



PROGRAM OF TALKS

(updated July, 22)

PLEASE NOTE THAT

- Five minutes of musical interval will play between talks as you take a moment to relax or move to other venues; the only exception are a few consecutive flash talks in uninterrupted succession
- A sound will indicate the beginning of the question time (between 2 and 5 minutes depending on the talk duration)
- Time intervals will be strictly enforced by the automatic system and by the chairs

23 July

14:00-18:45 **Registration and Welcome Cocktail**

Plenary Lecture (CT; streaming in AD1, AD2, and BC)

19:00-20:00 Philip Donoghue Telling evolutionary time

24 July

Plenary Lecture - Presidential Address (CT; streaming in AD1, AD2, and BC)

9:00-10:00 Kateryna D. Makova Telomere-to-telomere assemblies uncover secrets of ape sex chromosomes

COFFEE BREAK

15- Animal genomics goes wild (CT)

10:30 - 10:55 Susan Johnston Sexual dimorphism in recombination rates & landscapes in wild vertebrates.
11:00 - 11:15 Harrison Ostridge Local genetic adaptation in wild chimpanzees
11:20 - 11:35 Craig Primmer Beyond GWAS: Complex mechanisms underlie the simple genomic architecture of Atlantic salmon age at maturity
11:40 - 11:55 Angela Fuentes-Pardo Genomic adaptations in Atlantic herring to past, present, and future climate
12:00 - 12:12 Flávia Fernandes Late but good: genomic and plastic signals of adaptive mismatch in a long-lived sub-Antarctic species
12:12 - 12:24 Pierre Lesturgie Size matters: how a chromosomal inversion determining size shaped the demographic history of a chondrichthyan species (*Amblyraja radiata*)

6- Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict (AD1)

10:30 - 10:55 Manyuan Long Sexual conflict drive in new gene evolution
11:00 - 11:15 Cristina Berenguer Millanes Effect of inversion size on recombination landscape, and its impact on selection for recombination suppression in the early stages of sex chromosome evolution
11:20 - 11:35 Daniel Shaw Single-cell gene expression of spermatogenesis reveals evolution of post-meiotic gene repression and activation of amplicons on the threespine stickleback fish Y chromosome
11:40 - 11:55 Iulia Darolti The genomic architecture of sex-specific adaptation in stick insects
12:00 - 12:25 Max Reuter Sexually antagonistic genetic variation in *Drosophila melanogaster*

13- Polygenic Adaptation – Predictability and Pleiotropy (AD2)

10:30 - 10:55 Daniel Ortiz-Barrientos A systems view of polygenic adaptation in an Australian wildflower
11:00 - 11:15 Frederic Guillaume Predictability of gene expression evolution during climate adaptation
11:20 - 11:35 Grant Kinsler Phenotypic and evolutionary properties of large-effect adaptive mutations isolated from a two-step adaptive walk
11:40 - 11:55 Isabela do O The evolution of genetic covariance and modularity as a result of multigenerational environmental fluctuations
12:00 - 12:25 Jacqueline Sztepanacz The role of pleiotropy in generating evolutionary limits

23- Evolutionary approaches to understand cancer across scales (BC)

10:30 - 10:55 Ivana Bozic Evolutionary dynamics of tumor progression
11:00 - 11:15 Brian Johnson Estimating clonal dynamics in human blood using coalescent theory
11:20 - 11:35 Elisa Scanu A mathematical model in evolutionary medicine: ecDNA dynamics
11:40 - 11:55 Jorge Alfaro-Murillo Detecting pairwise and higher-order epistatic effects among somatic cancer mutations across oncogenesis
12:00 - 12:25 Alexander Cagan The impossibility of whales: somatic mutation across the tree of life

LUNCH BREAK

15- Animal genomics goes wild (CT)

