

Virtual Conference Agenda

Start (GMT)	Finish (GMT)	Presenter details
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Wednesday 9 February 2022

12:00 12:10 Welcome

Scientific Programme Committee:

[*Juliette de Meaux, University of Cologne, Germany*](#)

[*Brandon Ogbunu, Yale University, USA*](#)

[*Olivier Tenaillon, INSERM, France*](#)

[*Trisha Wittkopp, University of Michigan, USA*](#)

12:10 12:55 Keynote 1

Introduction to the session

Chair: Olivier Tenaillon, INSERM, France

12:10 12:40 Evolving adaptive reproductive capacity: a systems approach using Drosophila models

[*Cassandra Extavour, Harvard University, USA*](#)

12:40 12:55 Q&A

Chair: Olivier Tenaillon, INSERM, France

Moderator: Juliette de Meaux, University of Cologne, Germany

12:55 13:15 Break and networking in Spatial Chat

13:15 14:45 Session 1: Evolution of proteins

Introduction to the session

Chair: Juliette de Meaux, University of Cologne, Germany

13:15 13:35 An evolutionary synthetic biology approach to explore life's origins and early history

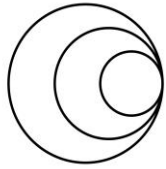
[*Betül Kaçar, University of Wisconsin-Madison, USA*](#)

13:35 13:55 Causes and consequences of epistasis in protein evolution

[*Nobuhiko Tokuriki, University of British Columbia, Canada*](#)

13:55 14:05 Compensatory mutations in proteins: which... where... how...?

Julien Dutheil, Max Planck Institute for Evolutionary Biology, Germany



14:05 14:15 Evolutionarily transient coding sequences influence cellular phenotypes and function
Aaron Wacholder, University of Pittsburgh School of Medicine, USA

14:15 14:45 Q&A
Chair: Juliette de Meaux, University of Cologne, Germany
Moderator: Olivier Tenailon, INSERM, France

14:45 15:10 Break and networking in Spatial Chat

15:10 16:00 Poster Session I

15:10 15:30 Poster session I lightning talks

15:30 16:00 Poster session I

16:00 17:30 Session 2: Evolution of molecular systems

Introduction to the session

Chair: Trisha Wittkopp, University of Michigan, USA

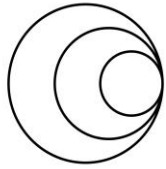
16:00 16:20 The molecular evolution of spermatogenesis across mammals
[*Henrik Kaessmann, Heidelberg University, Germany*](#)

16:20 16:40 A genome-wide screen for genes that “buffer” the effect of random mutations
[*Kevin Verstrepen, VIB-KULeuven Center for Microbiology, Belgium*](#)

16:40 16:50 The cis-regulatory effects of modern human-specific variants
David Gokhman, The Weizmann Institute of Science, Israel

16:50 17:00 Fitness landscape analysis reveals that the wild type allele is sub-optimal and mutationally robust
Tamar Friedlander, Hebrew University of Jerusalem, Israel

17:00 17:30 Q&A
Chair: Trisha Wittkopp, University of Michigan, USA
Moderator: Brandon Ogbunu, Yale University, USA



Thursday 10 February 2022

12:00 13:30 Session 3: Evolution of microbial systems

Introduction to the session

Chair: Juliette de Meaux, University of Cologne, Germany

12:00 12:20 A population genetic framework to understand evolution and transmission of drug resistance

[*Pleuni Pennings, San Francisco State University, USA*](#)

12:20 12:40 Epistasis and adaptation on rugged fitness landscapes

[*Claudia Bank, University of Bern, Switzerland*](#)

12:40 12:50 Evolution of genome architecture to divide labor through mutations

Renske Vroomans, Sainsbury Laboratory, University of Cambridge, UK

12:50 13:00 Wrinkly formation underlies bacterial adaptation to a host-associated lifestyle

