

EEBST 2021

Ecology and Evolutionary Biology Symposium, Turkey

16 - 21 August, ONLINE

ABSTRACT BOOK

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Organization and Scientific Committee:

Anıl Soyumert (Kastamonu University)

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Özge Erişöz Kasap (Hacettepe University)

Sibel Küçükyıldırım (Hacettepe University)

Tutku Aykanat (University of Helsinki)

Keynote Speakers:

Maria Paniw: Dr. Maria Paniw is a population ecologist, working at the Estación Biológica de Doñana, Spain as a Marie Curie Research Fellow. Her research focuses on how intrinsic (density) and extrinsic (environment) factors, biotic interactions, and individual traits interact to determine population structure and dynamics. She works with long-term data on animal and plant populations, and she is particularly interested in how population projections under global change can be improved by using mechanistic population models. She is the recipient of ESA's Outstanding Publication Award in Ecological Forecasting (Paniw et al. 2019, Science).

John McCutcheon: John McCutcheon is the associate director of the Biodesign Center for Mechanisms of Evolution and a professor in the School of Life Sciences at ASU (Arizona State University). McCutcheon studies endosymbiosis, the process by which one cell becomes a long-term resident inside another cell. He is interested in how and why symbioses form, how they are maintained and what happens as the associations become more and more intertwined. His work is also focused on the genomic, cell biological, and biochemical outcomes of these interactions. He is a fellow of the American Academy of Microbiology and the American Association for the Advancement of Science and is the recipient of the Presidential Early Career Award for Scientists and Engineers (PECASE, 2019).

John Linnell: Dr. John Linnell is a professor at the Inland Norway University of Applied Sciences and a Senior Research Scientist at Department of Terrestrial Ecology, Norwegian Institute for Nature Research. He obtained his doctoral degree in 1994 at University College Cork, Ireland. Dr. John Linnell is an ecologist who works with conservation related issues on large carnivores and wild ungulates. He conducts interdisciplinary research on the interactions between humans and wildlife with a view to promoting coexistence. He has worked in Norway, India, Myanmar, Turkmenistan, Kazakhstan, Brazil, Albania, Macedonia, Kosovo, Serbia, Bosnia & Herzegovina, Croatia, Estonia, Latvia, Lithuania, Greenland. He has been responsible for coordinating several interdisciplinary projects and his main focus is on human wildlife conflict and in combining ecology together with the human-dimension to come up with long term sustainable wildlife management programs. In addition to research he has also been involved in policy support projects for the government of Norway, the Council of Europe and the European Commission. He has published more than 400 scientific papers, 11 books, 8 book chapters and 29 scientific reports. He is an associate editor for Wildlife Biology, and a member of the Large Carnivore Initiative for Europe (LCIE-IUCN/SSC).

Torsten Günther: Dr. Torsten Günther is a Group Leader at the Department of Organismal Biology at Uppsala University. He graduated from the Friedrich-Schiller-University Jena in 2008 and received his M.Sc. in Bioinformatics. He did his PhD studying the population genomics of *Arabidopsis thaliana* and received his PhD in 2013 from University of Hohenheim. He joined the Mattias Jakobsson's laboratory at Department of Ecology and Genetics at Uppsala University as postdoctoral researcher between 2013 and 2015. Until now, he has published a total of 39 peer reviewed articles including those in prestigious journals such as Science, Nature Genetics and PNAS. His research is focused on understanding the migrations and adaptations of ancient human populations from Eurasia as well as domestication of wild animals in prehistory. He is pioneering the field not only by palaeogenomics research encompassing high quality population genomics analysis of large

genomic datasets but also developing new methods to analyze ancient DNA sequences such as methods for inference of kinship.

Stephen Woodward: He is currently working at the School of Biological Sciences of the University of Aberdeen, Scotland, UK. His main research is focused on alien invasive pathogens, their detection, the damage they cause, how they are spread globally and mitigation methods that can be used to reduce their impacts on natural ecosystems. He has worked in plant pathology for over 40 years, with 38 years in tree-pathogen interactions, initially on the physiological of root pathogen-host interactions. Following many years researching the ecological interactions between trees and pathogens or saprotrophs, his work transferred mostly to the impacts of alien invasive pathogens on trees and forest ecosystems in general. He has also published extensively on biological control of forest pathogens. He led seven EU-funded programmes and participated in many others, along with projects funded by UK Research Councils and charities, with funding in excess of £7 million. He is involved in several initiatives in collaboration with colleagues in Turkey.

Daniel Croll: Daniel Croll joined the University of Neuchâtel, Switzerland, in 2017 where he leads the Laboratory of Evolutionary Genetics as an Assistant Professor. Daniel Croll received his MSc in Biology in 2003 and his PhD in Life Sciences in 2009 from the University of Lausanne, Switzerland. He then joined the ETH Zürich as a postdoctoral fellow. Later, he received an Advanced Postdoctoral Fellowship from the Swiss National Science Foundation to work 2013-2014 at the University of British Columbia in Vancouver, Canada. In 2015, Daniel Croll was appointed as an Oberassistent (group leader) and lecturer at the ETH Zürich. At the University of Neuchâtel, Daniel Croll continues to investigate the evolutionary dynamics of disease emergence in agricultural ecosystems. The main interests include the dissection of phenotypic traits using genome-wide association mapping, the mechanisms of rapid genome evolution and the signatures of recent adaptive evolution.

Cindy Looy: Cindy Looy is an associate professor at the University of California, Berkeley, and a curator at the UC Museum of Paleontology and Herbarium. She describes herself as "a plant ecologist who works in the past" and studies the response of Paleozoic plants and plant communities to environmental change during periods of mass extinction and deglaciation, and their potential evolutionary consequences. In particular, her primary research is focused on terrestrial aspects of the end-Permian biotic crisis and its aftermath, and the transition from a glacial-dominated world to an ice-free one during the late Carboniferous to the middle Permian.

Luis Escobar: Luis Escobar is Doctor of Veterinary Medicine, Master in wildlife management and veterinary sciences, and PhD in disease ecology. His research has three focal themes, which in turn are the main lines of his academic program: Diseases Biogeography, Global Change, and Ecoinformatics. His work focuses on the application of ecology and biogeography to the study distribution and dynamics of infectious diseases. His laboratory explores classic and new theoretical frameworks and methods for investigating the linkages between environmental change and disease emergence. Escobar research includes multi-parasite, multi-host diseases systems for vector-borne diseases such as dengue and leishmaniasis, bat-borne diseases such as rabies and coronaviruses, and water-borne diseases such as cholera. Dr. Escobar's research generally includes additional studies of biodiversity conservation, biological invasions, and climate change.

A. Townsend Peterson: Town Peterson is a Ph.D. in evolutionary biology, and is University Distinguished Professor in the Department of Ecology and Evolutionary Biology and Curator of Ornithology in the Biodiversity Institute, both at the University of Kansas. Peterson works broadly across questions related to biological diversity, including broad biodiversity patterns, speciation mechanisms, distributional ecology, and disease risk mapping. Particular foci of his work at present include conceptual frameworks and empirical protocols for understanding geographic and environmental distributions of species, understanding the processes that interact to produce broad biodiversity patterns, and century-scale historical effects on distributions of species and ecosystems. Peterson's lab at the University of Kansas is large and diverse, including young scientists from around the world, all sharing interests in biological diversity.

Kathryn R. Elmer: Dr. Kathryn Elmer is an evolutionary ecologist who aims to understand the processes that drive adaptive genetic divergence and ecological speciation in the wild, using species complexes such as cichlids, lizards and salmonid fishes as models. Dr. Elmer completed her PhD in Queen's University, Canada in 2006. She later worked as a postdoctoral fellow in the University of Konstanz, Germany, where her research on Cichlids' parallel evolution were funded by Alexander von Humboldt and NSERC grants. She is currently a group leader and a professor in the College of Medical, Veterinary & Life Sciences, University of Glasgow, Scotland.

Anne Yoder: Dr. Anne Yoder is Braxton Craven Distinguished Professor of Evolutionary Biology at Duke University. Anne Yoder obtained her BA in Zoology from the University of North Carolina at Chapel Hill in 1981. Prior to obtaining her doctorate, she worked for the National Museum of Natural History of the United States and for the American Museum of natural history. She then obtained her Ph.D. in biology from Duke University in 1992. Over the next three years, she worked as a postdoctoral fellow in the Environmental Biology Program at Harvard University. Dr Yoder then worked as an Assistant Professor at Northwestern University Medical School and an Associate Professor at Yale University. Anne Yoder also served as a director of Duke Lemur Center. Yoder's research integrates field inventory activities with molecular phylogenetic techniques and geospatial analysis to investigate the biodiversity in Madagascar, with a special interest in lemurs. Dr. Yoder has a number of recognitions; she has been recently elected to the American Academy of Arts and Sciences.

Panel Speakers:

Meryem Beklioğlu: Meryem Beklioğlu is currently a full professor of limnology at Middle Eastern Technical University, Department of Biological Sciences. Her research concentrates on how freshwater ecosystems react to long term environmental and anthropogenic change using holistic approaches encompassing long-term monitoring, controlled experimentation and paleoecology. She is an associate editor for *Limnology and Oceanography Letter*, has over 200 publications and has been the recipient of numerous awards including the highest reward in limnology, the Naumann-Thienemann medal in collaboration with Erik Jeppesen's group.

Mustafa Yücel: Mustafa Yücel is a faculty member and Vice Director in the Middle Eastern Technical University Institute of Marine Sciences. Mustafa is interested in biogeochemical cycles in the ocean, geochemical drivers of seafloor ecosystems (vents, seeps, reducing sediments) and development of novel chemical sensors to study the dynamic environmental processes in situ. Since 2008 he (co)authored a total of 41 publications (10 as a first author). Mustafa also participated in 15 international ocean expeditions (in Pacific and Atlantic Oceans, Mediterranean, Black Sea and the Baltic Sea) and 5 submersible dives to the ocean floor. Mustafa holds young investigator awards from TUDAV (2017), TÜBA (2018), BAGEP (2019) and Mustafa Parlar Foundation (2020).

