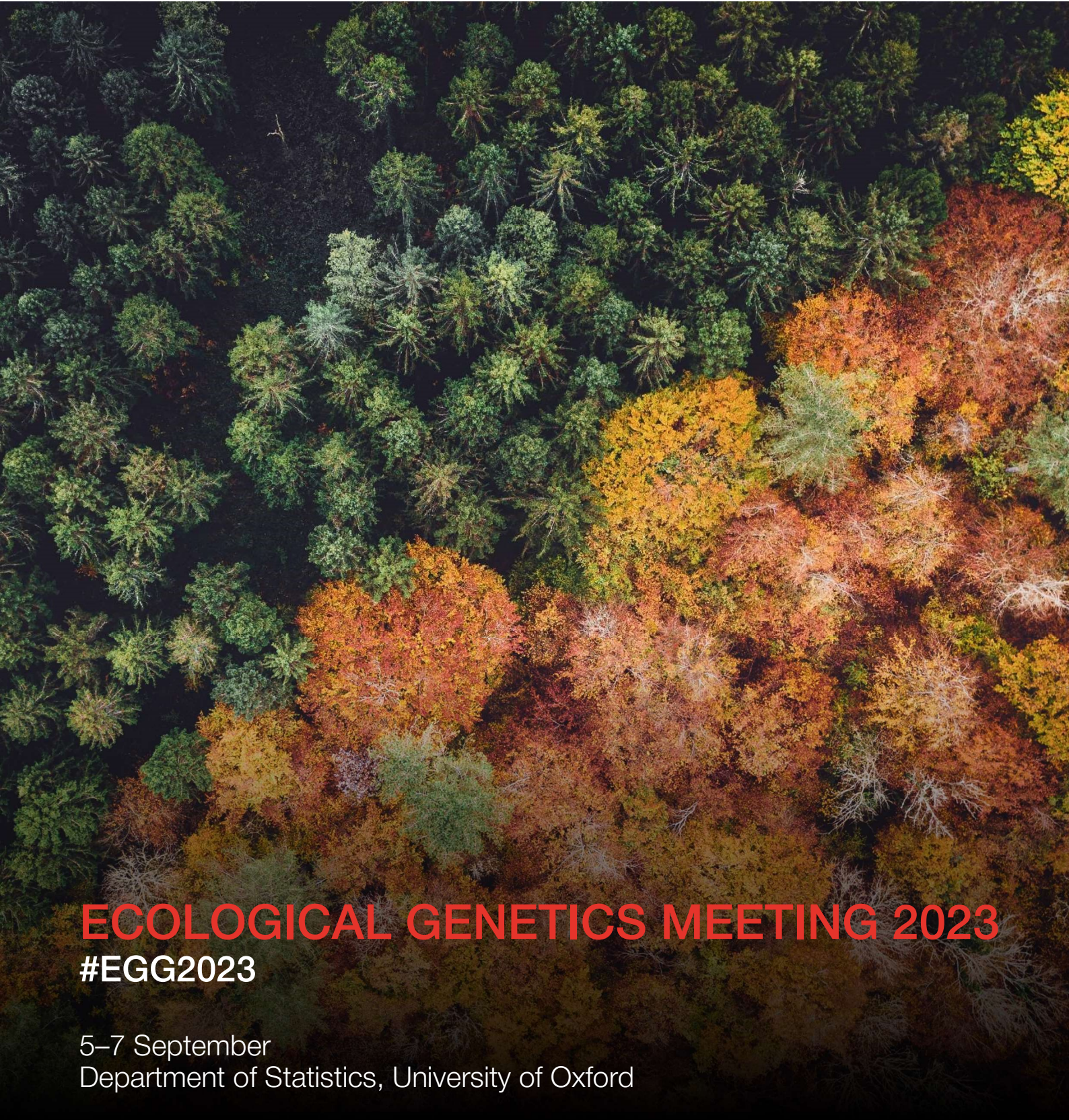


ECOLOGICAL
GENETICS
GROUP



ECOLOGICAL GENETICS MEETING 2023
#EGG2023

5–7 September
Department of Statistics, University of Oxford

P R O G R A M M E

Ecological Genetics Group Committee
(also the Organising Committee of #EGG2023)

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Thom Dallimore, Edge Hill University

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Sponsor



Declaration of competing interests: Cindy Tsai and Henry Hung are the Chief Scientific Officer and the Scientific Advisor of ZYTCA Ltd respectively. ZYTCA Ltd has no role in organising this meeting or influencing the work presented herein.

This programme is accurate as of 31 August 2023.

WELCOME

Welcome to #EGG2023!

I am overflowing with excitement as we gather once again for our annual meeting after the challenges posed by the pandemic. Although we successfully conducted remote meetings, such as the inaugural Climate Change Genomics Workshop last year, we have always cherished our in-person events. It also brings us immense pride to host the longest-running Special Interest Group and meeting since 1957.

Ecological genetics examines the intricate interplay between genetic variations and the biotic and abiotic elements of our environment. While the unwavering passion and dedication of ecological geneticists persist, our field confronts new and ever-changing challenges in these times of biodiversity loss and climate change. Additionally, we acknowledge the gaps that may separate academic research from practical application. However, opportunities also unfold. These include the advancement and affordability of novel genetic and ecological methodologies, along with interdisciplinary and transdisciplinary collaborations that even extend beyond our field.

Maintaining EGG as an ongoing platform for disseminating cutting-edge research, recognizing collaborative synergies, and exploring novel avenues for our field is of utmost importance.

I envision #EGG2023 as a space for like-minded individuals to reconnect while simultaneously propelling the boundaries of our discipline. This moment also affords me the chance to express my gratitude to my Co-Chair, Thom, for his enduring service. I extend my thanks to the committee members, Michelle, Brodie, Rebecca, and Cindy, who joined us last year and significantly invigorated EGG's activities.

With wholehearted sincerity, I extend a warm welcome to each of you and wish you very best in your endeavours.

