How can DNA legacy datasets contribute to developing best practices for CBD genetic diversity indicator estimation?

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Abstract Booklet

6TH EUROPEAN CONSERVATION GENETICS MEETING 2024

Lausanne
Switzerland
August 28-30, 2024

KEYNOTES

28 – 30 August 2024
Aula – Palais de Rumine

28 August, 9:00 – 9:45 – session 1: Biodiversity assessment through the study of environmental DNA. Promises and limitations of barcoding and metabarcoding approaches

Environmental genomic time series from seasons to millennia: impacts of climate and humans - and tools for long-term biomonitoring

Laura S. Epp(1)
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The current biodiversity crisis, caused both by direct human impact on species and habitats, as well as anthropogenically induced changes in abiotic factors, is causing tremendous turnovers on species, genomic and ecosystem levels. Several threats such as habitat loss, overexploitation, pollution, invasive species, and climatic changes are acting in synergy - but in many cases, neither the relative roles of these drivers, the pace of change nor the pre-impact community of the ecosystem are well mapped or understood. Monitoring time series of biodiversity typically extend back only a few decades, are available only for some organisms and are relatively scarce, given the substantial efforts and long-term infrastructure that they require.

Analyses of environmental DNA can provide such time series with relative ease and include both previously under sampled seasons and places, as well as information about organisms from across the tree of life, including taxa that do not leave behind visible traces. Archives of environmental DNA, such as sediments, also offer a view on biodiversity that reaches back into the past. By investigating ancient environmental DNA (ancient eDNA), we can retrieve (pre-)historical information on ecosystems as well as uncover cryptic changes not visible in morphology. Depending on the preservation conditions, such records can be globally retrieved on scales from hundreds to thousands and millions of years. Thereby, they can deliver information on natural variability of ecosystems since the Pleistocene, as well as on the onset of human impacts and their diverse and long-lasting consequences for current ecosystems.

The integration of environmental DNA into the study of past and present ecosystems is rapidly progressing, but both its full potential and its limits are yet to be conclusively established. To most efficiently sample environments and correctly interpret results, we need a better understanding of the provenance and taphonomy of eDNA in different substrates.

Through PCR-free shotgun sequencing, we can now increase our knowledge of the actual composition of the DNA in environmental samples and move to meta-taxonomic community analyses. At the same time, we can concentrate on an efficient utilization of this resource to inform conservation biology and devise simple measures that can be integrated into ongoing management efforts. In my talk, I will highlight how environmental genomic time series can contribute to conservation and management of ecosystems and species, which questions we can already answer and where we need a better understanding.

28 August, 14:00 - 14:45 – session 2 : Consequences of introgression on adaptive potential and conservation policies

Embracing hybridisation and introgression in practical conservation policies

Richard Ennos(1)
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Most conservation programmes are based on identifying species as the unit of conservation, with the implicit assumption that species can be treated as discrete biological entities for the purposes of management. However, the reality is that gene exchange commonly occurs between related species. Here, through hybridisation and introgression, the pool of genetic variation upon which a species can draw for adaptation and evolution extends across taxonomic boundaries. Hybridisation and introgression may have a number of consequences for a taxon of conservation concern. These include displacement by the hybridising species, introgression of genetic material that facilitates adaptation, the creation of a much wider gene pool from which differentially adapted lineages may evolve, and the evolution of novel hybrid taxa at the same or different ploidy levels. In these situations, where hybrids and introgressants may be integral to achieving conservation objectives, species-based approaches do not provide an appropriate framework for management. Instead, a policy approach that focusses on managing the evolutionary process of hybridisation and its consequences, rather the conservation of individual taxa, can be more valuable. The practicalities of implementing this approach will be illustrated with examples from ongoing conservation programmes.

29 August, 8:45 - 9:30 – session 3 : Inference of population dynamics to identify conservation measures

Genetic conservation in practice – rarity and resilience

Jeanette Hall(1)
1-Woodland Advisor at NatureScot, Inverness

As an ecologist at the Scottish Government's conservation agency, I need to be able to interpret research to inform conservation interventions on the ground, and policy at national and subnational level. Whilst I am also actively involved in carrying out research, this needs to be directly relevant to conservation practice. Working with policymakers and land-managers gives me insights into the needs of both, and opportunities for practical application of conservation genetics. This is a time of unprecedented challenge for biodiversity. The conservation movement needs to ensure that we are using the best tools and knowledge in our response to the twin nature and climate crises. Of the three strands of biodiversity (ecosystems, species, and genetics), genetic diversity has been neglected in monitoring targets, conservation practice and policy. Populations can only remain resilient in the face of multiple pressures when they have sufficient adaptative potential. Although conservation projects can be successful without considering genetic diversity, this is not always the case, and has led to missed opportunities. The importance of genetic insights is not restricted to conservation of very rare species. It can usefully inform conservation more generally, and is integral to ensuring resilience in the face of environmental change. Although genetic data are much more affordable than formerly, they're still expensive and, arguably, not always necessary. In many cases proxies are sufficient, especially for currently healthy populations, where the aim is to ensure resilience against the climate crisis and other environmental change. Elsewhere, especially for fragmented populations and where numbers are very low, direct genetic analysis will be vital to conservation interventions. At a continental level, I'll talk about opportunities provided by the EU's Nature Restoration Law.

At a national level I'll talk about Gene Conservation Units, which use population size as a proxy for genetic diversity, as well as nationwide analysis of genetic patterns to provide further information. At a regional level I'll talk about a successful collaborative project with farmers and foresters in the Scottish Highlands, to conserve a hitherto declining range edge population. This used an initial genetic analysis to provide an understanding of population structure, followed by habitat management to improve metapopulation functioning and thus dynamic genetic conservation. Finally, I'll introduce a much more intensive intervention, incorporating detailed genetic analysis and ex situ breeding followed by reintroductions, to restore populations of a Vulnerable plant.

These examples show how an understanding of genetic population dynamics can inform practical conservation measures at a range of scales. They also highlight a key opportunity for collaboration with different types of land manager. This will be particularly important in responding to the 30x30 commitment to reverse biodiversity decline and bolster resilience to climate change. Although genetics can seem quite daunting to the lay-person, many of the core concepts can be communicated effectively. This opens the potential for collaborations with people in other policy spheres, such as Natural Capital, planning and wider society.

29 August, 14:00 - 14:45 – session 4 : Harnessing genetic diversity and evolutionary principles for population resilience and ecological restoration

Managing genetic diversity for conservation and sustainable use

Dr Myriam Heuertz(1)
1-INRAE, Research Unit BIOGECO, Bordeaux, France.

I will provide an overview of how genetics and genomics applications can inform practitioners' actions for effective conservation, restoration and sustainable use of nature. Conserving large enough populations is important, but is only part of the picture. I will present a non-random view into conservation, restoration and management cases, based on 1. a review paper produced within COST action G-BIKE on genomics and ecosystem services, 2. conservation genetics applications in tropical trees from South America, and 3. a survey on practitioners' knowledge, perceptions and management actions regarding hybridization relevant to conservation in Europe. In our review paper, we observed that the keywords "genomics" and "ecosystem services" are rarely mentioned together in the scientific literature, exposing an "application gap".

Ecosystem services pertain to the conservation, restoration and sustainable use of nature; they can represent management goals that practitioners can pursue through targeted, genomics-informed management actions. These management actions can rely on genetic or genomic information and involve, for example, actions to supplement populations and reduce inbreeding, the definition of conservation/management units, the management of adaptive genetic variation or the selection of climate-adjusted provenances for habitat restoration. They can also rely on genetic information from interacting species, e.g., hybridizing species. Collaboration between practitioners and scientists is critical to co-construct the most effective conservation and management strategies. Much of my conservation genetics research focuses on tropical trees, mostly from French Guiana, an overseas territory of France covered up to 97% by tropical rainforest with a vast biodiversity.

This forest remains largely intact but suffers pressure from mining, climate change, and logging. Conserving the rainforest and achieving sustainable production of timber and non-timber forest products demands a better understanding of the evolutionary history and adaptive potential of harvested species, but also of other ecologically important species.

I will provide conservation genetic examples on the most harvested timber tree of French Guiana, Dicorynia guianensis (Fabaceae), the essential oil-providing trees Aniba rosaeodora (Lauraceae) and Carapa sp. (Meliaceae), and the ecologically important species complexes of the genera Symphonia (Clusiaceae) and Eschweilera (Lecythidaceae). To illustrate the need to co-construct conservation strategies with practitioners, I will focus on a study on practitioners' knowledge and views on the effects and management of hybridization relevant to conservation in Europe. Within COST Action G-BIKE we developed a questionnaire filled by ca. 150 practitioners, e.g., policy makers, natural areas managers, coordinators of species action plans and other relevant actors in conservation, from different European countries. We interpret the answers in the context of the legal framework pertaining to hybridization in nature management and derive recommendations combining common practices and current research findings for the management of hybridization in the most common cases of concern, in support of the conservation of genetic diversity and biodiversity more generally.

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30 August, 8:45 - 9:30 – session 5 : Monitoring genetic diversity and effective population size

Multinational evaluation of the genetic diversity indicators for the Kunming-Montreal Global Biodiversity Framework

Alicia Mastretta-Yanes(1)
1-Investigator, Mexican National Council of Humanities, Science and Technology (CONAHCYT)

Under the recently adopted Kunming-Montreal Global Biodiversity Framework, 196 Parties committed to report the status of genetic diversity for all species. To facilitate reporting, three genetic diversity indicators were developed, two of which focus on processes contributing to genetic diversity conservation: maintaining genetically distinct populations ("populations maintained" indicator) and ensuring populations are large enough to maintain genetic diversity ("Ne 500" indicator). The major advantage of these indicators is that they can be estimated with or without DNA-based data. However, demonstrating their feasibility requires addressing methodological challenges of using data gathered from diverse sources, across diverse taxonomic groups, and for countries of varying socio-economic status and biodiversity levels. To address these challenges, we conducted a pilot assessment of the indicators and co-developed guidelines through a collaborative effort involving nine countries, including megadiverse and developing economies. This included around 80 participants—students, practitioners, and researchers—who gathered data for the indicators, and feedback from over 10 international webinars, each attended by hundreds of participants. We assessed the genetic indicators for 919 taxa, representing 5 271 populations, of which 83% taxa had data available to calculate at least one indicator. Our results show that although the majority of species maintain most populations, 58% of species have populations too small to maintain genetic diversity.

Moreover, genetic indicator values suggest that IUCN Red List status and other initiatives fail to assess genetic status, highlighting the critical importance of genetic indicators. We hope our experience to become useful as a reference point, from which countries can adjust their protocols to their own needs and preferences.

TALKS

28 AUGUST 2024

AULA - PALAIS DE RUMINE

9:45 – 12:30 / session 1 : Biodiversity assessment through the study of environmental DNA. Promises and limitations of barcoding and metabarcoding approaches

Can airborne monitoring help to protect fungi?

Markus Schlegel(1), Artemis Treindl(1), Margaux Leisi(1), Andrin Gross(1)
1-Swiss Federal Institute for Forest, Snow and Landscape Research WSL

Fungi are increasingly recognised as a group of organisms in need of protection, but their inclusion in Red Lists is still a challenge due to the difficulties associated with monitoring fungi. The analysis of airborne eDNA from fungal spores has emerged as a promising tool to gain better knowledge on species distributions and to detect species that remain largely unnoticed. On the other hand, the interpretation of eDNA from the air is challenging due to the complex dynamics of wind dispersal as well as technical biases associated with sampling and analysis. For this reason, we are evaluating spore sampling in different projects, including the extensive field surveys carried out for the revision of the Red List of macrofungi in Switzerland. We found a strong spatial and temporal variation in spore composition and a structuring of the assemblages according to different habitat types. In a more comprehensive case study on small grassland fungi, we observed a pronounced decrease in spore concentrations within a short distance. Red-listed species were found to be generally under-represented in the air. Overall, our results demonstrate the effectiveness of the method but also highlight the difficulty of detecting rare fungi, not only by traditional methods. We provide an overview of the air-sampling methods and outline the opportunities and limitations of air monitoring with regard to fungal conservation.

Year-round monitoring and large-scale screening of native and invasive crayfishes in lotic systems using environmental genomic approaches

Franziska Chucholl(1), Gernot Segelbacher(2), Laura Epp(1)
1-Universität Konstanz, 2-Universität Freiburg

Freshwater crayfish are among the most threatened animal taxa in Central Europe. Effective conservation measures for endangered native and management of invasive alien crayfishes requires knowledge about distribution, monitoring of existing and early detection of newly established populations, as well as their connectivity. Genetic approaches hold great potential, both considering eDNA as a highly sensitive, non-invasive detection tool, and more traditional population genetic analyses to track the structure of populations.

To evaluate eDNA as detection tool for freshwater crayfish, we developed a novel set of specific eDNA-assays for all native (*Austropotamobius torrentium, Austropotamobius pallipes, Astacus astacus*) and the most relevant invasive crayfish species (*Pacifastacus leniusculus, Faxonius limosus, Faxonius immunis*) in Central Europe. To ensure specificity, each primer pair was tested in silico, in vitro, and in situ, including a total of 13 lotic and lentic waterbodies. Moreover, we assessed the influence of spatio-temporal variables (distance to upstream population, season, and stream size) on eDNA detection in seven streams using two different detection methods (qualitative endpoint PCR and quantitative droplet digital PCR, ddPCR).

The newly developed eDNA assays successfully detected all crayfish species across different lotic and lentic habitats. Multiple linear mixed-effects analysis revealed a significant effect of distance and season on eDNA detection rate (endpoint PCR) and eDNA-concentration (ddPCR). Year-round detection was successful up to 7 km downstream of the source population, although detectability was lowest in winter. eDNA detection rate further decreased with increasing stream size. Finally, eDNA concentration correlated positively with estimated upstream population size.

Overall, this study provides easily applicable eDNA assays for six crayfish species, enabling year-round detection, which represents a clear benefit over conventional methods. Due to its high sensitivity, eDNA detection is also suitable for the targeted search of as-yet unrecorded or newly emerging populations. Using quantitative ddPCR might further allow for a rough estimation of population size, provided that the identified spatio-temporal factors are accounted for. We therefore recommend implementing eDNA detection as a complementary survey tool, particularly for a large-scale screening of data-deficient catchments or a year-round monitoring. Combining this with information on population genetic structure will potentially provide insights into dispersal, connectivity and dynamics of crayfish populations.

Monitoring groundwater biodiversity in Switzerland with environmental DNA

Marjorie Couton(1, 2), Roman Alther(1, 2), Samuel Hürlemann(1), Mara Knüsel(1, 2), Nadine Locher(1), Florian Altermatt(1, 2)
1-eawag, 2-University of Zürich

Although groundwater is the largest type of freshwater ecosystem in the world, it is almost never mentioned as a conservation target in national and international strategies. The main reason for this disinterest is the lack of knowledge on biodiversity living in these habitats. In fact, gathering information on subterranean aquatic taxa is a challenge as our access to the groundwater is very limited, and is further complicated by the scarcity of organisms inhabiting it. To overcome these issues, we propose a method based on environmental DNA (eDNA) from water samples collected in drinking water wells in Switzerland. Combined with a metabarcoding approach, we investigated different aspects of biodiversity (i.e., genetic, taxonomic and phylogenetic diversity) for various taxonomic groups (i.e., bacteria, protists, metazoans). Since groundwater taxa are not well represented in reference databases and many of them are still undescribed or unobserved, the vast majority of our sequences could not be assigned to any particular species. We thus used a taxonomy-free approach to compare our samples with one another and link the patterns observed to the external factors such as the geology of the location or the surface land-use. We revealed that the various taxonomic groups and aspects of biodiversity responded differently to these external factors. We also demonstrated that eDNA could be a valuable tool to map biodiversity patterns of various groups in inaccessible environments and could be used as a first evidence to inform conservation strategies in the future.

Tracing the invasion: Using eDNA to track the spread of Dreissena mussels

Rebecca Dorendorf(1,2), Piet Spaak(3), Nathalie Dubois(3), Laura S. Epp(1)
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The invasion of non-native species is a major cause of biodiversity loss and ecosystem instability worldwide. The two *Dreissena* mussels, quagga (*Dreissena rostriformis bugensis*) and zebra (*Dreissena polymorpha*), are highly invasive freshwater bivalves that have spread rapidly across Europe in recent decades. To assess the distribution of zebra and quagga mussels within and between aquatic ecosystems, we use environmental DNA (eDNA) from sediments (sedDNA).

In our study, we use eDNA to combine the detection of dreissenid mussels in sediment cores and surface sediments to reveal the time of colonisation and spatial distribution. Sediment cores are used as an ecological archive to investigate the invasion history of the mussels. In a sediment core from Lake Constance, zebra mussel DNA is present in older sediment layers than the first mussel discovery, suggesting that sedDNA holds promise for early detection of Dreissenamussels. To quantify quagga mussel DNA in Lake Constance, we furthermore used a ddPCR assay. Surface sediment collected during the quagga monitoring campaign of the SeeWandel project in October 2022 was used. A total of 54 sites around the lake were sampled using a Ponar sediment grabber. The density of the quagga mussels was measured and the biomass per qm was quantified by Eawag (CH). For genetic quantification, the density and biomass data were used for comparison and reference. The distribution of the mussel could be described with the genetic quantification. This shows the potential of sedDNA for invasive species monitoring.

Our future goal is to use sedDNA to obtain genomic data that will provide us with information on the population structure of the dreissenid mussels in multiple perialpine lakes, both in the past and in the present. This will enable us to identify populations at different times and compare their genetic diversity and differentiation. This will help to understand historical and current invasive patterns of these bivalves.

Using environmental DNA and RNA to study the role of environmental stressors on aquatic multitrophic biodiversity

Julie Morgane Guenat(1)
1-Université de Lausanne

By fragmenting habitats and altering natural energy flows, anthropogenic activities are contributing to the unprecedented decline in biodiversity which threatens the functioning of ecosystems. The effects of environmental stressors on structural indicators, such as species composition, are well studied, although few studies have used a multitrophic approach, mainly due to methodological constraints. Recently developed environmental DNA and RNA approaches (jointly known as environmental Nucleic Acids (eNAs)) offer the potential to investigate the effect of environmental perturbations from a whole ecosystem approach. Here, we aimed at examining the effect of biotic (i.e., the absence of a predator) and abiotic (i.e., the addition of nutrients) stressors on multitrophic biodiversity using eNAs. We used 12 experimental lakes (15 x 30 m) located at the CNRS-ENS research station in Nemours (France). We collected water samples, co-extracted eDNA and eRNA, and recovered lake diversity using generic eukaryotic primers. By analyzing the co-occurrence of multitrophic networks, we highlighted structural and compositional differences in response to both treatments and the cascading effects of such disturbances.

Paleogenomic insights: Unraveling Phytoplankton Resilience in the Baltic Sea

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Our research investigates the genetic past of two key phytoplankton species involved in the Baltic Sea's spring bloom. The Baltic Sea is relatively young compared to other seas or large bodies of water, and its history is well-recorded. Throughout history, it has undergone several ecological shifts, alternating between freshwater and brackish states, with associated changes in oxygen levels and water temperatures. Currently, the Baltic Sea is facing many challenges due to anthropogenic activities, which risk destabilizing its ecosystem. To understand how key species might adapt to these changes, it is important to study how they have responded to environmental changes in the past. In this context, we are investigating changes in the genetic and genomic makeup within and among populations of these species over different periods of time. We do this by extracting and analysing DNA directly from sediment cores and from cultures grown from dormant resting stages found in these cores. The project focuses on the dinoflagellate *Apocalathium malmogiense* and the diatom *Skeletonema marinoi.* These primary producers are crucial to the ecosystem's adaptability. We have modified an existing index, the Dia/Dino-index, using these species as indicators to evaluate the ecosystem status over the past millennia. By investigating genetic and genomic changes at an intraspecific level, including changes related to key historical events, we can gain valuable insights into the resilience of the Baltic Sea ecosystem and its future under increasing anthropogenic pressure.

The role of pesticides and vineyard management on the soil arthropod community using eDNA

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1-Department of Ecology and Evolution, UNIL, 2-Agroscope ETH, 3-Agroscope Changins

Both conventional and organic viticulture use insecticides and fungicides but differ on the active compounds and dosages applied. This diversity complicates the association between a pesticide and its ecological impact on the soil ecosystem, as each product or combination affects the soil species differently. Soil arthropods provide key ecological services, and their role as soil health bioindicators is well studied. They are therefore an excellent reference community for studying the impact of pesticide use in the management of individual vineyards. To study whole communities, environmental DNA (eDNA) has become a robust approach as it captures the DNA present in the soil. Here, we applied this eDNA approach to sample the soil arthropod community in vineyards in two regions in Switzerland. We found the soil arthropod community of organic vineyards to have greater diversity compared to conventional ones. However, the community differences between regions indicated that the nature of the soil is a stronger driver of the sampled community than the management applied. Within each region, we were able to identify the active compounds which significantly correlated to the shifts in the arthropod community, i.e. highlight the pesticides with greater impact on the arthropod community. Overall, we provide an ambitious but scalable approach to monitor pesticide impact on the soil biological community and draw guidelines towards more sustainable vineyard management practices.

Coupling environmental DNA and hydrology-based modelling to advance monitoring of freshwater ecosystems

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1-University of Zurich, 2-Eawag

Freshwater ecosystems are among the most biodiverse but also affected by humans, and are thus subject to intense monitoring. Several approaches for their biomonitoring exist, which makes them hard to compare and difficult to scale in time and space. Crucially, current biomonitoring is exclusive to selected sample points, thus disregarding influences from upstream habitats. Novel environmental DNA (eDNA)-based approaches, especially when coupled with hydrology-based models, offer unprecedented opportunities to advance the evaluation of ecological indices. In particular, the eDITH model exploits spatially replicated eDNA measurements within a river to infer the spatial distribution of any taxon of interest. Its underlying concept is that eDNA particles are advected by streamflow, and hence an eDNA sample not only represents the sampling location but provides information for a certain upstream area. By exploiting multiple, spatially distributed sampling sites, and considering DNA transport and concurrent decay, eDITH can disentangle the various sources of DNA shedding. Therefore, eDITH complements pointwise eDNA measurements by projecting taxon distributions into space-filling catchment maps. Here, we demonstrate a proof of concept for spatially upscaling ecological indices based on eDNA and the eDITH model, demonstrating how the integration of molecular approaches with hydrological models allows upscaling eDNA biodiversity data for any river. As the eDITH model is now available as an R package, we expect this tool to strongly contribute to a more precise assessment of freshwater ecosystems, applicable across all riverine systems globally with minimal prior information, and thus also accessible for undermonitored regions.