Juli G. Pausas: Juli G. Pausas is a plant ecology scientist at Centro de Investigación sobre Desertificación (CIDE, Valencia, Spain) of the Spanish National Research Council (CSIC). His research focuses on ecology and evolution of mediterranean and fire-prone ecosystems, and specifically on understanding the role of fire in shaping populations, species (i.e., fire traits), communities (i.e., assembly processes), landscapes, and biomes. He has most experience in the Mediterranean Basin, but without forgetting the global perspective. He has participated in several successful international research projects and has experience in both field and modelling studies. He has written more than 200 scientific papers, co-edited an international book on the ecology of Cork oak woodlands (Island Press), co-authored a book on Fire ecology in Mediterranean ecosystems (Cambridge Press), and book in Spanish on fire ecology.

Program:

Monday 16 August 2021

Population Ecology

Chair: Arpat Özgül

Keynote Address:

14:00 - 14:45	Addressing the global challenges ahead using mechanistic insights from natural populations	Maria Paniw , Donana Biological Station, Spain
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Break & Discussion

15:00-15:15	How host switching can influence the ecological and evolutionary dynamics of parasites?	Elvira D’Bastiani , Laboratório de Interações Biológicas
15:15-15:30	Functional responses of wetland birds to habitat degradation and climate change: A case study from Turkey	Ibrahim Kaan Özgencil , METU, Dept. of Biological Sciences
15:30-15:45	Influences of Immediate Predation Risk on Agonistic Interactions Between Common Chaffinches (<i>Fringilla coelebs</i>) Living in Urban and Rural Habitats	Alper Yelimliç , Koç University, Dept. of Psychology
15:45-16:00	Seasonality effects on large-mammal co-occurrence patterns	Dilşad Dağtekin , University of Zurich, Dept. of Evol. Biol. and Emt. Studies
16:00-16:15	Tracking foraging outcome in the wild using accelerometers	Pritish Chakravarty , University of Zurich, Dept. of Evol. Biol. and Emt. Studies

Break & Discussion

Tuesday 17 August 2021

Genome Evolution

Chair: Sibel Küçükyıldırım & G. Ozan Bozdağ

Keynote Address:

9:00-9:45	The origins and endpoints of cell-in-cell relationships	John McCutcheon , Arizona State University, USA
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Break & Discussion

Tuesday 17 August 2021

Wildlife Ecology

Chair: Anıl Soyumert

Keynote Address:

10:00-10:45	Knowledge needs for large carnivore conservation in Europe: how to train a new generation of conservationists?	John Linnell , Norwegian Institute for Nature Research
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Break & Discussion

11:00-11:15	The spatial ecology of conflicts: Unraveling patterns of wildlife damage at multiple scales.	Carlos Bautista , Institute of Nature Conservation, Polish Academy of Sciences
11:15-11:30	Stopover ecology of some long distance migrants in Kızılırmak delta, Turkey	Kiraz Erciyas-Yavuz , Ondokuz Mayıs University, Ornithological Research Centre
11:30-11:45	Multi-modal signalling in the European robin	Çağla Önsal , Koç University, Dept. of Psychology
11:45-12:00	Is the black tie of Great Tits a signal in territorial interactions? An investigation with 3D printed models	Alican Avşar , Koç University, Dept. of Psychology
12:00-12:15	Snow leopard ecology in Bhutan: distribution and feeding ecology	Dechen Lham , University of Zurich, Population Ecology Research Group

Break & Discussion

Tuesday 17 August 2021

Ancient DNA

Chair: Gülşah Merve Kılınc

Keynote Address:

14:00 - 14:45	Opportunities and Challenges of using genomic ancient DNA in population genetic studies	Torsten Günther, Uppsala University, Dept. of Organismal Biology
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Break & Discussion

15:00-15:15	Complementing aDNA: Catching ancient signals within contemporary human genomes	Burak Yelmen , University of Tartu, Institute of Genomics
15:15-15:30	A new chapter of paleogenomics opens with million-year-old DNA	Patrícia Chrzanová Pečnerová , University of Copenhagen, Dept. of Biology
15:30-15:45	Tracking population structure of Southwest Asia human populations during Holocene	Dilek Koptekin , METU, Dept. of Biological Sciences
15:45-16:00	Metagenomic analysis of the DNA reads from the medieval warship crew	Emrah Kırdök , Mersin University, Department of Biotechnology
16:00-16:15	Kinship patterns among ancient genomes shed light on past social traditions of the last 10,000 years	Arda Sevkar , Hacettepe University, Dept. of Anthropology

Break & Discussion

Wednesday 18 August 2021

Ecological Crisis on Land and Water

Chair: İsmail K. Sağlam & Efe Sezgin

Panels:

10:00-11:00	Marine mucilage, drought and the ecology and biodiversity of lakes and coastal waters	
	Meryem Beklioğlu , METU, Dept. of Biological Sciences	Mustafa Yücel , METU, Institute of Marine Sciences

Break & Discussion

11:15-12:15	Forest fires across the Mediterranean	
	Juli G. Pausas Centro de Investigaciones sobre Desertificación, Valencia, Spain	

Break & Discussion

Wednesday 18 August 2021

Invasion Ecology

Chair: Kahraman İpekdağ

Keynote Address:

14:00 - 14:45	Changing Climate, Changing Pathogens: Threats to Forest Ecosystems Increase with Climate Change	Stephen Woodward , University of Aberdeen, UK
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Break & Discussion

15:00-15:15	Impact and control of a biological invader: the case study of <i>Dryocosmus kuriphilus</i> in NE Italy	Fernanda Colombari , University of Padova, DAFNAE
15:30-15:45	Tracking population structure of Southwest Asia human populations during Holocene	Oğuzhan Kanmaz , ITU, Eurasia Institute of Earth Sciences

15:30-15:45	Gene drives for vertebrate pest control: spatial modelling of eradication probabilities and time-to-eradication for invasive alien mammals in Australia	Aysegul Birand , University of Adelaide, Dept. of Ecol. & Evol. Biol.
Break & Discussion		

Thursday 19 August 2021

Microbial Evolution

Chair: Hilal Özkılınc

Keynote Address:

14:00 - 14:45	Drivers and brakes on pathogen emergence	Daniel Croll , University of Neuchâtel, Switzerland
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Break & Discussion

15:00-15:15	Eco-evolutionary Consequences of a Novel Trait in E. coli	Zachary D. Blount , Michigan State University, Dept. of Microbiol. & Mol. Gen
15:15-15:30	Draft Genome Assembly and Annotation of a novel Pseudomonas species	Uğur Çabuk , Bolu Abant Izzet Baysal University
15:30-15:45	Microbiome meta-analysis platform identifies host and microbiome interactions	Farid Musa , Izmir Institute of Technology, Food Engineering
15:45-16:00	Evolution of the mosquito-specific Culex pipiens densovirus and its interactions with endosymbiotic bacteria Wolbachia	Mine Altınlı , ISEM, Université de Montpellier
16:00-16:15	Mobile Elements in Mitochondrial Genomes of Monilinia Fungal Pathogens	Hilal Özkılınc , ÇOMÜ, Dept. of Mol. Biol. & Gen.

Break & Discussion

Friday 20 August 2021

Plant Evolution

Chair: Melis Aklam & Barış Özüdoğru

Keynote Address:

10:00-10:45	When conifers took flight: the evolution of wind dispersal.	Cindy Looy , UC Berkeley, Dept. of Integrative Biology
Break & Discussion		
11:00-11:20	Phylogenetics and Genome Evolution of the tribe Heliophileae (Brassicaceae)	Mert Doğan , Masaryk University, Central European Institute of Technology
11:20-11:50	Pollination Ecology, Specialization, and Genetic Isolation in Sympatric Bee-Pollinated Salvia (Lamiaceae)	Ferhat Celep , Kırıkkale University, Dept. of Biology
11:50-12:15	Digging up the past: tracking the domestication syndrome in sunflower using extant and ancient DNA	Melis Akman , UC Berkeley, Dept. of Plant and Microbial Biology
Break & Discussion		

Friday 20 August 2021

Biogeography

Chair: Özge Erişöz Kasap & Hakan Gür

Keynote Address:

14:00 - 14:45	Biogeography of Zoonotic Wildlife Diseases	Luis E. Escobar , FWC, Virginia Tech, USA
Keynote Address:		
15:00-15:45	Simple Processes Determine Complex Biodiversity Patterns on Global Scales	A. Townsend Peterson , KU, Biodiversity Institute
Break & Discussion		

16:00-16:15	Current status of Great Bustard <i>Otis tarda</i> in Turkey: population size, distribution, movements, and threats	Melisa Soyluer , METU, Dept. of Biological Sciences
16:15-16:30	Detecting Phenological shifts of different vegetation covers of Turkey with remote sensing	Tuğçe Şenel , ITU, Eurasia Institute of Earth Sciences
Discussion		

Saturday 21 August 2021

Molecular Ecology

Chair: Tutku Aykanat

Keynote Address:

10:00-10:45	Evolution of adaptive divergences in freshwater salmonids	Kathryns R. Elmer , University of Glasgow, UK
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Break & Discussion

11:00-11:15	Evolutionary History of Asexual Lizard Populations In Lake Van Area	Meric Erdolu , METU, Dept. of Biological Sciences
11:15-11:30	Heritability of immune traits of the pond snail, <i>Lymnaea stagnalis</i>	Cansu Çetin , ETH Zürich/Eawag
11:30-11:45	Genetic Structure of Sedentary and Migratory Bears (<i>Ursus arctos</i>) within Eastern Anatolia	M. Çisel Kemahlı Aytakin , Koç University, Dept. Molecular Biol. & Genetics
11:45-12:00	Examination of the possible role of DNA methylation on gene expression changes in response to acute osmotic stress in invasive Mediterranean Blue Mussel (<i>Mytilus galloprovincialis</i>).	Açelya Eren , Boğaziçi University Institute of Environmental Sciences
12:00-12:15	Investigation of the Effect of Floral Scents on Transcriptome Profiles of Antennal Chemoreceptors of <i>Bombus terrestris</i> L.	Tunç Dabak , İstanbul University Department of Biology

Discussion

Saturday 21 August 2021

Molecular Evolution & Bioinformatics

Chair: Ogün Adebali

Talks

14:00-14:20	Sex-specific phenotypic effects and evolutionary history of an ancient polymorphic deletion of the human growth hormone receptor	Ömer Gökçümen , State University of New York at Buffalo
14:20-14:50	Phylogeny-Aware Amino Acid Substitution Scoring	Nurdan Kuru , Sabancı University, Dept. Molecular Biol. & Genetics
14:40-15:00	Molecular evolution and population genetics of GAD system in <i>L. brevis</i> strains from different environments.	Burcu Tekin , Izmir Institute of Technology, Food Engineering
15:00-15:20	Variant stratified molecular population genetic analyses of SARS-CoV-2 Genome	Bahar Anıl Gürbüz , Izmir Institute of Technology, Food Engineering

Keynote Address:

15:30 - 16:15	Insights into patterns of cryptic speciation: Madagascar's mouse lemurs and the multi-species coalescent	Anne Yoder , Duke Center For Genomic And Computational Biology
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Break & Discussion

Abstracts:

POPULATION ECOLOGY

Keynote address: Addressing the global challenges ahead using mechanistic insights from natural populations

Maria Paniw

Donana Biological Station, Spain

Virtually all ecosystems are increasingly threatened by human activities, and ecologists are now faced with the Herculean task of understanding and projecting the impacts of these threats at various scales. Here, I want to discuss the opportunities of using methods from population ecology as a toolbox to rigorously and holistically assess human impacts on natural systems. Using various empirical examples across plant and animal systems that I was fortunate to work with. I will discuss how we can scale from phenotypes to populations to communities to gain a mechanistic understanding of key drivers of population and community dynamics. In particular, I will stress the importance of such mechanistic models for accurate forecasting and discuss the critical role of long-term studies that allow us to formulate mechanistic models in the first place.

