4th Annual Meeting in Conservation Genetics 2020

from Genomes to Application

Hosted by the Senckenberg Research Institute and

Natural History Museum Frankfurt am Main

February 26th – 28th 2020

SENCKENBERG
world of biodiversity

tbg translational biodiversity genomics

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Sponsored by:

Coordinators

- Alina von Thaden
- Carsten Nowak
- Stefan Prost

Scientific Committee

- Miklós Bálint, Frankfurt, Germany
- Niko Balkenhol, Göttingen, Germany
- Axel Hochkirch, Trier, Germany
- Rolf Holderegger, Zürich, Switzerland
- Sarah Mueller, Frankfurt, Germany
- Carsten Nowak, Frankfurt, Germany
- Stefan Prost, Frankfurt, Germany
- Tobias Erik Reiners, Frankfurt, Germany
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- Laura Hollerbach
- Julia Intemann
- René Meißner
- Sarah Mueller
- Carsten Nowak
- Stefan Prost
- Rudolf Putz
- Tobias Erik Reiners
- Alina von Thaden

About the Conference

The conference series “Annual Meetings in Conservation Genetics” was launched in 2015 with the aim to build a platform that helps bridging the gap between modern genetic/genomic research and applied nature and species conservation. While the general discrepancy between modern molecular technologies and their applications in conservation is a long-known problem, this gap is becoming even larger in the current era of rapid progress in genomics.

The conference serves as a platform for researchers and conservation practitioners interested in applying modern genetic and genomic tools to conservation. We will have different presentation and workshop sessions on diverse topics such as environmental DNA (eDNA), molecular wildlife forensics and landscape genetics, as well as policy, society & outreach (see sessions). Preference will be given – but is not limited – to presentations that have an explicit focus on applied conservation aspects.

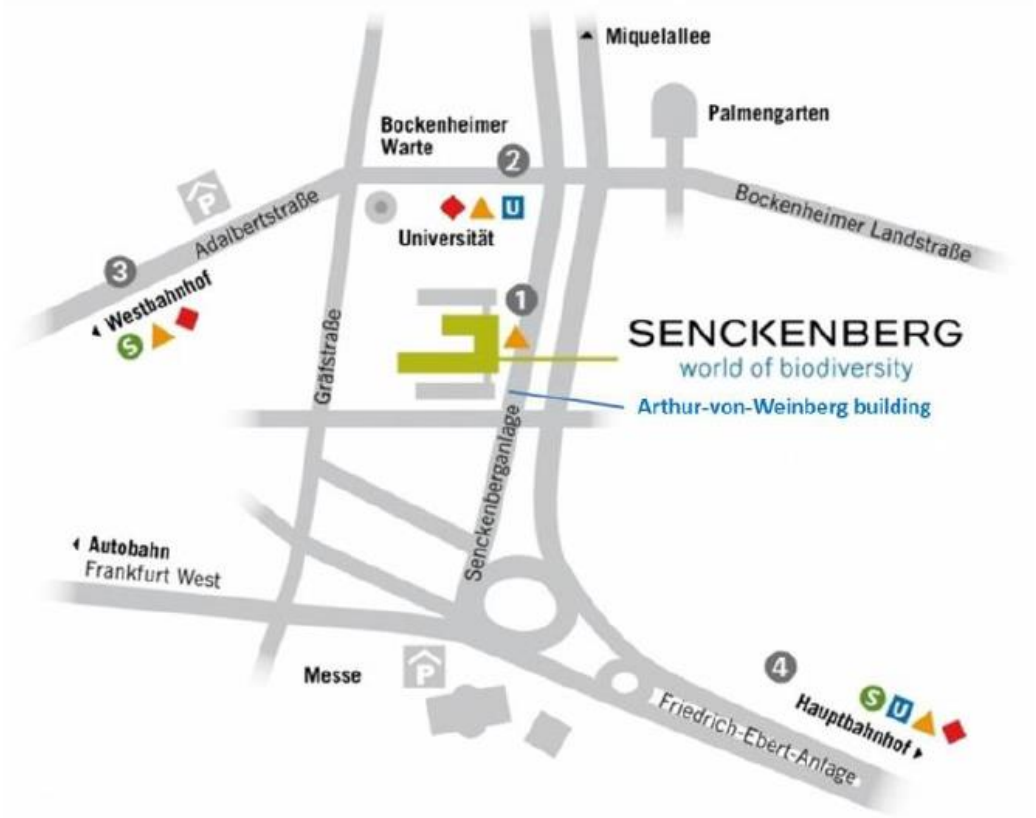
The meeting is intended for scientists and practitioners in the fields of conservation genetics, ecological genomics, and related fields, but also for those researchers, students, conservationists and environmental managers, who are interested in learning and/or applying conservation genetics & genomics themselves or want to come into contact with experts from these disciplines.

Venue

The meeting takes place at the Senckenberg Research Institute and Natural History Museum, one of Germany's largest institutions focusing on biodiversity research.

Street address

Senckenberg Forschungsinstitut und Naturmuseum Frankfurt
Senckenberganlage 25
60325 Frankfurt am Main
Germany



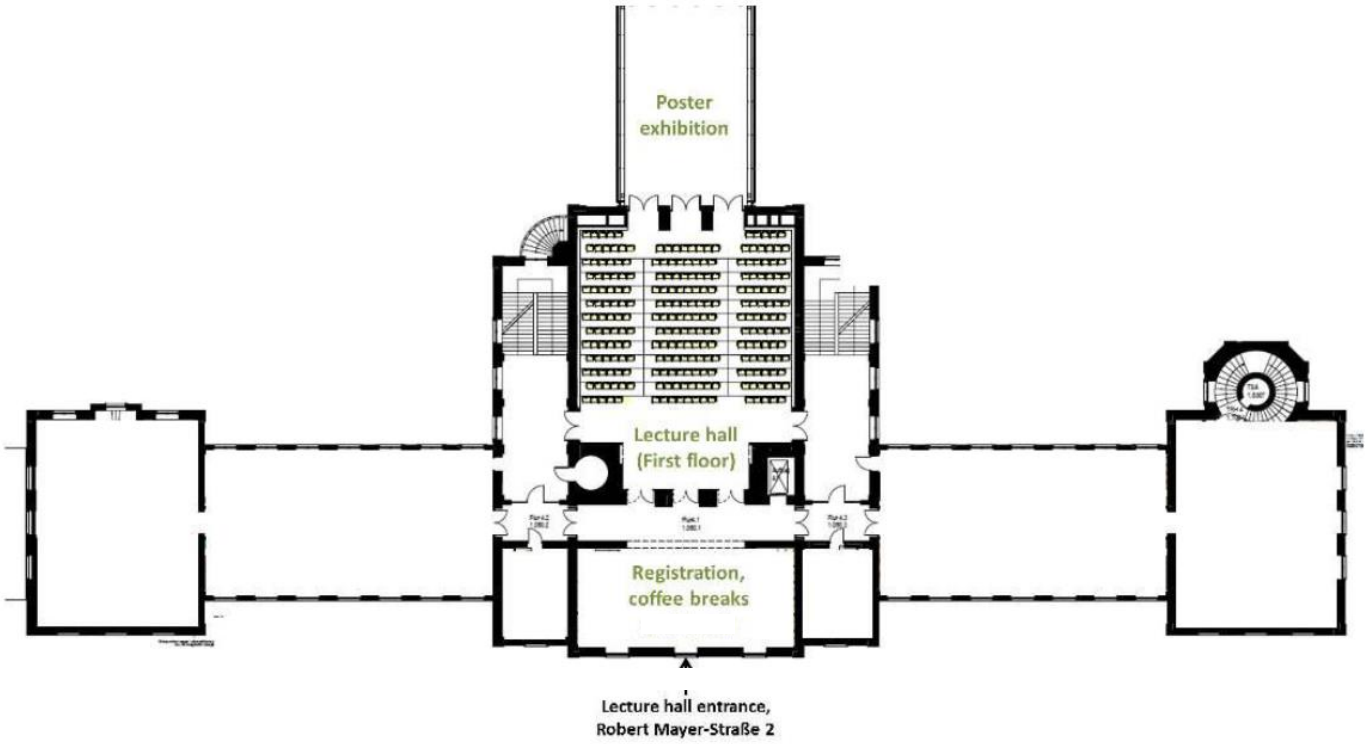
Get there

- By public transport:
  After the arrival at *Frankfurt Hauptbahnhof* (central train station), travel with the tram line U4 and exit at *Bockenheimer Warte (Senckenbergmuseum)*. Follow the signs for the exit to Senckenberg Museum.
- By car:
  We recommend traveling with public transport for environmental reasons and because parking space is very limited. There is paid parking in a parking garage available at Adalbertstraße 10, which is 10 min walk from the venue.

Floor Plans

Registration, Lecture Hall, Poster Exhibition

Arthur-von-Weinberg-Haus, Robert-Mayer-Straße 2

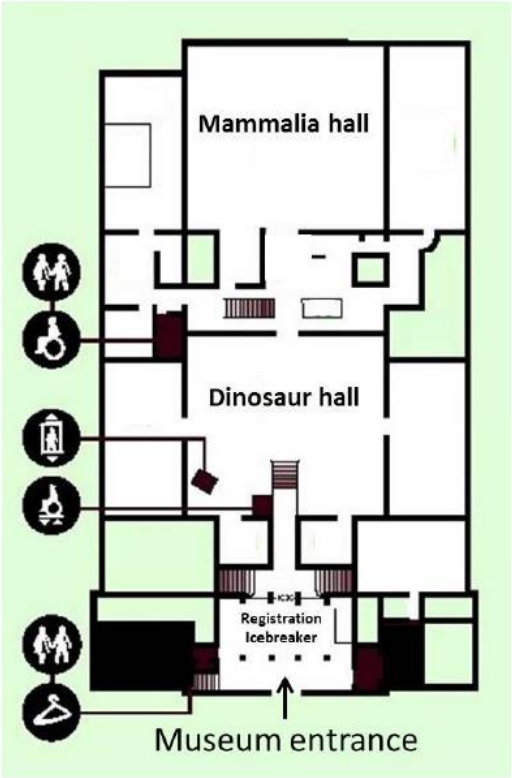


Icebreaker

2/26/2020, 20:00-22:00,
Exhibition “The Fascination of Diversity”,
Senckenberg Museum,
Senckenberganlage 25

Conference Dinner

2/27/2020, 20:00-22:00,
Dinosaur & Mammalia Hall, Senckenberg Museum,
Senckenberganlage 25



Exhibition – The Fascination of Diversity

Special Bicentennial Exhibition
Senckenberg Nature Museum Frankfurt
Wolfgang-Steubing-Saal, 2nd floor

For 200 years, the Senckenberg Gesellschaft für Naturforschung (society for natural history research) has studied the diversity in nature, whether animate or inanimate. To this end, the society collects and preserves biological and geological objects. There are approximately 40 million collection specimen to date, and their number grows every year. On the occasion of the anniversary year of 2017, Senckenberg grants a glimpse of these extensive archives of nature, encompassing plants, animals, fungi, microorganisms, rocks, minerals and even meteorites. The special bicentennial exhibition shows an impressive cross-section of this “geobiodiversity.” Approximately 1,000 objects – from tiny beetles, fascinating fossils, dazzling birds and glittering minerals to the majestic Okapi bull – can be admired in a tightly packed display 15 meters wide and 4 meters high. In this interactive display of diversity and geobiodiversity research at Senckenberg, visitors can explore a wide variety of ecosystems from the Mariana Trench in the deep sea to the lofty heights of Mount Everest.

Detailed Program

Wednesday, 26th February 2020

Registration		**09:00-13:00**
Workshop 1: Pamela Burger & Stefan Prost	**Cheetah Conservation Genomics**	**11:00-13:00**
Schmidt-Küntzel	Cheetah conservation genetics: origins and current applications	11:10-11:20
Prost	Conservation genomic analyses of African and Asiatic cheetahs (*Acinonyx jubatus)*	11:20-11:30
Magliolo	Validation of a Single Nucleotide Polymorphism marker set for forensic parentage verification in cheetah	11:30-11:40
Khalatbari	Assessing cheetah's population size, structure and diet in the central deserts of Iran with genetics	11:40-11:50
Maly	Determining genetic variability, kinship, and uniqueness in ex-situ cheetahs (*Acinonyx jubatus*) in North America	11:50-12:00
Czirják	The peculiar innate immune system of the cheetahs (*Acinonyx jubatus*)	12:00-12:20
Closed Session	For invited participants only	12:20-13:00
Welcome		**13:00-13:30**
Plenary I: Katerina Guschanski	**Time travel for conservation: Using museum collections to inform conservation decisions**	**13:30-14:00**
Session 1: Niko Balkenhol & Frank Zachos	**Landscape and Population Genetics**	**14:00-16:00**
Barratt	Long-term environmental stability, genomic diversity and demographic history of Pan-African chimpanzee populations	14:10-14:25
Brüniche-Olsen	Genomics and habitat reconstruction track climate-driven population dynamics in birds	14:25-14:40
Hepenstrick	Exploring the island biogeography of cryptogams on erratic boulders with a conservation genomic perspective	14:40-14:55
Traeger	Limited effects of woody overgrowth on genetic diversity and structure of *Primula veris* in semi-natural grasslands	14:55-15:10
Westekemper	Road density is the main driver of spatial genetic structure in European wildcats (*Felis silvestris*) across Germany	15:10-15:25
Geue	Landscape genomics as a useful tool for conservation prioritization: a multi-species study in Eastern Europe.	15:25-15:40
Bertola	Insights into the distribution of genetic diversity in the lion and implications for conservation	15:40-15:55
Coffee break		16:00-16:30
Session 2: Katerina Guschanski & Elisabeth Haring	**Ancient DNA and Museum Genomics**	**16:30-18:00**
von Seth	Sumatran rhinoceros genomes reveal the conservation implications of differential mutational load among the world's last remaining populations	16:40-16:55
Schulte	*Larix* chloroplast genomes assembled from sedimentary ancient DNA reveal past changes of Siberian forests	16:55-17:10

Lado	Detecting ancient dromedary-Bactrian and recent domestic-wild camel hybridization using shotgun sequencing	17:10-17:25
Open discussion		17:25-17:45
Free time	Hotel check-in and free visit to the Senckenberg museum	18:00-20:00
Icebreaker	in the museum (exhibition: fascination of diversity)	**20:00-22:00**

Thursday, 27th February 2020

Plenary II: Rob Ogden	**Wildlife DNA Forensics – from genetics to genomics on the front line of conservation**	**09:00-09:30**
Session 3: Rob Ogden & Stefan Prost	**Molecular Wildlife Forensics**	**09:30-11:00**
Pietsch	The African Wildlife Forensics Network (AWFN) – Challenges, experiences and opportunities of capacity building in wildlife forensics in Africa	09:40-09:55
Thakur	Using genetics and wildlife forensics in conservation of threatened vertebrates in the Indian Himalayan Region	09:55-10:10
Vasiljevic	Developmental validation protocol for species identification using the MinION nanopore sequencer	10:10-10:25
Morf	Animal forensics at the Institute of Forensic Medicine Zurich	10:25-10:40
Open discussion		10:40-11:00
Coffee break		11:00-11:30
Session 4: Klaus-Peter Koepfli & Sarah Mueller	**Reintroduction and Captive Breeding Genetics**	**11:30-13:30**
Loercher	Low genetic diversity and its consequences for the Alpine bearded vulture reintroduction project	11:40-11:55
Mueller	Genome wide evaluation of reintroduced Eurasian lynx populations in Central Europe	11:55-12:10
Koepfli	Genomic impact of founder history on ex situ populations of the critically endangered dama gazelle (*Nanger dama*)	12:10-12:25
Humble	Conservation genomics of scimitar-horned oryx: implications for future management	12:25-12:40
Biebach	Using genomics to inform genetic restoration of reintroduced populations	12:40-12:55
Grossen	Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex	12:55-13:10
Frandsen	Targeted conservation genetics of the endangered chimpanzee	13:10-13:25
Lunch break		13:30-15:00
Session 5: Carsten Nowak & Alina von Thaden	**Genomic Wildlife Monitoring**	**15:00-17:00**
Sharma	Monitoring Himalayan brown bear (*Ursus arctos isabellinus*) population by high-throughput noninvasive genotyping	15:10-15:25
Nowak	Reduced SNP panels allow for targeted genomic wildlife monitoring based on non-invasive sampling	15:25-15:40
Smith	What can genomic dietary analysis tell us about conflicts between conservation priorities and livestock herding practices?	15:40-15:55

Elbrecht	The Mobile Biodiversity Lab – DNA based ecosystem assessment in a backpack	15:55-16:10
Watsa	Portable sequencing for biomonitoring and capacity building in the Peruvian Amazon	16:10-16:25
Fischer	Genetic diversity monitoring: a feasibility study in Switzerland	16:25-16:40
Open discussion		16:40-17:00
Coffee break		17:00-17:30
Session X:	**Disease and Functional Genomics**	**17:30-18:30**
Hohenlohe	The devils' cancer: conservation genomics, rapid evolution, and adaptive potential in the face of a unique disease	17:40-17:55
Lyons	Whole genome and whole exome sequencing for felid conservation management	17:55-18:10
Muñoz-Fuentes	The International Mouse Phenotyping Consortium (IMPC): a functional catalogue of mammalian genes that informs wild species research	18:10-18:25
Poster session		**18:30-20:00**
Conference dinner	in the museum	**20:00-00:00**

Friday, 28th February 2020

Plenary III: Laura Epp	**Tracking the history of species and ecosystems with environmental DNA**	**09:00-09:30**
Session 6: Miklós Bálint & Florian Leese	**eDNA and Genomic Community Assessment**	**09:30-11:00**
Sander	An eDNA metabarcoding time series reveals high macroinvertebrate diversity and seasonal patterns in the Kinzig (Rhine-Main-Observatory)	09:30-09:45
Brasseur	Assessment of the macroinvertebrate community of the Vjosa river through non-destructive DNA-metabarcoding of preservative ethanol	09:45-10:00
Querejeta	The diet of the endangered Westland petrel: a DNA metabarcoding approach	10:00-10:15
Hartmann	The application of e-DNA methods for amphibian monitoring in a large scale ecological impact assessment	10:15-10:30
Kusanke	eDNA Monitoring of the endangered European Weather Loach (*M. fossilis*)	10:30-10:45
Martinez Arbizu	How 2bRad can help us to understand genetic connectivity and speciation in the oceans	10:45-11:00
Wrapping-up & Goodbye		**11:00-11:30**
Coffee break	For workshop 2	11:30-12:00
Workshop 2: Rolf Holderegger & Gernot Segelbacher	**Policy, Society and Outreach**	**12:00-14:00**
Pärli	Developing a genetic diversity monitoring program - What do the stakeholders say?	
Lunch break	For workshop 2	14:00-15:30
Workshop 3: Carsten Nowak, Stefan Prost, Alina von Thaden	At BikF auditorium	**11:30-15:00**
Tours	Botanical Garden or Frankfurt City tour	15:30-17:30

Plenary talks

Plenary I

Time travel for conservation: Using museum collections to inform conservation decisions

Katerina Guschanski

Evolutionary Biology Centre, Department of Ecology and Genetics/Animal Ecology, Uppsala University, Norbyvägen 18D, SE-752 36 Uppsala, Sweden

Limited by the available resources, one of the biggest challenges in conservation is prioritizing species for conservation interventions. Current estimates of population size and genetic diversity may not be accurate indicators of conservation needs, but instead reflect long-term demographic processes. However, species that have experienced rapid population declines accompanied by genetic diversity loss are highly vulnerable to genomic factors. Museum collections frequently span the last few hundred years, during which human impact on wild animal populations has dramatically increased. They thus allow us to travel into the past, before the most sever change took place, and provide a baseline against which current estimates of genetic diversity, inbreeding and genetic load can be compared. By quantifying the magnitude of change, we can identify species in greatest need of conservation action. The knowledge about changes in abundance and population-wide frequency of deleterious variants can inform about suitable conservation strategies, ranging from genetic rescue to captive breeding. Overall, the temporal approach that relies on museum collections can be crucial for informed conservation decision making.

Plenary II

Wildlife DNA Forensics – from genetics to genomics on the front line of conservation

Rob Ogden

Royal School of Veterinary Studies and the Roslin Institute, University of Edinburgh, Midlothian, EH25 9RG, UK

TRACE Wildlife Forensics Network, Edinburgh, EH12 6LE, UK

The illegal wildlife trade is having a devastating effect on the status of many endangered species, including some of our most charismatic large animals and plants. Tackling the trade has become an area of global concern and concerted international efforts are underway to address the issue, involving support for alternative livelihoods in source countries, law enforcement and the supply chain, and demand reduction for wildlife products in end-user countries. Law enforcement is a complex issue, requiring investigations at many different scales, from local bushmeat poachers through to international organized criminals. As with any other crime, investigators are using forensic science to detect and prosecute offenders. The use of molecular genetic analysis to identify human evidence has revolutionised forensic science and is now an established tool in law enforcement. The analysis and identification of wildlife DNA is used to address questions of species identity, captive breeding and geographic origin, as well as individualization across multiple species. The resulting evidence is used to provide intelligence concerning trade routes as well as prosecute individuals involved in wildlife trafficking. This presentation will introduce the field of wildlife DNA forensics, explain the key scientific questions involved, from phylogenetics to familial relatedness, and how the transition to genomics is providing increasing powers of detection. It will also take a look at how forensic science capacity is being developed for wildlife law enforcement in Africa and Southeast Asia, and how new laboratories are contributing to wildlife law enforcement and its role in biodiversity conservation.

