that population size alone guarantees genetic resilience and highlight the risk of overlooking internal fragmentation in populations that appear stable by demographic criteria alone. Our results demonstrate the critical value of integrating whole-genome data into conservation monitoring frameworks, particularly for species where management decisions depend on identifying functional genetic reservoirs, and provide actionable genomic evidence to refine translocation strategies for one of the most threatened small mammals in Western Europe.

33 GENOMIC RESCUE AS A TOOL TO RESTORE VULNERABLE POPULATIONS

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Abstract

Many wildlife species have been reduced to fragmented and isolated populations through Anthropogenic environmental change. Such populations are especially vulnerable to extinction, not only due to demographic stochasticity and environmental pressures, but also because of genetic factors. While the principles of drift, inbreeding, and mutation load are well established, their combined role in determining extinction risk is less well understood. This poses a challenge for conservation practitioners, who have to make an informed decision on how to manage such populations best.

Human-mediated gene flow, in an extreme case ‘genetic rescue’, is expected to become increasingly necessary in the future. Central to this intervention is the decision which populations or individuals to select as a source for genetic supplementation. Current practice often emphasizes demographic recovery, however even with an increase in population size, genetic erosion can still persist. Genetic load may accumulate further and eventually become expressed, especially when both source and target populations share deleterious alleles. Thus, interventions aimed at increasing diversity can inadvertently cause harm if the underlying evolutionary processes and resultant genetic patterns are not carefully understood.

To support decision-making, we have developed a unifying framework for genomic rescue, which integrates demographic history, standing genetic diversity, mutation load, and local adaptation. We implement this for a high-profile, real-world example: the pseudomelanistic tigers of Simlipal.

By bringing together theoretical, empirical, and applied perspectives, we aim to connect evolutionary principles with urgent conservation challenges. This type of collaboration between academic researchers and management authorities, leading to the co-design of an intervention and action-oriented approach, is still rare in the field of conservation genomics, yet much needed. We hope that this framework and its application will not only advance fundamental understanding of the vulnerability of small populations, but also improve the long-term outcomes of real-world interventions.

34 GENOMIC ASSESSMENT OF REINTRODUCED AFRICAN WILD DOGS INFORMS CONSERVATION TRANSLOCATIONS

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Abstract

Conservation translocations have become important assets in saving African wild dogs (*Lycaon pictus*) from local extinction, which have declined drastically due to anthropogenic pressures. In South Africa, wild dogs were eradicated except for a small, isolated population remaining in Kruger National Park. Due to reintroductions into private reserves, the country now holds a viable metapopulation of over 150 individuals that is used as a donor to repopulate other countries in southern Africa. This Range Expansion Project has become one of the most extensive efforts worldwide to recover population numbers of an endangered carnivore, allowing a unique opportunity to quantify the genomic effect of founder effects, population isolation, and conservation translocations. For this purpose, we re-sequenced 30 genomes of wild dogs from Kruger, private reserves, and outside protected areas. Demographic reconstructions indicate that populations were historically large (10,000-40,000 individuals) but began declining gradually ~500-100 kya, coinciding with Mid-Pleistocene climate shifts, followed by a sharp collapse ~0.8 kya. The negative correlation between nucleotide diversity and runs of homozygosity (ROH) suggests that low genetic variation is primarily driven by inbreeding rather than by demographic history. Reintroduced populations in private reserves exhibited the highest variation and lowest

deleterious load. The short ROHs and close genetic affinity to an individual from Kenya further highlight the effectiveness of ongoing translocations and population admixture. The absence of drift and relaxed selection on trait variance in translocated groups imply that genetic resilience can be restored within 10 generations, providing valuable guidance for managing genetic variation in threatened species. We also developed conservation translocation guidelines based on continent wide population structure to inform future reintroduction efforts. We recommend that wildlife managers prioritize maintaining overall genetic diversity rather than strictly preserving original genetic composition, thereby enhancing adaptive potential in a rapidly changing environment.

35 ASSESSING RISKS AND OPPORTUNITIES OF ASSISTED EVOLUTION IN EELGRASS RESTORATION.

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Abstract

The unprecedented rate at which climate change is altering ecosystems and accelerating biodiversity loss, raises concern that current restoration efforts may not enable species to adapt quickly enough. This concern has led to consider more direct interventions such as assisted evolution strategies, which aim to enhance resilience in vulnerable populations by introducing more tolerant or genetically diverse individuals. While such approaches are becoming technically feasible, the genetic risks and consequences of such interventions remain largely unexplored, particularly in marine ecosystems. To address this gap, we compiled and analyzed research evidence and case studies involving assisted evolution in seagrass and related systems to identify advantages, risks and decision-making factors that could promote evidence-based interventions in the future. Our goal was to synthesize relevant information that could serve to develop practical guidelines for conducting risk-benefit assessments before implementing assisted evolution in eelgrass (*Zostera marina*) meadows in Sweden.

36 PREDISPOSED OR JUST LUCKY? THE GENETICS OF AFRICAN SWINE FEVER SUSCEPTIBILITY

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Abstract

Over the past 50 years, many new wildlife epidemics have emerged. This phenomenon is currently poorly understood but appears to be affected by an increase in encounters with new pathogens and a decrease in the ability to adapt to emerging infectious diseases. Understanding the nature of population-level susceptibility to new diseases allows for predictions of local population declines and stimulates vaccine development. One newly emerged disease is African Swine Fever (ASF), a lethal disease to wild pig species. It is currently accepted that all non-African members of the Suidae family (including multiple threatened wild Asian pig species) are highly susceptible to the disease, resulting in high mortality (90- 99%). Susceptibility appears not to be affected by initial viral dose or ecological factors, suggesting a genetic component to susceptibility. We aimed to assess a genetic link to susceptibility using a genome-wide association study (GWAS) approach. To this end, Latvian wild boars that either died from (n=21) or survived (n=18) ASF were whole genome sequenced (12.9X - 25.2X). We sought to identify both associated single nucleotide polymorphisms (SNPs) and putatively causative genes. Significant SNPs based on the GWAS model were further assessed for relevance based on genetic divergence (F_{ST}), as well as evolutionary conservation and genome architecture (CADD scores). In total, we identified 197 significant SNPs spanning over 32 individual GWAS peaks. These peaks overlapped with 40 annotated genes, 12 of which contained SNPs with higher genetic differentiation and high putative impact. Focal genes are involved in regulating autophagy, immune cell differentiation, apoptosis, and/or protein translation. These processes are known to be actively modulated by the virus to increase virulence or prevent immune detection. To our knowledge, this is the first GWAS assessing ASF survival in European wild boar, simulating the relevance of genetic surveillance for understanding wildlife disease dynamics.