Contact: m.paniw@gmail.com

How host switching can influence the ecological and evolutionary dynamics of parasites?

Elvira D’Bastiani, Karla M. Campião, Sabrina LB Araujo

Laboratório de Interações Biológicas

A traditional idea about parasite-host association is that some parasites are highly specialized in their hosts and therefore, co-speciation can be expected. However, there is accumulated evidence that parasites are able to incorporate new hosts with independent evolutionary histories. The incorporation and sharing of hosts are mediated by compatibility and opportunity of interaction, but little is known about how they influence the ecological and evolutionary dynamics of parasite species. Therefore, here we examined how the host switching can structure the ecological and evolutionary dynamics of parasites. For this we propose a theoretical model based on parasite individuals that can switch among hosts during their evolution. Our model assumes that the intensity of the switching of host to parasites decreases with increasing divergence in the evolutionary time of the host. The model allows parasites to evolve over the host phylogeny and limits parasite reproduction to the individuals that use the same host and have a minimum genetic similarity. Parasite variability arises from genetic recombination

between parents and mutation rate. We compared the model's simulations with nine empirical data of host parasite association. Our results indicate that the host's evolutionary history does not represent a barrier to host switching, but there is a limit for the switching of resources. When compared to empirical data, the model could detect the most probable percentage of host switching. For endoparasites it varied from 0.01% to 11%, and for ectoparasites, the host switching average indicated by the model varied from 0.01% to 25%. Thus, the model shows that host switching is more frequent among ectoparasites, agreeing with the idea that these organisms are more capable of switching hosts due to their ability to disperse and because they are less related to their hosts when compared to endoparasites. These results support that the compatibility with the resources used and opportunity of interaction (dispersion, geographic isolation and ecological context) can be a useful proxy to understand the dynamics of parasite diversity.

Contact: elviradebastiani@ufpr.br

Functional responses of wetland birds to habitat degradation and climate change: A case study from Turkey

İbrahim Kaan Özgencil*, Mehmet Arda Çolak, Melisa Soyluer, Alaz Uslu, Melisa Metin, Gültekin Yılmaz, Meryem Beklioğlu, Korhan Özkan, Zuhale Akyürek, and Erik Jeppesen

*METU, Dept. of Biological Sciences

Human-caused habitat degradation and loss, and global climate change affect birds worldwide, altering their community structure and delivery of ecosystem services. We investigated how breeding wetland bird communities responded to two decades of wetland loss and degradation and climate change in Konya Closed Basin in Turkey, a closed basin larger than the Netherlands, by using two different breeding bird atlases. We found that the loss of functional diversity at the basin scale was three times more intense than the taxonomic loss. Changes in taxonomic and functional compositional beta diversity patterns were contrasting. Overall, functional richness and dispersion were lower at local scale. We also found that the larger species, late-breeders, reed-nesters, diving species, and species with smaller brain mass were the losers and that, unlike expectations, higher trait plasticity did not confer any advantage to their bearers. We offer earlier drying/shrinking of the lakes and resulting potential increases in competition as a novel mechanism for the decline of late-breeding endangered diving ducks.

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Influences of Immediate Predation Risk on Agonistic Interactions Between Common Chaffinches (*Fringilla coelebs*) Living in Urban and Rural Habitats

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Human-caused habitat degradation and loss, and global climate change affect birds worldwide, altering their community structure and delivery of ecosystem services. We investigated how breeding wetland bird communities responded to two decades of wetland loss and degradation and climate change in Konya Closed Basin in Turkey, a closed basin larger than the Netherlands, by using two different breeding bird atlases. We found that the loss of functional diversity at the basin scale was three times more intense than the taxonomic loss. Changes in taxonomic and functional compositional beta diversity patterns were contrasting. Overall, functional richness and dispersion were lower at local scale. We also found that the larger species, late-breeders, reed-nesters, diving species, and species with smaller brain mass were the losers and that, unlike expectations, higher trait plasticity did not confer any advantage to their bearers. We offer earlier drying/shrinking of the lakes and resulting potential increases in competition as a novel mechanism for the decline of late-breeding endangered diving ducks.

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Seasonality effects on large-mammal co-occurrence patterns

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While including seasonality in wildlife population studies is becoming more widespread, the majority of these studies consists of single-species investigations, generally overlooking species interactions. Species interactions, in turn, can vary among seasons and determine habitat-use and co-occurrence patterns of interacting species, e.g. spatial overlap of predator-prey pairs. We applied multispecies occupancy models with imperfect detection to 11 years of camera-trapping data from a human-dominated landscape in northwestern Turkey to investigate seasonality effects on the co-occurrence of 7 different large-mammal predator-prey pairs. We found seasonal differences in the gray wolf x roe deer, gray wolf x hare, and gray wolf x red deer interactions. We showed that the gray wolf's habitat use overlapped with all of the prey species, whereas the habitat use of the lynx overlapped mostly with the hare. Our results indicate that seasonal variation in species interactions must be accounted for in wildlife management of human-dominated areas.

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Tracking foraging outcome in the wild using accelerometers

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Foraging efficiency, a concept inspired from thermodynamics, views the entirety of foraging behaviour as a process where energetic investment by the animal is the input and the energetic content of ingested food is the output. Though this concept has proved to be a useful tool to investigate the link between foraging and fitness, it treats foraging as a black box, thereby occluding the actual mechanism of foraging. Since energy is distributed nonuniformly in the environment, and animals typically possess 'foraging toolkits' composed of multiple behavioural elements that can be combined together in different ways to find and harvest this energy, tracking foraging mechanism over time can yield valuable insights into how individuals interact with their environment. We quantified foraging mechanism through a new metric which we call 'foraging outcome', defined as eating duration (the behavioural result of the process of looking for food) divided by the energy invested in food acquisition (a single value that combines the duration and behaviour-specific energetic costs of the different fine-scale components of the process of looking for food). We tracked foraging outcome in ten Kalahari meerkats (*Suricata suricatta*) (five females, five males) by outfitting them with collar triaxial accelerometers, quantifying the durations of fine foraging modes (searching for surface prey, digging for below-ground prey, chewing) by applying validated behaviour recognition models to the accelerometer data, and quantifying behaviour-specific energetic costs using a new method linking accelerometry and energetics equations. We found that foraging outcome decreased with increasing body mass in females and with increasing age in males. Behaviour durations revealed that lighter females primarily searched whereas heavier females did more digging than searching. Given prey distribution in the Kalahari and foraging competition among meerkats, the contrasting foraging strategies in females imply that lighter females probably 'settled' for smaller surface prey to minimise risk of scrounging by heavier females. Our findings demonstrate that tracking foraging outcome in the wild using accelerometers can reveal new insights into how the mechanism of foraging mediates individual trait-dependent interactions of animals with their physical and social environment.

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GENOME EVOLUTION

Keynote address: The origins and endpoints of cell-in-cell relationships

John McCutcheon

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Mitochondria and chloroplasts are now called organelles, but they used to be bacteria. Understanding the genetic, biochemical, and cell biological events that happened during the transition from 'bacterial endosymbiont' to 'organelle' has been obscured by both time and by a lack of comparative examples. In this talk I will show how the long-term, stable endosymbioses of sap-feeding insects resemble the classic organelles in many ways, and describe some of the remarkably convoluted outcomes that occur when two (or more) cells become integrated with each other.

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WILDLIFE ECOLOGY

Keynote address: Knowledge needs for large carnivore conservation in Europe: how to train a new generation of conservationists?

John Linnell

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Despite being a very crowded and human-dominated continent, Europe has seen a dramatic recovery of large carnivores (wolves, lynx, wolverines and brown bears) during recent decades. This recovery has been due to a range of issues, including changes to legislation and landuse practices. As can be expected from such a diverse continent, there has been considerable local variation in this process of recovery, and in the manner in which some form of coexistence has been achieved. Studying the process of large carnivore conservation in Europe provides interesting insights into the way that science relates to policy. In this talk I will argue that the most essential types of knowledge are those that relate to the basic natural history of the species, and those that involve interdisciplinary activities on the borders between ecology, sociology and political science. Unfortunately, these are both areas of research that are challenging to fit into conventional modern day academia.

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The spatial ecology of conflicts: Unraveling patterns of wildlife damage at multiple scales

Carlos Bautista

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Human encroachment into natural habitats is typically followed by conflicts derived from wildlife damages to agriculture and livestock. Spatial risk modelling is a useful tool to gain understanding of wildlife damage and mitigate conflicts. Although resource selection is a hierarchical process operating at multiple scales, risk models usually fail to address more than one scale, which can result in the misidentification of the underlying processes. Here, we addressed the multi-scale nature of wildlife damage occurrence by considering ecological and management correlates interacting from household to landscape scales. We studied brown bear (*Ursus arctos*) damage to apiaries in the North-eastern Carpathians as our model system. Using generalized additive models, we found that brown bear tendency to avoid humans and the habitat preferences of bears and beekeepers determine the risk of bear damage at multiple scales. Damage risk at fine scales increased when the broad landscape context also favoured damages. Furthermore, integrated-scale risk maps resulted in more accurate predictions than single-scale models. Our results suggest that principles of resource selection by animals can be used to understand the occurrence of damages and help mitigate conflicts in a proactive and preventive manner.