Yours sincerely


T. H. (Henry) Hung
EGG CO-CHAIR

MEETING AGENDA

Tuesday, 5 September

DAY 1

12:30–13:00	Registration
13:00–13:15	Opening Remarks
13:15–14:00	Opening Keynote 1P-K 1P Chair: T. H. (Henry) Hung
14:00–14:20	1P-1
14:20–14:40	1P-2
14:40–15:00	1P-3
15:00–15:30	Tea Break
15:30–15:50	1P-4
15:50–16:10	1P-5
16:10–16:30	1P-6
16:30–17:00	Networking
17:30–19:30	EGG Social & Pub-quiz

Wednesday, 6 September

DAY 2

08:50	Please arrive 2A Chair: Michelle Davis
09:00–09:20	2A-1
09:20–09:40	2A-2
09:40–10:00	2A-3
10:00–10:20	2A-4
10:20–10:50	Tea Break
10:50–11:10	2A-5
11:10–11:30	2A-6
11:30–11:50	2A-7
11:50–12:10	2A-8
12:10–13:10	Lunch 2P Chair: Thom Dallimore
13:10–13:30	2P-1
13:30–13:50	2P-2
13:50–14:10	2P-3
14:10–14:30	2P-4
14:30–15:00	Tea Break
15:00–15:20	2P-5
15:20–15:40	2P-6
15:40–16:00	2P-7
16:00–17:00	Networking

KEY

Networking sessions
Keynote talks
Contributed talks
Social events

Thursday, 7 September

DAY 3

08:50	Please arrive 3A Chair: Rebecca Whitla
09:00–09:20	3A-1
09:20–09:40	3A-2
09:40–10:00	3A-3
10:00–10:30	Tea Break
10:30–10:50	3A-4
10:50–11:10	3A-5
11:10–11:30	3A-6
11:30–11:45	Closing Remarks
11:45–12:30	Closing Keynote 3A-K
12:30–13:30	Lunch
14:00–16:30	Wytham Woods Visit

EGG Social & Pub-quiz

At the end of Day 1, we will head to King's Arms, the oldest pub in Oxford since 1607, the first evening for our EGG Social & Quiz. Delegates pay for their own drinks and meals. Kudos to **Paul Ashton**, a long-valued member of EGG, for putting together the quiz!

Wytham Woods Visit

At the end of Day 3, we will have a guided walk around the famous Wytham Woods to refresh ourselves after the fruitful EGG2023. This is one of the longest ecological experiments in the UK. Credits to **Henry Hung** and **Cindy Tsai** for introducing the Wytham Oak Project and Wytham Badger Project. Also special thanks to **Nigel Fisher**, the Conservator of Wytham Woods since 2000, for giving a history of the Woods.

VISITING OXFORD

Nestled amidst the verdant landscapes of England, Oxford stands as an emblem of scholarly excellence, historic allure, and architectural grandeur. This venerable city, often referred to as the "City of Dreaming Spires," is renowned for its rich history that seamlessly intertwines with modern vibrancy.

Oxford Botanic Garden and Arboretum

Britain's oldest botanic garden, with plants from around the world, both indoor & outdoor. <https://www.obga.ox.ac.uk/>

Oxford University Museum of Natural History

Immense university museum of zoology, entomology and geology set in a grand neo-Gothic building. <https://www.oumnh.ox.ac.uk/>

Ashmolean Museum

Britain's first public museum on ancient & modern art & antiquities covering world civilisations, plus fine & applied arts. <https://www.ashmolean.org/>

Pitt Rivers Museum

A cornucopia of ethnographic treasures from shrines to shrunken heads, packed in according to type. <https://www.prm.ox.ac.uk/>

The Covered Market

Legendary 1770s indoor bazaar packed with artisan grocers, boutique clothing & buzzing cafes. <https://oxford-coveredmarket.co.uk/>

History of Science Museum

The university's diminutive science museum, curated around objects such as astrolabes and sundials. <https://www.hsm.ox.ac.uk/>

ST GILE'S FAIR & ACCESSIBILITY

St Giles Fair, one of the most celebratory festivals in Oxford, takes place on 4 and 5 September. We expect there may be noise and difficulty to access the meeting venue (Department of Statistics, University of Oxford) on Day 1 of EGG2023. We apologise in advance for any inconvenience and please let us know if there are any concerns of accessibility.

IMPORTANT NOTES TO ALL PRESENTERS

- The meeting supports **PowerPoint**. We can also support PDF presentations (but these will be locked down so edits will not be possible).
- 16:9 landscape mode is optimal.
- Please be present at least **10 minutes** before your scheduled presentation time, although you are encouraged to attend the meeting in full.
- **Your presentation is strictly timed**. Most contributed talks are given **17 minutes**. After the talk, there will be a maximum of **3 minutes** for questions. Please respect these timings and remember that the question time belongs to the audience, not to the speaker.

Please email your presentation to genetics@britishecologicalsociety.org by noon of Day 0 (4 September). The presentation file should be named your talk number (e.g. 1P-2).

IMPORTANT NOTES TO ALL DELEGATES

Entrance & Registration

The meeting venue is managed by the University of Oxford and will be staffed between 09:00–17:00 should you need to enter the venue.

The Registration Desk, located outside the Lecture Theatre, is open throughout the meeting. Committee members will welcome you at the Desk between 12:30 and 13:00 on Day 1. If you are arriving at a different time, please simply pick your name badge on the registration table.

Internet Access

Wi-Fi will be available throughout the University buildings and departments through eduroam. If you believe you have an eduroam account but unsure how to use, please consult the IT guide and staff of your institution.

If you do not have an eduroam account, you should be already provided an Oxford Wireless Lan (OWL) account for you that will remain valid for the meeting.

Mobile Phones

As a courtesy to presenters and other delegates, we ask that all mobile phones and electronic devices be changed to silent mode before entering the lecture theatre.

Social Media

All attendees are encouraged to join the discussion via social media (mainly Twitter), so please use the hashtag #EGG2023 to ensure that you are part of the conversation.

Name Badges

For security purposes, please wear your name badge at all times within the meeting venue. We recommend delegates continue to wear their badges at the social events as well.

Food and Refreshments

Your registration includes tea/coffee and lunches. Please refer to the meeting overview for exact times. We use local sustainable caterers in Oxford.

Smoking Policy

Please note that smoking is not permitted anywhere in the venue.

Currency

Oxford uses Pound Stirling (GBP).

Electricity Voltage

220–240 Volts, Type G electrical plug with three rectangular prongs.

Time Zone

Oxford is currently within British Summer Time (BST; UTC+1). All times listed are BST.

Insurance and Liability

It is recommended that participants arrange their own personal health, accident and travel insurance. The meeting organisers will not accept liability for personal injury or loss/damage to property/belongings of participants or accompanying persons, before, during or following the meeting, on tours or during your stay in Oxford.

Disclaimer

All the best endeavours will be made to present the programme advertised. However, the EGG reserve the right to alter or cancel, without prior notice, arrangements, timetables, plans or other items relating directly or indirectly to EGG2023, for any cause beyond its reasonable control. The EGG is not liable for any loss or inconvenience caused as a result of such cancellation. Delegates are advised to take out their own travel insurance and extend their policy to cover personal possessions as the EGG do not cover individuals against cancellation of bookings or theft or damage to belongings.

