European Conservation Genetics Meeting

August 30 – September 1
Edinburgh

Welcome

Fàilte, Bienvenue, Willkommen, Dobrodošli, Tervetuloa, Bienvenidas, Välkommen, Witamy or a very warm welcome to the

5th European Conservation Genetics Meeting – #ConsGen22

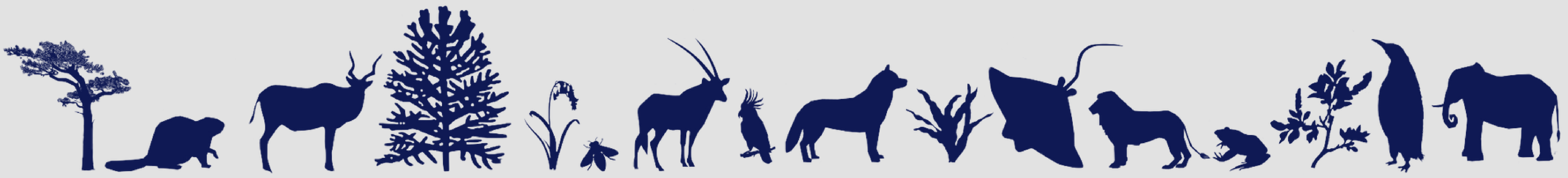
We have delegates attending from all corners of Europe and beyond, meeting here in Edinburgh, the historic capital of Scotland. We have a terrific schedule of conservation genetic delights including seven keynote speakers and over 130 attendees presenting their current research. And if you would like *even more* conservation genetic content we have three evening events organised so you can fit even more discussion time in and enjoy some true Scottish fun. Ceilidh anyone?

We hope you have a splendid three days catching up with colleagues after years of lockdowns, forging new partnerships, and discussing novel ideas. This year the event is being jointly hosted by the Royal Botanic Garden Edinburgh, the Royal Zoological Society of Scotland and the University of Edinburgh. It is the first time the meeting has been hosted in the UK and we hope you enjoy the Scottish hospitality as well as making time to explore the wider region.

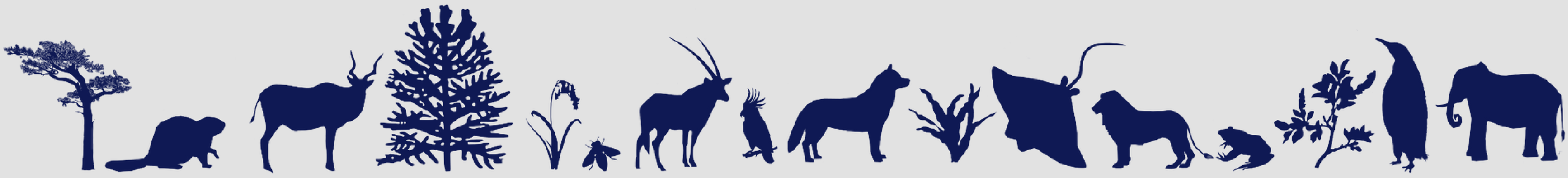
This booklet will hopefully provide you with all you need to know about this year's Conservation Genetics meeting but if you have any questions, do not hesitate to ask.

Have a fantastic conference,

ConsGen22 Organising Committee



Contents



Important Information

Transport in Edinburgh

Edinburgh is well connected through its public transport system which includes buses, and trams. Google Maps and a Transport for Edinburgh app can be used for planning travel and more information can be found at **transportforedinburgh.com**

Intercity travel is also possible by bus and train. Please be aware that some services may be reduced or cancelled due to industrial action.

Several taxi companies operate in Edinburgh including **City Cabs (0131 228 1211)** and **Central Taxis (0131 229 2468)**. Uber also operates in Edinburgh.

Accessibility and inclusion

At the conference venue we have a designated family friendly room as well as private space available for breastfeeding, and a quiet room for prayer and meditation.

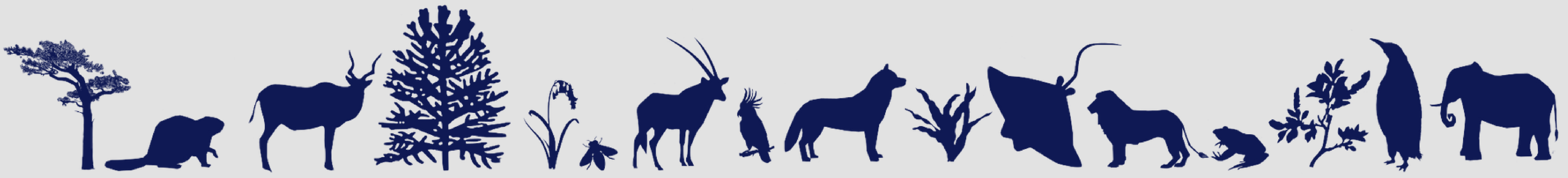
Additional information is available on the ConsGen22 website and please don't hesitate to contact any of our conference helpers for assistance.

Additional assistance

If you have any further questions or require any additional assistance please contact one of the conference helpers who can be identified by their green lanyards.

Covid-19 statement

All COVID-19 rules and restrictions have been lifted in Scotland. However, the virus has not gone away. We recommend that delegates think carefully about attending if they are feeling unwell and advise that you do not attend if you have symptoms of COVID-19. Hand sanitiser stations will be provided throughout the conference venue and masks will be available. For up-to-date COVID-19 guidelines please refer to the Scottish Government website.



Social Events

Poster session

Date: Tuesday 30 August
Time: 17:45-19:45
Location: Prestonfield Room, John McIntyre Conference Centre

Enjoy the first evening of the conference perusing posters and discussing exciting research. Every delegate will receive a drinks token that can be exchanged at the bar for a welcome drink (glass of wine, beer, or a soft drink). The bar will be open for the duration of the poster session but can only accept card payments.

Conference dinner and ceilidh

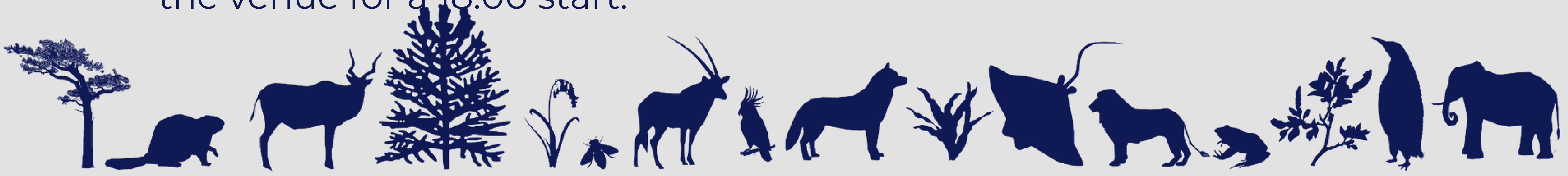
Date: Wednesday 31 August
Time: 18:00-Late
Location: John Hope Gateway, Royal Botanic Garden Edinburgh

Celebrate ConsGen22 in style on Wednesday 31 August with dinner at the Royal Botanic Gardens Edinburgh. Ticket holders to the conference dinner will be taken to the Royal Botanic Garden Edinburgh by buses that will leave the John McIntyre Conference Centre at 17:45. Attendees are also welcome to make their own way to the venue for a 18:15 start with dinner seating at 19:00. Tickets include a welcome drink and two glasses of wine with dinner. A bar will be open all evening but can only accept card payments.

Edinburgh Zoo evening soirée

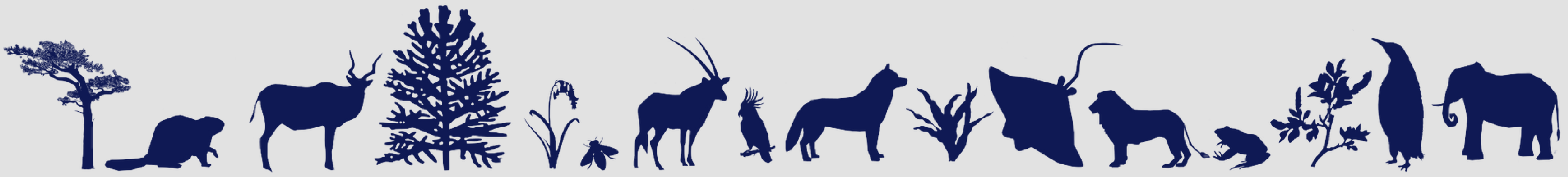
Date: Thursday 1 September
Time: 18:00-22:00
Location: Edinburgh Zoo

Enjoy the final evening of the conference with drinks and a delicious casual buffet at the Royal Zoological Society of Scotland's Edinburgh Zoo. A bar will operate all evening and a welcome drink is included in admittance. Ticket holders to the evening soirée will be taken to Edinburgh Zoo by buses that will leave the John McIntyre Conference Centre at 16:30. Attendees are also welcome to make their own way to the venue for a 18:00 start.



Venue Layout

Foyer: Conference Registration	Prestonfield: Poster Session
Boardroom1: Conference Organisers Only	Duddingston: Family-friendly Room
Boardroom2: Available for uploading talks	Salisbury: Available for general use
Concourse: Sponsors Tables	Holyrood: Quiet Room



TUESDAY

AUGUST

30

Schedule

PENTLANDS (EAST/WEST)

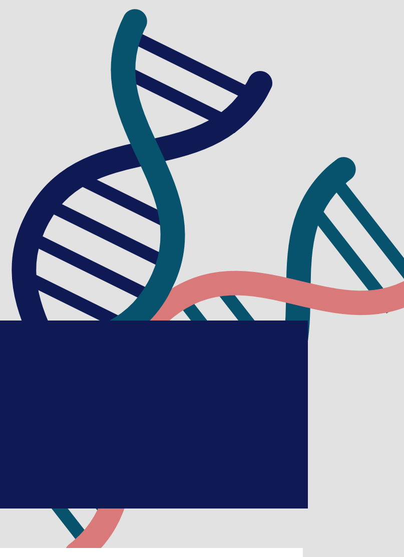
08:45	**ONT Workshop Registration**
09:00	ONT Workshop
10:15	**BREAK**
10:45	ONT Workshop
12:00	**LUNCH** **Registration Opens**
13:00	Welcome and housekeeping
	PLENARY - COLLECTIONS
13:20	**Rebecca Johnson** Smithsonian National Museum of Natural History, USA **Working as a wildlife detective from koalas to cockatoos - how museum collections illuminate dark data for conservation**
	COLLECTIONS
13:55	**59 Rasmus Heller** *Lessons, visions and challenges from 1000+ large African mammal genomes*
14:10	**19 J. Camilo Chacón-Duque** *Museum specimens reveal the genomic impact of recent population decline on Andean bears*
	SPEED TALKS
14:25	**92 Annika Mozer** *Developing Multiplex SNPSTR Marker Sets For Endangered Species* **10 Iva Bernáthoválva** *Conservation genetics of pangolins in the Congo Republic* **87 José Meléndez** *Genetic and phenotypic comparison of populations resulting from translocations and natural colonizations*

TUESDAY

AUGUST

30

Schedule



PENTLANDS (EAST/WEST)

11 **Roberto Biello**

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

14:40

BREAK

15:10

SPEED TALKS

86 **René Meißner**

Characterization of selected toll-like receptor genes in cheetahs (Acinonyx jubatus) *compared to the sympatric occurring leopard* (Panthera pardus) *and its implication for conservation*

82 **Prachi Masih**

Genetic divergence in wild populations of Indian major carp, Cirrhinus mrigala *(Hamilton, 1822) across India, an assessment from ATPase6/8 mitochondrial gene analysis*

80 **Melissa M. Marr**

Conservation genomics of red squirrels in Scotland: understanding diversity in a key stronghold

6 **Haidi Arbanasić**

Is extensive MHC class II diversity in striped dolphin (Stenella coeruleoalba) *in the Mediterranean Sea shaped by recent epizootics?*

COLLECTIONS

15:25

45 **Brigida Gallone**

Fungarium collections in the genomic era: the Mycena genus

15:40

102 **Catarina J. Pinho**

Digging in a 120 years-old lunch: what can we learn from collection

15:55

SPEED TALKS

25 **Simone D'Alessandro**

Understanding marine connectivity of scallop populations within Scottish and adjacent waters to inform marine management

129 **Gabriel Ulrich**

Sampling historical DNA to assess the impact of habitat loss on genetic diversity in a peatland-specialist

4 **Louise Arathoon**

Investigating inbreeding depression in a long-term study of Antirrhinum majus

18 **Emily Cavill**

When birds of the same feather flock together: a story of inbreeding in an endangered island bird species

84 **Claire McFarlane**

DNA-based methods for monitoring the Irish Damselfly (Coenagrion lunulatum)

TUESDAY

AUGUST

30

Schedule

PENTLANDS (EAST/WEST)

16:10

BREAK

COLLECTIONS

16:25

98 **Manabu Onuma**

Establishing a viable cell culture banking network for endangered species conservation in Asia

16:40

65 **Evelyn Jensen**

Surprises in the museum and arguments in the literature: how many Galapagos giant tortoise species are there?

SPEED TALKS

16:55

43 **Manuel Fonseca**

DNA Metabarcoding Is Not Magic: A Case Study With The Critically Endangered Highland Woolly Monkey

68 **Anubhab Khan**

What can you learn from a fly? Biting insects as non-invasive samplers

17 **Magdalena Butowska**

Novel Protocol for Diet Analysis of European Wildcat (Felis silvestris)

138 **Lucia Zanovello**

Exploring human-amphibian cohabitation with conservation genetics and landscape planning tools

75 **Olivier Lepais**

Fast sequence-based microsatellite genotyping development workflow for any non-model species

PLENARY - COLLECTIONS

17:10

Camila Mazzoni

on behalf of the European Reference Genome Atlas (ERGA) Consortium

Berlin Center for Genomics in Biodiversity Research, Germany

Establishing the European Reference Genome Atlas (ERGA) of Biodiversity

PRESTONFIELD

17:45

Poster Session

until 19:45

WEDNESDAY
AUGUST
31

Schedule

	PENTLANDS EAST	PENTLANDS WEST
09:00	Welcome back and housekeeping	
09:05	PLENARY - APPLICATIONS **Magda Bou Dagher Kharrat** Saint Joseph University of Beirut, Lebanon/ European Forest Institute, Spain **Plant conservation: insights from the East Mediterranean experience**	
09:40	PLENARY - TECHNOLOGIES **Mrinalini Watsa** San Diego Zoo Wildlife Alliance, USA / Field Projects International **Biodiversity Monitoring in the Peruvian Amazon via the In Situ Lab Initiative**	
10:15	**BREAK**	
	TECHNOLOGIES	APPLICATIONS
10:45	**40** **Maria Joana Ferreira da Silva** *The use of meta-barcoding tools to identify bushmeat consumed at bars in Guinea-Bissau, West Africa, and implications for non-human primates conservation*	**53** **Stefanie Grosser** *Resolving the genomic architecture of hatching failure in the Hawaiian crow* (Corvus hawaiiensis) *to improve conservation management*
11:00	**33** **Marianne Dehasque** *Temporal dynamics of genome erosion leading up to the extinction of the woolly mammoth*	**50** **Marc-Alexander Gose** *Population genetics of an elusive marine predator, the Atlantic white-sided dolphin* (Lagenorhynchus acutus), *across the eastern North Atlantic*
11:15	**77** **Samantha López-Clinton** *A field-friendly, low-cost genotyping approach for high and low quality DNA using the MinION portable sequencer*	**88** **Ronald Vincent Mellya** *Conservation genetics for the management of black rhinoceros* (Diceros bicornis michaeli) *in Tanzania*
11:30	**20** **F. Gözde Çilingir** *Chromosome-level* de novo *genome assembly for the Aldabra giant tortoise enables insights into the genetic health of a threatened population*	**107** **Mariana Ribeiro** *The value of captive wildlife in the conservation of species: Genetic diversity and admixture in the emblematic sable antelope* (Hippotragus niger)
11:45	**76** **Francesca Angela Lioce** *Diet and trophic niche overlap in chamois, red deer and domestic sheep in the Italian Alps*	**37** **Ettore Fedele** *Portable genomic tools for gorilla population dynamics and conservation*

WEDNESDAY

AUGUST

31

Schedule

	PENTLANDS EAST	PENTLANDS WEST
	TECHNOLOGIES	APPLICATIONS
12:00	**46** **Roberta Gargiulo** *Estimates of effective population size in plants with complex life-history traits*	**85** **Lydia McGill** *Genomic analysis of Flame Shells* (Limaria hians) *to inform nature conservation*
12:15	**131** **Raquel Vasconcelos** *Green matters: dietary reptile community assessment using DNA metabarcoding*	**74** **Deborah Leigh** *Sympatry of genetically distinct puffins in the High Arctic*
12:30	**LUNCH** Sponsor's talk - ONT and Basecamp	
	TECHNOLOGIES	APPLICATIONS
13:30	**122** **Steve Smith** *A creeping yet catastrophic threat: chytrid fungus presents a clear and present danger to amphibian populations in Europe and beyond*	**81** **Claudia Anne Martin** *Hybridization may aid genetic rescue across fragmented populations of an endangered East African passerine,* Zosterops silvanus
13:45	**57** **Heidi C. Hauffe** *The role of microbiodiversity in conservation: insights from ecosystem metataxonomics*	**71** **Klaus-Peter Koepfli** *Rescued, diminished, but hopeful: Severe genetic erosion revealed by genomic analysis in the endangered black-footed ferret* (Mustela nigripes)
	APPLICATIONS	APPLICATIONS
14:00	**31** **Michele De Noia** *Towards an in-situ non-lethal rapid test to accurately detect the presence of the nematode parasite,* Anguillicoloides crassus, *in European eel,* Anguilla anguilla	**1** **Sabhrina Gita Aninta** *Detecting purifying selection on endemic island ungulates and its implications for conservation*
14:15	**90** **Melissa Minter** *Using ddRAD seq to infer historical population changes and current isolation in a cold-adapted butterfly*	**41** **Aline Finger** *Putting genetic rescue to practice using the alpine blue-sowthistle* (Cicerbita alpina) *in Scotland*
14:30	**101** **Patricia Pečnerová** *Elephant task: Developing a genomic toolkit for research and conservation*	**116** **Yu Sato** *Conservation genomics of golden eagles on isolated populations of Scotland and Japan*

WEDNESDAY

AUGUST
31

Schedule

	PENTLANDS EAST	PENTLANDS WEST
	APPLICATIONS	APPLICATIONS
14:45	123 **Kasha Strickland** *Susceptibility to a sexually transmitted disease in a wild koala population shows heritable genetic variance but no inbreeding depression*	91 **Hernán E. Morales** *Genomic diversity decline over time in avian endangered species*
15:00	**BREAK**	
	APPLICATIONS	APPLICATIONS
15:30	105 **Orly Razgour** *Applying genomic approaches to identify historic population declines in British bats*	63 **Emily Humble** *Uncovering the mysteries of manta rays using genomics*
15:45	117 **Tanja Schwanck** *Using genomic tools to assess the efficacy of a Marine Protected Area designated to the critically endangered flapper skate*	93 **Annegret Moto Naito-Liederbach** *Major histocompatibility complex genes and age are associated with reproduction of the endangered Japanese Golden Eagle in captivity*
16:00	22 **Karen Cox** *Identifying landscape drivers of genetic variation of a pond-breeding amphibian on multiple spatial scales*	49 **José A. Godoy** *The ongoing contribution of genomics to the conservation of the once most endangered felid: the Iberian lynx*
16:15	121 **Cornelia Simon-Nutbrown** *Population genetics of Scottish maerl beds informing the need for targeted conservation management*	29 **Binia De Cahsan** *Road to extinction? Past and present population structure and genomic diversity in the koala* (Phascolarctos cinereus)
16:30	51 **Rachel Gray** *Investigating hybridisation between living and extinct Galapágos giant tortoises to inform a unique captive breeding programme*	24 **Love Dalén** *Conservation genomics of the Scandinavian arctic fox*
16:45	34 **Kara Dicks** *Genetic diversity in global populations of the Critically Endangered addax* (Addax nasomaculatus) *and its implications for conservation*	110 **Mathieu Robin** *Conservation genetics in bottlenecked species: Insights from ancient genomes of the Alpine ibex*
17:45	**BUSES TO CONFERENCE DINNER & CEILIDH AT ROYAL BOTANIC GARDEN EDINBURGH** 18:00 - LATE	

THURSDAY
SEPTEMBER
1

Schedule

	PENTLANDS EAST	PENTLANDS WEST
09:00	Welcome back and housekeeping	
09:05	PLENARY - POLICY **Robert Ekblom** Swedish Environmental Protection Agency, Sweden **Genetic population monitoring of Scandinavian large carnivores**	
09:40	PLENARY - APPLICATIONS **Laura Bertola** University of Copenhagen, Denmark **Harnessing genomic resources for lion conservation**	
10:15	**BREAK**	
	POLICY	APPLICATIONS
10:45	**97 David O'Brien** *Bringing together approaches to reporting on within species genetic diversity*	**62 Jo Howard-McCombe** *Whole genome sequencing dates the tipping point for genetic swamping of the critically endangered wildcat population of Scotland*
11:00	**100 Peter Pearman** *Monitoring population genetic diversity for conservation in Europe: Current situation and outlook in view of climate change*	**95 Paola Nogales-Ascarrunz** *Improving Jaguar conservation efforts through genomics*
11:15	**42 Martin C. Fischer** *Monitoring genetic diversity: a genomics-based pilot study for Switzerland*	**109 Heather Ritchie-Parker** *Genetic analysis of beavers* (Castor fiber) *in England and considerations for reintroduction*
11:30	**125 Rebecca Taylor** *The evolutionary history of caribou: implications of high intraspecific diversity for conservation*	**89 Antti Miettinen** *Following the trajectories of adaptive loci over time for conservation and management of Atlantic salmon*
11:45	**124 Helen Taylor** *Bridging the conservation genetics gap to improve conservation outcomes*	**44 Maëva Gabrielli** *Genomic variation and accumulation of deleterious mutations in the critically endangered Aeolian wall lizard*
12:00	**47 Julia Geue** *Genetic diversity and introgression in the Norway – Siberian Spruce Species Complex: implications in conifer management and conservation*	**8 Alex Ball** *Conservation genetics in the highlands; applications in Scotland and beyond*

THURSDAY
SEPTEMBER
1

Schedule

	PENTLANDS EAST	PENTLANDS WEST
12:15	**LUNCH** Sponsor's talk - Arbor Biosciences	
	POLICY	APPLICATIONS
13:15	128 **Samuel Turvey** *Species diversity and conservation priorities for Cuban hutias: insights from modern and ancient DNA*	52 **Christine Grossen** *Integrating ancient genomics and field-applicable protocols for sustained species conservation: the case of hybridization between Alpine ibex and domestic goat*
13:30	56 **Jeanette Hall** *Applying the Gene Conservation Units concept to taxa other than trees*	21 **Ivo Colmonero-Costeira** *The Western spot-nosed monkey* (Ceropithecus petaurista buettikoferi) *in Guinea-Bissau: combining genetic and social data to assess the conservation status and threats of the country's most unknown guenon*
	APPLICATIONS	APPLICATIONS
13:45	133 **Alina von Thaden** *Citizen science genomics guides conservation strategies of the rapidly declining garden dormouse* (Eliomys quercinus)	103 **Victoria Pritchard** *Parentage-based genetic tagging to monitor the success of conservation re-introductions*
14:00	58 **Sean Heighton** *Genomic insights and resources to aide in pangolin conservation*	61 **Karen Holm** *Improving ex situ conservation of the Endangered Red Siskin* (Spinus cucullatus) *through the use of genomic tools*
14:15	114 **Jordi Salmona** *The antique genetic plight of the Mediterranean monk seal* (Monachus monachus)	54 **Catherine Grueber** *Genomics and simulations to improve conservation breeding*
14:30	**BREAK**	
15:00	PLENARY - POLICY **Mike Bruford** Cardiff University, Wales **Honesty is the best policy: how genetic diversity has emerged from the shadows in conservation planning and what we all need to do to keep it in the spotlight**	
15:35	Closing session	
16:30	**BUSES TO EDINBURGH ZOO EVENING SOIRÉE** 18:00 - 22:00	

Plenary

Applications

Date: Thursday 1 September
Time: 09:40
Room: Pentlands (East/West)

Laura D. Bertola

University of Copenhagen, Denmark

Harnessing genomic resources for lion conservation

Population genomics and phylogeographic studies provide insights into the distribution of genetic diversity within and between species. These insights can then be used to guide conservation efforts, e.g. by prioritizing populations for conservation investments, by informing decisions regarding translocations, and by optimizing retention of genetic diversity in captive breeding.

Here, I present the lion as a case study, in which we started out exploring broad intraspecific diversity patterns, building on previous research based on mostly mtDNA and microsatellite data. Based on full genome data from individuals representing the main genetic lineages we designed a SNP panel, which allows us to genotype large numbers of samples more cost-effectively. This panel has been used to genotype lions from zoos, to inform captive breeding, focusing on the conservation of the northern subspecies in particular. The panel is also being used to assess patterns of lion genetic diversity throughout Kenya, and to support local decision-making on how to deal with translocations of problem animals. On a broader geographic scale, data on lion genetics and international trade data from CITES have been used to map translocations of lions and potential genetic consequences for resident populations. This resulted in a hierarchical decision-making tool, aimed to facilitate the integration of genetic considerations for the selection of source and/or target populations for conservation translocations. It should be emphasized that in order to make impact on the ground, long-lasting and balanced collaborations with local researchers and conservation practitioners are key.

These types of data can also provide insights into the processes driving these patterns to emerge. Data derived from one species can therefore be more broadly applicable, as it may be informative for a range of species. Co-distributed species often display congruence in these genetic patterns, and comparative research across communities helps to further highlight shared (or contrasting) patterns of diversity. The ongoing research program on population genomics of African mammals at Copenhagen University is producing data that can be used in this context, and we hope that it will provide a useful resource for researchers, practitioners and policy makers.

Plenary

Applications

Date: Wednesday 31 August
Time: 09:05
Room: Pentlands (East/West)

Magda Bou Dagher Kharrat

Saint Joseph University of Beirut, Lebanon
Mediterranean Facility (EFIMED)
European Forest Institute (EFI) , Spain

Plant conservation: insights from the East Mediterranean experience

The Mediterranean Basin is considered to be one of the most biodiverse regions in the world and an important site of floral exchange and active plant speciation. High level of vascular plant species richness and narrow endemism characterize its flora. Lebanon, a micro-hotspot for plant biodiversity in the Mediterranean Basin is characterized by the coexistence of plants with diverse biogeographical origins and a large number of narrow endemic taxa. It clearly exhibits differentiated center of endemism. Topographical relief and sharp climatic contrasts within a small geographical area may have driven micro-evolutionary diversification processes of newly evolved species while water availability was critical for the long-term persistence of ancient lineages in refuge areas of smoother topography.

As natural habitats continue to be lost and degraded, many plant species are becoming increasingly threatened especially endemic plant species that are usually more vulnerable to anthropogenic threats and natural changes. Therefore, they hold a higher extinction risk. The preservation of these species is a major concern on a worldwide context.

Our research group has carried out for the last few years an interdisciplinary, integrated approach to the conservation of threatened plants of the Lebanese flora and to ecosystem restoration. Investigations on plant distribution, systematic relationships, autoecology, genetic structure, and some plant-animal species interactions were conducted in order to plan conservation activities.

Knowing what taxonomic units (species, subspecies or populations) need to be preserved and how unique they are is a prerequisite to any conservation action. Since rescue from possible extinction could be performed through the reinforcement of populations, defining species and differentiating taxa is crucial in order to define conservation units. For this purpose, molecular and cytogenetic studies are conducted, targeting different species in need of *in-situ* and *ex-situ* conservation such as *Juniperus*, *Cedrus*, *Iris* and *Astragalus*.

DNA metabarcoding technique was also used to describe the seasonal plant diet composition of some mammal species to decipher important interactions necessary for community establishment in ecosystem restoration programs.

Plenary

Collections

Date: Tuesday 30 August
Time: 13:20
Room: Pentlands (East/West)

Rebecca Johnson

Smithsonian National Museum of Natural History, USA

Working as a wildlife detective from koalas to cockatoos - how museum collections illuminates dark data for conservation

From climate change to wildfires to floods, we are in a time of unprecedented global change largely attributable to human activity, especially with biodiversity loss. More than ever, we need planetary information to understand the rate and scale of these changes. Biological collections housed in natural history museums support foundational discovery science and collectively represent a baseline of biodiversity and ecosystem knowledge, including how these have changed over time, including how they might change in the future. With examples ranging from cockatoos to koalas, this presentation will explore the rich source of data in museum collections and how it can be translated into actionable conservation information.

At the Smithsonian's National Museum of Natural History (NMNH), we are custodians of the world's largest biological collections. The collections support foundational discovery science and collectively represent a substantial baseline of biodiversity and ecosystem knowledge, including how these have changed over time. Despite its vast holdings at NMNH, much of the information about these specimens is dark data – meaning that the data may not be discoverable or accessible. This presentation will share some of our future plans to create accessible collections records using new technologies. Illuminating the dark data in museum collection is urgent, not just to make data visible and shareable, but to use it to understand and mitigated the rapid changes to the Earth’s biodiversity and ecosystems.

Plenary

Collections

Date: Tuesday 30 August
Time: 17:10
Room: Pentlands (East/West)

Camila Mazzoni
on behalf of the European Reference Genome Atlas (ERGA) Consortium
Berlin Center for Genomics in Biodiversity Research, Germany

Establishing the European Reference Genome Atlas (ERGA) of Biodiversity

Biodiversity is being lost faster than science is able to catalogue and study the species of our planet. New Genomic technologies can help us describe the genome sequence of virtually any living species, and unveil the most basic and essential information that forms an organism. In 2020, hundreds of scientists got together to form an European-wide initiative to support the Earth BioGenome Project (EBP) mission of sequencing all complex life on Earth. The European Reference Genome Atlas (ERGA) is both a project and a network of projects, institutions and scientists. As a project, ERGA aims to sequence thousands of genomes of European critical biodiversity and to form an expandable sequencing and computational infrastructure, distributed across Europe. As a network, ERGA intends to connect projects, institutions and scientists as a synergistic hub of knowledge and resources exchange. The first major endeavour of ERGA has been a Pilot project that aimed to sequence at least one genome from every European country. The ERGA-Pilot has formed the basis of ERGA's infrastructure, including the association of several sequencing centres, support from stakeholders, development of SOPs and an initial computational infrastructure to assemble, annotate and submit data to public repositories. The path paved by the ERGA-Pilot will be expanded by the next ERGA core project, the Biodiversity Genome Europe (BGE) ERGA stream, which was recently funded by the European Commission. The BGE project will support the ERGA consortium in establishing a robust infrastructure to allow the network expansion and indirectly the sequencing of thousands of genomes. Conservation is one of the core BGE-ERGA topics, which aims to generate hundreds of genomes of endangered species and habitats and to generate proof-of-principle of the value of reference genomes for conservation applications.

Plenary

Policy

Date: Thursday 1 September
Time: 15:00
Room: Pentlands (East/West)

Mike Bruford
Cardiff University, Wales

Honesty is the best policy: how genetic diversity has emerged from the shadows in conservation planning and what we all need to do to keep it in the spotlight

The last three years have seen an active and at times challenging debate on the role of genetic diversity in the CBD post 2020 Framework, specifically around its inclusion in goals and targets for signatory countries. The CBD's COP 15 meeting is rapidly approaching, and even after a number of delays, the text for the Framework is still to be finalised. However, by concerted global action the signs are now looking positive that we will at last have a meaningful framework within which member states can measure, monitor and report on progress in genetic diversity for both wild and domesticated species, in a pragmatic way. In this presentation, I will discuss both the origin and progress of the debate which has led to this point, taking the IUCN Conservation Genetics Specialist Group as an example initiative that has contributed to the development of genetic diversity policy. I will also highlight the recent formation of the Coalition for Conservation Genetics, that brings together a number of similar initiatives to form a global alliance for the advocacy of genetic diversity. Finally, I will pinpoint a number of challenges that are actively being addressed around proposed genetic indicators, challenges that remain to be addressed and suggest what practising conservation geneticists can do to continue the advancement of genetic diversity in biodiversity monitoring and management into the future.