Plenary III

Tracking the history of species and ecosystems with environmental DNA

Laura Epp

Environmental Genomics, Limnological Institute, Department of Biology, University of Konstanz, Germany

The last centuries have seen tremendous turnovers in species distributions and biodiversity on a global scale, linked to direct anthropogenic modifications of the abiotic environment, heightened migration rates and climatic changes. In many cases, neither the relative roles of these drivers, the pace of change nor the original community of the ecosystem are well mapped or understood. Ancient environmental DNA (ancient eDNA) stored in sedimentary records contains historic information about organisms from across the tree of life, including taxa that do not leave behind visible traces. It can uncover cryptic changes not visible in morphology and offers novel possibilities to study biotic interactions and networks through time. Depending on the preservation conditions, genomic biodiversity records from sediments can globally be retrieved on scales from hundreds to thousands of years. At sites with exceptionally good preservation, such as the Arctic, records can even go back multiple hundreds of thousands of years, thereby spanning more than one glacial cycle of the Pleistocene. These high-latitude areas are of particular relevance for the study of current and past climatically induced ecosystem changes and offer a backdrop of natural variability of ecosystems since the Pleistocene. Complementary to this, sites from temperate and tropical regions have experienced more direct effects of human environmental history. While ancient eDNA thus has a lot to offer to the study of historical biodiversity change, both its full potential and limits are not yet conclusively established. For example, the DNA of macroorganisms is not uniformly distributed in the sedimentary environment, and its distribution is putatively linked to the biology of the organisms. However, for many organismic groups we can by now reliably trace community change through time by DNA metabarcoding as well as use more specific assays and genomic tools to track the dynamics of single species or populations. Current developments promise a more efficient utilization of this resource to inform conservation biology, identify restoration targets and offer an empirical body of data for ecological theory.

Sessions

S1. Landscape and Population Genetics

Population genetic data can provide important information on genetic diversity and functional connectivity in plants and animals. Furthermore, landscape genetic approaches can help to identify the environmental drivers of population genetic patterns observed in nature. The implementation of population and landscape genetics has undoubtedly changed management and conservation in many respects. This session will present novel approaches and interesting conservation applications of population and landscape genetics.

Chairs: Niko Balkenhohl & Frank Zachos

Long-term environmental stability, genomic diversity and demographic history of Pan-African chimpanzee populations

Barratt C[1,2], Fontserè Alemany C[3], Lester J[2], Gratton P[2], Onstein R[1], Kalan AK[2], White LC[2], Vigilant L[2], Dieguez P[2], Abwe EE[4], Aebischer T[5], Agbor A[2], Angedakin S[2], Assumang AK[6], Aubert F[7], Ayuk Ayimisin E[2], Bailey E[2], Barubiyo D[2], Bessone M[2], Bonnet M[8], Brazzola G[2], Chancellor R[9], Cipoletta C[10], Cohen H[2], Corogenes K[2], Coupland C[2], Danquah E[7], Deschner T[2], Dilambaka E[10], Dierks K[2], Dowd D[2], Dunn A[10], Dupain J[11], Egbe VE[2], Eno-Nku M[4], Granjon AC[2], Goedmakers A[12], Hedwig D[13], Imong I[10], Jeffery KJ[14,15], Jones S[2], Junker J[2], Kadam P[16], Kambere M[2], Kambi M[2], Kienast I[2], Kujirakwinja D[10], Langergraber KE[17,18], Lapeyre V[2], Lapuente J[2,19], Larson B[2], Laudisoit A[20], Lee K[2,17], Leinert V[7], Maretti G[2], Marrocoli S[2], Martín R[2], Murai M[2], Meier A[2], Mirghani N[21], Morgan B[4,22], Morgan D[23], Mulindahabi F [10], Neil E[2], Nicholl S[2], Nixon S[24], Niyigaba P[10], Normand E[25], Orbell C[26], Ormsby LJ[2], Orume R[27], Pacheco L[20], Piel A[28], Regnaut S[7,29], Rundus A[30], Sanz C[31], van Schijndel J[2,12], Sommer V[32,33], Sop T[2], Stewart F[28], Tagg N[34], Tickle A[2], Ton E[12], Vanleeuwe H[10], Vergnes V[25], Vyalengerera MK[2], Welsh A[2], Wessling EG[2], Willie J[34], Wittig R[2,35], Yuh YG[2], Yurkiw K[2], Zuberbuehler K[36,37], Marques-Bonet T[3], Arandjelovic M[2], Boesch C[2] & Kühl H[1,2]

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[5]*University of Fribourg*
[6]*Department of Wildlife and Range Management, Faculty of Renewable Natural Resources, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana*
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[8]*The Aspinall Foundation, Port Lympne Wild Animal Park, Hythe, Kent, UK*
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[11]*Africa Wildlife Foundation, 1400 Sixteenth Street NW, Suite 120, Washington, DC 20037, USA*
[12]*Chimbo Foundation, Amstel 49, 1011 PW Amsterdam, Netherlands*
[13]*Elephant Listening Project, Bioacoustics Research Program, Cornell Lab of Ornithology, Cornell University, 9 Sapsucker Woods Road, Ithaca, NY 14850, USA*
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[19]*Comoé Chimpanzee Conservation Project, Kakpin, Comoé National Park, Ivory Coast*
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[22]*Institute for Conservation Research, Zoological Society of San Diego, Escondido, CA 92025, USA*
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[24]*Chester Zoo*
[25]*Wild Chimpanzee Foundation (WCF) 23BP239 Abidjan, Côte d'Ivoire*
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[37]*School of Psychology and Neuroscience, University of St Andrews, St Andrews, UK*

It is unknown how Pleistocene environmental change has affected the evolutionary history of chimpanzees across Africa, even though this knowledge may be highly relevant for conservation efforts. Here, we examine the genomic diversity and demographic history of populations across the entire chimpanzee range representing all four recognized subspecies using high-throughput sequencing data (whole-exome and chromosome 21). Combined with high temporal resolution paleoclimate data (up to 1000 year intervals) to reconstruct chimpanzee distributions through time since the Last Interglacial (120 kya), our data yields novel insights into population size changes, gene flow, and contemporary levels of genomic diversity. With this new information we can examine the historical demographic processes that have occurred within and between populations, such as the role of landscape barriers, ecological gradients and forest refugia, in addition to detecting signatures of recent anthropogenic impacts. Together, this work strives for a deeper understanding of diversity patterns in chimpanzees and the mechanistic processes that drive them, enabling predictions to be made about how specific populations will respond to environmental change and anthropogenic impacts in the future.

Genomics and habitat reconstruction track climate-driven population dynamics in birds

Brüniche-Olsen A[1], Kellner KF[2], Belant JL[2] & DeWoody JA[1,3]

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Past climatic changes have had large effects on the distribution and abundance of species. During the Pleistocene, recurring glacial periods forced species to migrate, adapt or go extinct. These environmental changes varied in speed, duration and extent (e.g., glacial and inter-glacial periods). The current acceleration in climate perturbations raises concerns for how species may persist in the changing environment. We are just beginning to understand how species responded to past environmental perturbations (i.e., glacial periods), and this is important for conservation efforts as it enables us to make informed predictions on how they may respond to the ongoing environmental changes (e.g., changes in temperature, habitat availability). Birds have evolved a rich species diversity, successfully colonized most of the world's surface, and adapted to a range of niches. They are well-studied and thus form a well-suited system for studying evolutionary effects of past and ongoing climate change. Using whole genome sequencing and environmental niche modelling we track the population dynamics and habitat availability during the Pleistocene for >80 avian species. Life-history traits (e.g., diet, migration patterns) and IUCN status are used to assess how different groups of taxa responded to past environmental change, and to forecast potential responses to future environmental perturbations. This study may ultimately serve as an indicator for how avian species respond to future climate change, and the methodology are directly applicable to other systems.

Exploring the island biogeography of cryptogams on erratic boulders with a conservation genomic perspective

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Erratic boulders harbouring rock-dwelling cryptogams (bryophytes, ferns, lichens) contribute to total biodiversity in landscapes. In the calcareous Swiss lowlands, about 20 bryophyte, one fern and numerous lichen species occur exclusively on siliceous erratic boulders. Despite their significance for biodiversity, glacial history and island biogeography, the conservation biology of these spatially isolated communities has not been investigated so far. Moreover, they face threats such as encroaching vegetation and rock climbing (bouldering). We aim at creating the scientific basis for the conservation of these small and spatially isolated "terrestrial islands" by addressing: (i) their ecology, (ii) the impact of magnesia used in bouldering and (iii) their phylogeographic origin and connectivity of populations on erratic boulders. The latter is addressed with SNPs derived from ddRADseq. We studied the genetic structure of the regionally critically endangered fern *Asplenium septentrionale* and the moss *Hedwigia ciliata,* which are emblematic species of siliceous erratic boulders. We sampled all eight remaining "island" populations of *A. septentrionale* on erratic boulders, as well as "mainland" populations in adjacent mountain areas. For the more abundant *H. ciliata*, we conducted a congruent sampling, complemented with additional boulder populations of various spatial scales. We present and discuss the genetic results from this unusual island-mainland system.

Limited effects of woody overgrowth on genetic diversity and structure of *Primula veris* in semi-natural grasslands

Träger S[1], Reinula I[1], Holderegger R[2], Helm A[1], Aavik T[1]

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Fragmentation of semi-natural habitats due to management changes is one of the major threats to genetic diversity. In an era of severe environmental change, plants are particularly susceptible to the effects of habitat fragmentation as they are sessile and must cope with novel habitat conditions. Recent high-throughput genotyping enables the detection of numerous genetic markers distributed over the whole genome, including regions of adaptive relevance. We applied double-digest RADseq (ddRADseq) to collect about 3500 single nucleotide polymorphism (SNP) markers across 570 individuals originating from 32 populations of *Primula veris*, a plant species common to semi-natural grasslands. We worked in Estonian alvar grasslands, because of their high conservation value. However, alvar grasslands have experienced a drastic loss in habitat connectivity. We combined population genetic analyses with landscape analyses to evaluate the effect of habitat change due to woody overgrowth of grasslands on the genetic diversity and structure of *P. veris* populations. Our study showed that *P. veris* populations in overgrown habitats maintained a relatively high level of genetic diversity despite substantial change in environmental conditions. In addition, the genetic structure of study populations was related to geographic distance rather than habitat type, amount of barrier (forest cover) between populations, or connectivity. Our results indicate that the effect of habitat change and fragmentation is not genetically manifested in the study populations, yet, suggesting there is still time to counteract a potential tipping point in the genetic variation due to habitat loss in *P. veris*.

Road density is the main driver of spatial genetic structure in European wildcats (*Felis silvestris*) across Germany

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The impacts of anthropogenic habitat fragmentation on gene flow have long been recognized for a variety of species, including species of conservation and management concern. Here, we investigate the large-scale effects of various natural and anthropogenic landscape elements on the functional connectivity of wildcats (*Felis silvestris*) across Germany. We used a continuous dataset of 975 individuals genotyped with 14 microsatellites and distributed across the core range of wildcats in the country. We investigated landscape effects on individual-based genetic structure using multiple regression based on distance matrices in conjunction with commonality analysis. Specifically, we constructed landscape resistance surfaces from 17 different variables, estimated effective distances based on circuit theory and found that six variables have a significant impact on genetic structure (road density, distance to settlements, distance to undivided areas with low traffic volumes, slope, forest & agricultural areas, and straight-line geographic distances). In combination, these factors lead to a spatial bottleneck of low landscape resistances for wildcats in Germany, highlighting the dependence of the species on defragmentation measures, especially with respect to roads. Commonality analysis revealed that road density is by far the single most important driver of wildcat genetic structure, and that this effect is due to the combined effect of different road types (i.e., federal, state and county roads). These findings improve our understanding of functional landscape connectivity in wildcats and can be used to predict the future spread of the species and identify priority areas for connectivity conservation.

Landscape genomics as a useful tool for conservation prioritization: a multi-species study in Eastern Europe

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Classical conservation prioritization methods consider species richness as an indicator for the current level of biodiversity that should be protected. Within a changing environment however, the status quo of biodiversity can change and species need to respond to those changes by shifting their ranges to more favorable habitats or by changing plastically or adaptively. With increasing habitat fragmentation, adapting genetically is likely the only way of ensuring long-term survival of species. Rapid evolutionary responses rely on the standing genetic variation, representing adaptations to the environment, here termed “Environmentally Associated Variation” (EAV). Landscape genomic approaches have greatly facilitated our ability to map this genetic variation and help identify important areas for conservation. Exploiting this opportunity, I integrate genetic variation in spatial conservation planning in Romania and Bulgaria, two highly diverse eastern European countries. I identify major patterns of adaptive variation, ascertained from whole genome Single Nucleotide Polymorphism (SNP) data. I also test whether spatial patterns of EAV in functional genetic markers are well represented by those in non-functional markers. In addition, I evaluate the mutual representation of different measures of biodiversity, including species richness, habitat heterogeneity and EAV. Here, I will present the results for two species, the buff-tailed bumble bee (*Bombus terrestris*) and the house sparrow (*Passer domesticus*). Major patterns of variation were consistent among data types, but finer scale differences highlight the importance of specifically incorporating genetic variation in conservation prioritization. Also, I will present preliminary results on the mutual presentation of different biodiversity measures.

Insights into the distribution of genetic diversity in the lion and implications for conservation

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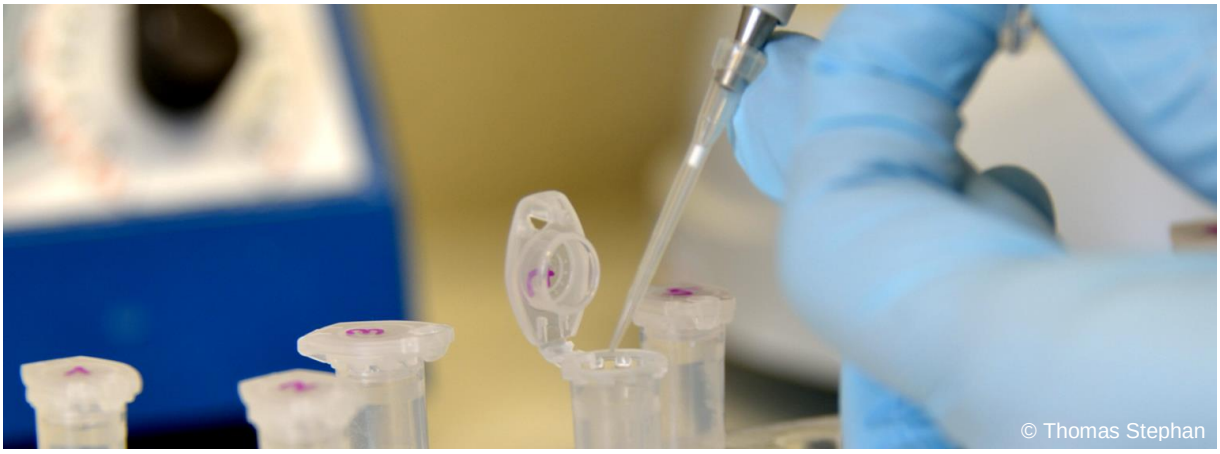
Phylogeographic studies have shown that there is a strong structure in the African lion. We describe here how we used whole-genome sequencing of 10 lions to generate a SNP panel which has been used to genotype ~300 individuals to date. This has improved our understanding of the geographic distribution of genetic diversity in the lion. Specifically, this has been applied in a country-wide effort to genotype Kenyan lions to inform conservation management locally. The SNP panel has also been used to genotype ~70 zoo lions from EAZA affiliated institutions, in order to inform future breeding strategy. Notably, populations in West/Central Africa are genetically distinct from their East/Southern African counterparts, which has led to a revision of the lion taxonomy. Now, we distinguish the northern subspecies *Panthera leo leo* (West/Central Africa + India) and the southern subspecies *Panthera leo melanochaita* (East/Southern Africa). With this revision, taxonomy covers the full diversity of the lion and is more in line with the evolutionary history of the species. This taxonomic revision has immediate implications for conservation, especially for populations in West/Central Africa. These populations are generally small, isolated and declining, a trend which has also been observed in other large mammals in the region. These lineages are also severely underrepresented in captivity, although several 'hybrid' individuals show traces of West/Central Africa origin. This is of value when considering a new breeding strategy. Insight into the distribution of genetic diversity can further contribute to conservation by making recommendations for translocations, reintroductions and reinforcement projects.

S2. Ancient DNA and Museum Genomics



The myriads of specimens contained in natural history collections hold vast potential to enhance biodiversity and conservation research. While genomic tools become increasingly accessible and cost-efficient, the application of these approaches to museum specimens opens up chances to complement ecological studies and inform recent conservation management. We invite contributors to present examples where studies of ancient DNA and museum specimens inform applied conservation.

Chairs: Katerina Guschanski & Elisabeth Haring

Sumatran rhinoceros genomes reveal the conservation implications of differential mutational load among the world's last remaining populations

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**These authors contributed equally to this work*

Recent studies on endangered species have shown that human-induced declines of the past 200 years have led to the accumulation of detrimental mutations in fragmented populations. The Sumatran rhinoceros (*Dicerorhinus sumatrensis*) used to be widespread over Southeast Asia but is now restricted to small and isolated populations on Sumatra and Borneo. We analysed 21 contemporary and historical Sumatran rhinoceros genomes from populations on Borneo, Sumatra as well as from the now extinct Malay Peninsula population. We find that the population on Borneo had already diverged from other populations by 300 ky BP, whereas the divergence between Sumatra and the Malay Peninsula was estimated to 13 ky BP. Contrary to expectations, we found significantly lower levels of inbreeding and mutational load in the two surviving populations on Borneo and Sumatra compared to the extinct popu-

lation on the Malay Peninsula. Moreover, there was no indication of a temporal increase in these parameters on Borneo. In contrast, our results show that the Malay Peninsula population experienced a significant increase in inbreeding during the last century, and had comparatively high levels of inbreeding and mutational load immediately prior to its extinction. Importantly, we found evidence for private detrimental mutations in each extant population. Taken together, these results suggest that managing the species as a single unit by translocation or exchange of gametes could potentially lead to an increase in deleterious mutations in each population and thus reduce the long-term survival of the species.

Larix chloroplast genomes assembled from sedimentary ancient DNA reveal past changes of Siberian forests

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Siberian larch (*Larix* Mill.) forests dominate vast areas of northern Russia and contribute important ecosystem services to the earth. It is important to understand the past dynamics of larches, in order to predict their likely response to a changing climate in the future. Sedimentary ancient DNA extracted from lake sediment cores can serve as archives to study how species reacted in the past to environmental changes. However, the traditional method of studying sedimentary ancient DNA – metabarcoding – focuses on small fragments, which cannot resolve *Larix* to species level nor allow the detailed study of population dynamics. Here we use shotgun sequencing and hybridization capture with long-range PCR-generated baits covering the complete *Larix* chloroplast genome to study *Larix* populations from a sediment core reaching back up to 6700 years from the Taymyr region in northern Siberia. In comparison to shotgun sequencing, hybridization capture results in an increase of taxonomically classified reads by several orders of magnitude and the recovery of near-complete chloroplast genomes of *Larix*. Variation in the chloroplast reads corroborate an invasion of *Larix gmelinii* into the range of *Larix sibirica* before 6700 years ago. Since then, both species have been present at the site, although larch populations have decreased to only a few trees remaining in what was once a forested area. This study paves the way for further studies aiming at using ancient DNA preserved in lake sediments to find possible adaptations to environmental changes or reconstruct ancient organellar genomes.

Detecting ancient dromedary-Bactrian and recent domestic-wild camel hybridization using shotgun sequencing

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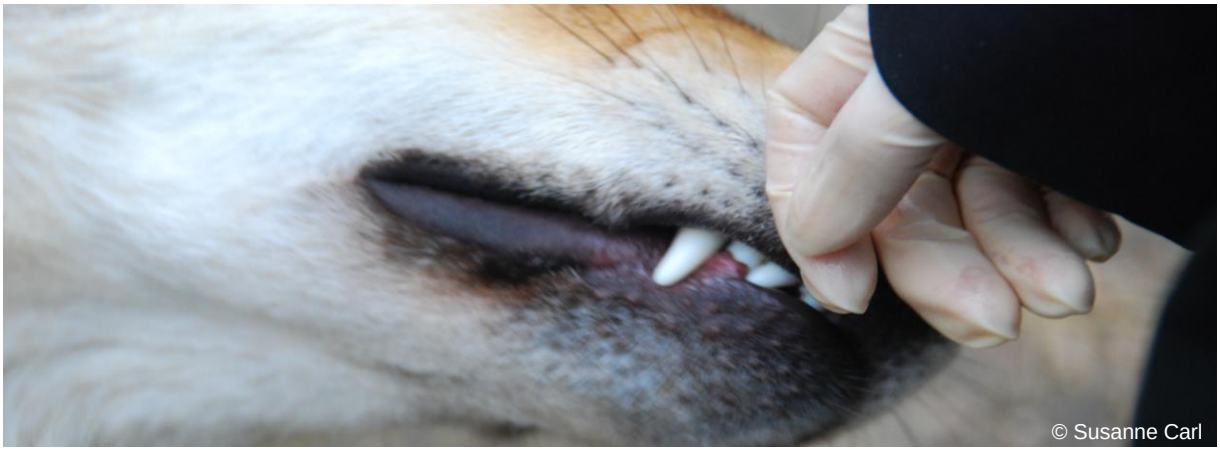
Anthropogenic hybridization is important to obtain specific traits in different species. One example is the hybridization between two domestic Old World camel species - dromedary (*Camelus dromedarius*) and domestic Bactrian camel (*Camelus bactrianus*). However, hybridization can also be a potential threat to endangered species such as between both domestic and wild (*Camelus ferus*) Bactrian camels. In case of dromedary-Bactrian hybrids, humans deliberately started to interbreed these two species, already in historic times, to create stronger and more robust animals. It is not clear when and where interbreeding began, but some postulate as early as pre-Roman times, resulting in ancient hybridization events that would not occur naturally. In order to understand when and where camels first were interbred, we combine history, zooarchaeology and genetics. We extracted DNA from camel bone fragments found at archaeological sites mainly from the Iron Age, following strict laboratory protocols for ancient DNA extraction and analysis. We then subjected DNA extracts to ancient DNA optimized library preparation and performed Illumina shotgun sequencing. We analyzed the resulting ultra-low coverage shotgun sequencing reads with the Paleomix and Zonkey pipelines with the later specifically developed for hybrid detection in archaeological contexts. Finally, archaeologically assigned sample dates were verified with direct radiocarbon dating of hybrid samples, enhancing the chronological emergence sequence and spread of hybrid camels. Finally, for fast detection of domestic - endangered wild Bactrian hybrids, we used whole-genome sequencing data to develop a method for non-invasive samples using PCR and restriction enzymes for thousands of potential RFLP sites.