PRESENTATIONS

OPENING KEYNOTE

1P-K

Life history and reproduction in the territorial Javan slow loris based on a decade of field data

KEYNOTE SPEAKER

Anne Nekaris, Oxford Brookes University

Reproduction is a key biological process modulating species demographics and regulating population trends over time. Energetic costs of reproduction may be direct, driven by increased demand on nutrients and energy, or indirect, related to the reallocation of resources invested in other tasks to maximize reproduction. The Javan slow loris is a highly territorial venomous primate which lives in small social uni-male uni-female family groups. I use life history data from 166 individuals alongside ~5200 hours of behavioural data collected in Indonesia from 2012-2023 to understand life history patterns as well as to explore the strategies adopted by wild Javan slow loris mothers (*Nycticebus javanicus*) to mitigate energetic costs incurred by reproduction, and to understand the role of fathers behaviourally and genetically. We calculated no seasonality of births, age at first birth (1006 days), gestation (190 days), and interbirth interval (370 days). Temperature positively influenced behaviour of females during gestation and lactation. During gestation and overlap (pregnant whilst lactating), consumption of insects increased, whilst exudate consumption decreased during overlap and cycling. Home range size of females decreased during lactation and overlap, but not for males. Parental and sibling care, especially from adult males, are critical for development of infants and link to dispersal ages of up to three years, and preliminary genetic data reveal that social fathers are also biological fathers. For Critically Endangered species subject to illegal wildlife trade, such data are vital to understand hunting-induced impacts on reproduction and on the social implications of translocations of confiscated animals.

CONTRIBUTED TALK

1P-1

Integrating metagenomics and metabolomics to study the response of microbiota in black soil degradation

Jia Yang, Northeast Forestry University
Jianhu He, Northeast Forestry University
Lin Jia, Northeast Forestry University
Huiyan Gu, Northeast Forestry University

PRESENTING AUTHOR

Jia Yang

As the largest commercial food production base and ecological security barrier, soil degradation in black soil areas seriously threatens various countries' food supply and natural ecosystems. As the key to restoring degraded soils, it is crucial to determine the response of soil microbiota in degraded black soils. This study combined

metagenomics and metabolomics to investigate the effect of degradation levels on microbial communities' composition and metabolic function in black soils. It was found that degradation in black soil areas increased microbial diversity and significantly altered the structure and composition of soil microbial communities. *Sphingomonas* and *Ramlibacter* were significantly affected by soil degradation and can be considered biomarkers of mild and moderate degradation in black soil areas, respectively. Soil nutrient concentrations decreased significantly with increasing black soil degradation, where the critical driver affecting microbial community structure was shown to be C. Microorganisms, in turn, responded to soil degradation by altering their abundance in the carbon cycle pathways involved. In addition, metabolomic analyses indicated that soil degradation significantly modified the soil metabolite spectrum and that the metabolic functions of most microorganisms responding to soil degradation were adversely affected. The combined multi-omics analysis further indicated that biomarkers play a dominant role in accumulating microbial metabolites in degraded black soils. With these findings, we verified that the microbiome is a crucial factor influencing black soil degradation and found the linkage and order between black soils with different degrees of degradation, providing theoretical guidance for the management and restoration of black soil areas.

CONTRIBUTED TALK

1P-2

Genetic diversity and spatial structures of snow leopards (*Panthera uncia*) reveal proxies of connectivity across Mongolia and northwestern China

Charlotte Hacker, Department of Biological Sciences, Duquesne University, Pittsburgh, PA, 15282, USA

Luciano Atzeni, Department of Biology, University of Oxford, Oxford, UK

Bariushaa Munkhtsog, Institute of General and Experimental Biology, Mongolian Academy of Sciences, Ulaanbaatar, Mongolia

Munkhtsog Bayaraa, Irbis Mongolia, Ulaanbaatar, Mongolia

Naranbaatar Galsandorj, Institute of General and Experimental Biology, Mongolian Academy of Sciences, Ulaanbaatar, Mongolia

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Charleen Gavette, Snow Leopard Conservancy, Sonoma, CA, 95476, USA
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PRESENTING AUTHOR

Luciano Atzeni

Understanding landscape connectivity and population genetic parameters is imperative for threatened species management. Such information is lacking for the snow leopard. This study explored hierarchical snow leopard gene flow patterns and drivers of genetic structure in Mongolia and China. A total of 97 individuals from across Mongolia and from the north-eastern edge of the Qinghai-Tibetan Plateau in China were genotyped across 24 microsatellite loci. Distance-based frameworks were used to determine a landscape scenario best explaining observed genetic structure. Spatial and non-spatial methods were used to investigate fine-scale autocorrelation and similarity patterns as well as genetic structure and admixture. A macro-division between populations in China and Mongolia was observed, suggesting that the Gobi Desert is a substantial barrier to gene flow. However, admixture and support for resistance scenarios suggest historical connectivity routes. Populations in Mongolia had greater connectivity, indicative of continuous habitat. Drivers of genetic structure in China were difficult to discern, and fine-scale sampling is needed. This study elucidates snow leopard landscape connectivity and helps to prioritize conservation areas. Although contact zones may have existed, and occasional crossings can occur, focus should be placed on maintaining high connectivity for snow leopard populations within Mongolia and increasing research efforts in China.

CONTRIBUTED TALK

1P-3

Population differentiation in *Carex ornithopoda* (Bird's foot sedge) Willd. using molecular characters

Alexander Gray, Edge Hill University
Jennifer Clayton-Brown, Edge Hill University

PRESENTING AUTHOR

Alexander Gray

Understanding population genetics and how information on variation of a species interacts with the environment is highlighted in studies that utilize molecular markers, such as microsatellites, to investigate variation because of restricting factors, such as geographical limitations or environmental changes. Isolation by distance (IBD) describes the trend of the geographical distance between populations and their genetic similarity. The establishment of a pattern in IBD could imply several restrictions on an organism, for example geographical distance or seed dispersal, which results in genetic drift. *Carex ornithopoda* Willd. is a member of the *Carex* sect. *Digitatae* that has light pigmentation and short, numerous spikes that has seeds dispersed via winds. *C. ornithopoda* provides a good case study to investigate IBD with *Carex* having a

complex genetic history and incomplete classification. Studies investigating population differentiation on a molecular level provide data on genetic frequency and diversity of populations, as well as geneflow between different populations. In the context of this study, microsatellites provide a good case study of high mutation rates leading to higher variation for better comparison to aid in easier classification and more depth. The study will also help bridge gaps in genetic literature of sect. *Digitatae*, and attain use in several future studies in subjects, such as evolutionary history and reviews of dispersal methods of the species.

CONTRIBUTED TALK

1P-4

Is it a bird? The phylogeny of the *Falco* genus

Sophia Gray, Writtle University College
Michelle L Davis, Writtle University College

PRESENTING AUTHOR

Sophia Gray

Traditionally, the biological and morphological species concepts have been used for species classification, a more recent approach is the phylogenetics species concept. Each species concept has rational for its use and limitations, in practice they are often combined to providing consensus support for species recognition. GenBank is an open access database with over 1.6 billion sequences, which is an underutilised resource for genetic analysis of evolutionary relationships. GenBank can be used to analyse and resolve the evolutionary history and taxonomic positioning of a species and/or subspecies. The genus *Falco* is currently composed of 39 species with global distribution and varying levels of conservation concern. The taxonomic standing of species and subspecies within the *Falco* genus is debatable. Traditionally *Falco* species classification has been based on phenotypic traits such as plumage characteristics. This study used the *Cytb* gene to evaluate genetic support for *Falco* species and subspecies, using sequences from GenBank and producing all a neighbour-joining consensus tree was produced. This found a lack of support for most *Falco* subspecies, evidence of hybridisation and possible inter-specific gene flow. Results highlight the importance and value of GenBank as a tool for resolving taxonomic questions, species and subspecies classification and managing conservation resources.

