2025
LOUIS-JEANTET SYMPOSIUM

Vertebrate Genome Evolution

FONDATION
LOUIS-JEANTET

PROGRAMME

08:15 – 08:50 **Registration and welcome coffee**

08:50 – 08:55 **Antoine Geissbühler,** Dean of the Faculty of Medicine, University of Geneva
Opening

08:55 – 09:00 **Denis Duboule,** President of the Board of Trustees of the Louis-Jeantet Foundation
Welcome

SESSION 1

9.00 – 9.30 **Margarida Cardoso-Moreira,** The Francis Crick Institute, London, UK
The evolution of new vertebrate cell types and organs

9.30 – 10.00 **Manuel Irimia,** UPF-CRG, Barcelona, ES
Tissue-specific transcriptomes in the origin and evolution of vertebrates

10.00 – 10.30 **Francisca Martinez Real,** Centro Andaluz de Biología del Desarrollo (CABD), Sevilla, ES
Elucidating the molecular basis of mammalian flight

10:30 – 11:00 **COFFEE BREAK**

11.00 – 11.30 **Patrick Tschopp,** University of Basel, CH
The gene regulatory logic of skeletal cell type specification and evolution

11.30 – 12.00 **Leif Andersson,** Uppsala University, SE
How the Atlantic herring colonized and diversified in the brackish Baltic Sea within the last 8,000 years

12:00 – 13:30 **LUNCH**

SESSION 2

13.30 – 14.00 **Dario Valenzano,** Leibniz Institute on Aging, Fritz Lipmann Institute, Jena, DE
Evolution and Ecology of Aging

14.00 – 14.30 **Pontus Skoglund,** The Francis Crick Institute, London, UK
Ancient genome evolution in short- and long-time series

14.30 – 15.00 **Jenny Tung,** Max Planck Institute for Evolutionary Anthropology, Leipzig, DE
The genomic consequences of hybridization in a living primate model

15.00 – 15.30 **COFFEE BREAK**

15.30 – 16.00 **Evan Eichler,** University of Washington, USA
Segmental duplication, inversion toggling and the rapid emergence of novel ape genes

16.00 – 16:30 **Pierre Vanderhaeghen,** VIB-KU Leuven Center for Brain & Disease Research, BE
Chi va piano va sano: linking developmental tempo and evolution of the human brain

16.30 – 16:40 **CONCLUDING REMARKS**

ORGANISING COMMITTEE

Svante Pääbo
Max Planck Institute for Evolutionary Anthropology, Leipzig, DE

Henrik Kaessmann
Centre for Molecular Biology (ZMBH), Heidelberg, DE

THE LOUIS-JEANTET SYMPOSIUM

First held in 2012, the Louis-Jeantet Symposium is chaired each year by leading scientists — former Louis-Jeantet Prize winners, members of the Scientific Committee, or other distinguished researchers — who, together with invited speakers, highlight advances in their fields and discuss current challenges. These symposia offer a unique opportunity for Master's students, PhD students, and post-doctoral researchers to engage with leading scientists and expand their networks. Over the years, the programme has explored a wide range of topics, including cancer, stem cells, immunity, developmental biology, and mRNA biology.

THE LOUIS-JEANTET FOUNDATION

Founded in 1983 in Geneva, the Louis-Jeantet Foundation advances medicine by supporting innovative projects in both fundamental and clinical research. Today, it is recognised as one of Europe's leading foundations in this field.

The Foundation awards the Louis-Jeantet Prize for Medicine and the Collen-Jeantet Prize for Translational Medicine, which recognise outstanding researchers working in member countries of the Council of Europe. These prizes are not intended to crown completed work, but rather to foster the continuation of promising projects across all areas of the life sciences related to human health.

Deeply rooted in its home city, the Foundation also provides annual funding to the Faculty of Medicine at the University of Geneva, enabling the recruitment of full professorial and tenure-track positions and strengthening local biomedical research.

