



## ***Newsletter July 2014***

Welcome to the 4<sup>th</sup> edition of the PopGen ALUMNI newsletter!

### ***Recent events***

#### **Summer 2014: Internships for high school students**

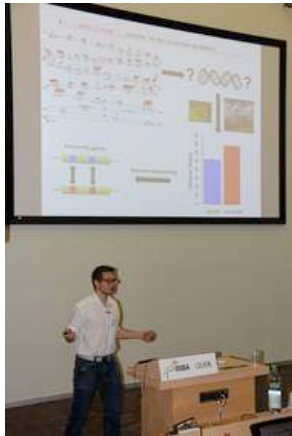
During Summer 2014, four high school students will be hosted at PopGen Vienna. Bernadette, Thomas, Julia and Clemens were selected from a number of interested high school students to spend one month during Summer at PopGen Vienna, collaborating with our PhD students to gain insight into hands-on science.

#### **June 2014: poster award**

Paul Herrera, one of our 2013 cohort students, has won the 2nd Prize for the Students' Award of the 8th International Wolbachia Conference in Innsbruck (Austria) for his poster entitled "Habitat-specific Fitness Dynamics among Wolbachia Clades in *Drosophila melanogaster*".

#### **June 2014: PopGen Vienna at Falling Walls Lab**

Final year student Daniel Fabian contended for participation to the Falling Walls Lab, a non-profit series of scientific conferences that aims at building and fostering interdisciplinary connections between young bright minds. This new and interdisciplinary format offers the opportunity to excellent young academics and professionals from all disciplines to present their outstanding ideas, research projects and entrepreneurial or social initiatives. Each participant is asked to present his/her work in 3 minutes, and a prestigious jury from science and business awards the best participants.



### May 2014: PopGen Vienna at Open University Day

At this year's Open University Day at Vetmeduni Vienna, Barbara Horvath, Tom Hill, Kerstin Gärtner and Ana Marija Jaksic represented the Vienna Graduate School of Population Genetics to visitors of all ages. The audience was quite fascinated by temperature-adapted fruit flies and different bizarre mutants.



### Mini-Symposium: Frontiers of Population Genetics II

The SAB meeting was concluded by a Mini-Symposium on **May 16**, featuring talks by Jean-Michel Gibert, John Parsch, Brian Charlesworth and Simon Tavaré:

#### *Frontiers of Population Genetics II*

10:00 Opening remarks

10:05-10:50 **John Parsch** – LMU München

*“Sex- and population-biased gene expression in the brain of Drosophila melanogaster”*

10:50-11:35 **Brian Charlesworth** - University of Edinburgh

*“Faster-X evolution in species of Drosophila”*

11:35-12:00 coffee break

12:00-12:45 **Jean-Michel Gibert** – CNRS Paris

*“Genetic bases of phenotypic plasticity in Drosophila”*

12:45-13:45 break

13:45-14:30 **Simon Tavaré** – University of Cambridge

*“A statistical problem arising in the study of tumour heterogeneity”*

### **May 2014: SAB meeting**

The yearly Scientific Advisory Board (SAB) meeting took place on May 14 and 15. Five of our SAB members (Brian Charlesworth, Simon Tavaré, Andy Clark, John Parsch and Jean-Michel Gibert) listened to our student's progress reports, discussed future steps and gave career advice to our last-year students. After the meetings, the students took the SAB members out for a few drinks and informal chats.

### ***Recent visitors***

Stefanie Walter, a bioinformatics master student from Berlin spent a 1 month internship at PopGen Vienna and worked with our PhD student Kerstin Gärtner. Stefanie ran simulations to get to know how LDhelmet and LDhat performed under different recombination rates and sample sizes.

Daniel Fischer, a PhD student and bioinformatician at the MTT Agrifood Research Finland spent a 3-week research visit at the Vienna Graduate School of Population genetics. He collaborated with Marlies Dolezal on the 'Identification of Signatures of Selection from Next Generation Sequencing Data'.

Giuseppina Schiavo is a PhD student from the Department of Agricultural and Food Sciences, Division of Animal Sciences at the University of Bologna, Italy. She just concluded her 2 months PhD-internship at the Vienna Graduate School of Population genetics. During her stay, Giuseppina studied Copy Number Variations in cattle and pig based on high density Illumina SNP array data.

### ***New associated faculty***

The following associated faculty members are to be appointed as full faculty, conditional on a new funding period:

**Andrea Betancourt** (*Institute of Population Genetics, Vetmeduni Vienna*)

**Marlies Dolezal** (*Institute of Population Genetics, Vetmeduni Vienna*)

**Angela Hancock** (*MABS/MFPL, Univ. of Vienna*)

**Alex Kalinka** (*Institute of Population Genetics, Vetmeduni Vienna*)

**Sylvain Mousset** (*MABS, Univ. of Vienna*)

**Ovidiu Paun** (*Department of Botany and Biodiversity Research, Univ. of Vienna*)

### ***Alumni careers***

Most students of our first DK cohort are nearly done with their PhDs and we hope to celebrate several defenses still this year: **Daniel Fabian** accepted a Postdoc position in Frank Jiggins' Lab in **Cambridge**, **Christian Huber** will move to **UCLA** to work as Postdoc with Kirk Lohmueller. **Johanna Bertl** will work in the group of Jakob Skou Pedersen in **Aarhus**, also as Postdoc. Congratulations to the new positions!

## ***Alumni lab portraits***

We feature a brief report about one of PopGen's graduate and faculty alumni in every Newsletter. Claudia Bank told us about her postdoc experiences in the last edition.