CONTRIBUTED TALK

1P-5

Dose the genetic differentiation of the gut microbiome of the endemic *Gallotia galloti* lizard reflect on their genetic differences

Dayna Cottam, Edge Hill University

PRESENTING AUTHOR

Dayna Elizabeth Cottam

The gut microbiome is made up of bacteria, fungi, and viruses that live within and upon organisms. Recently, research concerning is becoming increasingly addressed in non-

anthropogenic communities (Bahrndorfand et al, 2016) such as reptiles to understand how they have adapted to selective pressures in the environment (Webster et al, 2018). Gallotia galloti is a species of lizard that is native to the western Canary Islands and have shown inter – island phenotypic and genetic variation across Tenerife (Thorpe et al, 1989). Gallotia galloti are famously known in research for their subspecies on the northern (yellow) and southern (blue) sides of the island differentiated by their colouration. In May 2023, Edge Hill University Pielab visited Tenerife and collected 150 – 200 Faecal samples and 20 cloacal swabs from the Gallotia galloti lizard. DNA extraction will be conducted on both types of samples. A Polymerase chain reaction (PCR) will then be conducted followed by a PCR purification process. The samples will be sent off to Novogene for next gen sequencing, all data will undergo bioinformatics and specific statistical analysis. The aim of this study is to use metabarcoding to characterise the gut microbiome of the Gallotia galloti with respect to their sex, environment, and lizard subspecies. The importance of this study is to understand how the gut microbiome adapts to pressures within the environment to help guide our knowledge in conservation management.

CONTRIBUTED TALK

1P-6

Frequent long-distance marine migrations by anadromous trout (*Salmo trutta*) in the English Channel

R. Andrew King, Department of Biosciences, Faculty of Health and Life Sciences, Hatherly Laboratories, University of Exeter

Sophie Launey, ESE, Ecology and Ecosystem Health, Agrocampus Ouest, INRAe, Rennes, France

Jamie R. Stevens, Department of Biosciences, Faculty of Health and Life Sciences, Hatherly Laboratories, University of Exeter

PRESENTING AUTHOR

R. Andrew King

In order to effectively manage anadromous trout populations, accurate information on life history and migration patterns is needed. Reliable information about resident trout is now available for management of in-river populations. However, sea trout spend a significant proportion of their life at sea with relatively little known about this phase of their life cycle. Tracking studies have suggested that many sea trout stay close to their natal river with some individuals moving longer distances. However, such methods are typically restricted to single catchments (or a small number of rivers). Conversely, every fish carries its own unique genetic 'tag', which can be analysed and used to study the origins and movements of sea trout in the marine environment. We have constructed a genetic database incorporating DNA profiles, based on 95 SNP markers, of trout populations from 107 potential source rivers of sea trout from the English Channel. Initial findings indicate significant structuring across the region, with the identification of 14 genetic groups. This baseline has been used to determine the river of origin of adult sea trout sampled at sea in the English Channel and southern North Sea to understand the migration routes that sea trout take from their natal rivers.

Genetic diversity in UK populations of southern wood ant (*Formica rufa*, Linnaeus 1761)

Amy Turner, Edge Hill University
Elva Robinson, York University
Paul Ashton, Edge Hill University
Thom Dallimore, Edge Hill University

PRESENTING AUTHOR

Amy Turner

In contrast to general climate change expectations, the southern wood ant, *Formica rufa*, is in decline at its northern range edge in the UK. These northern populations are geographically remote from other healthy UK populations in central and southern Britain. While the ecological value of these ants to woodland ecosystems is well understood, for instance as the drivers of processes and functions in nutrient cycling, seed dispersion, etc., their patterns of population genetic diversity is poorly understood and may be contributing to their range edge decline. Using microsatellites and nest mapping this study investigated levels of genetic heterogeneity, population diversity and gene flow within and between nests in regions of contrasting latitude within the UK, including range edge populations. Here we discuss the interesting findings from the study and the possible implications for the species and their conservation

The extent of genetic variability of the invasive kingsnake species in the Gran Canaria

Al-fida M. Ahmed, Edge Hill University
Marcio Pie, Edge Hill University

PRESENTING AUTHOR

Al-fida Meer Ahmed

Invasive species pose a major threat to both local and global biodiversity. Additionally, these can have socio-economic implications and pose a risk to human health. Within islands, these species can inflict irreparable damage due to the fragile nature of these ecosystems. The Kingsnake (*Lampropeltis californiae*) is one such invasive species, introduced to the isle of Gran Canaria circa 2007. This species is currently consuming large quantities of the native and endemic fauna at an alarming rate due to efficient spread. Previous studies have analysed *L. californiae* aiming to quantify the spread and adaptations; this study hopes to build upon this research by incorporating phylogenetics alongside population genetics to determine variations amongst the populations. Sanger sequencing will be conducted to confirm the gene sequences. Next nanopore sequencing protocol will be followed next to then sequence all the samples using 13bp tags delivered by custom primers to keep track of all the samples during sequencing for bioinformatic analysis. This research will hope to inform

management techniques in the protection of local biodiversity and provide direction in relevant and effective approaches to eradication.

CONTRIBUTED TALK

2A-3

Are you keeping us together, or apart?!: Investigating the effects of landscape features on genetic connectivity in *Geranium pratense*

Tinu Adenegha, Edge Hill University
Michelle L. Davis, Writtle University College
Thom Dallimore, Edge Hill University
Paul Ashton, Edge Hill University

PRESENTING AUTHOR

Tinu Adenegha

Human activities, such as the expansion of agricultural lands and clearing of vegetation for rural development has exacerbated the natural fragmentation of landscapes. Landscape features have long been assumed to influence patterns of gene flow, in addition to the effects of geographical distance. The uni-direction flow of waterways in particular has been suggested to result in the accumulation of genetic diversity downstream compared to upstream and in contrast to artificial features such as roads which are assumed to allow bi-direction geneflow. *Geranium pratense* (Meadow Cranesbill) is an insect pollinated plant widespread throughout much of Eurasia. The broad geographical range makes it an ideal study species for the effects of natural and anthropogenic landscape features on geneflow patterns. Evidence for the impacts of landscape upon geneflow within this species was minimal, additionally there was no evidence of isolation by distance. Distinct patterns of genetic diversity were observed within river systems, however no support for the unidirectional genetic diversity hypothesis was found. Sites nearest to the source of the river system had similar levels of genetic diversity to those closest to the mouth of the river.