Using environmental DNA detection to inform control and eradication efforts for aquatic invasive plants in Ontario, Canada

Joanna Freeland(1), Chris Wilson(2), Francine McDonald(2), Stephanie Coghlan, Aaron Shafer(1), AllisonMarinich(1), Kristyne Wozney(2), Mary Gunning(3), Kaitlin Maurer(3)
1-Trent University, 2-Ontario Ministry of Natural Resources and Forestry, 3-Quinte Conservation

Environmental DNA (eDNA) is increasingly being used for early detection and surveillance of invasive species as well as general biodiversity applications, although applications for aquatic plant taxa have lagged behind those for vertebrate and invertebrate species. One of the earliest North American applications using eDNA to detect aquatic plants was in response to water soldier (*Stratiotes aloides*), an emergent, cold-tolerant aquatic plant that is native to Eurasia, and was introduced to North America in recent decades as an ornamental garden species. In 2008 the first known wild North American population of water soldier was identified in the Trent-Severn waterway of southern Ontario, Canada, and in 2015 a second population was identified in Black River. Prolific clonal reproduction in established populations leads to dense mats of floating vegetation that outcompete native species, alter water chemistry, and impede commercial and recreational activities; thus, water soldier is considered an invasive species in Canada. There is also a concern regarding continued range expansion into sites that include Lake Ontario (one of the Laurentian Great Lakes). Here we discuss eDNA barcoding and metabarcoding as a tool that can facilitate surveillance and management of invasive aquatic plants including water soldier. As of 2024, water soldier appears to have been eradicated from Black River, but populations in the Trent-Severn waterway have expanded into the Bay of Quinte (Lake Ontario). eDNA assays are providing a relatively time- and cost-effective means for ongoing water soldier surveillance, and are supplementing more traditional management strategies including visual surveys, manual removal, and herbicide applications.Although eDNA aquatic plant surveys have some limitations, this long-term (10+ years), multi-site case study illustrates the role of eDNA as part of a broader invasive species management program involving academic, government, and conservation organisations.

28 AUGUST 2024

AULA - PALAIS DE RUMINE

14:45 – 17:30 / Session 2 : Consequences of introgression on adaptive potential and conservation policies

Adaptive and maladaptive anthropogenic introgression into Alpine ibex

Christine Grossen(1)
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Anthropogenic hybridization, the unintentional hybridization with a non-native or domestic species in human-dominated environments, is a major concern for species conservation and a challenge for conservation management decisions. Genetically depleted species are expected to be particularly vulnerable to hybridisation and introgression, since hybridisation can restore or introduce new adaptive genetic variation and alleviate effects of inbreeding through hybrid vigour. However, defining the precise sets of deleterious or beneficial mutations resulting from anthropogenic hybridisation is complex and limited by the quality of genomic resources. The Alpine ibex (*Capra ibex*), a species native to the Alps, faced near-extinction two centuries ago, but conservation programs have successfully restored its populations. Alpine ibex are known to hybridise with the domestic goat (*Capra hircus*) occasionally leading to hybrid swarm formation. Introgression at immune-related genes has likely been adaptive. Alpine ibex also carry deleterious mutation load from the reintroduction bottlenecks, which could be alleviated through admixture. Here, we produced a chromosome-level reference genome for Alpine ibex based on Oxford Nanopore sequencing coupled with high-throughput chromosome conformation capture. The highly contiguous assembly of 2.66 Gbp reveals 30 chromosomes and is augmented by a 98.8% complete RNAseq-assisted gene model prediction. To determine the impact of recent admixture, we resequenced eight hybrids sampled from two hybrid swarms in Northern Italy. Hybrid individuals carried between 18-50% goat genome representing up to 3rd generation hybrids including one F1 hybrid. Combining the new data with 68 previously sequenced whole genomes representing Alpine ibex and related species (including domestic goat) we investigated the impact of admixture on the deleterious mutation load in Alpine ibex. We found that admixture introduced new deleterious mutations but also masked previously fixed deleterious mutations (candidates for hybrid vigor). We demonstrate how admixture results in complex selection to alleviate the mutational burden in Alpine ibex populations as well as likely introducing maladaptive genetic variation.

Recent increase in species-wide diversity in the highly endangered Iberian lynx following introgression from Eurasian lynx

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Interspecific admixture events can increase genetic variation in the recipient species' gene pool, but empirical examples of species-wide restoration of genetic diversity by admixture are lacking. The Iberian lynx (*Lynx pardinus*) is one of the most endangered felids and one of the most genetically eroded species, due to small long-term population sizes and serial bottlenecks. The analyses of multi-fold coverage whole-genome data from three ancient Iberian lynx specimens dated ca. 2,000-4,000 ybp show lower diversity and lower introgression levels from Eurasian lynx (*Lynx lynx*) than contemporary samples. This suggests a continuous or recurrent process of interspecies admixture that increased modern Iberian lynx genetic diversity above that occurring millennia ago. Our results add to the accumulating evidence for widespread natural admixture and introgression, and show that this can result in a substantial increase in the standing genetic diversity in highly eroded species. The strict avoidance of interspecific sources in genetic restoration measures may need to be carefully reconsidered, particularly in cases where no additional conspecific source population exists, so a closely related species might be the only source of novel genetic diversity.

SPATIO-TEMPORAL POPULATION GENETICS OF SOLITARY BEES

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Wild bees provide key ecosystems services through the pollination of many crops and wild plants. Due to the massive decline of pollinators, some bee species started to be managed to substitute biodiversity losses and the consequent shortage of pollination services. However, the introduction of managed populations may cause introgression with local wild populations and may disrupt local adaptations, compromising their resilience. In Europe, managed populations of solitary bees *Osmia cornuta* and *Osmia bicornis* are usually released to ensure crop pollination and to promote biodiversity. However, the consequences of the release of commercial *Osmia* spp. on the wild populations of these bees have not been investigated so far. The aim of this project is therefore to assess how the management of *O. cornuta* and *O. bicornis* can affect the diversity and the genetic structure of wild populations of these species through a spatio-temporal analysis. Samples of both species were collected using trap nests placed in different regions of Switzerland including urban, rural, and semi-natural areas and reflecting a gradient of Osmia spp. management. Samples from two commercial breeders active in the study areas were also analyzed. In addition, museum specimens of *O. cornuta* and *O. bicornis* collected in the same sampling areas before the beginning of Osmia spp. management (i.e., early 90s) were studied. 11 microsatellite markers were used to compare genetic diversity and population structure across sampled areas and time periods. The analysis of contemporary samples revealed strong genetic admixture between the bees sampled in the different areas and the managed populations of *O. cornuta* and *O. bicornis*, suggesting strong introgression caused by the management of these species. The ongoing analysis of museum samples will allow confirming these results. The data will be presented and discussed.

Lifting borders: Does genetic admixture in hybridizing oak (Quercus spp.) species enhance their adaptive potential under climate change?

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The current pace of climate change poses a threat to long-lived forest trees with long generation times, as they can only adapt slowly to environmental changes. Hybridization and introgression could increase the adaptive potential to a warmer and drier climate through the exchange of beneficial gene variants. Here we estimated levels of admixture in three European white oak species *Quercus robur, Q. petraea* and *Q. pubescens*. These ecologically, economically, and culturally important tree species generally occupy different ecological niches but are often found in sympatry and frequently hybridize. Using a newly developed diagnostic SNP set for accurate taxonomic assignment, we show that the three oak species, and especially *Q. petraea* and *Q. pubescens*, show evidence of extensive hybridization and backcrossing, resulting in a fine-scale taxonomic gradient among and within forest stands. Despite these high levels of admixture, the three taxa have largely retained their species integrity. We then demonstrate that topographic and soil properties are important factors influencing the taxonomic composition of trees and populations on regional and local scale. Even on the scale of a single stand, water availability and soil pH seem to drive the spatial distribution of pure and admixed individuals. Moreover, hybrids between *Q. petraea* and *Q. pubescens* appear to be as drought tolerant as the parental species *Q. pubescens*, which is known to be very competitive on dry soils. Our study suggests that hybridization can be an important component of adaptation to more severe and frequent droughts under climate change. Hybridization and introgression enhance genetic diversity and therefore adaptive potential of oak populations. In the future, conservation and management strategies for European white oaks should thus give priority to the species complex rather than focusing on single taxonomic entities. The same applies also to species of concern that form a naturally hybridizing species complex.

Genetic swamping of the critically endangered Scottish wildcat was recent and accelerated by disease

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Anthropogenic hybridisation poses a threat to wild populations. Genetic swamping following hybridisation with domestic populations can drive native species to the brink of extinction, as is the case for the critically endangered Scottish wildcat. Using genomic data from modern and museum samples representing 106 wildcats, domestic cats, and their hybrids, we reconstruct and date the catastrophic decline from a viable to a severely hybridised population. By identifying the haplotype structure of the domestic introgression, we demonstrate the onset of hybridisation was within the last 70 years. Introgression has accelerated in the late-20th century leading to the ‘hybrid swarm’ structure observed in Scotland today. We demonstrate that sufficient genetic variation exists for the recovery of the wildcat in Scotland. Our analyses also reveal that the domestic ancestry present in modern wildcats is over-represented in immune function genes, likely implying that domestic introgression is protective against the very diseases introduced by domestic cats.

Assessing effects of direct seeding on a dry meadow plant species using combined genomic resources

Jasmine Noëlle Tschan(1), Oliver Reutimann(1), Simone Fior(1), Patrick Ackermann(1), Alex Widmer(1), Martin C. Fischer(1)
1-ETH Zurich

Anthropogenic influences like land-use change, invasive alien species and climate change negatively impact biodiversity. Revegetation through direct seeding is a common and cost-effective measure to promote biodiversity around infrastructure projects. However, the seed provenance is highly relevant because different populations of the same species may be locally adapted to specific ecological conditions or belong to genetically divergent evolutionary lineages. Despite the popularity of direct seeding, the actual extent of direct seeding, the provenance of seed material, and its effects on natural populations remain largely unknown. We used a population genomic approach to identify evolutionarily significant units (ESUs), infer seed provenance, and quantify the extent of direct seeding in the dry meadow species *Dianthus carthusianorum*, which is widely used in revegetation projects. To achieve the large spatial sampling needed to identify ESUs, we combined datasets from different studies. Such heterogeneous genomic resources are increasingly common in conservation genetics, as projects are mostly carried out at a regional or national level and are challenging because of differences in e.g. sequencing type, quality, and coverage. We developed a SNP panel with >48,000 SNPs based on 446 samples that cover a large proportion of the species distribution range. We identified six ESUs of *D. carthusianorum* in Europe, five of which were found in Switzerland, four occurring naturally and one non-natively. In Switzerland, 48% of randomly sampled populations were inferred as direct seeding, of which 80% were seeded with naturally occurring ESUs. Evidence for gene flow between different ESUs was observed in 23% of the populations. The combination of heterogeneous genomic resources provides a powerful tool for conservation genomics and allows the detection of different ESUs and direct seeding to support decision-making for revegetation measures.

Monitoring distribution, density and introgression in European Wildcats in Switzerland

Beatrice Nussberger(1)
1-Wildtier Schweiz

Monitoring the population dynamics of elusive species in human-dominated landscapes helps conservation and management of these species. This is particularly relevant when wild species are potentially threatened by hybridization with a domestic species, as is the case for European wildcats and domestic cats.

We will present how the European wildcat, a nationally protected species, is currently monitored in Switzerland and why hybridization with domestic cats is a crucial, yet challenging conservation issue.

The impact of species hybridization and subsequent guidelines for conservation programmes

Laura Tensen(1)
1-University of Copenhagen

Hybridization is an important evolutionary force with a principal role in the origin of new species, known as hybrid speciation. However, ongoing hybridization can create hybrid swamping, in which parental genomes are completely lost. This can become a biodiversity threat if it involves species that have adapted to certain environmental conditions and occur nowhere else. Because conservation scientists commonly have a negative attitude towards hybridization, whether involving species or populations, it is important to improve understanding of its influence. We reviewed the literature on species hybridization to build a list of all known cases in the wild in the order Carnivora. To evaluate the conservation implications of hybrids, we developed a decision-making tree for status assessments. We further discuss three cases for which we generated empirical genomic data: African wild dogs *Lycaon pictus* (population level), leopards *Panthera pardus* (subspecies level), and Ethiopian wolves *Canis simensis* (species level). We found no evidence of genomic extinction in the order Carnivora, whereas positive outcomes of hybridization were common, such as novel genetic diversity, adaptation to extreme environments, and increased reproductive fitness. This may be particularly valuable in translocation programmes for counterbalancing the negative effects of genetic drift and enabling adaptation to human-dominated landscapes. The hybrid assessment showed that only the Ethiopian wolf faces immediate risk of genomic extinction, through hybridization with domestic dogs. Due to its small population size and narrow ecological niche, reduced fitness of hybrids seems inevitable and active elimination or restriction of domestic dogs is recommended as a conservation strategy.

Genomic and environmental insights and conservation challenges for the hybridizing crocodiles Crocodylus acutus and C. moreletii

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Hybridization is of key relevance for conservation of wild species, and yet it is still one of the most controversial issues in conservation. Identifying historical and contemporary factors promoting the formation and maintenance of hybrids is crucial for the management of endangered species, as well as characterizing the environmental factors and patterns of habitat use among parental species and their hybrids. Crocodiles are a conservation priority group since all 23 species recognized worldwide are in a protected category and hybridization occurs between many of their species, particularly between *Crocodylus acutus* and *C. moreletii*. Their hybridization system encompasses a geographically extensive hybrid zone, where two distinct hybrids and two *C. acutus* lineages have diverged and only a few geographically isolated populations of both parental species remain. We used a combined approach of genome-wide sequencing and ecological niche modeling to discern the geographic and temporal patterns of introgression, migration and demography, and to assess the ecological niches of the distinct lineages. We determined the spatial and temporal components of the divergence and admixture events of hybrids and non-admixed lineages, described the environmental characteristics and geographic extent of areas of sympatry, and confirmed human-mediated hybridization events. Our findings also showed overall distinct ranges and ecological niches among lineages, where hybrids presented a different set of environmental requirements from both parental species. Our approach can be readily applied to different taxa and ecological contexts, providing species information on genetics and the environment with direct conservation relevance. We additionally describe the various conservation challenges that *C. acutus* and *C. moreletii* currently face, highlighting that these distinct crocodile species and hybrid lineages warrant recognition and need urgent conservation effort.

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AULA - PALAIS DE RUMINE

9:30 – 12:30 / session 3 : Inference of population dynamics to identify conservation measures

A framework for identifying ESUs to support potential inclusion in the RedList

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The IUCN RedList is a global conservation tool, providing threat status labels (e.g. endangered) for species protection. The RedList does not consider genetic diversity loss or protection in any way. This oversight limits global conservation because genetic diversity is fundamental to self-sustaining populations, individual fitness, and population growth rates. Subpopulations - extremely isolated demographically independent units - can receive separate RedList listings. An achievable and rapid route to incorporate genetic diversity into the RedList, is a shift from “subpopulations” to “Evolutionary Significant Units” (ESUs). ESUs are lineages demonstrating limited gene flow within a species that also house unique genetic diversity (e.g. local adaptation).

Erroneously combining distinct ESUs in the RedList could drive genetic diversity loss, because extirpation of an ESU can occur silently, with minor impacts on global population trends but extinctions of alleles. Moreover, erroneous merging of ESUs can harm species-level conservation success through incorrect management decisions and falsely inflated population trends. The gold standard for ESU delineation requires genetic and genomic data; however, such data are expensive and any changes to the IUCN RedList cannot introduce barriers (i.e. cost) that limit access. Consequently, we have developed a framework of both genetic and nongenetic indicators to facilitate ESU identification and inclusion into the IUCN Redlist.

Do central populations have a higher genetic diversity than marginal ones? A re-analysis across 800 species

Katalin Csilléry(1)
1-Swiss Federal Research Institute WSL

The distribution of genetic diversity across the species range provides key insights into ecological, evolutionary, demographic, and biogeographic processes. Based on population genetic theory, one of the simplest predictions about the spatial distribution of genetic diversity is that populations at the center of their distribution range, where population size is large, harbor more diversity than populations at the edge, where population size is small and populations are isolated. This expectation is also commonly known as the central-marginal hypothesis (CMH). A myriad of empirical studies addressed this question over the past two decades, however, consensus about the generality of the CMH is still lacking. Here we use a novel database, GenDivRange, that integrates geo-referenced genetic diversity data from SSR markers for over 13,000 populations and over 800 species across all major taxa and habitats around the globe with species distributions and ecological data. A re-analysis of all data suggests that about 60% more species have a negative relationship between genetic diversity and distance from the center of their distribution than expected at random. While post-glacial colonization history commonly overrides this relationship, the most common factor for lacking support for the CHM was the power of the study. The number of populations sampled, their spatial distribution, and sample size affected most the validity of CMH. Overall our study suggests that the great amount of SSR data that accumulated during the past decades can be useful for testing evolutionary hypothesis. Based on our findings, we suggest sampling strategies for genetic diversity monitoring studies.

Whole genome sequencing of Sunda pangolin reveals population structure and provides insights into conservation management units in Thailand

Nattapong Banterng(1), Tim Bean(1), Rob Ogden(1)
1-University of Edinburgh

Pangolins are the most trafficked mammals globally, threatening their survival despite complete CITES protection. An insufficient understanding of the genetic diversity and connectivity between the population groups across the Asian region impedes attempts to protect Asian pangolin species. We analysed the genome sequences of 30 Sunda pangolins (*Manis javanica*) across Thailand alongside previously published sequences from neighboring countries to investigate their population structure.

The analysis identified five distinct pangolin populations, including those found in the northern regions (covering southern China and northern Myanmar) and separate populations located in Thailand and Malaysia. Moreover, divergence across Thailand and Malaysia was observed based on geographic region and forest complex. Within Thailand population genetic diversity was fairly constant, however, large inter-individual variation in inbreeding was sometimes observed. These baseline inferences identify genetically distinct Sunda pangolin populations providing information for conservation management across a fragmented natural landscape.

In addition to delineating possible management units, our findings will be used to develop wildlife forensic traceability tools that enable genetic assignment of confiscated pangolins to source populations in and around Thailand. More extensive geo-referenced genetic sampling from a broader habitat range is required to understand population structure and support traceability across the whole Southeast Asian continent.

Uncovering population structure in the endangered Northern rockhopper penguin (Eudyptes moseleyi) across islands in the southern Indian and Atlantic Oceans

Heather Ritchie-Parker(1), Alex Ball(1), Trevor Glass(2), Charly Bost(3), Antje Steinfurth(4)
1-Royal Zoological Society of Scotland, 2-Tristan da Cunha Government, 3-Centre d'Etudes Biologiques de Chizé, 4-Royal Society for the Protection of Birds

The Northern rockhopper penguin (*Eudyptes moseleyi*) is an 'Endangered' species (IUCN Red List) as populations have been in rapid decline for several decades. The species has a transoceanic distribution with breeding colonies found on five islands in the South Atlantic Ocean (Gough, Nightingale, Inaccessible, Alex, and Tristan da Cunha) and two islands in the southern Indian Ocean (Amsterdam, and St Paul) with seemingly no intermediary populations. Outside of breeding seasons the birds do forage widely in the southern oceans and vagrant individuals have been recorded in South Africa, Kerguelen Islands, Australia, and New Zealand. The origin of these vagrant birds is largely unknown, and it remains unclear to what extent birds move between islands and oceans. Understanding the connectivity, or lack thereof, of these (sub)populations is essential for developing appropriate conservation strategies. This is especially pertinent as some (sub)populations may be at greater extinction risk than others and source–sink dynamics may occur. Genetic data can provide insights into the movement of Northern rockhopper penguins and aid in the development of conservation strategies. Here we use a combination of mitochondrial DNA markers (CR and ND2) and a ddRAD sequencing approach to uncover population structure across the species' distributional range. Using this genetic data we; 1) investigate historic and contemporary patterns of gene flow, 2) estimate the extent and direction of migration between islands, and 3) overlay these patterns with ecological and environmental factors to better understand the driving forces shaping population structure.

Conservation genomics of Anodonta freshwater mussels in Switzerland

Julie Conrads(1), Ellika Faust(1, 2), Marco Giulio(1), Gwyneth Halstead-Nussloch(3), Philine Feulner(2, 4), Alexandra Anh-Thu Weber(1)
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Freshwater mussels of the family Unionidae provide important ecosystem services such as nutrient cycling and water purification. Yet, they are emblematic of the global biodiversity crisis observed in freshwater ecosystems, as they are one of the most imperiled groups of aquatic organisms worldwide. They are globally declining due to the combined effects of habitat degradation and destruction, climate change, pollution and invasive species. In Switzerland, there are three species of the genus *Anodonta*, the widespread *A. anatina* and *A. cygnea*, and *A. exulcerata* that is restricted to the southern part of the Alps. This study aimed to evaluate the four genetic essential biodiversity variables (EBVs: genetic diversity, genetic differentiation, inbreeding and effective population size) of Anodonta populations in Switzerland using high-resolution genomic data. We generated a 2.8 Gb de novo reference genome for *A. anatina*, the first reference genome of the Anodonta genus. We then conducted an extensive field campaign and collected non-lethally tissue samples of 423 Anodonta mussels (252 *A. anatina*, 153 *A. cygnea* and 18 *A. exulcerata*) from 31 populations occurring in lakes, ponds and rivers. Whole-genome resequencing data revealed the occurrence of hybrids between *A. cygnea* and *A. exulcerata* in a sympatric population, and the existence of a new undescribed *Anodonta* species south of the Alps. *A. anatina* metapopulation structure followed catchments area, with populations within catchment being more connected than populations among catchments. Interestingly, genetic diversity was positively correlated with the water body size, highlighting that populations in small ponds are more vulnerable to environmental disturbances than populations in large lakes. We found significant patterns of isolation-by-distance via river network, which is interesting given the patchy distribution of the species in lakes and ponds. Our study, informing about the vulnerability status of these three species, is particularly relevant in the context of the ongoing update of the Swiss mollusc red list and has therefore direct implications for management and conservation. Finally, our study provides important information on essential biodiversity variables for the three species, in line with the goals of the CBD to assess, maintain and safeguard genetic diversity.

