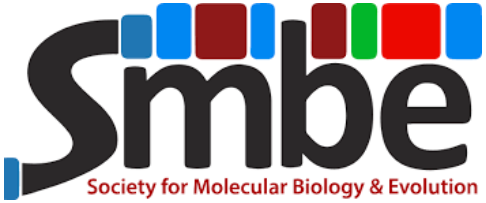

SMBE satellite meeting

‘Towards an integrated concept of adaptation: uniting molecular population genetics and quantitative genetics’

February 11-14, 2019

Vienna Austria

Monday 11th February 2019

09:00	**Registration**
09:20	**Michael Lynch**, Arizona State University, USA Drift, mutation, and selection and the evolutionary dispersion of mean phenotypes
10:00	**Henner Simianer**, University of Goettingen, Germany Breeding assisted genomics
10:40	**Coffee break**
11:20	**Neda Barghi**, Institute of Population Genetics, Vetmeduni Vienna, Austria Genetic redundancy fuels polygenic adaptation in *Drosophila*
12:00	**Luisa Pallares**, Princeton University, USA The role of cryptic genetic variation in regulating the transcriptional response to new and stressful environments in flies
12:25	**Ulla Kemi**, Max Planck Institute for Plant Breeding Research, Cologne, Germany Genetic basis of flowering time variation within a Scandinavian population of *Arabis alpine*
12:50	**lunch break**
13:50	**Felicity Jones**, Friedrich Miescher Laboratory of the Max Planck Society, Tübingen, Germany Clustered cis-regulatory elements underlie adaptive divergence in sticklebacks
14:30	**Max Reuter**, University College London, UK Genome-wide sexually antagonistic variants reveal longstanding constraints on sexual dimorphism in the fruitfly
14:55	**Esra Durmaz**, University of Fribourg, Switzerland A clinal polymorphism at *foxo* contributes to life-history adaptation in *Drosophila*
15:20	**Coffee break**
16:00	**Juliane Friedrich**, University of Edinburgh, UK Assessing the genetic contribution to complex behavioural traits in German Shepherd dogs
16:25	Wrap-up (1 hour)

Tuesday 12th February 2019

09:00	**Registration**
09:20	**Kavita Jain**, Jawaharlal Nehru Centre for Advanced Scientific Research (JNCASR), Bangalore, India Rapid adaptation dynamics of a polygenic trait
10:00	**Yang Li**, University of Chicago, USA Trans effects on gene expression drive the omnigenic patterns of inheritance
10:40	**Coffee break**
11:20	**Robert Maier**, Broad Institute, USA Polygenic adaptation signals are confounded by population stratification
12:00	**Joachim Hermisson**, University of Vienna, Austria Polygenic adaptation of a quantitative trait: analytical criteria for 'sweeps' and 'shifts'
12:40	**Lunch break**
13:40	**Christian Huber**, Australian Centre for Ancient DNA, University of Adelaide, Australia Human adaptation in the last 10,000 years: new insights from ancient DNA
14:05	**Hannes Svardal**, University of Antwerp, Belgium Tracing the genomic footprints of fisheries-induced adaptation in Lake Malawi cichlids
14:30	**Kevin Thornton**, University of California, Irvine, USA Polygenic adaptation and patterns of hitch-hiking
14:55	**Coffee break**
15:35	**Emily Josephs**, Michigan State University, USA Detecting adaptive differentiation in structured populations with genomic data and common gardens
16:00	Wrap-up
17:00	Poster session and informal discussion (1:30 hours)

Wednesday 13th February 2019

09:00 **Samuel Yeaman**, University of Calgary, Canada
Architectural motifs and the genetic basis of local adaptation: reconciling quantitative and population genetic perspectives

09:40 **Magnus Nordborg**, GMI Austria
The genetics of epigenetics

10:20 **Coffee break**

11:00 **Frederic Guillaume**, University of Zürich, Switzerland
The genetics of adaptive divergence: Models and experiments

11:40 **Nick Barton**, IST Austria
How best to distinguish selection on discrete loci from the infinitesimal model?

12:20 **Lunch break**

13:20 **Patrick Phillips**, University of Oregon, USA
Next generation experimental evolution: expanding the evolutionary toolkit in pursuit of the molecular basis of phenotypic evolution

13:45 **Layla Hirmatsu**, Friedrich Miescher Laboratory of the Max Planck Society, Tübingen, Germany
Tracking signatures of response over 20 generations of selection for long leg length in mice

14:10 **Rui Borges**, Institute of Population Genetics, Vetmeduni Vienna, Austria
A Bayesian method to detect targets of selection in Evolve-and-Resequence experiments

14:35 **Coffee break**

15:15 **Robert Kofler**, Institute of Population Genetics, Vetmeduni Vienna, Austria
Optimizing the power to identify QTLs with Evolve and Resequence

15:40 **Pierre deVillemereuil**, Centre d'Ecologie Fonctionnelle et Evolutive, CNRS, Montpellier, France
Local adaptation to spatio-temporal variation in salinity in the halotolerant micro-algae *Dunaliella salina*

16:05 3 discussion groups

18:05 Summary (1 hour)

Thursday 14th February 2019

09:00 **Reinhard Bürger**, University of Vienna, Austria
The effects of epistasis and pleiotropy on local adaptation and the detection of adaptive loci

09:40 **Himani Sachdeva**, IST Austria
Modeling introgression under linked, polygenic selection

10:05 **Tom Ellis**, GMI Austria
A quantitative framework for mechanisms of pleiotropic and genotype-by-environment interactions

10:30 **Coffee break**

11:10 **Luis-Miguel Chevin**, Centre d'Ecologie Fonctionnelle et Evolutive, CNRS, Montpellier, France
Adaptation to randomly changing environments

11:50 **Kaileigh Ahlquist**, Brown University, USA
Balancing selection and beyond: machine learning approaches for determining selection scenarios in a complex parameter space

12:15 **Lunch break**

13:15 **Margarita Takou**, University of Cologne, Germany
How do *Arabidopsis lyrata* ssp. *petreae* populations at the edge of the distribution adapt, while coping with decreased genetic variation?

13:40 **Fabrice Roux**, Université de Toulouse, INRA, CNRS, Castanet-Tolosan, France
Intermediate degrees of synergistic pleiotropy drive adaptive evolution in ecological time in *Arabidopsis thaliana*

14:20 **Coffee break**

15:00 3 discussion groups

17:00 Summary (1 hour)