CONTRIBUTED TALK

2A-4

Unstable environments create a greater epigenetic response compared to single stress exposure

Hollie Marshall, University of Leicester UK
Christian Thomas, University of Leicester UK
Lucy Day, University of Birmingham UK
Marine Bochsler, University of Birmingham UK
Maria Cuenca-Cambronero, University of Vic Spain
Henar Tomero, University of Birmingham UK
Eamonn B. Mallon, University of Leicester UK
Leda Mirbahai, University of Warwick UK
John K. Colbourne, University of Birmingham UK
Luisa Orsini, University of Birmingham UK

PRESENTING AUTHOR

Hollie Marshall

Climate change and anthropogenic impact are currently the major drivers of species loss. We need to understand how species adapt to rapid environmental change to mitigate these losses. Epigenetic mechanisms have recently been proposed to play a role in species adaptation. DNA methylation is the most well studied epigenetic mechanism, with gene-body DNA methylation found widely across animals. In this study we use the model organism, *Daphnia magna*, to begin to examine the role of DNA methylation in species adaptation to anthropogenic stress. We tested the hypothesis that pesticide-induced DNA methylation marks would revert to their original state after three generations of pesticide removal. We find that individuals from a population historically exposed to pesticides generally show a greater DNA methylation response than individuals from a population naïve to pesticides. We also find a greater number of DNA methylation changes after three generations of pesticide-removal compared to maintained pesticide exposure. These findings suggest that populations with previous experience of pesticides may be more primed for a DNA methylation response. Additionally, a less stable environment may create a greater DNA methylation response, compared to a single stressor. These findings have implications for the role of epigenetic mechanisms in species adaptation.

CONTRIBUTED TALK

2A-5

Standing genetic variation and de novo mutations drive the repeated evolution of body size in an island-colonising bird

Andrea Estandía, Edward Grey Institute of Field Ornithology, Department of Biology, University of Oxford, UK

Ashley T. Sendell-Price, Edward Grey Institute of Field Ornithology, Department of Biology, University of Oxford, UK

Bruce C. Robertson, Department of Zoology, Otago University, Dunedin, New Zealand

Sonya M. Clegg, Edward Grey Institute of Field Ornithology, Department of Biology, University of Oxford, UK

PRESENTING AUTHOR

Andrea Estandía

Repeated patterns of evolution are commonly observed across populations of island-dwelling birds; including changes in morphology, reduced dispersal capacity, and a slowed pace of life. This set of repeated evolutionary changes is known as the 'island syndrome'. However, whether these convergent phenotypes arise from standing genetic variation and potentially have the same genetic basis, or whether different new mutations are responsible, remains largely unexplored. Silvereyes, of the white-eye bird family Zosteropidae, show several features of the island syndrome, including an increase in body size. The species is a prolific natural coloniser of southwest Pacific islands: its island populations vary in age from very recent (<200 years) to intermediate (4000 years) to very ancient (>100 thousand years). To explore how the island syndrome unfolds at the genomic level, we have sequenced 377 silvereye whole genomes from 31 different silvereye populations. We identify de novo mutations associated with morphological variation (body size and bill size) in single lineages. Other associated polymorphisms are common across all populations, suggesting that

standing genetic variation also underlies rapid changes in morphology following island colonisation. We find inversions in Chromosomes 28, 29 and 30 and a neo-sex chromosome, but they are not associated with body size.

CONTRIBUTED TALK

2A-6

Dynamic conservation of genetic diversity in *Juniperus communis*

James Baker, The University of Edinburgh
Stephen Cavers, The UK Center for Ecology & Hydrology
Joan Cottrell, Forest Research
Richard Ennos, The University of Edinburgh

PRESENTING AUTHOR

James Baker

The common juniper, *Juniperus communis*, is one of only three conifers native to the UK. Despite being one of the most widespread conifers in the world, juniper populations in the UK and Europe have been in a state of decline for the past century due to habitat fragmentation, land use change, low regeneration and, most recently, the introduction of *Phytophthora austrocedrii*. This project aims to measure the impacts of these effects by quantifying the genetic diversity in juniper populations across the UK using genetic fingerprinting and a common garden trial. Our findings suggest distinct genetic groups within *Juniperus communis* spp. *communis* and spp. *nana*. Although these groups are significantly differentiated, both genetically and phenotypically, they are not entirely isolated from each other. These findings can provide valuable insights to conservation managers, who have been working without a thorough genetic survey of UK juniper populations. We will use our results to guide the inclusion of UK juniper populations as a Gene Conservation Unit (GCU) under the European Forest Genetic Resource Program (EUFORGEN) framework to preserve local adaptations and the adaptive capability of populations.

CONTRIBUTED TALK

2A-7

The association of the single nucleotide polymorphism C789A in the dopamine beta-hydroxylase gene (DBH) and aggressive behaviour in pitbull-type dogs

Zoe Thomson, Writtle University College
Michelle Davis, Writtle University College

PRESENTING AUTHOR

Zoe Thomson

Canine aggression poses serious public health and animal welfare concerns. The Dangerous Dogs Act 1991 protects the public by implementing restrictions on ownership and sales of breed 'types'. Bite statistics show that dog bite incidents continued to rise after its implementation, raising concerns about its ability to sufficiently protect the public. Research into canine genetics could highlight genes and single

nucleotide polymorphisms (SNPs) within a gene that predispose an individual or breed to aggressive behaviours. Previously, the DBH gene the C789A polymorphism has been linked to aggressive behaviour in canines. This study aims to determine if there is an association between C789A genotypes and aggressive behaviour in Pitbull type dogs. The results show no significant association in DBH genotypes and allele frequency between aggressive, nervous, and non-aggressive dogs ($\chi^2 = 6.23$, d.f. = 4, $p = 0.182$). Future research should focus on genome wide association studies (GWAS) to identify and confirm genetic markers that contribute towards aggression in Pitbull type dogs, although, epigenetic processes could contribute to altered phenotypes. The identification of multiple SNPs could allow for the development of a SNP chip, similar to those used in livestock production, to identify predispositions towards aggressive behaviour in Pitbull type dogs.

CONTRIBUTED TALK

2P-1

Interspecific behavioural interference and range dynamics in smokey rubyspots (*Hetaerina titia*)

Christophe Patterson, Durham University
Jonathan Drury, Durham University

PRESENTING AUTHOR

Christophe Patterson

An overlooked biotic interaction between species is interspecific behavioural interference: any aggressive, territorial, or mating behaviour by one species that has a negative impact on the fitness of another species. Behavioural interference can decrease population growth rates, cause exclusion from adequate habitat, and reduce or prevent dispersal into novel areas. It is yet to be demonstrated that variation in the degree of behavioural interference experienced between species has led to variation in the spatial distribution of those species. *Hetaerina* damselflies species experience varying levels of interspecific behavioural interference within and between species. Using ddRAD sequence data, we present our work on understanding how variation in behavioural interference across *Hetaerina* damselflies has influenced their phylogeography and historical demography.