S3. Molecular Wildlife Forensics



Over the last years genetics has become an integral part of wildlife forensics worldwide. Molecular methods can help with species identification, population sourcing (e.g. for illegally traded wildlife products), characterization of human-wildlife conflicts and even aid in human forensic case work. This session covers the current state and future directions of wildlife forensic genetics, with a special focus on newly emerging genomic methods.

Chairs: Rob Ogden & Stefan Prost

The African Wildlife Forensics Network (AWFN) – Challenges, experiences and opportunities of capacity building in wildlife forensics in Africa

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Developing access to wildlife forensic services in Africa has been identified as an enforcement need in the long-term fight against the Illegal Wildlife Trade (IWT). The African Wildlife Forensics Network (AWFN) was launched in Gaborone, Botswana in May 2016 as part of an initiative led by the United Nations Office on Drugs and Crime (UNODC) and the TRACE Wildlife Forensics Network (TRACE) supported by the United Kingdom Illegal Wildlife Trade (IWT) Challenge Fund. Since then it has expanded to include wildlife forensic scientists and law enforcement stakeholders from thirteen African nations and a range of international technical experts and donors.

The objectives of the AWFN are:

1. To provide and maintain network and training opportunities for wildlife forensics within and beyond Africa.
2. To facilitate interactions between the relevant stakeholders (law enforcement agencies and wildlife forensic practitioners).
3. To coordinate opportunities for wildlife forensics training in Africa.
4. To create an awareness of, and support for new technologies in wildlife forensics.
5. To build shared resources such as reference databases, reference samples, crime scene tools and training manuals.
6. To harmonize wildlife forensics methodologies, good practice, policies and procedures.

This presentation will describe the progress made over the past four years, as well as some of the challenges faced in working across multiple countries with varying capacities and capabilities. It will also introduce a broader strategy being developed for the future of wildlife forensics in Africa.

Using genetics and wildlife forensics in conservation of threatened vertebrates in the Indian Himalayan Region

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Species residing in transboundary landscapes often experience various risks due to lack of common strategies and different priority investment across the range states. The Indian Himalayan Region (IHR), formed by a series of climatic oscillations and temporal topographic metamorphosis, has disrupted the contiguous distribution of several widespread species and plausibly accelerated allopatric speciation. Hence, understanding landscape connectivity, mapping current habitat suitability and investigating population genetics parameters of the standing populations are pivotal to re-create the historic events and propose conservation management plans for widespread species. This paper will address the key findings of the ongoing efforts of Zoological Survey of India, Kolkata, in the field of conservation genetics, meta-genomics and wildlife forensics with special focus to red panda, and Indian & Chinese pangolin.

Red Panda (*Ailurus fulgens*): Briefly, we undertook STR analysis of red panda pellets in Kanchenjunga landscape (KL India-part), shared between India and Nepal, and evaluated functionality of the predicted red panda corridors using landscape genetic approaches. In the entire KL-India, we identified 24 unique genotypes, and results showed that red panda occurs in a meta-population framework in KL-India. Genetic analysis validated the patterns of longitudinal connectivity in the KL-India from West to East, by connecting the landscape in a crescent arc.

Chinese pangolin (*Manis pentadactyla*) and Indian pangolin (*Manis crassicaudata*): We investigated intra and inter species genetic variation by sequencing 624 scales of pangolin for the mitochondrial DNA cytb gene and obtained haplotypes unique to Indian and Chinese pangolins. Scales from the voucher specimens, which varied in the size, shape and weight, were measured for morphological features to establish species-specific signatures of Indian and Chinese pangolins. Further, we also developed a dinucleotide STR multiplex panel for discrimination and individualization of Indian and Chinese pangolins. The multiplex assay has power in forensic assignment of the seizure and for studying population genetic structure of Indian and Chinese pangolins. The present study facilitates law enforcement by enabling on-the-spot decision making by ascertaining species identity from the seized scales.

Developmental validation protocol for species identification using the MinION nanopore sequencer

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DNA barcoding is a powerful and effective tool for species identification in wildlife forensic cases, but remains largely reliant on generating single sequence reads using traditional Sanger sequencing. High-throughput (next generation (NGS) / third generation) sequencing is rapidly overtaking traditional methods in most areas of wildlife genetic research, but has not yet been routinely applied to international wildlife DNA forensics due to issues of platform cost and levels of sequencing error. Oxford Nanopore Technologies have recently developed the MinION, an affordable, small footprint NGS sequencer that has the potential to be distributed to laboratories at an affordable price worldwide. However, to date there has been no formal validation of forensic species identification using high-throughput (deep read) sequence data from the MinION. Here, we present a deep read sequence data validation pipeline for species identification. First, we developed and tested whether our clustering-based bioinformatics pipeline can be used to generate an accurate consensus sequences for species identification. Second, we systematically evaluated the read variation distribution around generated consensus sequence. Finally, we quantified result precision, result accuracy and result specificity using both bioinformatics pipeline and user-friendly software Geneious. Critically, we have applied this pipeline to cytb sequences generated using the MinION. We hope to expand this work across a broader range of taxa and mitochondrial markers and validate its use across labs worldwide. Ultimately, the development of this pipeline will address the pressing need for a portable, low-cost and validated method for species identification in the wildlife DNA forensic community.

S4. Reintroduction and Captive Breeding Genetics

Maintaining captive-breeding populations is of utmost importance for restocking and reintroduction projects and serves as an ark if species become extinct in the wild. While genetic tools play a crucial role in breeding management and monitoring reintroduction success, they are still not routinely applied in this field. The session focuses on outstanding research and application examples in the fields of breeding and reintroduction genetics.

Chairs: Klaus-Peter Koepfli & Sarah Mueller

Low genetic diversity and its consequences for the Alpine bearded vulture reintroduction project

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The ongoing bearded vulture *Gypaetus barbatus* reintroduction in the Alps, which started in 1986, is based on the release of young Bearded Vultures from an internationally coordinated breeding program. All captive bred birds were genotyped with 24 microsatellites using a blood sample. Wild birds are genetically monitored by a non-invasive sampling of feathers mainly collected in targeted searches below eyries. This monitoring enabled us to reconstruct most of the pedigree which is spanning now over five generations. This pedigree reveals a very skewed founder contribution in the wild-breeding population with more than half of the genetic information originating from only six founders and a genetic diversity in the wild population of only 13.5 founder genome equivalents. Therefore, inbreeding depression could put the population in danger without further influx of genetic information through natural immigration or releases. Based on these analyses the release strategy in the Alpine reintroduction project has been revised and carefully selected birds which contribute to the genetic diversity are now primarily released in the part of the Alpine arc where they have the highest probability to become a reproducing adult. In addition, releases in the French Prealps and the Massive Central should help to build-up a meta-population by connecting the Pyrenean and Alpine bearded vulture population. The genetic monitoring remains crucial not only for evaluating the success of this adapted release strategy but also for better understanding the biology of this species (e.g. family histories, native dispersal distances, etc).

Genome-wide evaluation of reintroduced Eurasian lynx populations in Central Europe

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While lynx have been successfully reintroduced within different Central European regions, most populations are currently stagnant or decreasing. Reintroductions run a high risk of encountering genetic problems, which contribute to the long-term failure of many (if not most) reintroductions. These problems arise due to a low number of founder animals and isolation from adjacent populations. This is the case for most Eurasian lynx (*Lynx lynx*) reintroductions, as they show significantly reduced heterozygosity levels. We assembled reference samples from six reintroduction areas and the autochthonous Carpathian source population and applied nextRAD sequencing to assess the extent of inbreeding and genome-wide loss of genetic diversity within the isolated reintroductions. We provide the first estimates of genetic diversity and inbreeding across all different reintroduced Central European lynx populations using 21,000 SNP loci identified through nextRAD sequencing. These samples will become the basis for better comparability of genetic diversity indices between studies and populations. The dataset is intended to provide a basis for lynx managers and researchers working on the implementation of effective management strategies to connect lynx populations in Western and Central Europe.

Genomic impact of founder history on *ex situ* populations of the critically endangered dama gazelle (*Nanger dama*)

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Dama gazelles are the world's largest and rarest gazelle species, with only about 200 animals remaining in the wild. They are native to the Sahara Desert and Sahel, with only remnant populations remaining in Chad, Mali, and Niger. However, more than 2,300 dama gazelles are managed *ex situ* in zoos and private collections around the world, with the largest number of animals found on private ranches in North America, mostly in Texas. Three geographic subspecies have been recognized based on color patterning differences among populations: addra (*Nanger dama ruficollis*), the nominate dama (*N. dama dama*), and mhorr (*N. dama mhorr*). The e*x situ* population of mhorr gazelles was founded by only a small number of individuals, before this subspecies had become extinct in the wild. In contrast, the addra gazelle *ex situ* population was founded by a larger group of individuals. We examined the genome-wide effects of these different founding histories by generating whole genome sequences of addra and mhorr gazelles, which included a chromosome-scale reference genome assembly from one addra gazelle. Mhorr gazelles had almost 50% less heterozygosity, a genome occupied by up to 45% of runs of homozygosity, and about three times the number of putatively loss-of-function mutations compared to addra gazelles. We also analyzed addra gazelle populations managed in zoos and private ranches in North America ddRAD-derived SNPs and found differences in levels of inbreeding and admixture among individuals. These genomic data help inform the conservation management, genetic rescue, and reintroduction of this critically endangered antelope.

Conservation genomics of scimitar-horned oryx: implications for future management

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Captive breeding programmes play an important role in species conservation. The growing move towards integrating *in-situ* and *ex-situ* conservation management requires sustainable and diverse zoo populations to act as sources for future reintroductions. Over the last two decades, genetic data has increasingly been used to improve and evaluate captive breeding programmes. However, advances in DNA sequencing technologies have enabled a transition towards genome-scale analysis and researchers are now able to address broad-reaching biological questions with more power and precision than ever before. For example, it is now possible to measure inbreeding in the absence of any pedigree information, to uncover population structure that had previously gone undetected and to reconstruct both recent and historical population size fluctuations. This has the potential to transform conservation programmes that rely on accurate measures of genetic diversity, inbreeding and demography. The scimitar-horned oryx (*Oryx dammah*) reintroduction programme provides an ideal opportunity to integrate genomic data from zoo populations into applied conservation. We have used whole-genome sequence data together with a chromosomal-level genome assembly to develop a dataset of over one million genomic markers in scimitar-horned oryx individuals originating from multiple captive populations. This has enabled us to a) compare levels of genome-wide diversity with other mammalian species, b) uncover genetic structure among captive populations and c) infer individual inbreeding and demography using runs of homozygosity. I will examine these results in light of what we know about the history of scimitar-horned oryx and discuss implications for the future management of the species.

Using genomics to inform genetic restoration of reintroduced populations

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Alpine ibex almost went extinct by the end of the 19th century with only one population of about 100 individuals surviving in northern Italy. The successful reintroduction of this species to large parts of its former habitat, with now more than 50 000 ibex living in 178 populations, is one of the success stories of conservation. However, the reintroduction events have left a genetic footprint of low genetic diversity and high inbreeding. In order to minimize the negative impact of these genetic deficiencies, e.g. on population growth rates, the management authorities in Switzerland aim to genetically restore several Swiss ibex populations, and to found additional populations. Here we use genomic data to inform the best conservation practice of how to found and restock ibex populations from a conservation genetic perspective. The influence of the number, source and sex of the founder individuals are explored with individual based simulations that take genomic data and life history parameters into account. Specific guidelines of how to found new and genetically restore existing populations are developed from these simulations.

Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex

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Human activity caused dramatic population declines in many wild species. The resulting bottlenecks have a profound impact on the genetic makeup of a species with unknown consequences for health. One key genetic factor for species survival is the evolution of deleterious mutation load, but how bottleneck strength and mutation load interact lacks empirical evidence. We take advantage of the exceptionally well-characterized population bottlenecks of the once nearly extinct but successfully restored Alpine ibex. We analyze 60 complete genomes of six ibex species and the domestic goat. We show that historic bottlenecks rather than the current conservation status predict levels of genome-wide variation. By retracing the recolonization of the Alps by Alpine ibex, we find genomic evidence of concurrent purging of highly deleterious mutations but accumulation of mildly deleterious mutations. This demonstrates how human-induced severe bottlenecks caused both relaxed selection and purging, thus reshaping the deleterious mutation load. Our findings also highlight that even populations of ~1000 individuals can accumulate mildly deleterious mutations. Hence, conservation efforts should focus on preventing population declines below such levels to ensure long-term survival of species.

Targeted conservation genetics of the endangered chimpanzee

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Populations of the common chimpanzee (*Pan troglodytes*) are in an impending risk of going extinct in the wild as a consequence of damaging anthropogenic impact on their natural habitat and illegal pet and bushmeat trade. Conservation management programmes for the chimpanzee have been established outside their natural range (*ex situ*), and chimpanzees from these programmes could potentially be used to supplement future conservation initiatives in the wild (*in situ*). However, these programmes have often suffered from inadequate information about the geographical origin and subspecies ancestry of the founders. Here, we present a newly designed capture array with ~60 000 ancestry informative markers used to infer ancestry of individual chimpanzees in *ex situ* populations and determine geographical origin of confiscated sanctuary individuals. From a test panel of 167 chimpanzees with unknown origins or subspecies labels, we identify 90 suitable non-admixed individuals in the European Association of Zoos and Aquaria (EAZA) *Ex situ* Programme (EEP). Equally important, another 46 individuals have been identified with admixed subspecies ancestries, which therefore over time, should be naturally phased out of the breeding populations. With potential for future re-introduction to the wild, we determine the geographical origin of 31 individuals that were confiscated from the illegal trade and demonstrate the promises of using non-invasive sampling in future conservation action plans. Collectively, our genomic approach provides an exemplar for *ex situ* management of endangered species and offers an efficient tool in future *in situ* efforts to combat the illegal wildlife trade.

S5. Genomic Wildlife Monitoring

Monitoring of elusive wildlife, such as large carnivores or game species, relies strongly on genetic analyses. The dependence on non-invasively collected samples with low DNA content hampers the methodological transfer from traditional multilocus genotyping techniques to genome-wide approaches. In this session we invite talks focusing on the implementation of NGS and other technologies in wildlife monitoring.

Chairs: Carsten Nowak & Alina von Thaden

Monitoring Himalayan brown bear (*Ursus arctos isabellinus*) population by high-throughput noninvasive genotyping

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The Himalayan brown bear (*Ursus arctos isabellinus*) population spanning the northern and southern flanks of Himalaya in Pakistan and India is considered Endangered in the IUCN's Red List under criterion D (very small or restricted population). The total population is estimated at 130-220 bears, but most live in isolated habitat patches with <10 individuals. It is among the least studied brown bear populations worldwide. The IUCN Bear Action Plan (1999) recommends development of efficient and reliable survey methods for regular monitoring of bears. To address this critical requirement, we used the new genotyping approach based on high-throughput sequencing (HTS) of amplicons of short tandem repeats (STR) and a sex marker to estimate abundance and sex-ratio of Himalayan brown bear population in Kugti wildlife sanctuary in India from samples collected non-invasively. We collected 72 fecal and 2 hair samples in spring 2019 (May-June) and could genotype over 90% of these samples successfully at 13 loci. We detected 18 individuals (7 males, 11 females), many of which were recaptured multiple times (average recapture rate 3.28 captures per individual). We present results of abundance estimate based on spatial (SECR) and non-spatial (Capwire) approaches and evaluate the efficacy of HTS genotyping for monitoring of bear populations in Himalaya.

Reduced SNP panels allow for targeted genomic wildlife monitoring based on non-invasive sampling

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Genome-wide sequencing data, collected using next-generation technologies, is becoming widely used in biodiversity research to answer a variety of questions concerning non-model organisms, including phylogenetic relationships, evolutionary history and population structure. In the case of endangered species, the application of genome-wide approaches in the context of monitoring is, however, still hampered by the reliance on non-invasively collected samples with low DNA content as well as the considerable effort needed in data analysis.

Here, we provide examples for reduced SNP panels (rSPs) designed for a wide variety of purposes related to species conservation and wildlife monitoring. The panels are optimized for their application using microfluidic arrays, allowing for fast and accurate data generation based on non-invasively collected samples.

The European bison, for instance, has extremely low levels of genome-wide heterozygosity, which has so far hampered genetic population monitoring and breeding genetics. A recently designed reduced 96-SNP panel allows for analyses of relatedness as well as breeding line discrimination, which provides new opportunities for conservation management. In the case of European wildcats and grey wolves, we apply two SNP panels per species, one optimized for individual discrimination and the other one for hybridization assessment. Based on an optimized 93-SNP panel for maximum discrimination between European wolves and domestic dogs, introgression can be detected up to the third backcross generation, without any potential bias from reference sample selection. For rodents such as the hazel or garden dormouse, reduced SNP panels facilitate distinguishing evolutionary lineages and conservation units, which has direct implications for reintroduction efforts.

Based on these examples we discuss the advantages and limitations of rSPs for their potential application in routine genetic wildlife monitoring.

What can genomic dietary analysis tell us about conflicts between conservation priorities and livestock herding practices?

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The Great Gobi B strictly protected area (SPA) is the final refuge for many species of conservation concern including the Asiatic wild ass or “khulan” (*Equus hemionus heminus*). The existence of threatened wildlife in this nature reserve in the extremely arid steppe region in the south-west of the Gobi Desert is complicated by conflicts with traditional grazing practices of the local herding community. It is unclear how the interaction between herders and wildlife affects the access to preferred vegetation sources and hence optimal forage for threatened fauna. Here we address this question using molecular tools to examine dietary composition of khulan from the Great Gobi B SPA and to compare that with dietary profiles from khulan in an area of contrasting herding activity in the south eastern Gobi. Our results show general concordance with previous work based on stable isotope data but give finer scale information on the genera of plants in the diet. We found different dietary niches between the two study areas and that a seasonal switch between grazing and browsing is less pronounced in the south eastern Gobi. Together these data provide a solid baseline for the management of wildlife-livestock conflicts and suggest scope for future work on feeding practices of other threatened taxa in the Gobi Desert.

The Mobile Biodiversity Lab – DNA based ecosystem assessment in a backpack

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Over the last years we have observed the widespread adoption of DNA based methods, especially metabarcoding, for species identification. Metabarcoding has been tremendously useful for assessment of whole communities across many groups. This method is well validated and has been scaled up in laboratory environments. Metabarcoding has revolutionized the way we asses and monitor global biodiversity. However, these methods require laboratory infrastructure and molecular expertise. Both is often limited in remote locations of the world, which harbor much of the world's biodiversity. Thus, we believe it's time to unlock the next frontier of biodiversity discovery: The mobile biodiversity Lab! Miniaturized laboratory equipment as well as mobile sequencing technology are readily available. Here, we introduce several concepts centered around Nanopore sequencing. Current Nanopore technology suffers from high sequencing error rates, limiting the usefulness of the data. However, using different consensus based approaches, we can drastically increase amplicon sequence quality. Combining optimized protocols and clever bioinformatics, does enable reliable metabarcoding using mobile sequencers. Thus, if successful, the mobile biodiversity lab will allow anyone to assess biodiversity at the point of sample collection without laboratory infrastructure.

Portable sequencing for biomonitoring and capacity building in the Peruvian Amazon

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As biodiversity loss continues to accelerate, there is a critical need for education and biomonitoring across the globe. Portable technologies allow for *in situ* molecular biodiversity monitoring that has been historically out of reach for many researchers in habitat nations. In the realm of education, portable tools such as sequencers facilitate *in situ* hands-on training in real-time DNA sequencing and interpretation techniques. In this study conducted between June and October, 2018, we a) implemented a broad-scale mark-recapture program sampling bats, birds, primates, small mammals and plants in the Madre de Dios region of Peru; b) created a unique field molecular genomics laboratory titled the Green Lab; c) used portable nanopore sequencing to conduct multi-marker DNA barcoding in the first large-scale molecular biomonitoring effort in the region; and d) integrated conservation training programs into both wildlife handling and genetic analyses to facilitate local capacity building. In total, we used nanopore sequencing on 581 samples across three libraries, including 37 primate, 95 bat, 69 bird, 142 small mammal, and 238 plant amplicons. We trained over 35 researchers across 6 countries in wildlife handling and conservation genomics. Finally, we created step-by-step protocols to be used as a blueprint for a conservation genetics field training program that uses low-cost, portable devices to conduct genomics-based training directly in biodiverse habitat countries.

