

SPEAKERS SESSION DETAILS TO PARTICIPANTS (ORAL)

SMBE 2026 - THE ANNUAL MEETING OF THE SOCIETY FOR MOLECULAR BIOLOGY & EVOLUTION



Opening with Local Chair Tom Gilbert

Date

Sunday, June 28, 2026

Chair

17:00

to

17:15

Room

Main

Times	Title	Speaker	Organisation	Country	Presentation type
17:00:0017:15:00	Opening with Local Chair Tom Gilbert	Tom Gilbert	University of Copenhagen	Denmark	Presentation

Times	Title	Speaker	Organisation	Country	Presentation type
17:15:00	18:15:00 Presidential adress	Prof Juliette De Meaux	University Of Cologne	Germany	Presentation

Times	Title	Speaker	Organisation	Country	Presentation type
09:00:0009:50:00	Bats: Genomes, phylogenies, fossils and cures ?	Emma C Teeling	School of Biology and Environmental Science, University College Dublin	Ireland	Plenary presentation

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	Understanding the roles of Endozoicomonas in marine animals: Mutualists, parasites, and everything in between?	Claudia Pogoreutz	Université De Perpignan Via Domitia	France	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:05:00	Streptococcus amylase-binding proteins in geladas and baboons reveal convergent oral microbial adaptation to starch-rich diets in humans and primates	Irina Velsko	Max Planck Institute for Evolutionary Anthropology	Germany	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:20:00	Holo-omic insights into host–microbiome dynamics during starvation and compensatory growth in zebrafish	Søren B. Hansen	University of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
11:20:00	11:35:00	Leveraging large-scale long-read sequencing data to understand the diversity, drivers and evolution of Lepidoptera cobionts at unprecedented resolution	Dr Julien Martinez	Wellcome Sanger Institute	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:50:00	Zooming into Host–Microbiome Evolution via Micro-Scale Spatial Metagenomics	Amalia Bogri	University Of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
11:50:00	11:55:00	What lives in, on, and around a lichen?	Merce Montoliu Nerin	Wellcome Sanger Institute	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
11:55:00	12:00:00	The New Zealand Butterfish - A model teleost to understand holobiome interactions	Qing Xiang Charles Mak	University Of Auckland & New Zealand Institute for Bioeconomy Science Limited	New Zealand	Flash Presentation (3 min. + 2 min. Q&A)
12:00:00	12:05:00	The role of Wolbachia in reproductive isolation and speciation in Drosophila paulistorum	Linnéa Ekström	Uppsala university	Sweden	Flash Presentation (3 min. + 2 min. Q&A)
12:05:00	12:10:00	Metagenome-derived population genomics of a vertically transmitted endosymbiont during ecological speciation of its insect host	André Bourbonnais	University of Copenhagen	Sweden	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	Disentangling the relationships between microbial taxa and metabolic outputs in a seaweed holobiont	Maximiliana Bogan	The University Of Chicago	United States	Flash Presentation (3 min. + 2 min. Q&A)
12:15:00	12:20:00	Ecology and evolution of the mammalian oral microbiome elucidated using museum specimen metagenomics	Markella Moraitou	University Of Edinburgh	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)

Open 1: Population genetics and genomics 1					Date	Monday, June 29, 2026		10:20	to	12:20
					Chair	Gopalakrishnan, Shyam		Room	Main	
Times	Title			Speaker	Organisation	Country	Presentation type			
10:20:00	10:35:00	tSNP: A dimensionality reduction algorithm for genetic data		Ori Sharon	The Hebrew University of Jerusalem	Israel	Oral Presentation (12 min. + 3 min. Q&A)			
10:35:00	10:50:00	Rethinking human AMY1 copy number evolution in light of demographic history		Andrea Soler I Núñez	Uppsala University	Sweden	Oral Presentation (12 min. + 3 min. Q&A)			
10:50:00	11:05:00	Strong bottlenecks constrain adaptive evolution in a host–parasite metapopulation		Pascal Angst	University of Basel	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)			
11:05:00	11:20:00	Fine-scale genotyping reveals assemblage-wide introgression in ants		Guillaume Lavanchy	Lund University	Sweden	Oral Presentation (12 min. + 3 min. Q&A)			
11:20:00	11:25:00	Deep-Time History of Balkan Brown Bears		Danijela Popović	Centre of New Technologies, University of Warsaw	Poland	Flash Presentation (3 min. + 2 min. Q&A)			
11:25:00	11:30:00	Local genomic adaptation to rabies in raccoons		Taylor Ackley	North Carolina State University	United States	Flash Presentation (3 min. + 2 min. Q&A)			
11:30:00	11:35:00	From Core to Periphery: Mapping Evolutionary Potential Across Species Ranges		Anna Brüniche-Olsen	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)			
11:35:00	11:40:00	Positive Selection Across Scales: Genetic Architecture of Adaptation and Connectivity in Wild Sunflowers		Zhiqin Long	The University Of British Columbia	Canada	Flash Presentation (3 min. + 2 min. Q&A)			
11:40:00	11:45:00	Massive genetic diversity loss within Asian elephant subspecies: new insights for determining conservation priorities		Jeroen Kappelhof	Wageningen University & Research	Netherlands	Flash Presentation (3 min. + 2 min. Q&A)			
11:45:00	11:50:00	The genomic basis and evolution of maternal genetic effects on early -life immunity in Soay sheep		Gina Henderson	University Of Edinburgh	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)			
11:50:00	11:55:00	Assessing dog introgression through structural variants in European refugial wolf populations		Daniele Battilani	Fondazione Edmund Mach	Italy	Flash Presentation (3 min. + 2 min. Q&A)			
11:55:00	12:00:00	Genomic signatures of recent inbreeding are associated with rarity and habitat specialisation among flies of the UK.		Elisa Mogollon Perez	University Of Oxford	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)			
12:00:00	12:05:00	Is genetic differentiation between species homogeneous across mammals?		Mathilde Barthe	Cnrs	France	Flash Presentation (3 min. + 2 min. Q&A)			
12:05:00	12:10:00	Effects of habitat arrangement on gene flow and genetic diversity in a grassland-specialist butterfly (Cupido minimus)		Danielle Clake	Lund University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)			
12:10:00	12:15:00	Adaptive evolution under extreme genetic erosion in invasive Spotted Lanternfly		Fang Meng	New York University	United States	Flash Presentation (3 min. + 2 min. Q&A)			
12:15:00	12:20:00	Gene expression and disease susceptibility of the genetically depauperate Channel Island fox (Urocyon littoralis)		Kimberly A Schoenberger	University of Southern California	United States	Flash Presentation (3 min. + 2 min. Q&A)			

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	Predicting interaction partners and generating protein sequences using protein language models	Anne-Florence Bitbol	EPFL	Switzerland	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:15:00	Molecular evolutionary analyses with protein foundation models from deep learning	Dr. Sudhir Kumar	Temple University	United States	Invited Speaker Presentation (20 min. + 5 min. Q&A)
11:15:00	11:30:00	Combining agentic AI with open infrastructure for reproducible analyses	Anton Nekrutenko	Penn State	United States	Oral Presentation (12 min. + 3 min. Q&A)
11:30:00	11:35:00	Adaptive Phylogenetic Tree Search via Machine Learning-Based Parameter Selection	Ella Baumer	Tel Aviv University	Israel	Flash Presentation (3 min. + 2 min. Q&A)
11:35:00	11:40:00	Likelihood-free inference of phylogenetic tree posterior distributions	Luc Blassel	Sorbonne Université	France	Flash Presentation (3 min. + 2 min. Q&A)
11:40:00	11:45:00	Molecular phylogenetics directly from deep learning protein foundation models	Rohan Alibutud	Temple University	United States	Flash Presentation (3 min. + 2 min. Q&A)
11:45:00	11:50:00	pIAlgue: An Artificial Intelligence Framework for Detecting Microbial Species in Ancient Human DNA	Annabel Perry	Harvard University	United States	Flash Presentation (3 min. + 2 min. Q&A)
11:50:00	11:55:00	TKF-based models with latent and hierarchical structure are competitive with parameter-heavy neural networks as models of protein sequence evolution	Annabel Large	University of California, Berkeley	United States	Flash Presentation (3 min. + 2 min. Q&A)
11:55:00	12:00:00	Scaling and Representation Learning for Deep Ancestral Sequence Reconstruction	Lys Sanz Moreta	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
12:00:00	12:05:00	Improved Power to Detect Sparse Episodic Positive Selection:A Protein Language Model-Informed Branch-Site Approach	Kabita Baral	University Of Calgary	Canada	Flash Presentation (3 min. + 2 min. Q&A)
12:05:00	12:10:00	Phylogenetic regression of sequence embeddings reveals genotypic basis of phenotypes	Zhenqiu Cao	Institute Of Zoology, Chinese Academy Of Sciences	China	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	Machine Learning Reveals Path-Dependent Functional Evolution in Animal Opsins	Dr. Todd Oakley	University of California, Santa Barbara	United States	Flash Presentation (3 min. + 2 min. Q&A)
12:15:00	12:20:00	Self-organizing map as a new AI algorithm for motif characterization	Xuhua Xia	University Of Ottawa	Canada	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	Beyond the Constant: Structural, Life-History, and Environmental Drivers of Germline Mutation Rate Variation	Prof. Dr. Markus Pfenninger	Senckenberg Biodiversität und Klima Forschungszentrum	Germany	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:05:00	Trinucleotide genome composition reflects context-dependent mutation spectra in plants	Ziyue Gao	University of Pennsylvania	United States	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:20:00	Transcription, Replication, and Recombination Shape Local Mutation and Sequence Variation at Human TSSs	Dr Fanny Pouyet	Université Paris-Saclay	France	Oral Presentation (12 min. + 3 min. Q&A)
11:20:00	11:35:00	Beyond Molecular Error: Developmental Selection Biases Germline Mutation Rates	Paco Majic	Embl Heidelberg	Germany	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:50:00	A Statistical Framework for Mutation Model Inference of Tandem Repeat Variants via the Ancestral Recombination Graph	Sebastián Iturbe	University Of Oregon	Mexico	Oral Presentation (12 min. + 3 min. Q&A)
11:50:00	11:55:00	Are Triallelic SNPs generated by trans-lesion synthesis?	Caitlin Price	University Of Kent	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
11:55:00	12:00:00	Germline mutation rate variation and its consequences for speciation in a cichlid adaptive radiation	Daniela Souza-Costa	University of Basel; Ludwig Maximilian University of Munich	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)
12:00:00	12:05:00	Heritability of germline mutagenesis in 40 large three- and four-generation pedigrees	Alexis Garretson	The University of Utah	United States	Flash Presentation (3 min. + 2 min. Q&A)
12:05:00	12:10:00	The mutational processes in primate spermatogenesis inferred from HiFi long read sequencing	Mikkel Heide Schierup	Aarhus University	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	Spontaneous mutation rate and spectrum are modulated by organismal fitness	Jianzhi Zhang	University of Michigan	United States	Flash Presentation (3 min. + 2 min. Q&A)
12:15:00	12:20:00	Transcription start sites experience a high influx of heritable variants fueled by early development	Donate Weghorn	Centre For Genomic Regulation (crg)	Spain	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title	Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00 Fatal entanglement: how a DNA satellite causes reproductive isolation in Drosophila	Mia Levine	University Of Pennsylvania	United States	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:05:00 The tdk family: an evolutionarily persistent single-gene killer meiotic driver family employing a toxin–antidote strategy	Yu Hua	Zhejiang University-University of Edinburgh Institute, Zhejiang University	China	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:20:00 Dissecting the genetic basis of the Paris SR meiotic drive system in Drosophila simulans	Cécile Courret	Cnrs	France	Oral Presentation (12 min. + 3 min. Q&A)
11:20:00	11:35:00 To purge or not to purge? How mating systems shape transposable element dynamics in Mimulus (monkeyflowers)	Eleanore Ritter	University Of Georgia	United States	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:50:00 An ancient allele directs epigenetic suppression of a selfish reproductive barrier in maize	Elli Cryan	University Of California, Irvine	United States	Oral Presentation (12 min. + 3 min. Q&A)
11:50:00	12:05:00 A large selfish mitochondrial deletion hints at an unexpected diversity of drive strategies	Alexandre Schifano	Uppsala University	Sweden	Oral Presentation (12 min. + 3 min. Q&A)
12:05:00	12:10:00 Nondisjunction and fitness costs in a selfish X chromosome that causes meiotic drive in both sexes in Drosophila testacea	Steve Perlman	University Of Victoria	Canada	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00 Natural variation in sex chromosome drive enables the discovery of a neo-X meiotic drive gene family	Jeffrey Vedanayagam	University Of Texas At San Antonio	United States	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title	Speaker	Organisation	Country	Presentation type
13:20:00	13:35:00 Epistasis between gene expression noise and functional mutations shapes cellular fitness	Wei-Han Lin	Institute of Molecular Biology, Academia Sinica	Taiwan	Oral Presentation (12 min. + 3 min. Q&A)
13:35:00	13:50:00 Insertion of an invading retrovirus regulates a novel color trait in swordtail fish	Nadia Haghani	Stanford University	United States	Oral Presentation (12 min. + 3 min. Q&A)
13:50:00	14:05:00 Extensive Reorganization of the Escherichia coli Chromosome Over 75,000 Generations of Laboratory Evolution	Ira Zibbu	Michigan State University	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:05:00	14:20:00 Evolutionary history of two X chromosome meiotic drivers and polymorphic Y chromosomes in Drosophila affinis	Anjali Gupta	University Of Kansas	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:20:00	14:35:00 Convergent genome evolution shaped the emergence of terrestrial animals	Jialin Wei	University of Bristol	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
14:35:00	14:50:00 Recovering Lost Kveik Diversity in Farmhouse Brewing with Ancient Metagenomics	Oya Inanli	University Of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
14:50:00	15:05:00 Intraspecific variation in the duration of epigenetic inheritance	François Frejacques	Institut de Biologie de l'ecole Normale Supérieure	France	Oral Presentation (12 min. + 3 min. Q&A)
15:05:00	15:20:00 The origins and molecular evolution of sperm	Arthur Matte	University Of Cambridge	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)