13:30 - 13:55 Michael Westbury Arctic marine mammals in a changing environment
14:00 - 14:15 Patricia Pecnerova STAMPEDE: Spatial and Temporal Analysis of Modern and Past Elephant Diversity
14:20 - 14:35 Xenia Wietlisbach 1000 full genomes of Darwin's finches reveal polygenic architecture of both beak morphology and individual fitness
14:40 - 14:55 Lara Urban A ghost of past selection: the evolution and conservation relevance of colour polymorphism in the critically endangered kākāpō
15:00 - 15:12 Xuejing Wang Islands of selective sweep in an ocean of genetic drift: genome-wide relaxation of selection of a big insular rodent
15:12 - 15:24 Jonas Oppenheimer Evolutionary history of bison revealed through ancient DNA

20- Evolutionary biology through a functional genomics lens (AD1)

13:30 - 13:55	Genevieve Housman	Cell culture systems to interrogate primate skeletal functional genomics
14:00 - 14:15	Alessandro Raveane	The influence of ancient ancestries on the immunological landscape of present-day Europeans
14:20 - 14:35	Andres Bendesky	Genetic causes and phenotypic consequences of a newly evolved adrenal cell type
14:40 - 14:55	Małgorzata Gazda	Evolution of the uterine epithelium in model mammals
15:00 - 15:25	Steven Reilley	The functional and evolutionary impacts of human-specific deletions in conserved elements

22- Experimental evolution of non-model species and systems (AD2)

13:30 - 13:55	Vaughn Cooper	Adaptation to overflow metabolism by mutations that impair tRNA modification in experimentally evolved bacteria
14:00 - 14:15	Yu-Ying (Phoebe) Hsieh	Fungal-mediated magnesium competition shapes bacterial fitness and the evolution of antibiotic resistance
14:20 - 14:35	Jan Engelstädter	The impact of natural transformation on adaptation to heterogeneous environments
14:40 - 14:55	William DeWitt	Evolutionary dynamics of antibody affinity maturation in replica germinal centers
15:00 - 15:25	Britt Koskella	Experimental evolution from populations to communities

24- Indels: computational methods, evolutionary dynamics, and biological applications (BC)

13:30 - 13:55	Gerton Lunter	The impact of indels on bioinformatics, health, and evolution
14:00 - 14:15	Jūlija Pečerska	Polynomial-time frequentist joint alignment and tree inference
14:20 - 14:35	Ian Holmes	Hidden Markov model generators of indel processes
14:40 - 14:55	Guillaume Beslon	Spontaneous regulation of non-coding sequences in bacteria through border effect duplications neutral bias
15:00 - 15:25	Benjamin Redelings	Indels, rate variation, and heterotachy

COFFEE BREAK

Open symposium (CT)

16:00 - 16:15	Siliang Song	Adaptive tracking generates quasi-neutral molecular evolution
16:20 - 16:35	Jennifer James	Within and between species variation in the distribution of fitness effects
16:40 - 16:55	Alessio Iannucci	Genome size evolution in squamate reptiles is influenced by ecological factors and parity mode
17:00 - 17:15	Karen Siu-Ting	How to become poisonous and avoid dying in the attempt: Investigating molecular adaptations in neotropical poison frogs
17:20 - 17:35	Christopher Wheat	miRNA targets: non-model species, false-positives, and functional coherence
17:40 - 17:55	Andrew Clark	Are expression levels of homologous alleles independent of each other?

Open symposium (AD1)

16:00 - 16:15	Eric Baptiste	Interactomics: dozens of viruses, co-evolving with humans, including the influenza A virus, may actively distort human aging
16:20 - 16:35	Jiansi Gao	Model misspecification misleads inference of the spatial dynamics of disease outbreaks
16:40 - 16:55	Eva Šatović Vukšić	Bivalves disclose novel pattern of satellite DNA organization, highly dispersed and closely connected to Helitron mobile elements
17:00 - 17:15	Esther Betran	Recurrent co-domestication of PIF/Harbinger transposable element proteins in insects
17:20 - 17:35	Alba Marino	Effective population size does not explain transposable elements and genome size variation in animals
17:40 - 17:55	Murillo Rodrigues	Shared evolutionary processes shape landscapes of genomic variation in the great apes

Open symposium (AD2)