Are dynamics of neutral genes and genes under selection different in translocation programs?

Xenia Münger(1), Carlo Pacioni(2, 3), Carly Cook(1)
1-Monash University, 2-Arthur Rylah Institute for Environmental Research, 3-Murdoch University

Anthropogenic pressures, such as habitat destruction, lead to increasingly isolated and small wildlife populations. The risks faced by small and isolated populations are well known. The small population paradigm indicates that very small populations are prone to losing their genome-wide variation and their ability to adapt to future environmental changes. Thus, it is generally assumed that their extinction risk is higher. Translocation of conspecifics is a powerful tool for conservation aiming to counteract these risks and to increase the genetic diversity of a population. However, from a genetic perspective, concerns associated with translocations are the potential risk of outbreeding depression and the introduction of maladaptive loci into a population with an already limited genetic diversity.

Since the adaptive value of alleles is rarely known in the wild, management guidelines are generally developed following the genetic theory for neutral genes. However, in small populations, random genetic drift has an increasingly greater effect on determining allele persistence compared to selective forces. In the genomics era where single nucleotide polymorphism (SNP) data become the norm, the assumption of neutrality is violated since SNPs can also be found in functional regions of the genome. Hence, it is critical to assess the potential effect of management practices on functional genes. Here, we follow the fate of alleles under selection with varying starting frequencies in a stochastic metapopulation model and use a critically endangered marsupial as a case study. The simulations include different sized populations, varying levels of gene flow as well as alleles experiencing positive and negative selection. We aim to determine management recommendations of gene flow threshold levels in terms of the number of individuals moved to retain alleles of certain frequencies. The model outcomes provide valuable insights for conservation managers, especially with genomic data becoming more and more accessible. Studies, such as this one, are important to further improve translocation programs and to obtain the best possible conservation outcomes.

Genomic legacy of human impacts on Scotland's red squirrels informs future conservation management

Melissa M. Marr(1), Emily Humble(1), Peter W. W. Lurz(1), Liam A. Wilson(1), Elspeth Milne(1), Katie Beckmann(1), Jeff Schoenbeck(1), Uva Fung(1), Andrew Kitchener(2), Kenny Kortland(3), Colin Edwards(3), Rob Ogden(1)
1-The University of Edinburgh, 2-The National Museum of Scotland, 3-Forestry and Land Scotland

The Eurasian red squirrel, *Sciurus vulgaris* L. 1758, is an icon of conservation science due to the text-book process of population replacement it experienced after the introduction of an invasive competitor, the north American grey squirrel, to the UK. Scotland is the last stronghold for the species in Britain, but it has a long demographic history of serial population fluctuations in the region, having been subject to repeated translocations, continental introductions and habitat fragmentation. It typifies a regionally endangered species highly modified by historic and ongoing human intervention.

We undertook the first whole-genome re-sequencing study for red squirrels to examine population structure, genetic diversity and demographic history in an applied context. We observed previously unknown patterns of spatial structure and connectivity related to landscape and gene flow. Levels of heterozygosity were amongst the lowest reported for any mammal. These were associated with abrupt and severe historical founder effects that were congruent with historical records of continental translocations into Scotland. Our results have key implications for future conservation management of red squirrels and for other regionally endangered taxa that contain a genetic legacy of past anthropogenic influence.

Assessing the genetic composition of cotton-top tamarins (Saguinus oedipus) before sweeping anthropogenic impact

Linett Rasmussen(1), Claudia Fontsere Alemany(2), Christina Hvilsom(1)
1-Copenhagen Zoo, 2-University of Copenhagen

During the last century, the critically endangered cotton-top tamarin (*Saguinus oedipus*) has been threatened by multiple anthropogenic factors that drastically affected their habitat and population size. As the genetic impact of these pressures is largely unknown, this study aimed to establish a genetic baseline with the use of temporal sampling to determine the genetic makeup before detrimental anthropogenic impact. Genomes were resequenced from a combination of historical museum samples and modern wild samples at low-medium coverage, to unravel how the cotton-top tamarin population structure and genomic diversity may have changed during this period. Our data suggest two populations can be differentiated, probably separated historically by the mountain ranges of the Paramillo Massif in Colombia. Although this population structure persists in the current populations, modern samples exhibit genomic signals consistent with recent inbreeding, such as long runs of homozygosity and a reduction in genome-wide heterozygosity especially in the greater northeast population. This loss is likely the consequence of the population reduction following the mass exportation of cotton-top tamarins for biomedical research in the 1960s, coupled with the habitat loss this species continues to experience. However, current populations have not experienced an increase in genetic load. We propose that the historical genetic baseline established in this study can be used to provide insight into alteration in the modern population influenced by a drastic reduction in population size as well as providing background information to be used for future conservation decision-making for the species.

Genomic Insights into the Decline and Resilience of Grayling in Switzerland

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2-Department of Aquatic Ecology, Swiss Federal Institute of Aquatic Science and Technology (Eawag), Dübendorf, Switzerland

Biodiversity loss is an ongoing planetary crisis with far-reaching consequences for ecosystems and human society as a whole. Freshwater systems are characterised by limited connectivity, temporal variability and often high anthropogenic impact. Consequently, biodiversity is declining at an alarming rate, often twice the rate seen in other systems. To preserve biodiversity, we need to know what is there and how it is changing, which is where genomic data plays an important part. However, there is an urgent need to develop well-described procedures and simplified pipelines to increase time efficiency and accessibility. Here we use the European grayling (*Thymallus thymallus*) as a case study to develop a conservation genomics framework in freshwater. The specific habitat requirements across the graylings' life stages have made it an important biological indicator species for riverine ecosystems. Unfortunately, this also makes the species very vulnerable, which has declined in many parts of its distribution. Here we conduct the first whole-genome population genomics study of grayling using resequencing data of >200 fish across Switzerland. Results reveal clear divergence both between and within river catchments as well as signs of inbreeding, influenced by human-led translocations and natural spatiotemporal variation. Interestingly, several contemporary hatchery fish significantly diverged from their wild counterparts. Overall, we show how genome-wide data can be effectively used within freshwater conservation frameworks despite a history of anthropogenic influence. Engaging with local stakeholders, our research aims to highlight the relevance of genomic insights for conservation management.

Genetic Diversity Can Be Maintained at High Levels with Proper Management During Fragmentation

Ohad Peled(1), Gili Greenbaum(1)
1-The Hebrew University of Jerusalem

One of the most detrimental processes induced by humans is the fragmentation of landscapes into small, isolated patches. Habitat fragmentation can erode genetic diversity within populations and increase genetic differentiation between them. A common approach for tracking the health of populations is through analysis of genetic data, i.e., genetic monitoring. However, the perspective with which genetic monitoring is interpreted often relies on simplistic models of between-population connectivity patterns , and assumes that genetic measures are trivially related to connectivity levels. We developed a computational framework for studying temporal dynamics of population genetic measures, accounting for real-world complexities and variability of fragmentation processes. We modeled populations as networks and simulated various fragmentation scenarios that correspond to typical anthropogenic processes leading to fragmentation (e.g., climate change, urban expansion, road construction, etc.). Using coalescent transformations of population networks, we tracked genetic diversity (expected heterozygosity) and genetic differentiation (Fst) during the fragmentation process. Our results indicate that under the same level of connectivity loss, genetic monitoring outcomes are markedly different, and strongly depend on the sequence of events leading to the fragmented landscape. In some scenarios, like road construction, a rapid decline in genetic diversity and increase in differentiation is expected, while in other processes, such as climate change in which connectivity loss is not spatially restricted, fragmentation is not as detrimental. Overall, our approach provides an important step towards linking theoretical population genetic models with the real-world complexities of genetic monitoring of wild populations. This framework can facilitate more effective use of genetic monitoring to track fragmentation and improve conservation efforts for at-risk populations.

29 AUGUST 2024

AULA - PALAIS DE RUMINE

14:45 – 17:45 / session 4 : Harnessing genetic diversity and evolutionary principles for population resilience and ecological restoration

Intra-specific diversity, inbreeding, and genetic load in caribou: implications for population resilience in the face of declines

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1-Environment and Climate Change Canada, 2-Trent University

High intra-specific genetic diversity and adaptive potential are key for resilience to global change. However, high variation may also support deleterious alleles through genetic load, thereby increasing the risk of inbreeding depression if population sizes decrease. Purging of deleterious variation has been demonstrated in some threatened species. However, less is known about the costs of declines and inbreeding in species with large population sizes and high genetic diversity even though this encompasses many species globally that are expected to undergo population declines. We use whole-genome sequences from caribou across Canada, a declining keystone species of cultural and economic importance, to reconstruct intra-specific genetic structure and measure key diversity metrics including heterozygosity, inbreeding, and genetic load. We found high genetic diversity and nine phylogenomic lineages across the continent, but also high genetic load among lineages. We found highly divergent levels of inbreeding across individuals, with the analysis of runs of homozygosity demonstrating some populations to be severely bottlenecked or having recently undergone strong declines. In inbred individuals, we see drops in heterozygosity including the loss of alleles by drift but not increased purging of deleterious variation. Caribou are thus particularly vulnerable to inbreeding depression upon declines such as those being observed in some areas. We discuss the implications of our results for the management of caribou to ensure the long-term resilience of the species, as well as the implications for other genetically diverse species-at-risk.

Multiple chromosomal inversions drive the genetic structure of king scallop (Pecten maximus): implications for management

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Chromosomal inversions play a crucial role in maintaining genome-wide divergence through local adaptation and speciation processes. They can independently accumulate private mutations in each orientation, suppressing recombination between heterozygous individuals and allowing sets of locally adapted alleles to be maintained despite gene flow. These rearrangements are increasingly associated with adaptive traits within species, which has relevance for management and conservation.

A previous study recently discovered, using restriction site-associated DNA sequencing, three large putative inversions in the commercially important king scallop (*Pecten maximus*). These inversions were associated with differences in the frequencies of temperature-related alleles and genes involved in gonad-specific expression and oocyte maturation, suggesting a role in regulating spawning time at small spatial scales.

Here, we determine scallop chromosomal structural variation by utilising medium-coverage whole-genome sequencing on 160 specimens from Scottish waters. Our findings reveal 17 chromosomal rearrangements, nine of which exhibit high linkage disequilibrium and homozygosity within, but not between, arrangements—consistent with the behaviour of large inversions. These inversions are independently segregated between individuals. Interestingly, patterns of genetic differentiation only show weak spatial structure, indicating a level of chaotic genetic patchiness, likely due to the biological traits of scallops (i.e. sweepstake reproduction events, larval dispersal).

Our study highlights the power of conducting whole-genome sequencing to investigate population structure at small spatial scales, providing insights into the appropriate spatial and temporal scale for management units.

Genetic diversity for population resilience in Scotland: capercaillie, beavers and pine hoverfly

Alex Ball(1), Heather Ritchie-Parker(1), Helen Taylor(1), Helen Senn(1)
1-Royal Zoological Society of Scotland

At the range edge of many terrestrial species, Scotland has been heavily affected by the large-scale declines that have impacted populations across Europe. As we build back the lost biodiversity it is therefore an imperative that genetic diversity is considered if we are to create resilient populations. At the Royal Zoological Society of Scotland's WildGenes lab we are using genetics and evolutionary theory on a case-by-case basis. We will discuss three of our approaches, 1) The use of target enrichment probes to develop non-invasive techniques for population monitoring of Capercaillie 2) Assessment of genetic diversity for Beaver translocations in the first successful reintroduction of a mammal to the UK and 3) Ex-situ breeding and monitoring of genetic diversity to create a resilient release population of Pine hoverfly. By taking a pragmatic and varied approach we are using genetics for targeted impact during species recovery in Scotland.

Angiosperms353 for population genetics of regionally threatened plant species

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1-Conservatoire et Jardin botaniques de Genève, 1 ch. de L'Impératrice, 1292 Pregny-Chambésy, Switzerland, 2-Department of Biology and Botanical Garden, University of Fribourg, Chemin du Musée 10, 1700 Fribourg, Switzerland

Intraspecific genetic diversity is a key component of biodiversity, but it has frequently been overlooked in conservation studies so far. Here we test the effectiveness of the targeted sequence capture approach using a standardized set of 353 nuclear genes (Angiosperms353) to capture the genetic structure and diversity of small regionally endangered populations of four distinct plant species for which conservation action plans are developed in Switzerland (*Clematis alpina, Blackstonia acuminata, Eryngium campestre, and Lythrum hyssopifolia*). For each species, we could successfully identify a minimum of 900 unlinked Single Nucleotide Polymorphisms (SNPs) in exonic and flanking intronic regions. The analysis of these SNPs allowed a clear differentiation of morphologically similar taxa (*B. acuminata and B. perfoliata*) and revealed patterns of population structure linked to different alpine refugia (*C. alpina*) or drainage systems even at a very local scale in the canton of Geneva (*E. campestre*). Signals of hybrid and polyploid taxa were also detected in *B. acuminata* and *L. hyssopifolia*. Altogether, our results demonstrate the usefulness of this method at the population level, despite the high conservation level and limited number of targeted genes selected in the *Angiosperms353* baits set. In addition, the many advantages of this method such as direct applicability, cost-effectiveness, compatibility with herbarium samples and a better data interoperability could facilitate the generation of sufficient data for rapidly assessing the genetic diversity and structure of endangered plants needed for informing conservation actions.

Genomics-driven monitoringfor genetic conservation and breeding in forest trees

Jill Hamilton(1)
1-Pennsylvania State University

In a rapidly changing environment, maintenance of genetic variation within and across populations is increasingly important for conservation and restoration. A species evolutionary potential is tightly linked to both the amount and distribution of genetic variation available through which natural selection may act. While there is growing emphasis on the importance of genetics in conservation, there is a need to pair genomic monitoring with range wide ex situ conservation collections as a foundation for breeding and restoration programs. Here, I will discuss the value of combining population genomic monitoring with conservation collections to understand species' evolutionary history, and the role different evolutionary mechanisms may play influencing neutral and adaptive processes across space and time using *Fraxinus* species as a case study. The decimation of eastern hardwood forests in North America in response to the Emerald Ash Borer and its continued expansion west emphasizes the need for proactive conservation of existing genetic resources and development of new genomic resources to pair with future breeding and restoration programs. I will discuss the need to safeguard biodiversity for species at risk, proposing genomic screening of seed and living collections for use in restoration, genecology, seed orchard establishment, and breeding program development.

Genome-level inference of reproductive isolation with implications for rare species conservation

Lionel Di Santo(1), Alayna Mead(2), Jessica Wright(3), Jill Hamilton(2)
1-University of Basel, 2-Pennsylvania State University, 3-USDA-Forest Service

Genetic rescue is a conservation strategy aimed at introducing novel genetic variability into populations to mitigate potential adverse fitness consequences associated with genetic and demographic decline. Despite its relevance to conservation, this approach remains controversial where species exhibit strong signatures of local adaptation as the introduction of novel variation may breakup coadapted gene complexes, ultimately accelerating population decline. Restricted to one island and one mainland population, Torrey pine (*Pinus torreyana*) is globally one of the rarest pine species in the world. It exhibits exceedingly low genetic diversity for a conifer and faces abiotic and biotic threats leading to population-level decline. Given these observations, Torrey pine has been a candidate species for potential genetic rescue. Here, we use phenotypic and genomic data from a common garden experiment of parental populations and F1s to test whether populations are evolving signatures of reproductive isolation. Insights into intra-specific genetic boundaries maintained between parental populations will help quantify potential risks of outbreeding depression following genetic rescue. Combining genomic simulations and genome-wide association analyses, we uncovered SNPs exhibiting low rates of admixture in F1s, annotated them using GO and PO terms, and associated them with fitness and fitness-related traits, including tree height and cone production. Overall, we found that SNPs with low rates of admixture were enriched for reproductive- and development-related functions, including growth or pollination. One SNP with low admixture strongly differentiated between populations was also significantly associated with differential fitness in all traits measured, suggesting it could play a role in promoting reproductive isolation. Concordant with previous observations of phenotypic and genomic differentiation between populations of Torrey pine, our research warrants caution if genetic rescue is considered as a conservation strategy as inter-population gene flow may disrupt local adaptation, reducing the species' fitness.

Providing new guidance to conserving plants ex situ: genetically resilient collections

Sean Hoban(1), Emily Schumacher(1), Austin Koontz(1), Kaylee Rosenberger(2), Patrick Griffith(3), Abby Meyer(4), Jeremie Fant(5), Lauren Eserman(6), Bethany Zumwalde(7), Gavin Salas(1), Murphy Westwood(1)
1-The Morton Arboretum, 2-University of Colorado Boulder, 3-Montgomery Botanical Center, 4-BGCI US, 5-Chicago Botanic Garden, 6-Atlanta Botanical Garden, 7University of Florida

Botanic gardens, arboreta, and seed banks conserve many plant species ex situ, helping forestall extinction and providing opportunities for research, ecological restoration, and education. However, due to limitations in space and resources, these institutions face a pivotal question: how can ex situ facilities maximize their conservation impact? In this talk, I will describe several methods to quantitatively assess whether ex situ populations adequately represent the genetic, geographic, and trait breadth of each species. I provide brief examples of three approaches to this problem: using GIS analysis of collection sources and species range maps; using simulations to determine minimum size; and using DNA based analysis of in situ and ex situ plant material. Each approach highlights that relatively few species' collections are genetically secure and emphasizes a need for ongoing collection and conservation efforts. Achieving the ex situ representation of genetic diversity will often require maintaining at least several hundred plants. Sampling requirements can be tailored to each species' biological traits. Insights from these approaches can help revise collection plans, and measure progress towards completing specific conservation goals. I close with future directions, including the necessity of incorporating collection duplication to enhance resilience to disasters.

Phylogenomic analysis of entire regional flora as a resource for biodiversity assessments

Sébastien Miche(1, 2), Charles Pouchon(2), Camille Christe(2), Maya Wells(2), Nicolas Wyler(2), Mathieu Perret(1, 2)
1-University of Geneva, 2-Conservatory and Botanical Garden of Geneva

Accurate knowledge of the phylogenetic relationships among the species composing the regional biota is crucial to understand how species were assembled and how much phylogenetic diversity they represent. However, phylogenetic information available for local species communities is still limited because of the poor resolution and uncomplete sampling of the tree-of-life at the species-level. Here, we demonstrate the feasibility of using Angiosperms353 target-enrichment and high-throughput genome sequencing on both fresh and historic DNA to estimate phylogenetic relationships among all species composing the regional flora of the Canton of Geneva. The analysis of over 1500 species provides a more resolved, supported and complete tree than available synthetic or plastid-based phylogenies. This new genomic reference for Swiss plants points to several disagreements with the current plant classification and provides a new framework to assess the evolutionary dynamics of a complete regional flora. In particular, the computation of several phylogenetic diversity indices (PD, RPD, CANAPE, EDGE…) brings new insights into the consequences of regional extinctions on phylogenetic diversity and the identification of areas that should be prioritized for long-term conservation strategies.

Assessing the impact of chemical pollution on the genetic profile of wild populations

Tiffany Scholier(1), Marissa B. Kosnik(1)
1-Department of Environmental Toxicology, Swiss Federal Institute of Aquatic Science and Technology, Eawag, 8600 Dübendorf, Switzerland

Humans alter the environment in numerous ways and force organisms to either adapt to the new living conditions or to perish and can therefore indirectly change the genetic pool of wild populations. One of the main drivers behind these human-induced changes and consecutive biodiversity loss is the release of numerous chemicals into the environment, including personal care products, pesticides, and pharmaceuticals. Yet while other environmental variables such as climate have been studied as a potential driver of genetic differentiation, chemical pollution has been largely overlooked up until now. In this study, we propose a new computational approach to overcome this knowledge gap. We combine several methodologies such as data scavenging, GIS programs, population genomics tools and multiple genome scan methods to discover SNPs that associate with environmental contaminants. As an example, by relating a SNP dataset of the bank vole to potential heavy metal contamination in its habitat, we found several variants in the genome of the bank vole that could be linked to genes that are involved in detoxification pathways. Interestingly, the majority of these detected genes of interest are also known to alter their transcription when exposed to heavy metals. Documenting changes in the genomes of several species over a large geographical range for multiple chemical pollutants will enable us to make an estimation of the genetic changes happening in wildlife due to chemical pollution. This approach can help develop environmental remediation strategies or set chemical threshold levels that do not affect the genetic diversity of wildlife populations.

The population genetic history of Bombus pascuorum in Sweden

Michael Mitschke(1, 2), David Díez-del-Molino(1, 2)
1-Centre for Palaeogenetics, Stockholm University, 2-Department of Zoology, Stockholm University

The past century's extreme anthropogenic environmental change, particularly the intensification of agriculture, led to reduced insect biomass, changes in arthropod species composition, and species extinctions. These changes impair essential ecosystem services like for example the pollination of crops, thereby having not only intrinsic, but also economic relevance. It is vital to understand the impact of anthropogenic global change on species to inform targeted conservation measures. However, studies are often limited to spatial comparisons or to relatively short timeframes. A promising approach to overcome this issue is to perform temporal comparisons using historical DNA from museum collections.