37 USING PREDICTED DELETERIOUS MUTATIONS FOR CONSERVATION MANAGEMENT

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Abstract

To improve or conserve the genetic health of threatened species, conservation strategies increasingly rely on predicting deleterious mutations from genomic data. These approaches allow conservation geneticists to estimate the mutation load based on genetic data alone, which can be used to monitor genetic health over time, identify vulnerable populations, and inform captive breeding programs. However, their utility ultimately depends on how well predicted mutation load translates to fitness in the wild. In my research, I disentangle mutation load dynamics by linking genomic mutation loads to sexual traits and fitness proxies in a wild lekking bird, the black grouse. We show that mutations predicted with functional annotation and evolutionary conservation differ in predictive power, that natural and sexual selection act on distinct functional elements of the genome, that heterozygous deleterious mutations contribute substantially to mutation load, and that selection varies across life-history stages. Together, these findings have important implications for the application of current prediction tools in conservation, and underscore the need to first establish how predicted deleterious mutations translate into fitness variation in wild populations before their value for conservation management can be properly assessed.

38 FORENSIC GENOMICS FOR RAPTOR CONSERVATION: GENOMIC EQUILIBRIUM AS A DIAGNOSTIC TOOL TO COMBAT SAKER FALCON TRAFFICKING

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Abstract

Effective conservation of raptors requires distinguishing wild from captive-bred individuals. This study proposes a novel framework based on the breakdown of drift-migration-mutation equilibrium in captive populations. Using whole-genome sequencing of 27 confiscated Saker Falcon (*Falco cherrug*) in Kazakhstan, alongside known wild and captive controls, we characterised "genomic benchmarks" of wild versus captive populations. We first defined a wild equilibrium via several parameters including divergence, heterozygosity, and Runs of Homozygosity (ROH) patterns. In contrast, we identified captive-bred individual using thresholds for Gyr Falcon-ancestry and longer-segment ROH, detecting either hybrid-induced heterozygosity or clear signs of inbreeding. We then validated our binary classification by testing whether confiscated individuals matched the landscape-level signatures of wild populations or the distinct profiles of known captive controls. This equilibrium-based approach allows us to provide authorities with robust evidence to separate local wild birds from captive individuals. Our results demonstrate how fundamental population genetics parameters can be repurposed into high-resolution forensic anchors to disrupt illegal wildlife trade and guide rehabilitation strategies.

39 WOLF–DOG HYBRIDIZATION: POPULATION STRUCTURE CONFOUNDS HYBRID CLASSIFICATION

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Abstract

Close relatedness between gray wolf and domestic dog may complicate reliable hybrid detection in routine monitoring, particularly where divergent wolf lineages meet and admix. Here, we develop and evaluate a conservative, monitoring-compatible workflow for wolf–dog hybrid detection in Czechia, a Central European contact zone at the intersection of differentiated wolf populations. Using four consecutive wolf years (2020/2021–2023/2024), we analyzed 2,413 field-collected samples (predominantly non-invasive), yielding 380 unique wolf genotypes based on 20 short tandem repeat (STR) loci. We demonstrated that hybridization testing without accounting for intraspecific wolf structure can inflate apparent admixture and bias assignment outcomes. We therefore implemented a framework that accounts for population structure by (i) inferring wolf population clusters, (ii) calibrating conservative assignment thresholds per cluster using HYBRIDLAB simulations and two Bayesian approaches (STRUCTURE and NewHybrids), and (iii) verifying individuals below thresholds with mitochondrial control-region haplotypes and a 96-marker wolf–dog single nucleotide polymorphism (SNP) panel. Cluster-specific thresholds flagged 20 individuals for verification, SNP analyses confirmed 19 as pure wolves, while one individual showed strong support for dog backcross ancestry and carried a mitochondrial DNA haplotype commonly reported in dogs. Our results show that accounting for wolf population structure is essential to avoid false-positive hybrid assignments in contact zones and that STR-based screening retains high practical value when embedded in a conservative, simulation-calibrated workflow with targeted confirmation steps. Because hybrid claims can influence management actions and public perception, and misclassification can have disproportionate consequences, reliable and reproducible detection methods are essential for conservation management.

40A CONSERVATION ROADMAP FOR THE ANTICIPATED EURASIAN LYNX (*LYNX LYNX*) METAPOPOPULATION IN CENTRAL EUROPE – MODELLING EFFECTIVE DEME SIZES AND CONNECTIVITY

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Abstract

Reintroducing wildlife into anthropogenic landscapes is challenging. Particularly for wide-ranging species, extensive habitat fragmentation and limited carrying capacities pose genuine risks of population isolation and subsequent genetic erosion. A current example are the fragmented populations of the Eurasian lynx (*Lynx lynx*) in Central Europe, where isolated demes currently rely on *ex situ* sourced releases to buffer inbreeding accumulation over short timescales. But due to management trade-offs, such assisted migration can only function as a transitional remedy, whereas long-term stability hinges on inherent growth rates and vital genetic exchange in a metapopulation framework. We here use analytic modelling to examine potential scenarios and requirements for a vital metapopulation of the Eurasian Lynx (*Lynx lynx*) in Central Europe. To inform conservation management in the early stages of formation, we considered scenarios that describe the current and near-future status of the metapopulation, as well as anticipated – but not yet established – scenarios that would ensure long-term genetic stability. We find that current and near-future effective sizes and migration rates among demes are far from sufficient to reach long-term stability ($N_{e_{meta}} > 500$) over hundreds of generations. Robust configurations would require significant increases in deme sizes (> 150%), and average pairwise migration rates (> 0.1), in order to advance towards stable metapopulation dynamics. This, however, entails potential distribution trade-offs from limited capacities in *ex situ* and/or wild population sourcing. Here, our model outcomes caution against diverting resources towards new introductions, and highlight the need for increased connectivity among existing demes.