16:00 - 16:15	Muthukumar Panachakaram	Bayesian clock model selection to distinguish evolutionary rate variation models for divergence time estimation
16:20 - 16:35	Nicolas Galtier	Distinguishing gene flow from incomplete lineage sorting via branch length analysis
16:40 - 16:55	Marta Álvarez-Presas	Assessing the origin of Bilateria with new genomic methods
17:00 - 17:15	Luca Ferretti	Trees grow while you aren't looking: an artefactual correlation of branch lengths with sample size in reconstruction of large phylogenies
17:20 - 17:35	Zachary Szpiech	Scanning for selection in unphased data
17:40 - 17:55	Georgette Fumerling	Testing for ancestral population structure in demographic models using linkage disequilibrium statistics

Open symposium (BC)

16:00 - 16:15	Lara R Arauna	Biological relatedness and social structure in an ancient Oceanian population
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16:20 - 16:35	Aida Andrés	The genetics and anatomy of face evolution in humans and other primates
16:40 - 16:55	Parul Johri	Developing an evolutionary baseline model for humans: jointly inferring purifying selection with population history
17:00 - 17:15	Hanaisa Sant'Anna	History of Sex-Biased Admixture: new method and insights on mating behavior in Brazil
17:20 - 17:35	Flávia Schlichta	How does genetic surfing impact genomic diversity? Predictions and applications to human genomes
17:40 - 17:55	Benjamin Vernot	The Dog in my Data: faunal aDNA that maps to the human genome
18:00-20:00	Poster session 1 (SP and EC)	

25 July

Plenary Lecture (CT; streaming in AD1, AD2, and BC)

9:00-10:00	Emilia Huerta-Sanchez	Archaic and modern humans: an evolutionary history of recurrent introgression and natural selection
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COFFEE BREAK

Graduate Student Excellence Awards (CT; streaming in AD1, AD2, and BC)

10:30 - 10:43	Matteo Sebastianelli	Genome-wide association study reveals the polygenic nature of rhythm in a wild non-passerine bird
10:43 - 10:56	Aurora Alvarez-Buylla	Dealing with a deadly diet: toxin binding proteins in poison frogs
10:56 - 11:09	Harvinder Pawar	Ghost admixture in eastern gorillas
11:09 - 11:22	Carmina Barberena-Jonas	Analyzing IBD segments in the MX Biobank to track the genetic structure of Mexico through time
11:22 - 11:35	Ujani Hazra	Differences in disease burdens across human populations are governed more by neutral evolution than by recent polygenic selection
11:35 - 11:48	Margaux Aubel	Comparing de novo emerged proteins with their unevolved random-sequence counterparts
11:48 - 12:01	Marianne Dehasque	Temporal dynamics of woolly mammoth genome erosion prior to extinction
12:01 - 12:14	Carlos Cortez	Simple mechanisms for the evolution of heterospecificity in the hemoglobin complex
12:14 - 12:27	Kai Yan	Modification of maternally defined H3K4me3 regulates the inviability of interspecific <i>Xenopus</i> hybrids

LUNCH BREAK

7- Computational evolutionary genomics in the era of machine learning (CT)

13:30 - 13:55	Sohini Ramachandran	Interpretable models for complex trait architecture via learning from population genetic datasets
14:00 - 14:15	Santiago Medina-Muñoz	Demographic modeling of admixed latin american populations from whole genomes
14:20 - 14:35	Luca Nesterenko	Phyloformer: towards fast and accurate phylogeny estimation with self-attention networks
14:40 - 14:55	Alex Mas-Sandoval	The genomic footprint of social stratification in admixing American populations
15:00 - 15:12	Cai Li	A generalizable deep learning framework for inferring fine-scale germline mutation rate maps
15:12 - 15:24	Letizia Lamperti	Using transformers to relate DNA sequence composition from eDNA to ecosystem properties

27- Regulatory evolution and the emergence of diversity (AD1)