CONTRIBUTED TALK

2P-2

Discerning adaptive haplotype blocks in goatgrass (*Aegilops*)

Ashley L. Tuffin, University of Edinburgh, Scotland's Rural College

PRESENTING AUTHOR

Ashley L. Tuffin

Goatgrasses (*Aegilops* spp.) are some of the closest wild relatives to bread wheat (*Triticum aestivum*), a crop with limited genetic diversity due to domestication and further human selection. Goatgrass has evolved into 9-11 diploid species over the last ~7 million years and represents a source of genetic and functional diversity for wheat

breeding. Large haplotype blocks and related chromosomal inversions are associated with ecotypic adaptation and speciation, recently identified in common ragweed, cultivated cotton, and sunflowers. These chromosomal regions of non-recombination can be several megabases long and may contain co-adapted genes. Outlined here is a study aiming to detect potentially adaptive haploblocks in goatgrasses. It will use ancestral recombination graphs to detect ancient introgression events within the genus, such as between *Aegilops speltoides* and subsection *Emarginata* (*Aegilops bicornis*, *sarsii*, *sharonensis*, and *longissima*) and between *Aegilops mutica* and the CU/MN clade (*Aegilops caudata*, *umbellulata*, *comosa*, and *uniaristata*). Investigating haploblock diversity in *Aegilops* not only illuminates the complex evolutionary history of the genus but also allows a greater understanding of the adaptive traits these species possess that would be beneficial to agriculture if transferred to bread wheat.

CONTRIBUTED TALK

2P-3

Carex muricata agg. - a modern approach to an age-old problem

Lorna Halliwell, Edge Hill University
Paul Ashton, Edge Hill University

PRESENTING AUTHOR

Lorna Halliwell

The *Carex muricata* aggregate (section *Phaestoglochin*) is a poorly understood, difficult to classify group of sedges (Cyperaceae). Globally it includes approximately 37 taxa with contrasting views as to how these are separated and ranked, with five of these taxa being native to the UK. Existing classifications are based solely upon morphological characteristics. Therefore, a reassessment of the section using molecular approaches is long overdue. Genetic analyses are being used to determine the phylogeny of the species using a combination of nuclear and chloroplast DNA markers. A population genetics approach, utilising microsatellite markers, is also being taken to identify potential differences in breeding system and assess connectivity between the populations within the UK. This work will provide genetic data which will provide a more informed phylogeny of the aggregate and enable landscape scale patterns of variation to be understood.

CONTRIBUTED TALK

Genomic signatures of sexual selection in the Yellow Fever mosquito *Aedes aegypti*

Claudia A. S. Wyer, Imperial College London; Lauren J. Cator, Imperial College London; Brian Hollis, University of South Carolina

Aedes aegypti mosquitoes are vectors of several arboviruses of public health concern. Promising new control methods involving the mass release of modified mosquitoes to induce sterility or pathogen resistance into wild populations critically depend on the ability of lab-reared males to successfully mate with wild-type conspecific females. A thorough understanding of the genetic basis of male mating success could help to increase efficacy of such control strategies and aid in the development of novel mosquito control interventions. In this study, we compare whole genome sequences from populations of recently colonised *Ae. aegypti* mosquitoes evolved in the presence and absence of sexual selection. Our data show that populations evolved under sexual selection retain greater genetic similarity to recently colonised field populations, and that populations evolving without sexual selection show greater genomic divergence from the ancestral population. We report that significantly diverging variants with functional impact on amino acid sequence were enriched for several gene ontology terms related to chemosensation. Further, we used RNAi to deplete expression of high-confidence candidate genes to determine a mating-related phenotype. Our results highlight the importance of sexual selection in mosquito rearing, and that sexual selection may be important in maintaining genetic similarity to field populations.

The presenting author, Claudia A. S. Wyer, has **withdrawn** this presentation.

Range-wide differential adaptation and genomic offset in critically endangered Asian rosewoods

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John J. MacKay, University of Oxford

PRESENTING AUTHOR

Tin Hang Hung

In the billion-dollar global illegal wildlife trade, rosewoods have been the world's most trafficked wild product since 2005. *Dalbergia cochinchinensis* and *Dalbergia oliveri* are the most sought-after rosewoods in the Greater Mekong Subregion. They are exposed to significant genetic risks and the lack of knowledge on their adaptability limits the effectiveness of conservation efforts. Here, we present genome assemblies and range-wide genomic scans of adaptive variation, together with predictions of genomic offset to climate change. Adaptive genomic variation was differentially associated with temperature and precipitation-related variables between the species, although their natural ranges overlap. The findings are consistent with differences in pioneering ability and in drought tolerance. We predict their genomic offsets will increase over time and with increasing carbon emission pathway but at a faster pace in *D. cochinchinensis* than in *D. oliveri*. These results and the distinct gene–environment association in the eastern coastal edge of Vietnam suggest species-specific conservation actions: germplasm representation across the range in *D. cochinchinensis* and focused on hotspots of genomic offset in *D. oliveri*. We translated our genomic models into a seed source matching application, *seedeR*, to rapidly inform restoration efforts. Our ecological genomic research uncovering contrasting selection forces acting in sympatric rosewoods is of relevance to conserving tropical trees globally and combating risks from climate change.

Ecological genetics of an invasive tree pathogen threatening a vulnerable native host

Daisy Crowson, University of Edinburgh
Stephen Cavers, UK Centre for Ecology and Hydrology
Joan Cottrell, Forest Research

Richard Ennos, University of Edinburgh
Sarah Green, Forest Research

PRESENTING AUTHOR

Daisy Crowson

Invasive plant pathogens can have devastating effects on natural ecosystems. Managing pathogen impact requires an understanding of the complex suite of evolutionary-ecological characteristics governing novel host-pathogen interactions. However, invasive pathogens are often previously unknown to science, and will undergo rapid adaptation to their novel host, presenting major challenges when it comes to studying and managing their impacts. Our research uses an ecological genetics approach to study the invasive tree pathogen *Phytophthora austrocedri*, which is causing widespread mortality in its UK-native host juniper (*Juniperus communis*). We used high-coverage PacBio HiFi data to determine that the pathogen is likely of hybrid origin, as k-mer spectra indicate *P. austrocedri* is an allotetraploid with highly homozygous subgenomes. We then assembled a high-quality draft genome, and used this as a valuable tool to implement population genomic approaches to address key questions regarding pathogen dispersal, mode of reproduction and evolutionary history. By exploring the ecological genetics of this novel pathosystem, we will provide important insights into managing the impact of an invasive pathogen on a vulnerable native tree.