Margarida Cardoso-Moreira
The Francis Crick Institute, London, UK

The evolution of new vertebrate cell types and organs

How do new cells, new tissues, and entire new organs arise during evolution? Our lab investigates these questions using an organ that has evolved independently many times and is remarkably diverse: the placenta. The placenta forms through the fusion of embryonic and maternal tissues, enabling the transfer of nutrients, gases, waste, and more during gestation. In placental species, such as mammals, the mother gestates her offspring inside her body and nourishes them via a placenta. Remarkably, placentas have evolved more than 100 times independently among vertebrates, including once in mammals. Within a family of small live-bearing fishes known as Poeciliidae, at least nine independent origins of the placenta have occurred. This makes them excellent models for studying how new organs emerge during evolution. We have combined whole-genome sequencing, single-cell RNA sequencing, spatial transcriptomics, and imaging to uncover the genetic and developmental basis of four independent origins of a placenta in Poeciliids. Our research revealed that the evolution of a novel cell type unique to Poeciliids allowed this family to transition from egg-laying to live-bearing through egg retention. This new cell type was subsequently co-opted to make up the bulk of the placenta in the four placental species. In two independent origins of a placenta, additional novel cell types also evolved. Our work illustrates the diverse genetic and developmental paths underlying the evolution of new organs, even among closely related species, and supports a link between cell-type innovation and the origin of new organs.

Biography

Margarida Cardoso-Moreira did her PhD research under the supervision of Manyuan Long at the University of Chicago. She then took a postdoctoral position in Andrew G. Clark's group at Cornell University. While at Chicago and Cornell, Margarida investigated the evolution of newly duplicated genes. Margarida then joined the group of Henrik Kaessmann (University of Lausanne and Heidelberg University), where she spearheaded a research program on the evolution of mammalian organs, for which she received the Otto-Schmeil prize from the Heidelberg Academy of Sciences and Humanities in 2020. Margarida established her group at the Francis Crick Institute in 2021. Her lab focuses on understanding how new cells, tissues, and organs originate.

https://www.crick.ac.uk/research/labs/margarida-cardoso-moreira

Manuel Irimia
University Pompeu Fabra - Centre for Genomic Regulation (UPF-CRG), Barcelona, ES

Tissue-specific transcriptomes in the origin and evolution of vertebrates

Understanding how transcriptomic diversity arises and evolves is key to deciphering the mechanisms underlying tissue identity and organismal complexity. Among the main contributors to this diversity are regulated gene expression and alternative splicing, two complementary yet distinct regulatory layers through which genomes specialize their transcriptomes and proteomes in a tissue- and cell type–specific manner. In this talk, I will present our results investigating how these two mechanisms have shaped the evolution of bilaterian transcriptomes, with a focus on vertebrates. Our work revolves around (i) a vast transcriptomic dataset covering eight tissues across a balanced phylogeny of twenty bilaterian species (enriched for vertebrates and insects), and (ii) a targeted analysis of ancestral genes. This framework enabled us to explore both conserved and lineage-specific patterns of tissue-specific gene expression and alternative splicing, revealing how these complementary regulatory programs emerged and diversified throughout bilaterian evolution. We show that the evolution of tissue-specific gene expression and alternative splicing is particularly prevalent at the common ancestor of vertebrates, coinciding with the two rounds of whole genome duplication. Moreover, we found that tissue-specific gene expression and alternative splicing typically act on distinct sets of genes with characteristic features, thereby contributing to transcriptome and proteome specialization through synergistic roles.