Genetic diversity monitoring: a feasibility study in Switzerland

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Genetic diversity is an integral component of biodiversity. The Swiss Biodiversity Strategy and CBD Aichi targets emphasize its importance and aim to prevent further loss and foster sustainable use of genetic diversity by 2020. Unfortunately, we are far from reaching these goals. In Switzerland, no concept of how genetic diversity can be monitored and how changes in genetic diversity over time can be inferred has previously been developed. However, recent progress in sequencing technology now allows sequencing the genomes of hundreds of individuals at low cost, providing robust estimates of the genetic diversity of populations and species. In a feasibility study we explored how extant genetic diversity and possible changes over time could be assessed across a variety of organisms to initiate a monitoring of genetic diversity, as a first step to its conservation and sustainable use. We propose that genetic diversity be monitored for 50 species from all major taxonomic groups using whole-genome resequencing. The proposed sampling encompasses about 17,000 individuals from all biogeographical regions of Switzerland. The selected species should meet a variety of criteria and include, e.g. rare and common species as well as species affected by climate change or habitat fragmentation. Since genetic diversity usually changes over extended time intervals, we further recommend a retrospective genetic diversity monitoring using samples from scientific collections. With the study of museum and herbarium samples we anticipate to reconstruct changes in genetic diversity over at least one century. We present the set-up of the proposed Swiss genetic diversity monitoring program.

SX. Disease and Functional Genomics

While conservation genetics has largely focussed on neutral genetic variation within populations and species in the past, modern genomic approaches allow for targeted assessments of functional and disease-related loci throughout the genome. Ultimately, conservation genomics must integrate functional traits in order to gain a comprehensive understanding of the effects of habitat fragmentation, inbreeding and genetic diversity loss on populations and species. In this session, the talks summarize the current state and practical applications in this research field.

The devils' cancer: conservation genomics, rapid evolution, and adaptive potential in the face of a unique disease

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Devil facial tumor disease (DFTD) is a transmissible cancer that threatens the persistence of Tasmanian devils (*Sarcophilus harrisii*). Using genomic techniques, we have detected evidence for rapid evolution in response to DFTD as well as a genetic basis to disease-related phenotypes. Recently a second independently derived transmissible cancer was discovered in devils, raising the hypothesis that this a recurring selective force. Using comparative genomic analyses across marsupials, we have found widespread evidence for historic selection in the devil genome, but it does not overlap significantly with candidate genes currently responding to DFTD. If transmissible cancers have appeared historically in the devil lineage, they have imposed selection on different genes, although perhaps similar functional groups, compared to the current DFTD epidemic. These results hold important implications for management of devil populations for the conservation of adaptive potential in the face of transmissible cancer and other threats.

Whole genome and whole exome sequencing for felid conservation management

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The management of species survival programs (SSP) is similar to working with domesticated breed populations. A felid SSP has limited founders, limited migration, limited population expansion and breeding is not always panmictic. Thus, like breeds, an SSP can have inbreeding depression that can lead to health concerns, reduced fecundity and fertility. Genetic advisors for the North American Felid Taxonomic Advisory Group (TAG) are working with SSP coordinators to use whole genome (WGS) and whole exome sequencing (WGS) to identify genetic causes for heritable diseases. WGS of a trio of black-footed cats (*Felis nigripes*) was used to identify a causal variant for a heritable progressive retinal atrophy in the gene, *IQCB1*. This variant is now being genotyped in the SSP breeding population to identify carriers and cats at risk for blindness to select appropriate mating types to reduce the incidence of the disease. The cost for WGS/WES is now sufficiently low to conduct genetic studies in felids. The cat genome has a strong genome assembly for comparison and many good genome assemblies are in development of other felids. Additional studies include Snow leopards (*Panthera uncia*) with eyelid coloboma, lions (*Panthera leo*) with vitamin A deficiency, Pallas cats (*Otocolobus manul*) with polycystic kidney disease, fishing cats (*Prionailurus vivverinus*) with transitional cell carcinoma, and black-footed cats with amyloidosis. These studies have implications for all captive breeding programs as the founder animals can be the origination of the disease variants. Updates on the WGS/WES genotyping efforts for the NA Felid TAG will be presented.

The International Mouse Phenotyping Consortium (IMPC): a functional catalogue of mammalian genes that informs wild species research

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The IMPC is an international endeavour to systematically identify the function of every mammalian gene. Despite having sequenced the entire genomes of many species, most genes remain understudied and their function unknown. To address this shortcoming, the IMPC (www.mousephenotype.org) aims to generate and phenotype a knockout mouse line for every protein-coding gene, thus constructing a catalogue of mammalian gene function; up to now, 7,000 mouse genes have been characterized. While the IMPC strives to generate data that ultimately helps to understand human health and disease, this data can also be useful for studies focusing on other mammalian species, including threatened ones. We will show how IMPC viability data combined with viability data from human cells allows the identification of genes that are essential for development. These genes might be essential in other mammals, too, and we show that they are enriched for genes associated with disease. In addition, the phenotypic data the IMPC systematically collects allows the identification of the physiological systems disrupted when a gene is disabled. This gene-phenotype data can be used to identify genes linked to adaptation in mammals and examples from gorillas, the cheetah, polar bear, wolf, panda and cattle will be presented. This methodology could be potentially applied to current breeding approaches by allowing researchers to identify the individuals that are most likely to produce healthy offspring or preserve genetic variation that is important for adaptation.

S6. eDNA & Genomic Community Assessment

We live in an era of unprecedented biodiversity loss. Large-scale monitoring projects are being carried out to better understand and subsequently counteract this rapid loss of biodiversity. Recent developments in high-throughput DNA sequencing have greatly facilitated the assessment and characterization of biological communities. In this session we will outline the current state and future direction of molecular-based biodiversity monitoring and assessment.

Chairs: Miklós Bálint & Florian Leese

An eDNA metabarcoding time series reveals high macroinvertebrate diversity and seasonal patterns in the Kinzig (Rhine-Main-Observatory)

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Environmental DNA (eDNA) metabarcoding is a new, promising and non-invasive method to detect biodiversity in aquatic environments. So far, it has mainly been used to screen for fish and amphibian diversity and rarely to detect macroinvertebrates. The aim of the project was to assess the potential of eDNA metabarcoding to assess macroinvertebrate diversity from eDNA filtered from a stream. Therefore, we performed a time series at the Kinzig (Hesse), a silica-rich low-mountain-range stream, which is part of the RhineMainObservatory (LTER site). A near-natural sampling location was sampled biweekly for 15 months at three different sites within the stream: 1. surface; 2. riverbed; 3. riverbank. Subsequent steps included the amplification of the extracted DNA using degenerate mitochondrial COI primers BF2/BR2 as well as a newly designed, more specific insect primer. We found 3919 OTUs with the degenerate COI primers, but the majority were diatoms and bacterial. Only 6.7 % were metazoans. With the specific primer, only 1161 OTUs were found but 99.7 % were metazoan. We found a strong seasonal pattern for all taxa detected: diatoms (spring/summer), bacteria (summer/autumn) and macroinvertebrates (winter). While several taxa reported were not found with eDNA metabarcoding, this study shows that long-term time series can be obtained relatively quickly with a great resolution only by analysing eDNA collected from the water.

Assessment of the macroinvertebrate community of the Vjosa river through non-destructive DNA-metabarcoding of preservative ethanol

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Streams and rivers represent hotspots of biodiversity in their natural state. This biodiversity is declining world-wide due to pollution, exploitation, land-use change. Furthermore, in most parts of the world, the natural flow of streams was modified through dams and water regulation, diminishing natural flow dynamics and associated processes such as sediment transport. One of the last big, natural rivers in Europe is the Vjosa in the Balkan region. The catchment is characterized by high habitat diversity and turnover and hosts several sensitive and endemic species (e.g. *Isoperla vjosae*). Here, we assessed stream biodiversity with focus on macrozoobenthic (MZB) taxa via a non-destructive, voucher-preserving DNA-metabarcoding protocol that uses DNA from storage ethanol as template. Samples were taken in spring and autumn 2018 at 48 sites allocated over the catchment. The ethanol used for preservation in the field was filtered through 0.43 um nitrocellulose membranes from which DNA was extracted. Subsequently, a 421 bp fragment of the COI gene was amplified with the primer pair BF2/BR2 and Illumina sequenced. After filtering for sequences with similarity to reference entries >85%, 4,123 OTUs were obtained (34.4%), of which 921 were identified as MZB taxa. Dipterans and ephemeropterans were most abundant, followed by plecopterans. Some taxa were not identified due to primer bias (e.g. molluscs) and over 7000 OTUs could not be yet be assigned above 85% similarity due to incomplete reference data bases. However, our comparison showed the power of non-destructive fixative metabarcoding for detecting MZB communities with highly increased taxonomic resolution.

The diet of the endangered Westland petrel: a DNA metabarcoding approach

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The study of dietary preferences may have important implications for the conservation of endangered species, as feeding ecology and food availability have consequences on their fitness and, hence, in their population dynamics. In the last years, metabarcoding approaches have become powerful tools to characterize the taxonomic diversity of animals' diet. Here, we applied this approach to characterize the diet of the Westland petrel (*Procellaria westlandica*). This seabird is endemic to New Zealand and breeds only in the West Coast of the South Island, spending the majority of its life at sea and returning to the coast only during the breeding season. Being an endangered species as it is, the preservation of the Westland petrel is essential in the conservation of New Zealand's biodiversity. In addition to describing its dietary preferences, we aimed to test whether there were differences in prey diversity and composition between the breeding and non-breeding seasons and, also, between different areas of the species' distribution range. To do so, we collected 99 fresh faecal samples on which we performed 16S metabarcoding Illumina sequencing, quality filtered the library and carried out several biodiversity and statistical analyses. Our results allowed us to describe accurately the diet of this seabird species, confirming previous results based on morphological identification, and, moreover, showing the existence of a clear effect of seasonality on the prey diversity and diet composition of the Westland petrel.

The application of e-DNA methods for amphibian monitoring in a large scale ecological impact assessment

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When amphibians are monitored in the framework of construction projects, field observations including morphological and acoustic methods are standard. However, environmental DNA samples have recently become a powerful tool to gain additional information on species identity or distribution. Yet, monitoring approaches applying genetic methods remain restricted to the scientific user mainly, whereas environmental consulting agencies rarely adopt these novel methods. Here we present an example where environmental DNA was used additionally to field monitoring data to unravel the presence and distribution of two amphibian species listed in the FFH annex IV, the great crested newt *Triturus cristatus* and the pool frog *Pelophylax lessonae* to contribute to a large scale ecological impact assessment in southwestern Germany. Whereas no evidence for the existence of *Triturus cristatus* was gained with traditional field monitoring of >100 waterbodies, the species was found genetically in one of the pools. Surprisingly, most samples of morphologically determined *Pelophylax lessonae* seem to represent *Pelophylax bergeri*, a species which started spreading throughout Switzerland from the south. This is the first indication it might have reached Germany already, possibly replacing *lessonae*. We will furthermore show a range of other species, which were differently represented in the field monitoring versus the genetic data. We therefore conclude that the combination of both methods is necessary to gain a thorough picture of the amphibian fauna in a given area and thus should become a standard method in environmental consulting.

eDNA Monitoring of the endangered European weather loach (*M. fossilis*)

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The European weather loach (*Misgurnus fossilis*) is classified as highly endangered in Germany because of severe habitat loss due to the drainage of swamps and a decreasing number of natural backwaters. To counteract this alarming development, reintroduction programs and intensive monitoring are needed. Because *M. fossilis* buries itself into the sediment, it is difficult to detect via conventional fishing methods. Therefore, environmental DNA (eDNA) monitoring appears particularly relevant for this species. In previous studies, *M. fossilis* was surveyed following unspecific eDNA water sampling protocols, although several studies suggested that eDNA workflows should be adjusted to the target organism. We created two full factorial study designs to investigate which eDNA workflows (sample preservation, DNA capture and DNA preservation) lead to maximum DNA yield for *M. fossilis* in water and sediment samples. To determine the optimal sampling period, we analyzed the DNA yield of samples from a ditch with a natural *M. fossilis* population monthly over the course of one year. Our results show that the eDNA workflow highly influence the target DNA yields, and we present the most suitable eDNA workflow for this species. Furthermore, total and target eDNA was higher in summer months and thus we recommend summer as the most advantageous sampling period. Based on an optimized monitoring protocol, protected areas can be created where human interventions such as sediment dredging, or machine weeding are reduced to a minimum. An efficient monitoring also helps to decide where to apply reintroduction measures and where to find suitable parents for breeding.

How 2bRad can help us to understand genetic connectivity and speciation in the oceans

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Genetic characterization of marine species using DNA-Barcoding is rapidly becoming an accepted standard. The most commonly used fragment belongs to the mitochondrial COI gene. The barcode of life library (boldsystems.org) contains over 7 million barcodes of over 650 thousand species (but mainly terrestrial). As COI is quickly evolving gene, there is enough variability to differentiate species using this gene, but genetic result not always match morphological evidence. On the other hand single nucleotide polymorphism in the COI region is often used to assess haplotype diversity and distribution and to infer genetic connectivity between populations. The caveat of using COI for species assignment and population connectivity is that the mitochondrial genome maternally inherited only, so there is no recombination. Results can be misleading. Restriction site–associated DNA (RAD) methods are based on sequencing the fragments produced by chosen restriction endonucleases. The 2bRAD method uses Type IIb restriction enzymes that cleave both sides of the double stranded DNA at specific distance, producing fragments that are uniform in length. This is an easy and cost effective way for genotyping the whole genome of many specimens from different populations.

In this talk we demonstrate the use of 2bRAD for two questions which are important for marine conservation:

1.) Do the specimens belong to the same species, in case that there is a contradiction between barcoding and morphology? (Brittle stars from the deep-sea and Seastars from the North Sea)

2.) How are the populations connected over long distances? (Hydrothermal Vent shrimps from Indian Ocean)

Workshops

W1. Cheetah Conservation Genomics

Cheetahs are majestic carnivores and the fastest land animals; yet, they are quickly heading towards an uncertain future. Threatened by habitat loss, human-interactions and illegal trafficking, there are only about 7,100 individuals left in the wild scattered across 33 subpopulations. Cheetah conservation is in dire need of comprehensive nations-wide genetic monitoring to aid in evidence-based conservation management decisions. In this workshop, we aim at summarizing the current state of cheetah conservation genetics and monitoring, and bringing together cheetah conservation stakeholders from many countries to facilitate collaborative genetic monitoring efforts.

Chairs: Pamela Burger & Stefan Prost

Cheetah conservation genetics: origins and current applications

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The cheetah is mostly known for its record-breaking speed which makes it the fastest land mammal. It is also the only living representative of its genus (*Acinonyx*) and was one of the first species to benefit from, and demonstrate the importance of, conservation genetics. As the techniques of the field progressed from 2D gels for allozymes to whole genome analyses, they were applied to this flagship species of conservation. All resulting conclusions pointed to a reduced genetic diversity consistent with a historic reduction in population size. We will present a brief overview of the international research efforts that paved the road for the knowledge we have today. Emphasis will be on the various studies assessing the levels of genetic diversity, starting with the first publication in 1983, and including studies on microsatellites, mitochondria, the MHC, and genome wide analyses. While the direct impact of the low genetic diversity remains difficult to assess, it has been linked to poor sperm quality and presents an additional threat to the cheetah's ability to adapt and survive, especially in light of the range-wide decline in cheetah numbers that we are witnessing today. Today the research efforts of the Cheetah Conservation Fund (CCF), and other international laboratories, are emphasizing a stronger application of genetics to conservation, including the optimization of markers to handle poor quality samples, and the identification of the provenance of samples obtained from the illegal wildlife trade of cheetah cubs.

Conservation genomic analyses of African and Asiatic cheetahs (*Acinonyx jubatus)*

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Cheetahs (*Acinonyx jubatus)* are majestic carnivores and the fastest land animals; yet, they are quickly heading towards an uncertain future. Threatened by habitat loss, human-interactions and illegal trafficking, there are only approximately 7,100 individuals remaining in the wild. Cheetahs used to roam large parts of Africa, and Western and Southern Asia. Today they are confined to about 9% of their original distribution. We generated genome-wide data for 55 individuals from all four currently recognized subspecies, along with mitochondrial DNA (mtDNA) data of 135 museum samples to investigate their genetic diversity and conservation status. We found clear genetic differentiation between the four subspecies, thus refuting earlier assumptions that cheetahs show only little population differentiation. We detected stronger inbreeding in the Critically Endangered *Acinonyx jubatus venaticus* (Iran) and *A. j. hecki* (Northwest Africa), and show that overall genome-wide heterozygosity in cheetah is lower than that reported for other threatened and endangered felids such as tigers and lions. We further developed and tested simple amplification based tests to monitor illegal wildlife trade in cheetahs, and developed field friendly research setups for local capacity building in cheetah range countries. Our results provide new and important information for efficient genetic monitoring, subspecies specific management and evidence-based conservation policy decisions, including recent plans to re-wild cheetahs in former range states.

Validation of a Single Nucleotide Polymorphism marker set for forensic parentage verification in cheetah

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Cheetah (*Acinonyx jubatus*) are listed as vulnerable on the International Union for Conservation of Nature (IUCN) Red List of Threatened Species. Export of wild cheetah is strictly prohibited, and captive trade must be managed. In order to monitor trade, it is thus important to develop a forensically validated molecular test that can confirm captive breeding and can be used for forensic investigations. In this study, we developed a 240 SNP array from Double Digest Restriction Associated DNA sequencing (ddRADseq) data and SNPs were genotyped using the Applied BiosystemsTM QuantStudioTM 12 Flex Real-Time PCR System. Here, we generated SNP data for unrelated individuals (n = 76) and known family groups (12 families consisting of 3-5 individuals) in order to validate the SNP array. In addition, the cross species amplification of the SNP array was tested on a variety cheetah subspecies and other feline species. From the array data, 218 SNPs reproducibly amplified in cheetah and the optimal concentration ranged from 10 and 30 ng.ul-1. Cross species amplification in other felids was limited; however the SNP array demonstrated a clear genetic separation of three cheetah subspecies. Further, the combination of 218 SNPs had a higher resolving power for individual identification compared to Short Tandem Repeats and provided high assignment accuracy in known pedigrees. We conclude that the described molecular test is suitable for accurate parentage assignment and provides a traceability tool for forensic investigations of cheetah.

Assessing cheetah's population size, structure and diet in the central deserts of Iran with genetics

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Cheetah populations have undergone massive range reduction over the past century, both in Africa and in Asia. The decline was more extreme in Asia and currently a single population persists in the central deserts of Iran. Despite being the most threatened felid in the world, the knowledge on status and ecology of Asiatic cheetah (*Acinonyx jubatus venaticus*) is scarce: they are divided into several subpopulations, but it is unclear the fragmentation level, and they are reported not to attack livestock but the actual main prey items of their diet is unknown. In this study we aimed to assess population size and structure, gene flow dynamics among the putative sub-populations, and their diet composition. We collected carnivore scat samples across the currently known Iranian distribution (N=382). Mitochondrial DNA sequencing was used to identify scat depositors, and those belonging to cheetah (N=139) were genotyped using 22 microsatellite loci to identify possible individuals and assessing the genetic diversity and population structure. DNA metabarcoding approach was then used to identify prey items in scats. In total, 15 individuals (11 males and 4 females) were identified. The population is structured into three subpopulations: northern (Touran), southern (Yazd) and eastern (Naybandan). Northern and Southern populations are geographically separated, however they can be connected indirectly through the eastern population. Cheetahs feed mainly on wild sheep (*Ovis orientalis*), wild goat (*Capra aegagrus*) and hare (*Lepus sp.*), the composition of prey items varies between male and females and in different regions depending on the availability of prey items.

Determining genetic variability, kinship, and uniqueness in *ex-situ* cheetahs (*Acinonyx jubatus*) in North America

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The cheetah is a charismatic ambassador for wildlife conservation. Due to poaching, habitat loss, and human conflict cheetah populations are dwindling. Only 7,100 wild individuals remain, illuminating the importance of maintaining captive populations against extinction. One major challenge is the low genetic diversity of cheetahs due to historic population bottlenecks. Currently, the North American Species Survival Plan (SSP) cheetah population is managed through a pedigree-based breeding program. Breeding recommendations aim to minimize the mean kinship of the *ex-situ* population and retain genetic diversity. However, founder assumptions, unresolved parentage, and inaccurate record keeping can decrease the accuracy of pedigree-guided breeding recommendations, which may lead to less optimal breedings, a loss of genetic diversity, and potentially an increase in inbreeding events. To mitigate these issues, we developed a panel of 16 highly polymorphic tetranucleotide microsatellite markers from the cheetah genome and genotyped 234 cheetahs to determine genetic variability, kinship, and identify unique individuals. Empirical pairwise relatedness values ranged from -0.732 to 1. Preliminary findings suggest a weak correlation between the empirical molecular and the pedigree-derived estimates of relatedness (r=0.179), which may reflect possible effects from founder assumptions. This study represents a step towards the inclusion of empirical data in captive breeding programs to help resolve unknown parentage and bolster the current pedigree-based system. As a species with severe genetic homozygosity, future management plans for captive and wild cheetah populations will directly benefit from molecular information to maximize breeding potential and genetic diversity.