Plenary

Policy

Date: Thursday 1 September
Time: 09:05
Room: Pentlands (East/West)

Robert Ekblom
Swedish Environmental Protection Agency, Sweden

Genetic population monitoring of Scandinavian large carnivores

I work in the interface between policy, management and research. In my presentation I will introduce and discuss how these areas can jointly contribute to monitoring and conservation of wildlife. I will focus mainly on projects on large carnivores in Scandinavia, such as wolverine (*Gulo gulo*) and brown bear (*Ursus arctos*), where genetic tools are currently being utilised and developed for such purposes. By yearly, extensive, non-invasive sampling of DNA we can follow individuals, identify genetically important long-distance migrants, and construct pedigrees. Data is collected and processed with harmonised methods across both Norway and Sweden, and we have a joint database including data on observations, individuals, and search efforts. We also use novel capture-recapture modelling to estimate precise carnivore densities from the DNA data. By applying these estimates to local geographic scales, we are currently developing a compensation system for livestock owners based on carnivore abundance. This relates especially to the reindeer herding indigenous Saami people, who experience substantial losses to semi-domesticated reindeer from carnivores. With the availability of large-scale genetic monitoring data, we can also calculate temporal trends in genetic diversity. In Sweden we are currently developing such monitoring programs of genetic variation for a large number of species. The results from this will be valuable for evaluating national environmental goals, as well as in reporting progress to international treaties such as the Convention on Biological Diversity (CBD).

Plenary

Technologies

Date: Wednsday 31 August
Time: 09:40
Room: Pentlands (East/West)

Mrinilini Watsa
San Diego Zoo Wildlife Alliance, USA
Field Projects International

Biodiversity Monitoring in the Peruvian Amazon via the In Situ Lab Initiative

Broad scale long-term active surveillance in biodiversity hotspots is a prerequisite to implementing year-round disease surveillance, as the resolution of taxonomy can have significant impacts on disease data. The In Situ Laboratory Initiative aims to create a decentralised biomonitoring and disease screening network in southeastern Peru. In 2021, the ISL Initiative launched the Wildlife Conservation Laboratory at the Los Amigos Biological Field Station as the first node in a network of connected biomonitoring facilities. Staffed and operated by regional scientists, the WCL is a BSL-2 laboratory that is entirely energy independent, with capacity for up to 8 working scientists at one time. To fully test the limits of the laboratory's capabilities, an annual mark-recapture program (2021/2022) on vertebrates allowed for high-quality sampling, while teams on foot deployed innovative conservation technology (such as automated hair-snares) to bank noninvasively collected samples. Protocols for sample preservation and processing, both manually and via automated pipelines, were developed on site for publication on protocols.io. Portable nanopore sequencing and a custom indexing strategy were utilised for highly multiplexed (11 x 96) amplicon sequencing of gene markers, resulting in the submission of over 1200 new sequences from the region to BOLD. Trace DNA from hair and footprints were amplified and barcoded to confirm species identity. Overall, we present evidence that field laboratories can be effective, sustainable, energy-independent, cutting-edge and innovative, and discuss common pitfalls to be considered in establishing similar laboratories globally.

Applications

Date: Wednesday 31 August
Time: 14:00
Room: Pentlands West

Abstract 1

Oral Presentation

Detecting purifying selection on endemic island ungulates and its implications for conservation

Sabhrina Gita Aninta1,2,3, Rosie Drinkwater1,3, Dwi Sendi Priyono4, Selina Brace2, Stephen J. Rossiter1, Nurul Winarni5, Jatna Supriatna5, & Laurent Frantz1,3

1 Queen Mary University of London, UK.
2 Natural History Museum, London, UK.
3 Ludwig-Maximilian-Universität, München, Germany.
4 Faculty of Biology, Universitas Gadjah Mada, Yogyakarta, Indonesia.
5 Faculty of Mathematics and Natural Sciences, University of Indonesia, Depok, Indonesia.

Small population paradigm on conservation biology indicates that a very small population is prone to losing their genome-wide variation and their ability to adapt to future environmental change. Several genomic studies on species of conservation concern found that, although small isolated populations do lose their heterozygosity, they have lower frequency of deleterious mutation due to purifying selection. We aim to test this on a meta-population of endemic ungulates, anoa (*Bubalus* spp., “dwarf buffalo”), and babirusa (*Babyrousa* spp., “pig-deer”). The two taxa are endemic to the Wallacea, an archipelago in Indonesia, Southeast Asia. Both had experienced population expansion at around the same time within the archipelago at ~2 Mya and have been adapted to live across the archipelago since. With increasing anthropogenic pressure, their population is currently at risk of extinction and knowledge on how their genome-wide variation is crucial for their management. Thus, we used likelihood-based SFS of these two taxa on the coding sequences of 67 anoa and 46 babirusa of 5-10x coverage to determine whether high impact deleterious mutations present in lower or higher frequency compared to deleterious mutations of lower impact. We found that smaller islands such as Togian and Buton has lower frequency of high impact mutation compared to larger island of Sulawesi, indicating the presence of purifying selection in smaller island and the tendency of larger population to retain deleterious mutations in high frequency. Consequently, individuals from larger islands might not be a viable source for translocation to increase the genome-wide variation of small islands.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 2

Poster Presentation

Insights to genomics of extinctions from inbreeding and mutation load of modern and ancient grey wolves

Sabhrina Gita Anintal[1], Alberto Carmagnini[1,2], Deborah Greer[1,4], Dave Stanton[1], Logan Kistler[3], Laurent Frantz[1,2]

1 Queen Mary University of London, UK
2 Ludwig-Maximilians-Universität München, Germany
3 Smithsonian National Museum of National History, US
4 Imperial College London, UK

Extinction has been happening throughout Earth's history as a result of natural disasters and extreme climate change. Recently, however, we have been increasingly aware of human-induced biodiversity loss that may be the precursor of the next mass extinction. Studying previous extinction events such as the megafaunal extinctions of Late Pleistocene and early Holocene (~100,000 to 8,000 years ago) and understanding their causes is pivotal for assessing the risks of extinction in contemporary populations and for guiding conservation policies. Grey wolves (*Canis lupus*) provide an excellent model of wild species to study as it is one of the few large canids that survived the megafaunal extinction and now exist in a relatively wide global distribution with its IUCN Red List Status as Least Concern. We developed a framework to detect inbreeding and mutation load in modern and ancient genomes of grey wolves that have been sequenced from various time points and locations. More specifically, we assess the distribution of runs of homozygosity (ROH) and abundance of deleterious mutations across different populations of grey wolves. Then, we determine whether extant grey wolves showed similar levels of inbreeding and mutation load with extinct grey wolves. By discussing the two genomic proxies in extant and extinct grey wolves, we can compare whether either recent changes or long term evolutionary history affect their survival.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 3

Poster Presentation

Extensive genomic data sheds light on the conservation status of the semi-captive population of Asian Elephants from Myanmar

Larissa Souza Arantes1,2, Diego de Panis1, Camila Mazzoni1,2, & Virpi Lummaa3

1 Berlin Center for Genomics in Biodiversity Research, Berlin, Germany
2 Leibniz Institute for Zoo and Wildlife Research, Department of Evolutionary Genetics, Berlin, Germany
3 University of Turku, Finland

Human-mediated environmental changes are leading to a rapid and unprecedented wildlife population decline. Asian elephants (*Elephas maximus*) are not an exception: they have disappeared from 95% of their historical range. Remarkably, one quarter of the remaining Asian elephants in the world now actually live in captivity, and are employed as draft animals or in tourism. By using a comprehensive longitudinal dataset of the largest semi-captive population of Asian Elephants in the world, located in Myanmar, we aim to combine Genomics information with phenotypes, health and life-history data of Asian Elephants to address fundamental questions in biology, disease and conservation of this endangered species. We obtained the first reference genome for the Asian Elephant in collaboration with the Vertebrate Genome Project, which is currently being annotated. The platinum genome showed a high assembly contiguity and completeness and showed to be a bit longer than previously estimated. We also generated 3RADseq data for 297 individuals. The genetic diversity observed in this population was relatively high and was not correlated to the different born locations, being all elephants from relatively close camps in Myanmar. Relatedness analysis showed the presence of three generations and several trios. Closer relationships were observed among captive compared to wild individuals. Whole genomes for 67 individuals are currently being analyzed to estimate the inbreeding level, to infer the demographic history and to investigate the genomic basis of tusk development or other traits. Our ultimate goal is to provide a powerful resource to contribute to the conservation of Asian Elephants.

Applications

Date: Tuesday 30 August
Time: 15:55 / 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 4

Speed talk & poster

Investigating inbreeding depression in a long-term study of Antirrhinum majus

Louise Arathoon1, Carina A. Baskett1, David L. Field2, Melinda Pickup1, Nicholas Barton1

1 ISTA, Austria.
2 Edith Cowan University, Australia

Self-incompatibility (SI) is an evolutionary mechanism of major importance that prevents inbreeding in flowering plants. However, it is theoretically predicted to be easily lost in a population with too low inbreeding depression (ID). Using a large dataset from a field population of the plant species *Antirrhinum majus*, we investigate whether ID is above the necessary threshold to maintain SI in this population. We estimate inbreeding depression through heterozygosity-fitness correlations (HFCs). For 11 years, we measured trait data for six fitness proxies, and genotyped a panel of 91 SNPs in 22,353 individuals. We first confirm that there is significant correlation in heterozygosity between markers, which implies that there is variation in inbreeding, providing the opportunity for inbreeding depression to cause HFCs. We then correlate fitness against heterozygosity in order to quantify inbreeding load for these traits. Despite significant variation in inbreeding, only one of six fitness proxies (number of flowering stems) increased significantly with heterozygosity, and has a high inbreeding load of 0.7.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 5

Poster Presentation

Experiment adjusted bioinformatics workflow reduces genotyping errors in polymorphic multilocus MHC systems

Haidi Arbanasić1, Krešimir Križanović2, Ida Svetličić1, Dejan Bugarski3, Jovan Mirčeta4, Dean Konjević5

1 Faculty of Science, University of Zagreb, Croatia
2 Faculty of Electrical Engineering and Computing, University of Zagreb, Croatia
3 Scientific Veterinary Institute Novi Sad, Remenački put 20, 21113 Novi Sad, Serbia
4 Vojvodinašume, Preradovićeva 2, 21000 Novi Sad – Petrovaradin, Serbia
5 Faculty of Veterinary Medicine, University of Zagreb, Croatia

The Major Histocompatibility Complex (MHC) is highly polymorphic genetic region involved in immune response and significant indicator of adaptively important genetic diversity. Due to extensive variability represented by large number of alleles in population and locus duplications, accurate genotyping of MHC genes may be challenging. Next Generation Sequencing (NGS) technologies are particularly applicable for the genotyping of highly polymorphic, multilocus MHC systems.

Here, we analyzed 227-bp part of exon 2 of the MHC class II DRB gene in 70 red deer (*Cervus elaphus*) individuals from Serbia, using Illumina platform. The major challenge in analyzing NGS data is to separate artefacts that include polymerase nucleotide misincorporation and chimeras, from true alleles. Namely, artefacts largely outnumber true alleles, which may be under-amplified due to primer mismatches. To identify alleles, we developed a workflow adjusted to our experiment, where 60% of individuals had amplicon replicates. We identified 26 DRB alleles, whose population frequency ranged from 0.4% to 11.9%, and found 1-6 alleles per individual. Within-amplicon allele frequency ranged from 1.2% to 79%, while the most frequent artefact was represented by 7% of amplicon reads. Two alleles were characterized by low intra-amplicon frequencies, suggesting low amplification efficiency. Further, we conducted genotyping analysis by Amplisas tool (Amplicon Sequencing Assignment) using default Illumina parameters. In comparison to our workflow, Amplisas dropped 19 allele assignments, all connected to low amplicon frequency or small number of reads. We conclude that lab developed workflow reduces genotype calling errors, particularly for extremely polymorphic genes, such as MHC class II DRB.

Applications
Date: Tuesday 30 August
Time: 15:10/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 6
Speed talk & poster

Is extensive MHC class II diversity in striped dolphin (Stenella coeruleoalba) in the Mediterranean Sea shaped by recent epizootics?

Arbanasić H1, Luis Medrano-González2, Ida S1, Gomerčić T3, D̄uras M3, Galov A1

1 Faculty of Science, University of Zagreb, Croatia,
2 Departamento de Biología Evolutiva, Facultad de Ciencias, Universidad Nacional Autónoma de México, México,
3 Faculty of Veterinary Medicine, University of Zagreb, Croatia

The major histocompatibility complex (MHC) are highly polymorphic genes important for adaptive immunity. Due to their association with adaptation and fitness traits, MHC genes have been largely explored in evolutionary ecology and conservation genetics. The maintenance of high genetic diversity on MHC genes is attributed to the action of balancing selection driven by pathogens. Here, analysis of MHC class II DQA and DQB loci in striped dolphin from the Mediterranean Sea revealed extraordinary diversity, with 29 unique genotypes detected in 31 individuals. Allelic diversity represented by 17 DQA and 18 DQB alleles, which form 27 two-locus haplotypes, was further extended to substantial functional diversity. Namely, translated alleles formed ten DQA and seven DQB structural supertypes capable of binding and presenting a broad range of antigens. The acting of balancing selection on both genes was indicated by homogenised allele and supertype frequencies, presence of rare alleles, and several tests of long-term positive selection. We have found intriguing results on DQA diversity comparable to DQB locus, which is atypical for usually less polymorphic MHC alpha genes. Moreover, Ewens-Watterson test provided compelling evidence of recent selective pressure acting on the striped dolphin’s DQA gene. Indeed, the Mediterranean striped dolphin population faced severe recurrent morbillivirus epizootics over the last decades, of which the first one recorded during 1990-1992 was particularly severe. We hypothesize that morbillivirus exerted selective pressure that shaped extensive MHC class II DQ genes diversity in striped dolphin, which potentially might be an interesting model to observe contemporary adaptation to environmental challenges.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 7

Poster Presentation

Hybridization of wolves and dogs: genomic interactions and artificial selection

Báčová A1, Lucas-Lledó JI2, Jindřichová M1, Boyko A3, Hulva P4, Černá Bolfíková B1

1 Department of Animal Science and Food Processing, Faculty of Tropical AgriSciences, Czech University of Life Sciences in Prague, Czech Republic
2 Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Spain
3 Department of Biomedical Sciences, Department of Biomedical Sciences, Cornell University, United States
4 Department of Zoology, Faculty of Science, Charles University, Czech Republic

The evolution of dogs is dated approximately to 15 – 40kya when the process of wolf domestication started. Since then, the wolves and dogs diverged into the distinct lineages, sometimes already considered as separate species, however, they lack complete reproduction barrier due to the incomplete lineage sorting and no establishment of isolating reproductive mechanisms. Introgressive hybridization is present in many species and usually is considered as a threat, especially for small and endangered wild populations.

The lack of reproductive barrier between wolves and dogs was lately used in several, mainly military, independent experiments when humans crossed wolves and dogs to create new dog breeds. The aim was to create strong, persevering wolf-alike individual with the tameness and trainability of dog. These experiments are known from Czech Republic (Czechoslovakian wolfdog), Netherlands (Saarloos wolfdog), Russia (Volkosob), United States (American wolfdog) or China (Kunming). These breeds are very good model organisms for studying the artificial selection, hybridization, and their effect on individual's genome. However, ubiquitous artificial selection may bring side effects which might be also negative. The artificial selection may in the end harm an organism with accumulated runs of homozygosity, selective sweeps, or genetic hitchhiking. Within these genomic regions, fixed harmful alleles can be transferred to next generations.

So far, we used 170k CanineHD BeadChip microarray (Illumina) SNPs shared within Saarloos wolfdogs, Czechoslovakian wolfdogs, German Shepherds and the wolves. Using the genomic data in domestic species, whose genome is well known, can predict the effect of hybridization on the genome also for wildlife.

The study was supported by IGA FTZ CZU 20223108.

Applications
Date: Thursday 1 September
Time: 12:00
Room: Pentlands West

Abstract 8

Oral Presentation

Conservation genetics in the highlands; applications in Scotland and beyond

Alex Ball1

1 Royal Zoological Society of Scotland

The Royal Zoological Society of Scotland's WildGenes Laboratory uses genetic data to inform conservation planning and action. With a focus on both native species restoration, and an international portfolio, the techniques, and partnerships we develop for conservation here in Scotland can differ with our international work. I will introduce some of our key projects, from the wildcats of the Scottish Highlands, across the wolves of the Himalayas, to the crocodiles of the Cardamom mountains in Cambodia. I will compare and contrast some of the methods we use, from small SNP panels to whole-genome sequencing, with an emphasis on the importance of tailored approaches and the vital role of trusted partnerships.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 9

Poster Presentation

Population genetic structure of Castanea sativa Mill. in the South Caucasus: conservation implications

Berika Beridze1,2, Łukasz Walas1, Katarzyna Sękiewicz1, & Monika Dering1,3

1 Institute of Dendrology, Polish Academy of Sciences, Poland
2 Adam Mickiewicz University in Poznań, Faculty of Biology, Poland
3 Poznań University of Life Sciences, Department of Silviculture, Poland

The Caucasus is a region of global significance with immense biological diversity and endemism, and yet the most highly anthropogenically threatened area. The area is vastly diverse in terms of habitats and includes two refugia of Neogene relicts; Colchis lowlands (western Caucasus) and Hyrcanian forests (southern coasts of the Caspian Sea). The Caucasus shares several important trees conspecific or congeneric to Europe species. The sweet chestnut (*Castanea sativa* Mill.) is one example of an economically, ecologically, and culturally significant tree species whose populations are seriously fragmented and devastated by the deadly fungal pathogen *Cryphonectria parasitica*, especially in Georgia. In contrast to the European range of the species, its genetic structure and demographic history are not fully understood across the Caucasus. Sweet chestnut are believed to survived in the Caucasus during the Last Glacial Maximum and played a prominent role in forest communities, implying unexplored evolution potential.

The project run at the Institute of Dendrology PAS aims to fill this gap and deliver information on population genetics and landscape structure of sweet chestnut in the region. What we found by employing genetic data and ecological niche modelling is that populations of sweet chestnuts from the western part of the Caucasus are of great significance for conservation efforts. Nevertheless, one easternmost population surveyed displayed different allelic distribution and vulnerability against climate change. We believe that the knowledge acquired will be used for future planning and possible genetic rescue of the species in its entire range.

Applications

Date: Tuesday 30 August
Time: 14:25/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 10

Speed talk & poster

Conservation genetics of pangolins in the Congo Republic

Bernáthová I1, Swiacká M1, Hulva P2, Loubassou CBV3, & Černá Bolfíková B1

1 Faculty of Tropical AgriSciences, Czech University of Life Sciences, Czech Republic
2 Faculty of Science, Charles University, Czech Republic
3 Institut National de Recherche Forestière, Brazzavile, Republic of Congo

Pangolins are currently considered the world's most illegally trafficked mammals and their numbers continue to decline. Furthermore, there is still a lack of knowledge on their population structure and dynamics. We provide the first population-level molecular study focused on pangolin populations in Odzala-Kokoua National Park in the Congo Republic. We sampled individuals of White-bellied pangolin (*Phataginus tricuspis*) and Giant pangolin (*Smutsia gigantea*) and analysed their mitochondrial (control region) and two nuclear markers (beta-fibrinogen, titin). The mitochondrial haplotype network in *P. tricuspis* indicates differences between sub-populations from western and central Africa which supports cryptic diversity of *P. tricuspis*. We detected population growth in *P. tricuspis* 500 kya. The population expansion started during a period of aridity which confirms that *P. tricuspis* is, to some extent, capable of adaptation to various conditions and is not fixed solely to rainforest habitat. In *S. gigantea*, we detected a slow decline that started around 500 kya, probably also driven by habitat changes. According to genetic distances between the samples from Odzala-Kokoua NP, we estimate the local origin of the pangolins at the trade market. The study provides data on population structure and dynamics of pangolins in the Congo Republic and can be used for better understanding the population biology of pangolins, the local trade dynamics and may contribute to conservation management planning.

The study was supported by IGA grant No. 20223108.

Applications
Date: Tuesday 30 August
Time: 14:25/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 11

Speed talk & poster

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

Roberto Biello1, Silvia Fuselli1, Elena Ramella Levis2, Caterina Spiezio3, Annalaura Mancia1, Andrea Benazzo1, Giorgio Bertorelle1

1 Department of Biotechnology and Life Sciences, University of Ferrara, Ferrara, Italy
2 Department of Biology, University of Padua, Padua, Italy
3 Research & Conservation Department, Parco Natura Viva, Bussolengo, Italy

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 local populations represent additional threats. Our previous genetic studies based on STR and ddRADseq markers were able to clearly distinguish two subspecies (the eastern *T. h. boettgeri* and the western *T. h. hermanni*) and to identify some major geographical groups, allowing also the development of practical genetic tools for geographic assignment. The genetic panels we developed can be cost-effectively and detect the geographic origin of confiscated individuals currently kept in captivity, thus helping their correct relocation in reintroduction plans. More recently, we generated a high-quality assembly and annotation of the *T. hermanni* genome using a combination of PacBio HiFi and Oxford Nanopore Technologies data. The assembled genome size was 2.26 Gb with a contig N50 of 58.76 Mb. The genome included 22,017 protein-coding genes, and repetitive elements constituted 45.5% of the assembled genome. The genome assembly and the set of annotated genes yielded 97% and 95% completeness scores, respectively when compared with the BUSCO Sauropsida dataset. In addition, we re-sequenced whole genomes at 20x coverage of six individuals from the two subspecies. These genomic resources will allow us to better understand the effective risks of translocation and hybridization in this species and propose management plans based on functional genomic regions.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 12

Poster Presentation

Increased Genetic Diversity via Gene Flow Provides Hope for an Endangered Wattle Facing Extinction

Colette Blyth1,2 , Matthew J. Christmas3, Doug Bickerton4, Renate Faast1,5, Jasmin G. Packer1,5, Andrew J. Lowe1, Martin F. Breed2,6

1 School of Biological Sciences, University of Adelaide, North Terrace, Australia
2 Group on Earth Observation Biodiversity Observation Network (GEO BON) Genetic Composition Working Group
3 Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden
4 Northern Territory Herbarium, Palmerston, Australia;
5 Environment Institute, University of Adelaide, North Terrace, Australia
6 College of Science and Engineering, Flinders University, Bedford Park, SA 5042, Australia

We apply a conservation genomics approach to make evidence-based management recommendations for *Acacia whibleyana*, an endangered shrub endemic to Eyre Peninsula, South Australia. We used population genomic analysis to assess genetic connectivity, diversity, and historical inbreeding across all known stands of the species sampling remnant stands, revegetated stands of unknown origin, and a post-fire seedling cohort. Our results indicate a degree of historical connectivity across the landscape, but habitat loss and/or pollinator community disruption are potential causes of strong genetic structure across the remnant stands. Remnant stands had low genetic diversity and showed evidence of historical inbreeding, but only low levels of intra-stand relatedness indicating that risks of contemporary inbreeding are low. Analysis of a post-fire first generation cohort of seedlings showed they likely resulted from intra-stand matings, resulting in reduced genetic diversity compared to the parents. However, admixed seedlings in this cohort showed an increase in heterozygosity relative to likely sources and the non-admixed seedlings of the same stand. Assisted inter-stand gene flow may prove an effective management strategy to boost heterozygosity and corresponding increases in adapting capacity in this endangered species.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 13

Poster Presentation

Reconstructing the demographic history of the endangered Hispaniolan solenodon, one of the most evolutionary distinct mammals on earth

Maria Zicos 1, Laurent Frantz 2, Samuel Turvey 3, & **Selina Brace 1**

1 Natural History Museum, UK
2 Ludwig-Maximilian-Universität, Germany
3 Institute of Zoology, UK

Island systems such as the Caribbean have been focal in researching evolutionary patterns and processes. Islands are particularly relevant for reconstructing colonisation and radiation events, but also for preserving ancient populations and biodiversity with important conservation implications for understanding the evolutionary history of insular species. The insular Caribbean was colonized by non-volant land mammals that diversified into more than 120 different species, however the region has suffered from a massive Holocene extinction event and very few terrestrial mammalian species remain. The extant fauna includes two representatives of the Solenodontidae, the Hispaniolan solenodon (*Solenodon paradoxus*) and Cuban solenodon (*Atopogale cubana*). Solenodons are nocturnal insectivores and the only living mammals with dental venom delivery systems, they form an ancient lineage that diverged from other living mammals c.73 million years ago. Solenodons are considered endangered and coupled with their evolutionary distinctiveness and current threats to survival, both species have been identified as global priorities for mammal conservation.

To explore the demographic history of these high priority species this study has generated six new solenodon genomes: five for the Hispaniolan solenodon, one of which is the first genome for the previously described south-western population, and the first genome for the Cuban solenodon. Our genome wide data supports structure of the Hispaniolan solenodon into three populations as previously suggested from mitochondrial only data, but goes further as we apply this whole genome dataset to explore gene flow, divergence dates, inbreeding coefficients and signs of genomic erosion.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 14

Poster Presentation

Beyond the host: balancing conservation of biodiversity with infectious disease risks

Stephanie Brien1, Katherine Mertes2, Erhan Yalcindag1, Marie Petretto3, Melissa Marr1, Ouled Ahmed Hatem4, Mahamat Hassan Hatcha5, Tchari Doungous6, Mahamat Saboun6, Moukhtar Defallah5, Mark Bronsvoort1, Rob Ogden1

1 University of Edinburgh (Royal (Dick) School of Veterinary Studies and the Roslin Institute, Edinburgh), UK
2 Smithsonian Conservation Biology Institute, USA
3 Marwell Wildlife, UK
4 Veterinary Research Institute of Tunis, Tunisia
5 Department for the Conservation of Wildlife and Protected Areas, Chad
6 Institute of Livestock Research for Development, Chad

In reintroductions, conservation genetic techniques are routinely applied to target species. The parasites reintroduced alongside their hosts are often overlooked despite being a crucial component of healthy ecosystems, contributing to and driving biodiversity1-5. Antelope reintroductions in the Sahelo-Sahara region lead to land sharing with livestock. Their parasites may well occupy overlapping ecological niches, leading to competition for hosts, alterations in parasite abundance and disruption of the ecological balance. The loss of host-adapted parasite species can also be detrimental to their hosts2,4,6-8 due to replacement with more pathogenic species9. Our study aims to (i) improve understanding of the haemoparasite infection status of endangered antelope populations in conservation reintroductions and (ii) identify infections that pose a risk at the wildlife-livestock interface. DNA was extracted from blood collected from endangered antelope in reintroduction programmes in Tunisia and Chad. The samples were screened for haemoparasites using PCR and sequencing. Infections with haemoparasite genera that also affect livestock were common, including Anaplasma, Ehrlichia and Theileria. However, the causative species showed differences from those recorded in livestock. Additionally, there is evidence of bacteraemia associated with novel, poorly characterised bacterial families identified as a cause of emerging infectious disease in wildlife and humans. Haemoparasite infections could present a risk at the wildlife-livestock interface due to interspecies transmission leading to shifts in pathogenicity, or biodiversity loss due to competitive exclusion. This has important implications for disease management and ecosystem-level dynamics in antelope reintroductions. Future work is planned to compare the haemoparasite infection status of antelope with sympatric livestock.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 15

Poster Presentation

Assessment of gene flow between red deer populations of Baden-Wuerttemberg and bordering states

Fritz Brockhaus1

1Forest Research Institute Baden-Wuerttemberg (FVA)

The genetic status of red deer (*Cervus elaphus*) populations in Germany and especially the gene flow between populations is of major concern. In Baden-Wuerttemberg, as in other federal states, the occurrence of red deer is restricted to certain areas due to forest management (potential browsing damage). Outside these (5) areas, the wildlife management policy advises that red deer must be shot. Due to this policy (since the 1950ies), the increasing habitat fragmentation and the distance between the areas, red deer are at risk of suffering from isolation effects through reduced gene flow. Isolation and small population sizes could result in decreasing genetic diversity, hence the expansion of defective genes in a population.

Based on a landscape genetic approach, we are assessing gene flow between the red deer populations of Baden-Wuerttemberg and bordering countries and federal states (France, Austria, Switzerland, Hesse, Bavaria, Rhineland-Palatinate) using a set of 28 microsatellite markers. The analyses give a deeper insight into the population's gene pool and the current inbreeding coefficient. The selected microsatellite markers are identical to other red deer genetic studies in Germany to obtain comparability of genotype data. Here we show preliminary results of our current red deer genetic study in south-western Germany.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 16

Poster Presentation

Low genetic diversity in adaptive immune response genes in the critically endangered wild two-humped camels (Camelus ferus) from the Mongolian Great Gobi desert

Pamela Burger1, Sara Lado1,2, Adiya Yadamsuren3, Anna Jemmet3,4, & Petr Horin5

1 Research Institute of Wildlife Ecology, University of Veterinary Medicine, Vienna, Austria
2 Medical University, Vienna, Austria
3 Wild Camel Protection Foundation, Ulaanbaatar, Mongolia
4 Durrell Institute of Conservation and Ecology, University of Kent, United Kingdom
5 Department of Animal Genetics, University of Veterinary Sciences, Brno, Czech Republic

Old World camels are known to be resistant to serious infectious diseases that threaten other livestock species inhabiting the same geographical regions, although they may contract other poorly studied diseases. Hence, as diversity in immune response (IR) genes may influence infectious disease susceptibility in populations, a better understanding of IR genomic diversity will support conservation and sustainable management of the "critically endangered" (IUCN) wild two-humped camels in the Mongolian Great Gobi and Chinese Taklimakan and Lop Nur deserts. When we compared nucleotide diversity among both two-humped camel species, wild camels had lower mean nucleotide diversity for both SNP and indels and nonsynonymous SNP analyses, except for the MHC class I and II genes, and for adaptive genes with nonsynonymous SNPs. In general, the domestic Bactrian camel had higher mean nucleotide diversity compared to the wild camel, except for the mean nucleotide diversity in adaptive genes with non-synonymous SNPs. One possible explanation for these results is that the wild camel suffered strong population declines leading to the current status of "critically endangered" species. Thus, with the number of individuals decreasing, loss of genetic diversity is unfortunately real. Examining genetic variation in diverse immune genes in camels should be a priority, not only because camels are well adapted to extreme environments even in contact with different pathogens, but also because both domestic species are economically very important. Studies focused on functionally important parts of the genes will be helpful to improve the understanding of the biology and evolution of these species.

Technologies

Date: Tuesday 30 August
Time: 16:55/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 17

Speed talk & poster

Novel Protocol for Diet Analysis of European Wildcat (Felis silvestris)

Magdalena Butowska1, Muhammad Ghazali1, Gill Murray-Dickson1, Elizabeth Heap1, Alex Ball1

1 Royal Zoological Society of Scotland, WildGenes Laboratory, UK

European Wildcat (*Felis silvestris*) is Scotland's most threatened mammal. Historically, they faced challenges from habitat loss, persecution, and hybridisation with domestic cats, with the latter remaining a major threat today. Its restoration in Scotland is led by Saving Wildcats, an RZSS initiative under the EU LIFE programme, who are currently captive breeding wildcats for planned releases into the Cairngorms National Park starting in 2023. To successfully establish, the wildcats need to be able to hunt wild prey. Due to legal restrictions, mechanical prey simulators will be relied on for promoting hunting behaviours. However, a method to assess diet of the wildcats after release will provide data on hunting preferences. Therefore, we have developed a DNA metabarcoding protocol for detecting prey species in wildcat faecal samples. We have extracted DNA from 94 samples from cats with known diets, collected in the wildcat enclosures in the RZSS Highland Wildlife Park. Environmental swab samples were collected to control for external contamination. We have also performed internal faecal swabs to compare the efficacy of this approach versus an extraction from a full sample. We used barcoded universal mammalian 12SV5 primers, combined with a blocking primer designed to inhibit wildcat DNA amplification. PCR was performed in triplicates to increase prey detection prior to sequencing on an Illumina platform. This allowed for detection of prey species which have been fed to the captive cats in the sample collection period. This methodology has been developed to allow for further analyses of both captive and in situ post-release wildcats.

Technologies
Date: Tuesday 30 August
Time: 15:55/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 18

Speed talk & poster

When birds of the same feather flock together: a story of inbreeding in an endangered island bird species

Emily Louisa Cavill1, Shyam Gopalakrishnan1, Mick Westbury1, Bronwyn Dunlop2, Wilna Accouche2, Nirmal Shah2, Anna Zora2, Licia Calabrese2, M. Thomas P. Gilbert1

1 Center for Evolutionary Hologenomics, The GLOBE Institute, University of Copenhagen, Denmark
2 S.M.A.R.T., coordinated by Nature Seychelles, Center for Environment and Education, Seychelles

The Seychelles magpie robin (*Copsychus sechellarum*) was once considered one of the rarest birds in the world with just 8 surviving individuals on a single island. This IUCN-Red-List Endangered species has made a promising recovery, largely due to conservation translocations to four new Seychelles islands over the past 25 years. However, we have only just started to explore the potential genetic consequences of the population crash and the species translocation history. We resequenced the genomes of ~180 individuals sampled before the historic population crash (museum specimens) and after modern translocations (blood samples). Our initial study uncovered signals of recent inbreeding as evident from very low levels of heterozygosity coupled with long homozygous segments across the genome. In light of this information, and as the population continues to grow, we ask: Has inbreeding resulted in inbreeding depression and affected life history traits? Are there other mechanisms in place allowing these populations to persist? How can we best manage this species from a genetic standpoint? To answer these questions, we annotated genetic variants of each resequenced genome to see if the discovered variants have strong biological effects (e.g. amino acid substitutions), we then compared the historic genetic architecture with the modern individuals, and cross-referenced long-term field observations with the genetic results. Ultimately, our results will be used to support the upcoming conservation translocation planned for the magpie robins, through donor selection, as well as in the consideration of genetic rescue between the existing five populations.

