



The European *Drosophila* Population Genomics Consortium (DrosEU)

generously funded by a **European Society for Evolutionary Biology (ESEB) Special Topics Network (STN)**



DrosEU consortium website: <http://droseu.net/>

Rationale

- This is an extremely exciting time for population genomic studies. The recent advent of powerful next-generation sequencing (NGS) techniques allows us researchers to examine genetic variation at unprecedented scale, at the whole-genome level and with single nucleotide resolution. The continuing technological improvements and the dropping costs of these methods means that even single labs can now generate terabytes of sequence data very rapidly a relatively low cost. However, the resulting data are typically used to address only a very limited number of specific questions, so that the overall value of these data sets for the community as a whole is somewhat limited. The best-suited organisms to track genetic changes and adaptation are those that are easy to collect, which are broadly distributed, possess a short generation time, have a well-annotated genome and for which hypotheses about climate adaptation can be tested in the laboratory. The fruit fly *Drosophila melanogaster* and its sibling species are ideally suited for this purpose and have already been shown to respond to global and local climatic changes over short periods of time. Indeed, the genus *Drosophila* is one of the most powerful model systems for studying adaptation. However, in contrast to other continents, population samples of *Drosophila* from Europe are so far available only from a few environments and from single time points of collection.

Objectives of DrosEU

- To foster the integration and exchange of population genomic information and data, we have founded in 2013 the *European Drosophila Population Genomics Consortium (DrosEU)*, a collaborative consortium of scientists and laboratories interested in evolutionary genetics and genomics of *Drosophila*. Our main objective is to cooperate closely in collecting, generating and analyzing genomic and environmental data for numerous *Drosophila* populations across Europe (and beyond). While our initial focus is on sampling and analysis of the most tractable species, *D. melanogaster*, we also plan in the future to include related species such as *D. simulans*, *D. subobscura* (a model for climate change adaptation) and *D. suzukii* (a recent invasive pest species). Our long-term goal is to regularly sample and sequence *Drosophila* populations through both space and time in order to track their eco-evolutionary dynamics. We plan this to be a continuing multi-year effort. Importantly, many of the sampled populations are being kept as isofemale lines by the members of the consortium as a resource for phenotypic, functional (genotype-phenotype mapping) work.
- A similar consortium already exists in the US: the *Drosophila Real Time Evolution Consortium (Dros-RTEC)*, coordinated by Alan Bergland (Virginia), Dmitri Petrov (Stanford) and Paul Schmidt (Philadelphia). The goal of *DrosEU* is to extend and complement the North American efforts by implementing a similar initiative focused on Europe. We are closely collaborating with *Dros-RTEC*.

What we have achieved so far & future plans

- To date, we are approximately 70 scientists from approx. 17 European countries and also including several North American colleagues from *Dros-RTEC*.
- Between 2014 and 2016 we have collected and pool-sequenced approx. 50-66 of population samples across all of Europe, from approximately 20-30 different locations, most of which have been sampled once in summer and once in fall; additional annual collections will be sequenced in the near future. The funds to generate the already existing sequencing data have all been raised internally within our consortium. The resulting population genomic data are being analyzed by our different internal working groups; our US colleagues from *Dros-RTEC* are actively contributing to some of our working groups.
- We are in the process of finishing a first joint consortium paper based on the first 2014 set of sequencing data, with everyone who has actively contributed being involved as co-authors.
- Some of us are also planning to extend sampling to *D. simulans* and *D. suzukii*, and we have active plans to improve our geographic coverage for *D. melanogaster*. For many populations we are keeping live isofemale lines.
- Currently we are planning to perform a comprehensive phenotyping effort for European *melanogaster*, to take place in 2018/2019.

Joining DrosEU

- We encourage scientists - especially members of ESEB (!) - interested in joining us to contact Josefa González (josefa.gonzalez@ibe.upf-csic.es), cc to Thomas Flatt (thomas.flatt@unifr.ch); we are now accepting applications for active consortium membership.
- Active consortium membership for a given year requires a commitment and contribution to a minimum of 2 out of the 3 requirements:
 - (1) to perform sampling in that year for a minimum of 1 geographic location and for a minimum of 2 timepoints (once in summer and once in fall/autumn), following our sampling protocol for pool-seq.
 - (2) to make a financial contribution to covering consortium-related costs.
 - (3) to make an other valuable contribution to the consortium effort in a given year. This could, for example, include: data analysis; maintenance of live isofemale lines; coordinating a working group; organizing and hosting a consortium workshop; data storage; coordination tasks within the network; developing, hosting and maintaining databases; developing, hosting and maintaining web-based communication tools for the consortium, e.g. websites, twitter, etc.; generating funding for the consortium, e.g. via grant writing; and so forth.
- Active membership entails being involved in all democratic decisions of the consortium, having access and being privy to all consortium-internal informations, communications, data, analyses outputs, and so forth.
- Statements of interest should be sent to Josefa González and/or Thomas Flatt; the commitment agreement form is available from us upon request.

Main consortium organizers

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