In this study, we analyze ~100 historical and ~60 modern genomes of *Bombus pascuorum*, an important pollinator. Historical samples were retrieved from the Naturhistoriska Riksmuseet, Stockholm, Sweden, and originate from southern and central Sweden, covering the past 150 years. The historical samples had a very short fragment length (average 58.3 bp) but high endogenous content (average 81%). We generated low-coverage genomes (depth 1.02x-18.93x, mean of 3.64x) and compared them with a dataset of high-coverage modern genomes. We performed PCA and admixture analysis to identify temporal changes in population structure and investigated how genetic diversity and inbreeding levels have changed over time.

Our results highlight the potential of accessing historical DNA from specimens in museum collections to investigate the genomic impact of global decline on insect populations. By providing insight into the past, historical DNA enables the formulation of a baseline or initial state and can inform the conservation practices of the future.

30 AUGUST 2024

AULA - PALAIS DE RUMINE

9:30 – 12:30 / session 5 : Monitoring genetic diversity and effective population size

Genomic monitoring of Orthoptera using a multi-locus barcode

Ines Carrasquer Puyal(1,2), Julia Bilat(1), Christian Monnerat(3), Jeremy Gauthier(4), NadirAlvarez(4)
1-Muséum d'Histoire Naturelle de Genève, 2-University of Geneva, 3-infoFauna, 4-Naturéum

Evaluating the conservation status of species and communities is essential for effectively informing conservation actions. As the biodiversity loss accelerates, there is an urgent need to monitor interspecific and intraspecific diversity. In insects, a single mitochondrial gene, COI, has been classically used as a barcode to determine samples at the species level. However, intraspecific resolution of such a barcode is limited and applications are strongly impacted by several biases. The inclusion of additional nuclear loci to the classical barcode could in practice overcome most of the limitations and allow direct evaluation of demographic and evolutionary trajectories of populations. In this study, we present a new set of multi-locus markers applied to Orthoptera, among which 40% of the species are currently threatened in Switzerland. This set, which includes universal single-copy orthologs [USCO] and ultraconserved elements [UCE], the mitogenome and the ribosomal DNA, was captured and sequenced in 750 samples including all Swiss Orthoptera species collected at the country-wide scale during the current update of the Red List. Our results assess the performance and limitations of this new set of markers when applied to an entire insect order encompassing lineages that diverged for a remarkably long time, i.e. 350 million years. The application of this multi-locus marker has enabled the resolution of the phylogeny of Swiss species and the clarification of complex taxonomic issues with direct consequences in conservation practice. In addition, we were able to identify patterns of intraspecific genetic diversity, according to the species' conservation status. These results are included for the first time in the forthcoming Red List update, setting a precedent for subsequent integration of genetic monitoring programs resulting in future national conservation policies.

Museomics to retrace the decline of insect populations throughout the 20th century

Jérémy Gauthier(1,2,3), Inés Carrasquer(2), Enolà Le Basle(2), Camille Pitteloud(2), Marylène Bacaicoa(2), Aristide Parisod(2), Nathan Cornide (2), Hélène Mottaz(2), Julia Bilat(2), Nadir Alvarez(1,3,4)
1-Naturéum, State Museum of Natural Sciences, Lausanne, Switzerland, 2-Museum of Natural History of Geneva, Geneva, Switzerland, 3-Département de Génétique et Evolution, University of Geneva, Geneva, Switzerland, 4-Department of Ecology and Evolution, University of Lausanne, Switzerland

The large-scale decline of insects in the past decades is increasingly evident and widely documented. Although the decline is evidently linked to the consequences of human activities, the specific factors driving it remain elusive, and its specific mechanisms and causes remain poorly understood. Studies documenting this decline are based on recent trends—since the 1970s—and generally rely on biomass estimations that do not fully reflect the state of populations. Yet an ample set of samples is available to undertake a large-scale study, both spatially and temporally (throughout the 20th century). Most museum collections comprise insects collected over this period, forming genuine time series. Thanks to recent developments in museomics, it is now possible to access the genetic information carried by these samples and, thus, to study the demographic evolution of populations over time. Following thorough databasing in the five main Swiss museums, we selected eight insect species among Ephemeroptera, Orthoptera and Lepidoptera. We then achieved a comprehensive sampling of insect tissues from museum specimens, yielding a total of nearly 1,504 historical samples spanning the entire 20th century, and covering a large number of localities in Switzerland. In addition, historical localities have been resampled in 2021-2022, resulting in 962 fresh specimens. Whereas a ddRAD approach was utilized to analyze fresh specimens, a hybridisation capture method, namely hyRAD, was applied to recover genetic information from historical samples. This innovative museomics approach, compatible with ddRAD data, recovered thousands of nuclear loci, enabling the estimation of various population genetic indices to assess population dynamics. Initial findings indicate an erosion in genetic diversity of approximately 40% in the species studied. Spatial demographic inferences are currently being conducted to highlight the dynamics of this decline in greater details as well as the potential correlation with shifts in agricultural practices and the use of new pesticides.

Population genomics of the muskox' resilience in the near absence of genetic variation

Edana Lord(1), Patrícia Pečnerová(2)
1-Centre for Palaeogenetics, Stockholm, 2-University of Copenhagen

Towards the end of the last ice age, many megafauna across the northern hemisphere went extinct. However, the muskox (*Ovibos moschatus*) is an Ice Age relic that persists today in fragmented populations in the High Arctic of Canada and Greenland. Thus, understanding how the muskox survives today whilst other species perished can provide insights on population decline and extinction dynamics. Here, we present 108 muskox genomes, from present-day individuals from across the current range of muskox and a 21,000-year-old ancient genome from Siberia. Demographic reconstruction suggests that past climate and post-glacial recolonisations were the primary drivers of changes in population size. Importantly, the white-faced muskox has the lowest genome-wide heterozygosity that has been observed in ungulates with more than 70% of the genome found in runs of homozygosity. However, despite this, there is no evidence of inbreeding depression, suggesting that long-term gradual population decline may have removed strongly deleterious mutations from the population. The muskox is an important case study in how a fragmented population with low effective population size and low genomic diversity can still persist, suggesting the mode of decline is important to consider in assessing population resilience.

Biodiversity Genomics Europe: advancing the use of genomic science for biodiversity

Robert Waterhouse(1)
1-SIB Swiss Institute of Bioinformatics

The Biodiversity Genomics Europe project, BGE, (https://biodiversitygenomics.eu/) aims to advance the use of genomic science to improve our understanding of biodiversity, monitor biodiversity change, and guide interventions to prevent its decline. To achieve this goal, BGE brings together two networks: iBOL Europe (https://iboleurope.org/) that focuses on DNA barcoding, and the European Reference Genome Atlas (ERGA: https://www.erga-biodiversity.eu/) that focuses on reference genome generation and is the European node of the Earth BioGenome Project. To achieve its applications-focused goals with respect to the use of reference genome resources in bioeconomy and conservation, BGE is running an array of case study sub-projects. Several ongoing case studies are developing their research programmes to demonstrate the potential of reference genomes and additional genomic data in biodiversity applications focused on species conservation efforts. These include Mediterranean gobies in Croatia, the European hamster in Hungary, and bath sponges in Greece, as well as several other case studies relevant to bioeconomy issues and additional projects spanning a range of taxa and countries across Europe. As well as the scientific aims of each study, these BGE actions are building bridges between genomic researchers, conservation practitioners, and citizens, linking case study activities to relevant stakeholders and the public. Working with the ERGA Data Analysis Committee and Citizen Science Committee, the teams involved are also contributing to building capacity and best practices in biodiversity application analysis toolkits as well as to wider stakeholder mapping efforts and engagement with genomics solutions applied to biodiversity research.

A perspective on the Swiss pilot study for a monitoring of genetic diversity

Martin C.Fischer(1), Oliver Reutimann(1), Gabriel F. Ulrich(1), Karim Clivaz(1), Jasmine Noëlle Tschan(1), Enrique Rayo(1), Niklaus Zemp(2), Felix Gugerli(3), Rolf Holderegger(1, 3), Alex Widmer(1)
1-Institute of Integrative Biology (IBZ), ETH Zurich, 8092 Zurich, Switzerland, 2-Genetic Diversity Centre (GDC), ETH Zurich, 8092 Zurich, Switzerland, 3-Biodiversity and Conservation Biology, WSL Swiss Federal Research Institute, 8903 Birmensdorf, Switzerland

Genetic diversity is the raw material of evolution and is essential for species to adapt to changing environments. At the international level, particularly in the context of the Convention on Biological Diversity (CBD) and the Global Biodiversity Framework (GBF), concerted efforts have been made to incorporate within-species genetic diversity—one of the three fundamental pillars of biodiversity—into monitoring projects and conservation initiatives. To date, there has been little systematic monitoring of genetic diversity at the national level, the scale at which most biodiversity conservation is funded. Therefore, capacity, knowledge and experience need to be built up first. We initiated a genomics-based pilot study for genetic diversity monitoring in Switzerland, with the aim of assessing genetic diversity indicators, thereby gaining the practical experience necessary for setting up a monitoring programme in Switzerland. For this pilot study we selected five focal animal and plant species based on multiple criteria, including their occurrence in habitats of national importance or in anthropogenically modified landscapes, as well as their red list status, genome size and availability of specimens in natural history collections for retrospective analysis. We developed a tailored sampling strategy to monitor genetic diversity, based on which we sampled >1,200 individuals from 158 populations across all biogeographic regions in Switzerland. For each species, we de novo assembled its reference genome and re-sequenced the whole genome of all sampled individuals. For two species and 400 specimens, we used a museomics approach to travel back in time (up to 200 years) to retrospectively assess temporal changes in genetic diversity, complementing the analysis of contemporary samples. The data from our pilot study allow detailed conservation-relevant analyses of not only the current spatial distribution of genetic diversity, but also of other genetic indicators such as genetic connectivity, inbreeding (FROH), adaptive genetic variation, and estimates of effective population size (Ne). These indicators will set the benchmarks against which future changes in genetic diversity will be compared, and they also provide unprecedented insights into recent changes in genetic diversity in wild populations of animals and plants in Switzerland. With the experience gained, we are creating a framework for monitoring genetic diversity in Switzerland that can serve as an example for other international initiatives.

Genetic erosion of a peatland specialist in space and time

Gabriel F. Ulrich(1), Enrique Rayo(2), Karim Clivaz(1), Alessia Guggisberg(1), Niklaus Zemp(3), Verena J. Schünemann(4), Alex Widmer(1), Martin C. Fischer(1)
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Anthropogenic habitat degradation, fragmentation and loss are among the key drivers of biodiversity decline. These can lead to population size reduction and isolation, and thus to genetic erosion, a decrease in genetic diversity over time through random genetic drift and inbreeding. Since genetic diversity provides the raw material for evolution, understanding the temporal dynamics of changes in genetic diversity and causes of genetic erosion is relevant for conservation. Here, we investigated habitat loss and changes in genetic diversity in space and time in a peatland specialist, *Eriophorum vaginatum*. Peatlands have drastically declined over the past two centuries due to drainage and peat extraction. We selected and sequenced 148 herbarium specimens from Switzerland, collected between the 1800s and 1940s. In 2022, we revisited the sites where they were collected to sample ten contemporary individuals from each population. Only 103 revisited populations could be recovered, and population extinction was greatest in densely populated and agricultural regions. Whole-genome re-sequencing data from 148 historical and 853 contemporary samples were used to infer temporal changes in genetic diversity and inbreeding based on runs of homozygosity (FROH). Genome-wide genetic diversity has declined by more than 6%, with frequent local increases in inbreeding. Interestingly, the region with the highest population extinction has not suffered the greatest loss of genetic diversity or increase in inbreeding. This may be a consequence of the large size and genetic diversity of the remaining populations, high historical genetic diversity, and an associated slow loss of genetic diversity. Our study shows that genetic diversity in wild populations of a peatland specialist has been declining for more than a century and is likely to continue to decline despite strict habitat protection. This is a consequence of past habitat destruction leading to increased isolation and inbreeding. Conserving large populations and restoring connectivity are necessary to prevent further genetic erosion.

Genetic indicators in plants and fungi: a botanical garden perspective

Roberta Gargiulo(1)
1-Royal Botanic Gardens, Kew

The inclusion of a headline genetic indicator based on effective population size (Ne) in the Kunming-Montreal Global Biodiversity Framework has fuelled more interest in improving the methods used to estimate genetic indicators, especially in light of known biases and methodological limitations.

Plants and fungi are among the groups in which such methodological limitations might be particularly exacerbated. Plants often exhibit complex life-history traits that influence Ne to census size ratios and violate several assumptions around which current estimation methods were built. Fungi have historically been neglected in conservation efforts due to their cryptic nature and the consequent scarcity of population genetic data, and therefore it is unclear whether population-based genetic indicators can be used in fungal species.

Additionally, the Kunming-Montreal Global Biodiversity Framework includes a complementary indicator for plant genetic resources in ex-situ conservation facilities. However, there is a poor link between this indicator and the actual genetic diversity levels of the populations preserved ex-situ.

Our contribution will (i) explore some of the limitations associated with the estimation of Ne in plants with complex life-history traits, (ii) describe the results from the first attempt to estimate contemporary Ne in fungi and finally, (iii) discuss the progress and challenges associated with finding genetic indicators for seed bank collections.

Demographic histories of two endangered warty pigs in the Malay Archipelago

Anna Schleimer(1), Alain C. Frantz(2), Lorraine Richart(3), Jörg Mehnert(4), Gono Semiadi(5), Wirdateti Wirdateti(6), Johanna Rode-Margono(7), Michel Mittelbronn(3), Stuart Young(8), Frank Drygala(4)
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The biodiversity of the Malay Archipelago is the product of the region's rich biogeographical history with periods of island connectivity and isolation during the Pleistocene glacial cycles. Here, the case of two endemic suid species, the Javan (*Sus verrucosus*) and Bawean (*S. blouchi*) warty pigs, was used to illustrate how biogeographic processes and recent anthropogenic pressures can shape demographic histories with significant implications for species conservation. We employed genome-wide single nucleotide polymorphisms from the Porcine SNP60 v2 BeadChip to assess interspecific genetic differentiation, to estimate divergence times and to perform demographic model selection.

In contrast to the hypothesis of recent divergence during the last glacial maximum, *S. blouchi* was found to have diverged from *S. verrucosus* at least 166k years ago following a founder event. The contemporary *S. blouchi* population was characterized by a recent bottleneck that reduced the effective population size to less than 20. The genomic assessment supports the single species status of *S. blouchi*, as was previously proposed based on morphometrics. The demographic history of *S. verrucosus* showed evidence of secondary contact with the sympatric banded pig (*S. scrofa vittatus*) that colonised Java 70 k years ago.

While the Javan and Bawean warty pigs have persisted throughout the Pleistocene climatic oscillations, contemporary pressures from human activities threaten their survival and immediate action should be taken to grant legal protection to both *S. verrucosus* and *S. blouchi*. This study highlighted the use of demographic history modelling using genomic data to identify evolutionary significant units and inform conservation.

Efficient estimate of effective population size from low coverage data through Approximate Bayesian Computation

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A key parameter for evaluating extinction risk is the population effective population size (*Ne*). The *Ne* is a proxy for the amount of genetic diversity lost due to random genetic drift within a population, and it reflects population structure and past demographic dynamics. In absence of genetic data, census size (*Nc*) is used as a proxy for Ne, which may provide biased estimates for highly drifted populations. With the increased availability of genomic data associated with decreasing costs, estimating *Ne* from whole genome sequencing (WGS) may become a possibility for a growing number of species. However, estimating current Ne from genetic data is still limited to higher coverage genomes from many individuals. This restricts its application in countries where WGS is still expensive and in critically endangered species. Here, we present results from a tool to measure contemporary *Ne* from low coverage genomes using Approximate Bayesian Computation. We discuss the power of our method to distinguish different simulated models (constant, bottleneck, expansion) using various locus length and number, coverage, and number of individuals per population. Besides proposing a method for estimating and monitoring current Ne, we also aim to provide a quick overview on the use of multiple genomic methods, comprising their limitations for monitoring adaptative potential under the Kunming-Montreal Global Biodiversity Framework (GBF), and under the context of the Genomics of the Brazilian Biodiversity, a genomics consortium based in a megadiverse country in the Global South.

Effective population size of two chamois (Rupicapra rupicapra) populations in the Bavarian Alps

Susanne Jacobs(1), Hendrik Edelhoff(1), Cornelia Ebert(2), Wibke Peters(1, 3)
1-Bavarian State Institute of Forestry, 2-Seq-IT GmbH + Co. KG, Kaiserslautern, 3-Wildlife Biology and Management Unit, Chair of Animal Ecology, Munich Technical University

The effective population size (Ne) and the effective number of breeders (Nb) are fundamental parameters in population and conservation genetic research, providing relevant information on adaptability and long-term viability of populations. In contrast, practical monitoring and management strategies commonly focus on estimates of census population size (N) without incorporating genetic data. Introducing genetically derived Ne estimates in wildlife management concepts could add an important layer of information on population viability. However, estimation of Ne is non-trivial, especially in long-lived species with overlapping generations, and may be influenced by sampling, e.g., if multiple non-distinguishable cohorts are sampled simultaneously. Additionally, population structure, especially in continuously distributed species, poses a major challenge when estimating Ne.

Northern chamois (*Rupicapra rupicapra*), an iconic mountain dwelling ungulate are widespread throughout the Alps. Here, we derived Ne and Nb for two populations in southern Bavaria based on 705 high-quality tissue microsatellite genotypes from samples of legally hunted individuals collected between 2016 and 2022. Concurrently, census population size estimates based on Bayesian spatial capture–recapture (SCR) from the same two areas allowed us to compare estimates of Ne and N. We contrasted both parameters with the ultimate goal to evaluate whether Ne can advance monitoring of Bavarian chamois.

Ne per generation in the two study areas were 514 (95% CI 388-737) and 179 (95% CI 154-211). Estimated Ne/N ratios were similar in both study areas but with considerably large confidence intervals: 0.50 (CI 0.35-0.78) and 0.56 (CI 0.39-0.80). Nb estimates suggested largely stable sizes over the sampling period. However, confidence intervals of Ne and Nb estimates varied substantially between the two study areas, presumably due to differences in population structure, in particular the level of population closure, and sample size. We conclude that estimation of Ne can be a valuable and versatile tool for monitoring genetic diversity in chamois, but caution is advised concerning population characteristics and sampling design.

POSTERS

28 – 30 August 2024
Everyday from 13:15 to 14:00 in the room
«Tissot» - Palais de Rumine

**Please be in front of your posters during the poster session time.*

1 - Novel insights from genetics into the ecology and evolution of deadwood-dependent invertebrates, and implications for conservation

Ryan Garrick(1)
1-Univesity of Mississippi, USA

Deadwood-associated (saproxylic) invertebrates are functionally important ecosystem engineers (they play key roles in decomposition and nutrient cycling processes in forests, and structuring microhabitats), yet their basic life history, population biology, and evolutionary history are often poorly known. Owing to convergent morphological features associated with adaptation to life in a rotting log (e.g., dorsoventral flattening, wing reduction or secondary loss), species boundaries have traditionally been difficult to demarcate, and many saproxylic taxa are known to be species complexes. Notwithstanding this tendency for "under-splitting", formally named saproxylic insect species are proportionately over-represented on threatened and endangered species lists. Molecular data can redress many of the knowledge gaps, including inferences about mating systems and family group structure, understanding the spatial scale of dispersal and gene flow, delimiting species using objective criteria (reproductive compatibility / genotypic cohesion, monophyly, etc.), and reconstructing species- or community-level response to past climatic change. Here, key take-home messages from a comprehensive review of how basic and applied research on saproxylic invertebrates has been informed by genetics, and the nature of remaining knowledge gaps, is presented.

2 - A new cryptic mammal species in Switzerland: when taxonomy illuminates conservation priorities

Manuel Ruedi(1)
1-Muséum d'histoire naturelle de la ville de Genève

Over the past decades, the use of molecular markers to assess population variation triggered the discovery of tens of new biological species, including in popular groups such as mammals, and in seemingly well—known areas like Western Europe. Most of these new species are morphologically cryptic, meaning that they chiefly differ by genetic characters, but can be hardly recognized by external or other phenotypic characters. One of these new species is a Hazel Dormouse, long considered as a single widespread and morphologically uniform species across most of Europe and western Asia.

Previous phylogeographic studies showed that populations from Western Europe and those from Northern or Eastern Europe were genetically very distinct but refrained to interpret data in terms of taxonomy. We showed that within Switzerland (and elsewhere in Central Europe), the distinct lineages maintain these differences despite close geographic proximity (parapatry). We therefore propose to consider them as two independent but cryptic species, the Western (*Muscardinus speciosus*) and the Eastern Hazel Mouse (*M. avellanarius*), respectively. Local authorities or protection organisations are sometimes reluctant to adopt such taxonomic novelties, especially when they involve cryptic species. However, failing to recognize them as two independent species would have far-reaching consequences as they are both globally protected and need specific plans for their conservation, including throughout population translocations. If such population reinforcements ignore the new taxonomic evidence, managed populations could lead to a failure or to local extirpation of the most threatened local taxon.

3 - The effective population size: do we know what we are estimating?

Joachim Mergeay(1)
1-Research Institute for Nature and Forest

In its simplest form, Ne depends on Nc and the reproductive variance among individuals. This variance in turn influences every aspect of genetic diversity in a population, such as inbreeding, kinship, linkage disequilibrium among loci, variance in allele frequencies, coalescence rates of alleles... Dozens of methods are available to estimate Ne from genotypic data, and all it takes is a “press on the button”. In truth, each method estimates a specific spatial or temporal aspect of Ne with its own assumptions, and estimates may easily differ an order of magnitude, highlighting the presence of large biases. This has led to a Babylonian speech confusion on Ne, and raises the question “do we know what we are estimating?”