Open 2: Comparative genomics and phylogenetics 1				Date	Monday, June 29, 2026		15:50	to	17:50
				Chair	Stiller, Josefin	Room	Main		
Times		Title	Speaker	Organisation	Country	Presentation type			
15:50:00	16:05:00	Evolution of a Diving Response: Divergent Transcriptomic Adaptations in Aquatic Versus Terrestrial Mammals.	Giovanna Selleghein-Veiga	University of Campinas	Brazil	Oral Presentation (12 min. + 3 min. Q&A)			
16:05:00	16:20:00	The Vertebrate Genomes Project Phase I: A global reference genome resource	Giulio Formenti	The Rockefeller University	United States	Oral Presentation (12 min. + 3 min. Q&A)			
16:20:00	16:35:00	Comparative Population Genomics of Two Pipefish Species in the Baltic Sea	Eli Taub	University Of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)			
16:35:00	16:50:00	Comparative genomics reveals chemosensory gene family evolution within a conserved genome architecture in Culex	Sonia Cebrián-Camisón	Estación Biológica De Doñana (ebd-csic)	Spain	Oral Presentation (12 min. + 3 min. Q&A)			
16:50:00	16:55:00	A deep-learning-based score to evaluate multiple sequence alignments	Ksenia Polonsky	Tel Aviv University	Israel	Flash Presentation (3 min. + 2 min. Q&A)			
16:55:00	17:00:00	Using petabase-scale sequence alignment to describe the host and phylogenetic diversity of microsporidian parasites	Aaron Reinke	University of Toronto	Canada	Flash Presentation (3 min. + 2 min. Q&A)			
17:00:00	17:05:00	CMAPLE 2: High-Performance Phylogenetic Inference for Millions of Pathogen Genomes	Nhan Ly-Trong	The Australian National University	Australia	Flash Presentation (3 min. + 2 min. Q&A)			
17:05:00	17:10:00	New genome assemblies from neglected phyla illuminate the evolution of Ecdysozoa	Alessandro Formaggioni	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)			
17:10:00	17:15:00	Testing the adequacy and the accuracy of models of amino-acid substitution across evolutionary timescales	Dr Mattia Giacomelli	University Of Barcelona	Spain	Flash Presentation (3 min. + 2 min. Q&A)			
17:15:00	17:20:00	An updated perspective: what genes make a tree a tree?	Siri Birkeland	Natural History Museum, University of Oslo	Norway	Flash Presentation (3 min. + 2 min. Q&A)			
17:20:00	17:25:00	A macroevolutionary gene network reveals diapause evolutionary dynamics beyond the circadian clock and predicts microevolution	Saurav Baral	Stockholm University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)			
17:25:00	17:30:00	The Toll-like receptor signalling pathway repertoire of cartilaginous fishes: loss of TLR4-LPS signalling as a case study	Zewei Yang	UCD	Ireland	Flash Presentation (3 min. + 2 min. Q&A)			
17:30:00	17:35:00	Tripling known fungal mitogenomes through large-scale public data reuse	Ammar Abdalrahem	Research and Development Institute (IRD)	France	Flash Presentation (3 min. + 2 min. Q&A)			
17:35:00	17:40:00	Genome characterization of rainbow trout-associated Midichloria-like organism reveals a novel, potentially pathogenic bacterial lineage in a vertebrate host	Argelia Cuenca	National Institute of Aquatic Resources (DTUaqua).Technical University of Denmark	Denmark	Flash Presentation (3 min. + 2 min. Q&A)			
17:40:00	17:45:00	Cellular Innovation through De Novo Gene Birth Driven by Promiscuous Protein–Protein Interactions	Yuxiang Huang	西湖大学	China	Flash Presentation (3 min. + 2 min. Q&A)			

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:20:00	Leveraging public data for comparative evolutionary genomics of arthropod biodiversity	Robert Waterhouse	SIB Swiss Institute of Bioinformatics	Switzerland	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:20:00	16:35:00	Rare variation in malaria parasites biases population-genetic inference	Amy Goldberg	UCLA	United States	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:50:00	Integration and comparison of public single-cell RNA-Seq data for animals in the Bgee database and the scFAIR consortium	Frederic Bastian	SIB Swiss Institute of Bioinformatics - University Of Lausanne	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	17:05:00	Completing the Tree of Life with High-throughput Phylogenetics	John Allard	Temple University	United States	Oral Presentation (12 min. + 3 min. Q&A)
17:05:00	17:10:00	Expanding the Mammalverse of Genomes	Jonathan Hughes	Arizona State University	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:10:00	17:15:00	Mining Public Metagenomic Archives Reveals Deep-Time Evolution and Hidden Diversity of the Human Oral Microbiome	Dr. Mohamed Sarhan	Eurac Research - Institute For Mummy Studies	Italy	Flash Presentation (3 min. + 2 min. Q&A)
17:15:00	17:20:00	FAIRness of polymorphism data matters for plant demographic inference	Maxence Brault	CNRS, ECOBIO (Ecosystems, Biodiversity, Evolution), Rennes, France	France	Flash Presentation (3 min. + 2 min. Q&A)
17:20:00	17:25:00	Developing open tools and datasets to uncover the role of whole genome duplications in early vertebrate evolution	Lukasz Niezabitowski	Trinity College Dublin	Ireland	Flash Presentation (3 min. + 2 min. Q&A)
17:25:00	17:30:00	RepeatOBserver: Tandem repeat visualisation and putative centromere detection in 2000 genomes from across the tree of life	Cassandra Elphinstone	University of Oslo	Norway	Flash Presentation (3 min. + 2 min. Q&A)
17:30:00	17:35:00	What do bats and belugas have in common? Comparative genomics reveals convergent anti-deafness adaptations in echolocating Cetacea and Chiroptera	Dr. Liliana M Dávalos	Stony Brook University	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:35:00	17:40:00	Understanding the diversity of adhesive proteins in sea stars (Echinodermata, Asteroidea)	Leandro Smacchia	University of Mons / University of Liège	Belgium	Flash Presentation (3 min. + 2 min. Q&A)
17:40:00	17:45:00	Characterizing HIF-pathway alteration across two early diverging metazoan lineages (Ctenophora, Porifora).	Zach Opoka	University Of Kansas	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00	Genomic fossils reveal hidden evolutionary processes underlying phylogenetic conflicts in avian radiations	Yulong Xie	Zhejiang University	China	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:20:00	Paralog interference contributes to the preservation of genetic redundancy	Dr. Christian Landry	Université Laval	Canada	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:20:00	16:35:00	The Gene Regulatory Evolution of the Human Skeleton	Nadav Mishol	Weizmann Institute of Science	Israel	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:50:00	Mapping the Local Biochemical Landscapes of TEM-1 β -Lactamase	Jia Zheng	Westlake University	China	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	17:05:00	Cumulative epistatic changes in fitness effects drove contingency and entrenchment in the billion-year evolution of Hsp90	Ricardo Muñiz-Trejo	University of Chicago	United States	Oral Presentation (12 min. + 3 min. Q&A)
17:05:00	17:20:00	Bacterial dynamics of evolution tracked by barcodes over 20,000 generations validate a century of theoretical models of adaptation	Olivier Tenaillon	Institut Cochin, Inserm, Université Paris Cité	France	Oral Presentation (12 min. + 3 min. Q&A)
17:20:00	17:25:00	Parsing nearly neutral theory at the protein level through experimental variation of effective population size and high-throughput biophysical measurements	Solomon McShea	University Of California, San Francisco	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:25:00	17:30:00	Tracking the evolution of protein fusion entrenchment via genomic directed evolution	Yiqiao Sun	University of Zurich	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)
17:30:00	17:35:00	Assessing Growth–Survival Trade-offs in Fluctuating Environments	Megan Behringer	Vanderbilt University	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:35:00	17:40:00	Experimental reconstruction of the domestication, evolution, and adaptive role of horizontal gene transfer in eukaryotes.	Florian Mattenberger	Gregor Mendel Institute	Austria	Flash Presentation (3 min. + 2 min. Q&A)
17:40:00	17:45:00	Understanding the rules of regulation: Rewiring gene networks with synthetic regulators from random sequence	Dr Arianne Babina	University of Glasgow	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00	Interplay of gene conversion and nucleotide skews is driving the evolution of macrolide antibiotics	Aleksandra Nivina	University Of Zurich	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:20:00	Devils, Disease and Defence: the immune system strikes back	Prof. Kathy Belov	The University Of Sydney	Australia	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:20:00	16:35:00	Understanding the evolutionary dynamics of host and pathogen through comparative transcriptomics	Dafna Tussia-Cohen	Tel Aviv University	Israel	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:50:00	Divergent cis-regulatory haplotypes at Tlr2 are associated with immune responsiveness	Lars Råberg	Lund University	Sweden	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	17:05:00	Evolutionary diversification of horizontally acquired pathogen-defence genes in bdelloid rotifers	Tim Barraclough	University Of Oxford	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
17:05:00	17:20:00	VIEWING IMMUNITY IN THE CONTEXT OF AGEING AND EVOLUTION	Imroze Khan	Ashoka University	India	Oral Presentation (12 min. + 3 min. Q&A)
17:20:00	17:25:00	Evolutionary Signatures of Host–Pathogen Interactions Revealed by Polygenic Adaptation in Ancient Genomes	Eduardo Amorim	Arizona State University	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:25:00	17:30:00	The evolutionary dynamics between viral mimics and host proteinss14	Rotem Fuchs	Tel Aviv University	Israel	Flash Presentation (3 min. + 2 min. Q&A)
17:30:00	17:35:00	The population-level mutation dynamics of SARS-CoV-2 spike under immune selection	Marina Escalera Zamudio	University College London	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
17:35:00	17:40:00	Intraspecific diversity shapes functional variability of bats innate immunity	Emeline Esnouf	MIVEGEC	France	Flash Presentation (3 min. + 2 min. Q&A)
17:40:00	17:45:00	The specialist – generalist trade-off for infection ability of a parasite	Dieter Ebert	University of Basel, Zoologie	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00	Integrating protein structure and population genomic data to detect diversifying selection related to immunity	Leonie J. Lorenz	EMBL-EBI	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)

Times		Title	Speaker	Organisation	Country	Presentation type
15:50:00	16:20:00	Evolutionary rescue under extreme selection: Linking adaptation and demography in agricultural weeds	Julia Kreiner	University Of Chicago	United States	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:20:00	16:35:00	Genomic and Phenotypic Differentiation of Cydia pomonella Populations Under Varied Pest Management Regimes in France	Hyerin An	DGIMI, INRAE, University of Montpellier	France	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:50:00	Unwanted evolutionary rescue: bidirectional adaptive introgression of pesticide resistance genes between native and invasive Helicoverpa crop pests	Dr Henry North	University Of Cambridge	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	17:05:00	Convergent and divergent genetic routes to persistence under thermal stress in the yeast genus Saccharomyces	Jennifer Molinet	Universidad Autónoma De Chile	Chile	Oral Presentation (12 min. + 3 min. Q&A)
17:05:00	17:20:00	Cooperative interactions between measles viruses facilitate rapid dissemination throughout the brain	Alexander Robertson	University Of Washington, Seattle	United States	Oral Presentation (12 min. + 3 min. Q&A)
17:20:00	17:35:00	Evolution of genetic variance and genetic architecture in the context of species' range dynamics	Jitka Polechova	University of Vienna	Austria	Oral Presentation (12 min. + 3 min. Q&A)
17:35:00	17:40:00	Occurrence and potential of inter- and intraspecific gene flow in rapidly adapting butterfly populations	Jana Olivia Weigel	Uppsala University	Germany	Flash Presentation (3 min. + 2 min. Q&A)
17:40:00	17:45:00	The effects of environmental stress on the genetic architecture of fitness	Max Reuter	University College London	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00	Evolutionary rescue via short-lived modifiers of genetic variation	Alexander Longcamp	Mississippi State University	United States	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title	Speaker	Organisation	Country	Presentation type
09:00:0009:50:00	Human societies, past and present, in light of ancient DNA	Mehmet Somel	Middle East Technical University	Türkiye	Plenary presentation

Open 3: Ancient and historical genomics					Date	Tuesday, June 30, 2026	10:20	to	12:20
					Chair	Fonseca, Dr Rute	Room	Main	
Times		Title	Speaker	Organisation	Country	Presentation type			
10:20:00	10:35:00	Evolutionary dynamics of extinct and extant moose hybridization in North America	Amanda V. Meuser	Stockholm University	Sweden	Oral Presentation (12 min. + 3 min. Q&A)			
10:35:00	10:50:00	Paleolithic prevalence of human color vision diversity	Yizhen Wang	The University of Tokyo	Japan	Oral Presentation (12 min. + 3 min. Q&A)			
10:50:00	11:05:00	Characterization of archaic ancestry in 63,000 Japanese individuals from the Tohoku Medical Megabank	Mikel Lana Alberro	Max Planck For Evolutionary Anthropology	Germany	Oral Presentation (12 min. + 3 min. Q&A)			
11:05:00	11:20:00	Functional characterization of archaic introgression reveals immune system adaptation in Near Oceania	Steven Reilly	Yale University	United States	Oral Presentation (12 min. + 3 min. Q&A)			
11:20:00	11:25:00	Pleistocene wolves genome revealed new insight on migration and hybridization in North American canids	Dr Alberto Carmagnini	LMU	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
11:25:00	11:30:00	Ancient DNA from birch tar artefacts: insights into population structure and gendered practices in Neolithic Alpine Europe	Dr Anna White	Globe Institute, University of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)			
11:30:00	11:35:00	The Green Sahara genomic landscape: tracing ancestries across North Africa and Sahel through joint analysis of modern and ancient genomes	Flavia Risi	Sapienza University Of Rome	Italy	Flash Presentation (3 min. + 2 min. Q&A)			
11:35:00	11:40:00	Gene regulatory signatures of archaic introgression across human tissues and cell types	Kitty Murphy	Globe Institute, University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)			
11:40:00	11:45:00	Archaic Introgression in ancient Eurasians	Marco Rosario Capodiferro	Trinity College Dublin	Ireland	Flash Presentation (3 min. + 2 min. Q&A)			
11:45:00	11:50:00	Multiple Denisovan lineages shaped the genomic diversity of Asian populations	Charlotte Antoine-Derouet	UMR7206 - Éco-Anthropologie, Muséum National d'Histoire Naturelle	France	Flash Presentation (3 min. + 2 min. Q&A)			
11:50:00	11:55:00	The Evolution of HLA Diversity in a Native American Population from Ancient to Modern Times	Diyar Hamidi	University Of Hamburg	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
11:55:00	12:00:00	An archaeogenomic study of Black Death victims from Southern Europe	Oguzhan Parasayan	Institut Pasteur	France	Flash Presentation (3 min. + 2 min. Q&A)			
12:00:00	12:05:00	Signals of hybridization between commercial and wild bumblebees revealed by temporal genomics	Michael Mitschke	Stockholm University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)			
12:05:00	12:10:00	Ancient DNA and functional genomics retrace the path to modern chicken productivity	Yuemin Li	Ludwig Maximilian University	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
12:10:00	12:15:00	ratePlacer: A Phylogenetic Framework for Molecular Dating of Ancient Environmental DNA	Maya Lemmon-Kishi	University Of California Berkeley	United States	Flash Presentation (3 min. + 2 min. Q&A)			
12:15:00	12:20:00	Paleogenomics Reveals Arctic Range and Aquatic Specialization in the American "cheetah", <i>Miracinonyx trumani</i>	Molly Cassatt-Johnstone	University Of California, Santa Cruz	United States	Flash Presentation (3 min. + 2 min. Q&A)			