41 FORENSIC PHYLOGEOGRAPHY UNCOVERS MULTIPLE ORIGINS OF THE LEOPARD CAT (*PRIONAILURUS BENGALENSIS*) IN THE ILLEGAL WILDLIFE TRADE

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Abstract

The leopard cat (*Prionailurus bengalensis*) is one of Asia's most widely distributed felids, yet its populations are increasingly threatened by habitat loss, human-wildlife conflict, and the illegal wildlife trade. In Hong Kong, a recognised wildlife trafficking hub, distinguishing locally poached animals from smuggled individuals is a critical enforcement challenge, as each case falls under different ordinances carrying distinct penalties. This study used the mitochondrial genome to determine the geographic origin of three confiscated leopard cats - two seized in Hong Kong and one intercepted at Singapore's Changi Airport. In addition, whole genomes were assembled for 19 Hong Kong individuals to establish a novel genetic database for the city's native population. The assemblies were then compared against 40 publicly available sequences spanning the species' range using maximum-likelihood phylogenetic trees and median-joining haplotype networks. Our analyses revealed three distinct trafficking routes - one Hong Kong seizure was traced to a Southern Chinese source, a second to an Indochinese or South Chinese source population, and the Singapore seizure was assigned to the Sundaic lineage, most likely originating from Malaysian Borneo or Indonesia. None of the confiscated individuals matched the local Hong Kong genetic cluster, indicating that these seizures represent cross-border trafficking rather than local poaching. Our results demonstrate that leopard cat trafficking in the region is considerably more complex than simple cross-border trafficking, and encompasses international maritime or aerial routes that funnel Sundaic animals through Singapore as a transit hub. By generating actionable intelligence, our work illustrates the power of forensic phylogeography to support wildlife crime prosecution and highlights the urgent need for expanded reference databases to further strengthen enforcement capacity across Southeast Asia.

42 BopCo: SPECIES IDENTIFICATION, HYBRID DETECTION, AND RELATEDNESS ANALYSIS IN SUPPORT OF POLICY FRAMEWORKS AND WILDLIFE CONSERVATION PROGRAMMES

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Abstract

DNA-based species identification, hybrid detection, and relatedness analysis provide the empirical foundation for functional wildlife conservation programmes and policy instruments (e.g., CITES). BopCo is a Belgian service that applies these molecular tools to handle on-demand requests from a broad range of stakeholders, including government agencies, research institutions and conservation organisations. BopCo is jointly operated by two Belgian Federal Scientific institutions, viz., the Royal Belgian Institute of Natural Sciences and the Royal Museum for Central Africa, and its work spans a wide range of policy contexts, from aiding the enforcement of CITES trade regulations to supporting ex situ breeding programmes.

Recent projects illustrate this approach. First, BopCo uses mitochondrial DNA sequencing combined with nuclear microsatellite profiling to identify *Tragopan* pheasants and detect hybridisation in captive populations, in collaboration with Aviornis International vzw and the World Pheasant Association - Benelux. Similarly, BopCo applies this approach to study Chilean (*Phoenicopiterus chilensis*) and American (*P. ruber*) flamingos at zoos. Both flamingo species and three of the five *Tragopan* species are CITES-listed in Appendix II and I, respectively. Maintaining genetically pure lineages in captive populations is critical to preserve their conservation value and their potential as a source for future management planning and eventual reintroductions in the wild. Additionally, a co-ancestry matrix derived from microsatellite data further quantifies kinship among individuals, informing breeding pair selection and population management.

Second, commissioned by the CITES management unit at FPS Health, Food Chain Safety and Environment, BopCo performs parentage verification for CITES-listed birds of prey, owls and parrots held by Belgian breeders. By comparing the DNA profiles of offspring with those of putative parents, using feather samples collected by CITES inspectors, BopCo confirms whether birds such as the peregrine falcon (*Falco peregrinus*), snowy owl (*Bubo scandiacus*) and barn owl (*Tyto alba*) were legally bred in captivity, thereby protecting wild populations from illegal collection.

More information on our identification services can be found at <https://www.bopco.be/>.

43 GENOMIC INSIGHTS INTO THE POPULATION STRUCTURE OF CETACEAN TOP-PREDATORS IN THE NORTH ATLANTIC OCEAN

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Abstract

Climate change is driving rapid shifts in marine species distributions, including northward expansions of temperate cetaceans into Arctic waters. Understanding how these shifts affect genetic connectivity is critical for defining effective management units. We conducted a genome-wide population-genomic analysis of three temperate cetaceans, long-finned pilot whales (*Globicephala melas*), Atlantic white-sided dolphins (*Leucopleurus acutus*), and white-beaked dolphins (*Lagenorhynchus albirostris*), to reassess population structure across the North Atlantic, including previously undersampled Greenlandic waters. Previous studies based on mitochondrial DNA, microsatellites, and ddRAD suggested contrasting patterns of structure, but were limited by uneven sampling or low genomic resolution. Our results confirm strong genetic differentiation between North Atlantic and Mediterranean pilot whales, alongside fine-scale west-to-east structuring within the North Atlantic and evidence of admixture. Atlantic white-sided dolphins show no significant population structure, supporting a panmictic North Atlantic population with low levels of inbreeding. In contrast, white-beaked dolphins form three distinct clusters, with Greenlandic individuals grouping within a western North Atlantic cluster alongside Canadian samples. We also detect elevated inbreeding among individuals from the North Sea and the waters surrounding the British Isles. These findings refine population boundaries across all three species and highlight the importance of genome-wide data for detecting subtle structure, with direct implications for conservation and management under ongoing climate-driven range shifts.

44A GENOMIC TOOLKIT FOR EX-SITU CONSERVATION ACTION: SUBSPECIES-LEVEL REFERENCE GENOMES TO GUIDE POPULATION MANAGEMENT OF THE ASIAN FOREST TORTOISE (*MANOURIA EMYs*)

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Abstract

Within the challenge of global biodiversity decline, populations of critically endangered animal species in zoos are increasingly more important as genetic reservoirs for long-term species survival. However, for many endangered species, breeding management based on morphological or historical "best-guess" data limits conservation potential that could be enhanced through high-resolution genomic data. This challenge is particularly evident in the Asian Forest Tortoise (*Manouria emys*), where the EAZA European Ex-situ Programme (EEP) manages two morphologically distinct subspecies with uncertain historical parental records of the individuals within the breeding programme. This study addresses this gap by establishing the first chromosome-level *de novo* reference genome assemblies for both *M. emys emys* and *M. emys phayrei*. Using Oxford Nanopore sequencing, we generated 2.3 Gb assemblies that revealed a 1.34% genetic divergence between the subspecies, supporting their taxonomic distinction and providing a genetic basis for breeding programme management. Our heterozygosity analysis found no evidence of recent inbreeding, indicating that current lineages maintain low, but decent genetic diversity for sustainable management. These reference genome assemblies can serve as the foundation for developing practical management tools, such as molecular subspecies verification and DNA-based parentage assignment to resolve uncertain pedigree records. While genomes alone do not directly solve management challenges, they enable practical tools that zoo programmes can routinely implement, providing a framework for *ex-situ* programmes managing taxonomically complex species. As captive populations become increasingly vital for species survival, such genomic foundations are essential for maximising conservation value through *ex-situ* management, research, and future reintroduction efforts.