Biography

Manuel Irimia obtained his PhD in 2010 at University of Barcelona. After postdocs at Stanford University and University of Toronto, he started his laboratory at Centre for Genomic Regulation (CRG) in 2014. He is an ICREA Research Professor since 2018, and in October 2023 his lab moved to the MELIS department at the Universitat Pompeu Fabra, with dual affiliation with the CRG. Since 2024, he is the coordinator of the CRG-UPF-IBE Joint Program on Evolutionary Medical Genomics. He is an EMBO Member (2025), and he obtained ERC Starting and Consolidators Grants in 2014 and 2020, among other competitive international grants.

https://www.crg.eu/en/programmes-groups/irimia-lab

Francisca Martinez Real
Centro Andaluz de Biología del Desarrollo (CABD), Sevilla, ES

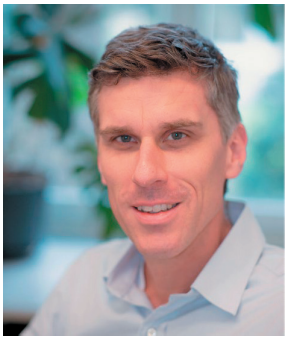
Elucidating the molecular basis of mammalian flight

Bats are the only mammals capable of self-powered flight, an evolutionary innovation based on the transformation of forelimbs into wings. The bat wing is characterized by an extreme elongation of the second to fifth digits and a wing membrane called chiropatagium connecting them. This adaptation enabled bats to conquer the aerial environment, contributing to the massive diversification of this taxonomic group. Yet, the molecular underpinnings of this evolutionary innovation remain obscure. In this study, we have explored the molecular basis of bat wing formation through a suite of genomic tools and single-cell analyses. We found that despite the substantial morphological differences between the species, there is an overall conservation of cell populations and gene expression patterns, including interdigital apoptosis. To trace the cellular origin of the chiropatagium, we performed single-cell and label transfer analyses on manually micro-dissected cells and identified a distinct fibroblast population, independent of the apoptosis-associated interdigital cells, as the source of this tissue. These distal cells express a conserved gene program including the transcription factors MEIS2 and TBX3, which are commonly known to specify and pattern the early proximal limb. Transgenic ectopic expression of MEIS2 and TBX3 in mouse distal limb cells resulted in the activation of genes expressed during wing development and phenotypic changes related to wing morphology, such as the fusion of digits. Our results elucidate fundamental molecular mechanisms of bat wing development and illustrate how drastic morphological changes can be achieved through repurposing of existing developmental programs during evolution.

Biography

Francisca is a Principal Investigator at the Andalusian Center for Developmental Biology (CABD, CSIC) in Seville, Spain, where she leads the Gene Regulation and Evolution group. She is a developmental and evolutionary biologist interested in how genomic changes shape developmental phenotypes and drive trait adaptation. Her group combines computational and experimental approaches, including in vivo transgenesis, with a particular focus on how the non-coding genome contributes to phenotypic diversity.

https://www.cabd.es/en/research_groups/gene-regulation-and-evolution/summary-458.html



Patrick Tschopp
University of Basel, CH

The gene regulatory logic of skeletal cell type specification and evolution

An articulated endoskeleton is one of the defining hallmarks of vertebrates, with variations in the size, number and shape of bones underlying much of the observed macromorphological diversity in this clade. During development, skeletogenic precursors give rise to a whole range of cell and tissue types, all essential for a fully functioning skeletal apparatus in the adult. However, depending on anatomical location, these cells originate from three different embryonic lineages, before they converge developmentally towards similar cellular phenotypes. Furthermore, the 'skeletogenic competency' of these three embryonic precursor lineages arose at distinct evolutionary timepoints, thus questioning to what extent different skeletal body parts rely on truly homologous cell types.

In my talk I will present single-cell functional genomics data describing how three developmentally and molecularly distinct precursor lineages are transcriptionally recoded, to allow for a skeletogenic cell fate convergence during vertebrate embryogenesis. From an evolutionary perspective, I will then discuss how these distinct gene regulatory dynamics might originally have been a necessity – i.e., to absorb and integrate lineage-specific molecular properties – but ultimately might have proven beneficial, by reducing pleiotropic constraints and allowing for individualized evolutionary trajectories, to define adaptive morphologies and biomaterial properties in different parts of the vertebrate skeleton.