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	Genetic load, drift debt, and the evolutionary management of vulnerable populations	Cock Van Oosterhout	University of East Anglia (UEA)	United Kingdom	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:05:00	Genomic diversity across 200 plant species of variable Red List status	Jules Perez	UC Berkeley	United States	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:20:00	A practical framework for identifying genetic subpopulations and ESUs: insights for IUCN assessments and broader management	Deborah Leigh	Senckenberg Nature Research/ Goethe University	Germany	Oral Presentation (12 min. + 3 min. Q&A)
11:20:00	11:35:00	Genera: An Integrative AI Framework for Conservation Management using Comparative Genomics at Scale	Ayshwarya Subramanian	Cornell University	United States	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:50:00	Functional genomic diversity and migratory survival: implications for evolutionary management of a critically endangered parrot	Soleille Miller	University of Sydney	Australia	Oral Presentation (12 min. + 3 min. Q&A)
11:50:00	11:55:00	Genomic Consequences of Translocations: Lessons from the Critically Endangered Pyrenean Brown Bear	Léa Auclair	National Museum Of Natural History Of Paris	France	Flash Presentation (3 min. + 2 min. Q&A)
11:55:00	12:00:00	Assessing adaptive potential in Scandinavian populations of Willow ptarmigan (Lagopus lagopus) using temporal genomics	Maja Svedberg	Stockholm University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)
12:00:00	12:05:00	Harnessing genetic rescue: from genomic evidence to management decisions	Aja Noersgaard Buur Tengstedt	Aarhus University	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
12:05:00	12:10:00	Detecting Vulnerability Early: Genomic Signals from Fragmented Landscapes	Mrs. Nathalie Puggaard Elkær Andersen Ibsen	Århus University	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	Costs and benefits of genetic rescue of the critically endangered helmeted honeyeater from another subspecies	Alexandra Pavlova	Monash University	Australia	Flash Presentation (3 min. + 2 min. Q&A)
12:15:00	12:20:00	Environmental effects on the origin and establishment of Arabidopsis arenosa	Yu Cheng	Department of Botany, Faculty of Science, Charles University	Czech Republic	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	What drives genome expansions in the fungal kingdom? From populations to deep timescales	Daniel Croll	University of Neuchatel	Switzerland	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:05:00	An in-vivo approach to population 3D genomics: age and sex affect 3D genome in a healthy controlled cohort of chickens.	Juan Antonio Rodríguez	Globe Institute, University Of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:20:00	Beyond the textbook centromere: genome evolution across monocentric–holocentric transitions in Drosera	Aaryan Bhatia	Max Planck Institute For Plant Breeding Research	Germany	Oral Presentation (12 min. + 3 min. Q&A)
11:20:00	11:35:00	An increase in chromosome copy number drives rapid adaptation in a cold-adapted bacterium	Macarena Toll-Riera	Institut de Biologia Evolutiva (IBE-CSIC)	Spain	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:50:00	Genome plasticity through a large chromosomal inversion structures phenotypic and regulatory responses to environmental variation	Ana Lindeza	University Of Helsinki	Finland	Oral Presentation (12 min. + 3 min. Q&A)
11:50:00	11:55:00	Chromosomal loss trajectories following whole-genome duplication in cancer	Máire Ní Leathlobhair	Trinity College Dublin	Ireland	Flash Presentation (3 min. + 2 min. Q&A)
11:55:00	12:00:00	An epigenetically induced hypermutator state reshapes genome architecture through elevated structural variation	Ivona Glavincheska	ETH Zurich	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)
12:00:00	12:05:00	Copy That: Exceptional Retrocopy Abundance in Sloths and Xenarthrans	Marcela Uliano Da Silva	Wellcome Sanger Institute	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
12:05:00	12:10:00	A theoretical perspective on the two-speed genome model	Julien Dutheil	Max Planck Institute For Evolutionary Biology	Germany	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	Construction of unbiased pangenomes to better characterize standing variation and structural rearrangements between closely related butterfly morphs	Ava Mackay-Smith	Duke University	United States	Flash Presentation (3 min. + 2 min. Q&A)
12:15:00	12:20:00	Alu-associated structural variation contributes to species-specific differences in genome organization across primate evolution	Shu Zhang	Gladstone Institutes	United States	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	Exploring Tree Space: Exact Transition Kernels and Proposal Efficiency in Bayesian Phylogenetics	John Huelsenbeck	University Of California, Berkeley	United States	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:05:00	Disentangling Ghost and Reciprocal Introgression in Four-Taxon Genomic Datasets	Evan Forsythe	Oregon State University	United States	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:20:00	Detecting balancing selection using ancestral recombination graphs	Debora Brandt	University College London	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
11:20:00	11:35:00	A New Technique for Ultra-Fast Maximum Likelihood That Gives Exact Phylogenetic Gradients for Free	Dr. Jason A.P. de Koning	University of Calgary	Canada	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:50:00	HOGPROP: transferring functional annotation and reconstructing ancestral function	Irene Julca	Aarhus University	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
11:50:00	12:05:00	Representing massive-scale phylogenetic uncertainty with phylogenetic networks	Dr Bui Quang Minh	Embl-ebi	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
12:05:00	12:10:00	The multi-species ancestral recombination graph reveals admixture dynamics in a hybrid baboon population	Iker Rivas-González	Max Planck Institute for Evolutionary Anthropology	Germany	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	The application of ancestral recombination graphs to understand the temporal dynamics of hybridization	Madeline A. Chase	Swiss Ornithological Institute	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)
12:15:00	12:20:00	Powerful inference of bacterial evolution from genome-wide genealogies	Hongjin Wu	Shanghai Institute Of Materia Medica	China	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	Primary cilia regulation linked to evolution of sex determination in vertebrates with and without sex chromosomess	Nicole Valenzuela	Iowa State University	United States	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:05:00	Drivers of primary sex ratio bias in dwarf willow	Sophie Karrenberg	Uppsala University	Sweden	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:20:00	Bagworm moths: a new model for studies of genome evolution across variable levels of sexual dimorphism, from mild to extreme.	Christina Watkins	The University of Florida	United States	Oral Presentation (12 min. + 3 min. Q&A)
11:20:00	11:35:00	A comparison of selection on autosomes and the young Xchromosome in diploid Mercurialis species	Suhaas Sehgal	University Of Lausanne	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:50:00	Diversity of dosage compensation mechanisms in squamate reptiles	Michail Rovatsos	Faculty of Science, Charles University	Czech Republic	Oral Presentation (12 min. + 3 min. Q&A)
11:50:00	11:55:00	Convergent evolution of genetic sex determination among species of stickleback fishes	Michael White	University Of Georgia	United States	Flash Presentation (3 min. + 2 min. Q&A)
11:55:00	12:00:00	A Tale of Skink Sex Chromosome Evolution	Paul Waters	University Of New South Wales	Australia	Flash Presentation (3 min. + 2 min. Q&A)
12:00:00	12:05:00	Causes and consequences of sex-chromosome turnovers in Diptera	Lorena Layana	Institute of Science and Technology Austria	Austria	Flash Presentation (3 min. + 2 min. Q&A)
12:05:00	12:10:00	Evolution of recent autosomic translocations to the X of iconic neotropical bats	Liliana M Davalos	Stony Brook University	United States	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	Alternative splicing and sex-specific adaptation in stick insects	Iulia Darolti	University Of Lausanne	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	Evolution of immunity across domains of life	Aude Bernheim	Institut Pasteur	France	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:05:00	Genomic constraints shape the evolution of alternative routes to drug resistance in prokaryotes	Chris Creevey	Queen's University Belfast	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:20:00	Dissecting the factors underlying sequence evolution by disentangled representation learning	Zhengting Zou	Institute of Zoology, Chinese Academy of Sciences	China	Oral Presentation (12 min. + 3 min. Q&A)
11:20:00	11:35:00	Mapping bacterial capsule diversity using protein structural homology	Dr Teodora Mateeva	Wellcome Sanger Institute	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:50:00	Deciphering and forecasting viral evolution via AI-augmented molecular evolution	Jian Lu	School Of Life Sciences, Peking University	China	Oral Presentation (12 min. + 3 min. Q&A)
11:50:00	12:05:00	Genomic Language Models for DNA sequence Analysis	Keith Crandall	George Washington University	United States	Oral Presentation (12 min. + 3 min. Q&A)
12:05:00	12:10:00	A random forest classifier to retrieve Insertion Sequences carrying antibiotic resistance genes from wastewater samples.	Alice Ledda	UKHSA	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	StrataBionn: a neural network supervised classification method for microbial communities	Omar Cornejo	University of California Santa Cruz	United States	Flash Presentation (3 min. + 2 min. Q&A)
12:15:00	12:20:00	LLM Reveals: Viruses Copy Synonymous Cell-Type Specific Patterns of Human Coding DNA	Noam Segal	Technion - Israel Institute Of Technology	Israel	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
13:20:00	13:50:00	Plant domestication under clonality and traditional management: perspectives from cassava collections	Logan Kistler	Smithsonian Institution	United States	Invited Speaker Presentation (25 min. + 5 min. Q&A)
13:50:00	14:05:00	ANCIENT PLANT DNA DOCUMENTS CEREMONIAL CONTINUITY AT PICURIS PUEBLO	Thomaz Pinotti	University Of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
14:05:00	14:20:00	Following the process of sunflower domestication through space and time with ancient DNA	Benjamin Blackman	University Of California, Berkeley	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:20:00	14:35:00	Two centuries of genetic diversity change in rice at different spatial scales	Rafal Gutaker	Royal Botanic Gardens, Kew	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
14:35:00	14:50:00	Tracking molecular mechanisms of plant adaptation to climate change with herbaria	Patricia Lang	UC Berkeley	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:50:00	15:05:00	Leveraging Herbarium Collections to access Natural Genetic Variation	Dr. Polina Novikova	Vib-ugent Center For Plant Systems Biology	Belgium	Oral Presentation (12 min. + 3 min. Q&A)
15:05:00	15:10:00	Historical Genomes Reveal a Centuries-Long Competition–Colonization Trade-off in Plant-infecting Pseudomonas	Prof. Hernán Burbano	University College London	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
15:10:00	15:15:00	A herbariomic approach to characterising medicinal black henbane (Hyoscyamus niger) populations in Britain	Natalia Przelomska	University Of Portsmouth	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
15:15:00	15:20:00	The phylogeography of the Wikstroemia genus – one phylogeny, 50 species, 60 islands, and 250 years of botany	Ruben Cousins-Westerberg	Lund University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)

Open 4: Molecular and genome evolution 1					Date	Tuesday, June 30, 2026	13:20	to	15:20
					Chair	Scherz, Mark D.	Room	Main	
Times		Title	Speaker	Organisation	Country	Presentation type			
13:20:00	13:35:00	Parallel Molecular Evolution Across Replicated Anolis Lizard Adaptive Radiations	Aryeh Miller	Washington University in St. Louis	United States	Oral Presentation (12 min. + 3 min. Q&A)			
13:35:00	13:50:00	The genomic underpinning of variation in vision across a global sample of ant workers	Joel Vizueta	University of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)			
13:50:00	14:05:00	The day after the drug: Investigating drug-induced cellular memory	Marina Khachaturyan	Tel Aviv University	Israel	Oral Presentation (12 min. + 3 min. Q&A)			
14:05:00	14:20:00	A fast-evolving C-terminus underlies species-specific function of an orphan gene required for sperm nuclear shaping	Geoff Findlay	College Of The Holy Cross	United States	Oral Presentation (12 min. + 3 min. Q&A)			
14:20:00	14:25:00	Functional characterization of the male-specific mitochondrial ORFan protein in DUI bivalves reveals a role in spermatogenesis	Julie Brémaud	Université de Montréal	Canada	Flash Presentation (3 min. + 2 min. Q&A)			
14:25:00	14:30:00	Single-cell phylodynamics reveal rapid late-stage colorectal cancer expansions	David Posada	University of Vigo	Spain	Flash Presentation (3 min. + 2 min. Q&A)			
14:30:00	14:35:00	Crossover and consequences: are individual recombination rates under selection?	Susan Johnston	University of Edinburgh	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)			
14:35:00	14:40:00	Disentangling patterns of variation in the human genome: the roles of mutation, recombination and selection revisited	Gustavo Valadares Barroso	University Of Wisconsin-Madison	United States	Flash Presentation (3 min. + 2 min. Q&A)			
14:40:00	14:45:00	What sets the upper bound on animal cell size?	Rachel Mueller	Colorado State University	United States	Flash Presentation (3 min. + 2 min. Q&A)			
14:45:00	14:50:00	Frequency-dependent immune selection in tumors inferred from neoantigen depletion patterns	Ryan Gutenkunst	University Of Arizona	United States	Flash Presentation (3 min. + 2 min. Q&A)			
14:50:00	14:55:00	Haplotype specific structural variation within a single human genome	Rebekah Rogers	UNC Charlotte	United States	Flash Presentation (3 min. + 2 min. Q&A)			
14:55:00	15:00:00	The origin and evolution of alkaloid sequestration in poison frogs	Julia Albuquerque de Pinna	Vrije Universiteit Brussel	Belgium	Flash Presentation (3 min. + 2 min. Q&A)			
15:00:00	15:05:00	Genomic Plasticity and Evolutionary Innovation in Avian Metabolic Adaptation	Xinyu Zhang	Zhejiang University	China	Flash Presentation (3 min. + 2 min. Q&A)			
15:05:00	15:10:00	A Blast from the Past: 'Living Fossil' Fish Genomes Bridge Gene Regulation Across Long Evolutionary Distances	Dr. Ingo Attendee7772	Michigan State University	United States	Flash Presentation (3 min. + 2 min. Q&A)			
15:10:00	15:15:00	Tandem repeat variation is functional with signatures for directional and balancing selection in humans and chimpanzees	Rori Rohlf	University Of Oregon	United States	Flash Presentation (3 min. + 2 min. Q&A)			
15:15:00	15:20:00	Profiling mutation rates and characteristics of somatic structural variants in the aging brain using long read sequencing	Caitlin F. Connelly	University Of California, Berkeley	United States	Flash Presentation (3 min. + 2 min. Q&A)			