45 LINKING SUSPECTS TO AN ILLEGALLY FELLED INCENSE TREE (*AQUILARIA SINENSIS*) USING DNA FORENSICS

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Abstract

The incense tree *Aquilaria sinensis* is an evergreen tree species that is extensively illegally harvested across Asia due to the high market value of the agarwood it produces. This problem is particularly prevalent in Hong Kong, where government agencies are actively working to reduce illegal harvesting by developing new deterrence measures and prosecuting criminal suspects. Here, we resolved the first criminal case of illegal incense tree harvesting in Hong Kong using forensic genomic analyses. We identified several plant particles collected from the clothing of suspects as *A. sinensis* using Sanger sequencing and further traced these back to a specific wild tree damaged by illegal harvesting. These results, presented as evidence, led to the prosecution of nine suspects, whose sentences ranged between 30–50 months in prison under the Hong Kong Organized and Serious Crimes Ordinance (OSCO). This was one of the first few times this Ordinance was used in illegal wildlife trade prosecution in Hong Kong, resulting in 25% longer sentences. The result demonstrates that even small, aged and poorly preserved wood particulates can yield sufficient genomic DNA for Sanger and whole genome analyses to be used as forensic evidence to support the prosecution of criminal suspects. This research also serves as an important case study for the application of genetics in real-life wildlife forensic prosecutions.

46 GENDIVA: A SIMPLE SITE-BASED GENETIC DIVERSITY ASSESSMENT TOOL

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Abstract

Genetic Diversity is the key foundational component of biodiversity, but is rarely recognised in policy. Since it is essential for adaptation in the face of climate change and other pressures, this is problematic. This is beginning to change with the development and implementation of national genetic diversity reporting under the Global Biodiversity Framework. However, whilst indicators have been developed for use at a national scale, they are not currently suitable for informing local management interventions. They may also be complicated to explain to land managers.

We thus identified a need for a simple tool facilitating inclusion of genetic diversity in policy and site management. We wanted this to be applicable to understanding genetic diversity within existing protected areas, Other Effective Area-based Conservation Measures (OECM), and any other areas managed with conservation in mind.

We worked with academics and practitioners from a range of countries across four continents, with different levels of education and experience, and working with diverse taxa, to develop a simple, proxy-based method, which relies on land managers' own knowledge and which they consider to be practical. This method also enables incorporation of genetic data where available.

We have used the resulting method with a range of communities in Scotland, Libya, Mexico and Australia, demonstrating that it is practical and useful on a range of scales, and that local people are both able and willing to incorporate genetic considerations into their management of land and species.

47 GENETIC DIVERSITY MONITORING FOR NATURE RESTORATION: INSIGHTS FOR POLICY AND PRACTICE FROM EUROPE AND BEYOND

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Abstract

Global commitments to halt biodiversity loss and restore degraded ecosystems have driven recent momentum for large-scale ecological restoration, including the Kunming-Montreal Global Biodiversity Framework and the recent EU Nature Restoration Regulation. Legislation and restoration initiatives typically focus on habitat recovery and ecological connectivity, but they overlook a key level of biodiversity: genetic diversity. Standing genetic diversity is critical for long-term resilience, adaptability, and persistence of populations and ecosystems. Consideration of genetic diversity in restoration initiatives is typically done at the very beginning, if at all. However, genetic diversity fluctuates over time, especially in the small populations that are often the focus of restoration projects. These changes can go unnoticed unless they are monitored. Genetic monitoring, the systematic tracking of genetic diversity changes over time and space, is a practical tool that can improve restoration outcomes. By analyzing changes within and among populations, genetic monitoring can reveal threats that are not captured by traditional measures such as monitoring species presence or evaluating habitat quality. It can act as an early-warning system for genetic erosion and fragmentation, inform functional connectivity, and help evaluate whether restored populations are stable or in need of genetic rescue. On the flipside, when genetic diversity is overlooked, restored populations may remain vulnerable to inbreeding,

reduced adaptive potential, or even maladaptation in the face of environmental change. In this talk, we present how genetic monitoring can support nature restoration in Europe and beyond, drawing on practical examples and outlining potential roadmaps for integration into restoration efforts. We identify key barriers to its uptake, including limited awareness among stakeholders and the disconnect between scientists and practitioners. By addressing these challenges, we demonstrate how genetic monitoring can directly inform conservation decisions and guide adaptive management, helping to improve long-term success of restoration efforts.

48 BEYOND THE FINE PRINT: HOW WELL DO NATIONAL AND EU CONSERVATION REGULATIONS ADDRESS GENETIC DIVERSITY?

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Abstract

Genetic diversity is one of the central pillars of biodiversity and is crucial for the adaptive potential and persistence of species in a changing environment, as recognised in the Convention on Biological Diversity (CBD) Kunming-Montreal Global Biodiversity Framework. However, for its effective and sustainable management to thrive, it is crucial that genetic diversity is also recognised in the core of legislation, i.e. legally binding documents, which should instruct and enforce the conservation of this natural resource. Within the EU COST-Action GENOA, we are evaluating if genetic diversity is truly considered within legislation documents of the EU as well as nationally in countries across Europe, spanning a wide spatial and political scale. Moreover, our analysis will enable to identify the legally binding documents that should address the protection and restoration of genetic diversity, which supports species survival and adaptation. Our preliminary results indicate that a direct implementation of genetic diversity is still lacking within legally binding national and EU documents. Instead, attention is given to general biodiversity aspects, i.e. habitats, or ecosystems, including the importance of ecological corridors promoting migrations, which might have indirect effects on maintaining genetic diversity. However, usually there are no specific actions or targets involved with the direct or indirect genetic diversity statements. This hampers the recognition and monitoring of genetic resources in conservation practices despite the shared obligation agreed upon. It is thus essential to clarify if the lack of direct recognition of genetic diversity with clear actions and targets is due to limited background knowledge, lacking monitoring or indicator tools in practice, or other reasons. Only by understanding the status and obstacles can we understand at which level a targeted engagement in policy and legislation is required to effectively protect one of biodiversity's core levels.