Nancy Obeng, Kiel University, Germany

13:00 13:30 Q&A

Chair: Juliette de Meaux, University of Cologne, Germany

Moderator: Olivier Tenaille, INSERM, France

13:30 14:00 Break and networking in Spatial Chat

14:00 14:50 Poster Session II

14:00 14:20 Poster session II lightning talks

14:20 14:50 Poster session II

14:50 16:20 Session 4: Evolution of developmental systems

Introduction to the session

Chair: Brandon Ogbunu, Yale University, USA

14:50 15:10 Evolution of sex determining mechanisms in the brown algae

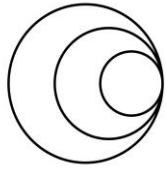
[*Susana Coelho, Max Planck Institute for Developmental Biology, Germany*](#)

15:10 15:30 HD-ZIPIII transcription factors are controlled by deeply-conserved START domains

[*Aman Husbands, The Ohio State University, USA*](#)

15:30 15:40 The evolution of developmental genetic biases explains the evolution of evolutionary trends

Joao Picao-Osorio, Institute of Biology of the École Normale Supérieure (IBENS), France



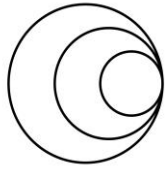
- 15:40 15:50 The cellular and molecular patterning dynamics of tetrapod digit diversification
Patrick Tschopp, University of Basel, Switzerland
- 15:50 16:20 Q&A
Chair: Brandon Ogbunu, Yale University, USA
Moderator: Trisha Wittkopp, University of Michigan, USA

Friday 11 February 2022

- 12:00 13:30 **Session 5: Evolutionary quantitative genetics and environmental interactions**
Introduction to the session
Chair: Brandon Ogbunu, Yale University, USA
- 12:00 12:20 Parallel reduction in flowering time from new mutations enabled evolutionary rescue in colonizing *Arabidopsis* lineages
[Angela Hancock, Max Planck Institute for Plant Breeding Research, Germany](#)
- 12:20 12:40 A genomic map of local adaptation of natural interactions between *Arabidopsis thaliana* and its leaf microbiota
[Fabrice Roux, Laboratory of Plant-Microbe Interactions – LIPM, France](#)
- 12:40 12:50 Selection and gene flow shape niche-associated variation of pheromone response
Erik Andersen, Northwestern University, USA
- 12:50 13:00 Evolution under changing environments in a laboratory evolution experiment of *Escherichia coli*
Maryl Lambros, Albert Einstein College of Medicine, USA
- 13:00 13:30 Q&A
Chair: Brandon Ogbunu, Yale University, USA
Moderator: Juliette de Meaux, University of Cologne, Germany

- 13:30 13:50 Break and networking in Spatial Chat

- 13:50 15:20 **Session 6: Evolution impacting human health**
Introduction to the session
Chair: Olivier Tenaillon, INSERM, France
- 13:50 14:10 Evolutionary dynamics of blood
[Jamie Blundell, University of Cambridge, UK](#)
- 14:10 14:30 Within-host diversity and transmission of SARS-CoV-2
[Katrina Lythgoe, University of Oxford, UK](#)



14:30 14:40 Exploiting convergent evolution to derive a pan-cancer cisplatin sensitivity gene expression
Jessica Scarborough, Case Western Reserve University, USA

14:40 14:50 Proteomic compensation by paralogs contributes to the genetic robustness of tumour cells
Anjan Venkatesh, University College Dublin, Ireland

14:50 15:20 Q&A
Chair: Olivier Tenaillon, INSERM, France
Moderator: Trisha Wittkopp, University of Michigan, USA

15:20 15:40 Break and networking in Spatial Chat

15:40 16:30 Keynote 2

Introduction to the session
Chair: Trisha Wittkopp, University of Michigan, USA

15:40 16:10 Understanding adaptation in an infinitesimal world
[Nick Barton, IST Austria, Austria](#)

16:10 16:30 Q&A
Chair: Trisha Wittkopp, University of Michigan, USA
Moderator: Olivier Tenaillon, INSERM, France

16:30 16:40 Closing remarks

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