13:30 - 13:55	Patricia J. Wittkopp	Evolutionary changes in gene regulatory networks inferred from patterns of co-expression
14:00 - 14:15	Thea Rogers	Novel regulatory units underlie the evolution of complex traits in coleoid cephalopods
14:20 - 14:35	Nataša Puzović	Make all the right noises: the evolution of gene expression mean and expression noise in changing environments is constrained by the gene position in the gene regulatory network
14:40 - 14:55	Antoine Fages	A single-cell perspective on the role of gene expression regulation in promoting ecological and dietary adaptations in Lake Tanganyika cichlid fishes
15:00 - 15:08	Riccardo Papa	High level of novelty under the hood of convergent evolution
15:08 - 15:16	Sandra Goutte	Regulatory variation leads to striking color polymorphism in a grass frog
15:16 - 15:24	Amanda Glaser-Schmitt	Population- and developmental stage-specific gene regulation in <i>Drosophila melanogaster</i>

11- Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics (AD2)

13:30 - 13:55	Victoria Mullin	Ten thousand years of cattle human interaction
14:00 - 14:15	Torsten Günther	the impact of human actions and wild introgression in the history of domestic cattle on the Iberian Peninsula
14:20 - 14:35	Elisabetta Canteri	An interdisciplinary analysis of the drivers and consequences of human mobility changes during the West Eurasian Holocene

14:40 - 14:55	Audrey Lin	Integrating genomics and Indigenous knowledge to illuminate the life, history, and loss of Coast Salish woolly dogs
15:00 - 15:25	Anders Bergström	The entangled genomic histories of humans and dogs

21- Science for everybody: education and outreach in Molecular Biology and Evolution (BC)

13:30 - 13:55	Laura MacDonald	Facilitating the inclusive classroom: building meaningful connections with and between students
14:00 - 14:15	Natasha Glover	Bringing science to the public in the light of evolution
14:20 - 14:35	Elaine Guevara	Teaching and outreach to broaden engagement and combat harmful misconceptions in human evolutionary genetics
14:40 - 14:55	Akos Dobay	How to teach computational biology to biologists and biomedical students
15:00 - 15:25	Natalia Pasternak Taschner	Supporting science is not the same as understanding science: teaching critical thinking for science-based policies

COFFEE BREAK

7- Computational evolutionary genomics in the era of machine learning (CT)

16:00 - 16:25	Yun Song	Advances in learning complex evolutionary constraints and predicting variant effects
16:30 - 16:45	M. Elise Lauterbur	Versatile detection of diverse selective sweeps in model and non-model organisms with flex-sweep
16:50 - 17:05	Erin Gilbertson	Using machine learning to predict 3D genome organization across thousands of diverse individuals reveals conservation and population differentiation.
17:10 - 17:25	Elias Dohmen	Resolving deep phylogenetic conflicts with deep learning
17:30 - 17:42	Burak Yelmen	Deep convolutional and conditional neural networks for large-scale genomic data generation
17:42 - 17:54	Ziyi Mo	Domain-adaptive neural networks improve supervised machine learning based on simulated population genetic data

27- Regulatory evolution and the emergence of diversity (AD1)

16:00 - 16:25	Tarang K. Mehta	Regulatory networks evolution underlying the rapid diversification of cichlids fishes in the Great African Lakes
16:30 - 16:45	Quentin Horta-Lacueva	Evolution of canalization: lessons from gene expression in an extreme case of divergence, the Arctic charr of Thingvallavatn.
16:50 - 17:05	Attila Placido Sachslehner	Hoxc13-dependent regulation of keratin genes facilitated the evolution of cornified claws and hair in terrestrial vertebrates
17:10 - 17:25	Fabricio Almeida-Silva	The impact of whole-genome duplications in the topology of angiosperm gene regulatory networks
17:30 - 17:38	Pamela Espíndola Hernandez	Signals of accelerated evolution in regulatory regions are linked to the emergence of diurnality in owls
17:38 - 17:46	Matthew Gouly	Evolution of monoaminergic cell types
17:46 - 17:54	Vincent Castric	Molecular control of dominance/recessivity interactions between self-incompatibility alleles in <i>Arabidopsis</i>

28- Host-pathogen co-evolutionary dynamics through the lens of paleogenomics (AD2)