49 GENSCOP: A PLATFORM FOR THE GENETIC ANALYSIS OF THREATENED SPECIES IN SWITZERLAND

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Abstract

GENSCOP is a platform, supported since 2024 by the Swiss Federal Office for the Environment and four research laboratories of Swiss institutions. It links geneticists, conservation practitioners, and governmental authorities for a better and more efficient conservation of threatened species. GENSCOP canalizes the demands of national/regional offices and practitioners and links them to the expertise of one of the laboratories. The platform further assures scientific and professional advice by an expert commission, including data interpretation and translation into conservation recommendations. GENSCOP therefore provides an interface between the scientists who produce and analyse the genetic data, the conservationists who want to preserve species in their natural habitat and need input from genetics for better informed decisions, and the national and cantonal offices which need to know how to invest their financial resources most efficiently to conserve threatened species. GENSCOP started with a pilot phase involving ten plant projects that address three types of concerns often raised by the cantonal authorities: i) estimate populations' genetic diversity and population differentiation of endangered species, ii) assess hybridization levels of threatened species with native congeners, cultivated or invasive ones, and iii) genetically delineate taxonomically unclear entities. We will present exemplary outcomes from these pilot studies in terms of their implementation in practical conservation.

50 MAKING GENETIC DIVERSITY COUNT: THE GENOA COST ACTION

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Abstract

Genetic diversity underpins population viability, adaptive potential and long-term resilience, making it a core focus of conservation genetics. Monitoring genetic diversity through population-level metrics such as effective population size (N_e), allelic diversity and temporal genetic change is increasingly recognised as essential for assessing conservation status and outcomes. However, across Europe, genetic diversity data remain fragmented, methodologically heterogeneous and insufficiently integrated into biodiversity monitoring frameworks and policy reporting. GENOA (CA23121 – Genetic Nature Observation and Action) is a European COST Action established to address these challenges by advancing coordinated, scalable and policy-relevant genetic diversity monitoring. GENOA brings together researchers, practitioners, policy-relevant organisations and early-career scientists to develop shared approaches for genetic nature observation across taxa, ecosystems and national borders. The Action focuses on three main objectives: (i) advancing genetic diversity indicators and best practices for long-term monitoring, including metrics relevant to population size, connectivity and adaptive potential; (ii) improving methodological harmonisation, data interoperability and integration with existing biodiversity observation systems; and (iii) strengthening capacity building and science–policy dialogue to support the uptake of genetic indicators in conservation assessment and decision-making. Through five working groups, training schools, short-term scientific missions, and stakeholder engagement, GENOA promotes the exchange of best practices and transdisciplinary collaboration. By linking genetic knowledge with biodiversity monitoring and policy needs, GENOA calls on the conservation genetics community to actively contribute to establishing genetic diversity as a measurable, actionable and policy-relevant component of biodiversity conservation in Europe.

51 HOW TO BEST ESTIMATE N_E WITH GENETIC DATA FOR CONSERVATION MANAGEMENT IN AGE- AND SPATIALLY-STRUCTURED SPECIES?

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Abstract

Effective population size (N_e) is a key parameter for understanding evolutionary processes, monitoring genetic diversity, and informing conservation strategies, as it shapes genetic drift, inbreeding, and adaptive potential. The “proportion of populations within species with N_e above 500”, a genetic indicator endorsed by the Kunming-Montreal Global Biodiversity Framework, can be estimated from DNA data. However, widely used estimators based on sibship frequency (SF) and linkage disequilibrium (LD) rely on assumptions rarely met in natural populations. Common challenges include age structure with overlapping generations and lifetime variance in reproductive success, as well as population structure with heterogeneous migration rates across species' spatial distributions. These factors influence estimations and interpretation of N_e and should be accounted for, with SF and LD methods expected to reflect local N_e unless migration is high, in which case estimates may approximate metapopulation N_e . It remains unclear where this shift occurs under realistic scenarios.

We outline simulations of demographic scenarios in order to assess how variation in life-history traits and migration rates jointly affect N_e estimates. Forward-in-time simulations are anchored in contrasted empirical case studies, and will integrate realistic variation in vital rates known to impact demographic N_e and migration to represent gradients of fragmentation across populations.

We will evaluate the statistical performance of genetic N_e estimates against demographic N_e estimates (“true” reference values) and identify the most appropriate methods for monitoring species under different scenarios. We also aim to specifically determine migration rate thresholds at which genetic N_e estimates shift from local to metapopulation N_e .

52 GENETIC INDICATOR ESTIMATION AND REPORTING IN FRANCE: THE FR-IDGE PROJECT

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Abstract

The Kunming-Montreal Global Biodiversity Framework (GBF), adopted under the Convention on Biological Diversity (CBD), calls on signatory countries to monitor and report genetic diversity using standardized genetic indicators — most notably the Ne500 indicator (proportion of populations within species with an effective size above 500) and the proportion of populations maintained (PM indicator). In France, the collaborative research-action project FR-IDGE (*Cadre Mondial de Biodiversité et Conservation de la Diversité Génétique en France: Indicateurs Génétiques en Hexagone et dans les Outre-mer*), aims to operationalize these indicators at national scale across metropolitan and overseas territories.

FR-IDGE pursues three interrelated objectives. First, it addresses the challenge of selecting a representative set of species across taxonomic groups and biogeographic contexts, including the distinctive biodiversity of French overseas territories. Second, it will compute genetic indicators for at least 300 species by 2029, in support of France's 8th National Report to the CBD, integrating best-practice workflows and leveraging both DNA-based genetic data and non-DNA proxy approaches. Third, and critically, FR-IDGE places capacity building at the heart of its approach — training and engaging biodiversity managers and conservation practitioners so that genetic indicators become operational tools for evidence-based decision making rather than reporting metrics alone.

The project is coordinated by INRAE (UMR Biogeco, Bordeaux) in partnership with the French Biodiversity Agency (OFB), the National Museum of Natural History (MNHN/Patrinat), the National Biodiversity Data Hub (PNDB), and GBIF France, who together are building a stakeholder network and consolidating species lists, genetic databases, and reproducible FAIR-compliant workflows. FR-IDGE represents a national-scale model for bridging the gap between research and practice, equipping managers and decision-makers to apply genetic indicators directly in nature management and contributing to the broader international effort to make genetic indicators a routine component of conservation reporting and action.

