

2 postdoctoral positions are available at the Institute of Population Genetics, Vetmeduni Vienna (Austria). The research focus of the Institute of Population Genetics is on understanding the genetics of adaptation. This central question in evolutionary biology is being tackled using up-to-date methods and a variety of approaches, including experimental evolution, quantitative genetics, functional genetics, empirical population genetics, bioinformatics and statistics.

The successful candidate will be part of a team of scientists studying adaptation of experimental *Drosophila* populations to temperature stress. Since our experimental evolution study is performed under controlled environmental conditions with a high level of replication we have a powerful system to successfully employ a combination of DNA sequencing, RNA-Seq and Chip-Seq to characterize the architecture of adaptation in an out-crossing species. With some of our populations having already evolved up to 100 generations, this project provides the opportunity to follow adaptive trajectories through time.

We are looking for a candidate with a good quantitative training and experience in handling large data sets. A background in population genetics and/or experience with the analysis of RNA-Seq and Pool-Seq data are a bonus.

The positions are available for at least two years starting April 2015 , but the exact starting date is negotiable. The application should be emailed to christian.schloetterer@vetmeduni.ac.at as a single pdf containing CV, list of publications, a statement of research interests, and the names of three references with contact details. While the search will continue until the position is filled, applications should be **received by 5.3.2015** to ensure full consideration.

Background:

- 1: Franssen, S.U., et al. (2015) Patterns of linkage disequilibrium and long range hitchhiking in evolving experimental *Drosophila melanogaster* populations. *Molecular Biology and Evolution* 32, 495-509
- 2: Orozco-terWengel, P., et al. (2012) Adaptation of *Drosophila* to a novel laboratory environment reveals temporally heterogeneous trajectories of selected alleles. *Molecular Ecology* 21, 4931-4941
- 3: Schlotterer, C., et al. (2015) Combining experimental evolution with next-generation sequencing: a powerful tool to study adaptation from standing genetic variation. *Heredity* in press

4: Schlötterer, C., et al. (2014) Sequencing pools of individuals - mining genome-wide polymorphism data without big funding. *Nature Reviews. Genetics* 15, 749-763

5: Tobler, R., et al. (2013) Massive habitat-specific genomic response in *D. melanogaster* populations during experimental evolution in hot and cold environments. *Molecular Biology and Evolution* 31, 364-375