16:00 - 16:25	Gaspard Kerner	A time-series aDNA approach detects genetic adaptation to pathogens in post-Neolithic Europe
16:30 - 16:45	Iseult Jackson	Contrasting evolutionary and adaptive histories revealed for three oral pathogens recovered from Bronze Age Irish remains
16:50 - 17:05	Michael Dannemann	Defend and adapt: the evolutionary impact on the genetics of the human immune response
17:10 - 17:25	Onur Özer	Spatio-temporal analysis of ancient HLA data reveals major effects of demography and admixture on immune gene diversity
17:30 - 17:55	Maria A. Spyrou	Investigating the genomic history of plague, from the Neolithic to the present

29- Leveraging evolution: controlling wild populations using gene drives and pathogens (BC)

16:00 - 16:25	Florence Débarre	Spatial structure and demographic feedbacks affect the spread of a gene drive
16:30 - 16:45	Nicky Faber	A two-target gene drive improves suppressive power when drive conversion is inefficient
16:50 - 17:05	Josh Reynolds	Exploring the potential of rare variants to help parameterise models of gene drive in <i>Anopheles gambiae</i> mosquitoes
17:10 - 17:25	Wenfeng Qian	CRISPR-mediated toxin-antidote system subverts mendelian inheritance in <i>Arabidopsis</i>
17:30 - 17:55	Paul Thomas	Using synthetic and natural gene drives for feral rodent population suppression

18:00-20:00 **Poster session 2 (SP and EC)**

26 July

19- Evolution of structural genomic variation in populations & species (CT)

9:00 - 9:25	Scott Edwards	Pangenomes of Scrub-Jays (<i>Aphelocoma</i>) reveal abundant structural variation and rapid shifts in the landscape of satellite DNA
9:30 - 9:45	Aurora Ruiz-Herrera	Unveiling patterns of 3D chromatin folding across the mammalian phylogeny - insights into genome evolution
9:50 - 10:05	William Murphy	Single-haplotype comparative genomics resolves the role of structural innovations during cat speciation.
10:10 - 10:25	Carina Mugal	The combination of HiFi and HiC sequencing technologies enables the investigation of structural variants in speciation of <i>Ficedula</i> flycatchers
10:30 - 10:38	Alexander Mackintosh	Have chromosome fusions in <i>Brenthis</i> butterflies evolved by positive natural selection?
10:38 - 10:46	Valentina Peona	Structural variation evolution during hybridisation in wheatears
10:46 - 10:54	Rishi De-Kayne	Evolutionary dynamics of a modular supergene in the African monarch butterfly (<i>Danaus chrysippus</i>)

5- New frontiers in conservation genomics (AD1)

9:00 - 9:25	Katerina Guschanski	Metagenomics of population declines in Scandinavian Brown Bears
9:30 - 9:45	Emily Patterson	Combatting illegal trade in animal products by rapid on-site DNA sequencing
9:50 - 10:05	Nicolas Alexandre	The High Stakes of Low Diversity – Predicting population-specific genomic consequences of dispersal barriers and inbreeding in California Mountain Lions
10:10 - 10:25	Christopher Kyriazis	Using computational simulations to model deleterious variation and genetic load in natural populations
10:30 - 10:55	Moises Exposito-Alonso	The population genetics of species range contraction in the Anthropocene

10- Integrating fossils and molecules to reconstruct the evolution of life in deep time (AD2)

9:00 - 9:25	Joanna Wolfe	The challenge and promise of integrating genomics and fossils in deep time phenotypic evolution
9:30 - 9:45	Giulia Campi	Tracing the evolutionary history of moulting genes across arthropod diversity
9:50 - 10:05	Eduard Ocaña-Pallarès	A fungal tree of life dated with fossil and horizontal gene transfer data
10:10 - 10:25	Maria Eleonora Rossi	Independent origins of spicules help disentangle the evolutionary history of sponges (Porifera)
10:30 - 10:55	Jeffrey Thompson	Using fossils, genes, and developmental biology to understand the evolution of Echinozoan body plans

30- IDEA symposium (BC)