53 VIOLATIONS OF SAMPLING ASSUMPTIONS BIAS N_e ESTIMATION AND N_{e500} INDICATORS IN RIVERINE FISH

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Abstract

Effective population size (N_e) is increasingly used as an operational genetic indicator for biodiversity reporting. For example, the proportion of populations within species with an effective size > 500 (N_{e500}) is the headline indicator A.4 of the Kunming–Montreal Global Biodiversity Framework. N_e is commonly estimated using single-sample methods such as linkage disequilibrium (LD) and sibship frequency (SF), which assume random mating and sampling. In conservation genetics studies of freshwater fish, populations are often assumed to be panmictic at the scale of tributaries or between two river structures. As a result, sampling units are frequently defined by logistical convenience rather than true biological breeding units. For example, three-spined stickleback migrate hundreds of meters within days, and sampling at similar spatial scales is often assumed to satisfy these assumptions. Here, we tested these assumptions using sibship inference with stickleback based on six microsatellite markers across 21 sampling sites in the Demer Basin (Belgium), and evaluated its implications for N_e estimation. Strong family structure was detected, particularly in upstream populations, indicating violations of random mating and sampling assumptions required by single-sample methods. We then compared the N_{e500} indicator derived from N_e estimates from LD (N_{eLD}), SF (N_{eSF}), and temporal methods (N_{eTV}). Single-sample estimates were consistently low (harmonic mean $N_{eSF} = 30$, $N_{e500SF} = 0$; harmonic mean $N_{eLD} = 60$, $N_{e500LD} = 0.29$). For a subset of seven populations with whole-genome pool-sequencing data spanning ~ 20 generations, temporal estimates were substantially higher (harmonic mean $N_{eTV} = 895$, $N_{e500TV} = 0.86$). Using the same subset, single-sample estimates remained low (harmonic mean $N_{eSF} = 30$, $N_{e500SF} = 0$; harmonic mean $N_{eLD} = 57$, $N_{e500LD} = 0.28$), although subsampling did not affect their magnitude. We call for a careful evaluation of the empirical data structure and its impacts on different genetic estimators for riverine fish.

54 FROM BOTTLENECKS TO MONITORING USING SLiM5

SIMULATIONS OF GENOMIC SIGNALS IN MANAGED MAURITIAN BIRD POPULATIONS

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Abstract

The loss of genetic diversity is a core component of the biodiversity crisis with lasting consequences for evolutionary potential and population persistence. However, genomic erosion is often difficult to interpret from present-day data alone because of delayed genomic responses to demographic change. In addition, different historical trajectories could produce similar contemporary outcomes. To improve genome-based monitoring and management, we are developing forward-in-time ‘digital twin’ models using known demographic and management histories to generate quantitative expectations for genome-wide signatures through time. We first focused on the Mauritius kestrel (*Falco punctatus*), which underwent an extreme bottleneck and intensive conservation management. Using SLiM5, we built an individual-based model that simulated a historically informed demographic trajectory and explicitly incorporated major management processes. The model was parameterised from species life-history data and empirical demographic records and was validated by its ability to reproduce observed population trajectories across replicated stochastic runs and to match empirical genome-wide patterns. Simulated heterozygosity and ROH-based inbreeding metrics showed close agreement with observed data, including the elevated long-ROH burden characteristic of heavily bottlenecked populations. We then used this digital twin model to explore counterfactual and prospective management histories (e.g. continued versus reduced intervention) and to quantify expected genomic trajectories under each scenario. Embedding real conservation histories into calibrated ‘digital twin’ simulations provides a practical way to forecast demographic and genome-wide trajectories under alternative management strategies. More broadly, this approach can help conservation practitioners identify when population recovery may still mask slow genomic recovery supporting more informed long-term monitoring and management of threatened species.

55 CHARTING A EUROPEAN ROADMAP FOR eDNA: THE FOUNDING OF eDNA EUROPE

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Abstract

Environmental DNA (eDNA) approaches are rapidly reshaping conservation genetics by enabling non-invasive detection of species, populations and genetic diversity across large spatial and temporal scales. Coupled with high-throughput sequencing, eDNA-based metabarcoding, metagenomics and emerging population-level applications offer new opportunities for genetic monitoring, assessment of population status, and early detection of genetic erosion under environmental change. These tools are increasingly relevant for long-term biodiversity observation and for informing conservation policy at national and European levels. Despite their potential, the development and uptake of eDNA approaches in conservation genetics across Europe remains

fragmented. Methodological heterogeneity, limited cross-border coordination, and uneven integration into regulatory frameworks hinder comparability, validation and long-term genetic inference. These challenges are particularly pressing as policy initiatives increasingly demand standardized, scalable genetic indicators to support conservation planning and evaluation. Here, we present eDNA^{Europe}, a newly founded European society dedicated to advancing the development, harmonisation and implementation of eDNA-based methods with relevance to conservation genetics, biodiversity monitoring and policy. The society aims to: (i) build an inclusive European community of eDNA researchers, practitioners and stakeholders; (ii) strengthen links between the European eDNA community and ongoing national, regional and global initiatives; (iii) promote technological advancement and share research findings and best practices; and (iv) facilitate mainstreaming of eDNA methods into policy and practice. By introducing eDNA^{Europe} to the conservation genetics community, we aim to foster engagement across science, industry and policy to support the development of eDNA^{Europe} as a unifying framework for harmonised eDNA-based monitoring and policy-relevant biodiversity assessment in Europe.

56 CHARACTERIZING SYSTEMATIC BIAS IN DEPOSITED WHOLE GENOME DATA OF WILD VERTEBRATE POPULATIONS

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Abstract

The generation of whole genome sequencing (WGS) data from wild populations is essential for addressing complex genetic questions. Many scientific journals require depositing data into online repositories, which in theory would enable secondary use of the data beyond the scope of the original research study. However, limited adherence to FAIR and open science principles, as well as biases in existing datasets, can constrain downstream research potential. Here, we used a targeted PubMed search to scan the published literature for WGS data of wild vertebrates (excluding reference genomes). In detail, SRA metadata were systematically downloaded from 28,497 studies and harmonized with the help of extracted accession numbers corresponding to the three major repository databases (NCBI, ENA, DDBJ). This effort enabled a quantitative assessment of metadata quality and open data compliance in population genomics and revealed substantial gaps and biases in the current datasets. For example, overrepresentation of domestic species (which were filtered out), certain wild species (112/922 wild species comprised about 80% of the data), geographic regions (European and North American species comprised 72% of the data) and taxonomic groups (mammals and bony fish comprised more than 80% of the data) were apparent in the final dataset. Additionally, metadata fields were not standardized across studies, and key variables (e.g., location) were often missing, even though this information could sometimes be recovered from the Supplementary Information or by contacting the authors. Our study highlights both the wealth of existing genomic data for wild vertebrates and its untapped potential for secondary reuse, and the limitations imposed by current practices. Therefore, we advocate for the field of population genomics to adhere to metadata standardization and deposit all available metadata alongside genetic data, and to prioritize targeted data generation for underrepresented species and geographic regions.