Using legacy datasets I show how even mild violations of assumptions can lead to large biases in Ne estimations, but also how we can deal with this. This highlights the need for very clear and practical guidelines on how to estimate Ne and diligently take implicit and explicit model assumptions into account when selecting a sampling design and choosing a method.

4 - Genetic rescue: Outbred or Inbred, who is the better rescuer?

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Anthropogenic changes mean that many populations are becoming increasingly small and isolated. The loss of fitness due to inbreeding, aka inbreeding depression, is a major concern for these populations, potentially contributing to their extinction. Genetic diversity can be introduced into the inbred population via the translocation of individuals (Genetic rescue), reducing inbreeding depression. However, the ideal rescuer to use in such situations is highly debated. Rescuers from a large, outbred population which will be more genetically diverse may also risk introducing recessive deleterious alleles. Alternatively, rescuers from other small, inbred populations will likely have purged deleterious alleles but will introduce less new genetic diversity. To explore this issue, we have performed experimental genetic rescue utilising the model species *Tribolium castaneum*. Inbred populations that have experienced three generations where they were bottlenecked to a single pair, were rescued by either an outbred individual or an inbred individual from another population. Control populations received no rescue. Fitness was measured as the number of offspring surviving to maturity at each generation, over a total of ten generations. After five generations, results show that all rescued populations had increased productivity compared to non-rescued control populations. Those populations rescued by outbred individuals also had increased productivity compared to those rescued by inbred individuals. Our study found that genetic rescue increased the productivity of inbred populations and was more effective utilising outbred rescuers rather than inbred rescuers.

5 - Effective population size of two chamois (Rupicapra rupicapra) populations in the Bavarian Alps

Susanne Jacobs(1), Hendrik Edelhoff(1), Cornelia Ebert(2), Wibke Peters(1,3)
1-Bavarian State Institute of Forestry, 2-Seq-IT GmbH + Co. KG, Kaiserslautern, 3-Wildlife Biology and Management Unit, Chair of Animal Ecology, Munich Technical University

The effective population size (Ne) and the effective number of breeders (Nb) are fundamental parameters in population and conservation genetic research, providing relevant information on adaptability and long-term viability of populations. In contrast, practical monitoring and management strategies commonly focus on estimates of census population size (N) without incorporating genetic data. Introducing genetically derived Ne estimates in wildlife management concepts could add an important layer of information on population viability. However, estimation of Ne is non-trivial, especially in long-lived species with overlapping generations and may be influenced by sampling, e.g., if multiple non-distinguishable cohorts are sampled simultaneously. Additionally, population structure, especially in continuously distributed species, poses a major challenge when estimating Ne.

Northern chamois (*Rupicapra rupicapra*), an iconic mountain dwelling ungulate are widespread throughout the Alps. Here, we derived Ne and Nb for two populations in southern Bavaria based on 705 high-quality tissue microsatellite genotypes from samples of legally hunted individuals collected between 2016 and 2022. Concurrently, census population size estimates based on Bayesian spatial capture-recapture (SCR) from the same two areas allowed us to compare estimates of Ne and N. We contrasted both parameters with the ultimate goal to evaluate whether Ne can advance monitoring of Bavarian chamois.

Ne per generation in the two study areas were 514 (95% CI 388-737) and 179 (95% CI 154-211). Estimated Ne/N ratios were similar in both study areas but with considerably large confidence intervals - 0.50 (CI 0.35-0.78) and 0.56 (CI 0.39-0.80). Nb estimates suggested largely stable sizes over the sampling period. However, confidence intervals of Ne and Nb estimates varied substantially between the two study areas, presumably due to differences in population structure, in particular the level of population closure, and sample size. We conclude that estimation of Ne can be a valuable and versatile tool for monitoring genetic diversity in chamois, but caution is advised concerning population characteristics and sampling design.

6 - GenDiB, a new database on genetic diversity in populations of wild species

Corine Buser(1), Benjamin Dauphin(1), Ionut Iosifescu-Enescu(1), Andrin Gross1, Rolf Holderegger(1), Evangelia Kolovou(1), Deborah M. Leigh(1), Rolf Meile(1), Meret Mosimann(1), Gian-Kasper Plattner(1), Christian Rellstab(1), Silvia Stofer(1), Lukas Wotruba(1), Felix Gugerli(1)
1-WSL

GenDiB aims to link conservation genetics with research data management to initiate a new database on genetic diversity in populations of wild species in Switzerland. An interactive map of existing studies on intraspecific genetic diversity in Switzerland already illustrates the richness and potential of these data, which were previously scattered or even inaccessible. Currently, GenDiB is being developed as a database prototype so that existing datasets can be systematically recorded. Newly created datasets, including comprehensive metadata, will be directly uploaded, and archived in a referenceable way. Our vision is that GenDiB will help to secure, process, and centrally archive the already existing treasure trove of data on the genetic diversity of wild species in Switzerland. Thereby, these data will become easily, long-term, and publicly accessible for research, teaching, and, especially, practical nature conservation—not least because such data were largely financed with taxpayers' money. GenDiB will be a useful tool to get an overview of genetic diversity data in Switzerland, but also to "assess, monitor and ultimately halt the loss of genetic diversity", as envisaged in the Swiss Biodiversity Strategy. This would make Switzerland the first country to have such a national database. We hope that GenDiB will raise awareness of this gap and inspire other countries to continue compiling georeferenced genetic diversity data and make them publicly available.

7 - Genetic evidence for a counterintuitive increase in black howler monkey dispersal in a fragmented landscape

Keren Klass(1), Sarie Van Belle(2), Julie Teichroeb(3), Eva Wikberg(4), Gwen Duytschaever(5), Hadjira Hamou(5), Anthony Di Fiore(2), Alejandro Estrada(6), Amanda Melin(5), Gili Greenbaum(1)
1-The Hebrew University of Jerusalem, 2-The University of Texas Austin, 3-The University of Toronto Scarborough, 4-The University of Texas San Antonio, 5-The University of Calgary, 6-The National Autonomous University of Mexico

Forest loss and fragmentation can alter dispersal patterns, which may lead to small, isolated, genetically depauperate animal populations at risk of extirpation. We examined fragmentation’s effects on endangered black howler monkey (*Alouatta pigra*) dispersal and population genetics, by comparing an unprotected population occupying forest fragments around Palenque National Park, Mexico (PNP), to the protected population within PNP. We extracted host-enriched fecal DNA from 158 monkeys and used ddRAD sequencing to generate a dataset of 9,567 SNPs. We analyzed population genetic structure, gene flow, diversity, and relatedness. Expected heterozygosity, observed heterozygosity, and inbreeding were higher in the fragments. Population structure analyses clearly differentiated between the populations, with PNP forming one cluster, while the fragmented forest was genetically structured, with considerable admixture. EEMS-derived maps of spatial variation in gene flow showed higher gene flow in the fragmented landscape, and lower gene flow in and around PNP. With kinship analyses, we identified dispersal events across the matrix, between fragments and from PNP into the fragmented landscape. Contrary to the accepted paradigm that habitat loss and fragmentation restrict movement and create isolated sub-populations, our results suggest that increasing levels of forest fragmentation force black howler to move through the landscape more, not less. The fine-scale genetic structure in the fragmented landscape indicates that black howlers preferentially remain and reproduce in higher-quality fragments, whereas those in smaller, more isolated fragments are obliged to disperse across the matrix for reproductive opportunities. Our results highlight the complex behavioral and genetic consequences of forest fragmentation for arboreal primates.

8 - Integrating genetic and habitat assessments for natterjack toad conservation

Karen Cox(1), Jeroen Speybroeck(1), An Van Breusegem(1), Leen Verschaeve(1)
1-Research Institute for Nature and Forest

The natterjack toad (*Epidalea calamita*) is endemic in Europe and is listed as a red-listed endangered species in Flanders, northern Belgium. To address this conservation concern, a species protection program has been implemented with the aim of fulfilling regional Conservation Objectives (G-IHD) through a comprehensive action plan. However, significant knowledge gaps remain, particularly regarding the genetic makeup of natterjack toad populations in Flanders.

In this study, we conducted genetic assessments of several natterjack toad populations, building upon previous investigations from 2014. Our findings shed light on the genetic structure, diversity, effective population size, and connectivity among different populations. These genetic insights were augmented by habitat assessments, providing a holistic understanding of the species' conservation status.

Our analysis revealed that several populations exhibit low genetic diversity, often associated with small and isolated habitats. Without intervention, these populations face an uncertain long-term viability, exacerbated by recent population declines. Conversely, larger populations in contiguous moorland areas demonstrate higher genetic diversity, suggesting their importance within a broader metapopulation framework.

Based on our integrated genetic and habitat assessments, populations were categorized as either favourable or unfavourable for conservation efforts. Management recommendations tailored to each population's specific needs were formulated, with a critical evaluation of past translocation efforts. Additionally, we present a comprehensive translocation plan for the natterjack toad in Flanders, identifying suitable source populations and potential reintroduction sites based on our assessments.

9 - Driving Conservation through Genomics: Australian Government's Role and Impact

Eilish McMaster(1, 2)
1-University of Sydney, 2-Botanic Gardens of Sydney

The state government of New South Wales (NSW), Australia, has implemented an advanced approach to conserving threatened plant species, incorporating conservation genomics as a key component. As a scientist involved in this initiative, I conduct conservation genomics research on endangered species and collaborate with field practitioners to develop effective management strategies.

In this presentation, I will provide an overview of the NSW government's organizational structure for integrating conservation genomics into its conservation framework. This will include outlining the roles of governmental entities and research institutions in the implementation of this strategy.

Additionally, I will discuss the cost-effectiveness of utilizing conservation genomics within the NSW conservation program. By leveraging genomic technologies, we optimize resource allocation and prioritize conservation actions, resulting in efficient use of funding and resources.

Finally, I will present case studies illustrating various management outcomes informed by conservation genomics. These examples will demonstrate how genomic insights have contributed to evidence-based management decisions and improved conservation outcomes for threatened plant species across NSW.

Attendees will gain insights into the operational framework, economic considerations, and practical applications of conservation genomics within a government-led conservation strategy. This presentation underscores the significance of interdisciplinary collaboration and data-driven approaches in addressing challenges related to biodiversity conservation.

10 - Genetic indicators for nature monitoring (GINAMO)

Christina Hvilsom(1), Joachim Mergeay(2), Linda Laikre(3), Gernot Segelbacher(4), Julia Geue(4), Joost Raeymaekers(5), Anja Westram(5), Alex Kopatz(6), Myriam Heuertz(7), Peter Galbusera(8), Cristiano Vernesi(9), Pauline Garnier-Gere(7), Marie-Gabrielle Harribey(7), Kristin Leus1, Christina Ritzl(1), Ian Brown(3), Francois Ehrenmann(7), Leslie Noble(5), Frederic Raspail(7), Anne-Sophie Archambeau(10), Sara Cousins(3), Annica Sandström(11), Carina Lundmark(11), Sean Hoban(12)
1-Copenhagen Zoo, 2-Research Institute for Nature and Forest, Own Capital, 3-Stockholm University, 4-University of Freiburg, 5-Nord University, 6-Norwegian Institute for Nature Research, 7-INRAE, 8-Royal Zoological Society of Antwerp, 9-Fondazione Edmund Mach, 10-MNHN, 11-Luleå university of technology, 12-The Morton Arboretum

Genetic diversity within species is key to maintaining adaptive potential and ecosystem resilience, and is one of the three pillars of biodiversity, but is widely ignored in both policy and management. In GINAMO, a Biodiversa+ funded project that started in March 2024, we follow a co-creation process to provide clear scientific guidelines and ready-to-use workflows to estimate genetic indicators. These indicators relate a) to a minimum effective population size, Ne, of 500, with Ne being an essential biodiversity variable enabling the quantification of genetic diversity loss, and b) to maintain genetically distinct populations within species. In GINAMO we first will determine best practices to obtain accurate and robust Ne estimates for species with reference DNA-based data. For species without such data, we will develop best practices to estimate Ne from proxies with publicly available data sources (e.g population size counts, occurrence data, and earth observation data). We co-decide from the outset with the stakeholder community for an optimal integration of all resources produced (i.e. databases, scripts, and guidelines) to meet their concerns, reporting duties and monitoring needs. This co-creation process will be evaluated and will strongly benefit from the multidisciplinary research team, including both natural and social scientists.

11 - From Herbarium Specimens to Contemporary Surveys: Tracing the Population Dynamics and Performance of Endangered Plant Species in Central Germany

Weronika Makuch(1,2), Isabell Hensen(1,2), Sabrina Träger(1,2), Christoph Rosche(1,2), Christine Römermann(2,3), Jochen Müller(4), Marcus Lehnert(2,5)
1-Martin Luther University Halle Wittenberg, Geobotany and Botanical Garden, Halle, Germany, 2-German Centre for Integrative Biodiversity Research (iDiv), Leipzig, Germany, 3-Friedrich Schiller University Jena, Institute of Ecology and Evolution, Jena, Germany, 4-Herbarium Haussknecht, Friedrich Schiller University, Jena, Germany, 5-Martin Luther University Halle Wittenberg, Herbarium, Halle, Germany

Anthropogenic activities are significantly contributing to a rapid decline in global plant biodiversity, primarily driven by extensive land-use changes. Factors such as habitat fragmentation, climate alterations, nitrogen overfertilization and the resulting changes in inter-specific competition are among the main causes of plant species extinction. To protect endangered species, population ecological studies are essential, which not only aim to assess the current state of populations, but also to investigate changes in their distribution over time and space. Since there is often a lack of long-term studies, herbarium records are a valuable source for tracking these changes. In this study, we analyze three endangered plant species (*Antennaria dioica, Viola pumila, and Omphalodes scorpioides*), which have different habitat preferences (dry grassland, riparian forest, and bog meadow, respectively) to examine the current status and performance of populations still extant in central Germany. Our results suggest that of several population factors categorized into four groups (population size, climate, soil parameters, and surrounding vegetation density), the number of individuals or patches, Palmer Drought Severity Index (PDSI), soil depth, and percentage of open ground exert the most significant influence on plant performance. However, the nature and strength of these correlations between population factors and traits vary considerably across species. Furthermore, the analysis of herbarium specimen spanning the last 200 years clearly shows the urgency of the problem of species extinction because for our three species, the loss of populations over the time could be shown. It underlines the imperative role of species conservation and the need of initiatives such as conservation breeding and reintroduction, which could lead to success even in small populations.

12 - ORG.one: supporting rapid sequencing of any endangered species, anywhere, by anyone

Kara Dicks
ORG.one, Oxford Nanopore Technologies

Understanding, mitigating, and reversing biodiversity loss requires a broad range of tools and approaches. There is increasing recognition of the importance of genetic diversity as a vital component of biodiversity and on the utility of genetic tools, such as DNA barcoding and eDNA, to assess and monitor species and communities. Yet, lack of access to genomic tools to generate the data required to guide and improve conservation efforts can prohibit their utility. ORG.one is a project designed to support equitable, faster, and more localised sequencing of endangered species.

Existing projects to sequence endangered species have made good progress; however, they can be limited by complex workflows and the requirement to send samples to centralised, often overseas, locations for sequencing. ORG.one enables biologists to rapidly study those species close to the sample's origin, using the latest sequencing approaches to develop high-quality de novo draft genome assemblies. In this talk, I will discuss how these genomes are forming the foundations for developing biodiversity monitoring efforts, identifying conservation challenges (e.g. hybridisation) and solutions (e.g. disease resistance alleles), and upskilling a community of conservation geneticists. With its partners, ORG.one is focusing on delivering and demonstrating the impactful benefits of genomics for conservation.

13 - Disentangling the evolutionary history of Howler monkeys at their northernmost distribution: population genetics and microbiome patterns

Ella Vázquez-Domínguez(1), Diego Zubillaga(1), Brenda Solórzano(1), Luisa Falcón(1)
1-Universidad Nacional Autónoma de México

The mantled (*Alouatta palliata mexicana*) and the black (*A. pigra*) howler monkeys wild populations represent the northernmost distribution of non-human primates in America, both critically endangered. Little is known about the gut microbiome in wild populations of New World monkeys. Our aims were twofold, to assess the genetic diversity, population structure and inbreeding of the two species and of hybrid individuals from a contact zone along their distribution in México (with microsatellite loci); and to evaluate the diversity and abundance of their gut bacterial communities (with the 16S rDNA V4 region). We used non-invasive sampling (fresh feces) of clearly differentiated individuals. We demonstrate negative genetic effects on both species because of isolation, fragmentation, and small effective population size, rendering significant differentiated genetic clusters, along with reduced nuclear genetic diversity, limited gene flow, and inbreeding. These patterns are associated with concurrent processes of historical dispersion, contemporary landscape changes and hybridization. Interestingly, results suggest that host's phylogeny is the main factor in the structure of their gut microbiome, while geographic distribution and diet are also important, where microbiome abundance and diversity patterns are consistent with their diet. The most abundant microbial Phyla are shared among species but differing at finer taxonomic levels and compared with hybrids, while significant differences by sex were identified in *A. pigra* but not in *A. palliata*. We documented the first overall microbiome data for these Mexican primates that, jointly with the population genetic data, provide crucial information for the maintenance of their adaptive diversity and long-term survival.

14 - Demographic histories of two endangered warty pigs in the Malay Archipelago

Anna Schleimer(1), Alain C. Frantz(2), Lorraine Richart(3), Jörg Mehnert(4), Gono Semiadi(5), Wirdateti Wirdateti(6), Johanna Rode-Margono(7), Michel Mittelbronn(3), Stuart Young(8), Frank Drygala(4)

1-Fondation Faune- Flore, Luxembourg, Luxembourg, 2-Musée National d'Histoire Naturelle, Luxembourg, Luxembourg, 3-Luxembourg Institute of Health (LIH), Luxembourg, Luxembourg, 4-Association for Nature and Biodiversity (ANB), Frankfurt am Main, Germany, 5-Research Centre for Applied Zoology, National Research and Innovation Agency, Cibinong, Indonesia 8Research, 6-Research Centre for Ecology and Ethnobiology, National Research and Innovation Agency, Cibinong, Indonesia, 7-IUCN SSC Wild Pig Specialist Group, Köln, Germany, 8-The North of England Zoological Society/Chester Zoo, Upton- by- Chester, Chester, UK Correspondence

The biodiversity of the Malay Archipelago is the product of the region's rich biogeographical history with periods of island connectivity and isolation during the Pleistocene glacial cycles. Here, the case of two endemic suid species, the Javan (*Sus verrucosus*) and Bawean (*S. blouchi*) warty pigs, was used to illustrate how biogeographic processes and recent anthropogenic pressures can shape demographic histories with significant implications for species conservation. We employed genome-wide single nucleotide polymorphisms from the Porcine SNP60 v2 BeadChip to assess interspecific genetic differentiation, to estimate divergence times and to perform demographic model selection.

In contrast to the hypothesis of recent divergence during the last glacial maximum, *S. blouchi* was found to have diverged from *S. verrucosus* at least 166k years ago following a founder event. The contemporary *S. blouchi* population was characterized by a recent bottleneck that reduced the effective population size to less than 20. The genomic assessment supports the single species status of *S. blouchi*, as was previously proposed based on morphometrics. The demographic history of S. verrucosus showed evidence of secondary contact with the sympatric banded pig (*S. scrofa vittatus*) that colonised Java 70 k years ago.

While the Javan and Bawean warty pigs have persisted throughout the Pleistocene climatic oscillations, contemporary pressures from human activities threaten their survival and immediate action should be taken to grant legal protection to both *S. verrucosus* and *S. blouchi*. This study highlighted the use of demographic history modelling using genomic data to identify evolutionary significant units and inform conservation.

15 - Population genetics for conservation of spadefoot toads, Pelobates fuscus, in Central Europe

Caroline Mouton(1), Karolin Eils(2, 3), Johan Auwerx(1), Paolo Eusebio Bergó(4), Wilbert Bosman(5), Angelica Crottini(6), Julia Dayon(7), Christophe Eggert(8), Christian Göcking(2), Wolf-Rüdiger Grosse(9), Werner Kloas(3), Spartak Litvinchuk(10), Katarina Ljubisavljevic(11), Claude Miaud(7), Norbert Menke(2), Maria Ogielska(12), Jeroen Speybroeck(1), Loïc van Doorn(1), Matthias Stöck(3), Richard Struijck(5), Joachim Mergeay(1)
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Worldwide, amphibian species are experiencing rapid population declines due to various factors such as habitat loss, urbanization and climate change. Despite extensive legislation to ensure conservation, European amphibians like the common spadefoot toad (*Pelobates fuscus*) exhibit alarming declines. Our study used newly developed microsatellite loci to investigate the genetic diversity and structure of this fossorial amphibian across most of its range, focussing on 66 populations. Using microsatellite markers, we revealed contrasting patterns of genetic diversity across the *Pelobates fuscus*' range, indicating that especially North-Western European populations appear genetically impoverished. Three major groups were revealed using clustering approaches, reflecting postglacial colonization patterns. The findings emphasize the dire conservation status of common spadefoot toad, underscoring the need for urgent conservation efforts. To address the ongoing declines and to safeguard the species, the significant importance of continued genetic monitoring and potential translocations is highlighted.