S01 Evolutionary-informed management of vulnerable populations in a rapidly changing world - Part 2					Date	Tuesday, June 30, 2026	13:20	to	15:20
					Chair		Room	Vandsalen	
Times	Title		Speaker	Organisation	Country	Presentation type			
13:20:00	13:35:00	Genomic legacy of near extinction and intensive management in the pink pigeon	Carolina Pacheco	Lund University	Sweden	Oral Presentation (12 min. + 3 min. Q&A)			
13:35:00	13:50:00	Phenotypic plasticity shapes genetic variation and patterns of inbreeding and extinction risk	Aleix Palahí i Torres	Uppsala University	Sweden	Oral Presentation (12 min. + 3 min. Q&A)			
13:50:00	14:05:00	Pedigree-based analysis reveals rapid de novo insertion and purging of retroviral integrations in the koala genome	Guilherme B. Neumann	Leibniz Institute for Zoo and Wildlife Research	Germany	Oral Presentation (12 min. + 3 min. Q&A)			
14:05:00	14:20:00	Parallel adaptation and genomic vulnerability of bottlenose dolphins in a changing ocean	Svenja Marfurt	University of Zurich	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)			
14:20:00	14:25:00	When Social Structure Shapes Genomes: Modeling Demography and Genomic Signals in Reef Fishes	Dr. Diego Hartasánchez	Cinvestav	Mexico	Flash Presentation (3 min. + 2 min. Q&A)			
14:25:00	14:30:00	Tracing the Genomic History of Spotted Owls and Their Relatives	Murillo Rodrigues	Oregon Health & Science University	United States	Flash Presentation (3 min. + 2 min. Q&A)			
14:30:00	14:35:00	Persistence and Resilience: Tracking the Genomes of North American Brown Bears	Joanna Kelley	University Of California Santa Cruz	United States	Flash Presentation (3 min. + 2 min. Q&A)			
14:35:00	14:40:00	The genomic consequences of introgression for an island-limited rail	Kees Wanders	University of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)			
14:40:00	14:45:00	Leveraging standardised frameworks for genetic monitoring of populations	Dr. Chris Barratt	Wageningen University And Research	Netherlands	Flash Presentation (3 min. + 2 min. Q&A)			
14:45:00	14:50:00	Predicting Mammal-Wide Variant Pathogenicity, Uncertainty, Gene Essentiality, and Genetic Load	Paulina Nuñez Valencia	Center For Genomic Regulation (CRG)	Spain	Flash Presentation (3 min. + 2 min. Q&A)			
14:50:00	14:55:00	Investigating Parallel Adaptation to Altitude and Response to Climate Change in Neotropical Butterflies	Dr Henry North	University of Cambridge	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)			
14:55:00	15:00:00	Restoring Vulnerable Populations via Genomic Rescue	Dr Laura Bertola	National Centre for Biological Sciences	India	Flash Presentation (3 min. + 2 min. Q&A)			
15:00:00	15:05:00	Using population structure and admixture analyses to inform management decisions of native caribou in Greenland	Nuno Filipe Gomes Martins	Department Of Biology, University of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)			
15:05:00	15:10:00	Structural variant load under demographic change: How a small fly can provide big insights	Jana Wold	Universite De Rennes	France	Flash Presentation (3 min. + 2 min. Q&A)			
15:10:00	15:15:00	Population Genomics of the Rice's Whale Reveals Long-term Isolation, Admixture, and Genetic Distinctiveness	Diana Aguilar Gomez	Ucla	United States	Flash Presentation (3 min. + 2 min. Q&A)			
15:15:00	15:20:00	Heterosis vs. adaptation: genomic insights from a 25-year mixed-source plant translocation program	Olivier Brisset	Muséum National D'histoire Naturelle	France	Flash Presentation (3 min. + 2 min. Q&A)			

S03 Genome Plasticity and Evolutionary Innovation - Part 2					Date	Tuesday, June 30, 2026	13:20	to	15:20
					Chair		Room	Lumbye (lower level)	
Times	Title		Speaker	Organisation	Country	Presentation type			
13:20:00	13:35:00	Macro-evolutionary perspectives on a large chromosomal rearrangement underlying alternative life-histories in seaweed flies	Dominique Hicks	CNRS	France	Oral Presentation (12 min. + 3 min. Q&A)			
13:35:00	13:50:00	Mobile chromosomes as drivers of clonal pathogen evolution	Cristina Barragan	University Of Kiel	Germany	Oral Presentation (12 min. + 3 min. Q&A)			
13:50:00	14:05:00	Transposable Elements in Ant Macroevolution	Lukas Schrader	University Of Münster	Germany	Oral Presentation (12 min. + 3 min. Q&A)			
14:05:00	14:20:00	Genome reorganisation and expansion shape 3D genome architecture and define a distinct regulatory landscape in coleoid cephalopods	Thea Rogers	University Of Vienna	Austria	Oral Presentation (12 min. + 3 min. Q&A)			
14:20:00	14:25:00	The contribution of epigenetic regulation to antimicrobial resistance phenotypes in Escherichia coli from antibiotic-free dairy farms	Adamandia Kapopoulou	University Of Bern	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)			
14:25:00	14:30:00	Programmed DNA elimination as a source of genomic plasticity in free-living nematodes	Dr Hend Abu-Elmakarem	Wellcome Sanger Institute	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)			
14:30:00	14:35:00	Extensive sex chromosome rearrangements in cichlid fish	Astrid Böhne	Leibniz Institute For The Analysis Of Biodiversity Change, Museum Koenig Bonn	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
14:35:00	14:40:00	When plasmids settle down: domestication and chromid-like evolution in Pantoea	Dr. Devani Romero Picazo	CAU Kiel	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
14:40:00	14:45:00	Structural variants and their contribution to successful and unsuccessful colonizations	Beatrice Sammarco	University Of Ferrara	Italy	Flash Presentation (3 min. + 2 min. Q&A)			
14:45:00	14:50:00	Telomere-Specific Transposable Elements and Host Fitness in Drosophila	Morteza Bajgiran	University Of Regensburg	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
14:50:00	14:55:00	Modeling the Evolutionary Advantage of Plasmid Persistence Strategies	Mario Santer	Kiel University	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
14:55:00	15:00:00	Genome-Wide Association Analysis reveals insights into Escherichia coli adaptation to specific clinical niches	Riccardo Nodari	University of Milan	Italy	Flash Presentation (3 min. + 2 min. Q&A)			
15:00:00	15:05:00	Transposable element islands at the interface of 3D genome architecture and karyotype evolution in ants	Janina Rinke	University Of Muenster	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
15:05:00	15:10:00	Exploring architectural diversity in fungal 3D genomes to uncover new perspectives on eukaryotic chromatin organization	Cecile Lorrain	ETH Zurich	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)			
15:10:00	15:15:00	Long-read sequencing reveals the genomic architecture of alternative reproductive tactics in swordtail fishes	Gabriel Preising	Stanford University	United States	Flash Presentation (3 min. + 2 min. Q&A)			

Times	Title		Speaker	Organisation	Country	Presentation type
13:20:00	13:35:00	From Sterility to Clonality: Linking Rapid Sex-Chromosome Turnover to Asexual Reproduction in a Vertebrate Hybrid Complex	Lucija Andjel	Institute Of Animal Physiology And Genetics Of The Czech Academy Of Sciences	Czech Republic	Oral Presentation (12 min. + 3 min. Q&A)
13:35:00	13:50:00	Functional verification of a genetic trigger for female sex determination in the Marsabit clawed frog (<i>Xenopus borealis</i>)	Ben Evans	Mcmaster University	Canada	Oral Presentation (12 min. + 3 min. Q&A)
13:50:00	14:05:00	Sex chromosome turnover: why some sex chromosomes never settle, and others never leave.	Paul Saunders	CEFE - CNRS UMR 5175	France	Oral Presentation (12 min. + 3 min. Q&A)
14:05:00	14:20:00	Sex-specific modifications of gametogenesis in natural and lab-bred <i>Fundulus</i> spp. hybrids	Anne-marie Dion-Côté	Université De Moncton	Canada	Oral Presentation (12 min. + 3 min. Q&A)
14:20:00	14:25:00	Reproductive morph specialisation facilitated by a maternal sex determining region in a fungus gnat (<i>Bradysia coprophila</i>)	Melany Henot	University Of Edinburgh	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
14:25:00	14:30:00	Evolutionary and Functional Consequences of W–Autosome Fusions in <i>Heliconius</i> Butterflies	Nicol Rueda	Wellcome Sanger Institute	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
14:30:00	14:35:00	Repeated losses of self-fertility shaped heterozygosity and polyploidy in yeast evolution	Nina Vittorelli	Sorbonne Université / Collège De France	France	Flash Presentation (3 min. + 2 min. Q&A)
14:35:00	14:40:00	Unveiling the Evolutionary Dynamics of the X Chromosome in Aphids	Gaorui Gong	INRAE IGEPP	France	Flash Presentation (3 min. + 2 min. Q&A)
14:40:00	14:45:00	Sex chromosome variation across vertebrate genome assemblies	Melissa Wilson		United States	Flash Presentation (3 min. + 2 min. Q&A)
14:45:00	14:50:00	Sex chromosome evolution mediated by a large inversion and a possible switch of the sex determination gene	Xiaomeng Mao	Stockholm University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)
14:50:00	14:55:00	Tetrapolar mating relaxes host boundaries through sexual recombination between wheat- and barley-adapted <i>Puccinia striiformis</i> rust fungi.	Julian Rodriguez Algaba	Aarhus University	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
14:55:00	15:00:00	Sex-chromosome evolution and speciation in the genus <i>Salmo</i>	Marte Sodeland	University Of Agder	Norway	Flash Presentation (3 min. + 2 min. Q&A)
15:00:00	15:05:00	Neo-sex chromosome evolution and reproductive isolation in hybridizing gazelle lineages	Thomas Bøggild	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
15:05:00	15:10:00	How and why genes survive on the human Y chromosome: Insights from telomere-to-telomere ape assemblies, long-read transcriptomes, and protein modeling	Kateryna Makova	Penn State University	United States	Flash Presentation (3 min. + 2 min. Q&A)
15:10:00	15:15:00	Experimental evidence that balancing selection maintains sexually antagonistic genetic variation in a polygenic trait	Martyna Zwoinska	Uppsala University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)
15:15:00	15:20:00	Sex chromosome turnover has dramatically different consequences between closely related cichlid fishes	Sophie Smith	Leibniz Institute For The Analysis Of Biodiversity Change	Germany	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
13:20:00	13:50:00	Biological Sequence Language Models for Prediction and Design	Yun Song	University of California, Berkeley	United States	Invited Speaker Presentation (25 min. + 5 min. Q&A)
13:50:00	14:05:00	From Likelihood to Fitness: Accounting for Phylogeny to Improve Variant Effect Prediction	Dr. Mafalda Dias	Crg	Spain	Oral Presentation (12 min. + 3 min. Q&A)
14:05:00	14:20:00	Learning protein interaction origination and evolution with sequence-based machine learning	Li Zhao	The Rockefeller University	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:20:00	14:35:00	From Sequence to Expression Across Evolution: Promise and Limits of AI Genome Models	Dr. Maria Chikina	University Of Pittsburgh	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:35:00	14:50:00	Nonlinearity in Complex Trait Genomics: Limits of Linear GWAS and Interpretable Deep Learning for Locus Discovery	Burak Yelmen	University of Tartu	Estonia	Oral Presentation (12 min. + 3 min. Q&A)
14:50:00	15:05:00	A new genomic foundation model and a sequence-only gene prediction model for plant evolutionary biology	Matt Pennell	Cornell University	United States	Oral Presentation (12 min. + 3 min. Q&A)
15:05:00	15:10:00	Functional impact prediction for single nucleotide variants in Drosophila melanogaster with FlyCADD	Katja M Hoedjes	Vrije Universiteit Amsterdam	Netherlands	Flash Presentation (3 min. + 2 min. Q&A)
15:10:00	15:15:00	Comparing archaic and modern human genomes using deleteriousness predictions from a DNA language model	Danat Yermakovich	Institute of Genomics, University Of Tartu	Estonia	Flash Presentation (3 min. + 2 min. Q&A)
15:15:00	15:20:00	The Evolutionary Ecology of Color Vision in Krill: Comparative Genomics, Machine Learning and Analysis of Standing Genetic Variation in Opsins	Andreas Wallberg	Uppsala University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:20:00	From Foundations to Futures: Building Equity in Genetics	Jazlyn Mooney	University Of Southern California	United States	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:20:00	16:30:00	Introducing the IDEA taskforce	Tugce Bilgin Sonay	Smbe Idea	Switzerland	Invited Speaker (10 min.)
16:30:00	16:35:00	Science Wise: Career mentorship through a storytelling interview podcast	Emilia Huerta-Sánchez	University Of Oregon	United States	Flash Presentation (3 min. + 2 min. Q&A)
16:35:00	16:50:00	Can evolutionary studies on social traits promote 21st-century eugenics?	Mehmet Somel	Middle East Technical University	Türkiye	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	16:55:00	Navigating Tribal Collaboration in Environmental and Genomic Research in California	Alexandra Sasha Nikolaeva	UC Berkeley	United States	Flash Presentation (3 min. + 2 min. Q&A)
16:55:00	17:00:00	From Specimen to Sequence: International Researcher Perspectives on Indigenous Data Sovereignty in Biodiversity Genomics	Jocelyn Chee Santiago	Arizona State University	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:00:00	17:05:00	EvoSur: Building an interconnected network for evolutionay biology in South America	Paco Majic	Embl Heidelberg	Germany	Flash Presentation (3 min. + 2 min. Q&A)
17:05:00	17:10:00	Mapping JEDI Challenges in the Earth BioGenome Project	Marcela Uliano Da Silva	Wellcome Sanger Institute	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
17:10:00	17:15:00	Biomedical and life science articles by female researchers spend longer under review	Dr. David Alvarez-Ponce	University of Nevada, Reno	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:15:00	17:20:00	Project Psyche: A case study of how to embed inclusivity within large -scale genomic projects	Charlotte Wright	Wellcome Sanger Institute	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
17:20:00	17:50:00	Panel discussion	Yichen (Serena) Dai Simone Andrea Biagini Hayley Free	Fudan University	China	Panel discussion (30 min.)

L06 From Ancient Pathogen Genomics to Palaeoepidemiology					Date	Tuesday, June 30, 2026	15:50	to	17:50
					Chair	Schroeder, Hannes Sikora, Martin	Room	Lumbye (lower level)	
Times	Title		Speaker	Organisation	Country	Presentation type			
15:50:00	16:05:00	Whole-genome sequencing of Black Death victims reveals an immune gene under natural selection	Harald Ringbauer	Max Planck Institute For Evolutionary Anthropology Leipzig	Germany	Oral Presentation (12 min. + 3 min. Q&A)			
16:05:00	16:20:00	On Inferring the Virulence of Ancient Pathogens, Especially Prehistoric Plague	Ruairidh Macleod	University Of Oxford	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)			
16:20:00	16:35:00	Ancient Genomic Analysis of a New Mycobacterium tuberculosis Lineage from Iron Age Britain	Megan Michel	Harvard University	United States	Oral Presentation (12 min. + 3 min. Q&A)			
16:35:00	16:50:00	Bayesian approaches to root phylogenetic trees under root uncertainty: evaluation using empirical and simulated ancient and modern pathogen data	Maria Lopopolo	Institute Pasteur	France	Oral Presentation (12 min. + 3 min. Q&A)			
16:50:00	16:55:00	First ancient genome of Streptococcus pyogenes from a pre-Columbian Bolivian mummy reveals its presence in the Americas before European contact	Frank Maixner	Eurac Research Institute for Mummy Studies	Italy	Flash Presentation (3 min. + 2 min. Q&A)			
16:55:00	17:00:00	Bacterial Disease and Viral Emergence in Holocene Hunter-Gatherers from Patagonia	Dr Maria C. Ávila-Arcos	Liigh-unam	Argentina	Flash Presentation (3 min. + 2 min. Q&A)			
17:00:00	17:05:00	Tracing the origin and evolution of early smallpox in South America	Bruno Romero	Trinity College Dublin	Ireland	Flash Presentation (3 min. + 2 min. Q&A)			
17:05:00	17:10:00	Insights from ancient DNA into deep-time evolution of oral microbes in the Cusco region of the Peruvian Andes	Dr. Tanvi Prasad Honap	University Of Zurich	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)			
17:10:00	17:15:00	Ancient Treponema pallidum genomes reveal phylogenetic diversity and lineage persistence through time in South American populations	Davide Bozzi	University Of Lausanne	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)			
17:15:00	17:20:00	Co-isolation of ancient DNA and RNA from non-formalin-fixed lung specimens reveals host-pathogen interactions during the Industrial Revolution in Great Britain.	Isabelle Du Plessis	Fred Hutchinson Cancer Center	United States	Flash Presentation (3 min. + 2 min. Q&A)			
17:20:00	17:25:00	Identifying the presence of Yersinia pestis in Medieval Turkey during the Second Plague Pandemic	Ravneet Sidhu	McMaster University	Canada	Flash Presentation (3 min. + 2 min. Q&A)			
17:25:00	17:30:00	A deeply divergent Yersinia pestis lineage identified in Early Iron Age Romania	Caitlin Mitchell	University Of Tuebingen	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
17:30:00	17:35:00	The deadly past of Yersinia enterocolitica: insights from paleogenomics	Margaux Lefebvre	Max Planck Institute for Evolutionary Anthropology	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
17:35:00	17:40:00	Genomic signatures of increasing disease burden in recent prehistory	Gili Greenbaum	The Hebrew University of Jerusalem	Israel	Flash Presentation (3 min. + 2 min. Q&A)			
17:40:00	17:45:00	Parvovirus B19 from early modern warships suggests genotype 2 continuity in Europe, bridging a millennium-long gap	Zoé Pochon	Centre for Palaeogenetics, Stockholm	Sweden	Flash Presentation (3 min. + 2 min. Q&A)			
17:45:00	17:50:00	Humans as reservoirs: Historical microbiomes uncover hidden zoonotic pathways	Kristen Rayfield	Stony Brook University	United States	Flash Presentation (3 min. + 2 min. Q&A)			