57 VIRAL TAGS AS KEYS TO ADVANCING INVASION GENOMICS

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Abstract

Biological invasions are accelerating worldwide, yet their effective management often requires resolving recent population dynamics at fine spatial and temporal scales. Traditional invasion genetics and genomics often struggles to capture these contemporary processes, as mutation rates and generation times of most non-native species preclude the detection of such rapid changes within their own genomes. We propose harnessing host-associated viruses as high-resolution “genetic tags” to overcome these limitations as virus evolution unfolds on timescales comparable to invasion dynamics. By applying molecular epidemiological frameworks, such as viral phylogeography and phylodynamics, viral genomes can be used to reveal fine-scale patterns of host dispersal, connectivity and introduction history that remain cryptic in host data. This poster will outline a conceptual framework highlighting this promising potential and arguing that integrating viral tagging into invasion genomics offers an alternative complementary and scalable approach to strengthen surveillance and inform spatially prioritised management of invasive species. *Intrigued? – Come by to have a fruitful discussion about this exciting topic!*

58 FROM FOREST TO CITY: HOW RECENT COLONIZATION RESHAPES THE MICROBIOME OF OPPORTUNISTIC AND GENERALIST SPECIES?

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Abstract

Urban expansion is driving profound ecological and biological changes in wildlife. Opportunistic and generalist species, such as the wild boar (*Sus scrofa*) and raccoon (*Procyon lotor*), are particularly successful in colonizing anthropized environments, where shifts in resource availability, population density, and interspecific interactions may influence their intestinal microbiome and associated health risks. Within a One Health framework, understanding the impact of recent colonization on host-associated microbial communities is essential to assess potential implications for pathogen transmission at the wildlife–livestock–human interface.

This study investigates the impact of environmental gradients—from forest to urban habitats—on the gut microbiome composition and diversity of these species in Belgium. Using non-invasive fecal sampling (n = 564 for wild boars and n = 226 for raccoons) across multiple sites representing contrasting habitats (forested, agricultural, and peri-urban), we apply high-throughput sequencing approaches to characterize bacterial communities and detect potential pathogens. Microbiome diversity (α - and β -diversity metrics) is analyzed in relation to habitat type, host ecology, and inferred dietary shifts derived from metabarcoding data.

Preliminary results suggest that urban populations exhibit increased dietary diversity and access to anthropogenic food resources, which may be associated with distinct microbial signatures compared to forest populations. These changes could reflect both ecological plasticity and altered exposure to environmental microbes and pathogens. Ongoing analyses aim to determine whether urbanization is linked to increased pathogen prevalence and to identify key microbial taxa driving community shifts.

By integrating ecological, dietary, and microbiome data, this work provides novel insights into how urban colonization shapes host–microbiome interactions in adaptable wildlife species. Ultimately, it contributes to a better understanding of the ecological and sanitary consequences of wildlife urbanization, informing management strategies in a context of increasing human–wildlife interactions.

59 ASSAYS TO ENABLE FIELD ID OF NON-INVASIVE FELIDAE SAMPLES IN PERU

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Abstract

The collection of non-invasive samples such as faeces or hair snags can be a fantastic source of biological data for conservation enabling population genetic and dietary analyses. Identifying the species a non-invasive sample originated from presents multiple challenges, especially in locations where closely related species co-occur. While methods such as DNA barcoding can be used, these approaches require access to Sanger sequencing and other molecular laboratory facilities. Rapid field-based identification would provide valuable knowledge to guide field work in real time throughout a season. This demand is especially evident in remote regions such as the Manu National Park in Peru, where mentoring of elusive Felidae and their diets is constrained by its location and limited laboratory facilities. We designed field deployable genetic assays capable of distinguishing between six species of Felidae which dominate the Manu National Park landscape. Each assay provides a PCR presence/absence for a target species with amplification assessed using gel electrophoresis. After developing these assays in a standard laboratory, we tested them on faecal samples using a portable laboratory set up. This project demonstrates an adaptable workflow enabling the development of similar assays for studies where lower tech, rapid in field species identification would be valuable.

60 EVALUATING LONG-READ RADSEQ FOR CONSERVATION GENOMICS

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Abstract

Emerging portable long-read sequencing technologies from Oxford Nanopore Technologies offer new opportunities for field-based genomic monitoring, yet their performance within reduced representation frameworks remains poorly understood. Here, we compare population genomic inferences derived from ddRAD datasets generated using short-read Illumina sequencing and long-read nanopore sequencing across individuals from three conservation-relevant bird species: Arabian bustard, Macqueen's bustard, and Peregrine falcon. For each species, we generated ddRAD datasets for five individuals across both platforms and benchmarked them against matched Illumina whole-genome sequencing data. Long-read ddRAD produced substantially higher numbers of raw SNPs (0.95–1.76 million per species) compared to short-read ddRAD data (37,000–90,000 SNPs), reflecting increased locus recovery and read length. However, successive filtering steps, including quality, minor allele count ($\text{MAC} \geq 2$), and missingness thresholds, dramatically reduced SNP counts in both datasets, resulting in more comparable final marker sets after linkage thinning (1,639–2,076 SNPs for Illumina and 2,071–3,968 SNPs for nanopore data). We further evaluated differences in variant discovery, locus recovery, genotype concordance, and summary statistics to assess how sequencing platforms influence biases inherent to reduced-representation approaches, and found largely congruent results across platforms. Although focused on avian taxa, this framework is readily extendable to a broad range of species with diverse genomic architectures. Our results demonstrate that differences in data generation and filtering strongly influence downstream genomic inferences, while portable sequencing represents a viable approach for democratizing conservation genomics.