The peculiar innate immune system of the cheetahs (*Acinonyx jubatus*)

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Cheetahs (*Acinonyx jubatus)* present little variation at the Major Histocompatibility Complex (MHC), a part of the adaptive immune system whose variability is thought to be crucial for recognizing a wide variety of pathogens. Cheetahs are therefore expected to have impaired resistance to infectious diseases. However, free-ranging cheetahs show no clinical or pathological evidence for disease despite being infected and/or exposed to various pathogens and parasites, suggesting an effective immune response. The immune system is highly complex and various other components apart from MHC participate to an adequate response. We therefore hypothesized that the immune system of cheetahs relies on such other components to compensate for the low variation at the MHC. To investigate this hypothesis, we measured six humoral effectors covering both innate and adaptive immune systems in cheetahs and leopards *(Panthera pardus*). The latter lives sympatrically, but has a higher MHC variability than the cheetah. We demonstrate that cheetahs had a stronger constitutive innate immunity than leopards, but a lower adaptive immunity. We conclude that cheetahs have shifted their immune investment towards a strong innate immunity, thus demonstrating that different species use different immune strategies to achieve similar levels of protection. Therefore, we conclude that the immune response of cheetahs is equally successful and their immune competence is higher than previously thought. Our results highlight the importance of combination of immunogenetic and functional immune methods in order to fully understand the health status of endangered species.

W2. Policy, Society & Outreach

A central part of conservation research and applications is the effective communication of results and recommendations to the general public, as well as policy and decision makers. This workshop aims at bridging the gap between policy and research, and explores effective ways to disseminate research results to the public via citizen-science and outreach.

Chairs: Rolf Holderegger & Gernot Segelbacher

Developing a genetic diversity monitoring program - What do the stakeholders say?

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Genetic diversity is a fundamental component of biodiversity and its conservation is considered key to ensure the long-term survival of species. The importance of safeguarding genetic diversity is reflected in Aichi target 13 of the United Nations Convention on Biological Diversity (CBD), which calls for the maintenance of genetic diversity and for strategies preventing further losses by 2020. However, no country is systematically monitoring the levels of genetic diversity in natural populations of wild species to date. Even Switzerland, who included genetic diversity in its national biodiversity strategy, only monitors species and landscape diversity. To explore the circumstances of implementing a genetic diversity monitoring program in Switzerland, we carried out a stakeholder analysis in the course of a feasibility study on genetic monitoring. We collected the data through expert interviews and an online survey. Based on this, we present the opinions and needs of different Swiss stakeholders regarding a nationwide genetic monitoring program for populations of wild species. Swiss stakeholders are overall aware of the lack of evidence regarding the status of genetic diversity in populations and species. Accordingly, a majority is interested in the development of a monitoring program and see opportunities to apply it in their work. Nevertheless, some stakeholders express concerns, such as limited resources of regional authorities and the fear that results may not be applied in practice. We propose to consider our findings in the future development of monitoring programs, which should be globally implemented at national levels in forthcoming years. Transparent communication about possibilities and limitations of a monitoring program and the involvement of concerned stakeholders might increase its acceptance.

W3. Einführung in die Naturschutzgenetik für Anwender, Entscheidungsträger und Behörden (in German)

Genetische Methoden finden im Arten- und Naturschutz, wie auch im Biodiversitätsmonitoring mittlerweile eine breite Anwendung. Vertreter aus dem angewandten Natur- und Umweltschutz sind daher immer häufiger mit Ergebnissen genetischer Studien konfrontiert und müssen entscheiden, welche genetischen Methoden zur Beantwortung einer naturschutzfachlichen Frage angewendet werden sollen. Dieser Workshop ist speziell für Anwender im deutschsprachigen Raum konzipiert, die Grundlagenwissen im Bereich der Naturschutzgenetik erlangen möchten, die ihnen in bei der Integration genetischer Methoden in ihre Projekte helfen. Im Rahmen eines initialen “Crashkurs: Naturschutzgenetik” wird dieses Wissen auf anschauliche Wiese vermittelt und dann im Rahmen einiger Praxisbeispiele vertieft (z.B. eDNA-Einsatz im aquatischen Biodiversitätsmonitoring, genetisches Monitoring großer Beutegreifer, (Meta-)Barcoding zur schnellen, standardisierten Biodiversitätserfassung).

Chairs: Carsten Nowak, Stefan Prost, Alina von Thaden

Detailliertes Programm separat.

Posters

Optimizing non-invasive genetic tools and DNA metabarcoding to assess the abundance and diet of the wild boar (*Sus scrofa*)

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The wild boar's (*Sus scrofa*) increasing abundance observed over the last decades in Europe and its widespread distribution are posing several threats to human safety, animal health, overall biodiversity (e.g. due to predation), among others. However, this elusive species is difficult to study and monitor using traditional ecological approaches. In this study, we have optimized genetic protocols to infer the abundance and diet of wild boar populations through the analysis of faeces. We used mitochondrial and nuclear markers to infer species, sex and individual ID, in order to further use this data on spatially explicit statistical models. In addition, a DNA metabarcoding approach was optimised to determine the range of species predated and/or consumed by wild boar. For that we used two pairs of primers: i) the trnl primer to amplify plants; and ii) the COI primer to amplify metazoan. So far, we have analysed 69 faecal samples from two distinct regions in the Iberian Peninsula: Castilla-la-Mancha county and Donãna National Park. 29 out of 32 faeces identified as wild boar amplified for nuclear markers, which together with our reference dataset of more than 400 wild boar and domestic pig genotyped in the Iberian Peninsula allowed estimating a probability to identity of 3.20×10^{-13} and probability to identity assuming siblings of 1.30×10^{-5}. Finally, the diet of the 29 individuals was characterized using the frequency of occurrence of family taxa. Overall, our results support for the inclusion of these genetic tools within the toolbox for population monitoring of this relevant species.

Can major histocompatibility complex genes be informative of golden jackal population dynamics?

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The golden jackal (*Canis aureus*) is currently undergoing a rapid range expansion throughout South-eastern and Central Europe. Genetic studies on neutral loci revealed low diversity among and within populations, and other markers were suggested for studying the origin and diversity of the present golden jackal European populations. Major histocompatibility complex (MHC) genes, which are crucial for adaptive immune response, represent functional, fitness-related genetic markers. Over short evolutionary time MHC diversity is maintained by diversifying selection, which promotes heterogeneous selective pressures over spatial and temporal scale. In this study, we examined genetic variability at MHC class II DRB, DQA and DQB loci in golden jackal population from Eastern Serbia. Using the cloning–sequencing method, we analysed 47 individuals collected between 2004 and 2016 and found four DLA-DRB, three DLA-DQA and three DLA-DQB alleles. Low allelic variability was compensated by six DLA-DRB1/DQA1/DQB1 three-locus haplotypes and substantial nucleotide diversity. Further, we found two intriguing haplotypes. The first one, DLA-DRB1*04503/DQA1*00101/DQB1*00806 that included newly identified DQA1 variant in jackals, was detected in only one individual, but as homozygous, suggesting its prevalence. Not being found on other locations so far, this haplotype raises question on Eastern Europe jackal population dispersal routes. The second haplotype, DLA-DRB1*04503/DQA1*00402/DQB1*02305 so far detected exclusively in ancient and genetically differentiated Dalmatian population, implies that there might be connection between continental and coastal jackal populations. Our results suggest that MHC genes might be informative and interesting markers in studying golden jackal population dynamics.

Evolution of the highly adaptable immune loci in dolphins

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Due to their crucial role in adaptive immune response, major histocompatibility complex (MHC) genes are considered essential for individual fitness and relevant to conservation. Distinctive feature of MHC genes is their exceptional polymorphism. However, studies on marine mammals revealed relatively low genetic diversity compared to terrestrial mammals, which was explained by different selection regime in the aquatic environment. In this study, we analysed genetic diversity at MHC class II DQA and DQB loci in three Mediterranean dolphin species: striped (*Stenella coeruleoalba*), Risso's (*Grampus griseus*) and bottlenose dolphin (*Tursiops truncatus*). Diversity indicators from our research were comparable to terrestrial mammals. Moreover, we found exceptional polymorphism in striped dolphin, with allelic richness and nucleotide evolutionary distance values notably exceeding those in Risso's and bottlenose dolphin. To investigate how much allelic diversity corresponds to functional diversity, multiple correspondence analysis was applied. Translated alleles were grouped by supertypes, considering physiochemical properties of the amino acids predicted to be under positive selection. We discovered an equal number of DQB supertypes comparing stripe and bottlenose dolphin, but notable difference at DQA locus where striped and bottlenose dolphin alleles clustered into ten and five supertypes, respectively, implying larger functional DQA diversity in striped dolphin. Small number of alleles found in Risso's dolphin was compensated by nearly equal number of supertypes, pointing to persistence of functionally divergent alleles in population. Eight DQA and eight DQB private supertypes might reflect species-specific parasite communities. Our results are indicative of distinct MHC evolution patterns and specific selective pressures across dolphin species.

Hybridization of wolf (*Canis lupus*) and dog (*Canis familiaris*): Introducing research on genome interactions and artificial selection

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The evolution of canids is deeply influenced by various rates of historical introgression. Recently, the hybridization between wolf and dog is considered as a potential threat. It could occur in small isolated wolf populations with low density of individuals or at the range edges (cf. history of Apennine population).

On the other hand, wolves were used to create new dog breeds. The aim was to create wolf-alike individuals that are tame and able to cooperate with humans. Such a crossbreeding experiments are known from many countries such as Czech Republic (Czechoslovakian wolfdog), Netherlands (Saarloos wolfdog), Russia (Volkosob wolfdog), United States (American wolfdog) or China (Kunming wolfdog). Our first studies based on Czechoslovakian wolfdogs revealed that wolves' genes are mostly linked to the wolfdog's morphological traits, meanwhile dog ancestry was observed mainly in physiological traits, in the regulation of circadian rhythms or cognitive functions. These crossbreeding experiments provide great opportunity to study interactions of genomes with known ancestry. Subsequent artificial selection represents a model enabling to study domestication process. Thus, the mapping of wolfdogs' genomes could help in our understanding of hybridization events and shed more light on the evolution of domestication.

The poster introduces a project focused on genomic selection within wolfdogs using 170k SNPs and whole-genome sequences. The aim is to determine the genomic composition and direction of gene selection in selected groups of wolf-dog hybrids such as Czechoslovakian wolfdog, Saarloos wolfdog or American wolfdogs.

Conservation genetics of gazelles in Iran

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Gazelles of the genus *Gazella* live in arid habitats in northern Africa, the Arabian Peninsula and Asia. Nine extant species are currently listed by the IUCN, and all except one are classified as “Vulnerable” or “Endangered”. Although these species occur in protected areas and are quite often bred in captivity, conservation on a national level remains difficult due to illegal hunting, habitat loss, and a lack of knowledge about the genetic makeup of the often small and widely separated populations.

Iran is home to at least three gazelle species: the widely distributed goitered gazelle (*G. subgutturosa*), the chinkara (*G. bennettii*) in desert areas in Central to Southeastern Iran, and the Arabian mountain gazelle (*G. arabica*) on Farur Island in the Persian Gulf. We collected fecal samples of gazelles in over 60 areas throughout the country. These were sequenced for cytochrome *b* for understanding subspecies patterning, population structure, and biogeography of the two wide-spread species (*G. subgutturosa* and *G. bennettii*) and evolutionary origin of *G. arabica* on Farur Island.

Surprisingly, the sequence data also revealed the possible occurrence of a fourth gazelle species, as mitochondrial sequences of sand gazelle (*G. marica*) were detected in two wild populations in south-western Iran. One of these is a mixed population of *G. marica* and *G. subgutturosa* that were introduced to the area from two (phenotypically similar) source populations. Furthermore, we detected natural hybrids of *G. subgutturosa* and *G. bennettii* in the Central Iranian deserts. Our results highlight the importance of genetic knowledge prior to re-introductions, and for improving captive breeding of gazelles in Iran.

Conservation genetics of pangolins in Congo

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Pangolins (Pholidota) are a unique group of mammals from the superorder Laurasiatheria with apomorphies related to myrmecophagy including protective scales, trophic adaptations and expansion to semi-fossorial or arboreal niche. Pangolins are often a target of poachers, they are hunted for their meat, which is considered a delicacy, and for their scales used in the Traditional Chinese Medicine. They are currently considered the world's most trafficked mammals. There are eight species of pangolins (four in Asia, four in Africa), all of them are listed on the IUCN Red List as threatened. Monitoring of pangolins using survey methods such as camera traps is difficult since they are mostly nocturnal and live either in burrows or treetops. Molecular methods are therefore a great tool to study them. Our study focuses on two most trafficked pangolin species occurring in Congo: the White-bellied Pangolin (*Phataginus tricuspis*) and the Giant Pangolin (*Smutsia gigantea*). We used 53 scales, 8 tissues and 3 buccal swabs collected from villagers in the area in Odzala-Kokoua National Park in Congo. The analyses were based on mitochondrial (d-loop) and nuclear markers (beta-fibrinogen, titin). The aim of the study is to assess and compare the genetic diversity, demographic parameters and phylogeographic history of the two pangolin species in the Odzala-Kokoua NP. This is the first detail population study of these species. Understanding the population biology of pangolins may contribute to better conservation management and in the fight with illegal trade with these endangered animals.

From conservation genetics to conservation genomics: the case of the endangered land tortoise *Testudo hermanni*

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For the past half century, it has been broadly perceived that the rate of species extinction is increasing and many species are in imminent extinction danger. In this context, genetics provides essential support to conservation biology because it helps to understand the evolutionary background of endangered species and enables the development of better management strategies. The Hermann's tortoise (*Testudo hermanni*) is an endangered land tortoise distributed in disjoint populations across Mediterranean Europe. Habitat reduction, intensive agricultural practices and forest fires are major causes of decline in different areas. Intense harvesting for the purpose of pet trade and the release of non-native individuals into autochthone populations represent additional threats. Our previous genetic studies based on a small panel of microsatellites and mtDNA markers were able to clearly distinguish two subspecies and to identify some major geographical groups, allowing also the development of a practical genetic toolkit for geographic assignment. More recently, we performed a ddRAD genomic sequencing that produced approximately 3,000 nuclear SNP markers and revealed further substructure in Western populations, especially in Calabria (Southern Italy). This genomic dataset was simplified into a panel of 48 informative SNPs that can be cost-effectively used to detect the geographic origin of confiscated individuals currently kept in captivity, thus helping their correct relocation in reintroduction plans. Moreover, this panel will be a useful resource to investigate patterns of illegal translocations and to assist forensic genetic applications.

Genome diversity and linkage disequilibrium in dromedary camels in Iran

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For the development of camel husbandry for protein production in desert climate, attention to genetic improvement is very important. Lack of records, pedigree, connectedness, size of herds and genetic evaluations are limitations for optimized camel breeding. Traditional camel breeding is difficult because of recording difficulty, disruption of herds and staff injures. Genetic diversity of Iranian dromedary camels was assessed by using 96 GBS data in 5 regions of central desert. Number of 14,522 SNPs (Average MAF=0.19) were discovered. Average observed heterozygosity was estimated 0.25 ± 0.03. Mean of LD at distances shorter than 40 kb was anticipated 0.089 ± 0.234. Principle component analyses and Genome Admixture indicate no deference among five populations in central desert in Iran (Bafgh, Khatam, Bahabad, Ardakan and Mehriz). Predicted Tajima's D (1.28) suggested a bottleneck or balancing selection in Iran's dromedary camels. This report is the first SNP calling report on nearly chromosome-level. Development of breeding programs in camels require genomic data to improve the production and performance traits. GBS based on whole genome sequencing could prove highly suitable for the analysis of relatedness and genetic diversity in camels.

Spatial distribution and risk of potential hybridization of the European wildcat (*Felis silvestris silvestris*) with the domestic cat (*Felis silvestris catus*) in Baden-Württemberg, Germany

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At the background of hybridization the main goal of this study was to assess if European wildcat presence in forest habitats attracts or scares away domestic cats. On one hand, wildcats excrete special sex pheromones during the mating season that might also attract domestic cats in the vicinity. On the other hand, aggressive territorial behavior of wildcats within their home range boundaries might chase domestic cats off. To investigate this, genetic data of 8 years of wildcat monitoring in Baden-Württemberg was used (2008 - 2016). Wildcat and domestic cat samples were assigned to one of the two subspecies based on mtDNA and microsatellite fragment analysis. Landscape related variables including forested areas, wildcat suitable habitat, settlement areas and data of single buildings outside of human settlement areas were created and calculated with ArcGIS. For statistical analysis a binomial mixed model (GLMM) was chosen and calculated in R. Domestic cat records at the lure stick were selected as response variable, whereas data on wildcat occurrences, distance to settlements, size of settlements and distance to the nearest single building outside of settlement areas were chosen as predictors. Main results displayed a significantly positive influence of wildcat occurrence in the close proximity to the lure stick on occurrence of domestic cat records. The probability of domestic cat records at a lure stick decreased significantly with increasing distance to the settlement. This study revealed some underlying mechanisms of wildcat and domestic cat occurrences at lure sticks to gain insight into potential risks of hybridization.

Landscape genomics of a widely distributed racer (*Dolichophis caspius*, Gmelin 1789) across eastern Europe and western Asia

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The Caspian whipsnake, *Dolichophis caspius*, inhabits a wide variety, but increasingly fragmented habitats from East-Central Europe to Western Asia. Until now, genetic studies on the species have been scarce. By double-digest restriction associated DNA (*ddRAD*) sequencing of 53 samples providing 17K single nucleotide polymorphisms (SNPs) we estimated genetic diversity, differentiation and effective migration patterns of populations sampled across the distribution range, and to detect genotypes and genes under selection by climatic factors. Principal component analysis (PCA), AMOVA, NeighborNet network and Admixture analysis identified eight clusters in the Caspian Whipsnake population. Estimated Effective Migration Surfaces (EEMS) revealed higher-than-average gene flow in most of the Balkan Peninsula, and lower-than-average gene flow along the middle section of the Danube River. These northernmost populations are located in small isolated patches along the western bank of the river. Landscape genomic analysis with Samßada identified a total of 751 selected genotypes that correlated with seven climatic variables (wind speed in April, annual mean temperature, isothermality, temperature annual range, mean temperature of the wettest quarter, annual precipitation and precipitation in the driest quarter). Isothermality correlated with the highest number of selected genotypes (478) found in 41 genes, followed by annual range (127) and annual mean (87) of temperature. Annual precipitation had the least correlation with only two genotypes in noncoding regions. We conclude that environmental variables, especially the day-to-night temperature oscillation in comparison to the summer-to-winter oscillation, have an important role in the distribution of Caspian Whipsnakes across their habitats.

A full chain-of-custody for big data as prerequisite of population-level conservation genomic tools

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Many conservation genetic tasks require the reliable identification of the geographic origin or within-species genetic lineage of individuals. In evolutionary systems dominated by a multitude of processes and noise, advanced population-level inference approaches continuously progress towards ever more finely identifying and extracting from large genomic datasets the genetic signal that is specific to a given question and its scale.

The collection of the thereby required global reference datasets of genetic diversity from natural populations is an extensive cooperative effort that requires many logistic and analytical steps. These cover the whole process, from project and sample design, sample collection and management, lab work and genomics to statistical analyses and reporting, as well as, finally, conclusions, which form the basis for further research and applied action.

Integrated into a single, user-friendly chain-of-custody of interoperable modules, these many steps can be managed even by smaller working groups focusing on non-model organisms from across the Tree of Life. Quality control and assessment are substantiated by standards and certified procedures, forming a data infrastructure and work environment. Throughout the chain, build-in functionality for efficient data cleaning and exploration, as well as, the reproducibility of analyses, allows for effective error detection and removal. Likewise, workflows for evaluations of model sensitivity and checks of model usefulness provide the basis for the validation of data and models.

Such a chain-of-custody provides the foundation for robust and reliable, as well as, scalable conservation genomic tools. These enable communities, governments and conservation activists to protect, manage and sustainably use biodiversity.

GEANS: Genetic tools for ecosystem health assessment in the North Sea region

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Several EU directives and OSPAR guidelines require transnational sustainable management of marine resources. Benthic organisms are key components in environmental impact assessments and the Marine Strategy Framework Directive. Currently, indicators are mainly based on morphological taxonomy, being time-consuming, labour-intensive and skills reliant. Novel, DNA-based tools promise cheaper, faster and more accurate methods, yet, different approaches between countries are used which hamper standard routine application. GEANS is a transnational co-operation among nine institutions aiming to implement mainstream fast, accurate, cost-effective DNA-based tools in routine monitoring programs enabling national authorities to adapt management measures in a transnational coherent way, resulting in improved management of human activities and protection of the marine environment across the North Sea Region. Within GEANS an open DNA reference library is developed serving as the backbone of all the molecular protocols. Furthermore, real time pilot studies, in close cooperation with managers, policymakers and involved stakeholders are implemented and will deliver proof of concept on the added value of genetic approaches in environmental health management. GEANS will provide a decision support framework including a fit for purpose choice of genetic tools and protocols, helping to translate genetic results into simple indicators.

Evaluation of eDNA as detection tool for imperilled native crayfishes

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Native stone (*Austropotamobius torrentium*) and white-clawed crayfish (*Austropotamobius pallipes*) are facing long-lasting, persistent population declines and are now among the most threatened animal groups in Germany. Effective conservation measures require knowledge on their distribution and remaining populations must be monitored regularly. However, conventional monitoring approaches are mostly disruptive for the animals, time consuming and require a high effort to detect populations at low densities. Detection by means of environmental DNA (eDNA) extracted from water samples represents a new promising tool for non-invasive and cost-efficient detection of freshwater crayfish. We are evaluating the reliability of eDNA as detection and monitoring tool for native crayfish. Particularly, we assess how detection probability is influenced by season, sampling location (within vs. downstream population) and population size. For this purpose, we developed a species-specific eDNA assay for each crayfish species, which was established in the laboratory by way of aquaria experiments. In addition, we took water samples from four wild crayfish populations using a spatial and seasonal sampling design. Preliminary results confirm detectability of both crayfish species in aquaria and field samples. For instance, stone crayfish were successfully detected via eDNA in the middle and 1.3 km downstream of the population in summer and autumn. Further investigations will show whether a year-round and consistent eDNA-detection of native crayfish is possible and whether population size can be estimated from eDNA samples using a quantitative approach (ddPCR).