Open 5: Population genetics and genomics 2				Date	Tuesday, June 30, 2026	15:50	to	17:50
				Chair	Poulsen, Michael	Room	Main	
Times		Title	Speaker	Organisation	Country	Presentation type		
15:50:00	16:05:00	Leveraging variation of matri- and patrilinear genomes reveals contrasting patterns of sex-bias dispersal in northern sea lions	Camille Kessler	LMU	Germany	Oral Presentation (12 min. + 3 min. Q&A)		
16:05:00	16:20:00	Coalescent-Based Introgression Inference: Theory, Biases, and Solutions	David Peede	Brown University	United States	Oral Presentation (12 min. + 3 min. Q&A)		
16:20:00	16:35:00	ARG-based inference of regional maize demographic histories	Regina Fairbanks	University Of California, Davis	United States	Oral Presentation (12 min. + 3 min. Q&A)		
16:35:00	16:50:00	Environmentally-driven asynchrony in genomic reconstructions of demographic responses to past climate change and human expansion across hundreds of bird populations	Ryan Germain	Aarhus University	Denmark	Oral Presentation (12 min. + 3 min. Q&A)		
16:50:00	16:55:00	The detection of selective sweeps associated with adaptation to lead (Pb) contamination in wild house sparrows	Yuheng Sun	Macquarie University	Australia	Flash Presentation (3 min. + 2 min. Q&A)		
16:55:00	17:00:00	Comprehensive Characterization of Inversions across the Human Population using Strand-seq Pooled and Long-Read Sequencing	Vasiliki Tsapalou	European Molecular Biology Laboratory (embl)	Germany	Flash Presentation (3 min. + 2 min. Q&A)		
17:00:00	17:05:00	From Drift Debt to Inbreeding Depression: Genomic Consequences of Population Decline in Ruffed Lemurs	Aryn Wilder	San Diego Zoo Wildlife Alliance	United States	Flash Presentation (3 min. + 2 min. Q&A)		
17:05:00	17:10:00	The westward expansion of Asian rice	Ornob Alam	New York University	United States	Flash Presentation (3 min. + 2 min. Q&A)		
17:10:00	17:15:00	Landscape barriers shape genetic connectivity in the Golden langur (Trachypithecus geei)	Ashika Dhimal	Indian Institute of Science	India	Flash Presentation (3 min. + 2 min. Q&A)		
17:15:00	17:20:00	Investigating the genomics of reindeer (Rangifer tarandus) domestication	Vanessa Bieker	Royal Botanic Gardens, Kew	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)		
17:20:00	17:25:00	Pangenomes Illuminate Genetic Diversity in Sheep and Their Wild Relatives	Brenda Murdoch	University of Idaho	United States	Flash Presentation (3 min. + 2 min. Q&A)		
17:25:00	17:30:00	Genomic Insights into Biodiversity Decline in Endangered Hallig Beetle, Pseudaplemonus limonii	Aryadevi Anitha Shaji	Leibniz Institute For The Analysis Of Biodiversity Change, Bonn	Germany	Flash Presentation (3 min. + 2 min. Q&A)		
17:30:00	17:35:00	Evaluating GWAS Power Using SLiM Simulations in Structured Populations	Diego Salazar	University Of Oslo	Norway	Flash Presentation (3 min. + 2 min. Q&A)		
17:35:00	17:40:00	Genetics of repeated ecotype separation in Malawi cichlid genus Labeotropheus	Moritz Blumer	University of Cambridge	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)		
17:40:00	17:45:00	Adaptive introgression from Pacific to Atlantic herring facilitates rapid niche exploration in the Baltic Sea	Mafalda Ferreira	Scilifelab, Stockholm University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)		

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:20:00	Diversity of recombination landscapes across taxa: from genetic control to genomic architecture	Prof. Aurora Ruiz-Herrera	Universitat Autònoma de Barcelona (UAB)	Spain	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:20:00	16:35:00	Rapidly Evolving Epigenetic Controlling Factors of Meiotic Recombination	Linda Odenthal-Hesse	Max Planck Institute For Evolutionary Biology	Germany	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:50:00	Tuning meiosis in different habitats: lessons from Arabidopsis arenosa	Marinela Dukic	ETH Zürich	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	17:05:00	Self-fertilization can reverse the selection coefficient on a recombination landscape modifier during experimental evolution	Tom Parée	New York University	United States	Oral Presentation (12 min. + 3 min. Q&A)
17:05:00	17:20:00	Heterogeneous evolution of effective recombination landscapes across percomorph fishes	Marion Talbi	Institute of Ecology and Evolution, University of Bern, Switzerland	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)
17:20:00	17:35:00	A holocentric pangenome links karyotype evolution to meiotic recombination	Dr. André Marques	Max Planck Institute For Plant Breeding Research	Germany	Oral Presentation (12 min. + 3 min. Q&A)
17:35:00	17:40:00	Fine-scale mapping of meiotic recombination in Saccharomyces cerevisiae unveils shifts in genetic exchanges driven by DNA heterologies	Irene Tiemann-Boege	Johannes Kepler University	Austria	Flash Presentation (3 min. + 2 min. Q&A)
17:40:00	17:45:00	Loci under balancing selection can change the recombination landscape around them	Lou Guyot	University Paris-saclay	France	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00	Turtles reveal novel insights into PRDM9's role in recombination rate landscape evolution	Laurie Stevison	Auburn University	United States	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title	Speaker	Organisation	Country	Presentation type
15:50:00	16:20:00 The phylogeny of Archaea as a case study of challenges in reconstructing very deep evolutionary relationships	Dr David Moreira	CNRS - Universite Paris-Saclay	France	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:20:00	16:35:00 Reconstructing the origin of the genetic code	Joanna Masel	University Of Arizona	United States	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:50:00 Ancient Reconstructed Proteins, inferring ancient proteins fromancient metagenomics samples	Gabriel Renaud	Université Laval	Canada	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	17:05:00 Comparative analysis of eukaryotic protein complex orthologs	Ore Francis	Wellcome Sanger Institute	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
17:05:00	17:20:00 Beyond conserved markers: enhancing deep node resolution via rigorous orthology filtering of 900 protein domains	Lina Uematsu	University of Bristol	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
17:20:00	17:25:00 NS-QMaker: Non-Stationary Amino-Acid Substitution Models Facilitate Deep Phylogenetic Inference	Thomas Wong	Australian National University	Australia	Flash Presentation (3 min. + 2 min. Q&A)
17:25:00	17:30:00 Eukaryote-like evolution of Asgard archaeal genomes	Julian Vosseberg	Wageningen University & Research	Netherlands	Flash Presentation (3 min. + 2 min. Q&A)
17:30:00	17:35:00 Reticulation dominates protein structural evolution in bacteriophages	Rachel Kavanagh	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
17:35:00	17:40:00 Rooting the deep divergence of land plants	Hengchi Chen	Georg-August-University Goettingen	Germany	Flash Presentation (3 min. + 2 min. Q&A)
17:40:00	17:45:00 Exploring Time-Nonreversibility in Deep Phylogenetics with ABYSS	Jasmine Saghafifar	University Of Auckland	New Zealand	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00 FastSpeciesTree: Fast and Scalable Species tree Inference	Dr Jonathan Holmes	University of Oxford	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:20:00	Late Neandertals of North-Western Europe	Mateja Hajdinjak	Max Planck Institute For Evolutionary Anthropology	Germany	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:20:00	16:35:00	Ancient DNA from Shimaο city records kinship practices in Neolithic China	Zehui Chen	Institute Of Vertebrate Paleontology And Paleoanthropology (ivpp)	China	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:50:00	Introgression from an unsampled lineage in Southern African genomes	Martin Kuhlwilm	University Of Vienna	Austria	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	17:05:00	Characterising and timing the four independent Denisovan admixture events in Asia and Oceania	Moisès Coll Macià	IBE (CSIC - UPF)	Spain	Oral Presentation (12 min. + 3 min. Q&A)
17:05:00	17:20:00	Genealogy-based analyses shows modern humans were formed through multiple deep admixtures	Hrushikesh Loya	University Of Oxford	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
17:20:00	17:25:00	Evaluation of a target capture approach for plant dietary identification from paleofeces	Miyabi Fujiki	Department of Biological Sciences, Graduate School of Science, The University of Tokyo	Japan	Flash Presentation (3 min. + 2 min. Q&A)
17:25:00	17:30:00	Uncovering previously unrecognized gene flow from modern humans into Denisovans	Lu Chen	Fudan University	China	Flash Presentation (3 min. + 2 min. Q&A)
17:30:00	17:35:00	Gene-culture coevolution in the European Upper Palaeolithic	Francesco Ravasini	Aarhus University	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
17:35:00	17:40:00	Genomic Landscapes of Oceania and Island Southeast Asia: Insights from 92 populations	Peter Gerlach	Stanford	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:40:00	17:45:00	Deep-Time Demographic Inference in the Americas Using Site Frequency Spectrum–Based Modeling	Epifanía Arango-Isaza	University of Wisconsin-Madison	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00	Natural selection acting on complex traits hampers the predictive accuracy of polygenic scores in ancient samples	Diego Ortega Del Vecchyo	National Autonomous University Of Mexico	Mexico	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
09:00:00	09:50:00	Presentation title: Evolution in the human gut microbiome	Nandita Garud	University of California (UCLA)	United States	Plenary presentation

Times	Title	Speaker	Organisation	Country	Presentation type
10:20:00	10:55:00 RESEARCH FUNDING OPPORTUNITIES WITH THE EUROPEAN RESEARCH COUNCIL	Nicolas Van Oostende	European Research Council EA	Belgium	Speaker (35 min.)
10:55:00	11:10:00 Highlights of ERC project and testimonial	Fernando Racimo	University Of Copenhagen	Denmark	Invited Speaker Presentation (12 min. + 3 min. Q&A)
11:10:00	11:25:00 Highlights of ERC project and testimonial	Dr Laura Eme	CNRS		Invited Speaker Presentation (12 min. + 3 min. Q&A)
11:25:00	11:50:00 Q&A	Nicolas Van Oostende	European Research Council EA	Belgium	Q&A (25 minutes)

Open 6: Comparative genomics and phylogenetics 2					Date	Wednesday, July 1, 2026		10:20	to	12:20
					Chair	Limborg, Morten		Room	Main	
Times	Title		Speaker	Organisation	Country	Presentation type				
10:20:00	10:35:00	Efficient Bayesian Phylogenetics under the Infinite Sites Model	Ivan Specht	Stanford University	United States	Oral Presentation (12 min. + 3 min. Q&A)				
10:35:00	10:50:00	Comparative Genomics of Syngnathiform Fishes	Jule Drewalowski	University Of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)				
10:50:00	11:05:00	Gene losses promoted skeletal innovation and cancer resistance in turtles	Leon Hilgers	Senckenberg Research Institute	Germany	Oral Presentation (12 min. + 3 min. Q&A)				
11:05:00	11:20:00	Ancestral introgression and the origin of a unique asexual vertebrate, the Amazon molly	Maximos Chin	University Of California, Davis	United States	Oral Presentation (12 min. + 3 min. Q&A)				
11:20:00	11:25:00	Evolution of the inflammasome pathway in bats: a comparative genomics perspective	Mridula Nandakumar	Senckenberg Research Institute	Germany	Flash Presentation (3 min. + 2 min. Q&A)				
11:25:00	11:30:00	Rapid chromosome evolution in parthenogenetic Panagrolaimus nematodes	Nadège Guiglielmoni	Université Libre De Bruxelles	Belgium	Flash Presentation (3 min. + 2 min. Q&A)				
11:30:00	11:35:00	Evidence for asynchronous rediploidisation following the 1R whole genome duplication in vertebrates	Róisín Long	Smurfit Institute of Genetics, Trinity College Dublin	Ireland	Flash Presentation (3 min. + 2 min. Q&A)				
11:35:00	11:40:00	Genome reorganisation in Ithomiini butterflies	Karin Nasvall	Wellcome Sanger Institute	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)				
11:40:00	11:45:00	A telomere atlas to study vertebrate chromosome evolution	Jack A Medico	The Rockefeller University	United States	Flash Presentation (3 min. + 2 min. Q&A)				
11:45:00	11:50:00	Genetic and transcriptional signatures of evolutionary mismatch in the Orang Asli of Peninsular Malaysia	Audrey Arner	Vanderbilt University	United States	Flash Presentation (3 min. + 2 min. Q&A)				
11:50:00	11:55:00	Root-symbiotic entomopathogenic fungi use distinct Pth11 G-protein coupled receptors for plant and insect recognition	Andi Wilson	University of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)				
11:55:00	12:00:00	New meiofaunal genomes reveal the diversity of animal Hox clusters	Dr. Madeleine Aase-Remedios	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)				
12:00:00	12:05:00	The genomics of miniature animals: the first genomes of the microscopic phyla Gnathostomulida and Micrognathozoa	Shoyo Sato	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)				
12:05:00	12:10:00	Maintenance of net deleterious mutations in polymorphism in fluctuating environments	Yuseob Kim	Ewha Womans University	South Korea	Flash Presentation (3 min. + 2 min. Q&A)				
12:10:00	12:15:00	Genome size: Did flight loss relax genome size constraints in birds?	Zeynep Oguzhan	Natural History Museum Of Denmark	Denmark	Flash Presentation (3 min. + 2 min. Q&A)				
12:15:00	12:20:00	Regulatory Plasticity as an Adaptive Strategy in Malaria Parasites	Elena Gómez-Díaz	Spanish National Research Council	Spain	Flash Presentation (3 min. + 2 min. Q&A)				