16 - Optimizing eDNA metabarcoding techniques for assessing arthropod communities in tree-related microhabitats

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1-Chair of Wildlife Ecology and Management, Institute of Forest Sciences, Faculty of Environment & Natural Resources, University of Freiburg, 2-Agricultural Sciences and Resource Management in the Tropics and Subtropics (ARTS), Faculty of Agriculture, University of Bonn

Understanding the diversity and ecological roles of arthropods within tree-related microhabitats (TreMs) is crucial for ecosystem management and conservation. We here aimed to identify the most effective eDNA metabarcoding approach for capturing ecologically important arthropod species primarily inhabiting the near-ground level TreMs. This study evaluated the use of COI and 16s primers for eDNA metabarcoding and compared direct and indirect eDNA sampling methods, including Lying Deadwood Sediment sampling (LDS), Standing Deadwood Sediment sampling (SDS), Soil Sampling (SS), and Tree Surface Roller Sampling (TSRS). Our results indicate significant biases and challenges, particularly in primer selection, with COI outperforming 16s in taxonomic resolution for most arthropod taxa. Moreover, direct sampling from sediments revealed a higher abundance of fungi than arthropods, impacting diversity estimates. We also observed habitat-specific preferences among arthropods, with certain sampling methods capturing distinct taxa. Despite similarities in community composition among sampling sites related to deadwood, high beta diversity suggests dissimilar species compositions across habitats. Our findings underscore the importance of careful method selection and primer validation in eDNA metabarcoding studies and provide insights into the complexity of arthropod communities in TreMs. These findings advance monitoring techniques for forest ecosystems and inform conservation efforts to preserve arthropod diversity in TreMs.

17 - Influence of an urbanized environment on the diet of wild vervet monkeys assessed by DNA metabarcoding

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Due to increasing habitat fragmentation and conversion, the range of wild vervet monkeys in urban areas has widened considerably, potentially leading to the presence of anthropogenic food in their diet. Due to their generalist and opportunistic feeding behaviour, studying urban vervet monkeys' diet is important to help understanding the impact of urban ecosystems on their foraging behaviours. However, accurately determining the variety of food types consumed by omnivorous species may in cases be complicated by mere observations. Consequently, environmental DNA (eDNA) based techniques provide complementary study options that can result in more complete assessments. In this study, we determined urban vervet monkeys' dietary components using DNA metabarcoding of faecal samples. 448 samples were analysed from 2 different monkey groups of respectively 23 and 21 individuals, collected during a 4-month period in an eco-estate in South Africa. We aim to define the proportion of natural food versus human food items ingested, and to compare diet variability between the two groups of monkeys, as well as between different sex and age classes.

18 - Large efective size as determinant of population persistence in Anostraca (Crustacea: Branchiopoda)

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The fairy shrimp *Branchinectella media*, because of its passive dispersal capacity and scarce and irregularly distributed habitats (temporary saline aquatic systems), is an intriguing organism from a population genomics and conservation perspective. Stochasticity of dispersal events and the irregular distribution of its habitat might lead to low levels of population connectivity and genetic diversity, and consequently, populations with limited persistence through time. Indeed, by using genomic data (SNPs), we found a strong genetic structure among some of the geographically isolated Iberian populations of *B. media*. Interestingly, we also obtained high estimates of effective population sizes. Lack of suitable habitat between populations (absence of a "stepping stone" network) and strong genetic differentiation suggest limited dispersal success in *B. media*. However, the high effective population sizes observed ensure persistence of *B. media* populations against genetic stochasticity (genetic drift). These results indicate that rescue-effect might not be essential for population persistence if they maintain high effective population sizes able to hold adequate levels of genetic diversity. Should high population sizes be reported in other low dispersing Anostraca, one might be optimistic with regard to their conservation status and fate, provided that their natural habitats remain undisturbed.

19 - States of eDNA (membrane-bound, dissolved and adsorbed) control its fate and transport at a watershed level

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Environmental DNA (eDNA) analysis holds significant promise as a tool for biodiversity monitoring, yet it faces critical challenges including the potential for false positives and negatives, and limitations in revealing population size and structure. To address these challenges, it is essential to understand the ecology of eDNA—specifically, its persistence and transport mechanisms in the environment. The degradation of eDNA is influenced by various factors including UV light, temperature, pH, and biological activity, while its transport is primarily dictated by the hydrological conditions of the landscape. The state of eDNA i.e. whether the eDNA is in its membrane-bound, dissolved, and adsorbed form, and the influence of its state on the fate and transport remains understudied.

This presentation will discuss results from extensive laboratory and field experiments that: 1) examine how the states of eDNA impacts its degradation, 2) demonstrate methods for sorting and analyzing different eDNA states from a single sample, and 3) present a field study of 729 state-sorted samples from 50 streams across eight Swiss watersheds, which explores variations in the biodiversity signals via metabarcoding from the three different states along these watersheds. Additionally, the presentation will consider whether lakes act as reservoirs for eDNA shed throughout a watershed and discuss strategies for effectively sampling lakes to gather comprehensive biodiversity data at the watershed level. This research highlights a pathway to enhance the reliability and reproducibility of eDNA analysis for biodiversity monitoring.

20 - Whole genome sequences of Asian elephants point towards subspecies status for the Bornean elephant

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This study presents whole-genome sequencing (WGS) data from mostly Asian elephants living in European zoos with a wild born origin, covering the distribution range of Asian elephants, aiming to validate their subspecies designation and address taxonomic ambiguities, particularly regarding Bornean and Sri Lankan elephants. Analysis reveals clear population structure with relatively recent splits, delineating three distinct genetic clusters: Borneo, Sumatra, and Mainland, with Sri Lanka forming an additional separation. While three clusters align with recognized subspecies, Borneo is currently identified as an Evolutionary Significant Unit (ESU), experiencing recent severe bottlenecks. However, this study is estimating the divergence time between Bornean and Sumatran elephants around 170,000 years ago, which is in line with earlier results. Hypotheses on Bornean elephants' origin—native dispersal or human introduction—are explored. Sri Lankan elephant divergence from the Mainland is estimated at 48,000 years ago. In our study, the Sri Lankan elephants cluster mostly with Myanmar elephants, possibly linked to historical trade networks. Furthermore, genetic management strategies for ex-situ populations are discussed, emphasizing the need for cluster-specific conservation measures. Despite data limitations and remaining questions, this study underscores the importance of recognizing Bornean elephants as a distinct subspecies, informing conservation strategies and highlighting avenues for further research.

21 - GINAMO - Genetic Indicators for NAture MOnitoring

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Genetic diversity within species is key to maintaining adaptive potential and ecosystem resilience, and is one of the three pillars of biodiversity, but is widely ignored in both policy and management, due to knowledge and implementation gaps. Two indicators in the Kunming-Montreal Global Biodiversity Framework are appropriate for monitoring and reporting on genetic diversity. These indicators relate a) to a minimum effective population size, Ne, of 500, with Ne being an essential biodiversity variable enabling the quantification of genetic diversity loss, and b) to maintain genetically distinct populations within species. In GINAMO, we follow a co-creation process to provide clear scientific guidelines and ready-to-use workflows to estimate genetic indicators that are understood and embraced by end users. In GINAMO we will determine best practices to obtain accurate and robust Ne estimates for species with reference DNA-based data. Genetic data will help designing realistic evolutionary scenarios for simulations, to understand how spatial distributions, life history traits, data quantity and types, sampling strategies and statistical methods affect Ne estimates. For species without DNA-based data available, GINAMO will develop best practices to estimate Ne from proxies with publicly available data sources (e.g. population size counts, occurrence data in observation portals, and relevant terrestrial habitat properties generated by earth observation data). A key component in GINAMO is to co-create from the outset with the stakeholder community in five European countries for an optimal integration of all resources produced from GINAMO activities (i.e. databases, scripts, and guidelines) to meet their concerns, reporting duties and monitoring needs and resources. These five countries will serve as pilots for wider global implementation. Standardised and automated workflows will be co-created for assessing genetic indicators on various transboundary geographical scales, enabling routine integration of genetic criteria and indicators into biodiversity monitoring and assessments, from policy on regional, national and EU levels, to global conventions and obligations.

22 - Genetic patterns of a grassland plant across a fragmentation gradient of semi-natural grasslands in Europe

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Habitat fragmentation is one of the major threats to European ecosystems and often leads to increased isolation of populations, which is expected to result in genetic impoverishment and reduced resilience to environmental changes in populations inhabiting fragmented landscapes. In particular, semi-natural grasslands are suffering from human-induced habitat fragmentation caused by intensification or abandonment of management. Grassland plant species that depend on external vectors for pollen and seed dispersal and exhibit a specific mating system for successful reproduction are particularly affected. In our study, we investigate the population genetics of the heterostylous, self-incompatible and insect-pollinated grassland plant *Primula veris* using RADseq. Samples were collected in five European countries spanning a wide range of the species' distribution. In each country, samples were taken from contrasting landscapes of fragmented vs. connected semi-natural grasslands, creating a gradient of grassland fragmentation sites on a European scale. We expect to find reduced genetic diversity in populations inhabiting fragmented landscapes compared to those in connected ones, depending on the landscape history. Genetic differentiation will be more pronounced among fragmented populations with the effect becoming stronger towards the margin of the species' distribution range. We hypothesize that those patterns are driven by a decline in potential mating partners in fragmented populations, possibly leading to an overall decrease in population size and individual performance. Our study will provide valuable insights to the consequences of ongoing habitat fragmentation on a European scale. We aim to contribute to develop new and reassess existing management strategies on a national and international scale to create, preserve and strengthen resilient populations.

23 - Best practices for genetic and genomic data archiving

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Genetic and genomic data are collected for a vast array of scientific and applied purposes. Despite mandates for public archiving, data are typically used only by the generating authors. The reuse of genetic and genomic datasets remains uncommon because it is difficult, if not impossible, due to non-standard archiving practices and lack of contextual metadata. But as the new field of macrogenetics is demonstrating, if genetic data and their metadata were more accessible and FAIR compliant, they could be reused for a vast array of purposes including an abundance of conservation applications. Previously published data could be irreplaceable baselines for genetic monitoring, collated multispecies data could guide large scale conservation initiatives (e.g. protected area design), and generally more accessible data would allow genetic information to be used by conservation managers in day-to-day decisions. In this talk, I will briefly discuss the main challenges with existing genetic and genomic data archives and give a detailed overview of our proposed best practices for archiving genetic and genomic data. Recognising that this is a longstanding issue due to little formal data management training within the fields of ecology and evolution, I will also highlight steps that research institutions and publishers could take to improve data archiving.

24 - Potential for evolutionary responses to climate change in the tropical tree species Dicorynia guianensis

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Essential ecosystem services are provided by rainforests, which play a pivotal role in sustaining life on Earth. Habitat and biodiversity loss is an imminent threat to tropical rainforest regions worldwide because of agricultural development, mining, overexploitation of timber, and climate change. To ensure their continued adaptability and resilience in a changing world, it is imperative to preserve genetic diversity within tropical rainforest species. Within the smaller context of French Guiana, the specters of climate change, affecting temperature and rainfall, pose unprecedented challenges to this ecosystem, including on the hyperdominant tree species, *Dicorynia guianensis* (Fabaceae). The genetic data suggests a significant differentiation of populations in the western part of French Guiana and a demographic history of populations that is regionally variable. New genome resequencing data allows us to examine regional-scale genomic signatures of adaptation to climate and soil in this drought-sensitive species and to model genetics-informed distribution range projections under future climate regimes. The local-scale family structure will be better understood with High-throughput SSR-Seq data, which may explain differences between sites in colonization dynamics and local-scale spatial genetic structure. We can develop conservation strategies that can adapt to the challenges posed by future climate scenarios by understanding genetic responses to climate change.

25 - The influences of paleogeography on the diversification and genetic diversity of Sulawesi tarsiers *(Tarsius)*

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The island of Sulawesi, within the Wallacea region of the south Pacific Ocean, is of profound and ongoing research interest due to its unique species assemblages and high proportion of endemic lineages. Situated at the geologic intersection of continental shelves, the biodiversity of Sulawesi consists of taxa with Asian evolutionary origins and taxa with Australian evolutionary origins. Additionally, the complex paleogeographic history of Sulawesi, along with historical sea-level fluctuations resulting in ephemeral land bridges within the proto-Sulawesi archipelago, has shaped the diversification of endemic taxa. Sulawesi tarsiers, small nocturnal primates, are emblematic of the biodiversity of this region, having diversified into 12 described species. The genus *Tarsius* is known only to Sulawesi and the surrounding islands, and its species are listed as either data deficient or of conservation concern by the IUCN. Past studies of Sulawesi tarsiers have highlighted a complex history of isolation, dispersal, and secondary contact among tarsier lineages which remains cryptic in many aspects and requiring of further study. Representing the first genomic-scale study of tarsiers from across Sulawesi, we used a reduced-representation genomic technique (Mig-Seq) to analyze 300 tarsier individuals from 32 sites across the island. In modeling ancestral ranges of diversifying tarsiers across Sulawesi we are coming to better understand how the diversification of tarsiers can be linked to the geologic history of the region, and how this contributed to the varying sizes of extant species ranges. The refined phylogeny enables us to gain detailed insight into the interspecific and intraspecific genetic relationships of extant Sulawesi tarsiers and understand the processes that led to the interesting pattern where species in close geographic proximity are not necessarily closely related. Our wider analyses of species identities and our analyses of population bottlenecks and gene flow contribute to our understanding of how the biogeography and genetic diversity of tarsiers has been shaped by the changing topography of Sulawesi and, further, is critical to prioritizing conservation efforts.

26 - The Subantarctic Rayadito *(Aphrastura subantarctica)*, a new bird species on the southernmost islands of the Americas

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We describe a new taxon of terrestrial bird of the genus *Aphrastura* (rayaditos) inhabiting the Diego Ramírez Archipelago, the southernmost point of the American continent. This archipelago is geographically isolated and lacks terrestrial mammalian predators as well as woody plants, providing a contrasted habitat to the forests inhabited by the other two *Aphrastura* spp. Individuals of Diego Ramírez differ morphologically from *Aphrastura spinicauda*, the taxonomic group they were originally attributed to, by their larger beaks, longer tarsi, shorter tails, and larger body mass. These birds move at shorter distances from ground level, and instead of nesting in cavities in trees, they breed in cavities in the ground, reflecting different life-histories. Both taxa are genetically differentiated based on mitochondrial and autosomal markers, with no evidence of current gene flow. Although further research is required to define how far divergence has proceeded along the speciation continuum, we propose A. *subantarctica* as a new taxonomic unit, given its unique morphological, genetic, and behavioral attributes in a non-forested habitat. The discovery of this endemic passerine highlights the need to monitor and conserve this still-pristine archipelago devoid of exotic species, which is now protected by the recently created Diego Ramírez Islands-Drake Passage Marine Park.

27 - Genetic monitoring in four keystone tree species, assessed in protected areas

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Genetic monitoring, the quantification of temporal changes in population genetic variation and structure, elucidates processes that maintain genetic variation in natural populations and introduces prognosis in the management and conservation of genetic resources. Genetic monitoring is vital in evaluating the maintenance of genetic diversity in natural populations and the impacts of environmental change. We applied genetic monitoring in natural forest tree populations mostly located in protected areas, based on the gene-ecological approach (assessment of genetic drift, gene flow, natural selection). We employed two methods: evaluation at different time intervals and evaluation of different age cohorts at the same time, using the same SSR and SNP markers across evaluations. Temporal evaluation in a time frame ranging from 5-16 years, included *Abies borissi regis, Quercus petraea* and *Q. robur* and a total of 25-200 samples. The simultaneous evaluation of different age cohorts was employed in *A. borissi regis* and *Alnus glutinosa*, assuming no effect of different ontogenetic state and competition status. We used 11 SSRs and 140 SNPs, as well as 450 (250 mature, 200 juvenile) plants in *A. borissi regis*. In *A. glutinosa*, we used 20 nSSRs and 600 (300 mature, 300 juvenile) plants. The temporal difference between cohorts was on the average 100 years for *A. borissi* regis and 50 years for *A. glutinosa*. Both temporal evaluation and simultaneous evaluation of different age cohorts, showed no statistically significant differences in genetic parameters, although in *Quercus* spp. genetic diversity declined to some extent. In hybrid fir, we detected some demographic instability in the recent assessment that might though be due to sampling in a non-masting year.

28 - Shedding Light on Historical Phytoplankton Biodiversity Trends in the Baltic Sea

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The reconstruction of past environments and their biodiversity is a challenging but important research field in time of global change. Sedimentary ancient DNA (sedaDNA) as molecular remains of past organisms is becoming increasingly prominent to reconstruct past marine ecosystems over time and, therefore, advantageous to investigate the impact of climate change and the anthropogenic pressures. Of special interest in sedaDNA studies are phytoplanktonic organisms that play a key role in the marine food web. Most sedaDNA metabarcoding studies have focussed on community composition and less on community abundance trends due to methodological biases. To address these methodological limitations, we investigated the reliability of abundance trends of sedaDNA metabarcoding by comparing them to long-term observation-based monitoring results. Here, the Baltic Sea serves as an exemplary “time machine” due to its extensive time series data and its facing multiple anthropogenic pressures for decades. Here, we demonstrate that metabarcoding can be used as a reliable tool to investigate long-term trends. However, careful consideration of methodological biases is essential for accurate interpretation of results at every location and taxonomic group. Confirming the reliability of sedaDNA for long-term data not only enhances our understanding of past marine ecosystems but also improves the development of new strategies for long-term biodiversity management in the face of global change.

29 - Monitoring genetic diversity in the oceans from space

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While the Convention on Biological Diversity advocates for better monitoring of genetic diversity, estimates of genetic diversity remain available only for a handful of wild and domesticated species. The main reason for this gap is that genetic diversity is directly measured via DNA sequencing, which is a time-consuming and expensive task—especially in environments that are difficult to sample such as our oceans.

Satellite earth observations offer a potential solution, since the remotely sensed characteristics of marine ecosystems (e.g., habitat size, bathymetric profiles, environmental conditions) are related to the spatial patterns of genetic diversity of species living in these ecosystems. Since earth observation is available worldwide in near-real time, this technology could be the foundation for rapid and cost-effective monitoring of changes to oceanic genetic diversity.

We are testing this approach on reef building corals, pillars of marine biodiversity undergoing a rapid decline under global change. We leverage public satellite-derived datasets to describe oceanic conditions at coral reefs worldwide. A database of coral DNA sequences—including more than 1,000 georeferenced samples—is then used to measure patterns of genetic diversity in coral populations around the world. These genetic data are finally used to train probabilistic models predicting genetic diversity from earth observations.

If demonstrating sufficient predictive power, our model could be used to monitor changes in the genetic diversity of corals worldwide without DNA sequencing. This *Genes from Space* framework (https://teams.issibern.ch/genesfromspace/) is currently being tested in other systems—on sea and land—and could open new avenues in biodiversity conservation.

30 - Using non-invasive genetic techniques to monitor Scimitar-horned oryx post-release in Chad

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Scimitar-horned oryx (SHO) *Oryx dammah* were once widespread in Chad's Ouadi Rimé-Ouadi Achim Game Reserve, one of the world's largest protected areas at over 78,000 km2. However, in the 1980's the population began to decline rapidly, largely due to overhunting. In 2000, the species was declared 'Extinct in the Wild' by the International Union for the Conservation of Nature (IUCN) Red List. In 2016 the first group of captive SHO were released, and as of 2023 over 285 SHO have been re-introduced resulting in wild herd numbers increasing to more than 600 individuals. SHO has since been reclassified as 'Endangered' by IUCN Red List.

We examined the diet and microbiome of both captive, pre-release and recaptured, post-release individuals in Chad across two years using non-invasive genetic techniques. Microbiome data was generated from a mixture of faecal samples collected from individuals during November 2021 and March 2022. Significant differences in the microbiome between captive and recaptured individuals were observed. Captive individuals had greater microbiota species diversity and richness than recaptured individuals. Additionally, significant differences in the microbiome between recaptured individuals across years was also observed which may be age or season related. Diet data were also generated from faecal samples collected from recaptured individuals during November 2021 and March 2022. Significant differences in diet were observed between years, with individuals in 2022 having a more diverse diet than individuals sampled in 2021. These differences in diet may be driven by season or age or a combination of both. Following this proof of concept, further work is underway to investigate these findings in more depth.

31 - Tracing the invasion: Using eDNA to track the spread of *Dreissena* mussels

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The invasion of non-native species is a major cause of biodiversity loss and ecosystem instability worldwide. The two *Dreissena* mussels, quagga (*Dreissena rostriformis bugensis*) and zebra (*Dreissena polymorpha*), are highly invasive freshwater bivalves that have spread rapidly across Europe in recent decades. To assess the distribution of zebra and quagga mussels within and between aquatic ecosystems, we use environmental DNA (eDNA) from sediments (sedDNA).

In our study, we use eDNA to combine the detection of dreissenid mussels in sediment cores and surface sediments to reveal the time of colonisation and spatial distribution. Sediment cores are used as an ecological archive to investigate the invasion history of the mussels. In a sediment core from Lake Constance, zebra mussel DNA is present in older sediment layers than the first mussel discovery, suggesting that sedDNA holds promise for early detection of *Dreissena* mussels. To quantify quagga mussel DNA in Lake Constance, we furthermore used a ddPCR assay. Surface sediment collected during the quagga monitoring campaign of the SeeWandel project in October 2022 was used. A total of 54 sites around the lake were sampled using a Ponar sediment grabber. The density of the quagga mussels was measured and the biomass per m2 was quantified. For genetic quantification, the density and biomass data were used for comparison and reference. The distribution of the mussel could be described with the genetic quantification. This shows the potential of sedDNA for invasive species monitoring.

Our future goal is to use sedDNA to obtain genomic data that will provide us with information on the population structure of the dreissenid mussels in multiple perialpine lakes, both in the past and in the present. This will enable us to identify populations at different times and compare their genetic diversity and differentiation. This will help to understand historical and current invasive patterns of these bivalves.

32 - Genetic Close-Kin Mark-Recapture as a Method for Assessing European Smelt Stock

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Sustainable fisheries management is crucial for maintaining healthy fish populations and ensuring long-term resource availability. The European smelt (*Osmerus eperlanus*) is a valuable species in both German rivers and the North Sea, but assessing its stock accurately remains challenging. Traditional methods often suffer from uncertainty due to limited data availability and complex population dynamics.