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Stopover ecology of some long distance migrants in Kızılırmak delta, Turkey

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Most of the migratory birds cover thousands of kilometres during their migration between breeding and wintering grounds. During these flights they spend most of their time at stopover sites to replenish their energy reserves prior to the next migration step. The critical decisions are when, where and for how long to stopover. With this study we aimed to investigate stopover ecology of Nightingale (*Luscinia megarhynchos*), Thrush Nightingale (*Luscinia luscinia*) and Garden Warbler (*Sylvia borin*) at Cernek Ringing Station (41°36'39" N, 36°05'39" E), nearly 40 km west of Samsun, in northern Turkey. We conducted standardised ringing, and recaptured birds have been evaluated for minimum stopover duration, fat and body mass change. Birds gained fat during stopover, which differed within species, season and age. The autumn stopover duration was longer than spring, and daily weight increase was higher in autumn than in spring. Minimum stopover duration, studied using ring recovery data, was different from radio telemetry data. The habitat use differed in both seasons and for all species. As Kızılırmak delta is an important stopover site before and after birds crossing the Black Sea, it is important to

understand the stopover strategy of migratory birds to develop a comprehensive conservation strategy.

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Multi-modal signalling in the European robin

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The effect on anthropogenic noise on acoustic signals is widely studied. Many animals however, have multi-modal signals which may offer flexibility in signaling under noise. In the present study we ask whether male European robins (*Erithacus rubecula*) use multi-modal signals flexibly in response to anthropogenic noise during territorial defense. Robins have territorial signals in both the visual (posturing) and acoustic (song) modalities. Previous studies found that robins respond both to song and visual signals and noise disrupts communication in the acoustic modality. We predict that during simulated intrusions, European robins will (1) respond with more posturing and fewer songs under experimental acoustic noise, and (2) this shift will depend on urbanization with urban birds displaying a greater shift than rural birds. Contrary to the multi-modal shift hypothesis we did not detect a shift from the acoustic signals to the visual signals under acoustic noise conditions. Instead, under experimental noise, robins sang at higher rates, suggesting that they increase serial redundancy of their acoustic signals under noise.

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Is the black tie of Great Tits a signal in territorial interactions? An investigation with 3D printed models

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Animals often use signals to resolve aggressive interactions without resorting to physical aggression. For instance, in many bird species, melanin-based plumage traits serve as “badges of status” in settling conflicts in dominance hierarchies in winter flocks. Whether such badges are also functional as a signal in territorial interactions however is less studied. Here we ask whether the “black tie” of the great tits, *Parus major*, is used to assess territorial intruders by male great tits. Specifically, we performed playback experiments on territorial males, in which we coupled song playback with 3D printed

Great Tit models with narrow and wide black ties. We also included a negative control (a monochrome gray 3D model) to ask whether great tits perceived the hand-painted 3D models as conspecific intruders. We predicted a more robust territorial response to the models with larger black-tie. Our study is expected to contribute to a better understanding the relationship between territory defense and plumage ornamentation in Great Tits. The use of 3D printed models also provide new opportunities to study the coloration signals in animals.

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Snow leopard ecology in Bhutan: distribution and feeding ecology

Dechen Lham

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The snow leopards (*Panthera uncia*) is one of the worlds most elusive felids. Globally, they occur in twelve countries: Afghanistan, Bhutan, China, India, Nepal, Kazakhstan, Kyrgyz Republic, Mongolia, Pakistan, Russia, Tajikistan and Uzbekistan. Its main threats are habitat loss and fragmentation, natural prey depletion, poaching, retaliatory killing. Therefore, it is important to understand the species distribution and its suitable habitats and also understand the feeding ecology of the snow leopards, in terms of how much wild and domestic are predated. Increased predation on livestock may result in retaliatory killing of the snow leopard. In Bhutan, the southern limit of the snow leopard's distribution range, reliable distribution and habitat suitability studies and the species feeding ecology are lacking, which impedes effective local conservation planning for the species. To understand the feeding ecology of the species, we conducted a micro-histological scat analysis. We found that most of the snow leopard diet consisted of wild ungulates (85%), mostly bharal (61%). We also observed that livestock depredation was higher in summer and differed markedly among four protected areas characterized by various wildlife densities and human activities. Next, to model snow leopard distribution and identify suitable habitat, we used data from 420 snow leopard occurrences and 12 ecological, climatic, or anthropogenic in an ensemble of species distribution modelling framework. Our model identified 21% (7,845 kmsq) of Bhutan as suitable for the snow leopard. Most of the suitable habitat are inside the network of protected areas. Moreover, suitable habitat for the snow leopard closely matches the distribution of its main wild prey, bharal, and had a mean livestock density of 1.34 per hectare and a mean slope of 25 degrees. Our results from both studies indicate the importance of bharal for the persistence of snow leopards in Bhutan. Our studies also establish baseline information on the distribution, suitable habitat and the diet of snow leopards to future species distribution and diet monitoring.

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ANCIENT DNA

Keynote address: Opportunities and Challenges of using genomic ancient DNA in population genetic studies

Torsten Günther

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Sequencing DNA extracted from ancient remains has opened the possibility for studies along the temporal dimension in macroscopic systems. This technological revolution has fundamentally changed the types of scientific studies performed in evolutionary biology and (pre-)history. I am going to show examples how these techniques made it possible to study several population transitions in Scandinavia during the last 10,000 years. Some migrations brought new technologies and are also associated with observations of cultural transitions in archaeological excavations. However, similar to other recently introduced scientific technologies, these opportunities come with some novel challenges for computational analysis partly stemming from specific properties of ancient DNA data such as contamination, fragmentation and post-mortem damage. I will illustrate computational issues arising from mapping short, damaged sequencing reads to linear reference genomes and discuss strategies of coping with these biases.

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Complementing aDNA: Catching ancient signals within contemporary human genomes

Burak Yelmen

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Although aDNA marked an important pinnacle for unravelling the intricate history of the human genome, its availability is limited due to geographical factors and DNA degradation through long periods of time. Thus, it is also important to utilize high-quality and abundant modern genomes to further our understanding in this subject. Contemporary human genomes can be seen as a jigsaw puzzle consisting of ancient components which can be extracted thanks to local ancestry inference algorithms. Studying admixed populations with this approach can help us identify the origin of these components and study them in terms of demography and functionality, which in return can pave the way for a better picture of the recent evolutionary history of the human species.

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A new chapter of palaeogenomics opens with million-year-old DNA

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Ancient DNA gave us the unique opportunity to study microevolutionary processes in various extinct and extant species. However, studying macroevolution and the origin of species was to some extent limited and out of reach for many mammals that evolved on the scale of millions of years ago. Using exceptionally well preserved mammoth teeth from Siberia, we now push the limits of what is possible with ancient DNA and we generate first DNA sequences that are more than one million years old. Our results demonstrate that doing ancient DNA research on such timescales is possible, and hopefully opens a new chapter of palaeogenomics. We also show that sequencing million-year-old genomic data is possible to the extent that it allows us to identify a new genetic lineage of mammoths and to look for the presence of cold adaptations, which are characteristic for woolly mammoths.

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Tracking population structure of Southwest Asia human populations during Holocene

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Southwest Asia was one of the world's first regions to experience the Neolithic Transition and associated demographic changes, most notably population growth. Analyses of genomic data from this region have further suggested increasing rates of population admixture since the Neolithic Transition. Here we present a spatiotemporal picture of human genetic diversity across the Zagros region, South Caucasus, the Levant, Anatolia, and the Aegean. We infer human movement dynamics among regions using different approaches, including sex-biased admixture. Our results reveal common trends as well as regional heterogeneity in the demographic history of Southwest Asia.

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Metagenomic analysis of the DNA reads from the medieval warship crew

Emrah Kırdök

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Researchers are working to unravel human history by examining ancient diseases and changes in the human microbiome over long periods. Ancient metagenomics helps to answer these questions by identifying the taxonomic origin of the sequenced DNA fragments that were extracted from historical human remains. However, these samples are usually contained in different environmental locations for an extensive period. So, they can contain critical amounts of environmental DNA contamination in addition to the human microbiome. Thus, assessing the environmental contamination and host-microbiome content in the ancient specimens could be valuable to understand ancient diseases and historical human microbiomes. In this study, we aimed to analyse the metagenomic composition of the DNA reads, sequenced from teeth samples of the crew from two Medieval warships: Mary Rose and Kronan. To do this, we identified the taxonomic profile of the samples by using metagenomic classification tools. To carefully assess the metagenomic composition of the ancient samples, we used contemporary DNA reads from Human Microbiome and Ocean Metagenome projects. We found that the metagenomic composition of the teeth specimens showed similarity to Ocean Metagenome samples. Moreover, we quantified the environmental contribution and oral microbiome content by using a Bayesian approach. We found that most of the samples contained remarkable amounts of environmental contamination, changing from 25% to 99%. However, the oral microbiome content was low, between 2% to 5% in the best cases. Also, we found an unidentified portion that can not be distinguished using the contemporary DNA reads. This high environmental contamination was expected since these specimens were exposed to seawater for more than 300 years. Finally, we identified DNA reads from several commensal oral bacteria. Using a reference-based assembly approach, we reconstructed an ancient oral bacteria *Desulfomicrobium orale* genome with more than 2x depth of coverage and 85% breadth of coverage. Furthermore, we authenticated these reads by showing the ancient DNA specific deamination damage at the ends of the fragments.

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Kinship patterns among ancient genomes shed light on past social traditions of the last 10,000 years

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The recent accumulation of published ancient genomes has opened up the opportunity to study genetic kinship among individuals buried in the same location and thereby infer past traditions. A major question is whether human societies that adopted agriculture and grew in social complexity over the last 10,000 years also changed their gender-related traditions, such as post-marital residence patterns and/or burial treatment of females and males. Here we investigate these questions using published genomes of more than 5000 ancient individuals spanning the Holocene Era (c.12,000 BP to present). We defined clusters of these individuals who could be possibly related, based on being buried within 200 kilometres and having less than 500 years difference between their archeological dates; we then estimated genetic kinship up to 2nd degree within each cluster. We thus determined 257 close kin pairs across 72,498 pairs tested. In this sample, we observed an overall trend of higher frequency of close kinship among male pairs, compared to female pairs or male-female pairs. This trend was observed consistently throughout the Holocene, with no observable sign of temporal change, and was present both for adults and for subadults. We argue that this pattern of higher male-kinship frequency among published genomes can be explained by two non-mutually exclusive phenomena: i) differences in burial treatment traditions for male and female individuals that creates a bias towards male kin to be discovered and genetically analysed; ii) patrilocality, i.e. adult males remaining with the family and females moving out, such that the latter are not sampled at the same site. Our study provides another example of how ancient genome analyses can contribute to anthropological theory.