Times		Title	Speaker	Organisation	Country	Presentation type
10:20:00	10:35:00	Miniaturization – a major player in Metazoan Evolution	Katrine Worsaae	University Of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
10:35:00	10:50:00	Balancing and Positive Selection Shapes the Spot Patterning Phenotype in the Masai Giraffe	Joy Love	Penn State University	United States	Oral Presentation (12 min. + 3 min. Q&A)
10:50:00	11:05:00	Pervasive and convergent changes in the kynurenine pathway contribute to sugar-diet adaptations in bats	Xueling Yi	Senckenberg Gesellschaft Für Naturforschung	Germany	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:20:00	Mutation bias is a key predictor of adaptation rate	Shazia Parveen	National Centre for Biological Sciences	India	Oral Presentation (12 min. + 3 min. Q&A)
11:20:00	11:25:00	Somatic mutation genomics to elucidate longevity in the extremely long-lived desert plant Welwitschia mirabilis	Michael Martin	NTNU University Museum	Norway	Flash Presentation (3 min. + 2 min. Q&A)
11:25:00	11:30:00	SELECTED TO SHINE:ENZYMES REPURPOSED FOR BIOLUMINESCENCE IN BRITTLE STARS	Wendy-Shirley Bayaert	University of Mons	Belgium	Flash Presentation (3 min. + 2 min. Q&A)
11:30:00	11:35:00	Not one Y, but five: evidence for mixed origins of Y haplotypes across the common frog's range	Wen-Juan Ma	Research group of Ecology, Evolution and Genetics, Biology Department, Vrije Universiteit Brussel	Belgium	Flash Presentation (3 min. + 2 min. Q&A)
11:35:00	11:40:00	The Hidden Cost of Speed: A Molecular Conflict Between Light Damage and Visual Recovery in Human Evolution	Gianni Castiglione	Vanderbilt University	United States	Flash Presentation (3 min. + 2 min. Q&A)
11:40:00	11:45:00	Pollen tube competition is mediated by a gene subject to Positive Selection in Arabidopsis	Peter McKeown	University Of Galway	Ireland	Flash Presentation (3 min. + 2 min. Q&A)
11:45:00	11:50:00	An Exploratory Assessment of Opsins in Pleurobrachia pileus	DaeNia La Rodé	University Of Leicester	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
11:50:00	11:55:00	Pervasive lateral gene transfer among grasses as a driver of metabolic innovation	Lara Pereira	University of Sheffield	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
11:55:00	12:00:00	Schistosoma mansoni single cell transcriptomics reveals recently duplicated genes specifically expressed in the host-parasite interfase.	Andres Iriarte	Facultad de Medicina, Universidad de la República	Uruguay	Flash Presentation (3 min. + 2 min. Q&A)
12:00:00	12:05:00	Molecular principles of iridescent color formation in bird feathers	Roberto Arbore	CIBIO - InBIO	Portugal	Flash Presentation (3 min. + 2 min. Q&A)
12:05:00	12:10:00	Trophic specialization drives contrasting evolutionary dynamics of chemosensory genes in blowflies	Tatiana Teixeira Torres	University of São Paulo	Brazil	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	Non-coding RNA regulation in differentiating ZW sex chromosomes	Ruben Olbrechts	Institute of Science and Technology Austria	Austria	Flash Presentation (3 min. + 2 min. Q&A)
12:15:00	12:20:00	Molecular mechanisms involved in homologous and intramolecular recombination in Coronaviruses	Sarah M. Metzger	Charité - Universitätsmedizin Berlin	Germany	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	Understanding the rate of somatic mutations and epimutations in trees	Frank Johannes	Technical University of Munich	Germany	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:20:00	Leveraging contemporary genotype-environment associations to predict maladaptation in pecan natural populations	Chloee McLaughlin	HudsonAlpha Institute for Biotechnology	United States	Invited Speaker Presentation (25 min. + 5 min. Q&A)
11:20:00	11:35:00	A Landscape Genomic story of the olive tree in the western Mediterranean : insights into local adaptation and future (mal-) adaptation	Philippe Cubry	IRD	France	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:50:00	Characterizing the DNA methylation landscape in O. sativa ssp indica	Isabel Bojanini	New York University	United States	Oral Presentation (12 min. + 3 min. Q&A)
11:50:00	11:55:00	Investigating Effects of Inversions and Recombination Modifiers to Ecotypic Differentiation in Wild Sunflowers	Yue Yu	University of British Columbia	Canada	Flash Presentation (3 min. + 2 min. Q&A)
11:55:00	12:00:00	Genome diversification and polyploidy in under-utilised, climate resilient millet crops in the grass genus Digitaria	Lizo Masters	Royal Botanic Gardens, Kew	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
12:00:00	12:05:00	Predicting Fitness in Future Climates: A Proof of Concept in Arabidopsis thaliana and Vitis vinifera subsp. sylvestris	Romain Villoutreix	Inrae	France	Flash Presentation (3 min. + 2 min. Q&A)
12:05:00	12:10:00	Genomic signal of local adaptation in UK silver birch (Betula pendula)	Phoebe Swift	Queen Mary's University London And Royal Botanical Gardens Kew	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	Genomic analysis reveals local adaptation and vulnerability to climate change of the African orphan crop finger millet (Eleusine coracana)	Margret Veltman	Institut de Recherche pour le Développement	France	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	Is my population locally adapted? Establishing the influence of natural selection in the real world.	Professor Aida Andres	University College London	United Kingdom	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:05:00	Disentangling drift and selection in an endangered plant using temporal genomics and language models	Dr Tahir Ali	University Of Cologne	Germany	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:10:00	Disentangling background selection from associative overdominance in structured populations using gene trees	Pierre Lesturgie	Centre for Ecology, Evolution and Environmental Changes (CE3C)	Portugal	Flash Presentation (3 min. + 2 min. Q&A)
11:10:00	11:15:00	Detecting local adaptation within chromosomal inversions	Karolina Wąchała	University Of Bern	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)
11:15:00	11:20:00	Parallel genomic adaptation promoting replicate range shifts of the blue-tailed damselfly, <i>Ischnura elegans</i> , in Scotland and Fennoscandia	Nicky Lustenhouwer	University Of Aberdeen	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
11:20:00	11:35:00	Detecting local adaptation to biotic and abiotic environmental conditions in the cosmopolitan ectomycorrhizal fungus <i>Cenococcum geophilum</i>	Dr. Benjamin Dauphin	Swiss Federal Research Institute WSL	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:50:00	The genomic architecture of rapid local adaptation under extreme demographic perturbations in native and invasive cichlid fish populations	Hannes Svoldal	University of Antwerp	Belgium	Oral Presentation (12 min. + 3 min. Q&A)
11:50:00	11:55:00	Genomic time-series of a butterfly biocontrol agent reveal selection under extreme demographic constraint	Gabriela Montejo-Kovacevich	Uppsala University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)
11:55:00	12:00:00	Early Interferon Pathways as Targets of Selection in an Anthropogenic Yellow Fever - Primate System	Joanna Malukiewicz	University Of Hamburg	Germany	Flash Presentation (3 min. + 2 min. Q&A)
12:00:00	12:05:00	Signals of positive selection on transposable element control genes across structured human populations	Roudin Sarama	Queen Mary University Of London	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
12:05:00	12:20:00	No evidence for recent selection on amylase copy number in humans	Laura Colbran	University Of Pennsylvania	United States	Oral Presentation (12 min. + 3 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
10:20:00	10:50:00	Concerted evolution and unorthodox recombination of human subtelomeres	Erik Garrison	University Of Tennessee Health Science Center	United States	Invited Speaker Presentation (25 min. + 5 min. Q&A)
10:50:00	11:05:00	Population-scale genotyping from low-coverage sequencing using pangenome graphs	Davide Bolognini	Human Technopole	Italy	Oral Presentation (12 min. + 3 min. Q&A)
11:05:00	11:10:00	Multidimensional variation and population stratification across 8000 complete human centromeres	Yanqing Sun	Zhejiang University	China	Flash Presentation (3 min. + 2 min. Q&A)
11:10:00	11:15:00	Population genetic analysis of G-quadruplexes across the human pangenome	Saswat Mohanty	Penn State University	United States	Flash Presentation (3 min. + 2 min. Q&A)
11:15:00	11:20:00	Pervasive inter-chromosomal recombination shapes human subtelomeric architecture	Andrea Guarracino	Translationa Genomics Institute (TGen)	United States	Flash Presentation (3 min. + 2 min. Q&A)
11:20:00	11:35:00	A Baltic Cod pangenome for population inference	Lingfeng Meng	GEOMAR Helmholtz Centre for Ocean Research Kiel	Germany	Oral Presentation (12 min. + 3 min. Q&A)
11:35:00	11:40:00	The Brassica super-pangenome uncovers novel exploitable genetic resources for crop breeding	Yuxi Hu	Crag	Spain	Flash Presentation (3 min. + 2 min. Q&A)
11:40:00	11:45:00	The role of structural variants during adaptation to whole genome duplication	Emma Curran	University Of Sheffield	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
11:45:00	11:50:00	Inferring ancestral alleles and signatures of selection in cattle from a pangenome graph	Guoli Li	ETH Zurich	China	Flash Presentation (3 min. + 2 min. Q&A)
11:50:00	12:05:00	Disentangling Reticulate Evolution in the Mediterranean Wall Lizards with a Super Pangenome	Natalia Zajac	Max Planck Institute For Evolutionary Biology	Germany	Oral Presentation (12 min. + 3 min. Q&A)
12:05:00	12:10:00	Pangenome-based investigation of genomic diversity in Kaolinonychus: A harvestmen lineage with deep admixture history and troglophilic adaptation (Arachnida, Opiliones, Paranonychidae)	Dongyoung Kim	Seoul National University	South Korea	Flash Presentation (3 min. + 2 min. Q&A)
12:10:00	12:15:00	Pangenome analyses for understanding adaptation to ash dieback disease in European ash populations	Dario Galanti	Royal Botanic Gardens Kew	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
12:15:00	12:20:00	A pangenomic approach to evaluate fate of ancestral and novel structural variants in a homopoloid hybrid sparrow.	Kalle Tunström	Lund University	Sweden	Flash Presentation (3 min. + 2 min. Q&A)

SMBE Business Meeting

Date **Wednesday, July 1, 2026**

12:20 *to* **13:20**

Chair De Meaux, Prof Juliette

Room Carstensen (lower level)

Times	Title		Speaker	Organisation	Country	Presentation type
12:20:00	13:20:00	SMBE Business Meeting presentation	Prof Juliette De Meaux	University Of Cologne	Germany	Presentation