9:00 - 9:25	C. Eduardo G. Amorim	SMBE IDEA Taskforce: achievements and future plans for inclusion, diversity, equity, and access
9:30 - 9:45	Sergio González-Mollinedo	The EvoBio Crash Course: a student-led project to bridge the knowledge gaps with the global south in evolutionary biology
9:50 - 10:05	Paula Adams	The inclusion of societally relevant concepts in biology education combats student misconceptions of science
10:10 - 10:25	Melinda Yang	Increasing accessibility to molecular biology and evolutionary concepts in an introductory biology classroom using a collaborative course-based undergraduate research experience through the genomics education partnership
10:30 - 10:55	Sadye Paez	Beyond absolutes: justice, equity, diversity, inclusion in the Earth BioGenome Project

COFFEE BREAK

19- Evolution of structural genomic variation in populations & species (CT)

11:30 - 11:55	Sissel Jentoff	The evolutionary role of genomic architectures in marine fishes
12:00 - 12:15	Tobias Lenz	Evolution of intra-specific copy-number-variation in the MHC and its role in local adaptation
12:20 - 12:35	Wesley Warren	Adaptation to extreme ecological change with structural variation in a cave-dwelling fish
12:40 - 12:55	Tuomas Hämälä	Impact of whole-genome duplications on structural variant evolution
13:00 - 13:08	Bohao Fang	Multiple long-read de novo assemblies of House Finches enable pangenome analysis of structural variants
13:08 - 13:16	Mafalda Sousa Ferreira	Old supergenes underly temperature adaptation in Atlantic herring
13:16 - 13:24	Kimberly Gilbert	Signatures of local adaptation within genomic inversions

3- The dark side of introgression (AD1)

11:30 - 11:55	Molly Schumer	The evolutionary origin of hybrid incompatibilities: insights from swordtail fish
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12:00 - 12:15	Juliette de Meaux	Interspecies introgression in low diversity endangered species: hybrid breakdown or potential for a supergenotype?
12:20 - 12:35	Mozes Blom	The genomic consequences of recurring hybridization between lekking Birds-of-Paradise species
12:40 - 12:55	Arielle Fogel	Assortative mating and offspring viability shape introgression along baboon hybrid genomes
13:00 - 13:25	James Mallet	Extraordinary case of hybrid speciation and ongoing introgression in the Amazon

14- Novel proteins and their emergence from LUCA until today (AD2)

11:30 - 11:55	Klara Hlouchova	Early proteins: could they do without all 20?
12:00 - 12:15	Ariane Babina	Investigating the de novo origins of small protein-coding genes: rescuing an <i>E. coli</i> auxotroph with novel proteins selected from random sequence
12:20 - 12:35	Lars Eicholt	From de novo a beginning - Identifying structures and activities of de novo proteins
12:40 - 12:55	David Rinker	No homologs? No problem! Functional characterization of de novo genes through alignment-free protein structure prediction.
13:00 - 13:25	Richard Goldstein	Principles of protein evolution from a biophysical perspective

30- IDEA symposium (BC)

11:30 - 11:55	Sarah Bay	Approaching diversity, equity, and inclusion as a scientific society: lessons learned at GSA
12:00 - 12:15	Joanna L. Kelley	Making connections across continents: virtual lab meeting training program
12:20 - 13:30	General Discussion	

LUNCH BREAK

16- From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology (CT)

14:30 - 14:55	Vincent Buffalo	The case for conducting a thousand more temporal genomics studies
15:00 - 15:15	Alexis Simon	The contribution of admixture, selection, and genetic drift to four thousand years of human allele frequency change
15:20 - 15:35	Olivia Johnson	The population genetic signatures of temporally fluctuating selection.
15:40 - 15:55	Benjamin Blackman	Sunflower domestication in space and time
16:00 - 16:08	Yilei Huang	Estimating population size trajectories with IBD time transect
16:08 - 16:16	Kwi Young Han	Looking for the smoking gun of fisheries induced selection using temporal genomic data
16:16 - 16:24	Johanna Pieplow	Long-term genomic consequences of thelytokous reproduction in the Cape Honeybee <i>Apis mellifera capensis</i>

31- Causation in protein evolution (AD1)