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INVASION ECOLOGY

Keynote address: Changing Climate, Changing Pathogens: Threats to Forest Ecosystems Increase with Climate Change

Stephen Woodward

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Stronger evidence for climate change emerges daily, with numerous wild fires burning, excessive heat waves and unprecedented storm events with catastrophic flooding in the news on an almost daily basis. The causes of such problems are clear: human activities; but details of the consequences less so. The aspect we focus on here is the impacts of environmental changes on the appearance of and damage caused by forest pathogens. Global trade over millennia, accompanied very recently with rapid technological advances in packing and shipping techniques, have led to inadvertent transfer of plant pests and pathogens from regions of co-evolution with plant hosts to areas with naïve plant populations, some of which are extremely susceptible to infection and damage. Examples of pathogens of trees which have been moved between continents include numerous *Phytophthora* species with wide host ranges, *Cryphonectria parasitica* attacking *Castanea* species, *Ceratocystis platani* killing *Platanus orientalis* and hybrids, and the pine wilt nematode, *Bursaphelenchus xylophilus*. In addition to these introduced species, changing climate leads to some apparently native pathogens causing much more significant damage than in the past, as with *Dothistroma septosporum*. There are many other alien pathogens attacking forest trees in different regions of the world. In this talk, we provide evidence of the significance of various tree pathogens, both introduced and endemic, causing increasing damage to our forest ecosystems as the climate changes. Where environmental effects on host and pathogen are known, we provide modelled prediction of changes in incidence and severity of the diseases, as the climatic envelope, where the pathogens may impact on tree growth and survival, is pushed northwards. Managing the problems is extremely difficult in the absence of true recognition of the seriousness of the situation in terms of both human responsibility for climate change, coupled with weak and careless control of intercontinental shipping of pests and pathogens.

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Impact and control of a biological invader: the case study of *Dryocosmus kuriphilus* in NE Italy

Fernanda Colombari

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The Asian Chestnut Gall Wasp (ACGW) *Dryocosmus kuriphilus* Yasumatsu (Hymenoptera: Cynipidae), native to China, is able to induce galls on chestnut. It represents an exception to the rule that only seldom gallmakers threaten plant health as, outside its natural distribution range, it is commonly recognized as the most harmful insect pest of chestnut species worldwide. As chestnut is a global commodity, being cultivated for nuts, timber, honey, and ornamental purposes, the species has been unintentionally transported to many countries arriving in Italy and in Turkey in 2002 and 2014, respectively. Invasion success and severe impacts of the pest are explained by the capacity of overwintering wherever chestnut species are present, the reproductive strategy, the combination of different mechanisms of dispersal, and the concept of 'niche opportunity'. ACGW is the only Palaearctic gallmaker able to develop on almost all *Castanea* species and their hybrids, taking advantage from resources unused or underused by native phytophagous species. Furthermore, it escapes from natural-enemy regulation as the low effectiveness of the native species of parasitoids associated to oak gall wasps.

In the Veneto Region (northeastern Italy) the ACGW was first reported in 2007 and, after the failure of some eradication attempts, in a few years the pest expanded its distribution throughout the region, perfectly overlapping the range of the European chestnut. Research studies assessed the negative impact of the ACGW on both nut and wood production (up to 80 and 60%, respectively) and the low mortality inflicted by native parasitoids (less than 2%). Thus, a classical biological program was implemented by releasing the non-native parasitoid *Torymus sinensis* Kamijo (Hymenoptera: Torymidae) and within 3 to 5 years after the establishment of the biocontrol agent the pest was successfully controlled. Currently, five years after the last releases, *T. sinensis* continues to strongly limit ACGW populations without adverse effects on non-target native gallmakers and their associated parasitoids.

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A Hybrid Modelling Framework for Biological Invasions under Climate Change

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Global environmental change is a multifaceted problem with many elements and complex interactions. Biological invasions, as one of them, are known to lead to various severe ecological and economical consequences. In the case of invasions, mitigation and control efforts are mostly labor and cost intensive and require careful planning. Reliable projections produced with computational models can be a highly valuable tool to

constitute a basis for these applications. In the recent decade the increasing number of studies using correlative species distribution modelling methods were conducted to determine the potential invasion ranges without addressing the dispersal mechanisms. On the other hand, agent based modelling as another common method, emphasizes the processes which are difficult to parametrize due to the scarcity of empirical data which connects the environmental variables and species. For this study, a hybrid modular framework was constructed by utilizing the best merits of aforementioned modelling methods to make yearly projections based on both empirical and correlative relations. The framework is spatially explicit and uses environmental data and projection layers as spatial input. In the model, species of interest are represented at the level of individuals as agents which are initially generated based on the occurrence records. The agents have multi-staged life cycles. The modules of the framework handle processes in and between the stages. Due to the flexible structure of the model, life cycle stages, modules and input layers can be determined in accordance with the species and/or the factors aimed to be emphasized in a study. To explain the framework, the results of the experiments which were conducted for a hypothetical invasive annual species and covering the period between 2020 to 2050 with RCP4.5 climate scenario, will be presented.

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Gene drives for vertebrate pest control: spatial modelling of eradication probabilities and time-to-eradication for invasive alien mammals in Australia

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Invasive alien species continue to threaten global biodiversity. CRISPR-based gene drives, which can theoretically spread through populations despite imparting a fitness cost, could be used to suppress or eradicate pest populations. However, gene drives in mammals are yet to be developed, and proof-of-concept studies have largely been restricted to modelling short-lived organisms. We develop an individual-based, spatially explicit, stochastic model to simulate the ability of CRISPR-based homing and X-chromosome shredding drives to eradicate populations of invasive alien mammals in Australia, using rodents (mice and rats), rabbits, cats, and foxes as target species. Through the model, we explored the interactive effect of the efficiency of the drive constructs and the spatial ecology of the target population on the outcome of a gene-drive release. Our results revealed that both drive strategies could be used to

eradicate large populations of these vertebrate pests; however, parameters related to drive efficiency and demography strongly influenced drive performance. We also show that highly efficient drives are not always optimal. When dispersal capabilities are low, rapid local population suppression around the introduction sites can cause loss of the gene drive before it can spread. We conclude that, although the design of efficient gene drives is undoubtedly important, accurate data on the spatial ecology of target species is critical for predicting the result of a gene-drive release.

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MICROBIAL EVOLUTION

Keynote address: Drivers and brakes on pathogen emergence

Daniel Croll

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The emergence of microbial plant pathogens poses severe challenges to global food security. Pathogens can rapidly evolve to overcome resistance in crops and tolerate pesticides. Illuminating the genetic basis and population context of such rapid adaptation is key to our understanding of crop diseases. Using experimental approaches and large-scale whole-genome sequencing of global pathogen collections, I show how fungal pathogen adaptation provides a fascinating case studies of rapid, contemporary evolution. I will be introducing examples of recent disease outbreaks, parallel gains of pesticide resistance and analyses of structural variation to identify drivers of pathogen emergence. Finally, I will propose that pathogens likely face constraints in their adaptation to their hosts. Such trade-offs may provide more sustainable means to control pathogen spread.

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Eco-evolutionary Consequences of a Novel Trait in *E. coli*

Zachary D. Blount

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Novel traits have played an outsized role in the history of life. As qualitatively new, ecologically relevant traits, novelties permit lineages to access new resources and niches, leading to increased ecological complexity and speciation. Experimental evolution with microorganisms provides a means with which to study the origins and consequences of novel traits at a level of depth that is often impossible to achieve in the

natural world. During a long-term evolution experiment (LTEE) with *Escherichia coli*, a novel trait, aerobic growth on citrate (Cit⁺), arose in one of 12 experimental populations owing to the duplication-mediated expression of a previously silent citrate-succinate antiporter (CitT). The Cit⁺ trait has had numerous ecological and evolutionary consequences. The large size of the citrate resource enabled the population to dramatically expand, and the Cit⁺ lineage has begun to diverge ecologically and genetically as it adapts to its new niche. The physiology of the CitT transporter has increased the resource complexity of the environment by causing the efflux of C₄-dicarboxylates into the medium, which the Cit⁺ lineage evolved to re-uptake in an unusual self-cross-feeding interaction. Unexpectedly, the Cit⁺ lineage displays high rates of cell death that are not ameliorated by tens of thousands of generations of further adaptation. Future work will examine how these eco-evolutionary consequences might vary under counterfactual scenarios in which the Cit⁺ trait is conferred by expression of alternative citrate transporters.

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Draft Genome Assembly and Annotation of a novel *Pseudomonas* species

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Pseudomonas species are gram-negative bacteria. They are one of the predominating inhabitants of soil and aquatic environments. Because of their vast distribution, it is expected to occur genome reduction, gene gain/loss in their genome since they tend to interact with plants, other bacteria, and organisms in surrounding environments. Several *Pseudomonas* species can act as plant growth promoting agent, especially by acting as a phosphate solubilizer. Whole genome sequencing gives comprehensive information about organisms including their evolution and biochemical mechanisms. In this study, we presented the draft genome of *Pseudomonas* spp. ESU1531 (stock code of the strain) that was isolated from the root of einkorn wheat (*Triticum monococcum* spp. *monococcum*) in Seben, Bolu. We performed whole genome sequencing using Illumina NextSeq 550 and obtained a total of 2,188,517 paired-end reads in average 76x depth. We used the pipeline for the assembly step that was previously designed to decrease number of contigs and obtain a more compact draft genome. The draft genome of *Pseudomonas* spp. ESU1531 comprise 252 contigs with a GC content of 61.03% and a length of 6,520,191. We were able to annotate 4547 of 5652 coding sequences predicted using PROKKA. We revealed that *Pseudomonas* spp. ESU1531 has several phosphate solubilizing genes in its genome. Moreover, as it is very close to *Pseudomonas thivervalensis*, we also examined whether there is a possible genome reduction or gene gain/loss in case of the same species. However, it is likely that *Pseudomonas* spp.

ESU1531 is a new species according to the results of average nucleotide identity and its position in phylogenetic topology. Our findings will contribute to comparative genomic studies of *Pseudomonas* genome evolution.