Times	Title		Speaker	Organisation	Country	Presentation type
13:20:00	13:35:00	170 million years of Y chromosome evolution	Diego Cortez	National Autonomous University Of Mexico	Mexico	Oral Presentation (12 min. + 3 min. Q&A)
13:35:00	13:50:00	The functional impact of adaptive variants in South Asian populations	Matteo Fumagalli	Queen Mary University of London	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
13:50:00	14:05:00	Increased survival of low-frequency lineages during fluctuations in resource abundance	Ruth Hershberg	Technion - Israel Institute Of Technology	Israel	Oral Presentation (12 min. + 3 min. Q&A)
14:05:00	14:20:00	Origin and host diversification of giant viruses infecting eukaryotes	Chuan Ku	Academia Sinica	Taiwan	Oral Presentation (12 min. + 3 min. Q&A)
14:20:00	14:35:00	A simulation framework for the study of population-level processes in phylogenetics	Carina Mugal	University Of Lyon 1	France	Oral Presentation (12 min. + 3 min. Q&A)
14:35:00	14:50:00	The evolution of exceptionally low mutation rates in plant mitochondrial and plastid genomes	Daniel Sloan	Colorado State University	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:50:00	15:05:00	Giant toxin genes, extreme genome variation, and repeated hybridization in harmful bloom-forming haptophyte golden algae	Jennifer Wisecaver	Washington State University	United States	Oral Presentation (12 min. + 3 min. Q&A)
15:05:00	15:20:00	You Don't Know What You've got 'Til It's Gone: Using non-biting mosquitoes to understand the evolution of blood-feeding.	Federico Hoffmann	Mississippi State University	United States	Oral Presentation (12 min. + 3 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
13:20:00	13:50:00	Using museomics to track the domestication of insects reared for feed and food	Pablo Librado	Institute of Evolutionary Biology (IBE)	Spain	Invited Speaker Presentation (25 min. + 5 min. Q&A)
13:50:00	14:05:00	Palaeogenomics and the multiverse of elephant ivory trade	Dr Patricia Pecnerova	University Of Copenhagen	Denmark	Invited Speaker Presentation (12 min. + 3 min. Q&A)
14:05:00	14:20:00	Paleogenomics and habitat modeling reveal temperate Eurasian origins of Late Quaternary woolly rhinoceroses	Xiao-Le Lei	Tsinghua University	China	Oral Presentation (12 min. + 3 min. Q&A)
14:20:00	14:35:00	Metagenomic Characterization of Canids from the Pre-Contact (3,475–360 yBP) Patagonian Coastal Region of Argentina	Miriam Bravo Lopez	Arizona State University	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:35:00	14:50:00	Ancient DNA Reveals Millennia of Morphological Stability Despite Climate-Induced Gene Flow in European Crows	Chyi Yin Gwee	State Museum Of Natural History Stuttgart / LMU Munich	Germany	Oral Presentation (12 min. + 3 min. Q&A)
14:50:00	14:55:00	Museum specimens characterize natural repertoire of antimicrobial resistance inwildlife and reveal human impact of antibiotic use.	John Richards	University Of Edinburgh	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
14:55:00	15:00:00	Pathogen-Host Genomic Interactions as Drivers of Invasion Success	Nasreen Broomand	University of Vermont	United States	Flash Presentation (3 min. + 2 min. Q&A)
15:00:00	15:05:00	Ancient-modern genomes reveal an impact-dependent erosion of functional diversity in Atlantic bluefin tuna	Piergiorgio Massa	University Of Bologna	Italy	Flash Presentation (3 min. + 2 min. Q&A)
15:05:00	15:10:00	A preliminary look into the paleogenomics of Anatolian big cats	Nisan Yıldız	Middle East Technical University	Turkey	Flash Presentation (3 min. + 2 min. Q&A)
15:10:00	15:15:00	Reconstructing the genomic history of Ice Age grey wolves	Mattias Sherman	Francis Crick Institute	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
15:15:00	15:20:00	Comet, a genome from the dawn of cattle breeding	Alex Siekmann	Trinity College Dublin	Ireland	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
13:20:00	13:35:00	A cross-linking enzyme underlies the development of feather structural coloration in birds	Simon Yung Wa Sin	The University of Hong Kong	Hong Kong	Oral Presentation (12 min. + 3 min. Q&A)
13:35:00	13:50:00	One Hundred Years of West Nile Virus Envelope Protein Adaptation	Jack Dorman	National Institutes of Health	United States	Oral Presentation (12 min. + 3 min. Q&A)
13:50:00	14:05:00	Single-cell analysis of prefrontal cortex differences in selectively bred tame and aggressive foxes (Vulpes vulpes)	Anna Kukekova	University of Illinois at Urbana-Champaign	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:05:00	14:20:00	Diverse Genomic Routes to the Same Protein: Evolutionary Mechanisms of New Gene Birth and Molecular Convergence	Xuan Zhuang	University of Arkansas	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:20:00	14:25:00	Deciphering Ion-Dependence of Fitness Effects of Protein Mutations	Haoli Gan	Westlake University	China	Flash Presentation (3 min. + 2 min. Q&A)
14:25:00	14:30:00	Identifying noncoding contributions to life history evolution with machine learning	Gregory Wray	Duke University	United States	Flash Presentation (3 min. + 2 min. Q&A)
14:30:00	14:35:00	Evolution of mutation rate in a simulation system with an explicit genome representation and a complex genotype-to-phenotype map	Quentin Fernandez De Grado	Université Grenoble Alpes	France	Flash Presentation (3 min. + 2 min. Q&A)
14:35:00	14:40:00	Convergent molecular evolution of thermal tolerance in mammals	Christopher Taylor	University Of Manchester	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
14:40:00	14:45:00	Evolutionary consequences of recombination suppression: the case of a chromosomal inversion in the seaweed fly	Léa Nicolas	University of Rennes	France	Flash Presentation (3 min. + 2 min. Q&A)
14:45:00	14:50:00	Selection on sexual chromosomes and circadian genes during speciation in two Amazonian butterflies	Riccardo Poloni	Cirb (collège De France Cnrs) - Paris	France	Flash Presentation (3 min. + 2 min. Q&A)
14:50:00	14:55:00	Public microbial single-cell RNA sequencing data reveal opposing transcriptional relationships at population and single-cell scales	Leandra Brettner	Arizona State University	United States	Flash Presentation (3 min. + 2 min. Q&A)
14:55:00	15:00:00	Quantifying DNA Methylation Consistency and Specificity Across Genomes	Stephanie McKay	University Of Missouri	United States	Flash Presentation (3 min. + 2 min. Q&A)
15:00:00	15:05:00	Quantifying the Genome-Wide Effect of Polygenic Selection over a Single Generation	Gabriele Sgarlata	University of California, Davis	United States	Flash Presentation (3 min. + 2 min. Q&A)
15:05:00	15:10:00	Multi-Omics Characterization of the Hibernation Phenotype in Ground Squirrels	Michele Albertini	Senckenberg Research Institute	Germany	Flash Presentation (3 min. + 2 min. Q&A)
15:10:00	15:15:00	Gene-by-gene evolution of dosage compensation in a neo-XY sex chromosome system	Vincent Mérel	University of Lausanne	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)
15:15:00	15:20:00	The genomic basis of hostplant usage in a rapidly radiating clade	Blair Stokes	University of South Carolina	United States	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
13:20:00	14:00:00	Functional analysis of proteins encoded in mammalian endogenous parvovirus	Gloria Arriagada	Universidad Andres Bello	Chile	Invited Speaker Presentation (35 min. + 5 min. Q&A)
14:00:00	14:15:00	Transposable Element Co-Option Drives Transcription Factor Neofunctionalization.	Olga Rosspopoff	Igbmc	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)
14:15:00	14:30:00	Ancient Epstein-Barr virus genomes from Mesolithic and Neolithic birch tar reveal early viral diversity and immune escape	Yuejiao Huang	Globe Institute, University of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
14:30:00	14:45:00	3,500 years of sheeppox virus evolution inferred from archaeological and codicological genomes.	Louis L'Hôte	University College Dublin	Ireland	Oral Presentation (12 min. + 3 min. Q&A)
14:50:00	14:55:00	Characterizing tumor-specific human endogenous retroviruses in clear cell Renal Cell Carcinoma patients	Sophie Kogut	Fred Hutchinson Cancer Center	United States	Flash Presentation (3 min. + 2 min. Q&A)
14:55:00	15:00:00	Recovery of an 18th Century Rhinovirus Genome through Ancient RNA Isolation of Human Lungs	Ms. Erin Barnett	Fred Hutchinson Cancer Center	United States	Flash Presentation (3 min. + 2 min. Q&A)
15:00:00	15:05:00	Co-option of long terminal repeats mediates endogenous retrovirus dysregulation in cancer	Margaret Chi	University Of Washington	United States	Flash Presentation (3 min. + 2 min. Q&A)
15:05:00	15:10:00	Tracing the spread of Beak and Feather Disease Virus over the past two centuries	Dr. Lucy Van Dorp	UCL Genetics Institute	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
15:10:00	15:15:00	Comparative analysis of KAP1 binding reveals species-specific KRAB-ZNF regulatory landscapes in primates	Katja Nowick	Freie Universität Berlin	Germany	Flash Presentation (3 min. + 2 min. Q&A)
15:15:00	15:20:00	Comparison of Methods for the Capture of Virus Genomes Using Formalin-Fixed Paraffin-Embedded Tissues	Lexi Keene-Snickers	Royal Veterinary College	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
13:20:00	13:35:00	Neglected microbial lineages and the birth of eukaryotic protein domains: A structural phylogenetics perspective	Dr. Paul Roginski	CNRS	France	Oral Presentation (12 min. + 3 min. Q&A)
13:35:00	13:50:00	Patterns of molecular evolution across prokaryotes	Giorgio Bianchini	University Of Bath	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
13:50:00	14:05:00	Plant terrestrialization: evolutionarily conserved mechanisms in UV acclimation in the closest algal relatives of land plants	Căcilia Kunz	Georg-August-Universität Göttingen	Germany	Oral Presentation (12 min. + 3 min. Q&A)
14:05:00	14:20:00	BLInG: Enabling Genomic Studies of Unicellular Organisms to Illuminate Major Evolutionary Transitions with Single-cell Genomics	Parker Crossland	Arizona State University	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:20:00	14:35:00	Diversity and integration of endosymbiotic associations in microbial eukaryotes	Anna Karnkowska	University Of Warsaw	Poland	Oral Presentation (12 min. + 3 min. Q&A)
14:35:00	14:50:00	Multilevel drift and selection in the evolution of prokaryotic plasmid	Pr. Dr. Tal Dagan	Kiel University	Germany	Oral Presentation (12 min. + 3 min. Q&A)
14:50:00	14:55:00	Evidence supporting a viral origin of the mitosing nucleus	Philip Bell	Microbiogen Pty Ltd	Australia	Flash Presentation (3 min. + 2 min. Q&A)
14:55:00	15:00:00	Epigenetics in Archaea: Chromosome conformation underlies heritable resistance to oxidative stress in Sulfolobus islandicus	Rylee Hackley	The Ohio State University	United States	Flash Presentation (3 min. + 2 min. Q&A)
15:00:00	15:05:00	Spatial proteomics reveals lipid droplet reorganization in symbiotic Paramecium bursaria cells	Jun-Yi Leu	Academia Sinica, Institute of Molecular Biology	Taiwan	Flash Presentation (3 min. + 2 min. Q&A)
15:05:00	15:10:00	An independent phylogenomic dataset sheds new light on the eukaryotic Tree of Life	Romain B. Leroy	Cnrs	France	Flash Presentation (3 min. + 2 min. Q&A)
15:10:00	15:15:00	Diversity of the protist world and the origin of animal multicellularity	Victoria Shabardina	Institue of Evolutionary Biology	Spain	Flash Presentation (3 min. + 2 min. Q&A)
15:15:00	15:20:00	Investigating cell type-specific gene expression in Salpingoeca rosetta	Maria Eleonora Rossi	University Of Galway	Ireland	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
13:20:00	13:50:00	The evolution of new vertebrate cell types and organs	Margarida Cardoso Moreira	The Francis Crick Institute	United Kingdom	Invited Speaker Presentation (25 min. + 5 min. Q&A)
13:50:00	14:05:00	Evolutionary conservation and rewiring of enhancer-promoter connectivity across mammals	Stephen Rong	Imperial College London	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
14:05:00	14:20:00	Cross-species chromatin accessibility maps reveal regulatory drivers of mammalian lifespan evolution	Erin Nicole Gilbertson	Yale School of Medicine	United States	Oral Presentation (12 min. + 3 min. Q&A)
14:20:00	14:35:00	A multi-omics approach to unravel the evolution of gene regulation in vertebrates	Laura González-Rodelas	Universitat Autònoma De Barcelona	Spain	Oral Presentation (12 min. + 3 min. Q&A)
14:35:00	14:50:00	Coevolution of microRNAs and their gene targets leads to novel traits – insights from across the vertebrate tree of life.	Jonathan Fenn	University Of Manchester	United Kingdom	Oral Presentation (12 min. + 3 min. Q&A)
14:50:00	14:55:00	A dog is not a wolf – how tiny differences have shaped man's best friend	Doreen Schwochow	School of Engineering Sciences in Chemistry	Sweden	Flash Presentation (3 min. + 2 min. Q&A)
14:55:00	15:00:00	Ancient Epigenetic Insights into Woolly Mammoth Adaptations	Yoav Mathov	Hebrew University Of Jerusalem and Tel Hai Collage	Israel	Flash Presentation (3 min. + 2 min. Q&A)
15:00:00	15:05:00	Cis and trans contributions to cell type–specific regulatory evolution in primates	Hsin-Chiao Huang	University Of Chicago	United States	Flash Presentation (3 min. + 2 min. Q&A)
15:05:00	15:10:00	An Evolutionary Multi-Omic Framework to Assess the Evidence for Adaptive Regulatory Evolution Across Diverse Molecular Traits	John Pool	University Of Wisconsin-Madison	United States	Flash Presentation (3 min. + 2 min. Q&A)
15:10:00	15:15:00	A statistical framework for DNA methylation repeatability in natural populations	Ioanna Garefalaki	Division Of Evolutionary Biology, Faculty Of Biology, Lmu Munich, Planegg-martinsried	Germany	Flash Presentation (3 min. + 2 min. Q&A)
15:15:00	15:20:00	Cell-Autonomous Adaptations in High-Altitude Human Populations	Ruthie Golomb	Weizmann Institute of Science	Israel	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title	Speaker	Organisation	Country	Presentation type	
15:20:00	15:50:00	Editors will be available for Q&A	Laura Katz	Smith College	United States	Q&A (25 minutes)

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:05:00	Bacterial ecospecies: extraordinary new models for studying complex adaption.	Prof Daniel Falush	Shanghai Institute Of Materia Medica	China	Oral Presentation (12 min. + 3 min. Q&A)
16:05:00	16:20:00	Modeling regulatory evolution under the assumption of local oligogenicity	Greg Gibson	Georgia Institute of Technology	United States	Oral Presentation (12 min. + 3 min. Q&A)
16:20:00	16:35:00	Tracing Protein Fold throughout Evolution using Synthetic Biology and Protein Design	Klara Hlouchova	Charles University	Czech Republic	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:50:00	Volcanic drivers of human demographic collapse and genetic divergence on New Britain Island	Prof. Hie Lim Kim	Nanyang Technological University	Singapore	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	17:05:00	Convergent Evolution in Tumor Genomes Targets Functional Domains from Ancient to Lineage-Specific	Li Liu	Arizona State University	United States	Oral Presentation (12 min. + 3 min. Q&A)
17:05:00	17:20:00	Transposable element exaptation as a source of novel genes in polyploid wheat evolution	Flavia Mascagni	Department of Agriculture, Food and Environment (DAFE), University of Pisa	Italy	Oral Presentation (12 min. + 3 min. Q&A)
17:20:00	17:35:00	Competition, compensation and inbreeding depression in the evolution of conifer polyembryony	Tanja Pyhäjärvi	University of Helsinki	Finland	Oral Presentation (12 min. + 3 min. Q&A)
17:35:00	17:50:00	Bayesian test of gene flow between sister lineages using genomic data	Tianqi Zhu	Chinese Academy Of Sciences	China	Oral Presentation (12 min. + 3 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:20:00	Socially Responsive Paleoproteomics: Scientific Advances, Challenges, and Ethical Pathways in African Hominin Research	Palesa Madupe	Maxplanck Institute	Germany	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:20:00	16:35:00	Characterisation of a male Neanderthal from Prado Vargas, Spain, via enamel paleoproteomics	Guillermo Carrillo-Martin	Universitat Pompeu Fabra	Spain	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:40:00	Time to rethink how to analyse ancient collagen	Matthew Collins	Globe Institute, Univeristy Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
16:40:00	16:45:00	Reconstructing the pre-Anthropocene evolutionary history of right whales	Yumeko Tarusawa	The Graduate University for Advanced Studies, Kyushu University	Japan	Flash Presentation (3 min. + 2 min. Q&A)
16:45:00	16:50:00	Evaluating protein preservation in dental calculus from natural history specimens for dietary reconstruction	Yoko Fukuhara	Integrative Evolutionary Science, The Graduate University For Advanced Studies	Japan	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:05:00	Novel examples of natural selection in ethnically and culturally diverse sub-Saharan Africans	Dr Jasmin Rees	University Of Pennsylvania	United States	Oral Presentation (12 min. + 3 min. Q&A)
16:05:00	16:20:00	Farming termites and microbial symbiont: enzymes and natural products in an evolutionary ecology context	Michael Poulsen	University Of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
16:20:00	16:35:00	Ancestral sequence reconstruction reveals simple genetic mechanisms for evolving octocoral bioluminescence	Emily Lau	University of Chicago	United States	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:50:00	Germline-specific patterns of hypomethylation of previously inaccessible regions of ape genomes	Dongmin Son	UC Santa Barbara	United States	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	16:55:00	Is sex-biased expression an evolutionary advantage – or a liability?	Carolina Barata	Institute Of Science And Technology Austria (ISTA)	Austria	Flash Presentation (3 min. + 2 min. Q&A)
16:55:00	17:00:00	Epigenetic variation of Y-chromosome palindromic regions across human populations revealed by nanopore sequencing	Monika Cechova	Faculty of Informatics, Masaryk University	Czech Republic	Flash Presentation (3 min. + 2 min. Q&A)
17:00:00	17:05:00	Homologous recombination in stationary phase bacteria	Pavel Payne	Institute Of Science And Technology Austria	Austria	Flash Presentation (3 min. + 2 min. Q&A)
17:05:00	17:10:00	Genomic reconstruction of the bacterial toolkit for plastic biodegradation	Pere Puigbò	Autonomous University Of Barcelona	Spain	Flash Presentation (3 min. + 2 min. Q&A)
17:10:00	17:15:00	Ancient microRNAs Reveal Regulatory Continuity in a 41,000-Year-Old Insect	Bastian Fromm	Uit - The Arctic University Of Norway	Norway	Flash Presentation (3 min. + 2 min. Q&A)
17:15:00	17:20:00	Hologenomic signatures of Arctic adaptation in Greenland sled dogs	Elsa Brenner	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
17:20:00	17:25:00	Hybrid zones and a deadly fungus: adaptive selection and microbiomes in Bombina toads	Isolde Van Riemsdijk	Globe Institute	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
17:25:00	17:30:00	Between fidelity and flexibility: host-specialist and generalist Helicobacter in Podarcis lizards	Dinah Parker	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
17:30:00	17:35:00	From post-glacial to the Anthropocene: the adaptation landscape dynamics of arthropod species in Denmark	Jilong Ma	Aarhus University	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
17:35:00	17:40:00	Ancient HLA Variation and Predicted Immune Responses During Epidemics in Colonial Mexico	Walter Nicolas Ortega	Liigh, UNAM	Mexico	Flash Presentation (3 min. + 2 min. Q&A)
17:40:00	17:45:00	Genome compartmentalization in a fungal insect pathogen reveals a second mating-type locus on an accessory chromosome	Henrik H. De Fine Licht	Københavns Universitet	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00	Different mutation rates, shared architecture: SNPs and SVs across the Neurospora crassa interactome	April Snøfrid Kleppe	University Of Jyväskylä	Finland	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:05:00	Molecular Insights into the Burmese Python Invasion of the Florida Everglades	Dr Margaret Hunter	U.S. Geological Survey	United States	Invited Speaker Presentation (12 min. + 3 min. Q&A)
16:05:00	16:20:00	Ecology-mediated demographic instability shapes genetic diversity in a cichlid adaptive radiation	Daniela Souza-Costa	University Of Basel	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)
16:20:00	16:35:00	Using genomics to predict inbreeding depression risk: Case studies in Hawaiian birds	Christopher Kyriazis	San Diego Zoo Wildlife Alliance	United States	Oral Presentation (12 min. + 3 min. Q&A)
16:35:00	16:50:00	Two decades of yellow-bellied marmot population sampling reveals physiological and regulatory resilience to the metabolic costs of seasonal climate change	Stavi Tennenbaum	Princeton University	United States	Oral Presentation (12 min. + 3 min. Q&A)
16:50:00	17:05:00	Biodiversity genomics research practices require harmonising to meet stakeholder needs in conservation	Chiara Bortoluzzi	Sib Swiss Institute Of Bioinformatics	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)
17:05:00	17:10:00	Genomic consequences of population collapse and recovery in European wolves	Claudia Fontserè	Globe Institute, University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
17:10:00	17:15:00	Four centuries of commercial whaling eroded 11,000 years of population stability in bowhead whales	Professor Eline Lorenzen	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
17:15:00	17:20:00	Combining environmental DNA with nuclear loci capture for genetic monitoring of endangered butterfly populations	Sarah Schmid	University Of Lausanne	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)
17:20:00	17:25:00	Whole genome resequencing enables temporal reconstruction of purifying selection in a highly bottlenecked avian population	Paige Byerly	Senckenberg Research Institute	Germany	Flash Presentation (3 min. + 2 min. Q&A)
17:25:00	17:30:00	How informative is demographic inference from genomic data for conservation?	Mael Le Gouellec	EPHE-MNHN	France	Flash Presentation (3 min. + 2 min. Q&A)
17:30:00	17:35:00	The frontier of genome SFS-based demographic inference	Abdelmajid Omarjee	College De France	France	Flash Presentation (3 min. + 2 min. Q&A)
17:35:00	17:40:00	Modeling repeats allows k-mer-based, alignment-free methods to calculate population genomic distances	Eduardo Charvel	Bioinformatics and Systems Biology Graduate Program, University of California San Diego	United States	Flash Presentation (3 min. + 2 min. Q&A)
17:40:00	17:45:00	High genomic connectivity and climate-linked demographic decline in the snowy owl	Helle Baalsrud	Norwegian University Of Life Sciences	Norway	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00	Habitat Specialisation Impacts Clownfish Demographic Resilience to Pleistocene Sea-Level Fluctuations	Théo Gaboriau	University Of Lausanne	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
15:50:00	16:20:00	Mechanistic fitness landscapes in random metabolic networks: from epistatic to ecological interactions	Djordje Bajic	Tu Delft	Netherlands	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:20:00	16:50:00	Mapping the immunity-dependent fitness seascape of influenza	Michael Lässig	University Of Cologne	Germany	Invited Speaker Presentation (25 min. + 5 min. Q&A)
16:50:00	17:05:00	Molecular mechanisms of gene regulatory evolution revealed by in vivo genotype–phenotype maps	Cauã Antunes Westmann	École polytechnique fédérale de Lausanne	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)
17:05:00	17:20:00	Inference of high-dimensional fitness landscapes with site-specific contributions to epistatic interactions	Carlos Martí-Gómez	Cold Spring Harbor Laboratory	United States	Oral Presentation (12 min. + 3 min. Q&A)
17:20:00	17:25:00	The shifting nature of the SARS-CoV-2 fitness landscape	Charlie Hamilton	Pandemic Sciences Institute, University Of Oxford	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
17:25:00	17:30:00	Temperature-Dependent Biochemical Landscapes of TEM-1 β -Lactamase	RuYi Ma	Westlake University	China	Flash Presentation (3 min. + 2 min. Q&A)
17:30:00	17:35:00	Modelling the genetic control of phenotypic stochasticity in genotype-phenotype-fitness maps	Jun Ishigohoka	Friedrich Miescher Laboratory Of The Max Planck Society	Germany	Flash Presentation (3 min. + 2 min. Q&A)
17:35:00	17:40:00	Indels in genotype-phenotype maps cannot simply be ignored because of their low rate	Manuela Giraud	Centre For Genomic Regulation (crg)	Spain	Flash Presentation (3 min. + 2 min. Q&A)
17:40:00	17:45:00	Epistasis informed protein fitness landscapes improve evolutionary modelling in bacterial genomes	Eamon Winship	Aarhus University	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00	Building realistic genotype-phenotype-fitness maps that predict mutant fitness in diverse environments	Kara Schmidlin	Arizona State University	United States	Flash Presentation (3 min. + 2 min. Q&A)