Collections

Date: Tuesday 30 August
Time: 14:10
Room: Pentlands (East/West)

Abstract 19

Oral Presentation

Museum specimens reveal the genomic impact of recent population decline on Andean bears

J. Camilo Chacón-Duque1,2,3*, Paola Pulido-Santacruz4, Adam Ciezarek5, Wilfried Haerty5, Federica Di-Palma6, Mailyn González4, Selina Brace1, Ian Barnes1*

1 Department of Earth Sciences, Natural History Museum, London, United Kingdom
2 Centre for Palaeogenetics, Stockholm, Sweden
3 Department of Archaeology and Classical Studies, Stockholm University, Stockholm, Sweden
4 Instituto de Investigación de Recursos Biológicos Alexander von Humboldt, Bogotá, Colombia
5 Earlham Institute, Norwich, United Kingdom
6 University of East Anglia, Norwich, United Kingdom

The Andean bear (*Tremarctos ornatus*) – the only extant bear in South America – is at risk of extinction (Vulnerable, IUCN). In order to assess the genomic impact of recent population decline, we used museum specimens collected during the last century in Colombia, and evaluated temporal changes in heterozygosity, inbreeding and genetic load. We sampled 34 specimens and applied ancient DNA techniques to extract and sequence the degraded DNA. All genomic libraries were shallow-sequenced screened and 15 samples – dating between 1913 to 2008 – were further sequenced to an average whole-genome coverage of 8X.

While population structure analyses display considerable geographical structure with temporal continuity, genome-wide heterozygosity declines sharply during the last century. Moreover, inbreeding intensifies throughout the same period, as evidenced by an increasing fraction of the genome contained within stretches of homozygosity. These results demonstrate that genetic diversity has decayed rapidly in Colombian Andean bears.

Distinguishing this recent demographic collapse – likely due to anthropic effects – from long-term and constant low population sizes is crucial for informing conservation and is only possible with the inclusion of historical genomic data. Furthermore, in the absence of genomic data from present-day populations (often the case for endangered and difficult to sample species), the combined use of ancient DNA techniques and museum collections constitutes an invaluable source of information for conservation genomics.

Technologies

Date: Wednesday 31 August
Time: 11:30
Room: Pentlands East

Abstract 20

Oral Presentation

Chromosome-level de novo genome assembly for the Aldabra giant tortoise enables insights into the genetic health of a threatened population

F. Gözde Çilingir1, Luke A'Bear2, Dennis Hansen3,4, Leyla R.Davis5, Nancy Bunbury2,6, Arpat Ozgul1, Daniel Croll7 & Christine Grossen1

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2 Seychelles Islands Foundation, Republic of Seychelles.
3 Zoological Museum, University of Zurich, Switzerland.
4 Indian Ocean Tortoise Alliance, Republic of Seychelles.
5 Zoo Zürich, Switzerland.
6 Centre for Ecology and Conservation, College of Life and Environmental Sciences, University of Exeter, Penryn, United Kingdom.
7 Institute of Biology, University of Neuchâtel, Switzerland.

The Aldabra giant tortoise (*Aldabrachelys gigantea*) is one of only two giant tortoise species left in the world. The species is endemic to Aldabra Atoll in Seychelles and is considered vulnerable due to its limited distribution and threats posed by climate change. Genomic resources for *A. gigantea* are lacking, hampering conservation efforts focused on wild and ex-situ populations. In this study, we used PacBio High-Fidelity sequencing and high-throughput chromosome conformation capture (Hi-C) to produce a 2.37 Gbp *de novo* genome assembly of *A. gigantea* with a scaffold N50 of 148.6 Mbp and a resolution into 26 chromosomes. RNAseq-assisted gene model prediction identified 23,953 protein-coding genes and 1.1 Gbp of repetitive sequences. Synteny analyses among turtle genomes revealed high levels of chromosomal collinearity even among distantly related taxa. To assess the utility of the high-quality assembly for species conservation, we performed a low-coverage re-sequencing of 30 individuals from wild populations and two zoo individuals. Our genome-wide population structure analyses detected genetic population structure in the wild and identified the most likely origin of the zoo-housed individuals. We further identified putatively deleterious mutations to be monitored. The high-quality chromosome-level reference genome for *A. gigantea* is one of the most complete turtle genomes available. It is a powerful tool for assessing the population structure in the wild and for the genetic management of rewilding efforts. Additionally, a high-quality genome will open avenues to investigate the genetic basis of the exceptionally long lifespan.

Applications

Date: Thursday 1 September
Time: 13:30
Room: Pentlands West

Abstract 21

Oral Presentation

The Western spot-nosed monkey (Ceropithecus petaurista buettikoferi) in Guinea-Bissau: combining genetic and social data to assess the conservation status and threats of the country's most unknown guenon

Ivo Colmonero-Costeira1234, Susana Costa4, Maria Joana Ferreira da Silva*123, Michael William Bruford*15; * shared last co-authorship

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2 CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Portugal
3 BIOPOLIS, Program in Genomics, Biodiversity and Land Planning, Portugal
4 CIAS, Research Centre for Anthropology and Health, Universidade de Coimbra, Portugal
5 Sustainable Places Research Institute, Cardiff University, UK

The Westernmost populations of the spot-nosed monkey (*Cercopithecus petaurista buettikoferi*) can be found in the Bijagós Archipelago (BA) in Guinea-Bissau. The primate is thought to have recently decreased in the mainland and is considered very rare. The insular spot-nosed monkeys are likely to be the last viable populations in the country but its current conservation status and threats are unknown. We conducted a non-invasive genetic survey in five large islands. We aimed to estimate genetic diversity and population sub-structure using a fragment of the mitochondrial control region and eleven autosomal microsatellite loci. Additionally, we conducted informal interviews and non-participative observations at Canhabaque island to assess the demographic trend and the main threats. Our genetic dataset was formed by 67 unique multi-locus genotypes and 65 mitochondrial sequences. The genetic diversity within islands was relatively high for both markers, especially at Canhabaque island. Populations are structured by island and gene flow between islands seems unlikely. Participants interviewed at Canhabaque island consistently reported a declining population trend. The main threat identified was commercial hunting to supply bushmeat markets at the country's urban areas. Furthermore, hunters are thought to target males as they have a bigger net worth. This work was the largest genetic study conducted on the taxon in Guinea-Bissau and highlights how local knowledge can be useful to investigate recent demography trajectory and conservation threats. Future research will estimate the effect of hunting on the long-term survival of these insular populations using genetic-based inferences.

Applications

Date: Wednesday 31 August
Time: 16:00
Room: Pentlands East

Abstract 22

Oral Presentation

Identifying landscape drivers of genetic variation of a pond-breeding amphibian on multiple spatial scales

Karen Cox1, Mathieu Denoël2, Hans Van Calster1, Jeroen Speybroeck1, Sam Van de Poel3, Iwan Lewylle3, Leen Verschaeve1, An Van Breusegem1, David Halfmaerten1, Dries Adriaens1, & Gerald Louette1

1 Research Institute for Nature and Forest (INBO), Belgium.
2 Laboratory of Ecology and Conservation of Amphibians (LECA), Freshwater and OCeanic science Unit of reSearch (FOCUS), ULiège, Belgium.
3 Natuurpunt Studie, Belgium.

The terrestrial landscape surrounding aquatic habitat influences the persistence of amphibian spatially structured populations (SSPs) due to its role in estivating, overwintering, migration, dispersal, and consequently the maintenance or loss of genetic diversity. To identify the landscape drivers of genetic variation, we investigated the relationship between the level of genetic variation measured within ponds of the great crested newt (*Triturus cristatus*), and the composition of the surrounding landscape at various spatial scales. Linear mixed models, with effects within and between SSPs incorporated, were used with genetic data from 40 ponds in thirteen SSPs. Model outcomes depended on spatial scale, with more significant associations between genetic variation, particularly allelic richness, and land use within radii of 50 and 100 m of core ponds. The availability of aquatic habitat had a positive effect, while tree cover, arable land and pasture had different effects depending on scale and on the genetic metric used as response variable. Total length of roads within a 250 m radius influenced effective population size negatively. Generally, the landscape affected genetic variation similarly within and between SSPs. This allowed us to provide general guidelines for the persistence of great crested newt populations, with an emphasis on the importance of the aquatic habitat.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 23

Poster Presentation

Laying the foundations for forensic timber identification of highly endangered and taxonomically challenging Madagascar rosewoods (Dalbergia L.f., Fabaceae)

Simon Crameri[1], Peter B. Phillipson[2], Nicholas Wilding[2], Richard Randrianaivo[3], Harisoa Ravaomanalina[4], Nivo Rakotonirina[4], Porter P. Lowry II[2], Alex Widmer[1]

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[3] Missouri Botanical Garden Madagascar Program, Antananarivo, Madagascar.
[4] Département de Biologie et Écologie Végétales, Université d'Antananarivo, Antananarivo, Madagascar.

The genus *Dalbergia L.f.* (*Fabaceae*) includes valuable timber species threatened by overexploitation. Conservation and establishment of sustainable management rely on viable taxonomy and correct species identification, including strategies and reference databases for forensic timber identification. Species identification of *Dalbergia* is particularly challenging in Madagascar due to a shortage of taxonomically informative characters and a large number of similar species. We sequenced DNA of all 51 currently accepted Malagasy *Dalbergia* species using target enrichment of 2,396 genomic regions. All except two species belong to two genetic supergroups of Malagasy taxa that markedly differ in flower characters. We further identified eleven well-supported clades within those supergroups, most of which are clearly associated with different eco-geographic regions of Madagascar. Phylogenomic and population genomic analyses indicated the presence of at least 84 evolutionary lineages or candidate species, of which 48 represent currently accepted species, excluding three species that should be regarded as synonyms of other species. We then integrated the phylogenomics data with morphological and eco-geographic information and inferred separate evolution of at least 22 additional species to be described or elevated to species rank, most of which produce large trees of potential economic interest. Our results demonstrate that the current taxonomy of Malagasy *Dalbergia* does not adequately account for the level and patterns of species diversity observed, and they provide insights that are highly informative for a taxonomic revision being conducted on this important genus, which is essential for the development of forensic timber identification strategies that depend on correctly identified reference collections.

Applications

Date: Wednesday 31 August
Time: 16:30
Room: Pentlands West

Abstract 24

Oral Presentation

Conservation genomics of the Scandinavian arctic fox

Love Dalén12, Malin Hasselgren2, Johanna von Seth12, Karin Norén2

1 Centre for Palaeogenetics, Sweden
2 Department of Zoology, Sweden

The arctic fox (*Vulpes lagopus*) used to be common in Scandinavia, with a population size of several thousands of individuals. However, by the beginning of the 20th century, intense hunting had brought the population size down to ca. 100 individuals. Despite legal protection, the population did not recover and instead remained very small for the subsequent 100 years. In the 1980s, the population size declined even further, to only a few dozen individuals. However, in the last two decades, intense conservation actions have resulted in a more than ten-fold recovery in population size. Using a combination of conservation genetic approaches and comprehensive field monitoring, we have investigated the genomic consequences of these demographic declines. These analyses have revealed a significant increase in inbreeding levels, and suggest that the population has also become fragmented into relatively isolated subpopulations. In at least one of these subpopulations, we find strong evidence of inbreeding depression that includes a direct link between individual mutational load and lifetime reproductive success.

Policy

Date: Tuesday 30 August
Time: 15:55/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 25

Speed talk & poster

Understanding marine connectivity of scallop populations within Scottish and adjacent waters to inform marine management

Simone D'Alessandro1, Emily Humble2, Rob Ogden23, Douglas Speirs4, Babette Hoogakker1, Joanne S Porter5, & Michel J Kaiser1

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2 Royal (Dick) School of Veterinary Studies and the Roslin Institute, University of Edinburgh, Edinburgh, UK
3 TRACE Wildlife Forensics Network, Edinburgh, UK
4 Department of Mathematics and Statistics, University of Strathclyde, Glasgow, UK
5 International Centre for Island Technology, Heriot Watt University Orkney, Stromness, UK

This study aims to combine whole-genome sequencing (WGS) and biogeochemical analysis to determine distinct scallop populations, infer their connectivity in Scottish and adjacent waters, and identify spatial scale for sustainable management of the fishery.

In Scotland, commercial fisheries land around 7000 tonnes with a value totalling almost £14 million in 2020. However, despite their importance, there is currently no common stock assessment and regional and local policy follows the assessment areas based on the ICES (International Council for the Exploration of the Sea) statistical rectangles. Moreover, effective marine management is hampered by knowledge gaps on population structure and complex interactions at the ecosystem- and population- levels, and the limited available information is difficult to interpret. Understanding connections between populations is a crucial step to determine management units and the appropriate scale at which to sustainably regulate the fishery.

Here, we illustrate the future steps of our project, which is to infer the marine connectivity of scallop populations in Scottish waters. We will examine the population structure and parental and geographic origins with multi-disciplinary approaches. Using isotopic signatures in the scallop shell,

we plan to determine scallop age and use shell chemistry signatures to investigate their geographic origins. WGS approaches will be used to explore population differentiation using both neutral and adaptive genetic markers, providing insights for local management units. Particular attention will be given to illustrating the strengths, weaknesses, and spatial and temporal resolution of the proposed methods in estimating marine connectivity of scallop grounds.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 26

Poster Presentation

Pleistocene glaciations explain the demography and distribution of Red Panda in eastern Himalayas

Supriyo Dalui1,2, Sujeet Kumar Singh1, Bheem Dutt Joshi1, Avijit Ghosh1,2, Shambadeb Basu1, Hiren Khatri1, Lalit Kumar Sharma1, Kailash Chandra1 & Mukesh Thakur1

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2 Department of Zoology, University of Calcutta, Kolkata, West Bengal 700019, India

Pleistocene glaciations facilitated climatic oscillations caused enormous heterogeneity in landscapes and consequently affected demography and distribution patterns of many mountain endemic species. In this regard, a recent genome based study on the red panda which is distributed along the geographical proximity to the southern edge of the Qinghai Tibetan Plateau have been classified into two phylogenetic species. However the study didn't cover Indian and Bhutan Himalayan region, therefore we collected samples from Indian Himalaya and demarcated the species boundary by proposing ‘Siang river’ as a potential boundary for species divergence between the Himalayan red panda (*Ailurus fulgens*) and Chinese red panda (*Ailurus styani*). We investigated demographic history and population genetic structure of red panda and Bayesian based phylogeny demonstrated that red panda diverged about 0.30 million years ago (CI 0.23–0.39) into two phylogenetic subspecies, that correspond to the middle-late Pleistocene transition. We observed intraspecific clades with respect to Himalayan and Chinese red panda indicated restricted gene flow resulting from the Pleistocene glaciations in the eastern and southern Tibetan Plateau. We found the Himalayan red panda population at least in Kanchenjunga Landscape (KL)-India declined abruptly in last 5–10 thousand years after being under demographic equilibrium. This study provides pragmatic genetic evidence and demonstrates the Siang River as a potential barrier for divergence of Himalayan and Chinese red panda. We suggest being associated with diverse habitats, threats and transboundary distribution, both species of red panda require regional as well as transboundary level conservation initiatives for a species survival plan.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 27

Poster Presentation

Use of genetic markers to improve management of a rare horse breed: Exmoor ponies

Deborah Davy1, Anubhab Khan1, Elizabeth Kilbride1 and Barbara K. Mable1

1 Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow

Conservation of endangered animals where resources are limited requires a targeted, informed approach to maximise effectiveness. Exmoor ponies, an endangered breed, are believed to have ancient origins, being descended relatively directly from Pleistocene wild horses. They underwent a genetic bottleneck in the 1940's, leaving fewer than fifty individuals as the breed's foundation animals, not all of whom have recorded descendants extant. This genetic bottleneck resulted in concerns about inbreeding depression and increased kinship values. Previously, planning of breeding programs relied solely on recorded pedigrees. To better inform Exmoor breeding programs we are investigating the mitochondrial haplotypes of descendants from all the extant recorded lines of descent from the foundation animals and are mapping mitochondrial haplotypes to recorded pedigrees. Our identification of multiple mitochondrial haplotypes suggests multiple maternal lineages for some lines, information which can improve pedigree resolution and the accuracy of the stud book records. We also have sequenced thirty Exmoor whole genomes, which we are using to investigate intra- breed relatedness, temporal trends in inbreeding and the genetic variation present in the current population. Additionally, inter-breed comparisons using these new and other published genomes will explore the relationship of Exmoor ponies to other breeds, thus exploring their potentially ancient origins. Increased accuracy of pedigrees and kinship values can improve the targeting of breeding programs for Exmoor ponies, a small and geographically diverse population where long generation time, low demand, and relatively high costs limit potential breeding pairings. Better understanding of their origins enhances their value in environmental restoration and rewilding schemes as ancient mega-herbivore analogs, thus improving their conservation potential.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 28

Poster Presentation

Are you a UK environmental researcher needing help and training in genetic techniques?

Deborah Dawson1, NERC Environmental Omics Facility (NEOF)1

1 NEOF Visitor Facility, University of Sheffield, UK

The NEOF Visitor Facility (NEOF-VF) at the University of Sheffield provides the following to UK-based researchers using molecular analyses to answer environmental questions:

- Training in wet lab molecular methods;
- Access to all necessary equipment and consumables;
- Next-generation sequencing data (to a maximum value of approx £10k);
- Training and assistance in data analysis and interpretation;

Researchers (including PhD students) visit the NEOF-VF for up to 6 months, to complete their own lab work following training and under the supervision of NEOF-VF staff.

NEOF will support any project that can benefit from access to NEOF's equipment and expertise. Please send us any questions, whether more general or about your specific project that will require support, via https://neof.org.uk/contact/. Applicants do not have to be NERC-funded (but the work needs to fall within the NERC remit, i.e. involve the environment).

Applications to access the Visitor Facility can be made at any time of year.

Applications

Date: Wednesday 31 August
Time: 16:15
Room: Pentlands West

Abstract 29

Oral Presentation

Road to extinction? Past and present population structure and genomic diversity in the koala (Phascolarctos cinereus)

De Cahsan, B.[1], Sandoval Velasco, M.[1], Westbury, M. V.[1], Duchene Garzon, D. A.[1], Lott, M.J.[2], Roca, A. L.[3], Greenwood, A. D.[4,5], Johnson, R. N.[6], Gilbert, M. T. P.[1]

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5 Department of Veterinary Medicine, Freie Universität Berlin, Berlin, Germany
6 Smithsonian National Museum of Natural History, Washington, U.S.A.

Koalas are arboreal herbivorous marsupials, endemic to Australia. During the 1800s and early 1900s koala numbers declined dramatically due to being hunted for their furs. Although the trade had ceased by the 1930s, when koalas were given complete legal protection in all Australian states, their current census population size represents only a small proportion of that prior to the fur trade. In addition, predation by exotic carnivores, the ongoing expansion of human infrastructure and the increase in frequency and intensity of annual bush fires due to anthropogenically driven climate change have further decimated available habitat and decreased population numbers.

Here, we utilise 37 historic and 25 modern genomes from across the past and present distribution range of koalas to gain insights into how their population structure and genetic diversity have changed through time, assess the genetic consequences of the detrimental culling period, and the current genetic status of this iconic Australian species. When comparing pre- and post-culling timespans, we found a decrease in genome-wide heterozygosity and uncovered mitochondrial haplotypes, as well as nuclear genotypes in the historic dataset, which are absent from today's koala populations.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 30

Poster Presentation

Does the extinct long-horned buffalo live on in Cape buffalo?

Deon de Jager1, Paulette Bloomer2, Eline Lorenzen1

1 University of Copenhagen, Denmark
2 University of Pretoria, South Africa

The African Cape buffalo (*Syncerus caffer caffer*) population in Addo Elephant National Park is the third-largest natural population in South Africa but harbours the lowest nuclear genetic diversity of the subspecies across its African range, due to a strong historical bottleneck and subsequent isolation. This population, threatened by high genomic inbreeding levels, is of high conservation value, as it is the only naturally occurring disease-free population of buffalo in South Africa. Consequently, Addo buffalo are often used to seed or supplement other buffalo populations in southern Africa. Despite its low nuclear diversity, the mitochondrial genome diversity is the highest of all populations across Africa. This is driven by the presence of a mitochondrial lineage that diverged ~2.14 million years ago from all other Cape buffalo mitogenomes. What is the source of this mitogenome? A plausible explanation is that it originated from introgression with the long-horned buffalo (Pelorovis antiquus) that went extinct in southern Africa at the end of the Pleistocene (~11,700 years ago). To test this hypothesis, we sampled long-horned and Cape buffalo subfossils from archaeological sites near Addo for ancient DNA analysis and comparison with extant Cape buffalo sequences. The results will settle the long-running debate about the taxonomic classification of P. antiquus – is it a distinct genus or species from, or simply a long-horned morph of, Cape buffalo? Do the genes of this extinct species survive in Addo Cape buffalo? If so, what are the conservation implications for the Addo buffalo population?

Applications

Date: Wednesday 31 August
Time: 14:00
Room: Pentlands West

Abstract 31

Oral Presentation

Towards an in-situ non-lethal rapid test to accurately detect the presence of the nematode parasite, Anguillicoloides crassus, in European eel, Anguilla anguilla

De Noia Michele 1, Poole Russell 3, Kaufmann Joshka 2-3, Waters Catherine 2-3, Adams Colin 1, McGinnity Philip 2-3, Llewellyn Martin 1

1 Institute of Biodiversity Animal Health and Comparative Medicine, University of Glasgow, Glasgow, UK
2 School of Biological, Earth and Environmental Sciences, University College Cork, Cork, Ireland
3 Marine Institute, Foras na Mara, Newport, Ireland

Anguillicoloides crassus is an invasive nematode parasite of the critically endangered European eel, *Anguilla anguilla*, and possibly one of the primary drivers of eel population collapse. The presence of the parasite has been shown to impact many features of eel physiology and life history. Early detection of the parasite is vital to limit the spread of *A. crassus*, and to assess its potential impact on spawning biomass. However, until recently, accurate diagnosis of infection could only be achieved via necropsy. To support *A. anguilla* fisheries management in the context of *A. crassus* we developed a rapid, non-lethal, minimally invasive and in-situ DNA-based method to infer the presence of the parasite in the swim bladder. Screening of 131 wild eels was undertaken between 2017 and 2019 in Ireland and the UK to validate the procedure. DNA extractions and PCR were conducted using both a Qiagen Stool kit at Glasgow University and in situ using Whatman qualitative filter paper No. 1 and a miniPCR DNA Discovery System™. Primers were specifically designed to target the cytochrome oxidase mtDNA gene region and in situ extraction and amplification takes approximately 3h for up to 16 individuals. Our *in situ* diagnostic procedure demonstrated Positive Predictive Values at 96% and Negative Predictive Values at 87% by comparison to necropsy data. Our method could be a valuable tool in the hands of fisheries managers to enable infection control and help protect this iconic but critically endangered species.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 32

Poster Presentation

Body mass, salinity and nematode parasite, *Anguillicola crassus*, infection induce microbial community changes in the critically endangered European eel, *Anguilla anguilla*

De Noia Michele1, Poole Russell3, Kaufmann Joshka2 - 3, Waters Catherine2-3, Adams Colins1, McGinnity Philip2-3, Bachar Chelib1, Llewellyn Martin1

1 Institute of Biodiversity Animal Health and Comparative Medicine, University of Glasgow, Glasgow, UK
2 School of Biological, Earth and Environmental Sciences, University College Cork, Cork, Ireland
3 Marine Institute, Foras na Mara, Newport, Ireland

The study of fish microbiome is an emerging means to understand the role of commensal microbes in modulating immune responses, improving digestion and pathogen colonisation resistance. Fish are constantly surrounded by the aquatic microbes that shape their gut and skin microbial composition, along with diet intake and pathogenic infection. The eel gut microbiome has only been studied in farm-reared fish under experimental conditions. This study provides characterization and association with life history traits, physiology and environmental drivers shaping the wild European eel microbiome. We sequenced sixty-two gut compartment samples from eels and 16 environmental samples using 16S rRNA gene from two lakes in Ireland over three consecutive years. We measured microbial species richness, diversity and variation between samples linking them with environmental and physiological factors. Effective Richness and Shannon Effective were strongly influenced by the health status of the fish, using weight and fat as a proxy. Diversity and richness were also influenced by infection the nematode *A. crassus* infection. Parasite burden reduces microbial diversity and richness (P value < 0.05). In healthier (heavier and fatter) eels we found an increase of diversity positively correlated with Oxyphotobacteria (P value < 0.05). The environment also plays in shaping the microbial community showing a core gut microbiome differing from the environment microbiome, the latter characterized mainly by free living bacteria. We didn’t detect any significant difference between microbial community diversity and composition and metabolic traits, although we found *Staphylococcus* and Oxyphotobacteria positively correlated with maximum metabolic rate. Our study opens a new field of study to investigate further the environmental and ecological factors driving the microbial composition and the connection between specific bacterial taxa and their function in fish heath, metabolism and ecology.

Technologies
Date: Wednesday 31 August
Time: 11:00
Room: Pentlands East

Abstract 33
Oral Presentation

Temporal dynamics of genome erosion leading up to the extinction of the woolly mammoth

Marianne Dehasque1
1 Centre for Palaeogenetics, Sweden

To understand the extent to which genetic processes contribute to extinction risk in small populations, time-series data over a wide temporal span can provide valuable insights. Yet, many studies focusing on the genetic burden in endangered species remain limited to data consisting of one or few generations since the population’s decline, making it difficult to distinguish between the initial genetic consequences of the rapid population decline and the theorised subsequent mutational meltdown. The woolly mammoth (*Mammuthus primigenius*) is an excellent model system to investigate the genetic extinction risk of declining populations. The mammoth population on Wrangel Island went through a bottleneck event in the early Holocene and survived as a small population for hundreds of generations before finally going extinct. To study the long-term genetic effects of these events, we analyzed whole-genome data from 21 woolly mammoths. Our analyses suggest that the Wrangel mammoth population size recovered quickly after the bottleneck, and subsequently remained stable during the ensuing 6,000 years. Interestingly, while inbreeding levels and genome-wide diversity changed rapidly due to the bottleneck, purging of highly deleterious mutations through purifying selection took place more gradually across thousands of years. These findings suggest that bottlenecks can lead to a “mutational debt” where, even despite fast demographic recovery, populations may continue to suffer from inbreeding depression for hundreds of generations.

Applications
Date: Wednesday 31 August
Time: 16:45
Room: Pentlands East

Abstract 34

Oral Presentation

Genetic diversity in global populations of the Critically Endangered addax (Addax nasomaculatus) and its implications for conservation

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7 Ministère de l'Environnement et de la Lutte Contre la Désertification, Niger
8 Noé au Niger, Réserve Naturelle Nationale de Termit et Tin-Toumma, Niger
9 San Diego Zoo Wildlife Alliance, San Diego, USA
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Threatened species are frequently patchily distributed across small wild populations, *ex situ* and reintroduced populations. Best practices advocate for integrated management across such populations, yet relevant data is rarely available to determine how. Africa's rarest antelope is the iconic desert-specialist addax (*Addax nasomaculatus*) with now less than 100 wild individuals remaining, and ex situ populations are a vital insurance against extinction. Despite the catastrophic declines in the wild, thousands remain in ex situ populations managed with of varying levels of intensity, and the species was reintroduced to Tunisia in the 1980s. We undertook to develop the genetic data needed to connect wild populations with ex situ populations that have incomplete knowledge of founder origins, management histories and pedigrees to assist conservation planning for this Critically Endangered species. Analysing mitochondrial DNA (723 bp of control region) from faecal samples of wild addax, we show that genetic diversity remains higher and more evolutionarily diverse than within a reintroduced population or ex situ populations. Additionally, we carried out double digest restriction site-associated DNA (ddRAD) to analyse 1704 SNPs from *ex situ* addax. We found that whilst population structure is limited, each population carries unique diversity, revealing that careful selection of founders is vital to ensure sufficient genetic diversity and minimise drift and inbreeding within reintroductions. Our results highlight a vital need to conserve genetic diversity within wild addax and provide a genetic foundation for determining integrated conservation strategies to prevent extinction and optimise future reintroductions.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 35

Poster Presentation

Identification of carcass use by predators and mammalian scavengers

Bettina Dobrescu1, Jens Seeger1, Felix Böcker1
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Predator identification at game and livestock carcasses plays a key role in human-wildlife-conflicts (HWC) but causes of death often remain uncertain, especially if the carcass was used by different mammalian scavengers. Since large carnivores such as wolves and lynx recolonize several parts of Germany and the federal state of Baden-Württemberg, potential large carnivore kills obtained more political and emotional stir (e.g. due to economic damages). However, many carcasses without obvious indication of being killed by large carnivore cannot be genetically analyzed within ongoing monitoring due to resource constraints and mammalian scavengers are often determined by experience. The main goal of this project is therefore, to figure out potentials and limiting factors of predator and scavenger species identification at game and livestock carcasses and enhance evaluation and information transfer to stakeholders. The project combines two methodological approaches. On the one hand data is collected by patho-morphological feeding traits and bite marks (based on standardized protocol and photo documentation). On the other hand, species identification is done based on genetic analysis via saliva traces from bite marks and feeding spots. Genetic species identification is done based on mitochondrial DNA analysis, amplifying several mammalian species. Specific blocking oligos were used for prey species to impede amplification of prey DNA. Furthermore, species identification success is also evaluated by (16S rDNA) metabarcoding. Camera trapping at specific kills is used for verification of patho- morphological traits and genetic results.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 36

Poster Presentation

How to build a low-cost decentralised wildlife disease surveillance network: Peru, Rwanda and Vietnam

Gideon Erkenswick1, Mrinalini Watsa1

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The In Situ Laboratory Initiative aims to accelerate wildlife conservation and disease surveillance by expanding in-country and on-site resources and capacity for applied genetic and genomic techniques. The core of the ISL missing is decentralization, including an emphasis on funding and leadership deriving from a diversity of stakeholders, both local and international, creating financial stability and the production of deliverables of high value internationally but limited relevance locally. Nearly 24 months into the initiative, programs are underway in Peru, Rwanda and Vietnam. The main foci include surveying animal health associated with wildlife trafficking and rescue centers in Peru, long-term ecological monitoring (including descriptions of diet and parasite/pathogen assemblages) of target species in Rwanda, and disease surveillance coalition building in wildlife critical habitat in Vietnam. While similar approaches were used in all countries, outcomes include distinct, country-specific actions, reflecting the specific needs of local partners. We believe this to be a strength of the model, and also anticipate program convergence as the initiative matures in each country, particularly during data analysis and deposition. Insights thus far include milestones (both expected and unexpected), obstacles to success, and an identification of underutilized toolkits that display great potential.

Applications

Date: Wednesday 31 August
Time: 11:45
Room: Pentlands West

Abstract 37

Oral Presentation

Portable genomic tools for gorilla population dynamics and conservation

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Non-human great apes are globally threatened by increasing habitat loss and fragmentation, diseases, hunting, and illegal wildlife trade. Their disappearance may trigger significant knock-on ecological effects, with far-reaching consequences for the stability of ecosystems that support millions of people. Therefore, monitoring changes in great ape populations is crucial for the development of sound and effective action plans that can help turn the tide on the future of these species. As a response, recent conservation efforts have seen an upsurge in the use of DNA testing to detect the effects of animal population shifts and assess the effectiveness of current preservation measures. We have been developing a portable DNA test to identify gorilla individuals and (sub)species in the wild. This is based on a robust autosomal 90-SNP marker panel suited for analysis of degraded DNA in non-invasive samples (e.g. faeces and hair) that, used in tandem with the Oxford Nanopore Technology™ (ONT) MinION™, facilitates rapid in-field sequencing. SNP validation was conducted using samples provided by collaboration with Twycross Zoo and the Aspinall Foundation. The approach reduces times and costs of sequencing while overcoming the need to ship precious samples overseas. In addition, the simplicity, portability, and affordability of this technology should allow researchers to conduct non-invasive DNA analysis virtually anywhere and assess population dynamics and structure in wild gorillas while offering support to the fight against poaching and illegal wildlife trafficking.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 38

Poster Presentation

Defining Evolutionary Significant Units (ESUs) in the salmonid species Arctic charr (Salvelinus alpinus)

Sam Fenton1, Kathryn R. Elmer1, Colin W. Bean1, & Colin E Adams1

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The incredibly high diversity amongst populations of the salmonid fish Arctic charr across its global range has led to this species being described as ‘the most variable vertebrate on Earth’. In the British Isles, this species, and the environments that continue to drive this variation, are of high conservation value. Rapidly changing climatic conditions increasingly threaten Arctic charr populations and the implementation of appropriate conservation measures for different populations across Scotland is vital to protecting this diversity. The high variation across populations both within and across catchments, means that identifying populations or groups of populations that can be defined as Evolutionarily Significant Units (ESUs) could create a viable system for managing this highly variable species in Scotland and elsewhere. However, many populations in Scotland have never been studied scientifically before, making the delineation of accurate ESUs across Scotland unrealistic.