Admixture patterns of Nile tilapia (*Oreochromis niloticus*) in East Africa and its conservation consequences.

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Translocation of natural populations may promote artificial admixture between groups, which may lead to outbreeding depression compromising their conservation status. This is particularly frequent on species with commercial value such as the Nile tilapia in East Africa. This species is native to the East African rift valley water bodies and the river Nile. To compensate losses due to overfishing, it was introduced in Lake Victoria and other lakes where it is not native. Native close related species were present in these lakes prior to the introduction so hybridization between them may have been promoted by these events. Additionally, stoking and aquaculture activities involving several water bodies are reported in the region which may have contributed to an artificial homogenization of Nile tilapia variation.

In the current work we evaluate if anthropogenic activities contributed to admixture of Nile tilapia both between populations and species. This was done using amplicon sequencing to genotype multiple microsatellite and mtDNA loci. We focused on native and introduced populations from Uganda. The results showed two major genetic units having each one of them contributed to the stoking of different waterbodies. Admixture between these groups is higher in non-native populations than in native's indicating multiple stoking events. Additionally, we found some mitochondria haplotypes to be shared between species which may be an indicative of hybridization has been promoted with the introductions of Nile tilapia. The results support that admixture is likely being promoted by anthropogenic activities which should be considered for conservation measures.

The genetics of reintroduced addax populations in Tunisia: moving towards a global management plan

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Populations of the addax (*Addax nasomaculatus*), a desert specialist antelope, are critically low and the last remaining wild populations are on the brink of extinction. Captive and reintroduced populations are therefore vital for the species' survival. Addax were reintroduced to Tunisia in the late 1980s from breeding programmes in Europe (EEP) and North America (SSP), and addax have since been translocated across three national parks. However, the small and isolated nature of these populations, which were formed from very few founders, make them susceptible to inbreeding and loss of genetic diversity, and so developing a meta-population management plan which incorporates genetic data is crucial for long-term sustainability.

Using biopsy darting, we were able to almost exhaustively sample the Tunisian population (104 of 108 addax sampled), and samples have been collected from captive populations in Europe, North America and Arabia. Reduced representation sequencing (ddRAD) was used to identify and genotype over 4000 SNPs across the sampled populations. Genetic diversity within Tunisian population was generally low, although a single national park which received a secondary augmentation of addax had substantially greater genetic diversity. Analysis of population structure revealed distinct genetic clusters and diversity was unevenly partitioned amongst captive populations, however all populations have the potential to act as a source for additional diversity to the reintroduced Tunisian population. This genetic data will now be used within population viability assessments to identify optimal management strategies for the Tunisian meta-population, exploring the impact of reinforcement and translocations on both population demographics and genetic diversity.

Metabarcoding of trap nests for bees and wasps to analyse multitrophic interactions in changing environments

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Insects and other arthropods are the largest animal group worldwide, occupying key positions in food webs and ecosystem processes, such as pollination. Their importance for ecosystem functioning and services is unparalleled, and estimations of their economic value reach billions of dollars per year alone for the US. Only recently, long-term studies have revealed a severe decline in arthropod diversity, biomass and abundance across Europe and other world regions. This excessive loss and its potential consequences for nature and mankind alarmed experts and society and engaged scientists in identifying the causes. Habitat change has been named a key factor, yet the complexity of insect ecologies hampers to elucidate the mechanism.

In the present project we want to analyse the impact of habitat change on trophic interactions between solitary, cavity-nesting bees and wasps, representing a highly diverse yet vulnerable insect group. In a nationwide effort in 2019, we collected trap nests from 320 sites across Germany, spanning gradients in urbanisation, habitat use and climate. Using a metabarcoding approach, we will now identify DNA within the trap nests allowing us to determine not only subadult bees and wasps, but also their plant and animal food resources and parasitic and parasitoid antagonists. Based on this information we will be able to unravel multitrophic interactions and food web architecture of the different sites. We expect that high diversity of basal resources in near-natural and high-latitude sites will be key in fostering high hymenopteran diversity through trophic interactions, while generalists will thrive at highly modified environments.

DNA barcoding methods for the detection of dragonfly species (Insecta: Odonata)

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Molecular genetic methods, such as environmental DNA barcoding (eDNA), offer great potential for the detection of species and have become increasingly important, particularly for the monitoring of aquatic organisms. In addition to eDNA barcoding, non-invasive methods for DNA sampling have gained in importance in molecular genetic studies and especially those with conservation purposes. The development of non-invasive sampling methods is essential when dealing with protected species groups such as dragonflies. Within the project "The dragonfly fauna of Vienna" an eDNA approach for the detection of five dragonfly species (*Calopteryx virgo, Erythromma viridulum, Cordulegaster heros, Leucorrhinia pectoralis* and *Sympetrum sanguineum*) was established. Filtrates from 53 water samples served as DNA source. They originated from five still and three flowing waters, whose dragonfly fauna was also investigated using traditional field methods. This allowed a comparison of the methods: *Leucorrhinia pectoralis* was detected via eDNA at two of three sites with sightings of adult individuals. *Sympetrum sanguineum* and *Erythromma viridulum* were detected at five and six of nine sites, *Calopteryx virgo* at three of seven. *Cordulegaster heros* was detected by eDNA even at one site more than by records of adult animals.

Exuviae offer great potential as a DNA source for species identification and further genetic studies. In the present study, we developed a DNA barcoding approach for species identification for dragonfly exuviae, covering all nine Central European dragonfly families. The method was tested with a total of 85 exuviae, 60 of which could be determined at species level and 22 at genus level.

Both methods (eDNA barcoding and the barcoding of exuviae) are to be further developed and extended in an application-oriented manner within the framework of the follow-up project "Crayfish and dragonflies in rural areas of Vienna" in order to test their applicability in aquatic ecological status assessments and the monitoring of FFH species. The results of the study form the basis for future management measures in the investigated waters.

Genetic monitoring of green frogs in Luxembourg using a NGS-based method

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Two species of green frogs are common in the Grand Duchy of Luxembourg: the pool frog *Pelophylax lessonae* and the edible frog *P.*kl. *esculentus*. Due to their complex mating system, which includes kleptogenesis and polyploidization, most *P.*kl. *esculentus* populations require the presence of *P.lessonae* for successful reproduction, while the reproduction of *P.lessonae* is independent from *P.*kl. *esculentus*. In some populations *P.*kl. *esculentus* can reproduce successfully by itself, but only if individuals are polyploids. Although both species are difficult to distinguish morphologically and the standard barcoding approach cannot be applied to this species complex, both are target species of the EU Habitats Directive (92/43/EEC) and thus have to be monitored individually. Here we analysed approx. 400 green frogs from 33 ponds throughout Luxembourg using ddRAD-sequencing. By sequencing a few thousand genetic markers per individual, we were able to identify each individual at the species level as well as to identify its ploidy level. We found co-occurrence of pool frogs and edible frogs in almost all analysed ponds, while polyploid populations of the edible frog, where reproduction was independent from the pool frog, were limited to a few ponds in the south of Luxembourg. This indicates that the protection of green frogs in Luxembourg largely requires the conservation and establishment of pools that are suited for both green frog species.

Assessment of MHC diversity in Central and Southeastern European grey wolf (*Canis lupus*) populations

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European grey wolf is considered a resident species in 36 European countries, and can be clustered into ten populations. The Carpathian population is mostly isolated from other populations by large areas where wolves have been exterminated by humans. The Dinaric-Balkan population represents border between Eastern European populations and largely extinct Western European populations. It is considered that a lack of MHC diversity can increase population susceptibility to infectious diseases with potentially deleterious consequences. We analysed allele distribution of MHC class II DQA, DQB and DRB loci in the population of European grey wolf from Carpathian Mountains and from the Serbian part of Dinaric Mountains with the aim of assessing their adaptive genetic diversity. We collected 99 wolf samples from Carpathian Mountains and 80 samples from Dinaric Mountains. Allele sequences were obtained using DLA - DQA, DQB and DRB specific PCR and sequencing. Obtained sequences were analysed in Seqscape software using a library of all known DLA alleles. Ambiguous heterozygotes were cloned, sequenced and reanalysed in Seqscape to resolve all alleles. In the Carpathian population, we found four different DQA, eight DQB and seven DRB alleles, while in the Dinaric population we found nine different DQA, 13 DQB and 13 DRB alleles. In both populations, we found previously unknown alleles. Preliminary results show relatively high diversity on MHC loci in both populations, while Dinaric population seems to be more diverse.

Historic pollen-metabarcoding on rare bumble bee species to investigate the role of floral resource availability upon rarity in Germany

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The occurrence and abundancy of bumblebees (*Bombus*) is drastically decreasing worldwide despite intensive conservation measures. Bumblebees are among the most specialized insect pollinators in both agricultural and natural habitats. Different bumblebee species do have different diet breadths and host plant preferences, however, until now, large scale testing for historical changes in floral resources to explain bumblebee decline is hampered by the lack of comparative data. However, natural history museums with their extensive bumblebee collections allow for the screening of old specimens for retrospective analyses.

We optimized the laboratory workflow for pollen metabarcoding, suitable also for pollen on historic specimen. We now can identify pollen on insects with a significantly higher accuracy, reproducibility and verifiability than earlier possible. The method can routinely be applied to small, partially degraded DNA starting materials that is up to 40 years old. The bioinformatic pipeline for species level pollen identification has been optimized. First experiments were conducted to analyze pollen host plant use of bumblebee species on a historic collection and we re-sampled the same places in Cuxhaven in a nature conservation area with adjacent gardens and settlements. We now investigate whether current and historic developments of bumblebee abundances and rarities coincide with changes in floral resources and how this affects rare and common species.

Current status and future direction of molecular pollen monitoring via metabarcoding approaches

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Plants are of enormous importance in all terrestrial ecosystems on earth. Global changes in climate and land use as well as a decline in global insect diversity and thus the number and frequency of pollinators in terrestrial ecosystems will also affect plants. The consequences are reduced gene flows between plants, which can lead to a reduction in the genomic diversity of the pollen obtained and ultimately to a reduced adaptation potential of the plant populations. In addition, climate change could cause flower tips in entomophilic plants to no longer match insect emergence periods.

This demands enhanced monitoring activities in a changing world to gain a better understanding of spatial and temporal aspects as well as the genomic basis and manifestation of plant-plant and plant-biome interactions. Understanding contemporary biotic and abiotic responses to perturbations as well as monitoring yet unknown relationships is immensely important in times of accelerating anthropogenic changes.

We conducted comparative metabarcoding analyzes of wind pollen samples from different wind pollen traps, locations and amounts of pollen during a pollen season (difficulty: different pollen traps, large amounts of pollen of some types and small amounts of other types, air pollutants). In addition, the metabarcoding of pollen on insects, also in a historical context, has been optimized (difficulty: extremely small amounts of pollen). We now can recommend field sampling, sample preparation, laboratory processes and bioinformatic pipelines for pollen metabarcoding analyzes for anemophilic and entomophilic pollen.

Development of techniques of forensic identification of wild and domestic animals on the basis of a study of genetic polymorphism of STR-loci

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The Scientific and Practical Centre of the State Forensic Examination Committee of the Republic of Belarus is engaged in the introduction of modern technologies in forensic examination in the investigation of crimes against wildlife. A set of measures to form a new expert area includes scientific research, the development of a scientific, technical and methodological base, the preparation of qualified expert staff.

Currently, the center is developing methods of DNA identification *Canidae* family (wolf, domestic dog, raccoon dog, red fox) during the study of polymorphism of animal populations living in the country.

In total, for forensic use, a technology has been proposed for species-specific PCR identification of wild animals of the *Cervidae* family and their differentiation from *Bovidae* and *Sus*, including 7 autosomal loci (source species: pig, deer, and cow); technologies of DNA identification for red deer (including of 16 autosomal STRs and 2 sex markers), Moose (18 STRs and 1 sex marker), roe deer (16 STRs and 2 sex markers), Wild boar (15 STRs and 1 sex marker) having the form of multiplex amplification of the target DNA followed by the study of allelic products using capillary electrophoresis.

Since 2015, the center conducted more than 300 forensic examinations on the facts of illegal hunting, theft of livestock and animal abuse. For the first time in the Republic of Belarus, DNA technologies have been created that guarantee the receipt of scientifically based information in the study of biological traces of wild and domestic animals selected to identify cases against nature.

Detecting the neozooic freshwater jellyfish *Craspedacusta sowerbii* with environmental DNA in sediments of Lake Constance

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Climate change is causing rising water temperatures in freshwater lakes, facilitating the establishment of new species, which can become invasive. Time series of the occurrences of neobiotic species along with temporal changes in overall community patterns can inform on the rate and mode of impacts of the establishment, but high-resolution monitoring data is often not available.

For Lake Constance, a number of neozoa have been recorded in the past decades. Among them, the freshwater jellyfish *Craspedacusta sowerbii*, which in other lakes of southern Germany has reached high population numbers, has been present in the lake since 1999. In recent years, higher water temperatures are causing the barely visible polyp of *C. sowerbii* to undergo a morphological change into the pelagic sexually reproducing medusa stage with a size of 2.5 cm.

We are analyzing *C. sowerbii*, as well as other neozoa, using environmental DNA extracted from lake sediments. We used species-specific primers that were designed and tested *in silico*. Analyzed samples from the top of sediment cores that were collected from multiple transects across Lake Constance. Initial results show that the *C. sowerbii* is detected in sediments, and its detection is highly congruent to reports of medusa sightings. Further analysis will test this on a higher number of samples and track the DNA through time. By analyzing a well monitored system such as Lake Constance for neozoa in sedimentary environmental DNA we will establish the sensitivity and utility of environmental DNA to track recent species establishments and invasions.

Of (s)cats and dogs: Detection dogs are a suitable tool for systematic non-invasive monitoring of Eurasian lynx

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As large carnivores like Eurasian lynx (*Lynx lynx*) are recolonizing parts of their historic ranges in Central Europe, solid monitoring strategies are necessary to survey population expansion, connectivity and genetic diversity. Non-invasive DNA sampling strategies are suitable to address this requirement, but genetic samples of lynx are generally hard to detect due to large home ranges and low densities of lynx as well as few characteristics for morphological identification of samples in the field.

In order to assess the suitability of detection dogs for lynx monitoring, we searched for scat samples with two detection dog teams in the Bavarian Forest National Park, Germany, for four weeks. Teams covered 440 km of forest road and trail transects in 44 grid cells of 2 x 2 km throughout the park. They found 52 genetically confirmed lynx samples, of which 26 were successfully genotyped and assigned to 11 individuals. Based on a single-season site occupancy model, we found that 10 km of transect search is required per grid cell to achieve a 70 % detection probability of lynx presence. In accordance with other large carnivore scat detection dog studies, our results indicate that detection dogs are an appropriate tool for systematic genetic lynx monitoring. In particular, the dog-based method may be used in addition to conventional monitoring strategies such as camera trapping to specifically address questions regarding genetic diversity and population connectivity.

De novo assembly of the Eastern mountain bongo genome as a modern genomic tool for conservation

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Eastern mountain bongo (*Tragelaphus eurycerus issaci)* is the largest species of mountain antelope in Africa. There are fewer than 100 individuals in five fragmented subpopulations in Kenya. Threats to their survival have included bush meat hunting and disease. The genetic diversity in the captive populations of North America, including the AZA SSP and private ranches, remains unknown. The genetic differences between this subspecies and the Western bongo, *T. eurycerus eurycerus* is also unknown. To address these conservation challenges, we generated a *de novo* assembly of a male eastern mountain bongo using 10X Genomics Chromium sequencing. The length of the pseudohaploid assembly was 2.9 Gb with a scaffold N50 of 13.37 Mb and a coverage of 56x. BUSCO analysis identified 89.3% complete genes. Our assembly is significantly more contiguous compared to a previous assembly generated for the species. This reference genome will be used to map and identify variant sites from sequences of additional individuals that will be whole genome re-sequenced. These will then be used to develop a targeted sequence capture array containing thousands of single-nucleotide polymorphisms, enabling us to genotype several hundred more individuals to investigate the inbreeding, genetic relatedness, and structure among the North American population of bongos. This genomic data will provide us with information needed to make breeding recommendations for conservation and herd management across North America for the possible reintroduction of genetically healthy individuals of this rare and elusive antelope.

Genetic monitoring of zooplankton communities in the German Bight (North Sea)

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Marine plankton respond rapidly to environmental changes, hence studying the diversity of planktonic fauna in different oceanic areas and over time is crucial to understand the dynamics of ecologically important planktonic species. However, the complexity of zooplankton assemblages, with numerous cryptic and closely related species and the lack of diagnostic characteristics for small plankton constitute important impediments to our understanding of patterns of plankton biodiversity and ecosystem function. DNA metabarcoding is an efficient method for measuring biodiversity considering the complete planktonic fauna and in contrast to more conventional approaches, metabarcoding has the potential to uncover the hidden diversity in marine planktonic communities and help distinguish between cryptic species. Here we developed and applied a molecular pipeline to isolate DNA from bulk plankton samples collected within 12 months from the 'Helgoland Roads' time-series location (one of the longest with highest taxonomically and temporary resolution time-series in Europe) as well as 11 different stations within the Doggerbank area and 2 stations near the Jade-Weser Harbor in Wilhelmshaven. An amplicon sequence variant (ASV) table has been produced by analyzing the high throughput sequencing reads from a MiSeq run. We developed a rich COI mtDNA reference library by barcoding individual zooplankton specimens which were identified morphologically, in order to enrich the existing databases. Taxonomic names have been assigned to each ASV blasting against available NCBI records and our own reference library. Diversity and composition of the planktonic communities have been compared between Doggerbank stations and long term monitoring results have been estimated over 12 months in Helgoland Roads area.

Temporal landscape genetic data indicate an ongoing disruption of gene flow in a relict bird species

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A major concern in conservation biology today is the loss of genetic diversity in structured populations, which is often a consequence of habitat contraction and restricted gene flow over time. These dynamic biological processes require monitoring with temporal environmental and landscape genetic data. We compared the spatial genetic variation of a relict, umbrella species, the capercaillie (*Tetrao urogallus*), in two different demographic periods, as represented by older museum specimens (1960–1990) and recent non-invasive samples (2011–2015) collected from the Carpathian Mountains, where habitat connectivity has dramatically decreased in the past decade. Using a combination of species distribution modelling and spatial genetic inference, we analysed how climatic and environmental constraints shaped population structures of the species. Environmental and climate niche models confirmed that relict Carpathian capercaillie populations are temperature sensitive, and they occur in a narrow range of mountain forest habitats at the highest altitudes. We found that the environmental and climatic constraints led to genetically isolated populations, but we also detected clusters that did not match relatively interrupted areas of niche habitats. We observed a similar disruption of gene flow in both periods; however, a stronger signal of genetic structuring in recent samples indicated ongoing processes that negatively affect connectivity. The effective population size in Carpathian population has declined in recent years but in Western Carpathians, it is low for at least the last five decades. This study demonstrates the usefulness and importance of temporal ecological and landscape genetic data for the conservation and management of wildlife species.

Estimating population size and connectivity of a fragmented capercaillie (*Tetrao urogallus*) population in the Black Forest

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As a result of habitat deterioration and fragmentation, the endangered capercaillie (*Tetrao urogallus*) has experienced a severe population decline in the Black Forest (Germany) over the past decades. The current population is threatened with extinction and highly fragmented. Thus, the connectivity between the spatially disjoint patches is of crucial importance for the long term survival of the local capercaillie population. To estimate and monitor population size and to study the connectivity between population patches as well as the functionality of the corridors connecting patches genetic analyses are conducted. Therefore, we use non-invasive genetic sampling and subsequent genotyping using 12 microsatellites to identify individuals in 3 consecutive years. We conducted a two-step analytical approach, first addressing the past pattern of population differentiation by comparing genetic diversity and structure of a historic dataset (1999-2000) with the recently repeated sampling (2013-2017). We hypnotized that the reported reduction in population sizes combined with increased fragmentation in the past centuries within our study area negatively affected genetic diversity and increased population differentiation. Additionally, we applied forward in time simulation on the historic data, to pinpoint whether we can recreate to the recent data comparable population differentiation applying various migration scenarios. Our results show that the spatially separated sub-populations in the Black Forest exhibit minor but significant genetic differentiation, as well as spatial patterning, suggesting possible barriers to gene flow due to fragmentation. Our results indicate the importance to keep corridors free of factors which might negatively affect connectivity between sub populations.