14:30 - 14:55	Joanna Masel	Birth, death and tinkering: levels of proteome selection at different timescales
15:00 - 15:15	David Liberles	A statistical analysis of clusters of amino acid substitutions to compare compensatory processes with directional selection
15:20 - 15:35	Jia Zheng	Lowered temperature accelerates Darwinian evolution
15:40 - 15:55	Claudèle Lemay-St-Denis	Adventitious catalytic activity promotes the emergence of a thermostable SH3 fold as a powerful antimicrobial resistance mechanism
16:00 - 16:25	Joseph Thornton	The epistatic architecture of proteins is simple, and it facilitates functional evolution

18- Modeling the genomic, social, and ecological drivers of speciation (AD2)

14:30 - 14:55	Guojie Zhang	Incomplete lineage sorting drove the phenotypic evolution in marsupials
15:00 - 15:15	Zhe Xue	Detecting environmental drivers of leopards speciation
15:20 - 15:35	Dabao Lu	Reticulate evolution and rapid development of reproductive barriers upon secondary contact pose challenges for species delineation in a forest fungus
15:40 - 15:55	Nicole Creanza	The interactions between socially learned song and speciation in songbirds
16:00 - 16:25	Tomas Marques-Bonet	A global primate sequencing initiative: lessons from conservation, evolution and speciation

17- Roles and evolution of oxygen sensing across kingdoms (BC)

14:30 - 14:55	Emily Flashman	Cysteinyldioxygenases: a molecular view of their role in oxygen sensing in plants, animals and evolution
15:00 - 15:15	Olivia Gray	Exploring Tibetan adaptations to high altitude hypoxia through functional genomics: insights from iPSC-based approaches
15:20 - 15:35	Noam Shtolz	Hypoxia shifts the mtDNA transcriptional pattern and alters mito-nuclear regulatory coordination

15:40 - 15:55	Laura Dalle Carbonare	Defining the molecular basis for the acquisition of a unique oxygen-sensing mechanism in vascular plants
16:00 - 16:25	Pierdomenico Perata	The many facets of hypoxia in plants

COFFEE BREAK

16- From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology (CT)

17:00 - 17:25	Leo Speidel	Zooming in on the ancient world with genealogy-boosted analyses of ancient DNA
17:30 - 17:45	Adam Andrews	Using ancient genomes to investigate responses to climate and anthropogenic impacts in the Atlantic bluefin tuna
17:50 - 18:05	Jan Laine	Ancient stickleback environmental genomes track adaptation across ecological transitions
18:10 - 18:25	Alexander Salis	Best-practice historical DNA extraction from formalin-fixed museum specimens
18:30 - 18:38	Lucas Anchieri	Assessing ancient DNA sampling strategies for natural selection inference with time-series data
18:38 - 18:46	Leonardo Iasi	The evolution of introgressed Neandertal segments through space and time: Insights from ancient and present-day human genomes
18:46 - 18:54	Xinyi Li	A new model-based method obtains less biased estimates of the selection coefficient while controlling for migration using aDNA

12- Evolution of sensory systems (AD1)

17:00 - 17:25	Marjorie Liénard	The evolution and function of insect visual opsins
17:30 - 17:45	Wendy Andrea Valencia-Montoya	Evolution of sensory receptors in octopus and squid
17:50 - 18:05	Maxime Policarpo	Highly dynamic evolution of chemoreceptor genes in Vertebrates
18:10 - 18:25	Alexander Van Nynatten	Adaptive evolution of Nearctic deepwater fish vision: a novel metabarcoding approach to monitor functional variation for conservation
18:30 - 18:55	Thomas Auer	<i>Drosophila sechellia</i> : a model for chemosensory system evolution

4- Origins, evolution and ecology of microbial hopeful monsters (AD2)

17:00 - 17:25	Gregorio Iraola	<i>Campylobacter fetus</i> : hopefully jumping through hosts and continents
17:30 - 17:45	Talia Karasov	A weaponized phage suppresses competitors in a metapopulation of pathogenic bacteria
17:50 - 18:05	Héloïse Muller	Investigating polyDNAviruses as a route of horizontal transfer from parasitoid wasps to their lepidopteran hosts
18:10 - 18:25	Fanny Mazzamurro	Causes and effects of the evolution of natural transformation in bacteria
18:30 - 18:55	Lucy Weinert	Predicting the emergence of hopeful monsters from the dynamics of genetic elements