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Microbiome meta-analysis platform identifies host and microbiome interactions

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The latest advances in microbiome research have enabled previously impossible studies on interactions between the host genome and its microbiome. Microbial interactions have a profound effect on the dynamics of the microbial populations. Microbes like bacteria, archaea, fungi, microalgae, and viruses can have commensal, mutualistic, and parasitic interactions either among each other or with the host. Genome-wide association studies between host variants and microbiome diversity metrics such as alpha and beta diversity (aka mGWAS) have identified interesting associations and provided understanding on how host genotype interacts or affects its microbiota profile. The studies on microbial interactions require large amounts of data to derive reliable conclusions. However, most of the studies that have produced microbiome data lack common standards, which are extremely important in performing meta-analysis studies. In this study we use our novel microbiome analysis framework called PhyloMAF to perform a microbiome survey study of microbial interactions with a phylogenetic perspective. Microbiota data of 83 inbred *Drosophila melanogaster* lines from two independent studies were processed in PhyloMAF and analyzed to find cooperation, communication, and conflict of OTUs. Processing of OTU-tables primarily consists of mapping taxon names to reference databases followed by taxon name corrections, sample wise merging, extracting reference phylogenetic tree topology and branch length estimation. Correlations of taxa at the genus level were then analyzed using non-metric multidimensional scaling (nMDS) to identify groups of closely related taxa. The results of our analysis suggested possible cooperation and conflict between OTUs based on manifested clusters of phylogenetically related taxa. In conclusion, we demonstrate that our microbiome meta-analysis platform can be a useful tool to study microbial interactions.

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Evolution of the mosquito-specific *Culex pipiens* densovirus and its interactions with endosymbiotic bacteria *Wolbachia*

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Often studied for the deadly viruses they transmit to humans, such as Dengue, West Nile and Zika Viruses, mosquitoes also host a diverse microbiome, including mosquito-specific viruses. The latter attracted scientific interest in the last couple of decades as they cannot infect vertebrates but can interfere with the transmission of mosquito-borne human pathogens. However, their ecology, evolution, and interactions with the rest of the microbiota are mostly unknown. Here, we studied the evolution and microbial interactions of a mosquito-specific virus, *Culex pipiens* densovirus (CpDV). CpDV is highly prevalent in natural *Culex pipiens* s.l. populations, and its worldwide diversity is grouped in two clades with possible recombination events between clades. Furthermore, laboratory experiments show that CpDV shares the same cells with the endosymbiotic bacterium *Wolbachia* within the mosquito ovaries and is transmitted vertically along with it. *Culex pipiens* s.l. populations are always infected with genetically diverse *Wolbachia* (wPip) that is transmitted vertically from mother to offspring and modifies its host phenotypes, including reproduction and survival. Focusing on mosquito populations in Northern Tunisia, we show an influence of different wPip genotypes on CpDV prevalence and a general positive correlation between wPip and CpDV loads. We further investigated whether CpDV and wPip co-diversified in nature due to their vertical transmission and observed a link between CpDV diversification and different wPip strains. However, this signal only exists when comparing sites where the same wPip group infected all mosquito larvae, but no such signal was detected where different wPip groups coexisted, suggesting CpDV horizontal transmission between larvae. Overall, our results provide good evidence for the influence of wPip on a mosquito-specific virus, CpDV, in natural mosquito populations and highlight the importance of integrating *Wolbachia* and mosquito-specific viruses in our understanding of vector ecology in nature.

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Mobile Elements in Mitochondrial Genomes of Monilinia Fungal Pathogens

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Mitochondrial genomes play an important role in many traits and evolution of the fungal pathogens. Genes related to respiration process are known highly conserved in the mitochondrial genomes. On the other hand, mobile genetic elements (or mobile introns) have been detected in many fungal mitogenomes and these sequences are considered the accessory parts of the mitogenomes. These elements have a significant role in resulting substantial variation and shaping the mitogenomes. *Monilinia* fungal plant pathogens are devastating on many stone fruits such as peach. Mitochondrial genomes of the sixteen samples of these pathogens were characterized in detailed and compared within and between the species. Mobile elements encoding homing endonucleases (HEGs) have been detected in the two prominent species of *Monilinia* genus (*M. fruticola* and *M. laxa*). Different LAGLIDADG and GIY-YIG families from group I introns of HEGs were found both in genic and intergenic regions throughout the mitogenomes. The mitogenome sizes of *M. fruticola* ranged from 158,607 to 167,838 bp, and approximately 18.1% of the whole mitogenomes were occupied by HEGs. The other species (*M. laxa*) had larger mitogenome sizes (from 178,351 to 179,780 bp) and carried HEGs with ~35.4% of the total mt-genomes. Those elements were the main reasons causing variation within and between species and expansion of the mitogenome sizes. Mobile introns may also play an important role in evolution of the fungal plant pathogens. This study supported by TUBITAK (Project no. 217Z134).

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PLANT EVOLUTION

Keynote address: When conifers took flight: the evolution of wind dispersal.

Cindy Looy

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Plants have evolved a variety of ways to disperse their diaspores. Each dispersal mode uses biotic and/or abiotic vectors, and often comes with a suite of associated morphological characters to promote dispersal via specific pathways. These so-called seed dispersal syndromes are commonly still visible in fossil remains that can thus be used to infer the dominant dispersal mode in extinct plant groups and inform us about aspects of ecology and migration. During the Late Paleozoic (~310-252 million years ago

(mya)) seeds with adaptations for wind and water dispersal appeared in several lineages. Also in early conifers a variety of seed morphologies existed, characteristic of wind dispersal. Some produced seeds with lateral or encircling wings, while others developed large wings indicative of autorotative flight. To examine the effects of various seed morphologies on aerodynamics and dispersal potential, we studied the flight performance of paper models of three morphotypes found in one species using high-speed cameras in a flight laboratory. These different morphotypes produced a wide variation in potential dispersal capacity. Overall, the results indicate that the evolutionarily novel autorotating winged seeds must have improved conifer seed dispersal, in a time when animals that could help dispersal were virtually absent. During the Mesozoic conifers diversified in their dispersal strategies through further modifications, using various tissues to perform similar tasks, especially in animal-dispersal. The very effective autorotative flight emerged independently at least seven times in extant lineages. Almost all functional morphotypes that we recognize today were present prior before the start of the Cenozoic (66 mya).

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Phylogenetics and Genome Evolution of the tribe Heliophileae (Brassicaceae)

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The unigeneric tribe Heliophileae encompassing more than 100 *Heliophila* species is morphologically the most diverse Brassicaceae lineage. The tribe is endemic to the southwestern South Africa, home of two biodiversity hotspots (Cape Floristic Region and Succulent Karoo). The monospecific *Chamira* (*C. circaeoides*), the only crucifer species with persistent cotyledons, is traditionally retrieved as the closest relative of Heliophileae. Our transcriptome analysis revealed a whole-genome duplication (WGD) ~26.15–29.20 million years ago, presumably preceding the *Chamira*/*Heliophila* split. The WGD was then followed by genome-wide diploidization, species radiations, and cladogenesis in *Heliophila*. The expanded phylogeny based on nuclear ribosomal DNA internal transcribed spacer (ITS) uncovered four major infrageneric clades (A–D) in *Heliophila* and corroborated the sister relationship between *Chamira* and *Heliophila*. We analyzed how the diploidization process impacted the evolution of repetitive sequences through low-coverage whole-genome sequencing of 15 *Heliophila* species, representing the four clades, and *Chamira*. Despite the firmly established infrageneric cladogenesis and different ecological life histories, repeatome analysis showed overall comparable evolution of genome sizes (288–484 Mb) and repeat content (25.04–38.90%) across *Heliophila* species and clades. Among *Heliophila* species, long terminal repeat (LTR) retrotransposons were the predominant components of the analyzed genomes (11.51–22.42%), whereas tandem repeats had lower abundances (1.03–12.10%). In *Chamira*, the tandem repeat content (17.92%, 16 diverse tandem repeats) equals the abundance of LTR retrotransposons (16.69%). Among the 108 tandem repeats identified

in *Heliophila*, only 16 repeats were found to be shared among two or more species; no tandem repeats were shared by *Chamira* and *Heliophila* genomes. Six “relic” tandem repeats were shared between any two different *Heliophila* clades by a common descent. Four and six clade-specific repeats shared among clade A and C species, respectively, support the monophyly of these two clades. Three repeats shared by all clade A species corroborate the recent diversification of this clade revealed by plastome- based molecular dating. Phylogenetic analysis based on repeat sequence similarities separated the *Heliophila* species to three clades [A, C, and (B+D)], mirroring the post-polyploid cladogenesis in *Heliophila* inferred from rDNA ITS and plastome sequences. Repetitive DNA, whole-genome duplication (WGD), ITS, plastome phylogeny, Brassicaceae

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Pollination Ecology, Specialization, and Genetic Isolation in Sympatric Bee-Pollinated *Salvia* (Lamiaceae)

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Previous pollination ecology studies in *Salvia* have demonstrated that there is low specialization to certain subgroups of bees and that pollinator number varies with species and locality. We studied twelve *Salvia* species (three clades with different corolla morphologies and staminal lever mechanisms) which in part co-occur and co-flower to examine pre-zygotic isolation mechanisms and the degree of specialization vs. generalization in pollination ecology. Field and statistical studies shown that mechanical, phenological, and ethological isolation occur among sympatric *Salvia* species. Morphological fit is evident between flower tube length and proboscis length of main pollinators. Pollinator networks indicate that most species are ecological generalists but only few are specialists. The twelve *Salvia* species, though phenotypically and functionally specialized due to their zygomorphic-bilabiate flowers and bee pollination syndrome, differ in the degree of ecological specialization. Most of the sympatric *Salvia* species tend to be ecologically generalized with two or more main pollinators and a few additional secondary pollinators, while a few *Salvia* species are clearly specialized. Some floral traits (e.g., flower color, morphology, size, corolla tube length and width of corolla tube entrance, type and size of the staminal lever mechanism, small numbers of flowers in the inflorescence), short flowering time, and small population size appear correlated to the degree of ecological specialization.