CONTRIBUTED TALK

2P-6

Exploring the uniqueness and shared origins of chalk stream Atlantic salmon (*Salmo salar*) in English and French Channel rivers

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Guillaume Evanno, DECOD (Ecosystem Dynamics and Sustainability), INRAE, Institut Agro, IFREMER, Rennes, France

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PRESENTING AUTHOR

R. Andrew King

Salmon populations in the chalk rivers of the Hampshire Basin have been shown to be some of the most genetically unique and distinctive populations in the eastern Atlantic distribution of the species. Separately, previous research has shown that the salmon populations from Upper Normandy are genetically distinct from French populations on more acidic geology. Here, using a recently developed suite of single nucleotide polymorphism markers, we investigate for the first time the relationships between salmon from rivers on both sides of the English Channel / La Manche. We highlight both the distinctiveness of chalk stream salmon and the precarious future of this unique component of diversity within the species. We corroborate the highly divergent nature of chalk-stream salmon and identify weak genetic divergence between populations inhabiting rivers with similar water chemistries and underlying geology. Additionally, we present evidence that there may be bi-directional straying of adult salmon between the Hampshire Basin and Upper Normandy rivers. Finally, we highlight a potentially bleak

future for both Upper Normandie and Hampshire Basin salmon, predicting significant future losses of genetic diversity.

CONTRIBUTED TALK

2P-7

Predicting landscape connectivity and prioritizing conservation areas for a small carnivore (*Leopardus guttulus*) in South America

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Ho Yi Wan, Department of Wildlife, California State Polytechnic University Humboldt

Flávia Pereira Tirelli, Programa de Pós-graduação em Biologia Animal, Universidade Federal do Rio Grande do Sul

Sérgio L. Altoff, Departamento de Ciências Naturais, Fundação Universidade Regional de Blumenau

Eduardo Eizirik, Escola de Ciências da Saúde e da Vida, Pontifícia Universidade Católica do Rio Grande do Sul

Tatiane Campos Trigo, Museu de Ciências Naturais do Rio Grande do Sul, Secretaria de Meio Ambiente e Infraestrutura

Thales R. O. de Freitas, Departamento de Genética, Universidade Federal do Rio Grande do Sul

PRESENTING AUTHOR

Caroline Charão Sartor

Human-induced habitat loss and fragmentation are one of the main threats to biodiversity conservation. Therefore, for the implementation of effective conservation actions it is imperative to spatially prioritize key areas able to sustain viable populations in the long term. Here, we identified and ranked the most important core areas and corridors for the maintenance of connectivity of *Leopardus guttulus* populations, a threatened Neotropical felid, and evaluate effective population size and genetic diversity, as well as the viability of the identified core areas in the long term. Our analysis demonstrate that populations are fragmented and the links between these areas are few and weak. Despite this, the species still presents moderate genetic diversity levels. However, due to their size, estimated density, and low connectivity, we predict that many current core areas will not be able to maintain viable populations in the long term and populations might be extinct. Also, the remaining populations will become even more isolated, and their size will reduce. This scenario is even more concerning when considered that only ~16% of the core areas' extent is under protection, demonstrating the urgency that exists in the adoption of more appropriate management actions for the species conservation.

The association of the single nucleotide polymorphism (SNP) C789A in the dopamine beta-hydroxylase gene (DBH) and aggressive behaviour in Pitbull type dogs

Amy Willats, Writtle University College
Michelle Davis, Writtle University College

PRESENTING AUTHOR

Amy Willats

Animal aggression is a response to stimuli or conflicts, impacted by their genetics or environment. Canine aggression prompted the introduction of legislation restricting particular aspects of dog ownership in the UK. Pitbull type dogs have been associated with high instances of human-directed aggression and dog-directed aggression and are commonly bred for fighting. The dopamine beta-hydroxylase gene (DBH) maintains the regulation of human and animal emotional states, motor coordination, and behavioural patterns. The aim of this study was to determine whether there was an association between the SNP variant C789A in the DBH and aggression in a dog that is banned within the UK, Pitbull type dogs. There was no significant association between identified genotypes in the DBH and overall aggression ($\chi^2 = 6.233$, $p = 0.182$, $DF = 4$), contradicting findings of a previous study. These results suggest that the genetic basis of behaviour is complex. Epigenetics alter the expression of specific genes without changing the base-pair sequence. This polygenic trait is influenced by a combination of genetic and environmental variants and controlled by simultaneous gene expressions. This indicates that the likelihood of significant variations of aggression and other behaviours within a breed are greater.

Unravelling the genetic basis of adaptation in a changing environment

Sir Erastus G. Rebero, College of Humanities and Social Sciences, University of Nairobi

PRESENTING AUTHOR

Sir Erastus G. Rebero

As the world continues to experience rapid environmental change, understanding the genetic basis of adaptation in natural populations is becoming increasingly important. Ecological genetics provides a powerful framework for exploring the relationship between genetic variation and ecological processes, and for predicting the evolutionary trajectories of populations in response to environmental change. The topic of the submission, 'Unraveling the Genetic Basis of Adaptation in a Changing Environment', refers to the study of how genetic variation within natural populations influences their ability to adapt to changing environmental conditions. With the world experiencing rapid and unpredictable environmental changes, understanding the genetic basis of adaptation is becoming increasingly important. This research seeks to identify the genetic traits that enable populations to thrive in their environment and to predict how

these traits may change over time in response to changing environmental conditions. Ecological genetics is a rapidly evolving field that combines principles of ecology and genetics to understand the evolutionary dynamics of populations. By studying the genetic basis of adaptation, researchers can gain insights into how populations respond to environmental stressors such as climate change, habitat loss, and pollution. This information is critical for predicting the potential impacts of environmental change on biodiversity and ecosystem functioning. Moreover, understanding the genetic basis of adaptation can help inform conservation and management strategies. By identifying the genetic traits that enable populations to persist in changing environments, conservationists can prioritize the protection of genetic diversity in threatened populations. Additionally, genetic tools can be used to monitor the genetic health of populations and inform translocation efforts to enhance genetic diversity. In summary, the study of the genetic basis of adaptation in a changing environment is critical for understanding the evolutionary dynamics of natural populations, predicting their responses to environmental change, and developing effective conservation and management strategies.

CONTRIBUTED TALK

3A-2

Molecular evolution of insect defence traits in forest tree populations

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Aris Janson, SILAVA, Latvia State Forestry Institute
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PRESENTING AUTHOR

Ernest T. Y. Wu

Forest trees are exposed to many insect pests, making their ability to defend insect attack important to ecosystem health. In *Picea glauca*, white spruce (WS), a defence related gene, β glu1, is responsible for releasing phenolic compounds (acetophenones) as a chemical defence against *Choristoneura fumiferana*, spruce budworm (SB), an insect defoliator. β glu1 is also expressed in *Picea abies*, Norway spruce (NS), although SB is not present within its range. The phenotypic variation of the acetophenone defence biomarkers is highly variable with trends suggestive of local adaptation found in previous regional landscape studies. We aim to understand the molecular underpinnings in response to the selective pressures that modulate this phenotypic variation on a range-wide scale in North America for WS and Europe for NS. Our results show that in eastern North American WS populations, which were historically associated with higher intensities of SB outbreaks, have higher β glu1 transcript levels. In western North American WS and in NS populations, where there is more diversity of other insect pests such as bark beetles but lower abundances or no SB, β glu1 transcript levels are comparatively lower. Therefore, selective pressure from a target species attack is key in modulating the phenotypic variation in foliar defence traits.