Biography

While Patrick Tschopp trained as a developmental biologist and molecular geneticist, he always had a keen interest in evolutionary questions and, thus, in comparative developmental biology, or EvoDevo. After undergraduate studies in molecular biology and a Master thesis at the Biozentrum in Basel, Patrick Tschopp pursued a PhD in molecular genetics, studying the transcriptional regulation of vertebrate Hox genes at the University of Geneva. During his postdoctoral research at Harvard Medical School in Boston, he trained in comparative functional genomics and single-cell transcriptomics, tools that we are now employed in an eco-evolutionary context in his research group at the University of Basel.

http://evolution.unibas.ch/tschopp/

Leif Andersson
Uppsala University, SE

How the Atlantic herring colonized and diversified in the brackish Baltic Sea within the last 8,000 years

The Atlantic herring is one of most abundant vertebrates on earth and sustains one of the top ten most important marine fisheries in the world. This species has developed into a gold mine for exploring the genetics of ecological adaptation in vertebrates because of the following reasons. Firstly, it is subdivided into many subpopulations adapted to different climate conditions, spawning time, migration and feeding behavior. Secondly, the huge population size and gene flow between populations essentially eliminate genetic drift even between geographically distant populations. Thirdly, the herring deposit sticky eggs on the sea floor or on vegetation which means that the developing embryo is exposed to the environmental conditions at the spawning site. Thus, herring is exposed to much more diverse environmental conditions during the sensitive early stage of development compared with a pelagic spawner, or a bird, or a mammal. Fourthly, the high fecundity leaves plenty of room for natural selection to act. Fifthly, the herring has recently (within the last 8,000 years) adapted to a new environment, the brackish Baltic Sea which is extreme as regards salinity in which this marine species is able to reproduce.

Here, I will review our current knowledge concerning how the herring has been able to adapt to the Baltic Sea. I will discuss the genetic architecture underlying adaptation, the importance of changes in protein sequence and gene regulation, and highlight some of the genes that have been particularly important for the successful colonization.

Biography

Leif Andersson has made ground-breaking studies on the relationship between genetic and phenotypic variation. Research on domestic animals has resulted in discoveries of genotype-phenotype relationships such as mutations affecting pigmentation, gaits in horses, comb morphology in chickens and muscle growth in pigs. He has also studied the genetic basis for domestication in rabbits, chickens and pigs. The research program has been expanded to natural populations including evolution of Darwin's finches and their beaks, a supergene controlling male mating strategies in ruff and the genetics of ecological adaptation in Atlantic herring. He is professor at Uppsala University and Texas A&M University.

https://www.uu.se/en/department/medical-biochemistry-and-microbiology/research/andersson-leif

Dario Valenzano
Leibniz Institute on Aging, Fritz Lipmann Institute, Jena, DE

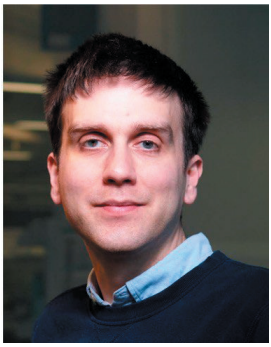
Evolution and Ecology of Aging

African killifishes have emerged as a powerful natural model to address fundamental questions in the biology of aging, development, and evolution. These fishes inhabit environments from rainforest pools to ephemeral savannah water holes that desiccate seasonally, surviving through an annual life cycle that includes embryonic diapause, a suspended developmental state enabling embryos to endure dry periods. Populations from arid habitats typically have naturally short lifespans and show diverse age-related changes such as neurodegeneration, inflammation, immune decline, and gut microbiome dysbiosis. Intense demographic fluctuations in the wild have shaped their genomes through drift and relaxed purifying selection on late-acting genes, influencing lifespan and life-history traits. Killifish studies reveal how ecological factors, particularly host–microbiome interactions, modulate homeostasis and aging; for example, microbiota transfers from young to middle-aged fish can extend lifespan and preserve function. By linking ecological context, demographic history, and molecular mechanisms, killifish offer a uniquely integrative view of aging evolution in vertebrates.