The CKMR (Close-Kin Mark-Recapture) method offers a promising alternative for estimating abundance and other demographic parameters using genomic information. It leverages kinship relationships determined from genetic samples to infer population size, survival rates, and connectivity. The underlying concept is straightforward: in larger populations, finding relatives becomes less likely, while smaller populations exhibit a higher likelihood of kinship. Recent refinements in statistical methodologies and advances in high-throughput sequencing have enhanced the efficiency of genomic analyses in stock assessment. CKMR can theoretically be applied to almost any species, provided sufficient knowledge of the organism’s life history and an adequate population size. For the European smelt, CKMR holds promise as a tool to assess stock dynamics and reduce uncertainty.

In our study, we applied CKMR to European smelt populations in German rivers and the North Sea. By analysing genetic samples, we are aiming to estimate abundance, population trends, and connectivity. Our preliminary findings suggest that CKMR can provide valuable baseline data for previously unassessed fish stocks and enhance assessments of regularly evaluated populations.

33 - *Gladiolus palustris* in Switzerland: from genetics to practical actions

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Wetland and marshes species are particularly threatened by global warming and land-use changes, which increase population isolation and fragmentation and consequently impact their genetic diversity through genetic drift. The sword lily (*Gladiolus palustris,* Iridaceae) is a typical species of Western-Central European wetland ecosystems, and its decline in the European Union and Switzerland has prompted legal protection measures. Swiss populations have faced decades of poor maintenance and management (e.g. abandonment of litter mowing or premature mowing) in conjunction with habitat loss (e.g. land improvements and drainage) and are now small-sized and isolated. For instance, in the first mid-twentieth century, only one population of *G. palustris* was preserved in the canton of Geneva before restoration actions were taken. This species tends also to hybridize with *G. communis*, locally introduced in some wetlands, which can highly affect its genetic diversity. In this context, genetic analyses, using SSR and NGS sequence capture, have been carried out on different populations of *G. palustris* and *G. communis* in the cantons of Geneva, Zurich and Zug, to assess their genetic diversity and identify the origin of a newly found population in Geneva. The two types of markers gave similar results and allowed to trace the origin of the new population while confirming the identity and genetic structure of *G. palustris* across Switzerland. Such results provided key information to guide practical actions.

34 - Linkages Between Diet, Microbes, and the Flexible Forager: Metabarcoding Insights into Roe Deer Nutritional Ecology

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Roe deer are an abundant yet often overlooked species in Scottish deer management, comprising nearly two-thirds of Scotland's annual woodland cull. As successful generalist herbivores, the plasticity of roe deer diet facilitates their widespread distribution across diverse habitats in Scotland and more broadly in Europe. However, their impact on commercial forestry and the biodiversity of heavily browsed areas across Scotland highlight the need to understand the nutritional strategies promoting their flexible foraging. The rumen microbiome assists ruminant nutritional adaptation and may enable utilisation of varied diets, supporting overwinter survival. We analysed rumen content from 200 culled free-ranging roe deer across six sites in Scotland using DNA metabarcoding. Sequencing of ITS2 and rbcL markers was performed to characterise plants in the diet, and 16s rRNA elucidated the rumen microbiome. Our results reveal seasonal shifts in dietary plant taxa and rumen microbial diversity and community structure that differ across geographical sites. These findings demonstrate rumen microbial associations that likely promote dietary plasticity in roe deer and should yield ecological and applied insights to inform the management of this prominent yet overlooked Scottish herbivore.

35 - Environmental genomic time series from seasons to millennia: impacts of climate and humans - and tools for long-term biomonitoring

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The current biodiversity crisis, caused both by direct human impact on species and habitats, as well as anthropogenically induced changes in abiotic factors, is causing tremendous turnovers on species, genomic and ecosystem levels. Several threats such as habitat loss, overexploitation, pollution, invasive species, and climatic changes are acting in synergy - but in many cases, neither the relative roles of these drivers, the pace of change nor the pre-impact community of the ecosystem are well mapped or understood. Monitoring time series of biodiversity typically extend back only a few decades, are available only for some organisms and are relatively scarce, given the substantial efforts and long-term infrastructure that they require.

Analyses of environmental DNA can provide such time series with relative ease and include both previously under sampled seasons and places, as well as information about organisms from across the tree of life, including taxa that do not leave behind visible traces. Archives of environmental DNA, such as sediments, also offer a view on biodiversity that reaches back into the past. By investigating ancient environmental DNA (ancient eDNA), we can retrieve (pre-)historical information on ecosystems as well as uncover cryptic changes not visible in morphology. Depending on the preservation conditions, such records can be globally retrieved on scales from hundreds to thousands and millions of years. Thereby, they can deliver information on natural variability of ecosystems since the Pleistocene, as well as on the onset of human impacts and their diverse and long-lasting consequences for current ecosystems.

The integration of environmental DNA into the study of past and present ecosystems is rapidly progressing, but both its full potential and its limits are yet to be conclusively established. To most efficiently sample environments and correctly interpret results, we need a better understanding of the provenance and taphonomy of eDNA in different substrates. Through PCR-free shotgun sequencing, we can now increase our knowledge of the actual composition of the DNA in environmental samples and move to meta-taxonomic community analyses. At the same time, we can concentrate on an efficient utilization of this resource to inform conservation biology and devise simple measures that can be integrated into ongoing management efforts. In my talk, I will highlight how environmental genomic time series can contribute to conservation and management of ecosystems and species, which questions we can already answer and where we need a better understanding.

36 - GENSCOP: A new platform for the genetic analysis of threatened species

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Understanding the distribution of genetic diversity and species' taxonomic delineation is pivotal for targeted biodiversity conservation and restoration. In its biodiversity strategy and the corresponding action plan, Switzerland has committed itself to the preservation of the genetic diversity of native species. However, while multiple Swiss academic laboratories hold the expertise to carry out genetic studies and to interpret them with respect to conservation issues, they are not sufficiently connected to the community of conservation professionals and regional authorities for practical implementation. GENSCOP is a new platform, supported by the Swiss Federal Office for the Environment and four research laboratories of Swiss institutions (CJBG, WSL, UniZh, UniFR), that aims at linking geneticists, conservation practitioners, and authorities for a better and more efficient conservation of threatened species This platform will serve as a proof-of-concept project and will canalize the demands of national/cantonal offices and practitioners and link them to the expertise and resource availability of suitable laboratories. It will assure a scientific and professional guidance of studies by an expert commission, including data interpretation and translation into conservation recommendations. By doing so, GENSCOP will provide an interface between the scientists who produce the genetic data and interpret them in terms of conservation recommendations, the conservationists who want to conserve species and need input from genetics, and the national and cantonal offices which need to know how to invest their financial resources most efficiently to conserve threatened species. In the next two years, GENSCOP will carry out several case studies on threatened plant and fungi species, identified as a priority by cantons.

37 - The tale of *Erebia palarica* : implications of novel genetic insights for the conservation of an Iberian montane endemic butterfly

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1-Universidade da Coruña

The knowledge regarding the biology of *Erebia palarica* Chapman, 1905 (Lepidoptera, Nymphalidae) is scarce, a fact that may compromise its conservation management. Here, we present a multidisciplinary study that addresses the population, conservation and evolutionary genetics of this montane pollinator restricted to northwest Iberia.

First, we undertake the phylogeography of *E. palarica* by combining genetics, morphometrics and ecological niche modelling. As a result, we obtain the first estimates of the genetic diversity and structure of the species and reconstruct its evolutionary history in the context of Pleistocene glaciations. Second, we provide an insight into the census (Nc) and effective (Ne) population sizes of *E. palarica* from genetic and capture-release-recapture data gathered in Courel, a relatively isolated locality in NW Spain. The application of IUCN criteria to these results led us to suggest the "Vulnerable" category for this butterfly. Third, we study the speciation of *E. palarica* and its sister taxon*E. meolans* (Prunner 1789). We discuss the putative reproductive barriers between both species as stemmed from phylogeny, Wolbachia infection, karyotype, wing size and genitalia morphology, and describe a pattern of asymmetric reproductive character displacement in areas where both species coexist.

Altogether, our findings support the consideration of two Evolutionarily Significant Units (ESUs) for *E. palarica*, which should be prioritised in present and future conservation strategies: (1) the Cantabrian Mountains-Montes de León, as they represent the largest genetic reservoir for the species, and (2) the Galician sites, given their higher degree of isolation and putative limited Ne. Among the latter, the peripheral population of Queixa (SE Galicia) stands as a conservation priority due to its genetic and morphometric uniqueness.

38 - Indirect evidence for outbreeding depression upon assisted gene flow: Insights from past introductions of Oriental beech

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European beech (*Fagus sylvatica ssp. sylvatica*) is a keystone European forest tree with immense ecological value providing habitat for over 6000 species. Its distribution is mostly limited by water availability: recent extreme drought events increased beech mortality, crown dieback and growth decline across Europe. Beech forests' resistance to drought could increase by introducing new alleles from more drought exposed regions of the species range, such as some parts of the Mediterranean or Minor Asia, where its sister subspecies Oriental beech (*F. sylvatica ssp. orientalis*) is growing. However, we lack knowledge about the long-term consequences of introgression between the subspecies.
We studied the extent and direction of introgression in two beech forests, one in Switzerland and one in France, where beech from Greater Caucasus was introduced next to *F. sylvatica* about 100 years ago. All adult trees of an approx. 0.5 ha area (N_CH = 216 and N_FR= 226) and a representative sample of seedlings (N_CH = 639 and N_FR = 423) were genotyped using 16 nSSR markers. Using NewHybrids, we found that 11.43% and 19.6% of the offspring, respectively, had some degree of introgression including F1s, F2s and *F. sylvatica* backcrosses. Using the neighborhood model of NMpi2, we found that pollen dispersal capacity is comparable between the two subspecies, but *F. sylvatica* ssp. *orientalis* receives more inter-specific pollen than *F. sylvatica*, suggesting that the lower abundance, pollen limitation, and the spatial configuration of *F. orientalis* influence the hybridization rates. Individual-based spatially explicit simulations using NEMO was used to estimate the expected proportion of hybrid classes with and without selection for or against hybrids. Our results suggest that hybridization between beech subspecies is frequency-dependent and may lead to outbreeding depression. However, with accelerating climate change, the relative importance of outbreeding depression versus the potential beneficial effects of more adapted alleles remains unknown.

39 - Building Raptor DNA databases: Profiling for Protection

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Despite peregrine falcons, hen harriers and golden eagles in the UK being protected by legislation, raptor persecution continues to be a significant problem for these species. Crimes, including shooting, trapping, poisoning and collection of either eggs or chicks from the wild, are notoriously difficult to detect and successfully prosecute and, particularly in the case of hen harriers, can lead to severe pressures on population viability. A critical part of the conservation of these species is the development of a reference DNA database to represent the wild population that can be used both as a tool to inform forensic criminal investigations and also for conservation genetic monitoring. Here we describe the ongoing development of reference DNA databases for these iconic raptor species and the development and application of DNA profiling methods that have been applied successfully in several criminal cases. They also have the potential to provide a crucial resource for the conservation of these species as repeated sampling allows the potential for following individuals, constructing pedigrees and the assessment of temporal genetic diversity. The success of sample collection relies on a network of licensed bird ringers from across the UK who implement a programme of yearly, non-invasive DNA sampling using buccal swabs from nest sites each breeding season. We are now in our sixth year of collection for hen harriers, fourth year for peregrine falcons and third year for golden eagles, with the aim to develop a comprehensive forensic and conservation resource in the UK for these species and provide investigative support for both enforcement and intelligence operations.

40 - Conservation Genomics for the Vulnerable Saker Falcon: Insights, Challenges, and Recommendations

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Conservation genomics focuses on developing and applying genome-scale data analyses dedicated to addressing questions that help the long-term preservation of population viability. These analyses, relying on high-quality reference genomes, support effective conservation by determining species identity, assessing hybridization, characterizing population structure, genetic diversity, and levels of inbreeding across the distribution range. Here, we illustrate how genomics can be applied to the conservation of the saker falcon, listed as vulnerable by the IUCN, through the assessment of conservation breeding programme established in Kazakhstan. We used wild reference samples collected throughout the distribution range to conduct a thorough evaluation of the genetic origin, status, relatedness, and inferred pedigree of potential founders of the breeding programme. Genetic clustering analyses reveals three distinct clusters among captive saker falcons, one of which originates from an unknown source, warranting further investigation. No evidence of introgression from gyrfalcons was found in these birds, dismissing the hypothesis of hybridization between sakers and gyrfalcons to account for the observed cryptic genetic diversity. While captive saker falcons exhibit slightly lower genetic diversity compared to their wild counterparts, their inbreeding levels are much higher which raise concerns about the potential release of their progeny. Relatedness analyses reveal full-sibling and half-sibling relationships among the captive individuals, which compensate for the limited documented parentage records (55% of the founders) and can inform pairing strategies. Implementation of a comprehensive genetic management plan, including prioritizing breeders with documented pedigrees, establishing a genomic benchmark, and careful introduction of new wild breeders, is crucial for the long-term success of the saker reinforcement programme.

41 - Molecular assessment of diet diversity in a wild primate, and implications of social factors on diet choice

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Diet studies of wild animals provide valuable information about their ecology and may also serve as biodiversity surveys. In primatology research, these are traditionally based on a variety of observation methods. However, it is difficult to obtain comprehensive observational data, as feeding habits are often difficult to observe in detail in the wild. The analysis of faecal samples using environmental DNA (eDNA)-based techniques opens further perspectives to investigate a species' diet. Recent DNA metabarcoding assays in primatology resulted in increased taxonomic resolution and coverage, i.e. revealed additional diet items and at lower taxonomic levels compared to observational data. In addition, and in particular for group living species, it can be valuable for conservation efforts to go beyond the species or population level and assess the effect of social factors on diet choice. For this purpose, we studied dietary variation of plants and arthropods inferred from DNA metabarcoding in an omnivorous primate, the vervet monkey (*Chlorocebus pygerythrus*). Faecal samples were collected in South Africa over 4 years and the attribution of samples to individuals with known life history data in our study system allows to assess the potential influence of social factors on feeding behaviour. We found a strong effect of season on variation in plant consumption and compared different diversity indices. Furthermore, we included social factors such as sex and age aiming to further understand individuals' foraging decisions. We will discuss the potential of this method to study behaviour, expressed as inter-group variation in diet as well as group-specific behaviour.

42 - Quaternary plant speciation in central Europe: evolution and conservation of the *Potentilla collina* aggregate

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Assessing and preserving the genetic diversity of species is one of the primary goals of the biodiversity strategy of Switzerland. In apomictic species complexes, conservation efforts are often hampered by our poor understanding of the evolution of the species, the genetic distinctness of populations, and taxonomic uncertainties. The *Potentilla collina* aggregate is one of these poorly studied apomictic species complexes, thought to be allopolyploid hybrids of sympatrically growing *Potentilla* species. They form many locally endemic and endangered or even already extinct species. There are conservation projects in several European countries, but they all need more clarity about which taxonomic groups and populations are most threatened. In this study, we focus on the populations in Switzerland and the upper Rhine area in France and Germany. Due to the lack of a reference genome, we use reduced-representation sequencing (ddRAD) to discover de novo SNPs. This allows us to compare the local hybridogenic species to the local putative parent species and confirm theories of their evolutionary history previously only based on morphology. We will infer the evolutionary history of the examined populations, in particular if they share a common ancestor or originated independently. First results confirm that the genome size of the hybridogenic species is in-between the genome size of the two putative parent species *P. argentea* and *P. verna*, and are therefore still the two most likely candidate parent species.

43 - How can DNA legacy datasets contribute to developing best practices for CBD genetic diversity indicator estimation?

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The 2022 Kunming-Montreal Global Biodiversity Framework (GBF) of the Convention on Biological Diversity (CBD) recognized the protection of genetic diversity (GD) as a major objective for biodiversity conservation. To monitor GD for the GBF, genetic indicators have been proposed, requiring the estimation of the effective population size (Ne), which relates to a healthy evolutionary status and adaptive potential (Ne>500).

Due to increasingly cost-effective DNA sequencing technologies and enhanced collaborations between researchers and conservation practitioners, an increasing number of DNA datasets are published. These datasets allow estimation of GD within and across species. However, Ne estimates from DNA data are sensitive to sampling designs and estimation methods applied, as well as to species features including population spatial genetic structure and life history traits such as reproductive system or life span. The best practices and workflows for Ne estimation need further development.

DNA legacy datasets are large population genetic datasets of well-characterized species including DNA data and metadata on census sizes, reproductive success and dispersal, sometimes with pedigrees. We present an approach to select and structure legacy datasets according to their features, resulting in a framework that will allow us to explore how contrasted evolutionary histories, biological characteristics and data features can impact Ne estimates. This framework will help us design simulation scenarios that mimic some of these features. It is intended to provide standardized workflows for reliable sampling and Ne estimating procedures to efficiently support conservation managers in their practice of assessing and reporting DNA-based GD indicators to meet management and policy requirements including those of the CBD.

44 - Genetic structure and diversity of Northern Chamois (*Rupicapra rupicapra*) in the Bavarian Alps: initial results from a large-scale study

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The Northern chamois (*Rupicapra rupicapra*) is a characteristic mountain ungulate with a distribution that spans across the European Alps. Like many wildlife species, chamois populations are impacted by a range of environmental and anthropogenic factors, including changes in habitat composition, land use, and climate change. It is further listed as appendix V species under the FFH (Fauna-Flora-Habitats) directive. Especially at the edge of its range in the Bavarian Alps, knowledge on the genetic status of present populations is lacking. This study aims to address timely questions on genetic diversity and population structure of chamois to inform potential conservation efforts, future monitoring, and management strategies in this area. Utilizing more than 2000 genetic samples from the Bavarian chamois hunting bag collected between 2021 and 2023, and employing 16 microsatellite markers, we conducted comprehensive genetic analysis. We applied several analytic techniques, including Bayesian clustering (STRUCTURE) and spatially explicit methods (Geneland, WINGEN), to assess population structure and genetic diversity. Considering the habitat requirements of the species and environmental heterogeneity within the species range in Bavaria, we expected varying levels of gene flow within and between populations, leading to hierarchical population structures.

We found a significant degree of isolation by distance with only the Inn valley presenting a critical genetic barrier, confirming trends observed in other recent genetic studies on chamois. We also observed a hierarchical population structure with discernible substructures that align well with prominent geographical features such as mountain ranges and natural landscape units. In addition to these substructures, a continuous examination of genetic diversity also revealed regional variation in heterozygosity and allelic richness. However, there was no evidence of critical conservation concerns like significant genetic diversity loss, inbreeding, or pronounced isolation and differentiation. This suggests that the Northern chamois populations in Bavaria can be considered metapopulations with generally intact gene flow at multiple levels.

To gain a deeper understanding of the potential drivers behind the observed hierarchical patterns of population structures, detailed landscape genetic analyses are necessary. This allows assessing the impacts of environmental and anthropogenic barriers on genetic diversity and gene flow potentially informing effective conservation strategies and ensuring the long-term viability of the Northern chamois in its native alpine habitat.

45 - Determinants of genetic diversity in an adaptive radiation of cichlid fishes

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Genetic diversity plays an important role for adaptation to environmental changes and is a key factor in maintaining ecosystem resilience. However, the determinants of genetic diversity remain poorly understood. While population size is often used as a proxy for genetic diversity, the amount of genetic variation within populations is not always reflected by their sheer size. Instead, factors such as selection at linked sites, the de novo mutation and speciation rates, as well as life history and ecological traits, may more strongly affect genetic diversity. Here, we examine the roles of these potential determinants of genetic diversity in the adaptive radiation of cichlid fishes from African Lake Tanganyika. The approximately 250 species exhibit an exceptional morphological, ecological, and behavioral diversity, with species richness positively correlating with genetic diversity. Using whole-genome sequencing data from population samples of 19 species spanning the entire range of species abundance, we assess genetic diversity, contemporary effective population size, and reconstruct their evolutionary history. Further, we sequenced parents and offspring to evaluate germline mutation rates. Complemented by an extensive dataset of 22 ecological and life history traits for all species, we investigate the key determinants of genetic diversity in cichlid fishes. Our results identify the role of the de novo mutation rate in shaping genetic diversity in cichlid fishes and provide valuable insights into the possibility to leverage ecological and life history data for the interpretation of genetic diversity in conservation management in general.

46 - Survey of the genetic diversity of steppe plants in Austrian dry habitats

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The random fluctuation of allele frequencies (genetic drift) can have a significant impact on evolution in small and fragmented populations and can lead to an extinction vortex, a feedback loop between reduced population size, loss of genetic diversity and inbreeding depression. As dry meadows and pastures in Austria are among the most species-rich habitats, but also among the most endangered ones due to changes in land use, we selected 14 rare "steppe plants" occurring in the Pannonian and partly also within the Alpine region for the genetic diversity survey: *Adonis vernalis; Artemisia pancicii; Astragalus exscapus; Carex supina; Crambe tataria; Dianthus serotinus; Dracocephalum austriacum; Iris humilis subsp. arenaria; Linum flavum; Onobrychis arenaria; Oxytropis pilosa; Phlomoides tuberosa; Pulsatilla vulgaris (s.lat.); Stipa capillata.* The populations will be genotyped using RADseq for a corresponding (long-term) comparison of genetic diversity (heterozygosity, inbreeding, gene flow). We expect that the data will provide valuable information for assessing the conservation status of the species themselves, but also of the habitats in which they occur. The project supports Austria's efforts as a party to the Convention on Biological Diversity to establish a national system for monitoring the status and trends of biodiversity and its components.