To address this, we conducted a national scale genetic study of approx. 50 different lake populations covering all 27 Hydrometric Areas known to contain this species in Scotland, the first study to do so. Our dataset of approx. 33,000 SNPs allows us to not only investigate patterns of genetic variation across all catchments in Scotland but also investigate variation within catchments and within lakes. I will present the most recent results of this study, discussing how patterns of genetic variation in both neutral and adaptive SNP markers might inform the definition of ESUs and discussing how Genomic Vulnerability might be used to identify vulnerable populations using both environmental and genetic data.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 39

Poster Presentation

Museomics in the lab: setup and best practices for not-so-ancient DNA

Giada Ferrari1, Peter Hollingsworth1, & Michelle Hart1

1 Royal Botanic Garden Edinburgh, Scotland

Natural history collections in museums and herbaria represent a vast repository of past biodiversity, with an estimated three billion specimens worldwide. Advances in laboratory and sequencing technologies have made these specimens increasingly accessible for genomic analyses, offering a window into the genetic past of species. Sequencing natural history collections adds a temporal component to conservation and evolutionary biology studies and often permits access to information that can no longer be sampled in the wild. DNA retrieved from intentionally preserved material can vary greatly in yield and quality, due to the age, preparation, and storage conditions of the specimens. Often resembling ancient DNA – heavily fragmented, biochemically modified, and low in concentration – it can present the same methodological challenges and susceptibility to environmental and laboratory contamination. Standards that are universally accepted in ancient genomics can be implemented to ensure the authenticity of DNA sequences obtained from natural history collections. However, these strict criteria greatly reduce the scalability of experiments and make them altogether inaccessible to institutions without access to a specialised laboratory. Attempts at establishing separate definitions and guidelines for younger historic DNA have been made, yet a consensus in the literature is lacking and often no precautions are followed or described. Here we give an overview of laboratory guidelines and setups at different levels of anti-contamination stringency, discuss when each strategy may be appropriate with respect to research questions and need for scalability, and make recommendations for implementing minimal precautions in existing laboratories.

Technologies

Date: Wednesday 31 August
Time: 10:45
Room: Pentlands East

Abstract 40

Oral Presentation

The use of meta-barcoding tools to identify bushmeat consumed at bars in Guinea-Bissau, West Africa, and implications for non-human primates conservation

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9 Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Rua do Campo Alegre FC4, 4169-007 Porto, Portugal
10 Department of Zoology, Faculty of Sciences, University of Johannesburg, 23, Auckland Park 2006, South Africa

Meta-barcoding techniques comprise the amplification of diagnostic DNA fragments and next-generation sequencing. Although not extensively used in food and wildlife forensic sciences, meta-barcoding tools has the potential to identity partially cooked meat or visually unrecognizable carcasses, in a fast and cost-effective manner, which can improve conservation efforts and law enforcement. In Guinea-Bissau, a small but biodiversity rich country in West-Africa, bushmeat is consumed as a snack while drinking alcoholic beverages at bars and restaurants (a practice locally named Abafatório). Since the bushmeat trade is illegal and may be subject to penalties, the location and details of these practices are usually concealed from outsiders of the local communities. We aimed to characterize the trade and consumption of bushmeat at bars/restaurants in a small town on the outskirts of a National Park without the direct observation of the activities. To collect information on traded species, type and prices of meals and carcasses' tissue samples, a research assistant and member of the local community visited six establishments every week for 15 months (2015-2017). We identified two hundred forty-nine tissue samples using cytb and 12S mitochondrial DNA regions and the miseq next-generation sequencing. Carcasses arrived fresh and non-processed, suggesting proximity of hunted areas. Meat was sold by the piece at monetarily accessible prices for locals. All the samples collected were successfully sequenced and identified Consumed species were mostly non-human primates (*Cercopithecus campbelli*, *Chlorocebus sabaeus* and *Papio papio*). Our results suggests that abafatório practices may have significant negative consequences to primate conservation in the country.

Applications

Date: Wednesday 31 August
Time: 14:15
Room: Pentlands West

Abstract 41

Oral Presentation

Putting genetic rescue to practice using the alpine blue-sowthistle (Cicerbita alpina) in Scotland

Aline Finger1, Mike Smedley2, Duncan Halley3, Natacha Frachon1, Martine Borge1, Antje Ahrends1

1 Royal Botanic Garden Edinburgh, UK
2 NatureScot, UK
3 Norsk institutt for naturforskning, Norway

We present a study that uses genetic rescue to help maximise the success of conservation translocations. Species in need of translocations often remain as small and isolated populations. This makes them vulnerable to genetic problems, such as genetic erosion, inbreeding depression and a lowered evolutionary potential. These genetic problems often decrease plant fitness and consequently make recovery work more difficult. Genetic rescue can help to overcome fitness declines in small populations and can consequently be a strong tool for creating more suitable plant material for conservation translocations. Here, we put genetic rescue to practice, including all associated steps, such as gathering genetic background information on the study species, cross-pollinations in a nursery, fitness measurements, and translocations. We're using the alpine blue-sowthistle (*Cicerbita alpina*) as an example, which is only left in four very small populations in Scotland, where it fails to reproduce. Like so many other species, *C. alpina* is unlikely to recover naturally and could be lost without human interventions. We demonstrate that genetic diversity is low and inbreeding high in Scotland, compared to larger, more continuous Norwegian populations. Cross-pollinations do improve plant fitness in the nursery, outbreeding depression is unlikely, and plants can establish at new sites (when micros-siting is correct) but grazing has strong negative impacts on plant growth. We demonstrate that genetic rescue and conservation translocations can indeed help plant conservation but will only succeed in conjunction with wider habitat conservation, enough space and time to grow enough plants, and considerable expertise on the study species.

Policy

Date: Thursday 1 September
Time: 11:15
Room: Pentlands East

Abstract 42

Oral Presentation

Monitoring genetic diversity: a genomics-based pilot study for Switzerland

Martin C. Fischer1, Oliver Reutimann1, Gabriel Ulrich1, Felix Gugerli2, Rolf Holderegger1,2 & Alex Widmer1

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Genetic diversity is the raw material of evolution and allows species and populations to adapt and persist in changing environments. Systematic and representative monitoring of genetic diversity has rarely been conducted, resulting in under-reporting to national and international authorities. Following our 2020 feasibility study on how genetic diversity and possible changes over time could be assessed across a variety of organisms, we initiated a pilot study for monitoring genetic diversity in five species across Switzerland. The pilot study aims to gain experience on how to implement a genetic diversity monitoring program using genomic approaches. We have selected five candidate species, each of which occurs in a specific habitat type of national importance and/or in anthropogenically modified landscapes. For each of the five species, we de novo assembled a reference genome. In 2021, we sampled >1,100 individuals from 135 populations across all biogeographic regions in Switzerland, applying a proportionally stratified random sampling strategy. We are currently whole-genome re-sequencing all individuals (~10x coverage). To explore possible changes in genetic diversity over time, we started a retrospective analysis of genetic diversity in two species, using specimens from natural history collections dating back up to 218 years. First results indicate that contemporary samples well represent the climate-space of each study species in Switzerland, and that retrospective monitoring based on historic DNA is feasible, but challenging. Another challenge remains to develop meaningful and intuitive indicators of change in genetic diversity for reporting to national and/or international authorities as well as practitioners.

Technologies
Date: Tuesday 30 August
Time: 16:55/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 43

Speed talk & poster

DNA Metabarcoding Is Not Magic: A Case Study With The Critically Endangered Highland Woolly Monkey

Manuel L. Fonseca12, Marcela A. Ramírez-Pinzón3, Kaylie N. McNeil4, Michelle Guevara5, Laura M. Gómez-Gutiérrez1, Klaus Harter6, Alvaro Mongui5, Pablo R. Stevenson1

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3 Laboratorio de Zoología y Ecología Acuática (LAZOEA), Universidad de Los Andes, Bogotá, Colombia
4 Department of Anthropology, University of Texas at San Antonio, San Antonio, TX, United States
5 Departamento de Ciencias Biológicas, Universidad de los Andes, Bogotá Colombia
6 Zentrum für Molekularbiologie der Pflanzen (ZMBP), Eberhard-Karls Universität Tübingen, Tübingen, Germany

DNA Metabarcoding is the use of genetic barcodes, polymerase chain reaction (PCR) and high-throughput sequencing (HTS) to detect organisms present in a sample. This non-invasive technique identifies multiple taxa in environmental samples (eDNA: scats, water, soil) by amplifying short conserved sequences by running a parallel sequencing of PCR amplicons. Metabarcoding has been used for unveiling the feeding ecology, food webs, and host-microbiota interactions of different sorts of organisms including in recent years primates. These sorts of studies will continue to increase in the near future but still, how reliable is published data? Although this NGS technique is being used broadly to answer all sorts of biological questions, it is not a recipe and requires a robust experimental design as well as bioinformatics analysis in order to avoid bias that could mislead to erroneous conclusions as is surprisingly common to find in the literature. From January to December 2018 we collected 247 scat samples from three groups of highland woolly monkeys (*Lagothrix lagotricha lugens*) at Cueva de Los Guácharos National Park, Colombia. We amplified two conserved

COI barcode regions for arthropods and included tags so we could differentiate the diet between adults and juvenile monkeys over time after sequencing in the Illumina Mi-Seq platform. Hereby we explore the feeding ecology of the highland woolly monkeys, an endemic and critically endangered subspecies, through the difficulties of planning, performing and analysing data through a metabarcoding approach, as well as suggestions that arise from our results and discussions.

Applications

Date: Thursday 1 September
Time: 11:45
Room: Pentlands West

Abstract 44

Oral Presentation

Genomic variation and accumulation of deleterious mutations in the critically endangered Aeolian wall lizard

Maëva Gabrielli1, Andrea Benazzo1, Alessio Iannucci2, Claudio Ciofi2, Giorgio Bertorelle1

1 University of Ferrara, Italy
2 University of Florence, Italy

Small populations give a unique opportunity to investigate the relative roles of drift and selection in evolution. In particular, small populations can show an accumulation of deleterious mutations (the genetic load) due to the strong effects of drift. The Aeolian wall lizard *Podarcis raffonei* is endemic to the Aeolian archipelago, located in the Mediterranean Sea, North of Sicily. The extremely restricted distribution range includes two small islets (La Canna, 1,800 m2, and Strombolicchio, 7,000 m2). Our project aims at investigating the genomic variation pattern and the genetic load in small populations of this species, and to compare them with those observed in the sister species *Podarcis waglerianus* (the Sicilian wall lizard), where the distribution range and the population size are much larger. A newly assembled genome was produced for the Aeolian wall lizard, and whole genomes were resequenced for ten individuals each from La Canna and Strombolicchio (estimated population size: 50 and 500 individuals respectively) and for ten individuals of the sister species. The Aeolian wall lizard shows a uniquely low level of polymorphism, in particular for the La Canna population that has 300 times less polymorphic sites than the Sicilian wall lizard. Annotation-based estimates of deleterious mutations revealed a high genetic load in the smallest La Canna population. Levels of variation and genetic load estimates are therefore clearly affected by the population size in this system, suggesting that more conservation actions should be implemented at least in the smallest islets.

Collections

Date: Tuesday 30 August
Time: 15:25
Room: Pentlands (East/West)

Abstract 45

Oral Presentation

Fungarium collections in the genomic era: the Mycena genus

Brigida Gallone1, Jorinde Nuytinck1

1 Naturalis Biodiversity Center, the Netherlands. Naturalis Biodiversity Center, the Netherlands

Understanding the taxonomic relationships among organisms and their evolutionary history is a critical step in establishing biodiversity conservation goals. Fungi are one of the most diverse group of eukaryotes, supporting the health of all ecosystems. Nevertheless, only 8% of fungal diversity has been currently described. Sampling and identification are often hampered by their elusive nature together with complex lifecycles. Over the past centuries fungal diversity has been preserved world-wide in Fungarium collections. The genomic revolution offers the opportunity to unlock this huge genetic repository to refine phylogenetic relationships, reconsider taxonomic assignments and describe new species.

Mycena is a large, yet under sampled, genus of small mushroom-forming fungi that lacks a robust phylogenetic framework. It exhibits high variability in morphology, broad ecological versatility and striking phenotypic diversity, with several bioluminescent members. In this project we are developing the first genome-based classification of Mycena, that integrates museum (type-)specimens, bridging taxonomy and evolution. We assessed the feasibility of generating whole-genome sequencing data from dried specimens and the efficiency of long-read high throughput sequencing for taxonomic identification of hundreds fungal specimens. Overall, the time has come to consistently integrate genomics in the study of fungal diversity and go beyond single-barcode approaches.

Technologies
Date: Wednesday 31 August
Time: 12:00
Room: Pentlands East

Abstract 46

Oral Presentation

Estimates of effective population size in plants with complex life-history traits

Roberta Gargiulo1
1 Royal Botanic Gardens Kew, UK

Effective population size (Ne) is a fundamental parameter in evolution and conservation, but notoriously difficult to estimate from demographic data and to interpret from genetic data. Effective population size provides an indication of the loss of genetic variation over time in natural populations. However, current baselines for effective population size to census size ratios are not representative of species with complex life-history traits, especially plants. The lack of reliable effective population size to census size ratios hinders our ability to predict loss of genetic diversity from the number of individuals in a population, and this misleads conservation efforts.

In this contribution, I will describe our research on Ne in orchids. Orchids are good models to investigate how Ne changes depending on different life-history traits and reproductive systems. In *Cypripedium calceolus*, we used RADseq and microsatellite data to calculate Ne with the linkage disequilibrium method. Ne estimates were up to 20 times smaller than the number of observed individuals, also because of the combination of different life-history traits and the occurrence of vegetative reproduction. To understand how different traits influence Ne, we are now focusing on the genus *Cephalanthera*, whose species have little vegetative spread and different mating systems, but also some traits in common with *C. calceolus* (i.e., overlapping generations, rhizomatous perennial life-cycle). As *Cephalanthera* spp. are either critically endangered (*C. rubra*) or vulnerable (*C. damasonium*, *C. longifolia*) in Britain, this study aims to advance our knowledge of Ne in plants and to provide practical recommendations for reintroduction and conservation.

Policy

Date: Tuesday 1 September
Time: 12:00
Room: Pentlands East

Abstract 47

Oral Presentation

Genetic diversity and introgression in the Norway – Siberian Spruce Species Complex: implications in conifer management and conservation

Julia C. Geue1, Alexis R. Sullivan1, Jade Bruxaux1, Wei Zhao1, David Hall1 and Xiao-Ru Wang1

1 Department of Ecology and Environmental Sciences, Umeå University, Sweden

Rapid environmental changes modify natural selection pressures, forcing populations to either shift their distributional range or respond plastically or adaptively to novel conditions. Forest tree species such as the Norway (*Picea abies*) or Siberian Spruce (*P.obovata*) may be particularly vulnerable to these changes because of long generation times, limited migration ability and adaptation to challenging environments. The ability to adapt to changing conditions largely depends on ‘standing genetic variation’. Thus, it is critical to map standing adaptive genetic variation in order to understand how species may be affected by environmental changes.

Norway and Siberian spruce are closely-related sister species, distributed across Eurasia, where Siberian spruce replaces Norway spruce around central Siberia and further to the east. Comparative studies on spatial genetic diversity and introgression in this species complex are scarce, leaving species delineation blurred, and conservation and breeding actions uninformed. This study conducts a genetic inventory of this species complex and unravels the extent of the introgression zone. We quantify genetic diversity in 1521 individuals from 156 populations using genotyping-by-sequencing. Additionally, we examine gene-environment associations across the species’ ranges. Knowledge about introgression and gene-flow between these species, as well as the spatial pattern of genetic diversity and its environmental correlates will provide key insights into the underlying selective pressures. An improved understanding of the processes driving adaptive variation in both species, and how they may be affected by human activities can benefit future forest conservation management strategies.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 48

Poster Presentation

How does forest management affect genetic and species diversity?

Marcel Glück1, Oliver Bossdorf2, Henri A. Thomassen1

1 Institute of Evolution and Ecology, Tübingen University, Germany
2 Plant Evolutionary Ecology, Tübingen University, Germany

Genetic variation is the most basic level of biodiversity, crucial for adequate responses of species to changing environments, and thus their long-term persistence. However, fuelled by an ever-increasing demand for timber, intense forest management might be depleting intraspecific genetic variation in many non-timber species. With the response to management being potentially species-specific, systematic insight into how forest management shapes genetic diversity might only be obtained using multiple species. We hence assess how forest management affects genetic diversity in ten plant and ten arthropod species. To do so, we sampled ~150 plots of the Germany-wide Biodiversity Exploratories research project, covering a management intensity gradient from undisturbed to heavily managed habitats. Insight into genetic variation is gained using reduced representation and whole-genome sequencing. Harnessing a landscape genomics approach and the wealth of information generated through the Biodiversity Exploratories, we will infer the most likely drivers of genetic variation. Additionally, because decreased genetic variation might be a precursor of the local extinction of species, we will relate genetic to species diversity to assess whether a loss in the former coincides with a loss in the latter. Following this holistic approach, we will contribute to a clearer picture of the processes shaping genetic and species diversity, which will allow us to protect remaining biodiversity as efficiently as possible.

Applications

Date: Wednesday 31 August
Time: 16:00
Room: Pentlands West

Abstract 49

Oral Presentation

The ongoing contribution of genomics to the conservation of the once most endangered felid: the Iberian lynx

Daniel Kleinman-Ruiz[1,3], María Lucena-Pérez[1], Raúl López-Torre[2], Lucia Mayor-Fidalgo[1], Aurora García-Dorado[3], Jesús Fernández[2] & **José A. Godoy[1]**

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The Iberian lynx was at the brink of extinction by the turn of the century, but thanks to ambitious and efficient conservation actions (which include conservation breeding, reinforcement and reintroduction programs) it is now growing and expanding. We have investigated the contribution of genetics to the species decline and recovery, first based on molecular markers and since 2016 with whole-genome sequence data. The Iberian lynx is one of the most genetically eroded species, due to small long-term population sizes and serial bottlenecks. This has also resulted in a lower load of highly deleterious variation, likely recessive, in comparison to its widespread sister species, the Eurasian lynx. Nevertheless, we also documented the accumulation of moderately deleterious variation in more bottlenecked populations within both species. Direct evidences for inbreeding depression are scarce, but some genetic diseases are segregating at moderate frequencies, including a juvenile epilepsy with high heritability and an apparently monogenic inheritance; its genetic basis is currently being investigated through linkage and association analyses. Accumulating evidence suggests a positive "rescue" effect of the admixture of the two remnant genetically differentiated populations in captivity and in the wild. The genetic management in the captive population based on the minimum kinship strategy is now being extended to the reintroduction program in the context of the ongoing LIFE "Lynxconnect" project, as allowed by an extensive individual-based monitoring program using non-invasive sampling and highly-informative SNP markers.

Applications

Date: Wednesday 31 August
Time: 11:00
Room: Pentlands West

Abstract 50

Oral Presentation

Population genetics of an elusive marine predator, the Atlantic white-sided dolphin (Lagenorhynchus acutus), across the eastern North Atlantic

Marc-Alexander Gose[1], Emily Humble[1], Nicholas Davison[2], Mariel Ten Doeschate[2], Andrew Brownlow[2], Rob Ogden[1]

[1] Royal (Dick) School of Veterinary Studies and the Roslin Institute, United Kingdom
[2] Scottish Marine Animal Stranding Scheme, United Kingdom

The Atlantic white-sided dolphin (*Lagenorhynchus acutus*) is an oceanic dolphin species inhabiting temperate and subpolar waters of the North Atlantic Ocean. Its restriction to a cold-water habitat makes it susceptible to impacts from climate change. However, monitoring these impacts and assessing the conservation status of this species is challenging due to its oceanic distribution. An accurate assessment of its conservation status is therefore urgently needed. Given the logistical and financial difficulties of obtaining data from free-ranging oceanic dolphins, obtaining tissue samples from stranded individuals provides an exceptional opportunity for studying elusive marine mammals across their geographic range. In this study, tissue samples from 92 Atlantic white-sided dolphin strandings that occurred between 1992 and 2020 along the coastlines of the eastern North Atlantic were used to resolve fine-scale population structure. We sequenced the mitochondrial control region and used a restriction-site associated marker approach (DArTseq™) to generate 41.000 nuclear markers, which were used to assess population structure, effective population size, genetic diversity, inbreeding, and relatedness across the sample set. The results of this study suggest that the eastern North Atlantic is habitat for a large, panmictic population of Atlantic white-sided dolphins. The population exhibits high levels of genetic diversity, low levels of inbreeding and a high effective population size. These results aid in assessing a more detailed conservation status of the species, but multidisciplinary approaches are needed to characterise potential threats to their long-term survival.

Applications

Date: Wednesday 31 August
Time: 16:30
Room: Pentlands East

Abstract 51

Oral Presentation

Investigating hybridisation between living and extinct Galapágos giant tortoises to inform a unique captive breeding programme

Rachel Gray1, Adalgisa Caccone2, Evelyn L. Jensen1

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Captive breeding programs are a valuable *ex-situ* conservation resource for increasing existing population sizes of threatened species or re-establishing extinct wild populations. Genetic analyses play a crucial role in these programs through monitoring genetic diversity and relatedness of the population. Here, we present the unique genetically informed captive breeding program of the Floreana Galápagos giant tortoise (*Chelonoidis niger*). The *C .niger* tortoise has been extinct since the 1800s, but its genome persists in hybrids with a living species from Isabela Island (*C. becki*). The program aims to increase representation of the *C. niger* tortoise in offspring and relies on accurate quantification of the proportion of *C. niger* ancestry in individuals to inform breeding groups. To achieve this, we employed whole genome sequencing of captive potential hybrid individuals and historical museum samples of Floreana tortoise ancestry to develop a single nucleotide polymorphism (SNP) panel. We used these data to identify the potential breeding individuals with high levels of *C. niger* ancestry. Individuals with high ancestry were then incorporated into breeding groups that maximised the representation of *C. niger* in offspring. Offspring from this captive breeding program will be repatriated to Floreana island as part of a re-introduction program to restore tortoise ecosystem services to the island. This work demonstrates the potential value of hyrbids in conservation and consideration of their presence on a case-by-case basis.

Applications

Date: Thursday 1 September
Time: 13:15
Room: Pentlands West

Abstract 52

Oral Presentation

Integrating ancient genomics and field-applicable protocols for sustained species conservation: the case of hybridization between Alpine ibex and domestic goat

Xenia Münger1, Mathieu Robin1, Noel Zehnder1, Alice Brambilla1, **Christine Grossen1**

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Hybridization with domestic species is a major concern in conservation biology. Endangered species are especially at risk of hybridization due to their small populations. Ancient samples from pre-bottlenecked populations can be a helpful tool to quantify the extent of widespread introgression and the study of concurrent cases of hybridization can help to estimate potential fitness effects in the wild.

Alpine ibex (*Capra ibex*) were at the brink of extinction two centuries ago, but recovered to stable numbers thanks to a successful reintroduction program. Current populations harbor substantial genetic signatures of low population sizes including low genetic diversity, inbreeding and increased mutation load. Furthermore, a previous study found signals of introgression from the domestic goat at an immune-relevant gene locus. We take advantage of two ancient and 29 recent whole-genomes of the Alpine ibex as well as 16 genomes representing domestic goat to examine the genome-wide extent of retained domestic goat introgression. We estimate about 2.5% recent domestic goat ancestry among concurrent Alpine ibex populations. Introgressed regions were enriched in immune-related genes where the generated genetic diversity may provide a selective advantage.

In order to investigate the extent of ongoing hybridization and potential fitness effects in the wild, we are currently developing a hybrid identification protocol applicable for in-field management situations, and we have sampled concurrent populations with repeated observations of suspected hybrids. The genetic analyses of our samples will give us important insights on how well hybrid individuals survive in the wild and help to inform decisions on hybrid management.

Applications
Date: Wednesday 31 August
Time: 10:45
Room: Pentlands West

Abstract 53

Oral Presentation

Resolving the genomic architecture of hatching failure in the Hawaiian crow (Corvus hawaiiensis) to improve conservation management

Stefanie Grosser1, Bryce Masuda2, Erin Datlof3, Yasmin Foster1, Catherine E. Grueber4, Oliver A. Ryder5, Jolene T. Sutton3, Bruce C. Robertson1

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2 Conservation Science and Wildlife Health, San Diego Zoo Wildlife Alliance, Volcano, Hawaiʻi, USA
3 Department of Biology, University of Hawaii at Hilo, Hilo, USA;
4 School of Life and Environmental Sciences, Faculty of Science, University of Sydney, Sydney, NSW, Australia;
5 San Diego Zoo Institute for Conservation Research, San Diego Zoo Wildlife Alliance, Escondido, USA

Egg-hatching failure is a common problem in endangered bird conservation and presents a major challenge to conservation breeding programmes. Many eggs fail to hatch due to inbreeding depression which is often a consequence of the limited breeding options available in small remnant populations of species that were once abundant in the wild. Despite decades of research, the genetic architecture of inbreeding depression and associated hatching failure is still not well understood, limiting our ability to take effective management actions. The “extinct in the wild” Hawaiian crow, or ʻalalā, presents a powerful model system for uncovering the causes of avian hatching failure as the managed breeding population suffers from high levels of inbreeding and up to 82% of eggs fail to hatch. Long-term pedigree data, detailed fitness records and a large number of samples, including embryos that died in the egg, have been collected through the dedicated long-term breeding programme, providing a rich resource to study embryo mortality. Here, we present a chromosome-scale genome assembly for the ʻalalā and whole genome resequencing data for more than 150 adults and embryos. With this exceptional data set we will elucidate the genomic architecture of hatching failure and aim to identify loci involved in this process. Using comparative genomics, we will further determine whether these candidate loci are universal drivers of variation in hatching outcome in birds. Our findings will directly inform ʻalalā breeding management and we will assess whether genomics-informed breeding strategies can reduce hatching failure in ʻalalā and other endangered avian species.

Applications

Date: Thursday 1 September
Time: 14:15
Room: Pentlands West

Abstract 54

Oral Presentation

Genomics and simulations to improve conservation breeding

Catherine E Grueber1

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Almost 2000 animal species rely on conservation breeding programs to prevent extinction, but how can we ensure these efforts deliver the genetic outcomes intended? Many evolutionary processes pose a risk to diversity in such programs, including small population size, founder effects, inbreeding and adaptation to captivity. In this presentation, I bring together tools from genomics, computational modelling and statistics to investigate the short-term genetic changes that can occur when we bring animals into controlled conditions, and breed for release to support dwindling wild populations. Taking lessons from a series of research projects focused on the large, Tasmanian devil insurance population, and through formal statistical comparison with species data generated all over the world, I show that genetic change can happen very rapidly, in sometimes just a single generation. Through collaboration with our partners in the broader conservation and zoo industry, this knowledge is now used to improve conservation outcomes.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 55

Poster Presentation

Tarsiers in the mist – Sulawesi`s mysterious mountain primate represents an ancient lineage

Laura Hagemann1, N. Grow2, Y. E.-M. B. Bohr3,4, D. Perwitasari-Farajallah5,6, Y. Duma7, S. L. Gursky8, S. Merker1

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2 Department of Anthropology, Washington State University, USA
3 Institute of Ecology, Diversity and Evolution, Johann Wolfgang Goethe-Universität Frankfurt, Germany
4 Institute of Zoology, Animal Ecology and Conservation, Universität Hamburg, Germany
5 Primate Research Center, IPB University, Bogor, Indonesia
6 Department of Biology, Faculty of Mathematics and Natural Sciences. IPB University, Bogor, Indonesia
7 Faculty of Animal Husbandry and Fisheries, Universitas Tadulako Palu, Indonesia
8 Department of Anthropology, Texas A&M University, College Station, USA

Sulawesi is the biggest island of the region Wallacea and located in the collision zone between major tectonic plates. Thus, the evolutionary history of the diverse flora and fauna of this biodiversity hotspot is inevitably linked to the complex geological past of the region. Tarsiers are small nocturnal primates which possibly arrived in the Sulawesi area in the early Miocene and split into two major lineages in the early Pleistocene, more than 13 MY later. Both of these lineages diversified further and today, 12 Sulawesi tarsier species are known. One of the 12 species is exceptional in many ways, it exclusively inhabits montane forests above 1800 m asl and is significantly smaller than its lowland relatives: *Tarsius pumilus*. This enigmatic primate was for the longest time known from only two museum specimens and its role in the evolution of tarsiers was very much unclear to date. Here we finally present first genetic data on Sulawesi's mountain tarsier and reveal that *T. pumilus* is not an aberrant lowland tarsier but in fact the sister taxon to all other Sulawesi tarsiers with a proposed split date of about 10 MYA. This coincides with the rise in sea level between the western and eastern parts of proto-Sulawesi but predates the presence of permanent mountains on the western part of islands. Our results allow for educated guesses on the mechanisms of speciation and foster our understanding of the evolutionary history of tarsiers and the spectacular biogeography of the Malay Archipelago.

Policy
Date: Thursday 1 September
Time: 13:30
Room: Pentlands East

Abstract 56

Oral Presentation

Applying the Gene Conservation Units concept to taxa other than trees

Jeanette Hall[1], Melissa Minter[2], David O'Brien[1], Joan Cottrell[3], Richard Ennos[4], Jane K. Hill[2]

1 NatureScot, UK
2 University of York, UK
3 Forest Research, UK
4 University of Edinburgh, UK

Genetic diversity is important for species persistence and to enable natural selection for adaptation to environmental change. Gene Conservation Units (GCUs) have been implemented for forest trees to protect genetic diversity and evolutionary processes in situ. GCUs have the potential to form OECMs (Other Effective area-based Conservation Measures) and thus contribute to the CBD's proposed 30x30 target. Furthermore, the Convention on Biological Diversity stipulates the protection of genetic diversity as an Aichi target, and so we explore the potential for GCUs to be implemented more widely in order to contribute towards this target.

Our global systematic review showed that GCUs are currently implemented primarily for plant species of economic importance (109/158 species studied), but a questionnaire sent to land managers and conservationists (60 U.K. participants) revealed strong support for fully integrating genetic information into conservation management (90% agree), and for creating GCUs for other plant and animal taxa.

Using four case studies of U.K. species of conservation importance which vary in genetic threat and population dynamics (two insect species, a fungus and a plant), we highlight that GCU implementation criteria need to be flexible to account for variation in effective breeding population size and geographic extent of target species. The wider uptake of GCUs would ensure that threatened genetic diversity is protected and support evolutionary processes that aid adaptation to changing environments.

Technologies

Date: Wednesday 31 August
Time: 13:45
Room: Pentlands East

Abstract 57

Oral Presentation

The role of microbiodiversity in conservation: insights from ecosystem metataxonomics

Giulio Galla[1], Nadine Praeg[2], Theresa Rzehak[2], Paul Illmer[2], Julia Seeber[2,3] & **Heidi C. Hauffe[1]**

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3 EURAC Research, Italy

As microbial communities hosted in various body niches (microbiota) are of recognized importance to individual health, the maintenance of such microbiodiversity in natural ecosystems could impact the conservation status of animal species. Metataxonomy using amplicon sequencing has become the standard for characterizing the diversity and composition of microbial communities associated with multicellular organisms and their environment, and numerous studies have now shown that human- and climate-mediated behavioural and dietary changes in wild animal populations are associated with changes in microbiota richness and composition. However, identifying the interactions between the microbiotas within the same ecosystem (i.e. those of water, soil, plants and animals) is essential for fully understanding the role of microorganisms in evolutionary and ecological processes. Comparative studies across such diverse biological samples are rare, due to potential biases during sample processing. Here we discuss the technical adjustments that can be applied to support direct comparisons of microbiota composition, using a terrestrial alpine ecosystem as a case study. We also show how microbial communities from 900 samples (1900 libraries) of wild vertebrates and invertebrates vary with those of domestic breeds and environmental microbiotas (soil and rhizosphere) across an altitudinal gradient, with implications for microdiversity conservation in light of climate and land use changes.