Biography

Dario Riccardo Valenzano is Professor at Friedrich Schiller University Jena and Scientific Director of the Leibniz Institute on Aging – Fritz Lipmann Institute, where he coordinates the research focus on Microbiome and Aging. An evolutionary biologist, he studies why we age, investigating how evolution shapes life-history traits across species. His group applies an ecological and evolutionary perspective to host–microbiome interactions in health, disease, and aging. Combining statistical modeling, genomics, experimental biology, and fieldwork in African killifish, his research aims to uncover fundamental mechanisms of aging and identify strategies to enhance resilience and promote healthy lifespan in vertebrates.

https://www.leibniz-fli.de/research/research-groups/dario-r-valenzano



Pontus Skoglund
The Francis Crick Institute, London, GB

Ancient genome evolution in short- and long-time series

All biology is the outcome of evolution—genetic change over time. Most approaches study evolution indirectly, by extrapolating present-day genetic variation into the past. Ancient genomics is currently the only way to study genetic evolution directly. I will present examples of how ancient genomes can be used to study genetic history and natural selection over both long- and short-time scales. In humans, we are studying evolution and natural selection in a fine-scale time series from the past few thousand years in Britain, for which fine-scale genome-wide association data linking traits and genomes is available through resources such as the UK Biobank. In ancient wolves, a favorable fossil record allows us to study natural selection over a much larger time scale of 100,000 years, or ~30,000 generations. I will use this to demonstrate a rare example of a hard selective sweep in a genomic time series from a vertebrate.

Biography

Pontus Skoglund is the group leader of the Francis Crick Institute's Ancient Genomics laboratory. He obtained his PhD in evolutionary genetics from Uppsala University in 2013 with Mattias Jakobsson, and thereafter did his postdoctoral research with David Reich at Harvard Medical School. His research has focused on developing new approaches to propel the field of ancient DNA into the genomic era. His PhD research revealed population migrations as catalysers for the transition from hunter-gatherer lifestyles to agriculture in Europe, and he expanded this to worldwide regions in his postdoc research. In 2018, he founded the first high-throughput ancient DNA laboratory in Britain at the Francis Crick Institute. His independent lab has used ancient DNA to pioneer research revealing the origin and evolution of dogs and their wild ancestors, the evolution of bacteria and human immunity in prehistory, and pioneered a new method to reconstruct genetic history in higher resolution than ever before in 2025. He is a Wellcome Trust Investigator, ERC starting and consolidator grantee, EMBO Young Investigator, Vallee Foundation Scholar and Blavatnik Award finalist.

www.skoglundlab.org

Jenny Tung
Max Planck Institute for Evolutionary Anthropology, Leipzig, DE

The genomic consequences of hybridization in a living primate model

Unlike most evolutionary processes, hybridization between divergent taxa can transform the structure and composition of the genome on a very rapid timescale. Recent work also shows that is common in primates and other vertebrates, including in our own lineage. However, genetic evidence alone provides an incomplete picture of the behavioral, ecological, and demographic processes that drive hybridization and explain its resolution. To address this gap, we study the process of hybridization in a long-term field study of baboons, now stretching over five decades, in which direct observations of behavior and individual fitness can be integrated with modern genomic data sets. Here, I will present results from our work showing how patterns of sex-biased dispersal and assortative mating combine with natural selection to explain genomic patterns of admixture in this population. Together, these findings help highlight the importance of other primates as living models for human evolution.important for the successful colonization.

Biography

Jenny Tung is the Director of the Department of Primate Behavior and Evolution at the Max Planck Institute for Evolutionary Anthropology and a Visiting Professor of Evolutionary Anthropology and Biology at Duke University. Jenny joined Duke University in 2012 after completing her post-doctoral training in the University of Chicago Department of Human Genetics and her PhD training in the Duke Biology department. She founded the Department of Primate Behavior and Evolution at MPI-EVA in 2022. Research in the department focuses on the intersection between behavior, social structure, and genes, primarily in nonhuman primates and other social mammals.

https://www.eva.mpg.de/primate-behavior-and-evolution/research-groups/genes-and-behavior/