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Digging up the past: tracking the domestication syndrome in sunflower using extant and ancient DNA

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Sunflower was domesticated around 4000 years ago in the Eastern North America. The wild progenitor of today's modern crop is a highly branched plant with small flowers and achenes. Resolving the timing and order of the domestication process in which this form was transformed into the modern crop is of great importance for agriculture, anthropology and evolutionary biology. In this study, we uncovered the timing and order of domestication of sunflowers through sequence analyses of extant wild and domesticated sunflowers and archeological specimens dating back to 3500 years ago. We first compared whole genome sequence data from extant wild sunflowers with early and modern domesticates. Through selection tests, we identified regions under selection, tested if these regions have genes associated with traits important for domestication by using homology. We also tested these genes for potential protein differences affecting function, and for expression differences for wild and domesticated forms. Altogether we selected 456 genes that were potentially selected by humans for beneficial traits, 50 of which representing a neutral pattern (no selection signature). We, then, used sequence capture methods to obtain high coverage data from 80 archeological sunflower specimens dating 500-3500 years old collected from 18 excavation sites. Our preliminary analyses show clear patterns of domestication for our domestication-related genes compared to the neutral genes captured. The allele frequency changes through time shows patterns of both rapid and protracted selection in important domestication genes related to flowering and growth. Further analysis will uncover details about domestication syndrome in sunflowers by revealing which genes and related traits were selected early on or later during domestication emphasizing their importance for humans.

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BIOGEOGRAPHY

Keynote address: Biogeography of Zoonotic Wildlife Diseases

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Infectious diseases do not occur at random across time, host species, or geographic areas. Instead, infectious diseases have patterns that make them predictable. Many infectious diseases, especially zoonotic diseases, have origins in wildlife and are transmitted accidentally to new host species. Classic epidemiological approaches may have limitations to capture important signals in complex zoonotic disease systems. Disease biogeography aims to understand major distributional patterns on the distribution of infectious diseases accounting for evolutionary and ecological signals from the taxa involved in the disease system. This talk will provide a comprehensive overview of the field of disease biogeography. Then, we will explore empirical applications of biogeography to understand zoonotic diseases, including the effects of climate and landscape change on the emergence and expansion of infectious diseases. Finally, ongoing biogeographic research and future research lines will be presented to promote intellectual exchange and collaboration among researchers.

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Keynote address: Simple Processes Determine Complex Biodiversity Patterns on Global Scales

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Biological diversity exists unevenly across the surface of the Earth, such that it manifests patterns (e.g., the latitudinal diversity gradient, Rapoport's rule) on global scales. These biodiversity patterns have been the subject of extensive speculation and commentary in the ecological and biogeographic literatures, with many complex hypotheses proposed to explain them that often invoke species interactions and evolutionary change as drivers. In this body of work, a multidisciplinary group (biodiversity scientists, paleontologists, computer scientists) has collaborated to create a "virtual world" simulation with which to test causal mechanisms. Specifically, we created a world in which species respond to real-world geography and climates, but (1) they do not interact, (2) they undergo only allopatric speciation, and (3) their ecological niches are constant (or evolve only in certain, predictable, controlled ways). With this novel, simulation-based approach, we show that global biodiversity patterns derive from very simple sets of processes, with the added insight that biological diversification is slowed by evolutionary change in ecological niches. This simple set of processes is able to explain global biodiversity patterns without any additional, more complex processes, such as species interactions and evolutionary change.

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Current status of Great Bustard *Otis tarda* in Turkey: population size, distribution, movements, and threats

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The Great Bustard *Otis tarda* is a globally threatened species with populations inhabiting the steppe zones of Turkey. Its populations in Turkey have suffered severe declines in range and size in recent decades. Despite the urgent need to protect remaining populations, no national-scale study on the species has been conducted since 2009, and huge information gaps remain concerning its range, abundance, and movements in the country. Here, we put together the data from five years of fieldwork with all available sight and literature records to reveal current estimates of distribution and population size in Turkey, to better understand its movement patterns, to declare its recent and historical population changes, and to assess national extinction risk and threats for the species. We found that the species' breeding population has declined by 20–29% over the last five years, and there remain only 559–780 breeding Great Bustards in Turkey distributed in two distinct subpopulations. By comparing our findings with historical records, we demonstrate that the species' range has decreased by at least 60% since the beginning of the 20th century. We suggest possible migratory routes within and through Turkey and that Turkey might have a higher regional prominence for the species than previously thought. The most serious threats for the species in Turkey could be listed as illegal hunting, agricultural intensification, shift to irrigated crops, overgrazing, collision with powerlines, and disturbance. Our national Red List assessment yields an Endangered categorisation. Further studies are required to explain the metapopulation structure and movements of the species and to conserve its remaining populations in Turkey.

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Detecting Phenological shifts of different vegetation covers of Turkey with remote sensing

Tuğçe Şenel

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Turkey has spectacular biodiversity in all three levels; gene, species and ecosystem diversity. However, being in the Mediterranean Basin region which is defined as one of the most vulnerable regions in the world to climate change and related effects together with anthropogenic threats (deforestation, land use/land cover change etc.), Turkey is and will be experiencing changes in climate and hydrology as indicated by different studies and global climate models. Thus assessing how different vegetation types respond to these effects is crucial for successful and accurate management and conservation plans.

Phenological shifts (in greening-up timing, flowering, etc.) are now accepted as one of the most reliable bioindicators of climate change and climate-related effects on vegetation. However, especially for natural vegetation, phenological studies often require continuous and long term data from broad-scale areas. Collecting data with such properties has many challenges led by labor and area coverage problems. Remote sensing data makes a major contribution to the solution of these problems with long term, spatially and temporally continuous data from global scale. In this study, we use red and near-infrared band data from MODIS daily surface reflectance data collection (MOD09GA, 500 m, from 2001 to 2018) to detect phenological shifts of three phenological parameters - start of season (SOS), end of season (EOS) and length of season (LOS), (derived from Normalized Difference Vegetation Index (NDVI) calculations for different vegetation types/species) and the direction of trends in 18 years. Results of the study will provide valuable insights about the phenological responses of different natural vegetation covers/species of Turkey.

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MOLECULAR ECOLOGY

Keynote address: Evolution of adaptive divergences in freshwater salmonids

Kathryn R. Elmer

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Instances of rapid and repeated evolution can provide important and novel insights to the ways that species can and do diversify. I will discuss an example wherein we explored the genomics and transcriptomics underlying evolution in a complex natural, postglacial system: the replicated divergences of a famously variable northern freshwater salmonid, Arctic charr (*Salvelinus alpinus*), into distinct sympatric ecotypes. We found that across Eurasia ecotypes show high levels of parallelism in key functional traits. Parallelism in gene expression was significant across population and we show that a component of gene expression is genetically based. Despite these high levels of parallelism and repeatability, genome-wide analyses suggested that genomic patterns of response to selection is mostly non-parallel across lakes. Interestingly, even at fine geographic scales, we found that the histories of demography, divergence, and introgression differed greatly across populations, and we suggest strongly influence contemporary ecomorph differentiation. Our findings overall show that under some environmental conditions, parallel eco-morphological evolution can overcome different evolutionary starting points and different demographic histories yet result in similar outcomes. These findings are important for advancing our understanding of the predictability of diversification.

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Evolutionary History of Asexual Lizard Populations In Lake Van Area

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Lizards which are hybrid of different bisexual species from genus *Darevskia* can reproduce clonally and create asexual populations. Different combinations of different bisexual *Darevskia* species can generate different asexual species in this genus. Among these asexual species, *Darevskia sapphirina* and *D. bendimahiensis* live in Lake Van area as a pair of populations and they are result of hybridization *D. raddei* females and *D. valentini* male lizards. Although combination of which bisexual species made these asexual species are known, which subpopulations of these bisexual species were included in the hybridization events are not known, and thanks to this, we can indicate most likely parental populations of these hybrid species and explore their evolutionary history more clearly. To do this, we collected lizard samples from different populations of *D. sapphirina*, *D. bendimahiensis*, *D. valentini* and *D. raddei* in Lake Van area. We performed population genetics analysis based on RADSeq data. We detected the autosomal alleles of hybrid individuals coming from either maternal or paternal side separately (i.e. diagnostic alleles) and in this way, we could determine the extent of genetic similarity of bisexual subpopulations with the asexual populations in both sides separately using ML phylogenies and coancestry matrix in fineRADstructure.

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Heritability of immune traits of the pond snail, *Lymnaea stagnalis*

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Parasites pose a serious threat to organisms by decreasing their fitness. Hence, understanding evolutionary potential of defence against parasites is very important. Since many immunological traits are not highly specific to certain parasites, they are predicted to evolve via selection on additive genetic variance. Quantitative genetics is a useful tool to understand evolutionary potential of phenotypic immune traits under natural conditions. High-marker density genotyping allows estimating genetic

relatedness of individuals and thus makes it possible to calculate quantitative genetic parameters of wild populations. Freshwater snail *Lymnaea stagnalis* (Gastropoda, Mollusca) is an important model organism in ecological immunology because the methods for quantifying its immune defense traits have been developed. Main aim of my research is to calculate additive genetic variance and covariance of phenotypic immune traits in *L. stagnalis* under field conditions. To this aim, immune traits (phenoloxidase activity, laccase activity and antibacterial activity) of 600 field collected individuals were measured. Genomic relatedness between those samples were calculated based on around 20.000 independent SNP markers. Heritability of these traits were estimated by combining phenotypic and ddRAD data. This provides a general understanding of the evolutionary potential of snail immune function.

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Genetic Structure of Sedentary and Migratory Bears (*Ursus arctos*) within Eastern Anatolia

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Genetic Structure of Sedentary and Migratory Bears (*Ursus arctos*) within Eastern Anatolia from Genome Wide Genetic Markers Large carnivores are known for altering life-history strategies in response to environmental change. One such shift was recently discovered in Eurasian brown bears (*Ursus arctos*) within eastern Turkey where the availability of city dumps as their food sources have led to the evolution of two distinct life strategists: sedentary bears that use city dumps as a primary food source and migratory bears that never use dumps and migrate in search of food. Understanding the demographic and genetic processes that have led to the establishment of these life-history strategies is vital for predicting which life history strategy will dominate in the future and the overall impact of anthropogenic pressures on wild carnivores forced to live in human-dominated landscapes. Adaptive and genomic processes responsible for the two life-history strategies were determined using genome sampling (RAD sequencing) from 57 blood samples collected from captured bears inserted with radio collars. Radio collared bears that have been tracked continuously for one year, therefore, provide information on bears' migratory behavior. 31 samples from these bears with known migratory behavior were used in a high-resolution genome-wide association study (GWAS). Moreover, 8 brown bears across the world, whole-genome sequences available, were included in the study to understand the genetic structure of the study population. We found that the Eastern Turkey population is genetically isolated from other brown bears, and comparable with Apennine (Italy) population, conserve due to being small and isolated. GWAS on RAD loci have identified many genetic variants associated with the transition between life-history strategies and indicated that "sedentary" and "migratory" bears have distinct genotypes, indicating that the change may have a genetic basis. Understanding the polygenic basis of a complex life-history trait, and how fast new

life-history strategies can be established in wild carnivore populations in response to anthropogenic factors, is vital to implement new and more effective conservation strategies to protect Eurasian bears and other large carnivores.