Assessing functional connectivity for a challenging ground-dwelling grouse species utilizing different landscape genetic approaches

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Variation in genetic pattern of species is believed to be driven by a landscape's spatial heterogeneity. Within landscape genetics, in recent years several methods to resolve these functional links have been published, yet studies predominately focused on well suited focal systems. We addressed whether we can attribute observed genetic pattern to isolation by distance or isolation by environment in a fine-scale metapopulation system of a ground-dwelling bird species of conservation concern, characterized by low genetic differentiation. The study was conducted in Styria, Austria, using 195 genotyped Alpine black grouse (*Tetrao tetrix*) individuals. To identify spatial genetic pattern, we applied a current density model based on estimated migration rates as well as multivariate regression approaches combined with Moran's eigenvector maps based on distance metrics derived from a correlative ecological niche model. Analyses were done between individuals and subpopulations using pairwise fixation and differentiation indices. Spatial genetic variation could be attributed to isolation by distance on individual level. On subpopulation level, the null model was the most parsimonious of the linear mixed effects models. The current density model pronounced areas connecting the eastern most occurrences of Alpine black grouse distributions. Black grouse in the Styrian Alps appeared to be shaped by isolation by distance within population genetic clusters. Although designed for weak structure within genetic pattern, current landscape genetic approaches struggled with the challenging focal system. Applying different theoretical approaches on hierarchical levels of genetic entities is a premise for disentangling effects of landscape heterogeneity to a species' genetic variation.

Genetic and phenotypic analysis of translocated and natural populations

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Conservation efforts for endangered populations are being implemented around the world. Translocations are a common strategy to create new populations. Consequently, translocations are often assumed to be successful if a new population is founded and begins to grow. However, we argue that there is also a need to understand the genetic consequences of translocations and how they affect the performance of individuals. This may help to better understand why some translocations are successful while other fail.

Here we present a genetic and phenotypic analysis of natural and translocated populations, using a spatially structured populations of the natterjack toad (*Epidalea calamita*) from northern Switzerland as an example. We combined microsatellites to study the genetic structure of the populations and a common garden experiment to study the life history phenotypes of individuals.

We found that the genetic structure and diversity of translocated populations was not different from natural populations (except for expected heterozygosity which was higher in translocated populations). Similarly, the experiment showed that the life history phenotypes mass at metamorphosis and length of the larval period of the toads from natural and translocated populations did not differ.

The results show that successful translocated populations and natural populations are genetically and phenotypically similar. This is good news for conservation practice as it shows that translocations can lead to new populations that are similar to natural populations.

Genomics and European mink: a new avenue for the species' conservation?

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European mink, *Mustela lutreol*a is one of the most endangered carnivores in Europe. In 2011, the species has been reassigned as "Critically Endangered" in the IUCN list because of an ongoing population reduction. The populations are distributed into three isolated areas: western (southwestern France and northern Spain), northeastern (Belarus and Russia) and southeastern (Romania) Europe. Genetic studies showed that the mink populations present a very high risk of inbreeding depression especially in the western part of its geographic distribution. Inbreeding depression is a critical concern for conservation efforts as it is common in small, declining or fragmented populations. This phenomenon is still poorly understood but it is usually caused by increased homozygosity at loci at dominant alleles and expression of recessive deleterious alleles which will likely results in a decline in reproduction and survival. One way to measure the extent of inbreeding is to scan genomes for runs of homozygosity (ROH). This method is becoming more commonly used to estimate inbreeding and could become a new index for conservation status in wild animals. For this study, we selected one European mink from Charente-Maritime (France) for whole genome sequencing (30x). We expect to find long stretches of ROHS that would indicate recent events of inbreeding. In addition, we will apply demographic inference from our genomic data. The results will be the preliminary steps of a bigger genomic project that might have a direct impact on the current conservation program for the European minks.

Genome-wide analysis of introgression from the domestic goat into the Alpine Ibex

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The demographic history of the Alpine ibex (*Capra ibex ibex*) is characterized by a near-extinction event in the 19th century caused by overhunting. A small population in Northern Italy was successfully protected. A captive-breeding and reintroduction program was initiated in the early 20th century. These days, the population has recovered to an estimated 50'000 Alpine ibex across the Alps. However, the genetic variability remains depleted.

Recent research found evidence for introgression from the domestic goat (*Capra aegagrus hircus*) into the Alpine ibex genome at the major histocompatibility complex. Understanding the extent of the retained goat alleles in the Alpine ibex is the aim of this Master thesis. Further, it is of interest to examine the potential negative consequences of introgression from a domesticated species into its wild relative.

Whole genome sequence data from 29 Alpine ibex and other *Capra sp*. are analyzed with various bioinformatic tools to determine genomic regions of introgression. Special emphasis is placed on the genomic regions of the immune system, since high genetic variability grants improved immune response. Hence, among these loci strong signals of positive selection for introgressed alleles are expected.

Genes and shapes: how concordant they are in the edible dormouse?

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In their 2006 seminal paper on the genetic criteria in species delimitation in mammals, Baker & Bradley observed that “genetically distinct populations … are distributed much like that implied in typical sub-species maps”. Indeed, species are structured morphologically and genetically, but little attempt has been made to assess the concordance, or lack of it, between patterns retrieved by different data sets. By sampling the edible dormouse *Glis glis* (Linnaeus, 1766) throughout its known range we explored the consistency among divisions produced by mitochondrial cytb sequence and geometric morphometric variation of skull and mandible. The match was perfect what gives us confidence that in our case the mitochondrial lineages are meaningful units for conservation management. Our study would not be possible without vouchers deposited in public museum collections. Over-impressed by recent advances in molecule-based techniques we are frequently too ignorant for the future of museum collections. As was repeatedly demonstrated over the last years, collections are declining in many countries due to neglect, ignorance, and lack of funding.

High frequency of sex reversal in Hungarian populations of the agile frog *(Rana dalmatina)* shown by novel genetic sex markers

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Amphibian populations are declining worldwide due to their outstanding vulnerability to climate change, chemical pollution and rapidly spreading pathogens. Previous experiments have shown that certain chemicals and high temperature during larval development can cause masculinization in some anuran species, resulting in genetically female individuals that are phenotypically males. However, we have very little information on sex reversals occurring in natural populations of anurans, mostly due to lack in availability of genetic sex markers.

We tested the reliability of three sex-linked DNA loci as potential sex markers on 125 agile frog individuals originating from three different populations that we reared in laboratory under environmental conditions that presumably do not cause sex reversal in anurans. Based on these results, we designed a suitable method for genetic sex identification that was used for exploring sex-reversal frequency among 162 adult individuals caught in 11 wild populations of North-Central Hungary.

About 10% of phenotypic males were genetically female among the laboratory-reared frogs, suggesting that a non-negligible frequency of masculinization could occur not only due to environmental effects, but randomly as well. In total, 20% of wild-caught males were genetically females, being 14% in natural, 17% in suburban and 34% in urban habitats. We found no feminized individuals. Higher masculinization frequency in urban populations may be explained by the urban heat island effect or chemical pollution in urban areas. Our results suggest that urbanization may increase masculinization rate in agile frogs, leading to significant male-biased sex ratios which might negatively affect long-term population stability.

Necessity of reliable identification as a baseline for conservation - an isopod case study on the genus *Haploniscus* Richardson 1908

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Why does conservation need species identification? During the first two IceAGE expeditions in 2011 and 2013, benthic macrofauna was sampled from various stations surrounding Iceland, specifically along depth transects including the Norwegian Channel, the Faeroe-Iceland-Ridge, South Iceland and East Greenland. Asselote isopods identified as *Haploniscus bicuspis* (Sars, 1877) were closely examined in an integrative approach to solve the question if *Haploniscus bicuspis* is a species complex or one species with different morphotypes. They were found to show high morphological variability in species-specific characters. Different morphological techniques (light, scanning electron and confocal microscopy) are complemented by multiple species delimitation methods based on genetics and proteomics. Preliminarily, a dataset for mitochondrial COI and nuclear ITS-1 was established. Furthermore, a ddRAD approach is applied, as well as a proteomic approach using the same set of specimens. All data sufficiently contribute to develop a database for the isopod species occurring around Iceland. So far, our results revealed that differences between male individuals regarding the pleopod 1 might represent developmental stages instead of different subspecies or male morphotypes within *H. bicuspis*. However, the analysis of the genomic and proteomic data is still ongoing. These different methodologies are steppingstones towards solving the *H. bicuspis* species' complex puzzle. A definitive and rapid species assessment is especially crucial around Iceland, as the subarctic waters are susceptible to climate change. In the future, this will aid efficient identification of various isopod species around Iceland.

The Eurasian beaver (*Castor fiber*) in France and the Greater Region : genetic consequences of different reintroduction strategies.

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During the 19th century, the Eurasian beaver (*Castor fiber*) was nearly extripated in many West European countries. In France, only one relictual population was present in the Rhône Valley at the dawn of the 20th century. In Belgium and Luxemburg, it had totally disappeared. While an official reintroduction program was implemented with the local lineage in France, an illegal reintroduction from various sources was carried out in the Greater Region (Belgian border). We investigated the genetic diversity and structure of those populations. Based on mt DNA and microsatellite data, we discuss the impact of these two opposite reintroduction strategies on the beaver populations and their future.

Population genomics delineate conservation units of the fire salamander (*Salamandra salamandra*) in the face of an expanding lethal pathogen

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Sophisticated species conservation management is required to protect a threatened species from genetic erosion or even extinction. Especially amphibian species are increasingly facing threats at a global scale, e.g. pollution, climate change, habitat destruction. Emerging infectious diseases such as chytridiomycosis are in fact killing entire species at an alarming rate. These threats commonly persist in the habitat for an unknown period, often making *ex situ* conservation the only feasible option to halt the ongoing biodiversity loss. The fire salamander (*Salamandra salamandra*) is severely affected by the introduced pathogenic chytrid fungus *Batrachochytrium salamandrivorans* (Bsal) which is rapidly expanding in Europe. Germany is the main area of distribution of the fire salamander but currently also the Bsal hotspot. In order to be prepared for a worst-case scenario requiring the prioritization of populations or *ex situ* conservation, we sampled fire salamanders across Germany and determined their genetic composition by microsatellite analysis, ddRAD sequencing, and mitochondrial sequence analysis. We identified two main genetic lineages (western, eastern) that were separated during the last glacial maxima and thus represent evolutionary significant units (ESU). The eastern ESU can further be divided into two management units (MU) that differ significantly in their allelic composition and that are demographically independent. The identified genetic units represent the most important populations worth being protected and the candidates for an *ex situ* project in Europe to save the genetic diversity and adaptations present. Here, we present the results of the study and how they are implemented into the first *ex situ* programs.

eDNA reveals detrimental predator prey interactions between endangered amphibians and invasive carnivorous fish

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Understanding biotic interactions and population dynamic processes is a central challenge in the field of ecology. Invasive species, for instance, may have considerable effects on population dynamic processes of their prey species and cause severe changes in biological communities and ecosystem processes. Revealing biotic interactions, including predator prey interaction however, is a difficult task, in particular for species and biological systems that are difficult to monitor. Here we present an assessment of predator prey interactions between two invasive fishes (*Lepomis gibbosus* and *Pseudorasbora parva*) and two potential prey species, the great crested newt (*Triturus cristatus*) and the spadefoot toad (*Pelobates fuscus*). We used species-specific TaqMan-assays for the quantitative assessment of DNA-concentrations from water samples collected across 30 ponds from a local amphibian hotspot, the Bingenheimer Ried area north of Frankfurt am Main, Germany. We found a strong negative relationship of pairwise comparison between DNA concentrations from predators (fishes) and prey (amphibians). Our finding confirms the hypothesis that the local decline of amphibians is at least partly caused by recently introduced invasive fishes. Our findings have important consequences for local conservation management and provide an example of the feasibility of eDNA-based approaches beyond simple species detection.

Genetic monitoring of wolf (*Canis lupus*) conservation status in Slovakia

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The grey wolf (*Canis lupus*) is both hunted and protected in Slovakia. This dual status calls for reliable data on key population parameters to inform management decisions. Estimates of abundance produced by hunters differ by an order of magnitude compared to those of environmentalists, while both lack robust methodology. To improve the accuracy of information available to decision-makers, since 2013 the Slovak Wildlife Society has conducted genetic monitoring in collaboration with the University of Ljubljana. We train 'citizen scientists' to help implement non-invasive sampling (http://slovakwild-life.org/en/activities/whitewilderness). Laboratory work and data analysis are financed from volunteer contributions and crowdfunding (https://www.gofundme.com/f/carpathian-wolf-watch). Samples are genotyped at 16 canine unlinked autosomal microsatellite loci. Two additional loci are used to determine sex. In 2015/16, for the first time in Slovakia, using the Capwire mark-recapture model we obtained a robust estimate of wolf abundance: 45 individuals (36–66, 95% CI) in a study area of c.2,000 km2. Further CMR estimates in 2017–2018 indicated the population to be stable. Extrapolating to the national level, we estimate c.315–510 wolves in Slovakia (excluding pups of the year). This fulfils criteria for favourable conservation status, but the population is transboundary and a large percentage of packs are shared with neighbouring states.

Reconstruction of the deep temporal genetic and demographic past of Alpine ibex (*Capra ibex*)

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As mankind started to expand, pollute and exploit their surrounding nature, demographic changes in large variety of species occurred. Some species, which were not able to cope with anthropogenic changes on their environment, went extinct; others survived only in small and bottlenecked populations. Even though some of these species recovered from the edge of extinction due to intense conservation efforts, a substantially altered genetic composition remained. In the light of the rapid global change and ongoing mass extinction of a large variety of species, but also of growing awareness of the intrinsic values of such, it is crucial to understand the effect of bottlenecks on populations. We present here the study-design to shed light on the topic by looking at a species, which already underwent the process of population decline until near extinction to the recovery to high census size. This species is the Alpine ibex (*Capra ibex ibex*), which encountered a reduction in census size since the 15th century resulting in a strong bottleneck in the 19th century. Although the species census size recovered, the recent populations inherited extremely low levels of genetic variability. We will combine genetic data from ancient and historic genomes, recovered from caves and museums with recent Alpine ibex genomes and population genetic approaches to investigate the pre- and within- bottlenecked diversity of the Alpine ibex.

Whole genome resequencing of the European wildcat provides comprehensive insights into their population history and hybridisation with the domestic cat

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Whole-genome resequencing can be a powerful tool to answer questions in conservation that have not yet been fully resolved through traditional methods. An understanding of a species' historical distribution, population structure, and past levels of hybridization remain important to current conservation as past events have great influence on the genetic structuring of contemporary populations. Given the advancement of sequencing technology and the reduced cost, it is more feasible than ever to resequence non-model organisms, especially when reference genomes are available. The European wildcat (*Felis silvestris*) is an ideal candidate to tackle remaining uncertainty in regard to historical and present genetic structuring and hybridization levels, because the reference genome from domestic cats (*Felis catus*) can be utilized for analysis.

Here, we use individual whole genome resequencing data of 37 domestic cats from around the world and 47 European wildcats from Germany to shed light on historical and current demographic history and historical hybridization rates. We show the regional sub-structuring of known wildcat populations, verify low hybridization rates and confirm the genetic structure found by traditional methods and even retrieve further fine scale information. Our results show that whole genome data can further illuminate the demographic history and hybridization rates, both historical and current, which can help inform the conservation of the European wildcat in the future.

Tracking individuals and potential hybridization in mountain hare (*Lepus timidus*) using noninvasive genetic sampling

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Systematic monitoring of individuals and their abundance over time has become an important tool to provide information for conservation. For genetic monitoring studies, noninvasive sampling has emerged as a valuable approach, particularly so for elusive or rare animals. Here, we present the five-year results of an ongoing noninvasive genetic monitoring of mountain hare (*Lepus timidus*) in a strictly protected area in the Swiss Alps. We used nuclear microsatellites and a sex marker to identify individuals and assign species to noninvasively collected feces samples. We found that male abundance in the area showed high fluctuations and apparent survival for males was lower than for females over time. Males and females showed only little temporary migration into and out of the study area. Using genotyped tissue samples from mountain hares, European hares (*Lepus europaeus*) and their hybrids, we were able to provide evidence for the first occurrence of a European hare in the study area at an elevation of 2300 m a.s.l. in spring 2016. For future monitoring studies, we suggest to include species assignment and thereby assess the potential threats given through competitive exclusion by and hybridization with the European hare.

Low genetic diversity and connectivity in a critically endangered batoid population residing in a Scottish marine protected area

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At present, only one marine protected area (MPA) located in West Scotland is designated for the critically endangered flapper skate *Dipturus intermedius*, and limited knowledge is available about its connectivity to other populations in the North East Atlantic. Recent tagging studies in the MPA show it to be a mix of siteattached (resident) and transient individuals. Using mitochondrial DNA (mtDNA) sequencing analyses, this study investigates the variability and recruitment of the residing population, as well as potential philopatric tendencies. When studying elasmobranchs, many studies inferred the reproductive connectivity from partial mtDNA control region gene sequences. This particular sequence did not show sufficient variability in the flapper skate, thus several full mitochondrial genomes were assembled to locate a suitable gene region. After successfully identifying a variable marker region, population structure and haplotype variability in several sites of the North East Atlantic within and outwith the MPA were analyzed with DNA sourced from fin clips, mucus and egg case samples of the flapper skate. Low haplotype diversity was revealed in the marine protected area, as well as what appears to be an exclusive haplotype. This apparent likelihood of site fidelity and lack of admixture in the population needs to be taken into consideration when evaluating and adapting management measures for the flapper skate.

Quantification of past arctic herbivore populations from ancient sedimentary DNA by metabarcoding, hybridization capture enrichment, and droplet digital PCR

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The Arctic is currently experiencing dramatic ecosystem changes with immediate effects on biodiversity. Palaeorecords (e.g. sedimentary ancient DNA) are a unique and valuable source of data on long-term ecosystem development, which may help understanding the relative impacts of climate, herbivory, and anthropogenic effects on ecosystems. In the project “Future ArcTic Ecosystems” (FATE), we aim to assess changes in past herbivore abundance over large spatial (circumarctic) and temporal (Last Glacial Maximum until today) scales using three (semi-)quantitative methods on sedimentary ancient DNA of plants, herbivores, and herbivore proxies (i.e. coprophilous fungi and parasites): metabarcoding, hybridization capture enrichment, and droplet digital PCR (ddPCR). Metabarcoding is useful for assessing biodiversity, however, quantification of specific taxa may be problematic due to inherent methodological biases (e.g. amplification efficiency). As an alternative, hybridization capture enrichment omits problems such as amplification bias. Both methods can be applied to a vast taxonomic range and may be used quantitatively based on relative sequencing read abundance; however, read abundance may be confounded by random and systematic errors and other biases. In contrast, ddPCR is taxon-specific but facilitates highly accurate quantification of template DNA molecules in a given sample. The combination of these methods will be used to generate datasets with high taxonomic resolution of vegetation and herbivores, allowing us to make detailed inferences on herbivore abundance and to reconstruct past ecological conditions, which may be important for ecosystem management and species conservation. We present our approaches along with an evaluation of taxonomic resolution and explanatory power of our molecular methods.

Genetic analyses favour an ancient and natural origin of elephants on Borneo

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The origin of the elephant on the island of Borneo remains elusive. Research has suggested two alternative hypotheses: the elephant stems either from a recent introduction in the 17th century or from an ancient colonization several hundreds of thousands years ago. Lack of elephant fossils has been interpreted as evidence for a very recent introduction, whereas mtDNA divergence from other Asian elephants has been argued to favor an ancient colonization. We investigated the demographic history of Bornean elephants using full-likelihood and approximate Bayesian computation analyses. Our results are at odds with both the recent and ancient colonization hypotheses, and favour a third intermediate scenario. We find that genetic data favour a scenario in which Bornean elephants experienced a bottleneck during the last glacial period, possibly as a consequence of the colonization of Borneo, and from which it has slowly recovered since. Altogether the data support a natural colonization of Bornean elephants at a time when large terrestrial mammals could colonise from the Sunda shelf when sea levels were much lower. Our results are important not only in understanding the unique history of the colonization of Borneo by elephants, but also for their long-term conservation.

Landscape genetics of Himalayan brown bear (*Ursus arctos isabellinus*) in India

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Landscape genetics is an approach for understanding how geographical and environmental features structure genetic variation at both the population and individual levels. Hence quantifying drivers which determine suitable habitats are crucial to assess the functional genetic connectivity between the suitable habitats. The threatened Himalayan brown bear (Ursus arctos isabelenus) has a fragmented range in the Himalayas and its habitat has never been documented, which hinders conservation efforts in Western Himalaya of India. The conservation and management strategies not only focus the protection of habitat areas, but also the spatial distribution of these areas across the landscape. Therefore, the present study is aimed the most comprehensive population and landscape genetic study of the Himalayan Brown bear in three states (Jammu and Kashmir, Himachal Pradesh and Uttarakhand) of western Himalaya in India. We genotyped 271 individual bear samples at 14 microsatellite loci. Bayesian and multivariate clustering methods demonstrated genetically structured brown bear population across the Himalaya, with potentially distinct differentiation observed between Jammu and Kashmir and Uttarakhand (Fst =0.130). Here, we have characterized the geographical distribution of genetic patterns in Himalayan brown bear living in four isolated patches of the western Himalaya. Three geographic distance definitions were used with the "isolation by distance theory": Euclidean distance (EUD), least-cost path distance (LCD) defined by food resources, and LCD defined by habitat suitability. This result identified geographic distance and resource availability (food) as the primary drivers of genetic differentiation, in keeping with brown bear exhibiting high levels of female philopatry. Landscape-based genetic analysis suggests that gene flow will be enhanced if the connectivity between currently fragmented brown bear habitat is increased. By providing a more accurate picture of Himalayan Brown bear population structure and the factors effecting it, these data can guide current efforts to manage and conserve the species in India.

