Newsletter April 2019

Welcome to the 18th edition of the PopGen ALUMNI newsletter!

Follow us on Twitter @PopGenViennaPhD

Do you know of suitable PhD candidates for PopGen Vienna?

Our call for PhD students is open – please help us spread the word!

Application deadline: May 13, 2019

([Flyer for download on the website](#))

Recent events and news

April 2019: New associated faculty

We're happy that **Neda Barghi**, junior group leader at Vetmeduni Vienna, just joined the Vienna Graduate School of Population Genetics as associated faculty.

Neda is an evolutionary biologist focusing on the genomics of complex adaptive traits. She is specifically interested in the genomic signatures of adaptive evolution in response to biotic and abiotic environmental changes. She uses an array of tools from Pool-Seq time-series data, molecular and phenotypic assays, and computer simulations to investigate the genetic basis of adaptation in experimental evolution populations of *Drosophila*.

April 2019: Alumni career news

Congratulations to our Alumna **Claudia Bank**, group leader of the Evolutionary Dynamics laboratory at the Instituto Gulbenkian de Ciência (IGC), on winning the SMBE Allan Wilson Junior Award 2019!

January 2019: New associated faculty

We're happy that **Kelly Swarts** joined the Vienna Graduate School of Population Genetics as associated faculty. Kelly is group leader affiliated with the Gregor Mendel Institute of Molecular Plant Biology (Austrian Academy of Sciences) and the Max F. Perutz Laboratories (Univ. of Vienna).

Kelly is a quantitative and computational geneticist focusing on understanding the genetic basis of complex traits using modern and ancient populations. Much of her past work

has focused on understanding temperate adaptation in maize, including predicting flowering in 2,000 year old archaeological maize. Her program in Vienna uses similar approaches to understand adaptation in conifers in light of climate change. While not focused on tool development, her group generates computational tools as needed to solve biological questions.

January 2019: PhD defense
Ilse Höllinger just defended her thesis "Mathematical models of speciation and polygenic adaptation" at University of Vienna. Congratulations, and all the best for your further career!

December 2018: Alumni career news
Our Alumna **Claudia Bank**, group leader of the Evolutionary Dynamics laboratory at the Instituto Gulbenkian de Ciência (IGC), received a 2018 EMBO Installation grant. Congratulations!

Out of sight, out of mind?
Experiences of our students abroad

Many of our students choose to spend three to six months in foreign labs during their study time. **Anna Maria Langmüller** (advisor Christian Schlötterer) was hosted by Philipp Messer at Cornell University as guest student researcher:

"Last semester (August 2018 to February 2019), I joined the research group of Philipp Messer at Cornell University. I was funded by the Institute of Population Genetics (Veterinary University, Vienna) and a Marshall Plan Scholarship. The goal of my work with Prof. Messer is to assess the potential fitness costs of CRISPR gene drive constructs in experimental *Drosophila* populations. The idea to use genetically modified organisms to fix distinct alleles in a population has been fascinating scientists for decades. The recently developed CRISPR-Cas9 gene editing technology allows targeted cleavage of genomic sequences, thereby facilitating the spread of alleles with super-Mendelian inheritance via engineered gene drives. CRISPR gene drives have versatile putative applications, like invasive population control, reversal of insecticide and herbicide resistance, species protection or correcting disease-causing mutations. Experimental and theoretical work have shown that the probability of a successful drive depends crucially upon the fitness effects of the gene drive construct. These fitness effects can be caused by a payload effector gene, the off-target cleavage of Cas9, or Cas9 expression and cleavage at the target site per se. By tracking the frequencies of different marker constructs in experimental *Drosophila* populations, we asses both costs of expression and possible off-target effects.

The Messer lab already revealed astonishing aspects of gene drive dynamics and provided an amazing framework for the planned research. I particularly enjoyed my contribution to the early phases of the project, for example the experimental design and the implementation of the maximum likelihood framework that we use to analyze the data. Parts of my work got already published (Liu et. al, 2019) - more to follow :) Cornell University is home of various exceptional research groups and programs. I had the opportunity to attend numerous scientific talks, statistical workshops, and attend lab meetings, journal clubs, and code reviews. One personal highlight was the seminar talk of

Nobel prize laureate Richard Axel about "Order from Disorder: The Imposition of Meaning on Odor Representation".