47 - Unraveling the demographic history of *Abies* species by applying spatio-temporal kriging to ancient pollen and climate data

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Climate change is a major threat to temperate forests that requires urgent action. Fir species (*Abies* spp.) are the third most important coniferous species in the growing stock of European forests after pines and Norway spruce, however, fir species may gain increased importance in the future. This is not only because of increasing spruce die-back but also because fir species are often associated with high biodiversity and have a much broader ecological niche than their current distribution may suggest. Indeed, the distribution of Abies species was drastically reduced by human impact since the mid-Holocene, mainly due to logging, fires, and grazing. Quantifying the effect of human impact is extremely challenging in the lack of quantitative data, for which reason past species distribution models and dynamic vegetation models often failed to accurately predict the current distribution of European fir species. In this study, we propose a purely statistical approach to (i) estimate the past demographic history of Abies species across Europe, the Mediterranean basin and Minor Asia and (ii) predict their future potential distribution under different climate change scenarios. We combined fossil pollen records from 201 sites across Europe with paleo-climate data to estimate the percentage of forest cover by fir species from the Last Glacial Maximum (LGM) till today using spatio-temporal kriging. This statistical approach allowed us to model the climate–species presence relationship across the past 20'000 years, thus including times when humans were absent. Among the climate variables, daily and yearly temperature amplitudes and maximum precipitation were best predictors of Abies presence, outperforming mean climate variables across the studied time period. Our results show that since the LGM, the realized climatic niche of Abies spp. expanded omnidirectionally, suggesting that the species is capable of growing and reproducing under a wide range of environmental variation.

48 - Survey of the genetic diversity of endemics of the north-eastern Limestone Alps as a basis for monitoring

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Austria is home to approximately 50 endemic, non-apomictic flowering plant species, predominantly located in the Alpine regions, particularly near known glacial refugia. Of these regions, the Northeastern Limestone Alps (NLA) stand out as being particularly rich in endemic plants. This project aims to create the basis for genetic monitoring of eight selected endemic plant species of the NLA (*Achillea clusiana, Alyssum neglectum, Callianthemum anemonoides, Campanula pulla, Draba stellata, Euphorbia saxatilis, Noccaea crantzii, Pulmonaria kerneri*). To do so, genomic data from each species will be obtained from individuals representing each species' entire distribution range. These data will be used to characterize the current state of populations, and to identify particularly diverse or vulnerable populations. The results of this project should serve as a basis for evidence-based nature conservation planning and management. Finally, we also aim at contributing to the establishment of systematic genetic monitoring of wild plants in Austria.

49 - Purging and the genetic paradox of invasions

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Invasive species threaten global biodiversity and pose major risks to human societies. To mitigate their impact and spread, colonisation routes and genetic processes involved with successful invasions must be understood. Using high-throughput sequencing, we will address the "paradox" of biological invasions: how can some species spread to new habitats very efficiently, when their invading populations should often suffer from inbreeding and loss of genetic variation due to low numbers of founder individuals? We will investigate a novel hypothesis proposing that "purging" (removal of deleterious recessive alleles exposed to selection in homozygotes because of inbreeding) is a decisive factor in invasiveness. We assume that without purging of strongly deleterious variation, inbreeding depression frequently leads to failure of invasions. We test our hypothesis by analysing levels of inbreeding and deleterious alleles in populations of the invasive zebra mussel (*Dreissena polymorpha*) that poses a threat to freshwater ecosystems worldwide. Our preliminary results suggest high and recent inbreeding in invasive zebra mussel populations in Denmark and are therefore in line with our hypothesis. We will study populations from the native range and at different steps of the invasion process to better understand the possible role of purging in the spread of the species. We will also study if the invasive populations show evidence for genetic adaptation to their local environments, despite low founder numbers. The improved understanding of genomic processes underlying biological invasions will be broadly relevant across taxa. It could fundamentally change our understanding of the dynamics of invasions and of the risks associated with populations at different invasive steps. This may help guide conservation to prevent and reduce the impact of invasive species.

50 - Measuring Distinct Genetic Diversity to identify Key Biodiversity Areas

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Key Biodiversity Areas (KBAs) are sites that contribute significantly to the global persistence of biodiversity. Traditionally, KBAs are determined via population data of species, but distinct genetic diversity is also permitted as an assessment parameter. So far, distinct genetic diversity has not been applied for KBA identification as potential methods have not been thoroughly compared. Here, we tested the applicability of AMOVA, the diversity index Simpson's λ, average taxonomic distinctness (AvTD, Δ+) and effective population size (Ne), calculated with the two different programs Speed Ne and Ne Estimator for identification of KBAs. AMOVA, the only method evaluating genetic distinctiveness exclusively, provides different results compared to the other methods. λ is not well suited to distinguish genetic diversity among areas if the diversity is high and if λ was corrected for sample size. When using Ne, valuable data about areas is lost frequently, and areas could be underestimated by KBA criteria. As a general recommendation, Ne Estimator is preferred over Speed Ne. However, for microsatellite datasets of a limited size, or when Ne Estimator calculations fail, utilizing Speed Ne can prove beneficial. Δ+ encompasses distinctiveness and functional diversity in addition to diversity. Furthermore, it can be calculated and applied smoothly. Since the method is new to a genetic context it should be further explored, but with the current state of knowledge it is the most suitable method to determine KBAs.

51 - Characterization of Toll-Like Receptor Gene Diversity in the Genus *Giraffa*

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Wildlife populations are increasingly impacted by shrinking habitats and are pushed to co-exist near humans and their livestock species, leading to an elevated risk of infectious diseases. Therefore, knowledge of a species' immune system is essential to assess its resilience and adaptive potential in a changing environment. The high variability in the genes of the innate immune system (IIS), e.g., toll-like receptor (TLR) genes, seems to be associated with resistance to infectious diseases. Therefore, the IIS is considered the first line of defense against pathogens. The IIS relies on TLRs to recognize pathogen-associated molecular patterns (PAMPs) and mount effective responses against pathogens. Despite the crucial role of TLRs in an organism's defense against these pathogens, research has mainly focused on humans, model organisms, and livestock, leaving non-model species like giraffes (*Giraffa spp.*) understudied. This study utilized a comprehensive dataset of giraffe whole-genome data to investigate immune gene diversity across giraffe taxa, specifically targeting TLRs. We identified three previously incomplete TLRs (TLR1, TLR6, TLR8) in the Masai giraffe (*G. tippelskirchi*) genome and extracted the sequences of the ten TLR genes from nearly 300 giraffe individuals. This study provides the first in-depth analysis of immune gene diversity in giraffids, unveiling crucial insights into the evolutionary dynamics of toll-like receptors (TLRs) within giraffes. These findings illuminate the giraffes' adaptive capacity in response to changing environments and various pathogenic challenges, underscoring the significance of giraffe conservation in safeguarding their distinctive genetic diversity and adaptive resilience against emerging threats.

52 - Conservation of the Tiny Mousetail

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The Tiny Mousetail (*Myosurus minimus*) is an annual herbaceous plant species from the buttercup family (*Ranunculaceae*). It is native to the Northern Hemisphere and grows in ruderal sandy-loamy sites that are occasionally flooded. In Switzerland, the species belongs to the highly endangered habitat type Nanocyperion (Typo CH). *M. minimus* is endangered in several European countries, threatened with extinction and a priority species in Switzerland (level 2, high national priority with a great need for action). The main threats are habitat loss and degradation, land drainage, urbanization and changes in water balance. Currently there is only a single viable population left in Switzerland, located in Solothurn.

In order to ensure the survival of the species in Switzerland, in collaboration with the Canton Solothurn we are planning a translocation to establish one or more new populations. The translocation will be backed up by three subprojects to determine: 1) the genetic structure of the population; 2) the role of soil-biota; 3) the presence of specialized phytopathogens.

To determine the genetic structure of the population, we will use the restriction site associated DNA (RAD) sequencing technique to infer different metrics like FST (population differentiation) and FIS (inbreeding coefficient). In particular, we will compare the inbreeding coefficient to two other populations in Germany and France. These results will help to optimize the translocation and to determine if mixing seed-material from different origins could be beneficial.

To determine if a soil-inoculation could help germination and establishment, we will perform a greenhouse study comparing germination in home-soil, translocation-site-soil and translocation-site-soil inoculated with home-soil.

Lastly, we monitor the population for the presence of two specialized phytopathogens: *Entyloma myosuri* and *Peronospora myosuri*. While these phytopathogens do not seem to affect reproductive output of the Tiny Mousetail, due to their specialization they are themselves rare and endangered.

53 - Developing new strategies to characterise genomic variation for biodiversity conservation

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Genetic diversity is one of the three basic elements of biodiversity and understanding the full extent of this diversity within species is fundamental for their conservation. However, despite the ongoing advances in DNA sequencing technologies, conservation genomics is lagging behind in using whole-genome data efficiently. In contrast, other fields, such as human genomics, have developed theoretical and computational approaches to tackle this. If applied to endangered species, these approaches could provide a better understanding of their genetic diversity, particularly regarding the structure of this diversity across populations and its effect on adaptation to changing environments. By leveraging two types of genetic data currently overlooked in conservation genomics—haplotype information and structural genomic variation—, we are developing new analysis strategies to characterise genomic variation in endangered species. Using the Arctic fox as a model species, we are using whole-genome data from both present-day and historical samples to: 1) infer subtle patterns of population structure and gene flow, 2) quantify temporal changes in genomic structural variation and 3) assess the ability of these types of genetic data to inform on adaptation to local environments. With these strategies, we expect to provide not only a comprehensive characterisation of genomic diversity in Arctic foxes—with a direct impact on the Swedish Arctic fox conservation programme—, but also new analytical tools for conservation genomics, unlocking the full potential of whole-genome data for biodiversity conservation.

54 - POPcontinuity : an R package to test continuity in structured populations

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Researchers analyzing genetic samples from different time periods often need to assess genetic continuity between populations across these periods. This is notably the case when delineating evolutionarily significant units for conservation settings. The POPcontinuity R package addresses this need by enabling the testing of structured population continuity. The specificity of this approach is that it takes into account the continuous gene flow between the populations under study and neighboring populations, a factor that has proved important when assessing genetic continuity through time. The package's main feature is the analysis of observed and simulated genetic data of different types (SNPs, microsatellites, or DNA sequences) while taking into account both spatial and temporal dimensions of the population. POPcontinuity relies on an Approximate Bayesian Computation (ABC) analysis to optimize the accuracy of the test. The integration of simulations and analysis into a single, simple-use R package simplifies the user approach to population continuity testing. POPcontinuity is a flexible tool, adaptable to various evolutionary and conservation research contexts when population molecular data in temporal series are available.

55 - Genetic Insights into Feline Immune Responses: Implications for Conservation

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One of the strongest evolutionary pressures shaping the genome is natural selection by pathogens, which challenge the immune system of any organism. To ensure a functional immune response, highly polymorphic gene families evolved that encode key receptor molecules, which recognize and, for example, present foreign peptides to phagocytic immune cells as part of adaptive immunity. When variability in adaptive immune receptor genes is reduced, as seen in some wild felid species, other immune system components must be selected to secure an effective immune response. Within the innate immune system, natural killer (NK) cells form a highly heterogeneous cell population due to the differential expression of NK receptors (NKRs), which are functionally linked to adaptive immune genes, allowing for potential functional compensation.

The toll-like receptors (TLRs) are an essential component of innate immunity that recognize pathogen-associated molecular patterns and play a crucial role in enhancing the immune response, e.g., against blood parasites such as *Babesia* and *Hepatozoon*. Despite their functional significance, NK cells and TLRs' capabilities and the underlying genetic diversity in felids remain largely unexplored. The feline innate immune system has undergone rapid changes during domestication and adaptation to diverse environments and changing habitats, leading to the evolution of specific properties in innate immunity genes, including those expressed in NK cells and TLRs. Preliminary results from next-generation sequencing efforts have been instrumental in characterizing and comparing innate and adaptive immunity genes in European wildcats, jaguars, cheetahs, and African leopards. This research project addresses knowledge gaps regarding innate immunity genes' existence, function, and (co-)evolution within the Felidae family and beyond. This study will facilitate effective genetic monitoring in wild-ranging felids by uncovering immunogenetic diversity and identifying selected haplotypes.

56 - The Intraspecific Diversity of Macrophytes in European Pondscapes

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European ponds support up to 70% of the regional freshwater species pool and are increasingly acknowledged as key habitats due to their abundance on Earth. Besides, ponds' biological diversity suffers both from more threats than lakes and rivers and from a lack of consideration in conservation policies, despite the key ecosystem services they provide. This lack of awareness comes with a deficit of monitoring which, if filled, could become a fundamental asset to assess freshwater biodiversity trends due to the cost-efficient nature of studying pondscapes. As part of the Biodiversa+ project « TRANSPONDER », this research's aim is threefold. First, understanding the intraspecific diversity of two different macrophytes (*Lemna minor* and *Potamogeton natans*) to get insights into signs of genetic erosion of these abundant species in European pondscapes. Second, understanding the differences and potential advantages of pooling individuals versus studying them as separate entities to assess the genetic diversity between populations. Finally, developing transnational standardised biodiversity monitoring guidelines for permanent and temporary ponds in Europe. The first two objectives will be met by using a genomic approach (ddRAD sequencing) and subsequent analysis to map genetic diversity. The third objective will be met by compiling the work of various other European working groups on different monitoring aspects. These three objectives will contribute to the development of a standardised methodology to assess the biodiversity and ecological status of ponds as it already exists for lakes and rivers.

57 - Using Nanopore sequencing for DNA-methylation-based sex identification in Aldabra giant tortoises

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Understanding the life history of wild species is critical for effective conservation management. One of the most important tools for this purpose is non-invasive sex identification, particularly for species that do not exhibit sex-specific phenotypic features until certain life stages. Among such species, the Aldabra giant tortoise (*Aldabrachelys gigantea*), one of the last remaining giant tortoise species globally, exhibits temperature-dependent sex determination and is increasingly vulnerable to the projected effects of climate change. Although DNA methylation is implied, the underlying molecular mechanisms of sex determination have been poorly understood. In this study, we employed Oxford Nanopore sequencing to perform comprehensive whole-genome DNA methylation profiling on 73 Aldabra giant tortoises, ranging in age from 20 to 110 years. Our preliminary analysis identified distinct sex-specific methylation patterns. Hypomethylation in females was primarily noted in genes associated with cellular metabolism and organization. In contrast, genes linked to tissue and organ development, including those involved in embryonic and morphogenetic processes, were predominantly hypermethylated, indicating a potential epigenetic regulation of sexual dimorphism in developmental programming. These findings not only contribute to our understanding of epigenetic regulation in a non-model species but also aim to establish epigenetic biomarkers for effective sex identification in the wild and rewilded colonies of a tortoise species for the first time. The novelty of the methodological approach and the originality of its application can open a new door for the effective use of epigenetic tools in conservation biology and significantly contribute to the emerging and much-needed scientific field of applied conservation epigenomics.

58 - Hybrids in conservation policy and species management

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Hybridisation has long been a central topic in evolution and conservation. Recent developments in genomics have increased the ability to detect hybridisation, defined here as breeding between species, subspecies or distinct populations, and assess levels of introgression between taxa. For decades, hybrids were typically considered only as threats to conservation, and current regional and national environmental policies largely focus on their potential negative effects. Nevertheless, new evidence indicates that hybrids can, at times, bring benefits, especially for maintaining or increasing species or population genetic diversity. In the context of the latest global conservation policy goals, we call for science-based, reflective and nuanced management of hybrids, applying a framework that shifts focus towards measuring the impact of hybrids, and assessing potential risks and benefits. Alongside demographic and ecological information, it is crucial for impact assessments to consider genetic information. Given new findings on how some hybrids may aid genetic adaptation to rapid environmental changes, conservation management of hybrids needs to be more case-specific.

59 - Exploring human impact on Swiss butterfly populations: a genomic perspective across more than a century

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Insects are facing a worldwide decline caused by various anthropogenic factors such as land-use change, contamination, and climate warming. In Switzerland, butterfly population reduction has been observed in several species, but the lack of long-term population monitoring makes it challenging to reconstruct their historical trajectories.

Museum collections house billions of historical specimens, a high-value record of entomological data. The genomic information carried by those individuals has recently been made available by advances in museomics. Here, we investigate the temporal dynamics of three butterfly species (*Polyommatus icarus, Pieris napi, Vanessa atalanta*) since the early 20th century in Switzerland. To finely track temporal genetic changes, we performed an extensive sampling comprising 665 historical specimens collected in museums and spanning more than a century, alongside with 351 fresh samples, totaling 1016 individuals. Using cutting-edge methods allowing to recover thousands of genomic loci from historical (leveraging the HyRAD protocol) and fresh (applying a ddRAD approach) specimens, we aim at comparing population genetic parameters across multiple space and time points, including present-day.

Establishing population dynamics using estimates such as genetic diversity, effective size and inbreeding along the last century and all over Switzerland offers a retrospective view on the human impact on butterfly population through decades, providing valuable guidelines for future environmental management strategies.

60 - Illegal Animal Trade Monitoring in Czechia

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Wildlife trade significantly impacts global biodiversity and contributes to the dramatic declines in animal populations, with some species facing extinction due to intense poaching and trafficking. Illegal animal trade also facilitates the spread of pathogens that affect wildlife, domestic animals, and human health. Although Czechia is not a traditional destination for illegal wildlife trade, it likely serves as an important transit route for the transportation of various animals and animal products to markets in Western Europe and Eastern and Southeastern Asia. To assess the risks posed by the illegal trade of animal products in Czechia, we analyzed items confiscated by the Customs Administration at Václav Havel Airport, the nation's largest international airport. Our focus was primarily on unprocessed raw meat, which can only be identified through molecular genetic methods. Using DNA barcoding, we determined the species origin of these items and screened the samples for pathogens typical of the identified source animals using RT-qPCR and LAMP methods. Our findings reveal that animal products of various origins are smuggled through Václav Havel Airport, including products from conventional meat-producing animals such as cows, pigs, and sheep, as well as from dogs, various fish species, and in one instance, softshell turtles (*Trionychidae*) listed in CITES Appendix II.

61 - Characterization of the silky feather phenotype in the European Bearded Vulture population

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The bearded vulture (*Gypaetus barbatus*) experienced an absence within the entire Alpine range for over 80 years. Based on a captive breeding program, the species has been reintroduced to the Alps and currently counts over 300 individuals. Unfortunately, between 2009 and 2017 three wild fledglings were recaptured due to their inability to fly caused by feather abnormalities. To the current knowledge, various factors can impact feather development and further may potentially interact. For instance, an excessive burden of mites or viral infections can induce feather abnormalities. Nevertheless, the affected birds underwent examinations that yielded no pertinent findings. Since after moulting the abnormality remained, an environmental factor (e.g., toxins, nutrient deficiencies) seems less likely. In the context of genetics, many feather variations from chicken and pigeon breeding are described. In chickens, a recessively inherited point mutation within a cis-regulatory region causes the silky feather phenotype, characterized by the absence of the interlocking hooklets crucial for wing formation. Conversely, in pigeons, a dominantly inherited mutation leads to abnormally thickened hooklets, yet the specific genetic region responsible remains unidentified. Electron microscopy revealed the presence of hooklets in the affected bearded vulture feathers, however, their orientation and quantity seem to influence the interlocking and subsequentially flying capability. The likelihood of expressing recessively inherited alleles increases with inbreeding, suggesting a potential explanation for the observed feather malformation. A pedigree analysis identified a shared common ancestor of the affected individuals on which all three individuals are inbred. Further genomic analysis now should help to clarify the genetic basis of the abnormality and its implications for conservation of the reintroduced bearded vulture population.

62 - Uncovering the Genetic Landscape: Population Structure of Highly-trafficked Pangolins in the Congo Basin

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African pangolins are hunted for their meat and for use in local traditional medicine, as well as for their scales, which are trafficked internationally to growing Asian markets. Pangolin's population genetic structure can be used to trace the geographic origins of trafficked scales, but substantial sampling gaps across pangolins' ranges hinder these efforts. We documented population structure and dynamics in the two species of African pangolin, the white-bellied pangolin (*Phataginus tricuspis*) and the giant pangolin (*Smutsia gigantea*) in the underexplored Congo-Brazzaville. Using the combination of matrilinear and biparental markers, we identified high genetic diversity in both species. We explored the distribution of mitochondrial lineages of the white-bellied pangolin in the Congo Basin. Their distribution was most likely shaped by river barriers together with dynamics of forest refugia related to the climatic shifts during the Pleistocene. We detected population growth in the white-bellied pangolin coinciding with a dry period during the Pleistocene, suggesting some ability for this typically forest-dwelling species to persist under diverse environmental conditions. Using landscape genetics, we found all but one of the pangolins we sampled at bush meat markets originated locally. A single individual, sampled near the border, appeared to have been imported from Cameroon. These findings significantly contribute to our understanding of pangolin population biology and local trade dynamics. In addition, our data from a previously unstudied part of pangolins' ranges will help us to better understand international wildlife trafficking patterns and to target conservation and protection strategies for these highly vulnerable species.

63 - What can we learn from dendrochronological and whole-genome data on the resilience of Limousin pedunculate oaks to future climatic conditions?

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Observations of dieback from oak forests across Europe have become more common in recent decades, fuelling concerns for their long-term evolutionary potential and resilience to future selection pressures. Evidence of decline, however, greatly varies among populations from different regions and can be species-dependent, with a crucial lack of knowledge regarding genetic diversity in some regions of both ecological and economic interests, such as the Limousin region in Central France. The wood harvested in this region comes mainly from private estates, consists mostly of *Quercus robur*, and harbours properties that are highly valued by the spirit industry such as large ring width and high tannin levels. Our objective is to gain a better understanding of the origins of Limousin oaks' specific properties, whether due to genetic divergence from other provenances or to their local interactions with particular climatic and ecological conditions, by following two complementary approaches. We sampled ~300 trees across 25 populations, following generally a latitudinal climatic gradient and including populations at increasing ecological or geographic distances from the focus region. We first present our progress using a dendrochronological approach that allows a detailed retrospective study of both historical and recent growth by testing correlations between variations of annual growth and climatic variables. We also follow a landscape genomics approach for a) assigning each individual to their genetic species (*Q. robur, Q. petraea, or Q. pubescens*) and assess their introgression levels in each region, b) testing genome-wide selection signatures between populations and species, and c) exploring differentiation between oak provenances for genes involved in biosynthetic pathways leading to aromatic wood compounds. We discuss the challenge of conserving and renewing these populations, given future changes in both climatic conditions and diverse management practices.