Genetic analyses and field monitoring of wolves from Bosnia and Herzegovina

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Wolves from Bosnia and Herzegovina, representing a subpopulation of the Dinaric-Balkan wolf population, have been insufficiently explored in the past. Recently, comprehensive genetic analyses were combined with field monitoring in order to study the Bosnian wolf population in depth. Genetic analyses were conducted by applying (i) 18 microsatellite loci of nuclear DNA, by which the level of genetic variability, population structure, kinship, bottleneck, and inbreeding were estimated, and (ii) control region of mtDNA by which phylogeography was analysed. Analyses of microsatellites showed moderately high genetic heterozygosity and structuring of wolves from Bosnia and Herzegovina into two genetic clusters. Observed structuring, representing an east-west gradient, might reflect structuring at the larger Dinaric-Balkan scale. Thus, it is necessary to continue analyses via extending the study area and enlarging sample size. Analyses of the control region mtDNA revealed the distribution of haplotypes into two haplogroups, without clear phylogeny patterns. Field monitoring, via the use of photo traps, has been implemented with the aim of detecting the presence of wolves at specific localities across Bosnia and Herzegovina, and to draw conclusions about their behavior and abundance. Continuously combined genetic and field monitoring has shown to be very successful in providing data necessary for the creation of a conservation management plan for species at both regional and national levels. This is the ultimate aim of all previous analyses.

Filling the gap: genetic structure and connectivity of vulnerable migratory elasmobranchs in oceanic islands in the Atlantic

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The survival of elasmobranchs is a major marine conservation concern, with 25% of all species currently at risk of extinction due to their exceptional vulnerability and low resilience to high levels of exploitation. However, our extremely limited knowledge of their basic ecology hampers the implementation of proper management and conservation actions. This is especially true for migratory species that depend on the restricted coastal habitats of oceanic islands. The location and role of Essential Fish Habitats (EFHs) around islands, especially nursery areas, for the sustainability of migratory elasmobranch populations is virtually unknown. This situation is particularly worrying in oceanic islands like the Azores, the most isolated archipelago in the North East Atlantic (NEA). Elucidating EFH role for elasmobranch ecology and conservation in the Azores and the wider Atlantic requires investigating the connectivity between populations and their patterns of habitat use. To fill this knowledge gap, we propose a research plan focused on three key migratory and vulnerable species, of contrasting life histories and behavior: tope shark (*Galeorhinus galeus*), smooth hammerhead shark (*Sphyrna zygaena*) and chilean devil ray (*Mobula tarapacana*). Adequate data to evaluate population structure and assess connectivity of populations between the Azores and other regions at different spatial scales – from the ocean basins to the island groups within the Azorean archipelago - will be generated through the analysis of Single Nucleotide Polymorphism (SNP) markers and Mitochondrial DNA (mtDNA). The expected results of this project will provide science-based knowledge to support sound management and conservation actions, regionally and globally.

Small population of spiral horned antelopes in semi-captivity - how far they have gone from wild?

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Tribe*Tragelaphini* are an essential part of the fauna across the entire African continent. Increasing landscape fragmentation negatively affects natural gene flow, there is a risk of loss of genetic diversity due to genetic drift or inbreeding. Similar effects can be noted in breeding systems in zoos and safari parks. However, in these artificial conditions, the breeding can be controlled and thus appropriate management can be applied. Another factor that can affect breeding is the occurrence of interspecific hybrids in mixed enclosures, which has been previously demonstrated in several bovid species.

This study aims to monitor genetic diversity in selected populations in human care, to compare genetic parameters of managed and non-managed animals; and test the presence of interspecific hybrids. Six species of spiral horned antelopes were commonly found in European breeds (common eland, lowland nyala, Western sitatunga, Eastern bongo, greater and lesser kudu) and one was bred in semi-captive condition in Senegal (Derby eland). All these species differ in a breeding management, conservation status and number of founding individuals and their origin. In total, 573 blood, tissue and hair samples were investigated using 10 microsatellite markers in fragmentation analysis and sequencing of control region of mitochondrial DNA. The current study provide useful practical information to the breeders about genetic status of the respective species and may help prevent mating of closely related individuals by evaluation of kinship among the individuals.

Detection of wildcat hybrids is a matter of monitoring effort

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In Southwest-Germany, the European wildcat is recently recolonizing its former habitat, where the species was considered to be extinct for over 100 years. Since the first evidence of wildcat presence in 2006 and 2007, a monitoring program has started to detect wildcat distribution in the federal state of Baden-Württemberg. Therefore, any indices of wildcat presence were recorded and checked for plausibility. Indices include the collection of hair samples (e.g. from lure sticks), sightings, pictures and video clips, captured animals and dead found animals (e.g. road kills). The latter is often the first evidence of the presence of a rare species in a distinct region. Hence, because we do not know where wildcats are present, we raise awareness for the monitoring to collect road kills that are suspected to be wildcats. Since 2006 we collected almost 200 carcasses, half of them turned out to be wildcats after a morphometric and genetic analysis. We found several wildcat hybrids, especially in human-dominated landscape. Some are very different in their phenotype and morphometric compared to pure wildcats. These hybrids would not be detected if only wildcat phenotypic cats were collected.
In conclusion, wildcat hybrids might be more often detected when monitoring effort is high and the collection of wildcat phenotypic cats is more conservative. In addition, the detection of hybrids with standard genetic analysis methods should be an accessible and reliable service.

The importance of including relevant reference samples when evaluating interspecific hybridization versus population admixture

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Interspecific hybridization linked to human-induced landscape changes is a global concern. However, it can be difficult to distinguish such gene flow, typically considered a conservation threat, from intraspecific exchange among areas where organisms show genetically divergent profiles. The latter process is generally considered beneficial, and dispersers and their descendants must therefore rapidly and accurately be distinguished from interspecific hybrids and their offspring.

Wolves (*Canis lupus*) at times hybridize with dogs (*C. familiaris*), which is seen as a long-term risk to genetic integrity and human-wildlife relationships. We use recent wolf data from Slovenia to illustrate the challenge in distinguishing hybridization from intraspecific gene flow. There is evidence of increasing gene flow between wolves in Slovenia and the Italian Alps, and between wolves in Slovenia and other parts of the Dinaric-Balkan region.

We show that analyses of wolf-dog hybridization with and without relevant wolf reference profiles produce divergent results, with potentially important management consequences. Our analyses include descendants of a wolf pair with ancestry from Italy and the northwestern Dinaric Mountains, where offspring are now migrating from Italy to Slovenia. We also examine a female wolf deemed to have dispersed into Slovenia from further south in the Dinaric-Balkan region, after which she reproduced with a local dog. Her pups are considered a conservation threat and managers are working to remove them. Our results underline how inclusion of relevant reference profiles is vital for research and management, and that omissions can produce erroneous conclusions with negative consequences for conservation management and public communication.

Population structure and genetic diversity of common terns (*S. hirundo*) from Slovenia and Croatia

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Common tern is a colonial seabird species whose breeding grounds include both freshwater and marine sites. Freshwater colonies are under a significant negative anthropogenic influence, mainly due to river regulations. Consequently, freshwater colonies throughout Europe are currently located mostly on artificial breeding sites, including rafts and gravel islands. Common terns in inland Croatia and Slovenia breed in the areas of the rivers Sava and Drava, whereas numerous marine colonies are scattered along the Adriatic coast. In order to explore their population potential for adaptation and environmental change, it is important to assess genetic diversity indices. Furthermore, the spatial pattern of genetic structure could contribute to future management decisions. Therefore, we aimed to inspect genetic diversity and degree of differentiation among common tern colonies. We analysed 52 samples from freshwater colony sites in Croatia and Slovenia and a coastal colony site in Slovenia. We amplified 7 previously published microsatellite loci. The mean allelic diversity per microsatellite locus was 6.095, ranging from 5 to 8 alleles and the mean expected heterozygosity was 0.72, ranging from 0.638 to 0.782. The results indicate relatively high genetic variability of the study populations. Structure analysis revealed two distinctive clusters - corresponding to the areas of the rivers Sava and Drava, and the coastal colony site Sečovlje Salina. Our findings illustrate the importance of those habitats as the reservoirs of genetic diversity and calls for their further protection and management.

Population structure and genetic diversity of wolves (*Canis lupus*) recolonizing Western Poland

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The gray wolf (*Canis lupus*) was extirpated from most of Europe, but recently recolonized big part of its historical range, including the western part of the Great European Plain. However, genetic consequences of this process have not yet been fully understood. We aimed to assess genetic diversity and population structure of this recently established wolf population in Western Poland (WPL). We utilized Bayesian and multivariate methods to infer genetic structure in a large dataset of wolf microsatellite genotypes. We found low mtDNA diversity, but moderate microsatellite allelic richness, relatively high observed heterozygosity and no detectable inbreeding in the newly recolonized areas. Interestingly, we discovered relatively strong west-east structuring in lowland wolves, probably reflecting founder-flush and allele surfing during range expansion, resulting in clear distinction of WPL, eastern lowland and Carpathian genetic groups. Thus, we conclude that the process of dynamic recolonization of Central Europe lead to the formation of a new, genetically distinct wolf population.

To better understand recolonization dynamics, we currently study interpack relatedness and analyze diversity of additional genetic markers. Our initial results suggest relatively high variability of both neutral, paternally-inherited loci (Y-STRs) and autosomal immunogenetic markers in WPL wolves. As it stands in stark contrast with low diversity of maternally-inherited mtDNA haplotypes, we speculate that gene flow from Eastern to Central Europe may be male-biased. This hypothesis is in line with preliminary results of relatedness analyses showing that breeding females from adjacent wolf family groups are usually more closely related than breeding males.

Molecular defense mechanisms of the crayfish immune system against the crayfish plague pathogen *Aphanomyces astaci*

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The noble crayfish (*Astacus astacus*) is a keystone species in European freshwater ecosystems and has a high economic value as a delicacy. Unfortunately, its populations are declining. The main threat are invasive North American crayfish, which are vectors of the crayfish plague pathogen *Aphanomyces astaci*. These North American vector species, such as the marbled crayfish (*Procambarus virginalis*), are resistant towards the disease, while it is lethal for the noble crayfish. However, recent reports from laboratory and wild indicate that *A. astaci* exposed noble crayfish can in some cases resist an acute crayfish plague infection. It seems that this susceptibility is genetically defined. Here I present our strategies to identify target genes and molecular pathways that potentially confer resistance in crayfish against an *A. astaci* infection. This project consists of 1) the *de novo* assembly of the noble crayfish genome as first genome in the family Astacidae, which will be a reference tool for gene expression analyses; 2) a controlled infection experiment with susceptible noble crayfish and resistant marbled crayfish, 3) subsequent gene expression analysis to compare the transcriptomes. The results will aid the understanding of gene functioning in the context of the crayfish immune system, which might play a key role in crayfish conservation efforts. In perspective, the results might become the basis of targeted breeding and subsequent reintroduction programs of plague-resistant noble crayfish into their original habitats.

Specialization does not affect genetic diversity in four species of copper butterflies

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Genetic diversity is considered to be of crucial importance for population fitness and the potential of populations to adapt to environmental changes. Random and deterministic factors may influence genetic diversity, which is expected to be reduced in specialists occurring at low abundances. We analyzed genetic differentiation and diversity in four species of copper butterflies, differing in their degree of habitat specialization (*Lycaena helle* > *L. hippothoe* > *L. virgaureae* > *L. tityrus*) by using five microsatellite loci and two nuclear genes (MDH, GADPH) in 11 populations with 20 individuals each per species. In *L. helle*, populations differed strongly in their genetic make-up but without clear spatial genetic structure, while the other species showed little genetic differentiation among sample locations. Despite substantial variation among genetic markers and molecular indices, genetic diversity and thus evolutionary potential tended to be highest in *L. hippothoe* and lowest in *L. tityrus*. These results do not match our a priori prediction of a high genetic diversity in *L. tityrus* and a particularly low one in the glacial relict species *L. helle*. We argue that locally high densities may foster high levels of genetic diversity, even in relict species. Therefore, the evolutionary potential to respond to climate change may not be generally reduced in rare relict species, and it is more relevant to focus on specific populations of concern to assess the genetic vulnerability to climate change.

Challenges in pine marten monitoring

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The European pine marten (*Martes martes*) is widely distributed across most of Europe, the Caucasus, and northern Asia. Until the 1980s the pine marten population in Northern and Central Europe declined, mainly due to hunting, but is now recovering. The pine marten is subject to conservation legislation in many countries, raising the need for reliable monitoring methods. Recent studies from Scotland suggest a combination of collecting hair and scat samples for molecular analysis as a preferred method for population estimation. We conducted a pilot study on the feasibility of hair traps in a state forest in southwest Germany. We applied 45 hair traps over an 8 week period. Preliminary results suggest limited success of this method. Collected hair samples originated predominantly from mice (*Apodemus sp.*) or dormice (*Glis glis*). However, camera traps recorded pine martens entering the hair traps but we were not able to collect hair samples from all observed events. We currently revise the design of the hair trap. Additionally, we plan further investigation in using camera traps as well as wildlife detection dogs for scat collection to design a cost and time efficient pine marten monitoring.

Solving the ElioMystery: Combining citizen science and conservation genomics to reveal the causes of rapid population decline in the garden dormouse (*Eliomys quercinus*)

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The garden dormouse (*Eliomys quercinus*) is a native European rodent species that has suffered extensive range contraction and severe population decline during the last decades. While disappearing from 50% of its former distribution range during the last 30 years, the species has deserted large parts of Eastern Europe and is now considered extinct in some countries. At the same time, contrasting population dynamics are observed in its western distribution range, where garden dormice are regionally abundant and even occupy synanthropic habitats. As reasons for these opposing range dynamics and drastic declines remain unknown, we have started a long-term cooperation project, joining the efforts of different research institutions and conservation NGOs to investigate the underlying causes. Our research activities include the involvement of citizen scientists via an online reporting tool to assess the current distribution, regional diet composition, phenology as well as the pathology of the species. Further, we conduct RADseq analysis to infer phylogeography and delineate different conservation units. Preliminary genomic data show the existence of highly divergent genetic lineages, even on a local scale. Based on these findings, we aim to develop a reduced SNP panel allowing for distinguishing these lineages. This tool will aid animal rescue centers with appropriate reintroduction of displaced *Eliomys* foundlings but also when establishing or reconnecting isolated populations of garden dormice. Ultimately, the joint project efforts aim to resolve the biology and ecology of *Eliomys* in order to develop a suitable conservation strategy and implement effective conservation measures for a species that has long been neglected in the legislation of European species conservation.

Bullshit makes sense now: A reduced SNP panel for non-invasive genetic assessment of a genetically impoverished species, the European bison

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The European bison (*Bos bonasus*, Linnaeus 1758) was saved from the brink of extinction due to considerable conservation efforts since the early 20th century. The current global population descends from a total of 12 captive individuals, which represents a severe bottleneck event. Although the population size increased to more than 7,500 individuals worldwide by successful *ex situ*-breeding and reintroductions into the wild, the species is still threatened by an extremely low level of genetic variability and high inbreeding. Due to the low allelic diversity, traditional molecular toolsets, such as microsatellites, fail to provide sufficient resolution for accurate assessments of genetic diversity, individualisation and relatedness in this species. This has so far hampered genetic assessments of *ex situ* breeding management as well as non-invasive population monitoring.

Here, we present a reduced SNP panel for microfluidic genotyping of low-quality and degraded samples from European bison. The panel accommodates 96 informative markers allowing for (i) sex determination, (ii) individualisation, (iii) parental assignment, (iv) breeding line discrimination, (v) assessment of genetic diversity and (vi) cross-species detection. We successfully genotyped various non-invasively collected sample types, such as faeces, hairs and saliva from approx. 300 captive and wild living wisent individuals, representing the most extensive genetic study of extant European bison. Due to the low costs, high marker resolution and the suitability for various sample types our new SNP assay will allow to tackle crucial tasks in bison conservation management, including the accurate genetic monitoring of reintroduced wild populations, as well as the molecular assessment of pedigree data documented in the world’s oldest studbook of a threatened species.

The invasion of the lime swallowtail in Australasia and its effect on endemic populations in the Lesser Sunda Islands

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The original range of the lime swallowtail (*Papilio demoleus* L.) consisted of two parts: (1) continental South and SE Asia, including the islands of Sri Lanka, Hainan and Taiwan; and (2) Australia (ssp. *sthenelus*), SE Papua New Guinea (ssp. *novoguineensis*), and the Lesser Sunda Islands (ssp. *sthenelinus*). Populations in the Australian region are well differentiated genetically from Asian ones, in adult phenotype, larval colour pattern and foodplant choice. Whereas larvae of Asian populations are a pest on *Citrus* (Rutaceae), those in the Australian region only feed on *Cullen* (Fabaceae).

Since the 1950s, *Citrus* feeding populations have invaded most of the previous distributional gap, starting from the Phillippines through the Greater Sunda Islands, and also reaching the Lesser Sunda Islands (Flores in 1997) and Papua New Guinea (in 2004) with their indigenous *Cullen* feeding populations.

Molecular analyses of mitochondrial DNA (*COI* & *COII*) prove that the indigenous populations in PNG and Flores are well differentiated genetically from invasive ones and closely related to Australian populations while all invasive populations are very similar genetically and originate from Southeast Asia. The most common *COI* haplotype which spread across most SE Asian islands and which was also introduced into the Caribbean originates from the SE Asian mainland or Hainan (China), a second haplotype spread from Taiwan via the Philippines to the Lesser Sunda Islands, and a third haplotype with as yet unknown origin was only found in Sumatra, the Lesser Sunda Islands and West Papua.

Despite the invasion into the Lesser Sunda Islands, indigenous populations still exist on the west coast of Flores and the nearby islands of Komodo, Rinca and Padar, where they feed on the endemic *Cullen gaudichaudianum*. Whereas no evidence of mitochondrial introgression was found at Labuanbajo, where indigenous and invasive populations occur in sympatry, genetical admixture could be established at the nuclear locus *ef-1α*.

Nevertheless we suspect that the taxon *sthenelinus* constitutes a distinct species, but further studies are needed to clarify the taxonomy of the *Papilio demoleus* complex and the extent of gene flow between indigenous and invasive populations, which might pose a threat to the endemic island taxa.

Combining collection specimen with genetic information using deep learning to assist IUCN conservation assessments

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Automated conservation assessments using species occurrence data from herbaria and museum collections are currently emerging as a time- and data-effective complement to full Red List assessments of the International Union for the conservation of Nature (IUCN). However, it is unclear how well these automated methods represent full assessments and how they can be developed beyond geographic occurrence data. Here, we present results from a case studie of different taxa across the tree of life, including the bromeliad (Bromeliaceae) and orchid families (Orchidaceae), showing that automated conservation assessment methods can reach an accuracy between 60 and 80% compared with full IUCN assessments, in a fraction of the time. A novel method, based on neural networks (IUC-NN) that can include information beyond geographic occurrences, for instance organism traits reached the highest accuracy. Furthermore, we will outline a route forward to harness the current increase in the availability of genetic and genomic data from large data aggregators for the global IUCN Red List, by including genetic population structure into automated assessments, and thereby increase the link between IUCN conservation assessments and conservation genetics.

Conservation genetics at the Cheetah Conservation Fund

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The Cheetah Conservation Fund (CCF) is based in Namibia and dedicated to saving the cheetah in the wild. CCF's Life Technologies Conservation Genetics Laboratory was established in 2008 and is the only fully-equipped genetics laboratory *in situ* at a conservation facility in Africa. From this facility, CCF collaborates with scientists around the globe. The laboratory's main aim is to contribute to CCF's on-going multi-disciplinary research and conservation efforts to save the cheetah. The key genetics projects are focused on cheetah conservation, including population structure, census, relatedness, and assignment of individual ID to non-invasive samples such as scat. To allow us to integrate such poor-quality samples, we have optimized markers to work specifically with cheetah scat.

One of the major projects on cheetah genetics is our Namibian Population Study, which has been running since CCF's inception in 1990. With over 750 blood and tissue samples, as well as over 1000 scat samples being part of the analyses, we have the opportunity to analyze the Namibian cheetah population not only in the state of today, but over a time span of 30 years and counting. Through various collaborations, we have similar, yet smaller-scale, projects in other African countries, such as Kenia or Angola. Besides the focus on cheetah population genetics, the CCF genetics laboratory is part of national and international collaborations such as black and white rhinoceros population management, or disease studies covering the effect of genetics on amyloidosis.

Sex-biased dispersal in the asp viper: only males care about their environment

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Dispersal is an important life history trait, and differences between sexes can affect the genetic structure and spatial distribution of populations. Sex-biased dispersal is frequent in vertebrates, with a general tendency of male-biased dispersal in mammals and female-biased dispersal in birds. In reptiles, male-biased dispersal seems to be prevalent, but only a few studies were conducted in this group. Moreover, most of these studies considered only a single study site, although one investigation demonstrated interpopulation variation in sex-biased dispersal in snakes. We investigated sex-biased dispersal in the asp viper (*Vipera aspis*) in 4 study sites in Switzerland using microsatellite markers and predicted a higher dispersal in males than females. In 2 of the 4 study sites, females were more spatially autocorrelated and showed a stronger isolation by distance compared to males, results that suggest male-biased dispersal. In the other 2 study sites, the lack of sex-biased dispersal could be explained by habitat fragmentation (a road and a stream, respectively). Indeed, detailed analyses of subpopulations in both fragmented sites also demonstrated male-biased dispersal. Surprisingly, the dispersal ability of females was similar in the 4 sites, independent of habitat fragmentation. This finding suggests the limited impact of habitat on female dispersal and the opposite to male dispersal. Our study demonstrates the importance of inferring sex-biased dispersal in different habitats because local barriers can impact the outcome of such studies. Hence, general conclusions about patterns of sex-biased dispersal should be drawn with caution when studies are conducted in a single study site.