This time, graduate **Florian Clemente** gives us some insight into his postdoc research in **Cambridge** (Group of Toomas Kivisild):

*"After my studies of bioinformatics in Munich, I received my Ph.D. degree in population genetics in Vienna.*

*In general, my research interests are focused on forces driving evolution on the molecular level. I am particularly interested in the relative roles of genetic drift and natural selection in the process of adaptation to different environments.*

*Former projects:*

*During my Ph.D., I studied genome-wide putatively selectively unconstrained DNA sequences in Drosophila, i.e., short introns and fourfold degenerate sites. Unconstrained sequences are of importance to infer selection in another sequence class, but also to reconstruct the demographic history of a population. Our results showed that in Drosophila, short introns may in fact evolve without selective constraints, but underlie a complicated mutational pattern, creating non-equilibrium. Fourfold degenerate sites, on the other hand, are governed by more complex selectional forces than typically assumed in the biallelic model of codon usage bias.*

*Current project:*

*The large amount of newly sequenced world-wide human genomes allows the study of human adaptation to different environments and life styles. For instance, Northeast Siberians are exposed to extremely cold temperatures and a resulting high-fat diet. Thus they provide a unique and interesting case in the study of adaptation. Our projects involve the detection of (unique) candidate regions, presumably driven by positive selection in the population of interest. Candidate regions are then inspected in more detail, trying to distinguish between patterns created by genetic drift and natural selection."*



Florian in Puerto Rico (SMBE 2014)

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

Many of our students choose to spend 3 months in foreign labs during their study time. In each of the Newsletters one of them tells us about their experiences.

**Johanna Bertl** (advisors Andreas Futschik and Carolin Kosiol) was hosted by Michael Blum as guest student at the **J. Fourier University of Grenoble** from October 2012 to January 2013:

*“In autumn 2012, I went to Grenoble, France, for 3 months to work with Michael Blum. I had already stumbled across his papers about Approximate Bayesian Computation when I wrote my master thesis and had followed his work during my PhD, so I was happy about the opportunity to join his group for three months.*

*During the analysis of DNA data sampled from plant species across the whole range of the Alps, Michael and his PhD student Nicolas had come across an interesting question: How can the molecular footprint of secondary contact after isolation, like it has been reported for many species whose habitats were split up during the Quaternary ice-ages, be distinguished from the footprint of reduced gene-flow, caused for example by a geographical barrier like a mountain range or a deep valley that inhibits migration? I set out to find out more about this with simulations of different evolutionary scenarios. It was very enjoyable and productive to work in a group where everyone was doing statistical population genetics and I learned a lot from my colleagues.*



*Apart from population genetics, programming and statistics, everyone seemed to be very much into hiking, skiing and whatever you can do on a*

mountain. That was no coincidence: Grenoble is in the heart of the French Alps and the surrounding mountain scenery is really impressive. So already on my first weekend there I went on a hiking tour, and on many of the following weekends I explored the mountains around Grenoble – with and without snow – with my colleagues.

So all in all, I had a very good time in Grenoble: I learned a lot, worked on a very interesting project, but I also enjoyed the scenic surroundings of Grenoble and learned to talk about “la génétique des pop” in French from my colleagues.”

### ***Upcoming events***

The 2014 **Introductory Course** schedule is now fixed. We already received several expressions of interest for participation from international students from Brasil, Italy and Germany. <http://www.popgen-vienna.at/training/lectures.html>

This year’s **retreat** will be held from October 3-5 at Altaussee, similar to last year. We’re expecting around 35 participants for a weekend of seminars, socialising and hiking.

After the big success of the NGS course in May 2011 we’re organising a **practical course on next generation sequencing for population genetics and experimental evolution** in October. We received around 70 applications and 25 successful candidates will be notified by mid of July.

A big date is coming up for the DK: the **FWF hearing** on November 4 will decide about a second funding period of 4 years, starting from January 2015. We’ll take the opportunity to bring our alumni back for a **Mini Symposium** on November 5 – we hope that many of you will be able to come to Vienna for that!

### ***Upcoming seminars***

We’re preparing a new seminar schedule starting from October. **John Huelsenbeck, Patrik Nosil** and **Andreas Wagner** have already signed up.

### ***Publications of our students***

2014 publications of our students:

**Ada Akerman** and R. Bürger: The consequences of gene flow for local adaptation and differentiation: a two-locus two-deme model. *J Math Biol* 68, 1135-1198 (2014)

**Ada Akerman** and R. Bürger: The consequences of dominance and gene flow for local adaptation and differentiation at two linked loci. *Theor Popul Biol* 94, 42-62 (2014)

**Ludwig Geroldinger** and R. Bürger: A two-locus model of spatially varying stabilizing or directional selection on a quantitative trait. *Theor Popul Biol* 94, 10-41 (2014)

**Peter Klepsatel**, M. Galikova, **Christian D. Huber** and T. Flatt: Similarities and Differences in Altitudinal Versus Latitudinal Variation for Morphological Traits in *Drosophila Melanogaster*. *Evolution* (2014)

E. Versace, V. Nolte, R.V. Pandey, **Raymond Tobler** and C. Schlötterer: Experimental evolution reveals habitat-specific fitness dynamics among Wolbachia clades in *Drosophila melanogaster*. *Mol Ecol* 23, 802-814 (2014)

**Raymond Tobler**, S.U. Franssen, R. Kofler, P. Orozco-terWengel, V. Nolte, J. Hermisson and C. Schlötterer: Massive Habitat-Specific Genomic Response in *D. melanogaster* Populations during Experimental Evolution in Hot and Cold Environments. *Molecular Biology and Evolution* 31, 364-375 (2014)

***Have a good summer!***