The scaly male ferns: how many sets of chromosomes?

Alison J. Evans, Edge Hill University
Roger Golding, Fell View, Bowness-on-Solway
Libor Ekrt, University of South Bohemia, Czech Republic
Sven Batke, Edge Hill University
Paul Ashton, Edge Hill University

PRESENTING AUTHOR

Alison Jean Evans

The taxa in the *Dryopteris affinis* complex of scaly male ferns have arisen through hybridisation and reticulate evolution, which is ongoing, making it difficult to untangle their evolutionary relationships. Current taxonomic treatment of the group in the UK and Ireland is inconsistent, with Sell and Murrell (2018) describing eight species, and Stace (2019) listing one species with four subspecies. There is a lack of morphometric evidence to justify either approach. How species should be defined in a complex such as this is open to question. A European-wide study of the *D. affinis* complex led by Michael Kessler, University of Zurich, uses the GoFlag target enrichment probes to generate phylogenetic information. My contribution to this project is to produce descriptions of the UK and Irish taxa, informed by morphometric analysis, flow cytometry, and cytological investigation. Ecological and genetic studies on these ferns depend on reliable identification of taxa, and knowing ploidy is a great help in identification. Average stomatal length is thought to increase with ploidy level. My study examines this relationship to try to find a way of estimating ploidy that is more easily accessible than flow cytometry. Identification guides will be made available online.

Patterns of genetic variation in the riparian plant *Carex aquatilis* (water sedge)

Jennifer Clayton Brown, Edge Hill University
Paul Ashton, Edge Hill University

PRESENTING AUTHOR

Jennifer Clayton Brown

Riparian systems are diverse and widespread within the UK. Water borne seed dispersal (hydrochory) helps shape the genetic diversity of the associated flora. Despite its potential significance, the role of this distribution method in genetically structuring populations has not been fully addressed. *Carex aquatilis* is a riparian sedge species restricted to a few rivers systems in the UK with some outlying populations. This study focuses upon the three regions: the Scottish Highlands, the Scottish Borders and Wales. Genetic analysis utilising SSRs was used to determine the genetic diversity and isolation by distance (IBD) in populations downstream vs upstream within the same river system and between adjacent catchments. Isolated populations were incorporated both within the mainland and on adjacent isles. IBD is evident, with unique gene pools

present in isolated sites and a distinction between genetic portfolios present in the different regions. However, no significant difference genetic variation was observed between upstream and downstream populations or between the adjacent river systems. These findings indicate dispersal methods outside of hydrochory are being utilised bypassing geographical barriers between catchments. This has implications for broader connectivity within the landscape.

CONTRIBUTED TALK

3A-5

All sedges have edges, but do the rare ones have low genetic diversity?

Michelle Davis, Writtle University College

PRESENTING AUTHOR

Michelle Davis

There is generally an assumption that rare species must, by virtue of their rarity, have lower genetic diversity than related species within the same genus with this is especially true within highly modified and/or fragmented habitats such as are found within much of the British Isles. However, it is not common that these assumptions are tested and where it has been results are mixed suggesting that the landscape and life history of the species also plays a significant role. *Carex*, also called true sedges, are a genus with global range and found on every continent except Antarctica. Within the UK there are 90 recognised native and two non-native species making them particularly interesting for studies on comparative genetic diversity. This study compared the rare *C. filliformis* and the common *C. flacca*, within the same geographical region, to determine what difference there was in population differentiation and genetic diversity between the two species, and what this could suggest about the genus more broadly.

CONTRIBUTED TALK

3A-6

Genome-wide methylation patterns in European badgers (*Meles meles*) are associated with pre-natal weather conditions and early-life weight and reveal adaptive hotspots in 47S rDNA

Ming-shan Tsai, Wildlife Conservation Research Unit, University of Oxford
Tin Hang Hung, Department of Biology, University of Oxford
Chris Newman, Wildlife Conservation Research Unit, University of Oxford
David Macdonald, Wildlife Conservation Research Unit, University of Oxford
Christina Buesching, Department of Biology, University of British Columbia

PRESENTING AUTHOR

Ming-shan Tsai

Adversity experienced in early life can cause permanent changes in individual phenotypes through epigenetic modification, such as DNA methylation. There is particularly a growing interest how prenatal conditions can exert developing stress on phenotypes. In this project, we utilised blood samples from a natural population of European badgers (*Meles meles*) studied systemtically at Wytham Woods for more than

30 years and analysed methylation patterns in ~4-month-old 95 individuals between 2003 and 2011 using reduced representation bisulfite sequencing. Incorporating sliding time-window approach, gradient forest model, and latent factor mixed-effect model, we detected that temperature- and precipitation-related variables in early pre-implantation had the largest importances in explaining methylation variation. Most of the significant CpG sites were located in the 47S rDNA region on chromosome 16. In a parallel analysis, we also found that 1,641 CpG sites were significantly associated with early-life weight. Enrichment analysis revealed three significantly over-represented KEGG pathways: phospholipase D signaling pathway, GABAergic synapse, and morphine addiction. Methylation of two rDNA CpG sites (61089 and 68845) were concurrently associated with weather variables and early-life weight, implying a plausible mechanism that might relay environmental stress to phenotype stress. Our study provided critical insights into early-life adaptation to environmental changes in badgers.

CLOSING KEYNOTE

3A-K*

Genomic fruits from the Darwin Tree of Life project

KEYNOTE SPEAKER

Alex Twyford, University of Edinburgh

The field of ecological genomics is at a turning point, where many unresolved questions can now be addressed using high quality reference genomes for non-model species. The Darwin Tree of Life (DToL) project has recently hit the milestone of generating 1,000 reference genomes for diverse wild collected British species. Here, I consider how plant genomes generated by DToL can be integrated with the wealth of knowledge on the diversity of the British flora. My focus is on illustrating why complete taxon coverage, as well as high quality genomes, are both important for addressing ecological and evolutionary questions. Complete sequencing of the 1500 native vascular plant species for DNA barcoding loci have enabled the first large-scale integrated analyses of hybridisation, showing parental genetic distance is more important than geographic range overlap in determining the outcomes of hybridisation. High quality genomes from focal species have enabled 'deep dives' into genome biology, including revealing the repeat landscape in the largest genome ever sequenced, the 90Gb genome of the European mistletoe. Future large-scale floristic analyses promise to combine the benefits of broad-scale analyses of diverse species, with the precision to infer evolutionary process from whole genome sequence data.

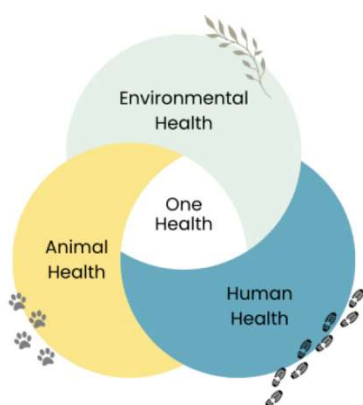
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