Applications

Date: Thursday 1 September
Time: 14:00
Room: Pentlands East

Abstract 58

Oral Presentation

Genomic insights and resources to aide in pangolin conservation

Sean P. Heighton1, Rémi Allio2, Jérôme Murienne1, Jordi Salmona1, Hao Meng3, Celine Scornavacca2, Armanda D.S. Bastos4, Flobert Njiokou5, Darren W. Pietersen4, Marie-Ka Tilak2, Shu-Jin Luo3, Frédéric Delsuc2, Philippe Gaubert1,6

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2 ISEM, Univ Montpellier, CNRS, IRD, Montpellier, France
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4 Mammal Research Institute, Department of Zoology & Entomology, University of Pretoria, Pretoria 0002, South Africa
5 Laboratoire de Parasitologie et Ecologie, Université de Yaoundé I, Faculté des Sciences, Cameroon
6 CIIMAR/CIMAR, Centro Interdisciplinar de Investigação Marinha e Ambiental, Universidade do Porto, Terminal de Cruzeiros do Porto de Leixões, Av. General Norton de Matos, s/n, 4450-208 Porto, Portugal

Pangolins form a unique group of scaly mammals that are being trafficked at record numbers for their meat and supposed medicinal properties. The limited genomic resources currently available for the eight extant species hamper global conservation genetic endeavors for sustaining their rapidly declining populations. We aim to provide a detailed assessment of the evolution, demographic history, and genetic diversity among the eight African and Asian pangolin species using orthologous genes and whole genome polymorphisms. Robust gene-based phylogenies recovered previously reported patterns, but suggested incomplete speciation or cryptic diversity within South-East Asian pangolins. New genome-wide divergence estimates indicate a strong influence of the rise of the Himalayan plateau on the early diversification of Asian pangolin species. Continental populations display earlier declines in demographic trajectories through changes in glacial-cyclicity, whilst island populations were likely influenced later by sea level fluctuations. Genome-wide homozygosity and heterozygosity estimates were variable, with some equal to those of mammalian species of great conservation concern. The most trafficked pangolin species, *Phataginus tricuspis*, had higher genome diversity estimates likely because of a stable demographic history and high population densities. However, we warn that the effect of recent and dramatic trafficking trends may not yet be realised in this species' genome, as well as others. Finally, we produce the first reference genome for the genus *Smutsia* (*S. gigantea*; ~87x) and draft genomes (~43x–77x) for four additional species. These data will be integral for future conservation management, genetic and forensic endeavors required for conserving pangolins, including tracing their illegal trade.

Collections

Date: Tuesday 30 August
Time: 13:55
Room: Pentlands (East/West)

Abstract 59

Oral Presentation

Lessons, visions and challenges from 1000+ large African mammal genomes

Rasmus Heller1, Vincent Muwanika2, Ida Moltke1, Hans Siegismund1, Anders Albrechtsen1, et al1

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2 Makerere University, Uganda

We recently embarked on an ambitious effort to sequence several 1000s of whole genomes from different populations of ~25 large mammal species in Africa. The aim is to bring our understanding of the phylogeographic and demographic history of the African megafauna to a new level, and to put this knowledge to the best possible use to inform conservation decisions on this fascinating and unique faunal assemblage. This will be achieved through a standardization of methods and analyses together with the synergies arising from a large and diverse cross-species data set from the same geographical setting. The first batches of this data has been analyzed, and in this talk I will present some highlights of what we have found. These include what we believe to be a best-practices (or at least decent practices?) pipeline of bioinformatics for such data, a few methods developed in the process, some important lessons about caveats in analyses and some important biological insights from such species as leopards, waterbucks and warthogs. I will also mention some analytical challenges that we do not currently have good solutions for, including limitations related to reference genome quality and annotation. Finally, I will end on a more forward-looking note and discuss how we can get a broader involvement in and application of our work, as well as how to squeeze the maximum amount of conservation-relevant information out of a data set such as this.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 60

Poster Presentation

A novel approach to investigate chromosome-specific inbreeding depression in red deer

Anna Hewett 1, Josephine Pemberton1, Martin Stoffel1
1 University of Edinburgh

Lowered fitness as a result of inbreeding, so-called inbreeding depression, is of significant concern for the conservation of both wild and livestock species. Previous studies have used genome-wide SNP genotypes to gain accurate measures of genomic inbreeding coefficients (Fgrm and FROH) in order to estimate inbreeding depression in certain traits. However, to identify particular genomic regions or certain chromosomes conferring excess inbreeding depression, a number of different approaches have been used. Here we present a novel approach to estimate chromosome-specific inbreeding depression using >35,000 autosomal SNPs genotyped in >3,000 individuals of a wild population of red deer. We use multi-membership models to estimate the effect each chromosomes inbreeding coefficient (FROHChr) has on fitness traits. We show that using this method is a more conservative measure of chromosome-specific inbreeding depression and demonstrate that such effects could easily be overestimated.

Applications

Date: Thursday 1 September
Time: 14:00
Room: Pentlands West

Abstract 61

Oral Presentation

Improving ex situ conservation of the Endangered Red Siskin (Spinus cucullatus) through the use of genomic tools

Karen M. Holm1,2, Kathryn M. Rodriguez-Clark2, 4, Brian J. Coyle2, Rebecca M. Gooley3, Erica Royer2, E. Emperatriz Gamero García2,4, H.C. Lim5,6

1 School of Systems Biology, George Mason University, Manassas VA , USA
2 Smithsonian's National Zoo and Conservation Biology Institute, Washington DC, USA
3 Smithsonian-Mason School of Conservation, Front Royal, VA, USA
4 Centro de Ecología, Instituto Venezolano de Investigaciones Científicas, Caracas, Venezuela.
5 Biology Department, George Mason University, Biology Department, Fairfax VA, USA
6 Center for Conservation Genomics, Smithsonian's National Zoo and Conservation Biology Institute, Washington, DC USA

Red siskins (*Spinus cucullatus*) are one of Venezuela's most endangered passerine songbirds with less than 1000 remaining in the wild. Known threats to the wild population include unsustainable harvest for the pet trade and loss of habitat, while cryptic hybridization with canary breeds and inbreeding maybe additional threats in *ex situ* populations. These pressures will have an effect on captive populations as a source for their eventual reintroduction. Here, we investigate the genetic structure and diversity of the ex situ conservation breeding populations and of the wild red siskins, as well as assess the accuracy of the pedigree derived from behavioral observations. We used genomic data, Single Nucleotide Polymorphisms (SNPs) derived from UltraConserved Elements (UCEs) and whole genome sequencing to perform a Principal Component and phylogenetic network analysis and found no evidence of general introgression with canaries in the captive populations examined. The captive populations are genetically more diverse than the sampled wild populations, indicating that current breeding recommendations based on mean kinship (MK) values are effective at maintaining genetic diversity and avoiding inbreeding. Through a pedigree analysis, we confirmed behavioral observations match the molecular data and that extra-pair copulations or egg dumping did not occur. We also established 10 triads of putative parent-offspring relationships and all had genotype inheritance that agree. Therefore, this study has provided us with the information to make better informed decisions and recommendations for breeding in ex situ populations. This will allow us to breed in captivity without hesitation to support in situ populations.

Applications

Date: Thursday 1 September
Time: 10:45
Room: Pentlands West

Abstract 62

Oral Presentation

Whole genome sequencing dates the tipping point for genetic swamping of the critically endangered wildcat population of Scotland

Jo Howard-McCombe1, Alex Jamieson2,3, Alberto Carmagnini3,4, Isa-Rita M. Russo5, Carsten Nowak6, Violeta Muñoz-Fuentes7 , Michael Bruford5, Andrew C. Kitchener8,9, Greger Larson2, Laurent Frantz3,4, Helen Senn10, Daniel J. Lawson11, Mark Beaumont1

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2 The Palaeogenomics & Bio-Archaeology Research Network, Research Laboratory for Archaeology and History of Art, The University of Oxford, UK
3 Palaeogenomics Group, Department of Veterinary Sciences, Ludwig Maximilians University of Munich, Germany
4 School of Biological and Behavioural Sciences, Queen Mary University of London, UK
5 School of Biosciences, Cardiff University, UK
6 Senckenberg Research Institute and Natural History Museum, Centre for Wildlife Genetics, Germany
7 European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), UK
8 Department of Natural Sciences, National Museums Scotland, UK
9 School of Geosciences, University of Edinburgh, UK
10 Conservation Department, Royal Zoological Society of Scotland, UK
11 School of Mathematics, University of Bristol, UK

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

Applications

Date: Wednesday 31 August
Time: 15:30
Room: Pentlands West

Abstract 63

Oral Presentation

Uncovering the mysteries of manta rays using genomics

Emily Humble1,2, Jane Hosegood2,3, Guy Stevens2, Mark de Bruyn3,4, Simon Creer3, Gary Carvalho3, Amelia Armstrong5, Ramon Bonfil6, Mark Deakos2,7, Daniel Fernando2,8, Niv Froman2, Lauren Peel2,9, Stephen Pollett2, Joshua Josh Rambahiniarison10, Alessandro Ponzo10, Helen Senn11, Joshua Stewart2,12, Sabine Wintner13,14, Rob Ogden1

1 University of Edinburgh
2 The Manta Trust
3 Bangor University
4 The University of Sydney
5 University of Queensland
6 Océanos Vivientes A. C.
7 Hawaii Association for Marine Education and Research (HAMER)
8 Blue Resources Trust
9 Save Our Seas Foundation, D'Arros Research Centre
10 Large Marine Vertebrates Research Institute Philippines
11 RZSS WildGenes
12 Oregon State University
13 KwaZulu-Natal Sharks Board
14 University of KwaZulu-Natal

Oceanic (*Mobula birostris*) and reef manta rays (*Mobula alfredi*) are among the most vulnerable species in our oceans yet significant knowledge gaps remain about fundamental aspects of their biology. For example, it remains a mystery both how their widespread distributions have arisen and the extent to which populations are connected within them. This information is crucial not only for establishing appropriate spatial scales for management, but for assessing population viability into the future. We address this using high-resolution genomic data from over 200 manta ray samples (*M. alfredi*: n = 126, *M. birostris*: n = 120) collected from across their entire distribution. We show that despite their recent divergence, oceanic and reef mantas display striking differences in population structure at a global scale, which was associated with significantly different levels of genetic diversity both between and within species. These findings indicate fundamental differences in colonisation strategy and migratory behaviour and highlight potentially vulnerable populations in need of heightened protection. I will examine these results in light of what is currently known about manta rays and discuss our findings in the context of global conservation management.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 64

Poster Presentation

Long-term, landscape genetic management of the wild camel (Camelus ferus) in Mongolia, the last surviving representative of an old-world camelid

Anna Jemmett1,4,5, Jim Groombridge1, Pamela Burger2, Deborah Dawson3

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2 University of Veterinary Medicine Vienna, Austria
3 University of Sheffield, UK
4 Institute of Zoology ZSL, UK,
5 Wild Camel Protection Foundation UK/Mongolia

The wild camel (*Camelus ferus*) is critically endangered. With less than 1,000 estimated to remain in the wild, it is further threatened by desertification due to climate change, habitat loss and degradation due to human encroachment and hybridisation with the domestic Bactrian camel (*Camelus bactrianus*). There is only one captive population, of 35 individuals, which is situated in Mongolia. Using non-invasive sampling techniques and microsatellite analysis we aimed to better understand the threats faced by *C. ferus* and how they are impacting the wild populations in the Great Gobi A Special Protected Area (GGASPA) in Mongolia. We conducted a population genetics study on the wild population in the GGASPA, estimating genetic diversity in the population and monitored levels of intogression from the domestic Bactrian. In the captive population genetic diversity was monitored to determine how much of the remnant wild diversity is held in the captive stock. Analysis of this data was also used to confirm parentage in the studbook. Together this analysis allows for better understanding of the species and for improved conservation management both in captivity and in the wild.

Collections

Date: Tuesday 30 August
Time: 16:40
Room: Pentlands (East/West)

Abstract 65

Oral Presentation

Surprises in the museum and arguments in the literature: how many Galapagos giant tortoise species are there?

Evelyn Jensen1, Stephen Gaughran2, Rachel Gray1, Nicole Fusco3, Adalgisa Caccone3

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2 Department of Ecology & Evolutionary Biology, Princeton University, USA
3 Department of Ecology and Evolutionary Biology, Yale University, USA

The Galapagos giant tortoises are charismatic emblems of evolutionary biology, and conservation icons. Despite decades of study, new discoveries about them are being made, and old arguments about their taxonomic status have yet to be settled. To address the seemingly simple question “how many Galapagos giant tortoise species are there?” we must first consider how many lineages are living and extinct, and then consider whether these lineages are “species”. In this talk I will sum up recent developments on the diversity and taxonomy Galapagos tortoises, from the discovery of museum specimens belonging to additional, undescribed extinct lineages, to the arguments for and against species or subspecies status, and what all this means for their conservation.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 66

Poster Presentation

Development of a genetic monitoring tool to assist conservation management of North-east Atlantic benthic elasmobranchs

Catherine S. Jones1, Tanja N. Schwanck1, Fenella Wood1, James Thorburn2, Jane Dodd3, Peter J. Wright4, David W. Donnan5 & Leslie R. Noble6

1 School of Biological Sciences, University of Aberdeen, UK
2 Scottish Oceans Institute, University of St. Andrews, UK
3 NatureScot, Cameron House, Oban, UK
4 Marine Scotland Science, Marine Laboratory, Aberdeen, UK
5 NatureScot, Battleby, Perth, UK
6 Faculty of Biosciences and Aquaculture, Nord University, Bodø, Norway

North-east Atlantic (NEA) elasmobranchs represent a minor but valuable component of marine fisheries, with many species suffering significant declines from targeting and bycatch. The protection and monitoring of genetic diversity in highly mobile elasmobranchs present management challenges across multi-legislative areas like the NEA. Genetic assessments are often rare and temporally separate, yet ongoing re-evaluation by workers in different states remains key to ensuring efficacy of protection. Declines in the critically endangered flapper skate (*Dipturus intermedius*) prompted designation of a marine protected area (MPA) on the Scottish west coast, affording incidental protection to the endangered spurdog (*Squalus acanthias*), a benthic aggregating shark species. Yet knowledge of the genetic connectivity and variability of populations within and outwith the MPA is limited. Next-generation sequencing provides large numbers of genetic markers but often requires considerable quantities of high-quality DNA, a problem for wildlife monitoring where available material typically yields low-quality/quantities of DNA. Dedicated reduced marker panel assays could offer simple, cost-effective tools, for cross-laboratory comparisons for routine genetic monitoring. We are establishing reduced panels of Single Nucleotide Polymorphic (SNP) markers to allow high throughput genotyping to monitor flapper skate and spurdog populations. Monitoring the status of the current MPA population(s), and connectivity with individuals at other locations in the NEA, is important to affirm its current siting, and to assess the need and location of future MPA placements.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 67

Poster Presentation

Applying genetics to the conservation of the Asian elephant (Elephas maximus) and Siamese crocodile (Crocodylus siamensis) in Cambodia

Sophorn Keath 1,2, Alex Ball3, Jenny Kaden3, Pablo Sinovas2, On Norong Uk1, Seanghun Meas1,2, & Saveng Ith1

1 Royal University of Phnom Penh, Cambodia
2 Fauna and Flora International, Cambodia
3 The Royal Zoological Society of Scotland, Scotland

Cambodia is one of the most valuable biodiversity countries in Southeast Asia. Low genetic diversity can have negative consequences for endangered species and it is important for conservation efforts to consolidate the knowledge from genetic studies. The conservation genetics laboratory at the Royal University of Phnom Penh (RUPP) is a research laboratory working on the study of two flagship species, the Asian elephant (*Elephas maximus*) and the Siamese crocodile (*Crocodylus siamensis*). The Asian elephant is highlighted as endangered on the IUCN red list, having declined by at least 50% in the last 60-75 years (Choudhury *et al*. 2008). Furthermore, Siamese crocodile conservation through captive breeding and re-introductions into the wild is required to boost numbers of this critically endangered species (Balaji *et al*. 2019). Recent work has focused on the elephant population in the Prey Lang Landscape for strengthened management, and the assessment of crocodile hybridization using single nucleotide polymorphisms and DNA sequencing analysis. The aim of our work is to determine the first elephant population size estimate for the Prey Lang Landscape.We will also present the results of species identification of crocodiles being screened prior to use in a Siamese crocodile breeding and release programme.

Technologies

Date: Tuesday 30 August
Time: 16:55/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 68

Speed talk & poster

What can you learn from a fly? Biting insects as non-invasive samplers

Anubhab Khan1, Ryan Carter1, Harriet Auty1, Barbara K. Mable1
1 IBAHCM, University of Glasgow, UK

Genomics-based studies are providing important new perspectives on the conservation of wild populations because of the scale of inferences possible, not only about population genetic structure but on the impacts of habitat fragmentation and management practices on inbreeding and the accumulation of deleterious mutations. However, one of the fundamental challenges for such studies remains the procurement of good samples. For endangered elusive species, good quality DNA from invasively collected tissue samples are exceptionally rare. Non-invasive sampling remains the popular choice for studying such species but obtaining faecal samples, hair or saliva can still be challenging. We are currently investigating whether blood sucking insects can be potentially used to study population genomics of the host mammal species. We used a whole genome shotgun approach to sequence pools of DNA extracted from tsetse fly abdomens for which the blood meals had been previously characterised to host species. Although the purpose was to test whether we could assemble genome-scale data from pools containing blood meals from single or multiple host species collected from different sites, we found that the vast majority of reads were from tsetse flies. As well as generating unique data on tsetse fly population genetics in relation to hosts fed on, we have been working on bioinformatics approaches to determine what scale of single nucleotide polymorphism calling will be possible from the non-tsetse reads. We further discuss the tools and technologies that could enable direct use for conservation genetics in field sites of biodiverse tropical countries with low resource settings.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 69

Poster Presentation

Population genomics of the waterbuck (Kobus ellipsiprymnus)

Corey Kirkland1, Carla Canedo-Ribeiro1, Tony King2, Marta Farré1

1 University of Kent, United Kingdom
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The waterbuck (*Kobus ellipsiprymnus*) is a species of antelope found throughout central and southern Africa. Two subspecies are currently recognised, the common (*K. ellipsiprymnus ellipsiprymnus*) and Defassa (*K. ellipsiprymnus defassa*), with the latter listed as “Near Threatened” by the IUCN Red List. Karyotypes are variable within and between the subspecies, ranging from 2n = 50 to 2n = 54. These have been caused by Robertsonian fusions between chromosomes 6 and 18 (the common waterbuck) and chromosome 7 and 11 (both the common and Defassa waterbuck). Chromosome polymorphisms have not been shown to cause reproduction isolation between the different karyotypes, as introgression has been seen within the hybrid zone where the two subspecies distributions overlap. Previous studies have used mitochondrial DNA and microsatellites to determine the population structure of the species but lack resolution due to limited genetic markers and sampling. In this study we present the first long-read genome assembly of the waterbuck using PacBio HiFi sequencing from a captive sample of the Defassa subspecies with a standard karyotype of 2n = 54. Furthermore, we utilise 24 skin samples from museum specimens dating back over 100 years and carry out low-coverage resequencing to determine the historical phylogeography and genetic diversity of the species. These samples will be supplemented with modern samples, to compare temporal shifts in genetic diversity. Our newly sequenced genomes will provide a resource for studying the evolutionary history and speciation of the waterbuck, with implications for future conservation management of the subspecies and further understanding of speciation.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 70

Poster Presentation

Implication of genetic rescue in the European ground squirrel conservation translocations

Peter Klinga1, Matúš Hrivnák1, Ervín Hapl2, Denisa Lobová3, Branislav Tám4, Diana Krajmerová1

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2 NGO Živá Planina, Slovakia
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4 National Zoological garden Bojnice, Slovakia

Translocations of native species has become increasingly important conservation tool for recovery of rare species and restoration purposes. However, despite interests in implication genomics into conservation management, genomic rescue components are rarely implemented in conservation translocation efforts. We showcase how genomics data could be used to inform conservation translocation planning of rare species. Using ddRAD sequencing data of 11,280 loci we elucidate genetic diversity and population structure in donor and reintroduced colonies fourteen years since the last translocation. We screened spatially isolated colonies to identify the donor colonies as well as the most genetically eroded colonies of European ground squirrel that need genetic rescue in Slovakia. We identified genetically distinct isolated colonies of European ground squirrel. Reintroduced colonies where individuals were translocated in the past matched the same genetic cluster as the donor colonies. However, genetic diversity of reintroduced colonies declined. We searched for local adaptations in autochthonous colonies across the altitudinal gradient but in a preliminary analysis we did not detect any signal of loci linked to climate variables. We stress the need for post-translocation genetic monitoring for early detection of genetic erosion risks due to founder effect in spatially isolated colonies of species threatened by habitat loss. Genetic data collected prior the translocation provide the base for temporal post-translocation genetic monitoring and its implication for further genomic-based conservation actions.

Applications

Date: Wednesday 31 August
Time: 13:45
Room: Pentlands West

Abstract 71

Oral Presentation

Rescued, diminished, but hopeful: Severe genetic erosion revealed by genomic analysis in the endangered black-footed ferret (Mustela nigripes)

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The black-footed ferret (*Mustela nigripes*, hereafter BFF) narrowly avoided extinction in the 1980s to become an oft-cited example of the benefits of intensive management, research, and collaboration to save a species and reintroduce it to the wild. Since species collapse and rescue of the last 18 animals (an estimated 7 founders) to initiate conservation breeding, more than 10,000 kits have been born over the last three decades, with ferrets released into 29 sites in the USA, Canada, and Mexico. Despite the resilience of BFF populations, the species remains at risk of extinction due to a high susceptibility to disease and multiple health challenges, including male fertility. To better understand the impact of the founder bottleneck on genetic diversity, inbreeding, and deleterious mutation load, we sequenced and analyzed whole genomes of 54 BFFs representing wild (pre-captive, n=6), captive (n = 26), and reintroduced (n = 22) individuals. Analyses revealed extremely low levels of mean genome-wide heterozygosity, high realized inbreeding as measured by runs of homozygosity, and an extreme reduction in singletons across individuals from the captive and reintroduced populations. Despite the extensive genetic erosion across the genome caused by the bottleneck, BFFs still retain variation in genes important for long-term fitness. Loss-of-function mutations were observed in genes associated with spermatogenesis and sperm cell function. Understanding what and where genetic diversity has been retained and lost in the BFF genome provides a foundation for a more nuanced understanding of genetic diversity and for resurrecting and restoring lost diversity, thereby mitigating extinction risk.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 72

Poster Presentation

Harmonizing DNA-based brown bear (Ursus arctos) transnational monitoring in northern Europe using SNPs

Alexander Kopatz1, Oddmund Kleven1, Anita J. Norman2, Göran Spong2, Mia Valtonen3, Ilpo Kojola3, Jouni Aspi4, Øystein Flagstad1, & Jonas Kindberg5

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3 Natural Resources Institute Finland, Finland
4 University of Oulu, Finland
5 Norwegian Institute for Nature Research, Norway & Swedish University of Agricultural Sciences, Sweden

The population of brown bears in Fennoscandia consists of the Scandinavian (Sweden, Norway) and Karelian (Finland, northeastern Norway) subpopulations, with estimates of about 2,700 bears in each population. For more than a decade, the brown bear populations of Sweden and Norway have been monitored using DNA from feces, hairs, and tissue samples, applying the same eight microsatellite (STR) markers. While these few STRs may be informative to identify individuals, the small number applied pose limitations to assess closer genetic relationships, such as family groups. With the current process of introducing DNA-based monitoring of bears also in Finland, transnational monitoring of brown bears across Finland, Sweden and Norway using advanced SNP-technology is feasible. We tested an available SNP-chip, developed to study Scandinavian brown bears, on a set of representative individuals sampled across Finland to assess its suitability as a marker set for monitoring of brown bears in all of Fennoscandia. We found that the SNP-panel provided higher resolution for individual identification and relatedness estimation in Finland compared with the same STR marker set used in Scandinavia. Genetic diversity estimates based on SNPs were however lower in Karelia compared with Scandinavia, unlike STR-based estimates, indicating ascertainment bias in the Finnish population. Although the currently available SNP panel can be used for individual identification in Finland, we provide suggestions for how to improve the SNP-panel to enhance its suitability as a general genetic marker system for transborder monitoring of brown bears in Fennoscandia.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 73

Poster Presentation

Using the past to understand the present: how museum collections can help with protecting endangered species?

Beatriz Lacerda, Selina Brace, Laurent Frantz

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Over 40,000 species are currently threatened with extinction. Zoos play a huge role in mitigating this biodiversity crisis through ex-situ conservation. Captive breeding has become the strongest conservation tool to prevent the disappearance of sub-species, populations or even entire species. However, high levels of inbreeding and adaptation to captivity in confined populations can potentially increase their vulnerability to extinction when released in the wild. By comparing genetic information from ancient (museum collections) and modern individuals (zoos), it is possible to address not only historical levels of genetic diversity and population structure, but how they change over time due to anthropogenic pressures.

Applications

Date: Wednesday 31 August
Time: 12:15
Room: Pentlands West

Abstract 74

Oral Presentation

Sympatry of genetically distinct puffins in the High Arctic

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2 University of Oslo, Norway
3 NINA, Norway
4 High Arctic Institute, USA
5 Wolf Creek Operating Foundation, USA
6 Environment and Climate Change Canada, Canada

Arctic biodiversity is rapidly shifting with climate change, yet missing Arctic taxonomic baselines limit our understanding of how species are responding. The conservation of Arctic seabirds in particular, faces longstanding challenges from limited genetic information and rarity of Arctic samples. The Atlantic puffin is an iconic seabird present across the North Atlantic and High Arctic. Using whole genome sequencing, we recently identified four (previously undetectable) genetic units across the puffin’s distribution that were each geographically and/or phenotypic distinct. The most distinct genomic unit was present in the Arctic, though this was based only on East Atlantic individuals, leaving a significant information gap for conservation managers.

To address this knowledge gap, we sequenced six puffins from Thule (West Greenland). Interestingly, unlike all other sequenced puffin colonies, Thule is comprised of two distinct size phenotypes. Our sequencing data revealed this is because members of three distinct genetic units are present at Thule: the High Arctic unit, as well as the West and East Atlantic boreal units. Phenotypic differences corresponded with genetic divisions. Despite colony sharing and longstanding contact-mediated hybridization between genomic units in the East Atlantic, no recent interbreeding was visible at Thule. Reasonable genetic differentiation was also present between the West and East Atlantic High Arctic populations, warranting further investigation. We hypothesise that Thule could be a recent contact zone resulting from a climate change-mediated northward range shift of boreal puffins in the West Atlantic.

Technologies

Date: Tuesday 30 August
Time: 16:55/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 75

Speed talk & poster

Fast sequence-based microsatellite genotyping development workflow for any non-model species

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2 ECOBIOP, INRAE, Université de Pau et Pays de l'Adour, France
3 LAPAPEZA, University of Batna 1 Hadj Lakhdar, Algeria
4 EABX, INRAE, France
5 DECODE, Agrocampus Ouest, INRAE, France

Application of high-throughput sequencing technologies to microsatellite genotyping (SSRseq) has been shown to remove many of the limitations of electrophoresis-based methods and to refine inference of population genetic diversity and structure. However, early proof of concept and species specific development studies resulted in dispersed information making it cumbersome for prospective users to identify a clear path to SSRseq approach set up in species of new interest. To overcome these difficulties, we present here a streamlined SSRseq development workflow that includes microsatellite development, multiplexed marker amplification and sequencing, and automated bioinformatics data analysis. The access to allele sequence make it possible to derive haplotype-based genotypes accounting for all linked polymorphisms observed along the sequence. The workflow was successfully applied to develop powerful multi-allelic genotypic datasets in tens of species for both basic and applied studies in ecology, evolution and conservation.

Technologies

Date: Wednesday 31 August
Time: 11:45
Room: Pentlands East

Abstract 76

Oral Presentation

Diet and trophic niche overlap in chamois, red deer and domestic sheep in the Italian Alps

Francesca Angela Lioce, 1, 2, 3, Crestanello B.1, Pertoldi C.3, Traba J. 4,5, Donini V. 6, 7, Partel P. 8, Mustoni A. 9, Bertorelle G.2, Hauffe H. C.1

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5 Centro de Investigación en Biodiversidad y Cambio Global (CIBC), Universidad Autónoma de Madrid, Facultad de Ciencias, Madrid, Spain
6 Stelvio National Park, Sustainable Development and Protected Area Service, Autonomous Province of Trento, Cogolo di Peio (TN), Italy
7 Stelvio National Park, Bormio, Italy
8 Paneveggio - Pale di San Martino Natural Park, Primiero San Martino di Castrozza (TN), Italy
9 Adamello-Brenta Natural Park, Strembo (TN), Italy

Understanding the process underlying interspecific competition is pivotal to investigating the future ability of animal species to adapt to changing environments. Coexisting species can avoid competition by partitioning resources, but when these are limited a potential for competition can occur, possibly producing a decrease of fitness. In the Alps, red deer numbers have been increasing, which was hypothesized to impact chamois populations through interspecific competition. In addition, as domestic sheep are moved to Alpine pastures in summer, chamois share the habitat with this livestock, potentially leading to multispecific competition.

In this study, we used DNA metabarcoding of the chloroplast trnL intron and the ITS1 and ITS2 internal transcribed spacers to describe the diet and to evaluate dietary niche overlap of the chamois, red deer and domestic sheep. 520 fresh fecal pellets were collected for each species from seven areas characterized by one of three combinations of species interaction: i) areas where only chamois graze; ii) areas where chamois coexist with red deer; iii) areas where chamois is present with both red deer and sheep.

At family and genus level, we detected high similarity in diet between the three species, but we observed diet segregation between chamois and domestic sheep and between chamois and red deer in periods when resource availability was expected to be limited. However, in general, the presence of competitors did not significantly affect the composition of chamois diet. We discuss the results considering ongoing climate change and habitat fragmentation and possible applications to wildlife management.

Technologies

Date: Wednesday 31 August
Time: 11:15
Room: Pentlands East

Abstract 77

Oral Presentation

A field-friendly, low-cost genotyping approach for high and low quality DNA using the MinION portable sequencer

Samantha López-Clinton1*, Mrinalini Watsa2*, Rachel A. Voyt3, Axel Jensen1, Gideon Erkenswick5, Katerina Guschanski6

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6 University of Edinburgh, Ashworth Laboratories, United Kingdom

Genetic and genomic research is important for the conservation of biodiversity and threatened species worldwide. It is clear that most of the world's biodiversity is found in developing countries, which incidentally possess limited sequencing services, technologies and access to information. Thus, in situ conservation holds the key to more inclusive, accessible and successful conservation efforts, and for conservation genetics research to be able to respond better to local needs. In addition, it is rarely straightforward and often expensive to obtain high quality DNA from threatened species in the wild. With all of this in mind, we decided to develop a robust field-friendly approach for genotyping two species of Amazonian primates using both high and low-quality samples. Our approach makes use of informative SNPs that are numerous, found throughout the genome, and can be amplified from degraded DNA, which is a common feature in low quality and/or non invasive samples. We used 14 high-quality Illumina sequenced genomes to construct a set of 226 SNPs that are informative of species (18 SNPs), sex (15 SNPs) and individual identity (193 SNPs). Of the latter set, 44 are shared between species and the rest are species-specific. We designed primers for these SNPs in a Genotyping-in-Thousands by sequencing approach, which uses multiplexed PCR products of several hundred SNPs, generating genotypes for thousands of individuals in a single run. To make our pipeline more reproducible, we are modulating our entire workflow with Snakemake.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 78

Poster Presentation

Characterizing the stability of and identifying differences in the fecal microbiome between two cheetah (Acinonyx jubatus) populations

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The health of endangered animals is critical for their future survival. Gut health and its relationship to gut microbiota are important aspects that may be influential in the care and well-being of endangered species, such as the cheetah. With only 7,100 cheetahs in the wild, it is important to maintain captive populations as insurance policies against extinction. Unfortunately, cheetahs in human care experience several health conditions, including gastrointestinal (GI) diseases, which pose significant risks to survival, welfare, and breeding success. In contrast, these potentially terminal GI diseases are rarely observed in wild cheetahs. We hypothesize this is due to the notable difference in diet between wild cheetahs and those in managed facilities. In this study we characterized the stability of the fecal microbiota for best sampling practices and characterized and identified differences in cheetah fecal microbiota between two captive populations (Front Royal, VA, USA and Otjiwarongo, Namibia) consuming different diets. Fresh fecals from 16 cheetahs (Virginia, n = 8; Namibia n = 8) were analyzed every 24 hours for five days for bacterial content using 16S rRNA sequencing. Fecal microbiota stability was longer in Namibia. Cheetahs in Namibia also had higher number of bacterial taxa, more phylogenetically diverse bacteria and were compositionally distinct from cheetahs in the USA. We also found significant differences in predictive functions of the fecal microbiota related to dietary metabolism and disease. Overall, these findings warrant further investigation into the influence of diet and population origin on the gut microbiota and health of cheetahs.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 79

Poster Presentation

Uncovering Amazonian Biodiversity: Genomics of Linnaeus’s two-toed sloth (Choloepus didactylus) supports three distinct lineages

Luísa Schlude Marins1,2,3*, Larissa Souza Arantes1,2,* , Benoit de Thoisy4, Marta Svartman5, Fabrício Rodrigues dos Santos5, Flávia Miranda6, Mariluce Rezende Messias7, Camila J. Mazzoni1,2

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6 Laboratório de Biodiversidade e Saúde, Universidade Estadual de Santa Cruz, Ilhéus, Brazil
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*Larissa Souza Arantes and Luísa Marins contributed equally to this work.