2- Editors Symposium (BC)

17:00 - 17:12	Connie Mulligan	Epigenetics, gene expression, and stress in mothers and offspring in the Democratic Republic of Congo: biocultural investigation of the intergenerational effects of stress
17:12 - 17:30	Rebecca Zufall	Amitosis, asexuality, and adaptation: evolutionary effects of genome structure in the ciliate <i>Tetrahymena thermophila</i>
17:30 - 17:50	Irina Arkhipova	Non-canonical base modifications of bacterial origin in a eukaryotic genome
17:50 - 18:10	Angela Hancock	Genetic architectures of complex traits differ between populations with contrasting demographic and selective histories
18:10 - 18:30	Deepa Agashe	Mutation rate and bias jointly determine evolutionary dynamics
18:30 - 18:42	Yuseob Kim	Positive feedback between demographic and fitness fluctuation greatly amplifies population size oscillation and causes long-term, multi-locus oscillation of allele frequencies
18:42 - 18:54	Yoko Satta	A new method for excavating Denisovan segments in unphased diploid sequences of East Eurasians

27 July

26- Genomics of adaptations to extreme environments (CT)

9:30 - 9:55	Joanna Kelley	Fish tales: convergent adaptation to extreme environments
10:00 - 10:15	Khaled Hazzouri	The genome of the mimosoid legume <i>Prosopis cineraria</i> , a desert tree
10:20 - 10:35	Maeve Perez	Evolutionary history of deep-sea clam symbionts
10:40 - 10:55	Juliana Vianna	Adapting to extreme environment: vertebrate genomics from the Atacama Desert to Antarctica
11:00 - 11:25	Andres Moreno Estrada	Latin American genomes tell extreme tales on isolation, adaptation, and migration

9- Evolution on repeat in the genomics era (AD1)

9:30 - 9:55	David Baum	The parallelism-convergence continuum and its implications for homology assessment
10:00 - 10:15	Emily Lau	Predictable genetic recruitment in the convergent evolution of bioluminescent substrate storage in fireflies, sea pansies, and ostracods
10:20 - 10:35	John Allard	Genetic models of convergent evolutionary traits by sparse learning
10:40 - 10:55	Frédéric Delsuc	The fundamental role of historical contingency and evolutionary tinkering in the convergent evolution of ant-eating mammals
11:00 - 11:25	Nathalie Feiner	The genomic basis of a repeatedly evolving sexually-selected syndrome in Mediterranean wall lizards

8- Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution (AD2)

9:30 - 9:55	Daniel Sloan	Contrasting mechanisms of mitochondrial DNA repair and transmission bottlenecks across eukaryotes
10:00 - 10:15	Yongsung Lee	Multipartite mitochondrial genomes in red algae
10:20 - 10:35	Dennis Lavrov	Mitochondrial tRNA gene loss and its consequences for evolution of animal mtDNA.
10:40 - 10:55	Kendra Zwonitzer	Copy number explains extreme evolutionary rate variation of mitochondrial DNA across plants
11:00 - 11:25	Sophie Breton	The mitochondria-derived alternative proteome

25- The puzzle of eukaryotic cellular origins (BC)

9:30 - 9:55	Courtney Stairs	Anoxychlamydiales and the origin of anaerobic metabolism in eukaryotes
10:00 - 10:15	Julian Vosseberg	Genome evolution of Asgard archaea: a window into eukaryogenesis?
10:20 - 10:35	Tara Mahendrarajah	ATP synthase evolution in the light of a cross-braced dated tree of life
10:40 - 10:55	Laura Katz	Foraminifera as a model of eukaryotic genome dynamics
11:00 - 11:25	Robert Robinson	The functional origins of the eukaryotic cytoskeleton

BRUNCH

Plenary Lecture (CT; streaming in AD1, AD2, and BC)

12:15-13:15	Michael Lynch	Principles of evolutionary overdesign and underperformance
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13-15-14:30 **Awards Ceremony and Introduction to SMBE 2024**