S22 Evolution of gene regulation: insights from novel molecular and statistical approaches - Part 2					Date	Wednesday, July 1, 2026	15:50	to	17:50
					Chair		Room	Lumbye (lower level)	
Times	Title		Speaker	Organisation	Country	Presentation type			
15:50:00	16:05:00	The regulation of evolutionarily new genes	Nicolas Svetec	Rockefeller University	United States	Oral Presentation (12 min. + 3 min. Q&A)			
16:05:00	16:20:00	Mechanisms for how cis-regulatory elements arise from transposable elements illustrated by repeated domestication in snake venom genes	Siddharth Gopalan	University of Texas, Arlington	United States	Oral Presentation (12 min. + 3 min. Q&A)			
16:20:00	16:35:00	Polygenic traits adaptation leads to selection of beneficial alleles in local regulatory hubs	Maud Fagny	Inrae	France	Oral Presentation (12 min. + 3 min. Q&A)			
16:35:00	16:50:00	How DNA methylation changes shaped recent human evolution	Dr. David Gokhman	Weizmann Institute of Science	Israel	Oral Presentation (12 min. + 3 min. Q&A)			
16:50:00	16:55:00	Evolution of dominance modifiers over 16 million years	Vincent Castric	CNRS	France	Flash Presentation (3 min. + 2 min. Q&A)			
16:55:00	17:00:00	Consistent signatures of selection on gene expression level at different evolutionary scales	Dr. Thibault Latrille	Université De Lausanne	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)			
17:00:00	17:05:00	RegEvol: detection of directional selection in regulatory sequences through phenotypic predictions and phenotype-to-fitness functions	Marc Robinson-Rechavi	University Of Lausanne	Switzerland	Flash Presentation (3 min. + 2 min. Q&A)			
17:05:00	17:10:00	Comparative inference of regulatory mechanisms driving age-related splicing changes across vertebrate species	Zoe Chervontseva	University Of Hamburg	Germany	Flash Presentation (3 min. + 2 min. Q&A)			
17:10:00	17:15:00	Measuring selection on regulatory networks combining population transcriptomics and experimental evolution	Eddy Mendoza-Galindo	UC Berkeley	United States	Flash Presentation (3 min. + 2 min. Q&A)			
17:15:00	17:20:00	Transcriptional Reprogramming as a Primary Driver of Long-Term Cold Adaptation in Wild Yeast	Luis A. Saona	Universidad De Santiago de Chile	Chile	Flash Presentation (3 min. + 2 min. Q&A)			
17:20:00	17:25:00	Identifying phenotype- and tissue-associated regulatory elements across species using public genomic and transcriptomic data	Wynn Meyer	Lehigh University	United States	Flash Presentation (3 min. + 2 min. Q&A)			
17:25:00	17:30:00	Salmonids reveal principles of regulatory evolution following autotetraploidization	Gareth Gillard	Norwegian University of Life Sciences	Norway	Flash Presentation (3 min. + 2 min. Q&A)			
17:30:00	17:35:00	Investigating gene regulatory underpinnings of human-great ape divergence: Insights from new models	Nathan Schaefer	University Of California, San Francisco	Denmark	Flash Presentation (3 min. + 2 min. Q&A)			
17:35:00	17:40:00	Decoding gene essentiality from cross-species transcriptional constraints	Matteo Zambon	Centre For Genomic Regulation	Spain	Flash Presentation (3 min. + 2 min. Q&A)			
17:40:00	17:45:00	Evolutionarily dynamic enhancer transcription links chromatin regulation to drought response in rice (Oryza sativa)	Zoé Joly-lopez	Université Du Québec À Montréal	Canada	Flash Presentation (3 min. + 2 min. Q&A)			
17:45:00	17:50:00	Gene expression variation underlying local adaptation in silver birch (Betula pendula)	Jenni Sirén	University of Helsinki	Finland	Flash Presentation (3 min. + 2 min. Q&A)			

Times	Title		Speaker	Organisation	Country	Presentation type
16:50:00	17:20:00	Gene editing livestock for sustainable agriculture	Simon Lillico	University Of Edinburgh	United Kingdom	Invited Speaker Presentation (25 min. + 5 min. Q&A)
17:20:00	17:25:00	Potential for alleviating inbreeding depression using gene editing	Richard Frankham	Macquarie University	Australia	Flash Presentation (3 min. + 2 min. Q&A)
17:25:00	17:40:00	Engineering Hope: How Genetic Rescue Biotechnologies are Reshaping Wildlife Conservation	Ben Novak	Revive & Restore	United States	Oral Presentation (12 min. + 3 min. Q&A)
17:40:00	17:45:00	Evaluating the efficiency of captive genetic rescue versus genome editing of ancestral variation	Thomas Birley	University Of East Anglia	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
17:45:00	17:50:00	ARIA's Accelerating Adaptation programme: Engineering Resilience in a Changing World	Yannick Wurm	Advanced Research + Invention Agency	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)

Times		Title	Speaker	Organisation	Country	Presentation type
09:10:00	10:00:00	Rapid adaptation vs. the Anthropocene	Moises Exposito-Alonso	University of California Berkeley and Howard Hughes Medical Institute	United States	Plenary presentation

Times	Title		Speaker	Organisation	Country	Presentation type
10:00:00	10:05:00	Introduction	Dr. Diego Hartasánchez	Cinvestav	Mexico	Introduction (5 minutes)
10:05:00	10:30:00	DAFNEE: a database of academia-friendly eco-evo journals to facilitate transitioning towards responsible publishing.	Nicolas Galtier	Cnrs - Université Montpellier	France	Invited Speaker Presentation (20 min. + 5 min. Q&A)
10:30:00	10:45:00	Where to Publish? Building a database of for-profit and non-profit journals in life sciences.	Dr. Thibault Latrille	Université De Lausanne	Switzerland	Oral Presentation (12 min. + 3 min. Q&A)
10:45:00	11:00:00	The Tie That Binds Us? Challenging the Primacy of DNA in Kinship Studies and Re-Centering Community in Defining Human Connections	Hannah Moots	Centre For Palaeogenetics	Sweden	Oral Presentation (12 min. + 3 min. Q&A)
11:00:00	11:15:00	Stay in your lane: developing effective approaches to multidisciplinary research and publishing to address twenty first century challenges.	Michael Dills	UiT-The Arctic University Of Norway	Norway	Oral Presentation (12 min. + 3 min. Q&A)
11:15:00	11:30:00	Scientist as a citizen-subject in a collapsing habitat	Asst. Prof. N. Ezgi Altınışık	Hacettepe University	Türkiye	Oral Presentation (12 min. + 3 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
10:30:00	10:45:00	The trans-Pacific voyage that shaped the pattern of genetic variation and enrichment of functional alleles in Native Hawaiians	Charleston Chiang	University of Southern California	United States	Oral Presentation (12 min. + 3 min. Q&A)
10:45:00	11:00:00	Collapse, recovery and future uncertainty: temporal genomics and simulations of genomic erosion in the Mauritius kestrel	Xuejing Wang	University of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
11:00:00	11:05:00	Population boom or bust? Kraken the population connectivity and demographic history of Octopus vulgaris	Qiaz Hua	CNRS	France	Flash Presentation (3 min. + 2 min. Q&A)
11:05:00	11:10:00	Heavy-tailed dispersal and its impact on local adaptation: Revisiting the British peppered moth	Sherif Negm	University of Chicago	United States	Flash Presentation (3 min. + 2 min. Q&A)
11:10:00	11:15:00	Repeatable genomic responses to climate during global invasion	Kathryn Hodgins	Monash University	Australia	Flash Presentation (3 min. + 2 min. Q&A)
11:15:00	11:20:00	Eco-evolutionary drivers of the emergence of the major wildlife pathogen, Ranavirus	Cedric Tan	University College London	United Kingdom	Flash Presentation (3 min. + 2 min. Q&A)
11:20:00	11:25:00	Population history and migration in sub-Saharan African Drosophila melanogaster	Austin Daigle	UNC Chapel Hill	United States	Flash Presentation (3 min. + 2 min. Q&A)
11:25:00	11:30:00	Comparing population genomic variation across ploidy levels	Nikita Tikhomirov	VIB-UGent Center for Plant Systems Biology	Belgium	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
10:30:00	10:45:00	The origins of domestic sheep and wool production in the Nordic Bronze Age	Laura Viñias Caron	University Of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
10:45:00	11:00:00	Have arctic wolves adapted to the arctic environment?	Harvinder Pawar	Department of Biology, University Of Copenhagen	Denmark	Oral Presentation (12 min. + 3 min. Q&A)
11:00:00	11:05:00	Whole-Genome Population Genomics Reveals Lineage Structure and Adaptive Potential of <i>Philaenus spumarius</i> , the Principal Vector of <i>Xylella fastidiosa</i> in Europe	Roberto Biello	University of Copenhagen	Italy	Flash Presentation (3 min. + 2 min. Q&A)
11:05:00	11:10:00	Thriving against the odds: bottlenecked invaders show evidence for purging	Antti Miettinen	Aarhus University, Department of Biology	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
11:10:00	11:15:00	Spatial and temporal patterns of genetic variation in Northern European pedunculate oak populations	Maxi Muessig	University of Copenhagen, IGN	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
11:15:00	11:20:00	Genome association studies of range-wide introduction of Douglas fir in Europe	Dimitra Sergiadou	Copenhagen University	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
11:20:00	11:25:00	Population and Gene Flow Decline Following Landscape Fragmentation and it's Consequences for Genetic Load in Soil Arthropods	Jeppe Bayer Pedersen	Aarhus University	Denmark	Flash Presentation (3 min. + 2 min. Q&A)
11:25:00	11:30:00	Palaeogenomic insights into late Quaternary African faunas	Deon de Jager	University Of Copenhagen	Denmark	Flash Presentation (3 min. + 2 min. Q&A)

Times	Title		Speaker	Organisation	Country	Presentation type
11:30:00	12:55:00	SMBE Awards Announcements	Prof Juliette De Meaux	University Of Cologne	Germany	Presentation
12:55:00	13:00:00	Final words from SMBE 2026	Tom Gilbert	University of Copenhagen	Denmark	Presentation
13:00:00	13:10:00	SMBE 2027	Nadia Aubin-Horth	Université Laval	Canada	Presentation