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Examination of the possible role of DNA methylation on gene expression changes in response to acute osmotic stress in invasive Mediterranean Blue Mussel (*Mytilus galloprovincialis*).

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Rapid adaptation capabilities and invasive characteristics of some organisms cannot be solely explained by the selection of the genetic variants. In recent studies, it has been shown that epigenetic mechanisms might be responsible for the rapid response of these organisms to emerging environmental stimuli without the alteration of their DNA sequences. Additionally, in some of these studies, it is also shown that these epigenetic variations on the genome could be transgenerationally inherited and result in the generation of new stable phenotypes. When the recent drastic changes and fluctuations in the environmental stimuli due factors such as climate change are taken into consideration, the search for the underlying mechanisms of increased phenotypic plasticity and rapid adaptation of these organisms becomes essential. In this study, the role of an epigenetic regulation mechanism, DNA methylation, on the adaptation of the invasive blue mussel *Mytilus galloprovincialis* to acute osmotic stress was investigated. For this purpose, methylation sensitive amplified polymorphism method was utilized from in order the detect the changes in DNA methylation patterns at the whole-genome level under the exposure to acute osmotic stress condition.

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Investigation of the Effect of Floral Scents on Transcriptome Profiles of Antennal Chemoreceptors of *Bombus terrestris* L.

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Insects use the chemical information around them to survive by performing actions such as nest site determination, mate selection, foraging, prey detection and hiding from predators. In other words, insects must be able to distinguish between different type of scents in their environment and differ in odor-oriented behavior. The foraging activity carried out by bees enables the pollination of flowering plants in agricultural and natural vegetation. In this study, gene expression differences observed in the antennae of

commercially reared *Bombus terrestris* (L.) species which is frequently used as pollinator bee in agricultural production in greenhouses when conditioned to eugenol, were compared by using RT-qPCR method. Thus, the differences caused by a specific odor and the effect of odor-related learning behavior were discussed at the gene level. In addition, the genes that should be focused on in order to direct the bees to the desired plant groups in greenhouse and agriculture as well as suggestions for the more effective use of bees in greenhouses were presented. Keywords: RT-qPCR, Olfactory receptors, odor-conditioning, PER.

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MOLECULAR EVOLUTION AND BIOINFORMATICS

Keynote address: Insights into patterns of cryptic speciation: Madagascar's mouse lemurs and the multi-species coalescent.

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Our understanding of the speciation process has been in constant flux since the time of Darwin, with species concepts offering philosophical mirrors of shifting theory. Whereas Darwin envisioned that speciation was initiated by natural selection within an interbreeding population—and by implication, with gene flow—the introduction of Mayr's Biological Species Concept shifted the conceptual focus to reproductive isolation resulting from geographic separation. These two views of speciation have long been considered to be fundamentally opposed, though the burgeoning field of speciation genomics has clarified the surprising extent to which species integrity can be maintained in the face of either episodic or ongoing gene flow. I will focus on Madagascar's mouse lemurs (genus *Microcebus*) as an emerging system for studying the process of “speciation with gene flow”. These endemic primates occur across all habitats throughout Madagascar, and though genetic data reveal deep evolutionary divergence among the named species, they are morphologically cryptic. At present, the ecological and geographic forces driving this species radiation are unknown. My talk address current understanding of mouse lemur species diversity and also present data from new and ongoing studies of lineage diversification across an ecological and geographic spectrum in Madagascar. Using a combination of whole-genome sequencing and RADseq analysis we have found that patterns of speciation in mouse lemurs range from cases of complete reproductive isolation in sympatry, on one end of the speciation spectrum, to incipient population divergence within a single species on the other. We have also identified examples of intermediate levels of lineage diversification finding that effective population size, both past and present, can have enormous impacts on inferred patterns of gene flow and incomplete lineage sorting. In summary, there is no question that mouse lemurs

are extraordinarily diverse, and with the benefit of genomic data and powerful statistical tools, we are entering a new phase of increased understanding of the patterns and processes that are shaping species diversity in these cryptic primates.

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Sex-specific phenotypic effects and evolutionary history of an ancient polymorphic deletion of the human growth hormone receptor

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The common deletion of the third exon of the growth hormone receptor gene (GHRd3) in humans is associated with birth weight, growth after birth, and time of puberty. However, its evolutionary history and the molecular mechanisms through which it affects phenotypes remain unresolved. We present evidence that this deletion was nearly fixed in the ancestral population of anatomically modern humans and Neanderthals but underwent a recent adaptive reduction in frequency in East Asia. We documented that GHRd3 is associated with protection from severe malnutrition. Using a novel mouse model, we found that, under calorie restriction, Ghrd3 leads to the female-like gene expression in male livers and the disappearance of sexual dimorphism in weight. The sex- and diet-dependent effects of GHRd3 in our mouse model are consistent with a model in which the allele frequency of GHRd3 varies throughout human evolution as a response to fluctuations in resource availability.

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Phylogeny-Aware Amino Acid Substitution Scoring

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With the advancement in high throughput sequencing technologies, our ability to detect genetic variation, and to predict the effect of a variant in the clinical diagnosis have been revolutionized. Single nucleotide polymorphisms (SNPs) in coding regions might cause the change of a single amino acid into another in the resulting protein (i.e., missense mutations). Since these mutations can alter protein function which might result in disease, understanding the effect of a missense mutation helps to diagnose rare diseases. Here, we introduce a novel phylogeny-dependent probabilistic approach, Phylas (Phylogeny-Aware Amino Acid Substitution Scoring) to predict the functional effects of missense mutations. Our approach exploits the phylogenetic tree information to measure the deleteriousness of a given variant. Independent evolutionary events and phylogenetic relationship among species are driven from the gene-based phylogenetic

trees. We obtain the probability of observing any amino acid at the given position of the protein in question by traveling through the nodes and leaves of the phylogenetic tree. This traveling process helps us to analyze the location of substitutions and their effects over query sequence which is human for our experiments. We compare the predictive performance of our algorithm against SIFT and PolyPhen-2 which are the most widely used tools in terms of predicting the effect of missense variants. On the benchmark dataset including variants from different databases such as Clinvar, Humsavar and Gnomad, our algorithm outperforms SIFT and PolyPhen-2 in predicting the pathogenicity of missense mutations by improving the AUROC values by around 3% and 7% respectively.

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Molecular evolution and population genetics of GAD system in *L. brevis* strains from different environments.

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Lactic Acid Bacteria (LAB) are common, non-pathogenic, commercially important microorganisms widely used in food and biotechnology industries. LABs have several acid resistance pathways (ARP) in their genomes used to survive in low pH environments by adjusting their cytoplasmic pH. Glutamate decarboxylase (GAD) system is the most common ARP reported in LABs. Genus and species level phylogenetic analyses with different LABs suggest adaptive protein evolution in GAD system proteins. However, thorough molecular evolution and population genetic analyses of GAD genes sampled from LABs adapted to diverse environments is lacking. We focused on the *L. brevis* GAD system consisting of *gadR*, *gadC*, *gadB*, *gadA* genes. Intraspecific molecular population genetic analyses compared *L. brevis* sampled from different environments. *L. sakei* and *L. buchneri* were used as outgroups for interspecific comparisons. Of the 294 total mutations observed 15% were replacements, and 46% were singletons. *gadC* showed the highest nucleotide diversity primarily driven by singletons, however, highest replacement diversity was observed in *gadA*. Comparison of populations isolated from different environments showed that feces population had the highest overall and replacement nucleotide diversity, where non-neutral patterns of allele frequencies were suggested by statistically significant Tajima's D. Highest genetic differentiation was observed between feces and other population, however no fixed differences were observed between the populations. Interspecific comparisons with *gadC* and *gadB* using *L. buchneri* as an outgroup showed that the ratio of nonsynonymous to synonymous divergences is significantly higher than the ratio of nonsynonymous to synonymous polymorphisms suggesting positive selection. Moreover, neutrality index and alpha values were both less

than one again suggesting positive selection on *gadC* and *gadB*. In conclusion, GAD system in *L. brevis* shows genetic adaptation to different environments.

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Variant stratified molecular population genetic analyses of SARS-CoV-2 Genome

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COVID-19 is a disease caused by the Sars-CoV-2 virus, which has caused many deaths since the first case was detected, and is still a threat to humans. As the virus keeps mutating, many new variants are emerging. Understanding the evolution of SARS-Cov-2 genome is important for identifying new virus variants, tracking the spread, and possibly predicting future outcomes of the pandemic. Most studies have focused on the utilizing phylogenetic methods to track the evolution of the virus from a genomic epidemiology perspective. A thorough statistical and population genetic analysis of the virus genome evolution is lacking. We aimed to perform comprehensive molecular population genetic analyses of virus genomes, all viral genes, and populations of viral Variants of Concern (Alpha, Beta, Gamma, Delta) associated with faster spread. Intraspecific comparisons focused only on human specific Sars-Cov-2 variants. We used bat RaTG13 as an outgroup virus for interspecific comparisons. Of the 492 total mutations observed 60% were replacements, and 83% were singletons. Delta variant showed the highest nucleotide diversity primarily driven by replacement changes ($P = 0.006$). All synonymous and replacement changes observed in the Gamma variant genome were singletons. ORF1a had the highest number of singletons and haplotype diversity, whereas ORF6 and ORF10 showed the lowest nucleotide and haplotype diversity. Comparisons using RaTG13 showed that, ORF1b, M, and N genes have significantly more negative Alpha values ($P=0.002$) and more positive neutrality index estimates ($P=0.002$) compared to other genes suggesting negative selection acting on these genes. High neutrality index and alpha values for ORF1b was driven by Gamma variant, however Delta variant was responsible for the M and N genes. On the contrary, Spike, ORF3a, ORF7a genes showed positive selection ($P < 0.05$) primarily driven by Delta variant. In conclusion, variant stratified analyses showed different selection pressures on Sars-CoV-2 genes. Selection was evident on the later emerging variant of concern, genomic surveillance of virus evolution using our approach can be useful for tracking the dynamics of COVID-19 pandemic.

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