I found it inspiring to hike next to the beautiful lakes and gorges surrounding the campus. Ithaca is home of countless little restaurants that offer regional cuisine from all over the world. Surrounding the city are various wineries that you can visit - they are particularly famous for their white wines. My colleagues (and now friends) were very welcoming and made sure I had an amazing time in Ithaca. Thanks to all of them, the Messer lab, and my advisor Prof. Schlötterer for this amazing experience."

Impressions from Ithaca

Upcoming events

The **SAB meeting 2019** will take place on May 13, 14 and 15 at Vetmeduni Vienna. We're looking forward to welcome Virginie Courtier-Orgogozo, John Parsch, Nick Barton and Andy Clark.

Upcoming seminars

The Summer Term seminar series includes talks by Juha Merilä, Simon Boitard, Andrew Kern, Matthias Steinrücken, Charles F. Baer, Patrick Phillips, Mike Ritchie, Trudy Mackay, Thomas Wicker, Kirk Lohmueller and Guy Sella.

Have a sunny Spring and Summer!

Publications of our students so far in 2019

Howie JM, Mazzucco R, **Taus T**, Nolte V and Schlötterer C: DNA motifs are not general predictors of recombination in two Drosophila sister species. *Genome Biol Evol.* evz082 (2019) https://academic.oup.com/gbe/advance-article/doi/10.1093/gbe/evz082/5454723

Höllinger I, Pennings PS and Hermisson J. Polygenic adaptation: From sweeps to subtle frequency shifts. *PLoS Genet.* 15(3), e1008035. (2019) doi: 10.1371/journal.pgen.1008035 https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1008035

Spitzer K, **Pelizzola M** and Futschik A. Modifying the Chi-square and the CMH test for population genetic inference: adapting to over-dispersion. *ArXiv* (2019) arXiv:1902.08127 https://arxiv.org/pdf/1902.08127.pdf

Jakšić AM, Karner J, Nolte V, **Hsu S-K**, Barghi N, Mallard F, Otte KA, Svečnjak L, Senti KA and Schlötterer C. Neuronal function and dopamine signaling evolve at high temperature in *Drosophila*. *bioRxiv* 585422. (2019) doi: 10.1101/585422 https://www.biorxiv.org/content/10.1101/585422v1.full

Vlachos C and Kofler R. Optimizing the power to identify the genetic basis of complex traits with Evolve and Resequence studies. *bioRxiv* 583682. (2019) doi: 10.1101/583682 https://www.biorxiv.org/content/10.1101/583682v1

Bergman J and Eyre-Walker A. Does adaptive protein evolution proceed by large or small steps at the amino acid level? *Mol. Biol. Evol.* (2019) doi: 10.1093/molbev/msz033 https://academic.oup.com/mbe/advance-article/doi/10.1093/molbev/msz033/5319976?guestAccessKey=fa3fff8d-08a6-40e9-a3e3-cc25065b22ec

Barghi N, **Tobler R**, Nolte V, **Jakšić AM**, Mallard F, Otte KA, Dolezal M, **Taus T**, Kofler R and Schlötterer C. Genetic redundancy fuels polygenic adaptation in Drosophila. *PLOS Biol.* 17(2), e3000128. (2019) doi: 10.1371/journal.pbio.3000128 https://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.3000128

Hsu S-K, **Jakšić AM**, Nolte V, Barghi N, Mallard F, Otte KA, Schlötterer C. A 24 h age difference causes twice as much gene expression divergence as 100 generations of adaptation to a novel environment. *Genes* 10(2), 89. (2019) doi: 10.3390/genes10020089 https://www.mdpi.com/2073-4425/10/2/89

Rogers J, Raveendran M, Harris RA, Mailund T, Leppälä K, Athanasiadis G, Schierup MH, Cheng J, Munch K, Walker JA, Konkel MK, Jordan V, Steely CJ, Beckstrom TO, Bergey C, Burrell A, **Schrempf D**, … Consortium BGA. The comparative genomics and complex population history of *Papio* baboons. *Sci. Adv.* 5(1), eaau6947. (2019) doi: 10.1126/sciadv.aau6947 http://advances.sciencemag.org/content/5/1/eaau6947

Liu J, Champer J, **Langmüller AM**, Liu C, Chung J, Reeves R, Luthra A, Lee YL, Vaughn AH, Clark AG and Messer PW. Maximum likelihood estimation of fitness components in experimental evolution. *Genetics* genetics.301893.2018. (2019) doi: 10.1534/genetics.118.301893 http://www.genetics.org/content/early/2019/01/24/genetics.118.301893

See all publications here