61 APPLYING GENOMICS TO THE MANAGEMENT OF WALLACEAN FLAGSHIP TAXA: EVALUATING THE EVOLUTIONARY POTENTIAL OF INSURANCE POPULATIONS

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Abstract

The anoa (*Bubalus* sp.) and babirusa (*Babyrusa* sp.) are iconic flagship taxa endemic to Wallacea, Indonesia. Facing severe threats from anthropogenic activities such as habitat fragmentation and poaching, these species are now managed under a Global Species Management plan (GSMP). The GSMP bridges in-situ protection with ex-situ insurance populations and to safeguard their future, the GSMP prioritises genomically informed practices to ensure population viability.

We sequenced 53 anoa and babirusa from Indonesian zoos and breeding centres, and analysed their ancestry and relatedness. We also evaluated metrics of genomic erosion, including heterozygosity, inbreeding, and mutational load, and compared this to wild populations. Ancestry analysis revealed relatively "pure" lineages in ex-situ anoa, whereas babirusa populations were highly admixed across zoos. While we identified strong kinship within each zoo, overall levels of inbreeding and mutational load in the ex-situ populations remain comparable to wild counterparts, highlighting their potential to maintain the long-term survival of wild populations.

Using these metrics, we can provide genomic-based breeding recommendations for the GSMP. This work includes active consultation with the studbook keepers and local stakeholders to familiarise conservation practitioners with a localized, evidence-based framework for breeding recommendations. This collaborative approach ensures long-term evolutionary resilience for these vulnerable species in a rapidly changing world.

62 ESTIMATING THE EFFECTIVE POPULATION SIZE ACROSS SPACE AND TIME IN THE CRITICALLY ENDANGERED WESTERN CHIMPANZEE IN GUINEA-BISSAU: CHALLENGES AND IMPLICATIONS FOR CONSERVATION MANAGEMENT

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Abstract

The western chimpanzee (*Pan troglodytes verus*) is a Critically Endangered subspecies. In Guinea-Bissau (GB), it faces increasing conservation threats, yet the extent of genetic risk to its populations remains poorly understood. This knowledge gap limits the development of effective conservation strategies and the prioritization of management actions by national authorities. In this study, we combined microsatellite data from populations from four protected areas in southern GB with five whole-genome sequences to estimate effective population size (N_e) and reconstruct recent and ancient demographic history using complementary

analytical approaches. We also integrated N_e estimates across methods to improve our understanding of the evolutionary history and current demographic status of this great ape, while assessing the strengths and limitations of each estimator for conservation planning. A large ancestral N_e is suggested by PSMC analyses, which likely reflect ancient meta-population structure across the subspecies' range. Results from MSVAR suggested that reduced connectivity, a demographic decline, or a combination of both appears to have decreased the N_e from around 10,000 breeding individuals to 1,000–6,000, approximately 10,000–15,000 years ago. This reduction may potentially correspond to more recent fragmentation into coastal and inland subpopulations. Estimates of the contemporary N_e suggest a global population of below 500 individuals (GONE: 395–583; NeEstimator: 107–549), highlighting a substantial risk of extinction. Our study suggests that coastal populations from Cantanhez National Park and Cufada Lagoons Natural Park remained small or isolated for several generations and are therefore particularly vulnerable, whereas inland populations (from Boé and Dulombi National Park) maintain higher long-term N_e and represent important conservation strongholds. By integrating different molecular markers and analytical methods, we overcame many of the challenges associated with obtaining high-quality DNA from wild threatened populations and generated N_e estimates across multiple temporal and spatial scales. This integrated framework provides robust information to support evidence-based conservation planning and management at both local and regional scales.

63 SAVING ASIAN ELEPHANTS THROUGH PANGENOMICS

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Abstract

Habitat loss and fragmentation are harming endangered animals, resulting in isolated and small populations. These populations risk accumulating harmful mutations through genetic drift, while inbreeding increases homozygosity exposing harmful recessive alleles, reducing individual fitness. Translocating individuals between populations could counteract this, but mixing distinct populations can lead to a loss of unique genomic variation and their associated local adaptations. To assess the relative risk of inbreeding and outbreeding in such populations, standard genomic approaches rely on a single reference genome. This systematically misses much of the genomic variation absent from the reference genome. By incorporating multiple genomes, a pangenome can capture the full genomic diversity within the species. In our project we aim to show the benefits of using a pangenome for a species that is facing extinction: the Asian elephant (*Elephas maximus*). By constructing 9 whole-genome assemblies, one for every major lineage, we aim to build the first pangenome for this species. Compared to single reference genomics we expect to find previously undetected genomic variation in the populations, including large structural variants. These structural variants are often associated with large phenotypic differences between lineages and could be lost if populations are mixed. By predicting the functional impact of the genomic variants found in the different populations we will identify variants of conservation concern. Together these analyses will guide future translocations and demonstrate how novel genomic methods can be implemented to improve genomics-informed conservation practice.

64 UNRAVELLING HYBRIDIZATION BETWEEN BLUE AND BLACK WILDEBEEST IN SOUTH AFRICA

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Abstract

Biological diversity is being lost at unprecedented rates, with admixture and introgression presenting major threats to species. To this end, our ability to accurately identify introgression is critical to the management of species. The genetic integrity of black wildebeest (*Connochaetes gnou*) and blue wildebeest (*Connochaetes taurinus*) populations in South Africa is threatened by introgressive hybridization. Black wildebeest is endemic to South Africa, whereas, blue wildebeest are widely distributed in southern and east Africa. Hybridization between the species was first reported in the 1960s and the hybrid offspring was observed to be fertile. Extensive translocation of both species and also keeping the two species on the same property has led to a potential hybrid dilemma, as reproductive isolation may- disappear. The extent of hybridization is not known, and it was estimated that ± 120 properties in South Africa contain both species. In a previous study, a molecular marker panel consisting of 13 cross-species and 11 species-specific microsatellite markers, could in some instances not detect second generation backcross individuals. In this study we report on whole genomes that were generated for South African black- and blue wildebeest as well as one known F1 hybrid. The genomes were used to identify diagnostic SNPs that can distinguish between the two species and potential hybrids. Subsequently an Open Array (240 SNPs) was used to screen blue- and black wildebeest and potential introgressed individuals. To conserve viable populations, conservation management strategies must preserve the genetic integrity, as well as high levels of genetic diversity in both species. This study will ultimately contribute to better management of black-and blue wildebeest.