As the single mammalian lineage to have evolved exclusively in the Americas, Xenarthrans are an intriguing but still understudied taxon. Linnaeus’s two-fingered sloth (*Choloepus didactylus*) inhabits the dense rainforest canopies of the Amazon and rarely comes to the forest floor, making it a challenging species to study and sample. The goals of our project are to investigate the evolutionary history and phylogenetic relationships within the genus Choloepus, and how they correlate to the history and biogeography of Amazonia. With this purpose, we have generated the first genomic dataset for the species. We present three low coverage genomes of Linnaeus’s two-toed sloths from distant Amazonian regions (French Guyana, Rondônia and Pará) and reduced representation genome data obtained with the method 3RADseq comprising ~23.000 SNPs for 27 sloths from 4 populations. Phylogenomic analysis including over 900 orthologous genes and population genetic clustering support

over 900 orthologous genes and population genetic clustering support three distinct sloth lineages, with different levels of heterozygosity and inbreeding. The genetic distance between the Rondônia population and the others is similar to that of two different three-fingered sloth species, and this population was found to have diverged from the others 2-5 Mya. Studies including other sources of data - such as morphology, ecology and behaviour - will be essential to confirm the taxonomic status of the populations investigated here and other potential divergent populations that remain unsampled. Obtaining a more accurate understanding of the taxonomic composition of the genus *Choloepus* is essential for the Genomics of Linnaeus's two-toed sloth (*Choloepus didactylus*) supports three distinct Amazonian lineages assessment of their threat level and thus to the conservation of these elusive tree-dwellers.

Applications

Date: Tuesday 30 August
Time: 15:10/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 80

Speed talk & poster

Conservation genomics of red squirrels in Scotland: understanding diversity in a key stronghold

Melissa M. Marr1, Peter W. W. Lurz1, Liam Wilson1, Elspeth Milne1, Katie Beckmann1, Emily Humble1, Rob Ogden1

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The Eurasian red squirrel, *Sciurus vulgaris*, is an icon of conservation science. In Britain, the species has suffered catastrophic declines due to habitat loss and ecological and disease-mediated competition from the introduced North American grey squirrel, *Sciurus carolinensis*. This species has supplanted the red squirrel throughout the majority of its historic range in what is one of the best-known examples of a native species being replaced by an invasive congener. Scotland is a key stronghold for red squirrels, harboring over 80% of the remaining British population and the majority of remnant genetic diversity. However, to date, little genomic research into red squirrels in Scotland has been attempted. This study presents results from the first whole-genome research into the conservation genetics of red squirrels in the region. An ambitious program of WGS from spatially-distributed red squirrels across Scotland has been undertaken with the aims of determining population structure, demographic history and genetic diversity within and among populations. This information will be used to assess current management practices and to inform future applied conservation strategies of this regionally endangered species.

Applications

Date: Wednesday 31 August
Time: 13:30
Room: Pentlands West

Abstract 81

Oral Presentation

Hybridization may aid genetic rescue across fragmented populations of an endangered East African passerine, Zosterops silvanus

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6 University of Würzburg, Germany.

Habitat loss and fragmentation is having a devastating effect on endemic tropical species, where land conversion due to urbanisation and logging continue to encroach on many natural forests. While for many species this results in population bottlenecks and consequent loss of genetic diversity, in some cases this may enhance dispersal propensity. In such instances, introgressive hybridization may enable gene flow across species barriers, which may result in new genetic material relevant for adaptation. Consequently, hybridization has been suggested as an important mechanism for enabling evolutionary rescue, i.e. the recovery of threatened populations through rapid adaptation to novel environments. Here, we use *Zosterops silvanus*, an endangered East African highland species suffering severe habitat fragmentation in the Taita Hills, to investigate if evolutionary rescue, and associated increased genetic diversity, occurs with the lowland congener *Zosterops flavilateralis*. Empirically parameterised individual-based modelling of these species reveals that evolutionary rescue via dispersal and hybridization is likely. Using whole genome resequencing of *Z. silvanus* and *Z. flavilateralis* populations, we then present population genomic results to test these findings. At the population level, we show admixture propensities across seven remnant forest fragments inhabited by *Z. silvanus*, and the lowland congener *Z. flavilateralis*. We then assess pairwise divergence and genetic diversity across individual genomes to determine the nature and extent of hybridization between these species. Our results provide evidence of introgressive hybridization in a species experiencing continued habitat loss, and demonstrate the potential utility of targeted gene flow to accelerate adaptation of endangered species to novel environments

Abstract 82

Speed talk & poster

Genetic divergence in wild populations of Indian major carp, Cirrhinus mrigala (Hamilton, 1822) across India, an assessment from ATPase6/8 mitochondrial gene analysis

Prachi Masih1, Rajeev K. Singh1, Vindhya Mohindra1, Rupesh K. Luhariya1, Rakhi Das, Arti Gupta1, J. K. Jena1, Kuldeep K. Lal1

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Cirrhinus mrigala or mrigal (Family: Cyprinidae) is a native inhabitant of the Indus and Ganga River systems and is an important aquaculture species of south Asia. During 2019, mrigal contributed 0.44% to global aquaculture production. The knowledge of the genetic diversity of wild relatives is important for the conservation of genetic resources and the genetic improvement of aquaculture species. The present study evaluated ATPase6/8 gene sequence (842 bp) of MtDNA for determining genetic variation demographic history and identifying stock in (n=285) from thirteen rivers of four river systems. Average nucleotide frequencies were A>C>T>G and is A+T rich. High haplotype diversity and low nucleotide diversity observed, indicates loss of haplotype diversity due to bottleneck and accumulation of new haplotypes during population expansion. Out of twenty-six haplotypes, five haplotypes were shared and twenty-one were unique. They radiate from h1 (the most common in all populations) or from subsequent haplotypes showing mutations during the time. The overall significant FST (0.098) showed that the population is moderately structured indicating the presence of detectable genetic differentiation in the population. The differentiation among populations was partitioned and found to be 10.46% within-group and 90.16% within populations. The present results indicated that the ATPase6/8 gene can be a useful marker for determining genetic diversity in *C. mrigala*.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 83

Poster Presentation

Evolution of individual chromosomal crossover rate variation in a wild house sparrow population (Passer domesticus)

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4 Department of Ecology and Genetics, Uppsala University, Uppsala, Sweden

Chromosomal crossing-over during meiosis is an essential part of sexual reproduction and an important driver of novel genetic diversity. Understanding this process may have important outcomes for conservation efforts in systems with small population sizes, as having more crossovers prevents the accumulation of deleterious alleles, allows faster responses to selection, and protects against errors in chromosome segregation, a leading cause of infertility. However, forming crossovers also increases the risk of local mutations, chromosomal rearrangements, and/or can break down of favourable allele combinations previously built up by selection. This cost-benefit dynamic is likely to vary depending on evolutionary context leading to an expectation of variation in crossover rate at the individual, population, and species levels. Understanding these contexts will improve our ability to monitor and respond to changes in a population's genetic diversity. Here, we investigate individual crossover rate variation in a wild population of Passer domesticus by characterising individual Autosomal Crossover Counts (ACC), estimating its heritability, and investigating genomic variants associated with ACC through genome wide association studies (GWAS). We found that crossover rates varied both between and within chromosomes and that females had higher crossover rates than males. In addition, we found that crossover rates were heritable in both sexes and likely to be controlled by many small effect loci throughout the genome. These findings add to the growing body of research on trends in crossover rate variation and serve as a stepping-stone for further analysis into associations between individual crossover rate and individual reproductive success and survival.

Applications

Date: Tuesday 30 August
Time: 15:55/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 84

Speed talk & poster

DNA-based methods for monitoring the Irish Damselfly (Coenagrion lunulatum)

Claire McFarlane1, Sarah Helyar1, Lesley Lancaster2, Paul Caplat1

1 Queens University Belfast, Ireland.
2 University of Aberdeen, Scotland.

Odonates (dragonflies and damselflies) have long been established as important bioindicators of freshwater habitat quality due to their high sensitivity to environmental change and position at the top of the invertebrate food chain. Global assessment has concluded that 16% out of the 6,016 species are at risk of extinction (categories CR, EN, VU and NT combined), largely due to habitat loss and eutrophication of their freshwater habitats from pollution. One of these, the Crescent Bluet or 'Irish' Damselfly (*Coenagrion lunulatum*), is IUCN listed as Vulnerable in Ireland and has shown significant declines across much of its' European range. This project is a collaboration with stakeholders across Ireland to increase our understanding of this species' biogeography and life history with the goal of informing conservation management strategies. Restriction-site associated DNA sequencing (RADseq) will be used to investigate the population genetic structure of *C. lunulatum* in Ireland to establish levels of genetic diversity, population connectivity and investigate dispersal abilities. Phylogeographic analysis will be used to investigate the relationship of Irish populations to others across their global range, which is important for management due to the recent discovery of *C. lunulatum* in Ireland (1981) and its' patchy distribution. Lastly, development of an eDNA assay to detect *C. lunulatum* from pond water samples will overcome the difficulties of larval identification and increase efficiency in identifying breeding ponds. Finally the genetic information will be combined with ecological data via Species Distribution Modelling to predict the future distribution across Europe, and facilitate appropriate species management.

Abstract 85

Oral Presentation

Genomic analysis of Flame Shells (Limaria hians) to inform nature conservation

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2 NatureScot, Scotland

Flame shells (*Limaria hians*) are a species of bivalve present across the northeast Atlantic. They have high ecological importance due to the dense beds that they form; they use byssal threads to bring together debris, raising and stabilising the sea floor and thus creating habitat for hundreds of species. Increasingly more of these beds are being discovered off the west coast of Scotland, and elsewhere. Little is known about the biology of flame shells. I am using a genomic approach to understand population connectivity and design a set of genetic tools that can be used to inform flame shell management throughout their range. I used RAD-seq to assay genomic variation across 6 populations from Scotland and the Republic of Ireland. Results revealed little genetic differentiation among the populations sampled in Scotland, but clear differentiation between Scottish and Irish populations. I am using the RAD dataset to develop targeted genotyping-by-sequencing assays for a subset of SNPs, with the aim of including more populations into this study and potential for use in future research. With this knowledge we can begin to understand flame shell populations' potential for recovery, and we can consider MPA design for the future of this species.

Applications
Date: Tuesday 30 August
Time: 15:10/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 86

Speed talk & poster

Characterization of selected toll-like receptor genes in cheetahs (Acinonyx jubatus) compared to the sympatric occurring leopard (Panthera pardus) and its implication for conservation

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3 World Wide Fund for Nature South Africa, Newlands, South Africa
4 Senckenberg Biodiversity and Climate Research Centre, Frankfurt am Main, Germany
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6 Department of Behavioural and Cognitive Biology, University of Vienna, Vienna, Austria
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Cheetahs are long known for their genetic impoverishment and many conclusion have been drawn to the species decreasing populations. Nevertheless, recent studies indicate more genetic diversity and structure than previously thought. A good indicator for diversity and a species' health is the innate immunity system, since it represents the initial 'firewall' of an organism against viruses and other pathogens. The more diverse the system, the higher the innate immune response. Toll-like receptors (TLRs) are important membrane-spanning proteins and play a key role in recognition of microbes at physical contact zones such as the mucosa. Little is known about TLRs in felids, and we compare four selected TLR genes in cheetahs to sympatric occurring leopards to evaluate the observed diversity. Understanding the immune competence of threatened species is especially important for conservation management, because it is a critical aspect of disease resistance and the resilience of a population. Maintaining the diversity of immune response genes as functionally important genomic regions for local adaptation to pathogens contributes to the species' fitness and potentially to its long-term survival. Considering the ever-increasing impact of humans, their livestock and pets on protected habitats, the adaptive potential of wild endangered species at the human-wildlife interface will be essential for preserving biodiversity in a functional ecosystem.

Applications

Date: Tuesday 30 August
Time: 14:25/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 87

Speed talk & poster

Genetic and phenotypic comparison of populations resulting from translocations and natural colonizations

José F. Meléndez-Cal-y-Mayor1

1 University of Zurich, Switzerland

There is a need to understand the genetic consequences of natural colonizations and conservation translocations and how they affect the performance of individuals. This may lead to a better understanding of why some colonizations and translocations are successful while others fail. Here we compare the genetic diversity of populations resulting from natural colonizations and conservation translocations and compare them to natural populations (colonizations occurred after the construction of new ponds). We use Midwife and Natterjack toad populations as examples because both species are undergoing population declines in Europe. Additionally, we used a common garden experiment to quantify differences in the life history traits of Natterjack toad individuals taken from natural and translocated populations. We found that although some populations had a bottleneck event and parameters such as distance, open lands, large roads, hedgerows and small roads were found to reduce genetic diversity, translocated and colonized populations show similar genetic diversity as natural population. The comparison of life history traits of translocated and natural populations showed that survival of translocated individuals was reduced in translocated populations. Taken together, the results suggest that differences between natural and translocated populations are small. This suggests colonization and translocation as conservation strategy seem to be successful.

Applications

Date: Wednesday 31 August
Time: 11:15
Room: Pentlands West

Abstract 88

Oral Presentation

Conservation genetics for the management of black rhinoceros (Diceros bicornis michaeli) in Tanzania

Ronald. V. K. Mellya 1,2, J. Grant C. Hopcraft1, Emmanuel S. Machа2, Elizabeth Kilbride1, Moses Otiende4, Ernest M. Eblate3, Anubhab Khan 1, Barbara K. Mable1

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2 Tanzania National Parks, Tanzania
3 Tanzania Wildlife Research Institute, Tanzania
4 Kenya Wildlife Services, Kenya

Molecular genetic analyses provide a means to study some unknown critical aspects of species biology that are difficult to determine directly and are important for conservation of threatened species. In Tanzania, poaching removed almost 10,000 rhinos, resulting in a small number of isolated populations. Following intensive protection and reintroduction, as of 2018 there were 161 individuals remaining in six populations that are managed separately. However, the genetic structure of these closed populations was not known. In this study we have combined observational pedigree data, mtDNA control region and whole genome sequences to assess the genetic diversity of all extant Eastern black rhino populations in Tanzania in relation to the following questions: What is the current population genetic structure of Tanzanian populations and how have past translocations impacted genetic diversity and inbreeding? How can we use this information to inform current and future management practices? Based on the mtDNA, we found loss of genetic diversity in the extant populations lack of allele sharing between geographically close populations but that recent translocations have restored some of the past genetic diversity. Observational pedigree data indicate that native populations have higher mean kinship than translocated populations. Whole genome sequencing has revealed high level of inbreeding in the native rhinos. Therefore, this study has revealed the genetic relationships among the Eastern black rhinoceros in Tanzania, and the information can be used to inform population viability models, assist with planning translocations and reintroduction policies and the management strategy for maximizing distribution of genetic variation across populations.

Applications

Date: Thursday 1 September
Time: 11:30
Room: Pentlands West

Abstract 89

Oral Presentation

Following the trajectories of adaptive loci over time for conservation and management of Atlantic salmon

Antti Miettinen1, Johan Dannewitz2, Tapani Pakarinen3, Stefan Palm2, Lo Persson4, Craig Primmer1,5, Atso Romakkaniemi6, Johan Östergren2, & Victoria Pritchard7

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2 Department of Aquatic Resources, Institute of Freshwater Research, Swedish University of Agricultural Sciences, Drottningholm, Sweden
3 Natural Resources Institute Finland, Helsinki, Finland
4 Department of Wildlife, Fish and Environmental Studies, Swedish University of Agricultural Sciences, Umeå, Sweden
5 Institute of Biotechnology, University of Helsinki, Helsinki, Finland
6 Natural Resources Institute Finland, Oulu, Finland
7 Rivers and Lochs Institute, Inverness College, University of the Highlands and Islands, Inverness, United Kingdom

How organisms are adapted to their local environment at the genomic level is a key question in evolutionary biology. It is also essential to consider for the conservation and management of threatened populations, such as many harvested Atlantic salmon (*Salmo salar*) stocks. An archive of salmon scales spanning almost a century provided us with a window to the past, allowing us to compare historical and contemporary adaptive genetic diversity and to interpret how human-induced selective pressures have influenced the genetic variation of salmon populations in the northernmost Baltic Sea region. Using genome-wide SNP data, we identified candidate loci under local selection in the largest wild Baltic salmon population. Some of these loci are known to underlie important life-history variation in salmonids. Changes in the allele frequencies of the loci may indicate signals of evolutionary responses in these genomic regions. To understand the impact of spatially and temporally varying fishing pressure on these loci over time, we monitored their allele frequency trajectories by studying the genetic composition of salmon harvested in a commercial and recreational fishery between 1928 and 2020. We observed strong temporal changes in the allele frequencies of large-effect loci linked with ecologically important

traits, which has potential conservation and management implications for Baltic salmon. Our study provides an example of using genomic approaches to improve our understanding of adaptive differentiation in wild populations, and applying this information to infer, monitor and mitigate human impacts on adaptively important genetic variation in nature.

Applications

Date: Wenesday 31 August
Time: 14:15
Room: Pentlands East

Abstract 90

Oral Presentation

Using ddRAD seq to infer historical population changes and current isolation in a cold-adapted butterfly

Melissa Minter1,2*, Kanchon K Dasmahapatra1, Chris D Thomas1, Mike D Morecroft3, Athayde Tonhasca4, Gavin J Horsburgh2, Kathryn Maher2, Króna McMonagle1 & Jane K Hill1

1 Leverhulme Centre for Anthropocene Biodiversity, Department of Biology, University of York, United Kingdom
2 NERC Environmental Omics Facility, University of Sheffield, Western Bank, Sheffield, United Kingdom
3 Natural England, York, United Kingdom
4 NatureScot, Battleby House, Perth, United Kingdom

Cold-adapted species are at considerable risk from climate change, and our study examines how historical population changes influence current patterns of genetic diversity. The current UK distribution of the cold-adapted butterfly *Erebia epiphron* represents post-glacial colonisations and subsequent upslope retractions in mountainous regions in England (Lake District) and Scotland (Grampian mountains). We use ddRAD seq data to understand genetic differences in UK populations, along with understanding population changes over time. Our data confirm genetic separation of England and Scotland populations and demonstrate 17% less genetic diversity in English populations than in the larger Scottish populations, and reveal genetic separation of England's Lake District into distinct east and west populations. Our genetic analyses infer population changes over time with respect to post-glacial climate fluctuations and Neolithic human land-use changes. We reveal butterfly population declines during post-glacial colonisation of Britain (~80-95% reduction), followed by population increases in line with Neolithic tree clearances (~5kya), creating more open grassland habitat for *E. epiphron*. Our findings suggest the importance of open grassland habitat for future conservation of *E. epiphron*, and highlights potential risks of further genetic isolation in England which could be exacerbated under future climate change.

Applications

Date: Wenesday 31 August
Time: 14:45
Room: Pentlands West

Abstract 91

Oral Presentation

Genomic diversity decline over time in avian endangered species

Hernán E. Morales1, Georgette Femerling Romero1, Xufen Liu1, Cock Van Oosterhout2, & Tom Gilbert1

1 Globe Institute, University of Copenhagen
2 School of Environmental Sciences, University of East Anglia

Population decline has put many species on the path of collapse and extinction. Stopping this decline ("Reverse the Red") is not enough to tackle the associated hidden evolutionary costs, most notably genomic erosion which compromises the long-term viability and resilience of species. Crucially, the conditions that lead to genomic diversity decline in response to population decline are currently largely unknown. Here we use a population genomics approach to compare re-sequenced whole-genomes of three pre-decline (100+ years old) vs. post-decline (contemporary) endangered bird species (Seychelles paradise flycatcher – Vulnerable-, regent honeyeater -Critically Endangered -, and whooping crane – Endangered-). The three species suffered distinct population collapse and conservation management in the last few decades. We show that loss of genomic diversity and extinction risk depends on the demographic trajectory, mode of collapse, connectivity, and conservation management. We developed a forward-in-time simulation approach to better understand how genomic erosion have likely impacted these species and to project expected trajectories into the future, to show the importance of incorporating genomics into species conservation assessments.

Abstract 92

Speed talk & poster

Developing Multiplex SNPSTR Marker Sets For Endangered Species

Annika Mozer1, Albia Consul1, Jonas Astrin1

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Overexploitation is one of the major drivers of the biodiversity loss we experience today. One aspect of overexploitation is the illegal trade of wild animals, which is estimated to account for 7-23 billion USD annually.

To better detect and counteract wildlife crimes, the BMBF-funded FOGS project (Forensic Genetics for Species Protection) is establishing novel marker sets for species illegally traded in Europe. Further, an online portal is being set up, which researchers and authorities can consult to gain access to the published marker sets. FOGS collaborates with customs, nature conservation authorities, and NGOs to target species recently affected by illegal wildlife trade and thus prevent population declines and ultimately extinction.

The developed marker sets are conceived as multiplex reactions containing 20 validated SNPSTR-markers per species. They combine microsatellites with SNPs in the flanking region. Such markers can be used e.g. for individual identification when a smuggled product or a carcass at a crime scene needs to be matched, in kinship analyses for certifying breeds, or population studies.

To establish a new SNPSTR set the genome is first screened for suitable STRs. Subsequently, a multiplex reaction is designed and carried out for 10 animals per species. After sequencing, the samples are analysed for their variation and 20 markers with a variable STR and SNPs in the flanking region are selected.

FOGS has successfully established SNPSTR sets for several species of vertebrates and continues to expand the list.

Applications

Date: Wednesday 31 August
Time: 15:45
Room: Pentlands West

Abstract 93

Oral Presentation

Major histocompatibility complex genes and age are associated with reproduction of the endangered Japanese Golden Eagle in captivity

Annegret Moto Naito-Liederbach1, Yu Sato2, Rob Ogden3, & Miho Murayama1

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2 National Institute for Environmental Studies, Japan
3 The Royal (Dick) School of Veterinary Studies, University of Edinburgh, United Kingdom

The Japanese Golden Eagle (*Aquila chrysaetos japonica*) is an endangered subspecies of the Golden Eagle, with ca. 500 individuals remaining in the wild. Captive breeding is taking place in 11 zoos across Japan (N = 48), but only a few pairs are reproducing successfully. To address this issue, we examined the major histocompatibility complex (MHC) DRB exon 2 region, which is known to influence immunocompetence and reproduction in vertebrates. We obtained DRB genotypes from 10 captive pairs (10 males, 8 females) of Japanese Golden Eagles using next generation amplicon sequencing. The number of DRB alleles, mean amino acid distances and proportion of shared alleles between males and females of each pair were calculated. Studbook relatedness, years paired, and age were also obtained for a total of 19 pairs (including the abovementioned 10). Using generalized linear mixed models, we tested the effect of these variables on clutch size, proportion of fertilized and hatched eggs. We found the proportion of fertilized eggs to decrease with male age, which may be due to fewer mating and lower fertility in older males. In addition, the proportion of hatched eggs increased with the number of DRB alleles in females, although statistically non-significant. Higher MHC diversity can positively affect body condition, so females with more DRB alleles may be able to allocate more resources towards egg production and post-laying care, increasing the chances of hatching. We hope these results can inform captive breeding strategies and assist in improving reproductive success of captive Japanese Golden Eagles.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 94

Poster Presentation

High Molecular Weight DNA extraction protocols for non-model plant species – the first step in long-read sequencing

Kanae Nishii1, Laura L Forrest1, David Bell1, Markus Ruhsam1, Pete M Hollingsworth1, Caroline Howard2, Maja Todorovic2 & Michelle L Hart1

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2 Wellcome Sanger Institute, UK

Advances in genome sequencing technologies are a powerful catalyst for realising ambitious genome-level projects such as The Darwin Tree of Life (DToL). The aim of DToL is to sequence the genomes of all c. 70,000 species of eukaryotic organisms in Britain and Ireland, producing fully annotated, chromosome level genome assemblies. To obtain this level of sequence accuracy, long-read sequencing technology such as PacBio HiFi must be employed, and employed at scale. High quality, high molecular weight (HMW) DNA is a must in the successful utilisation of long-read technologies. However, many plant species are rich in secondary metabolites that often co-precipitate with DNA during DNA extraction, and these can be a block in Next Generation Sequencing (NGS) protocols. Teams at the Royal Botanic Garden Edinburgh (RBGE) and The Wellcome Sanger Institute have developed several HMW DNA extraction methods suitable for NGS. The main steps of the DNA extraction protocol have been investigated individually and optimized, and pre-treatments and crude extraction steps added to remove contaminating compounds. The effects of commonly used DNA extraction buffers on downstream library preparation and sequencing have also been investigated. We summarize the keys steps and recommended modifications for obtaining high quality HMW DNA from several non-model plant species, and comment on their application in high-throughput genomic studies.

Applications

Date: Thursday 1 September
Time: 11:00
Room: Pentlands West

Abstract 95

Oral Presentation

Improving Jaguar conservation efforts through genomics

Paola Nogales-Ascarrunz1,2, Enzo Aliaga -Rossel 3, Rosie Drinkwater2,4, Stefan Prost 5,6,7 Laurent Frantz2,4

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4 Paleogenetics Group, Department of Veterinary Sciences, Ludwig-Maximilian-Universität, Germany
5 Department of Behavioural and Cognitive Biology, University of Vienna, Austria
6 University of Veterinary Medicine, Konrad Lorenz Institute of Ethology, Austria
7 Natural History Museum Vienna, Central Research Laboratories, Austria
8 South African National Biodiversity Institute, South Africa

The jaguar (*Panthera onca*) is a keystone species in the Neotropics and the only representative of the genus *Panthera* found in the Americas. Their historical distribution ranged from the southwestern United States all the way south to central Argentina. In recent times however, they have lost more than half the original range. The main threats for this species are habitat loss and fragmentation, persecution, human-wildlife conflict, and illegal trafficking of body parts. In Bolivia, the illegal trafficking of jaguar parts for Traditional Chinese Medicine has increased in the last years which is likely to be a major driver of the population decline. Moreover, information on jaguar genetics is incomplete for Bolivia. The National Conservation action plan for Bolivia indicates that there is an urgent need to obtain genetic data for this species to be able to make evidence-based decisions and develop management strategies. During 2017 and 2020 we collected 29 samples of jaguar skins provided by local hunters, traffickers, and cattle ranchers across the Bolivian jaguar distribution. We performed low coverage whole-genome sequencing to investigate population structure, potential gene-flow between regions, and genetic diversity/health. These data will form the base for future conservation action plans in Bolivia. Furthermore, the insights gained from population structure might also help us to identify possible source regions for the illegal trade in jaguar body parts. Finally, this is the first animal genomics project in Bolivia and highlights the importance of genomic analysis as a tool to directly inform conservation actions in Bolivia.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 96

Poster Presentation

Origin and admixture of Indonesian cattle

Casia Nursyifa1, Xi Wang1, Laura Bertola1, Genis Garcia Erill1, Mikkel Holger Strander Sinding1, Rasmus Heller1

1 Section for Computational and RNA Biology, Department of Biology, University of Copenhagen, Copenhagen, Denmark

Genetic diversity is a crucial resource in livestock breeds, determining their genetic load and ability to adapt to new environments or respond to artificial selection. Indonesian cattle breeds potentially have high genetic diversity due to having admixed ancestry from zebu (*Bos indicus*) and banteng (*Bos javanicus*). We performed whole genome sequencing on 215 local cattles from Aceh, Pesisir, Pasundan, Jabres, Madura, Sumba Ongole, Bali cattle breeds. Our results show that Indonesian cattle breeds have the highest reported genetic diversity of any cattle populations worldwide. This is caused by surprisingly large amounts of banteng ancestry, reaching up to 40% in the Madura breed. We discuss the implications of such large amounts of wild bovine ancestry in domesticated cattle breeds, including whether or not it is beneficial for the recipient cattle. Our results have implications for understanding the sources of genetic diversity in domesticated species and the dynamics of livestock/wildlife admixture.

Policy

Date: Thursday 1 September
Time: 10:45
Room: Pentlands East

Abstract 97

Oral Presentation

Bringing together approaches to reporting on within species genetic diversity

David O'Brien1,2, Linda Laikre3, Sean Hoban4, Michael W. Bruford5, Robert Ekblom6, Martin C. Fischer7, Jeanette Hall1, Christina Hvilsom8, Pete Hollingsworth2, Francine Kershaw9, Cinnamon S. Mittan10, Tarek A. Mukassabi11, Rob Ogden12, Gernot Segelbacher13, Robyn E. Shaw14, Cristiano Vernesi15, Anna J MacDonald16

1 NatureScot, UK
2 Royal Botanic Garden Edinburgh, UK
3 Stockholm University, Sweden
4 Morton Arboretum, USA
5 Cardiff University, UK
6 Swedish Environmental Protection Agency, Sweden
7 ETH Zurich, Switzerland
8 Copenhagen Zoo, Denmark
9 Natural Resources Defense Council, USA
10 Michigan State University, USA
11 Benghazi University, Libya
12 Edinburgh University , UK
13. Freiberg University, Germany
14 Murdoch University, Australia
15 Fondazione Edmund Mach, Italy
16 Australian Antarctic Division, Australia

Genetic diversity is one of the three main levels of biodiversity recognised in the Convention on Biological Diversity (CBD). Whilst it is fundamental for adaptation to environmental change, genetic diversity is nonetheless under-reported within global and national indicators. When it is reported, the focus is often narrow and confined to domesticated or other commercial species. Several approaches have recently been developed to address this shortfall in reporting on genetic diversity of wild species. Whilst multiplicity of approaches is helpful in any development process, it can also lead to confusion amongst policy makers and heighten a perception that conservation genetics is too abstract to be of use to organisations and governments. The developers of five of the different approaches have come together to explain how various approaches relate to each other and propose a scorecard, as a unifying reporting mechanism for genetic diversity. We believe the proposed combined approach captures the strengths of its components and is practical for all nations and subnational governments. It is scalable and can be used to evaluate species conservation projects as well as genetic conservation projects.

Collections

Date: Tuesday 30 August
Time: 16:25
Room: Pentlands (East/West)

Abstract 98

Oral Presentation

Establishing a viable cell culture banking network for endangered species conservation in Asia

Manabu Onuma[1], Takaharu Kawashima[1]

[1] National Institute for Environmental Studies, Japan

A viable cell culture banking is one option that could support and promote endangered species conservation. The Frozen Zoo in San Diego Zoo Wildlife Alliance has pioneered this kind of activity. The National Institute for Environmental Studies in Japan has been cryopreserving genetic resources from endangered species (mainly avian and mammalian species) since 2002. To date, around 4,000 individuals have been accepted, and 75,000 tubes have been cryopreserved. The NIES collections include viable cells from the Okinawa rail (*Gallirallus okinawae*), the Japanese crested ibis (*Nipponia nippon*), the Tsushima leopard cat (*Prionailurus bengalensis euptilurus*), etc. NIES has also attempted to expand the viable cell culture banking project to other countries, encompassing the biodiversity hotspots of Asia, to support ex-situ conservation activities for endangered species distributed in the area including the Asian rhinoceros, primates, tigers, and Asian bears. NIES has established a network among three countries, Nepal, Malaysia, and Singapore so far. Among them. the viable cell culture banking program has already started in Singapore. Once the viable cell culture bank is established, cryopreserved viable cells will be used for various kinds of research on endangered species, including reproductive research, cell biology research, infectious disease research etc. The results of such research will be applied to improving endangered species conservation in-situ and ex-situ. If this cyclic pattern of conservation activities (viable cell banking-research-field application) works well, some endangered species may be removable from endangered species categories. I propose to call this field "Conservation Cell Biology".