Evan Eichler
University of Washington, USA

Segmental duplication, inversion toggling and the rapid emergence of novel ape genes

The discovery and resolution of genetic variation is critical to understanding disease, adaptive traits and evolution. I will present our most recent work providing the most complete sequence of hundreds of diverse human and nonhuman primate (NHP) genomes, using both ultra-long and high-fidelity long-read sequencing (LRS) technologies. This allows us to develop pangenomes truly representative of human genetic diversity, as well as to detect and sequence resolve most structural variants irrespective of size or complexity. These studies shed new insights into genetic diversity and mutational processes, shaping primate genomes and the genetic differences that distinguish humans and non-human apes. I will present evidence of hundreds of novel protein-coding genes emerging in each of the African ape lineages and show that the emergence of these ape-specific genes is tightly linked to large-scale “toggling inversions” flanked by segmental duplications. LRS allows the expression and selection properties of these loci to be interrogated for the first time. Our results challenge the notion that the most significant changes distinguishing ape phenotypes involve mutations of regulatory DNA. Instead, large-scale SVs result in qualitative and quantitative lineage-specific changes in duplicated genes at the edges of inversions, which in turn create multiple novel genes and fusions (supergenes) that predispose humans to genomic disorders associated with neurodevelopmental disorders.

Biography

Evan Eichler is a Professor of Genome Sciences and Howard Hughes Medical Institute Investigator. He received his Ph.D. from Baylor College of Medicine. After his postdoctoral fellowship at Lawrence Livermore National Laboratory, he joined Case Western Reserve University in 1997 and the University of Washington in 2004. His research group provided the first genome-wide view of segmental duplications within human and primate genomes. He is a leader in identifying and sequencing normal and disease-causing structural variation and applied long-read sequencing to generate the first telomere-to-telomere (T2T) human genome. He is a co-chair and PI of the Human Genome Structural Variation, Human Pangenome Reference, and T2T primate sequencing consortia. The long-term goal of his research is to understand the evolution and mechanisms of recent gene duplication and its relationship to copy number variation and human disease.

https://eichlerlab.gs.washington.edu/

Pierre Vanderhaeghen
VIB KU Leuven Center for Brain & Disease Research, BE

Chi va piano va sano: linking developmental tempo and evolution of the human brain

The cerebral cortex has undergone rapid expansion and complexification during recent hominid evolution, which is thought to be at the origin of some of the higher cognitive and social skills characteristic of the human species. One striking feature of human corticogenesis is that it is highly protracted in time, from prenatal stages of neuronal generation (taking months, instead of days in the mouse), to postnatal stages of neuronal maturation and circuit formation (taking years, instead of weeks in the mouse). This neotenic neural development may contribute in an important fashion to human brain specialized functions, through enhanced cortical circuit plasticity and/or complexity.

In vitro and xenotransplantation models indicate that the species-specific developmental timing of corticogenesis is at least in part intrinsic to cortical cells. The underlying mechanisms include divergence in gene regulatory networks, the neofunctionalization of human-specific gene duplicates, as well as species-specific cell properties such as mitochondria metabolism. The newly discovered human-specific modifiers of cortical neuron development and function shed light on human brain evolution, and provide unexpected links to brain diseases.

Biography

Pierre Vanderhaeghen graduated as an M.D. and Ph.D. from the University of Brussels. He worked as a postdoctoral fellow at Harvard Medical School and then as a faculty member at the University of Brussels, before joining the VIB KU Leuven Center for Brain and Disease Research. He and his team study the mechanisms of development of the cerebral cortex and their links to human brain evolution and diseases. They pioneered in-vitro and in-vivo models of corticogenesis from pluripotent stem cells, through which they discovered the key influence of cell-intrinsic properties of neural stem cells and neurons on human brain evolution.

https://pvdhlab.org/

FONDATION
LOUIS-JEANTET

Maison des Fondations
17 chemin Rieu, CH-1208 Geneva
Tel. +41 22 704 3636 – info@jeantet.ch

www.jeantet.ch