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 99

Poster Presentation

Combatting illegal trade in animal products by rapid on-site DNA sequencing

Emily Patterson1, Jon Wetton1, & Mark Jobling1

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The illegal wildlife trade (IWT) is a key driver of species extinction. One challenge in combating this multi-billion-dollar industry is the difficulty in recognising protected species, particularly once processed. In such cases, DNA barcoding is the method of choice for species identification. This requires the transfer of samples to a laboratory for analysis using bulky and expensive equipment, with results obtained weeks later. Advances in sequencing technologies mean it is now possible to undertake this process outside of a laboratory, enabling rapid species identification on-site. This project aims to establish methods for the rapid identification of vertebrate species using cheap and simple methods for DNA extraction, amplification, and sequencing using Oxford Nanopore Technologies' MinION device. To make the method as 'universally' applicable as possible we designed primers for four barcodes (cytochrome c oxidase subunit 1, cytochrome b, and 12S and 16S ribosomal RNA) using mitogenome sequences of >200 vertebrate species. We tested barcode performance across 83 known vertebrate species (45 mammals, 19 birds, 12 fish, 6 reptiles, one amphibian), and obtained successful species- (n=69) or genus- (n=14) level identification. We additionally tested the developed methods with a portable laboratory (the BentoLab) at Twycross Zoo, where we successfully identified all three species (two primates and one bird) during a blind trial in just over five hours, including DNA extraction, amplification, sequencing, and database query.

Policy

Date: Thursday 1 September
Time: 11:00
Room: Pentlands East

Abstract 100

Oral Presentation

Monitoring population genetic diversity for conservation in Europe: Current situation and outlook in view of climate change

Peter Pearman1, Olivier Broennimann2, Paulo Alves3, Laura Bertola4, Elena Buzan5, Vlatka Cubric Curik6, Ancuta Fedorca7, José Godoy8, Christina Hvilsom9, Peter Klinga10, Maciej Konopinski11, Alexander Kopatz12, Linda Laikre13, Charalambos Neophytou14, Snæbjörn Pálsson15, Ivan Paz-Vinas16, Diana Posledovich13, Barbora Rolečková17, Dainis Rungis18, Gernot Segelbacher19, Katia Kavčič Sonnenschein20, Henrik Thurfjell21, Sabrina Träger22, Cristiano Vernesi23, Carles Vilà24, Marjana Westergren20, Frank Zachos25, Antoine Guisan2, & Michael Bruford26

1 University of the Basque Country / IKERBASQUE, Spain
2 University of Lausanne, Switzerland
3 University of Porto, Portugal
4 University of Copenhagen, Denmark
5 University of Primorska, Slovenia
6 University of Zagreb, Croatia
7 National Institute for Research and Development in Forestry "Marin Dracea", Romania
8 Consejo Superior de Investicaciones Científicas, Spain
9 Copenhagen Zoo, Denmark
10 Technical University in Zvolen, Slovakia
11 Institute of Nature Conservation of the Polish Academy of Sciences, Poland
12 Norwegian Institute for Nature Research (NINA), Norway
13 Stockholm University, Sweden
14 Institut für Waldbau, Austria
15 University of Iceland, Iceland
16 Colorado State University, United States of America
17 Institute of Vertebrate Biology of the Czech Academy of Sciences, Czech Republic
18 Latvian State Forest Reserch Institute "Silava", Latvia
19 University of Freiburg, Germany
20 Slovenian Forestry Institute, Slovenia
21 Swedish University of Agricultural Sciences, Sweden
22 Martin Luther University, Germany
23 Fondazione Edmund Mach, Italy
24 Doñana Biological Station, Spain
25 Natural History Museum Vienna, Austria
26 Cardiff University, United Kingdom

Genetic monitoring of populations currently attracts great interest but needs long-term planning and investments. It requires temporally replicated sampling and involves an accounting of observed genotypes or time series of estimated population genetic parameters. Monitoring these parameters supports conservation by detecting changes in genetic

diversity in small populations, assisting management of harvested populations, verifying efficacy of breeding programs, guiding directed gene flow and (re-)colonization, assessing impacts of environmental decline and climate change, etc. However, no overview of the extent of genetic monitoring in Europe exists. Such an overview, combined with projections of climate-driven environmental decline, would indicate opportunities for implementing population genetic monitoring in the context changing environmental suitability. We ask: 1. Where is genetic monitoring effort found in Europe, as current monitoring suggests sufficient infrastructure, political willingness and resources (together, ‘capacity’) for future monitoring. 2. Which factors explain among-country variation in realized monitoring capacity? 3. How will countries likely differ in climate-driven environmental change experienced by species of conservation interest? 4. How does realized capacity for monitoring coincide with anticipated impacts of climate change on populations? We identify patterns of realized monitoring capacity and increasing climatic marginality within the European ranges of species. Overall, we find surprisingly little documented population genetic monitoring in Europe. Country area extent, resource availability, and conservation policy will likely impact future capacity for monitoring, which partially coincides with increasing climatic marginality in species current ranges. The results suggest opportunity and need for increased population genetic monitoring across Europe and notably in its southeastern countries.

Applications

Date: Wednesday 31 August
Time: 14:30
Room: Pentlands East

Abstract 101

Oral Presentation

Elephant task: Developing a genomic toolkit for research and conservation

Patrícia Pečnerová1, Yasuko Ishida2, Alfred L. Roca2, Hans Siegismund1

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Genome-wide data is becoming an integral resource for conservation of species. In African elephants, a handful of genomes has been used to strengthen the case of recognizing savanna and forest elephants as two separate species. Here, we generate and analyse 165 genomes from African savanna and forest elephants in 13 countries, covering most of their current range. Compared to the previously-used traditional genetic markers like microsatellites and mitochondrial DNA, this genome-wide data allows us to infer: 1) a finer-scale population structure and the main trajectories of gene flow, 2) differences in genetic make-up of elephant populations in the different parts of the continent, and 3) demographic processes which resulted in the present-day patterns of genetic diversity. Besides providing essential insights for conservation genetics, this data serves as a valuable resource for conservation management. We identify and optimize a set of standardized genetic markers that will be implemented in genetic monitoring of wild elephant populations, thus, providing a resource for future research and conservation of elephants in Africa.

Collections

Date: Tuesday 30 August
Time: 15:40
Room: Pentlands (East/West)

Abstract 102

Oral Presentation

Digging in a 120 years-old lunch: what can we learn from collection specimens of extinct species?

Catarina J. Pinho1,2,3, Vicente Roca4, Ana Perera1,3, Amanda Sousa1,3, Michèle Bruni5, Aurélien Miralles6, Raquel Vasconcelos1,3

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2 Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal
3 BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, Vairão, Portugal
4 Departament de Zoologia, Facultat de Ciències Biològiques, Universitat de València. València, Spain
5 Collections scientifiques (Direction du Développement), Musée océanographique de Monaco, Monaco
6 Institut de Systématique, Évolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, Paris, France

Studying collection specimens is often the only way to unravel information about recent extinctions. These can reveal knowledge on threats and life traits related to extinction, and contribute, by extrapolation, to the conservation of extant species. However, high-throughput sequencing methods have rarely been applied to extinct species to reveal information on their ecology. Insular species are especially prone to extinction. We studied the gut contents of three specimens of the extinct giant skink *Chioninia coctei* of the Cabo Verde Islands using microscopy and DNA-metabarcoding. The presence of *Tachygonetria* adult nematodes suggests plants as important diet items. Our metabarcoding approach also identified plants and, additionally, invertebrates, supporting the hypothesis of *C. coctei*'s generalist diet. The absence of vertebrates in the digestive contents may reflect the decline of seabirds on the Desertas Islands that could have contributed to the debilitation of the giant skink, already depleted by persecution and severe droughts. Even with a small sample size, this study contributes to shedding light on the trophic roles of this enigmatic extinct species and emphasizes the need to develop holistic conservation plans for island threatened taxa. Additionally, it illustrates the potential of integrating up-to-date molecular methods with traditional approaches to studying collection specimens to help to solve ecological puzzles in other ecosystems.

Applications

Date: Thursday 1 September
Time: 13:45
Room: Pentlands West

Abstract 103

Oral Presentation

Parentage-based genetic tagging to monitor the success of conservation re-introductions

Victoria L. Pritchard1, Agata Drywa1 Silvia Ferreira Carvalho1, Dasha Svobodova1

1 Institute for Biodiversity and Freshwater Conservation, UHI Inverness, Scotland

Parentage-based tagging – connecting individuals to their parents through their multilocus genotypes – is a less invasive and more cost-effective alternative to traditional physical tagging for monitoring of captive-bred individuals released into the wild. We demonstrate the utility of this method to monitor the success of wild salmonid reintroductions in Scottish rivers. Using a panel of 95 microsatellite markers, assayed through high-throughput genotyping-by-sequencing, we monitor the short-term movement and long-term survivorship of Atlantic salmon released as juveniles within three different rivers. The results enable us to assess the impact of the conservation stocking programmes, both in terms of restoration of the target population and in terms of interactions with adjoining populations of wild fish. The flexibility of the sequencing methodology also enables simple extension of the genotyping panel, for example to add markers for known life-history relevant genes in the target species.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 104

Poster Presentation

Comparative Conservation Genomics of an Endangered Cooperative Breeder, The African Wild Dog

Amelia Ramage1, Rosie Woodroffe1, Julia Day1

1 Institute of Zoology and University College London

Small populations face elevated extinction risks due to processes such as genetic drift and inbreeding. These processes work to homogenise small populations, reducing their adaptive potential and exposing recessive deleterious alleles. These genetic processes may be exacerbated in cooperatively-breeding species, where the social suppression of reproduction can greatly reduce effective population size (Ne). At the same time, behavioural avoidance of inbreeding can halt reproduction in exceedingly small populations. Understanding these impacts of social behaviour on the genetics and viability of small populations, may have great conservation importance. The African wild dog (*Lycaon pictus*) is a globally endangered cooperatively-breeding canid. Most populations <10 packs, and most packs include a single breeding pair. In reintroduced populations, genetic diversity is maintained throughout managed translocations, but such genetic management has never been conducted elsewhere. Drawing on samples from small populations in Senegal and Kenya, and larger populations in southern Africa, this project will quantify genetic structure and loss of genomic diversity following known bottlenecks, assessing impacts of inbreeding and inbreeding avoidance in populations of varying size and degree of isolation. In so doing, it will help inform conservation decisions about the genetic management of this highly endangered species.

Applications

Date: Wednesday 31 August
Time: 15:30
Room: Pentlands East

Abstract 105

Oral Presentation

Applying genomic approaches to identify historic population declines in British bats

Orly Razgour1, Cecilia Montauban2, Francesca Festa1, Daniel Whitby3, Michael Bekaert4, Sandra Afonso5, Gareth Jones6, Pedro Horta5, Hugo Rebelo5, Carlos Ibañez7, Javier Juste7, & Katherine Boughey8

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6 University of Bristol, UK
7 Doñana Biological Station CSIC, Spain
8 Bat Conservation Trust, UK

Anecdotal evidence suggests British bat populations have suffered substantial declines during the previous century. However, there is little empirical evidence of these declines, which can be used to put more recent population changes into historic context and set appropriate targets for species recovery. This project is a collaboration between academic researchers, NGOs and conservation practitioners to develop molecular approaches capable of providing quantitative evidence of historic population change that would inform accurate definitions of Favourable Conservation Status and conservation management. We generated a genomic dataset (ddRADseq) for the Western barbastelle bat, *Barbastella barbastellus*, a globally Near Threatened and regionally Vulnerable species, including colonies from across the species' British and Iberian ranges. We used a combination of landscape genetics and Approximate Bayesian Computation model-based inference of demographic history to identify both evidence of population changes and possible drivers of these changes. We found that levels of genetic diversity and inbreeding were related to broadleaf woodland cover around colony home range, while genetic connectivity was affected by artificial lights and the combination of rivers

and broadleaf woodland cover. The demographic history analysis showed that the southern England barbastelle bat population has declined by 91% in the past 400 years (95% CI: 28-1052). This decline may be attributed to loss of native woodlands and spread of artificial lights. The results of this project will be used to inform the Favourable Conservation Status definition for the barbastelle bat. The approach will now be applied to inform the conservation status of other British bats.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 106

Poster Presentation

Sampling design for the monitoring of genetic diversity in Switzerland: Considerations and outcomes

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Many efforts have been made to integrate genetic diversity, one of the three main pillars of biodiversity, into monitoring projects and conservation efforts. The development and improvement of genetic diversity indicators is an intensively discussed topic. The type of genetic indicators that can be inferred from genetic monitoring is strongly dependent on the underlying sampling design. Here, we developed a universally applicable proportionally stratified random sampling strategy optimized for population genetic inferences. We tested and validated this protocol in a pilot study for a monitoring of genetic diversity in Switzerland. Our aim was to sample 30 populations from each of five species with 10 individuals each. Based on a 5x5 kilometer grid with 3,700 cells, we randomly selected 40 cells with recently documented occurrence data of the species, taking into account the species' distribution across the five major biogeographic regions of Switzerland, which we treated as sampling strata. The sampling design thus accounts for the unequal sizes of the five biogeographic regions while having a random sampling design within these regions. To avoid sampling bias within the 5x5 km cells, the order of locations at which to attempt sampling was again randomized based on available occurrence data. We show that samples obtained by a proportionally stratified random sampling design cover the entire environmental climate-space (temperature and precipitation) of the corresponding species in Switzerland. The developed sampling design provides the foundation to infer population genetic indicators such as e.g. neutral and adaptive genetic diversity, inbreeding, connectivity or adaptive potential.

Applications

Date: Wednesday 31 August
Time: 11:30
Room: Pentlands West

Abstract 107

Oral Presentation

The value of captive wildlife in the conservation of species: Genetic diversity and admixture in the emblematic sable antelope (Hippotragus niger)

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As defined by the IUCN, a species' conservation status considers population numbers both in the wild and in *ex-situ* captive populations. Although genetic diversity is not formally included in these classifications, it may be pivotal to optimal conservation management. A case in point is the sable antelope (*Hippotragus niger*), whose population numbers are dwindling in the wild, but occurs in high numbers in captivity, especially on privately-owned farms and ranches. Sable is a large African antelope that comprises five phylogroups and is classified as "least concern", despite the current paucity of evaluation of genetic diversity. To understand the importance of monitoring and preserving genetic diversity in captive sable that could serve as a source to restore wild populations, we evaluated diversity, inbreeding and admixture using microsatellite markers in 7,900 captive sable from 358 farms, representing the largest data set for a wildlife species analyzed to date, and compare results with 320 wild specimens. Our results revealed only two phylogroups were present in farm populations, with 80%

revealed only two phylogroups were present in farm populations, with 80% of the animals being admixed. Pure phylogroup animals are restricted to a few farms, making the future conservation of sable dependent on a small number of private owners. Farm populations showed decreased genetic diversity and higher relatedness and inbreeding relative to wild populations. Our study demonstrates the usefulness of comprehensive genetic analyses of captive populations that can serve as stocks for the conservation of wild species such as the sable antelope.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 108

Poster Presentation

Non-invasive genetic monitoring of a controversial carnivore

Robin Rigg1,2, Barbara Boljte2, Maja Jelenčič2, Marjeta Konec2, & Tomaž Skrbinšek2

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Reliable data on key population parameters are fundamental to wildlife conservation and management. EU Member States are legally obliged by the Habitats Directive to monitor species of Community interest to assess whether they are at 'favourable conservation status'. In Slovakia, there has been considerable controversy regarding the grey wolf (*Canis lupus*). Estimates of abundance in official game statistics (OGS), compiled from annual hunters' reports, differ by an order of magnitude from those of environmentalists. We used noninvasive sampling, genotyping and mark-recapture modelling to estimate wolf numbers in a model area in 2015–2020. Trained volunteer 'citizen scientists' conducted non-invasive sampling (http://slovakwildlife.org/en/activities/whitewilderness). Laboratory work and data analyses were financed from crowdfunding (https://www.gofundme.com/f/carpathian-wolf-watch) and other donations. We genotyped samples (n=761) at 16 canine unlinked autosomal microsatellite loci and the Amelogenin locus for sex determination. Using the Capwire mark-recapture model we obtained, for the first time in Slovakia, a statistically robust estimate of wolf abundance: 49 individuals (40–69, 95% CI) in c.14% of occupied wolf range in 2015/16. Results for the following four seasons indicated the population to be stable or slightly increasing, with an estimated 58 individuals (46–70, 95% CI) in 2019/20. OGS for the same area were more than 5-times higher than genetic mark-recapture estimates in all five sampling seasons. Using this quotient to recalibrate OGS on the national level produces an estimate of 609 wolves in Slovakia in 2019/20. Sampling in additional study areas or, if resources permit, throughout the occupied range is desirable to corroborate our findings.

Applications

Date: Thursday 1 September
Time: 11:15
Room: Pentlands West

Abstract 109

Oral Presentation

Genetic analysis of beavers (Castor fiber) in England and considerations for reintroduction

Heather Ritchie-Parker1, Alex Ball1, Róisín Campbell-Palmer2, Helen Taylor1, Helen Senn1

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2 Independent Beaver Consultant, UK

Eurasian beavers (*Castor fiber*) were once widespread across Europe, but populations severely declined across the mainland and the species went extinct in Britain over 400 years ago. Beavers were recently reintroduced back into Britain at a site in Knapdale, Scotland through the Scottish Beaver Trial (2009-2014), as well as unlicensed releases into a separate population in the River Tay (2006) which was allowed to remain after extensive studies and a government consultation. Unlicensed releases of beavers have subsequently been discovered in at least eight counties in England but the number of beavers and their breeding status in these locations are currently unknown. In response to the presence of beavers in England, Natural England is gathering advice to help inform the government's decision and future policy on the legal status, ecological benefits and impacts, future reintroduction and management of beavers more widely throughout England. To maximise the success of beaver reintroduction into England, genetic aspects that will increase the likelihood of success in the long term need to be considered. Here we have utilised genetic tools in order to; estimated the genetic diversity of beavers currently residing in England and compared these to established populations in Scotland and mainland Europe, examine relatedness between individuals, determine the origin populations of beavers currently in England (both free-living and in enclosures), investigate congruence between genetic data and translocation management decisions based on field observations. With this genetic information we can contribute to best practices for future reintroductions and the management of beavers in England.

Applications

Date: Wednesday 31 August
Time: 16:45
Room: Pentlands West

Abstract 110

Oral Presentation

Conservation genetics in bottlenecked species: Insights from ancient genomes of the Alpine ibex

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3 Institute for Evolutionary Medicine, University of Zürich, Switzerland
4 Department of Bioinformatics and Genetics, Swedish Museum of Natural History, Stockholm, Sweden
5 Royal Botanic Garden Edinburgh, Scotland

Understanding the genetic consequences of population bottlenecks is crucial for species conservation. Low genetic diversity in bottlenecked populations has been reported repeatedly and historic population size trajectories can be modelled using genetic data of contemporary individuals. However, such approaches have a limited temporal resolution in the recent past and pre-bottlenecked population structure, genetic diversity and genetic load are difficult to assess. Here, ancient DNA approaches allow shedding light on the pre-bottlenecked genetic past and could give valuable insight into the long-term genetic health of a species. We present the analysis of 57 ancient and 29 recent high quality whole genomes of the once nearly extinct Alpine ibex covering its species distribution range and spanning 12'000 years. The powerful dataset is complemented with 30 previously published whole genomes from related *Capra* species. We identify several extinct Alpine ibex lineages and our results suggest that the low genetic diversity of present-day populations is attributable both to overhunting over centuries but also environmental change over millennia. We find that population structure was stable over millennia indicating relatively small, isolated populations persisting over long time ranges. In accordance, we find high levels of mildly deleterious mutations in ancient and recent Alpine ibex when compared to related species but a deficit (and possible sign of purging) of highly deleterious mutations. We underline that ancient DNA approaches can be a valuable tool for setting genetic patterns of a bottlenecked species into conservation genetic context.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 111

Poster Presentation

Identification and removal of nuclear mitochondrial pseudogenes (numts) for accurate use of mitochondrial sequences in conservation

Alida de Flamingh*1,2, Angel G. Rivera-Colón*3, Tom P. Gnoske4, Julian C. Kerbis Peterhans4,5,6, Julian Catchen 2,3, Ripan S. Malhi1,2,7 & **Alfred L. Roca1,2,8**

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Nuclear mitochondrial pseudogenes (numts) may hinder the reconstruction of mtDNA genomes and affect the reliability of mtDNA datasets for phylogenetic and population genetic comparisons, or for forensics use. We have developed a program, Numt Parser, which allows for the identification of DNA sequences that likely originate from numt pseudogene DNA. Sequencing reads are classified as originating from either numt or true cytoplasmic mitochondrial (cymt) DNA by direct comparison against cymt and numt reference sequences. Classified reads can then be parsed into cymt or numt datasets. We tested this program using whole genome shotgun-sequenced data from lions (*Panthera leo*), because the genus *Panthera* is known to have numt pseudogenes. Numt Parser decreased sequence disagreements that were likely due to numt pseudogene contamination and equalized read coverage across the mitogenome by removing reads that likely originated from numts, improving the reconstruction of true mitogenomes, allowing for more accurate and robust biological inferences. Results will be placed in the context of using mtDNA to examine the provenance of confiscated trafficked samples of lions, and of other protected species subject to poaching such as elephants.

Link: https://biorxiv.org/cgi/content/short/2022.04.04.487049v1

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 112

Poster Presentation

Gauging DNA degradation among common insect trap preservatives

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2 Ecological Networks, Technische Universität Darmstadt, Germany

Genetic methods are being increasingly used for species identification and monitoring but obtaining good DNA quality from insect trap specimens remains a challenge for field studies. As alternatives to ethanol, ethylene glycol, propylene glycol and Renner solution have been previously suggested as suitable preservatives for the collection of genetic material, but a systematic overview of their performance under compromising field conditions is lacking. Here we experimentally test the three preservatives for their ability to preserve DNA over 27 days in different dilutions and temperatures using the house cricket *Acheta domesticus* (Orthoptera: Gryllidae). DNA quality was measured as DNA fragmentation and success rates in PCR amplifying a COI fragment of 658, 313 or 157 bp. Undiluted propylene glycol and ethylene glycol always retained high molecular weight DNA at room temperature. However, at 37°C or in any dilution no high molecular weight DNA was preserved and DNA fragmentation was substantial. Nevertheless, the COI sequence could be amplified from samples at every condition. Renner solution did not preserve high molecular weight DNA and fragmentation increased over time at 37°C until amplification was impossible. The results suggest that propylene glycol and ethylene glycol are suitable preservatives for collecting both genetic and morphological material, but dilution or hot temperature compromise their ability to preserve high molecular weight DNA. Considering the prerequisites for genetic methods more demanding than metabarcoding this could prove to be a limiting factor for certain applications.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 113

Poster Presentation

Historical and Contemporary Evolutionary Processes Interact to Drive the Genetic Structure of a Polymorphic Arctic Fish (Salvelinus alpinus)

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5 School of Biological Sciences, University of Aberdeen, Aberdeen, United Kingdom

Effective conservation of polymorphic species requires knowledge of the genetic characteristics and evolutionary drivers of intraspecific morphs. While both historical and contemporary processes may have shaped morph genetic structure, their relative influence is largely unknown for many species, including Arctic Charr (*Salvelinus alpinus*). This Arctic fish has anadromous, resident, and landlocked morphs that experience differences in selective pressures, gene flow, and genetic drift. Historical colonization may have also shaped charr genetic structure given the recent founding of most populations from five glacial lineages existing in allopatry during the Pleistocene. To investigate the evolutionary processes shaping charr morphs we used an 87k SNP chip to genetically characterize anadromous, resident, and landlocked charr in 45 locations from eastern Canada. Strong isolation by distance suggested charr genetic structure is primarily shaped by geographic distance. Landlocked populations had lower genetic diversities than anadromous populations. However, genetic diversities in landlocked populations were temporally stable, while recent decreases in some anadromous populations suggested their increased vulnerability. Genetic diversity also correlated with latitude in anadromous populations, potentially reflecting the threat climate change poses to southern

anadromous populations and the greater introgression between two glacial lineages in northern Labrador. Across all populations, we found functionally relevant outlier genes associated with climatic variation, suggesting environmentally driven adaptation also shapes genetic structure. Gene flow, colonization history, and local adaptation have therefore collectively shaped the genetic variation and evolutionary trajectory of each population. Our results emphasize the importance of considering the interactive effects of these evolutionary processes when making conservation decisions.

Applications

Date: Thursday 1 September
Time: 14:15
Room: Pentlands East

Abstract 114

Oral Presentation

The antique genetic plight of the Mediterranean monk seal (Monachus monachus)

Jordi Salmona[1], Julia Dayon[1,2], Emilie Lecompte[1], Alexandros A. Karamanlidis[3], Alex Aguilar[4], Pablo Fernandez de Larrinoa[5], Rosa Pires[6], Giulia Mo[7], Aliki Panou[8], Sabrina Agnesi[7], Asunción Borrell[4], Erdem Danyer[9,10], Bayram Öztürk[9,11], Arda M. Tonay[9,11], Anastasios K. Anestis[8], Luis M. Gonzáles[12], Panagiotis Dendrinos[3], Philippe Gaubert[1]

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3 MOm/Hellenic Society for the Study and Protection of the Monk seal, Athens, Greece
4 Universitat de Barcelona, IRBio and Department of Evolutionary Biology, Ecology and Environmental Sciences, Faculty of Biology, Barcelona, Spain
5 Monk Seal Conservation Program, Fundación CBD-Habitat, Madrid, Spain
6 Instituto das Florestas e Conservação da Natureza IP-RAM, Jardim Botânico da Madeira, Caminho do Meio, Bom Sucesso, Funchal, Madeira, Portugal
7 Istituto Superiore per la Protezione e la Ricerca Ambientale (ISPRA), Rome, Italy
8 Archipelagos - environment and development, Kefalonia, Greece
9 Turkish Marine Research Foundation (TUDAV), Beykoz, Istanbul, Turkey
10 Veterinary Control Central Research Institute, Ankara, Turkey
11 Istanbul University, Faculty of Aquatic Sciences, Istanbul, Turkey
12 Subdirección General de Biodiversidad Terrestre y Marina, Ministerio para la Transición Ecológica y el Reto Demográfico, Madrid, Spain

Assessing the impact of human activities on the local extinctions of species can have crucial implications in conservation. We investigated the population genetic diversity of the Mediterranean monk seal (*Monachus monachus*), one of the world's most endangered marine mammals, through an unprecedented dataset encompassing archeological (neolithic), historical (extinct) and extant populations throughout the species' range.

We recovered a population structure that is likely the consequence of recent drift, combined with long-term isolation by distance, resulting from prevailing short-distance (< 500 km) and infrequent long-distance dispersal (< 1,500 km). All populations (Madeira especially), show high levels of inbreeding and low levels of genetic diversity, seemingly declining since historical time, but surprisingly not being impacted by the 1997 massive

die-off in Cabo Blanco. Approximate Bayesian Computation analyses support scenarios combining local extinctions and a major effective population size decline in all populations during Antiquity. Our results suggest that the early densification of human populations around the Mediterranean Basin coupled with the development of seafaring techniques were the main drivers of the decline of Mediterranean monk seals. We further develop on the contribution of recently obtained genomic results to these patterns, and their potential implications for the species' global conservation plan.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 115

Poster Presentation

Genetic diversity of introduced farmed and native wild tilapia

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Tilapia are among the most important farmed fish species worldwide; in Nigeria, they are the second most farmed species after the catfish. Tilapias belonging to the Oreochromis, Sarotherodon and Tilapia genera are endemic to Nigeria and constitute the major catch in the wild. The species are of great importance to Nigeria's economy and contribute to the nation's food security. However, the development of the tilapia aquaculture industry has been impeded by the lack of a specific breeding programme to develop native tilapia species. Farmers have to rely on genetically improved farmed tilapia that are introduced from other countries, which takes care of the unwanted rapid reproduction of wild-type tilapia. Tilapia strains have therefore been introduced into Nigeria mainly from Thailand, Egypt, and the Netherlands for aquaculture purposes, but these sometimes escape into the wild. There is no record to show when the first introduction was made and no study has investigated the levels of genetic diversity in introduced farmed and native wild tilapia in Nigeria. To investigate this, we collected tilapia fin clips (targeting 30 per population) from 18 populations consisting of introduced farmed and native wild tilapia from three regions in Nigeria and obtained partial sequences of the mitochondrial cytochrome oxidase subunit 1 gene. Sequence analysis and clustering patterns from the phylogenetic relationship showed extensive variation among the populations and overall very high genetic diversity. Resolving the taxonomy of these tilapia would provide better insight into understanding the population structure and proper management and conservation of the species.

Applications

Date: Wednesday 31 August
Time: 14:30
Room: Pentlands West

Abstract 116

Oral Presentation

Conservation genomics of golden eagles on isolated populations of Scotland and Japan

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3 Wildlife Research Center, Kyoto University, Japan

The golden eagle (*Aquila chrysaetos*) is a circumglobal raptor species in the northern hemisphere. The Scottish population of European subspecies (*A. c. chrysaetos*) and the Japanese subspecies (*A. c. japonica*) are both considered to be endangered because of either past bottleneck due persecution in the early 20th century (Scotland), or the ongoing decline of breeding success (Japan). Previous studies revealed that these island populations are isolated from geneflow among continental populations, and therefore an understanding of genetic diversity and inbreeding is important for effective conservation management. We conducted whole genome re-sequencing of European golden eagles and some Japanese birds. Genomic data were analysed with principal component analysis (PCA), pairwise sequential Markovian coalescent (PSMC) modelling, and Runs of Homozygosity (ROH). Results of these analysis suggested isolated population clustering at a genomic scale, a continuous decline in effective population size, more recent inbreeding, and loss of genetic diversity in both island populations. Currently, the population size of Scottish birds has been increasing with effective conservation management and monitoring the genetic diversity might help to understand the population health and sustainability. On the other hand, the population size of Japanese birds continues to decrease and further loss of diversity and elevated inbreeding depression is anticipated. Effective conservation genetic management must be conducted as soon as possible, and integration of *in-situ* (wild) and *ex-situ* (captive) conservation is a plausible approach.

Applications

Date: Wednesday 31 August
Time: 15:45
Room: Pentlands East

Abstract 117

Oral Presentation

Using genomic tools to assess the efficacy of a Marine Protected Area designated to the critically endangered flapper skate

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After overfishing caused severe population declines of the critically endangered flapper skate *Dipturus intermedius* in the Northeast Atlantic, Scotland designated the ‘Loch Sunart to the Sound of Jura’ Marine Protected Area (MPA) to this species. High levels of site affinity found in the area favoured the spatial protection, but also questioned if this management measure would benefit the wider metapopulation. The lack of movement could mean that this MPA would not act as a potential source population that replenishes other populations. As there was insufficient knowledge about genetic diversity and connectivity across the species range, it remained unclear if this MPA would preserve the adaptive capabilities of the species or if populations outwith would benefit from it through migrants and genetic admixture.

Analysing mitochondrial DNA, low diversity and connectivity were found in the MPA in comparison to other populations, raising concerns about potential inbreeding risks within the most protected population of flapper skates, as well as for the conservation of the species’ overall genetic diversity. Single Nucleotide Polymorphisms were used to gain more insights into diversity and geneflow between the MPA and other populations. The MPA was found to be characterised by a reassuring degree of diversity, but also high levels of relatedness and significant differentiation to other areas. First and second-degree kin relationships confirmed low dispersal as relatives almost exclusively remain in relatively short distance from each other. While the MPA protects genetic diversity, there is little admixture with other populations.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 118

Poster Presentation

Genetic viability of a reintroduced population of south-western common brushtail possum (*Trichosurus vulpecula hypoleucus*), Western Australia

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This study focused on a reintroduced population of south-western common brushtail possum (*Trichosurus vulpecula hypoleucus*) to assess genetic variability and inform future management strategies. Individuals were translocated to Matuwa Kurarra-Kurarra Indigenous Protected Area, Western Australia, from four source populations, but subsequent monitoring has indicated a 50% reduction in population size from original founder numbers in the eight years since establishment. Tissue samples from three of the four source populations and an additional four comparative sites (n = 140 animals total) were analysed using 13 microsatellite loci. Inbreeding was lower and heterozygosity was higher in the translocated Matuwa population than in two of the source populations studied, highlighting the benefits of promoting outbreeding through the use of multiple source populations in translocations. However, allelic richness at Matuwa is low relative to two of the source populations, suggesting the impact of population bottlenecks on genetic diversity, which was supported by significant allele frequency mode shift and Wilcoxon rank sign test for heterozygosity excess tests for genetic bottlenecks. Despite the genetic health of the population being stronger than predicted, this population is still at risk due to environmental factors, small size and fragmentation. This is the first study to document patterns of genetic diversity and to highlight issues with translocation for this subspecies and adds to the limited literature illustrating how outbreeding can be used for conservation purposes.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 119

Poster Presentation

A phylogeny of pied and black oystercatchers reveals two new species

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Oystercatchers (order Charadriiformes, family Haematopodidae) are a genus of globally distributed shorebirds with eleven currently recognised extant species. Phylogenetic reconstruction and species delimitation of this group has been a longstanding challenge due to their morphological similarity and inconsistent sampling. The purpose of this study was a complete reconstruction of the evolutionary history of taxa inclusive of all recognised oystercatcher species. Nuclear and mitochondrial DNA were isolated from feathers and toepads of specimens and sequenced for phylogenetic reconstruction. Based on a combined alignment of mitochondrial and nuclear markers, a robust time-calibrated phylogeny was constructed, resulting in an improved understanding of the evolutionary history of the genus. It was found that oystercatchers separated into two ancient clades approximately 24.13 mya (CI: 19.86-28.24 mya) representing the New and Old Worlds. Within the New World, the endemic Galapagos Oystercatcher (*Haematopus galapagensis*), previously treated as a subspecies of the American Oystercatcher (*Haematopus palliatus*) likely represents a valid new species. Likewise, in the Old World clade, the Pacific Oystercatcher (*Haematopus osculans*), previously a subspecies of the widespread Eurasian Oystercatcher (*Haematopus ostralegus*), should be treated as a separate species. We subsequently recommend several changes to be made to oystercatcher taxonomy.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 120

Poster Presentation

A genetic assessment and functional analysis of the effects of retention forestry on saproxylic insects in a multifunctional forest system in southwestern Germany

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Deadwood is considered a key habitat for saproxylic species of which several are endangered. Retention of deadwood and habitat trees has become a common forest management practice in Central Europe to mediate forest biodiversity preservation and human interest. However, the prospect of forest retention in the aspect of species richness and genetic connectivity across forest landscapes needs more assessment. In this study, forest invertebrate diversity will be characterized through a metabarcoding approach. Metabarcoding has become a promising tool for molecular biodiversity monitoring studies over the past decade because it allows fast and standardized species identification. Combining characterized datasets on flying insect species and ground-dwelling arthropod communities from 135 plots in the southern black forest area, a low mountain range in southwestern Germany, will allow us to investigate the local habitat diversity. Furthermore, Low-coverage whole genome sequencing (lcWGS) will be used for selected saproxylic species to measure gene flow among the patches. By using these genomic variables, correlation with habitat and previously obtained landscape matrix characteristics (tree species composition, height, horizontal and vertical structuring) will facilitate landscape genomic analysis to identify connectivity pathways across the landscape and their local adaptation. This work will bring a valuable contribution to identifying the effects of retention forest management practice on forest invertebrate communities, affected by the available amount of deadwood and habitat trees, and identify potential drivers for the ongoing insect decline in forest ecosystems.

Applications

Date: Wednesday 31 August
Time: 16:15
Room: Pentlands East

Abstract 121

Oral Presentation

Population genetics of Scottish maerl beds informing the need for targeted conservation management

Cornelia Simon-Nutbrown1,2, Peter Hollingsworth2, Teresa Fernandes1, John Baxter3, Lisa Kamphausen4, Heidi L. Burdett1

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2 Royal Botanic Gardens Edinburgh, Scotland, UK
3 Ocean Perspectives, Scotland, UK
4 NatureScot, Scotland, UK

Maerl, free-living red coralline algae, that form reef-like ecosystems (maerl beds) which support high biodiversity including many rare, endemic and commercially important species, are found throughout the world's coastal oceans. Listed as 'Vulnerable' or 'Endangered' on the IUCN Habitats Red List, Scotland is a European hotspot for maerl beds but they face an uncertain future because of destructive human activities and climate change. Current understanding of Scottish maerl bed distribution relies on limited data and morphological species identification. There is little understanding of factors that control apparent distribution patterns, and knowledge of genetic diversity and species assemblages is almost non-existent. Here, we use a whole genome genotyping approach to explore the population genomics of maerl across Scotland. We present data that doubles the number of maerl species previously thought to be in Scotland and identify the extent of genetic connectivity both within and between maerl beds at a local to national scale. Coupled with species distribution modelling, we project how maerl species may be differentially affected by climate change over the coming century. Using this information, we provide recommendations for their targeted conservation management, such as identifying which species are at most risk from climate change, and identification of priority conservation areas for genetic refuge.

Technologies

Date: Wednesday 31 August
Time: 13:30
Room: Pentlands East

Abstract 122

Oral Presentation

A creeping yet catastrophic threat: chytrid fungus presents a clear and present danger to amphibian populations in Europe and beyond

Smith S1, Dittrich C1,2, Chloe Fouilloux2, Munimanda G1, Preininger D3 & Rojas B12

1 Konrad Lorenz Institute of Ethology (KLIVV), University of Veterinary Medicine, Vienna, Austria
2 Department of Biology & Environmental Science, University of Jyväskylä, Finland
3 Tiergarten Schöbrunn, Seckendorff Gudent Weg, Vienna, Austria

Chytrid fungus (*Batrachocytrium dendrobatidis*) has long threatened frog populations across the globe. In recent years, a new variant of the fungal pathogen, *B. salamandrivorans*, has entered northern Europe and is spreading southwards with catastrophic effect on local salamander populations. The international pet trade is the main suspect for its introduction. The key to managing outbreaks of both diseases is early detection of the two pathogens. We have conducted ddPCR-based screening of salamander populations from the wild and the pet trade in Austria since 2017. To date we report no detection of *B. salamadrivorans* in Austria and only occasional instances of *B. dendrobatidis* sub-clinical infection in captive salamanders. We combine this data with recent screening for *B. dendrobatidis* of wild populations and eDNA samples from French Guiana to assess the level of threat of illegal imports of amphibians from South America. Our data highlight the need for constant screening of imported animals to ensure the safety of European amphibian populations. While the spread of chytrid throughout Europe seems inevitable, early detection is the best way to ensure a rapid and effective response to new outbreaks.

Applications

Date: Wednesday 31 August
Time: 14:45
Room: Pentlands East

Abstract 123

Oral Presentation

Susceptibility to a sexually transmitted disease in a wild koala population shows heritable genetic variance but no inbreeding depression

Kasha Strickland1, Romane H Cristescu2, Anthony J Schultz3, Loeske E B Kruuk1, Deidre de Villiers4, Céline H Frère5

1 University of Edinburgh, UK
2 University of the Sunshine Coast, Australia
3 Icelandic Museum of Natural History, Iceland
4 Endeavour Veterinary Ecology, Australia
5 University of Queensland, Australia

The koala, one of the most iconic Australian wildlife species, is facing several concomitant threats that are driving population declines. Some threats are well known and have clear methods of prevention (e.g. habitat loss can be reduced with stronger land-clearing control), whereas others are less easily addressed. One of the major current threats to koalas is chlamydial disease, which can have major impacts on individual survival and reproduction rates, and can translate into population declines. Effective management strategies for the disease in the wild are currently lacking, and to date we know little about the determinants of individual susceptibility to disease. Here we used a powerful dataset to investigate the genetic basis of variation in susceptibility to chlamydia using one of the most intensively studied wild koala populations. We combine data from veterinary examinations, chlamydia testing, genetic sampling and movement monitoring. Out of our sample of 342 wild koalas, 60 were found to have chlamydia. Using genotype information on 5007 SNPs to investigate the role of genetic characteristics in determining disease status, we found no evidence of inbreeding depression, but a heritability of 0.14 (95%CI: 0.06 – 0.23) for the probability that koalas had chlamydia. Heritability of susceptibility to chlamydia could be relevant for future disease management, as it suggests the potential to select for disease resilience through assisted breeding.

Policy

Date: Thursday 1 September
Time: 11:45
Room: Pentlands East

Abstract 124

Oral Presentation

Bridging the conservation genetics gap to improve conservation outcomes

Helen R. Taylor1

1 Royal Zoological Society of Scotland, UK

Genetic data is of proven importance to conservation practice, but genetic factors are frequently overlooked in conservation planning and management. This divide between conservation genetics and conservation practice has been termed the conservation genetics gap. As a trained conservation geneticist who has become a conservation practitioner, I will take a three-pronged approach to discussing this research implementation gap, based on my own research and that of others. 1. A review of the continually evolving understanding of the drivers behind the conservation genetics gap, including the importance of talking to practitioners about these drivers, and some of the additional problems that genomic work may introduce. 2. A summary of some of the solutions that have been suggested and have, in some instances, been put into place to attempt to bridge the gap. 3. Examples of projects that firmly integrate conservation genetics into conservation practice from both the RZSS WildGenes team and various other international projects. The talk will finish with a brief outline of some of the skills that need to be cultivated within the conservation genetics community to successfully and routinely integrate genetics into conservation, improving conservation outcomes.

Policy
Date: Thursday 1 September
Time: 11:30
Room: Pentlands East

Abstract 125

Oral Presentation

The evolutionary history of caribou: implications of high intraspecific diversity for conservation

Rebecca S. Taylor1, Micheline Manseau1, Sonesinh Keobouasone1, Gabriela Mastromonaco2, Audrey Steedman3, Allicia Kelly4, Nicholas C. Larter5, Mary Gamberg6 Helen Schwantje7, Caeley Thacker8, Jean Polfus1, Leon Andrew9, Dave Hervieux10, Deborah Simmons9, Paul J. Wilson11

1 Environment and Climate Change Canada, Canada
2 Toronto Zoo, Canada
3 Parks Canada, Canada
4 Government of Northwest Territories, Canada
5 Retired, formally Government of Northwest Territories, Canada
6 Gamberg Consulting, Canada
7 Retired, formally British Columbia ministry of Forest, Lands, Natural Resource Operations, and Rural Development, Canada
8 British Columbia ministry of Forest, Lands, Natural Resource Operations, and Rural Development, Canada
9 ʔehdzo Got’ı̨nę Gots’ę́ Nákedı (Sahtú Renewable Resources Board), Canada
10 Government of Alberta, Canada
11 Trent University, Canada

Uncovering the evolutionary history of a species is important for conservation, for example the designation of conservation units. A good understanding of a species’ phylogenetic history is also needed when undertaking many analyses, and in particular when looking for adaptive variation. Caribou (*Rangifer tarandus*) in Canada are currently divided into 11 extant Designatable Units (DUs), similar to conservation or evolutionary significant units, all listed under the Federal Species At Risk Act. In this study, we reconstructed the phylogenomic and demographic history to uncover the evolutionary history of caribou using whole genome analysis and tested for genes under positive selection within the reconstructed lineages using an annotated chromosome scale caribou reference genome. Our whole chromosome phylogenies revealed a high level of intra-specific diversity including multiple lineages, gene flow between some lineages, and inconsistencies with current designations. We found a number of genes under positive selection in caribou, including lineage specific genes,

indicating adaptive differences between our reconstructed intra-specific lineages. Our chromosome scale assembly is an invaluable resource for conservation genomic research. Coupled with the most in depth reconstruction of the evolutionary history of caribou, our results provide vital knowledge for the refinement of conservation units as well as the baseline needed to study adaptive variation.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 126

Poster Presentation

Molecular tracking and prevalence of the red colour morph restricted to a harvested leopard population in South Africa

Laura Tensen1,2, John Power3, Gerrie Camacho4, Raquel Godinho2,5, Bettine Jansen van Vuuren2, Klaus Fischer1

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2 Department of Zoology, University of Johannesburg, Johannesburg, South Africa
3 Directorate of Biodiversity Management, Department of Economic Development, Environment, Conservation and Tourism, North West Provincial Government, Mmabatho, South Africa
4 Mpumalanga Tourism and Parks Agency, Nelspruit, South Africa
5 CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal

The red leopard (*Panthera pardus*) colour morph is a colour variant that occurs only in South Africa, where it is confined to the Central Bushveld bioregion. Red leopards have been spreading over the past 40 years, which raises the speculation that the prevalence of this phenotype is related to low dispersal of young individuals owing to high off-take in the region. Intensive selective hunting tends to remove large resident males from the breeding population, which gives young males the chance to mate with resident females that are more likely to be their relatives, eventually increasing the frequency of rare genetic variants. To investigate the genetic mechanisms underlying the red colour morph in leopards, and whether its prevalence in South Africa relates to an increase in genetic relatedness in the population, we sequenced exons of six coat colour associated genes and 20 microsatellite loci in twenty Wildtype and four red leopards. The results were combined with demographic data available from our study sites. We found that red leopards own a haplotype in homozygosity identified by two SNPs and a 1 bp deletion that causes a frameshift in the tyrosinase related protein 1 (TYRP1), a gene known to be involved in the biosynthesis of melanin. Microsatellite analyses indicate clear signs of a population bottleneck and a relatedness of 0.11 among all pairwise relationships, eventually supporting our hypothesis that a rare colour morph in the wild has increased its local frequency due to low natal dispersal, while subject to high human-induced mortality rate.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 127

Poster Presentation

Phasing Alleles Improves Network Inference with Allopolyploids

George P Tiley1 2, Andrew A Crowl1, Paul S Manos1, Emily B Sessa3, Claudia Solís-Lemus4, Anne D Yoder1, J Gordon Burleigh3

1 Duke University, USA
2 Royal Botanic Gardens Kew, UK
3 University of Florida, USA
4 University of Wisconsin, USA

Accurately reconstructing the reticulate histories of polyploids remains a central challenge for understanding plant evolution. Although phylogenetic networks can provide insights into relationships among polyploid lineages, inferring networks may be hampered by the complexities of homology determination in polyploid taxa. We use simulations to show that phasing alleles from allopolyploid individuals can improve inference of phylogenetic networks under the multispecies coalescent. Phased allelic data can also improve divergence time estimates for networks, which is helpful for evaluating allopolyploid speciation hypotheses and proposing mechanisms of speciation. To achieve these outcomes, we present a novel pipeline that leverages a recently developed phasing algorithm to reliably phase alleles from polyploids. This pipeline is especially appropriate for target enrichment data, where depth of coverage is typically high enough to phase entire loci. We provide an empirical example in the North American *Dryopteris* fern complex that demonstrates how phasing can help reveal the mode of polyploidization and improve network inference. We establish that our pipeline (PATÉ: Phased Alleles from Target Enrichment data) is capable of recovering a high proportion of phased loci from both diploids and polyploids, and that these data improve network estimates compared to using haplotype consensus assemblies. This approach is shown to be especially effective in reticulate complexes where there are multiple hybridization events.

The pipeline is available at: https://github.com/gtiley/Phasing

Policy

Date: Thursday 1 September
Time: 13:15
Room: Pentlands East

Abstract 128

Oral Presentation

Species diversity and conservation priorities for Cuban hutias: insights from modern and ancient DNA

Roseina Woods1, Ian Barnes1, Selina Brace1, **Samuel T. Turvey2**

1 Department of Earth Sciences, Natural History Museum, United Kingdom
2 Institute of Zoology, Zoological Society of London, United Kingdom

The Caribbean non-volant mammal fauna has experienced the world's greatest number of mammalian extinctions throughout the Holocene and historical eras. Most surviving species are threatened with extinction, and the region is recognised as a global priority for mammal conservation. Cuba retains the highest number of extant native land mammals, including seven hutias (large-bodied capromyid rodents) in three endemic genera: *Capromys* (1 recognised species: Least Concern), *Mysateles* (1 recognised species: Vulnerable), and *Mesocapromys* (5 recognised species: 1 Vulnerable, 1 Endangered, 1 Critically Endangered, 2 CR Possibly Extinct). *Mesocapromys* is therefore identified as a conservation-priority group, with its possibly extinct species (*M. nanus* and *M. sanfelipensis*) included within the EDGE of Existence's Top 100 mammal list and Re:wild's list of 25 "most wanted" lost species. We conducted genetic analysis of all extant and historically extinct Caribbean hutias, including samples from multiple individuals of most species, to reconstruct patterns of interspecific divergence and intraspecific diversification. We demonstrate that *Capromys pilorides* represents at least two distinct living species. Conversely, divergences between *Mesocapromys* species are much more recent, and *M. nanus* and *M. sanfelipensis* should potentially be reinterpreted as conspecific with closely related extant Cuban species. A similar pattern of recent differentiation is also seen between extant and recently extinct populations traditionally interpreted as different species in another Caribbean hutia genus, *Geocapromys*. These findings provide a potentially more optimistic perspective on species-level losses in the Caribbean, and raise important questions about conservation prioritisation for this mammal fauna: what taxonomic units do we want to save?

Policy

Date: Tuesday 30 August
Time: 15:55/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 129

Speed talk & poster

Sampling historical DNA to assess the impact of habitat loss on genetic diversity in a peatland-specialist

Gabriel Ulrich1, Enrique Rayo1, Alessia Guggisberg1, Simone Fior1, Martin C. Fischer1 & Alex Widmer1

1 Institute of Integrative Biology (IBZ) - ETH Zurich, Switzerland

Genetic diversity is the basis for adaptation to changing environmental conditions such as climate change. Human-induced habitat loss and landscape fragmentation are important drivers of population size reduction which can lead to genetic diversity loss. As a peat bog specialist, the cottongrass *Eriophorum vaginatum* has undergone major habitat loss in Switzerland during the past two centuries as a consequence of wetland drainage and peat extraction. Habitat loss has mainly occurred in the central plateau, a densely populated and relatively warm biogeographic region of Switzerland. In the pilot study for a monitoring of genetic diversity in Switzerland, *E. vaginatum* is monitored retrospectively using samples from natural history collections to understand the potential loss or change of genetic diversity during the last century. We developed a sampling scheme to select available *E. vaginatum* vouchers and corresponding contemporary samples for whole-genome re-sequencing (WGS) to assess whether past habitat loss has mediated the extinction or isolation of genotypes that are potentially adaptive under future climate change. From >700 vouchers available in seven different Swiss herbaria, we selected 226 specimens from across Switzerland considering age, spatial distribution, and habitat change. We tested and optimized DNA extraction protocols and performed WGS to identify methodological challenges and possible limitations of the data. With this project, we aim to measure genetic diversity change in *E. vaginatum* and to better understand consequences of habitat loss on the potential of species to adapt to climate change.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 130

Poster Presentation

Landscape genetics of the endangered White-Faced Darter (Leucorrhinia dubia) in fragmented habitats across Scotland

Sebastian van Hellemondt1, Kate Peters1, David O'Brien2, Robert Jehle3, Matt Geary1, Naiara Sales1

1 University of Chester, United Kingdom
2 NatureScot, United Kingdom
3 University of Salford, United Kingdom

The white-faced darter, *Leucorrhinia dubia*, is a small dragonfly that is highly specialised to environments containing acidic bog pools. While the global population is listed as least concern on the IUCN Red List, this species is endangered throughout the United Kingdom due to the destruction and fragmentation of its habitat. *Leucorrhinia dubia* can mostly be found within the Scottish Highlands, however little is known about the connectivity between habitat patches and corresponding sub-populations. Landscape genetic techniques and genetic analysis can provide critical information for the conservation management of this species. Understanding the gene flow, genetic drift, and possible inbreeding depression within *L. dubia*, in tandem with the structural accessibility and functional connectivity between habitats, is therefore crucial for future conservation efforts. Data obtained might also be able to help create predictive models for *L. dubia* as possible bioindicators to assess changes within local environments and specific ecosystem stressors. Due to the endangered status of this species, non-invasive (exuvia) and non-lethal (partial leg) samples have been collected from bogs within the Scottish Highlands for DNA extraction by means of the Qiagen Blood & Tissue Kit, adapted for insect tissue. This study therefore aims to use five *L. dubia* polymorphic microsatellite loci to investigate the genetic diversity and the occurrence of gene flow between sub-populations, and further evaluate how the white-faced dater navigates its habitat. Laboratory based experiments are currently underway, with results to be expected within the next couple of months.

Technologies

Date: Wednesday 31 August
Time: 12:15
Room: Pentlands East

Abstract 131

Oral Presentation

Green matters: dietary reptile community assessment using DNA metabarcoding

Catarina J. Pinho1,2,3, Mohammed Darwish4, Jiri Smid5,6, Salvador Carranza7, **Raquel Vasconcelos1,2,***

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2 BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal
3 Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Rua do Campo Alegre 1021/1055, 4169–007 Porto, Portugal
4 Wildlife and Natural Heritage Department, Royal Commission For AlUla, AlUla County, Saudi Arabia
5 Department of Zoology, Faculty of Science, Charles University, Viničná 7, 12844 Prague, Czech Republic
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7 Institute of Evolutionary Biology (CSIC-Universitat Pompeu Fabra), Passeig Marítim de la Barceloneta 37-49, Barcelona 08003, Spain
*corresponding author

DNA metabarcoding is widely used to characterize the diet of species, and it is becoming very relevant for biodiversity conservation, allowing the understanding of ecological networks. AlUla is a city in the Medina Region in north-western Saudi Arabia, with diverse habitats that once thrived with life. Currently, local authorities are committed to re-establishing the rich diversity of plant communities and wildlife in the area. With this work, we aimed to investigate the dietary preferences of the reptile community of Wadi Ashar in AlUla. To better understand the trophic networks involving plants, invertebrates and reptiles at a community level in this restricted area, we collected pellets of reptiles and applied a DNA metabarcoding approach using two genetic markers, one specific for plants and another for invertebrates. With this revolutionary tool for conservation and management, we were able to obtain rapid and holistic information on the community diet composition, diversity, and ecological links at relatively low costs. In this way, we can inform local authorities about which elements are central for Wadi Ashar reptile community.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 132

Poster Presentation

Wildlife population assignment using low-coverage whole-genome sequencing

Nina Vasiljevic1, Iris Biebach2, Lukas Keller2, Adelgunde Kratzer1, Rob Ogden3

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2 Department of Evolutionary Biology and Environmental Studies, Switzerland
3 Royal (Dick) School of Veterinary Studies, United Kingdom

One of the most serious threats to the survival of animal and plant populations is the illegal wildlife trade. Identification of geographic origin of poached animals could facilitate the detection of poaching “hotspots” and trade routes and is thereby an important means of informing law enforcement related to wildlife crime. Geographic origin assignment tests often rely on moderate- to high-coverage sequence data to genotype SNP panels, and require large numbers of geo-referenced samples per locality. These can be difficult to obtain for fields such as ancient DNA and wildlife DNA forensics, where DNA sample quality and number are limited. Here, we use low-coverage whole-genome sequence (lcWGS) data to investigate our ability to simultaneously assign a sample to a particular population, while excluding it from others, when we have different levels of background population structure. We re-sequenced the genome of 80 Alpine ibex individuals from six populations with different levels of pairwise Fst (0.02-0.14) across Switzerland. To examine the use of lcWGS to characterise assignment power we want to answer three questions: (1) how many population reference samples do we need? (2) what read depth is required? (3) how many markers do we need? The development of this method will address the pressing need for affordable and validated methods for identification of geographic origin in the wildlife DNA forensic and conservation genetic communities.

Applications

Date: Thursday 1 September
Time: 13:45
Room: Pentlands East

Abstract 133

Oral Presentation

Citizen science genomics guides conservation strategies of the rapidly declining garden dormouse (*Eliomys quercinus*)

Alina von Thaden 1,2, Sven Büchner 3, Johannes Lang 3, Holger U. Meinig 3 & Carsten Nowak 1,2

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2 LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG), Frankfurt am Main, Germany
3 Justus-Liebig-University Giessen, Clinic for birds, reptiles, amphibians and fish, Working Group for Wildlife Research, Giessen, Germany

In times of accelerating biodiversity loss, the involvement of citizen scientists is gaining importance for large-scale conservation projects. Here, we present how the combined efforts of research institutions, citizen scientists and conservation NGOs enables the generation of genomic data towards applied conservation of a rapidly declining rodent, the garden dormouse (*Eliomys quercinus*). The species occupies divergent habitats and shows contrasting population dynamics across its range. RADseq analysis of 103 samples revealed the existence of distinct genomic lineages within Germany and neighboring countries. We used these results to infer regional phylogeography, assess the genetic status of populations and to delineate different conservation units. Genomic data was further used to develop a reduced SNP panel suitable for non-invasive genotyping, geographic assignment of displaced garden dormouse foundlings and the identification of isolated populations in need of connectivity measures. Importantly, the active involvement of citizen scientists did not only facilitate a genomic characterization of the endangered garden dormouse, but also a comprehensive collection of data on its current distribution, ecology in different habitats and the underlying causes for its rapid declines.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 134

Poster Presentation

Experimental tests of factors affecting genetic rescue using a model system

George West1, Rebecca Lewis1, Jennifer C Perry1, & David S Richardson1

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Inbreeding depression is a severe challenge faced by many endangered species. A reduction in genetic diversity can lead to an increase in the realised genetic load of a population and a loss of adaptive potential. These factors can reduce a populations fitness and make them more vulnerable to extinction. Genetic rescue - the introduction of new genetic diversity to a population to alleviate these problems has been implemented successfully in several instances. However, there are still many questions and risks, including outbreeding depression and genetic swamping, associated with genetic rescue. As such it is important to improve our knowledge of what factors affect the success and long-term consequences of attempted genetic rescue. A key question is what makes a good genetic rescuer? For example, the sex of the genetic rescuer may be important. Females are often limited in the number of offspring they can produce, which may result in less of the rescuers genome making it into later generations. Conversely, males are usually limited by the number of mates available, which could enable faster introgression of the rescuer genome. Utilizing the model species Tribolium castaneum, a promiscuous species, I generated small, inbred populations which showed greatly reduced productivity. I then attempted genetic rescue with an outbred ancestral stock, using either a male or female rescuer. The results of these experiments including short- and long-term effects (such as assessing the potential negative effects of genetic load introduced through genetic rescue) will be discussed.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 135

Poster Presentation

Population genomic analyses of southern giraffe (Giraffa giraffa) reveal discrepancies in taxonomic assignment and the genetic impact of previous translocations in southern Africa

Sven Winter[1, 2, *], David Prochotta[1, 3, *], Emma E. Hart[4, 5], Julian Fennessy[4] & Axel Janke[1, 3, 6]

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2 Research Institute of Wildlife Ecology, Vetmeduni Vienna, Vienna, Austria
3 Institute for Ecology, Evolution, Diversity, Goethe University, Frankfurt am Main, Germany
4 Laboratory of Wildlife Ecology and Behaviour, School of Biology and Environmental Science, University College Dublin, Dublin, Ireland
5 Giraffe Conservation Foundation, Eros, Windhoek, Namibia
6 LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG), Frankfurt am Main, Germany

Giraffe (*Giraffa* spp.) have been traditionally assigned to subspecies by morphological markers e.g., pelage pattern or shape and number of ossicones, and geographic distribution. However, recent genetic and genomic studies have not just shown multiple giraffe species but have also shown that morphological and geographic markers are unreliable for taxonomic assignments. Yet, accurate taxonomic assignment, is crucial for conservation and assessments of extinction risk, especially in southern Africa where translocations of giraffe are common. Mitochondrial DNA was recently used to identify a population of Angolan giraffe (*Giraffa giraffa angolensis*) in southern Zimbabwe that was previously considered South African giraffe (*G. g. giraffa*). Here, we used whole-genome-resequencing of Angolan and South African giraffe to study discrepancies in taxonomic assignment across major giraffe populations in southern Africa and the impact of a 1990s translocation of giraffe from Etosha National Park, Namibia to the Namib desert approximately 200 km to the west. The analyses of the genome-wide SNP dataset grouped individuals of large giraffe populations in Botswana and Zimbabwe with South African giraffe, despite possessing mitochondrial DNA haplotypes of Angolan giraffe. In addition, the analyses verified the release location of the translocation from Etosha National Park to the Hoarusib river catchment and showed an uneven admixture of Etosha giraffe into desert-dwelling giraffe of different river catchments, despite the lack of geographic barriers and known movements. The results of this study call for a large-scale genomic assessment of giraffe across southern Africa and a reevaluation of geographic ranges, census population numbers, and extinction risk.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 136

Poster Presentation

Characterization of selected innate immunity genes in the European wildcat (Felis silvestris) and domestic cat (Felis catus)

Sven Winter1,2, Stefan Prost3,4,5,6, René Meißner1, Carsten Novak7,8, Petr Horin9, Pamela Burger1

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2 Senckenberg Biodiversity and Climate Research Centre, Frankfurt am Main, Germany
3 Department of Behavioural and Cognitive Biology, University of Vienna, Vienna, Austria
4 Konrad Lorenz Institute of Ethology, Vetmeduni Vienna, Vienna, Austria
5 Central Research Laboratories, Natural History Museum Vienna, Vienna, Austria
6 South African National Biodiversity Institute, National Zoological Garden, Pretoria, South Africa
7 Conservation Genetics Group, Senckenberg Research Institute and Natural History Museum Frankfurt, Gelnhausen, Germany
8 LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG), Frankfurt am Main, Germany
9 University of Veterinary and Pharmaceutical Sciences Brno, Brno, Czech Republic

One of the strongest natural selection pressures on the genome are pathogens, which challenge the immune system. In response, highly-polymorphic multigene families encode key receptor molecules that recognize and present foreign peptides to phagocytic immune cells as part of the adaptive immunity. If the variability in adaptive immune genes is reduced like in some wild felid species, other components of the immune system should be selected to provide an adequate immune response. As part of innate immunity, natural killer (NK) cells are a highly heterogeneous population due to the differential expression of NK receptors (NKRs). These are functionally related to adaptive immune genes. Despite their functional importance, the capacities and genetic heterogeneity of NK cells in felids are mainly unknown. The feline innate immune system has been challenged by rapid changes during the process of domestication and by adaptation to different environments. In response, specific properties of feline innate immunity genes have evolved, which differ from other mammalian families and are expressed in NK cells. Here, we present preliminary results based on next-generation sequencing, characterizing, and comparatively analyzing innate and adaptive immunity genes in European wildcats and domestic cats. This project fills a knowledge gap on the existence, function, and (co-)evolution of innate immunity genes in the family Felidae and beyond. Novel information on immunogenetic diversity and selected haplotypes will enable effective genetic monitoring in wild-ranging felids.

Date: Tuesday 30 August
Time: 17:45
Room: Prestonfield

Abstract 137

Poster Presentation

Genomic investigation and kinship provide insights into a highly mobile shark

Fenella R. Wood1, Tanja Schwanck1, James Thorburn2, Andrew Meharg3, Leslie R. Noble4, Catherine S. Jones1

1 School of Biological Sciences, UK
2 University of St. Andrews, UK
3 Queens University Belfast, UK
4 Nord University, Norway

Spurdog are a wide-ranging, highly mobile, K-selected small shark found in temperate seas across the globe. Once a commercially important species, they have experienced severe declines and are now listed as Endangered in the Northeast Atlantic. Despite a zero total allowable catch, they can be caught as bycatch, which as an aggregating species, can comprise of up to <10 tonnes in a single catch. This may impact population size, with subsequent effects on genetic diversity.

Previous research using microsatellite markers suggested that aggregations may contain closely related individuals. As the loss of kin groups can rapidly erode selectable genetic diversity, understanding the genetic composition of spurdog across the British Isles is crucial to assess the potential impact of their removal by fishing on population sustainability. Single Nucleotide Polymorphism (SNP) markers are being used to understand the genetic diversity and population structuring of spurdog across the British Isles. Kinship will also be investigated to reveal whether relations are found within sampled aggregations. This may subsequently provide insight into their aggregating behaviour, in terms of origin and persistence as a group, as well as the genetic diversity of the spurdog that they represent.

Technologies

Date: Tuesday 30 August
Time: 16:55/ 17:45
Room: Pentlands (East/West)
Prestonfield

Abstract 138

Speed talk & poster

Exploring human-amphibian cohabitation with conservation genetics and landscape planning tools

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Land use changes in combination with increasingly frequent droughts associated with climate change are impacting amphibian populations worldwide, causing dramatic declines even within highly protected areas. In the Mediterranean basin, artificial sites have been shown to be critical for the resilience of species that rely on ephemeral ponds for reproduction. With the aim of defining specific guidelines for habitat creation and restoration, we have developed innovative protocols for environmental DNA-based monitoring of species and genetic diversity of alpine amphibian communities. The protocols have been applied to 40 wetland sites in the Province of Trento (Italy), 20 natural areas (e.g., national and local reserves, Natura 2000 Network sites) and 20 of artificial origin or otherwise co-opted for human use (e.g., water basins and agricultural ditches, alpine pasture pools, sports fishing ponds). Species richness and mtDNA sequence data collected with the eDNA protocols will be used to verify the presence and haplotype diversity of these species in both protected and human-impacted water bodies. Architectural parameters and indices of habitat heterogeneity linked to amphibian presence are being measured at each site using remote sensing data and drone photography. In addition, landscape features will be reconstructed using GIS software to identify architectural and landscape characteristics preferred by amphibians in the sampled wetlands.