PhD position in Population Genomics and Adaptation
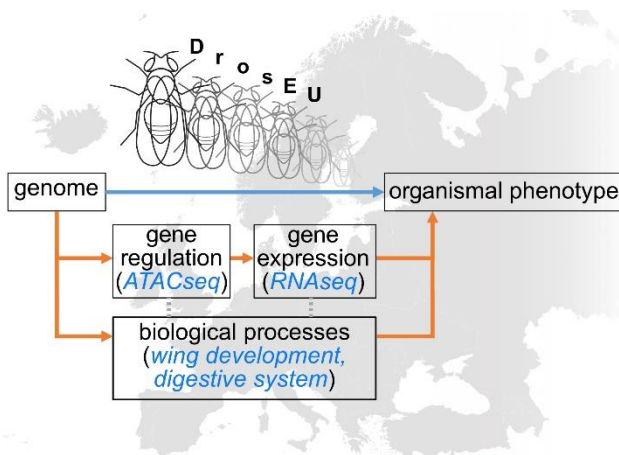## @ University Göttingen within the IMPRS-Genome Science program
3-years position (65%) | E13 TV-L | contact: nposnie@gwdg.de

Project Title:
Identification of loci underlying local adaptation in European *Drosophila* populations

Project Description:

Organisms must cope with an ever-changing environment. Due to adaptations to local biotic and abiotic conditions, individuals within and between populations differ at the genomic and phenotypic level and population diversification is shaped by selection, as well as neutral events, such as genetic drift and migration. Most of our current understanding of genetic diversity in populations is based on analyses of specific genes or restricted genomic loci. The advent of population genomics based on next generation sequencing technologies facilitated assessing genetic differentiation on a genome-wide scale. In contrast, the assessment of quantitative population differences in organismal phenotypic traits is often hampered because high-throughput screens are time consuming, and they require specialized equipment and expertise. Therefore, the phenotypes influenced by locally adapted genomic loci often remain elusive.

The European *Drosophila* Population Genomics Consortium (DrosEU) [1] has been collecting natural *D. melanogaster* populations across Europe since 2014 and first population genomics analyses revealed patterns of local adaptation [2,3]. In 2018, the consortium established 168 isofemale lines representing nine European *D. melanogaster* populations for an extensive phenotyping effort to quantify 18 life history, physiological, morphology and behavioral organismal traits. The analysis of this phenotypic dataset revealed clinal patterns for multiple traits, indicating local adaptation at the phenotypic level. We will harness this exciting resource by sequencing the genomes of all 168 isofemale lines to link observed phenotypic variation to genomic divergence. To gain mechanistic insights into the consequences of genetic diversity, we will study genome wide patterns of gene expression (RNAseq) and chromatin accessibility (ATACseq) for two tissues with relevance for observed adult phenotypes, namely the gut and wing imaginal discs.

The results of these experiments will shed light on local adaptation of natural populations. In addition, the use of state-of-the-art genomic and epigenomic methods will provide novel mechanistic insights into gene function in the context of local adaptation.

Research environment:
This project is a collaboration between the host lab at the University Göttingen and Sonja Grath (LMU Munich), Claudia Fricke (University Halle) and additional members of the DrosEU consortium. This highly interdisciplinary team provides an excellent research environment for

this project. The position will be hosted at the Department of Developmental Biology at the University Göttingen and the successful candidate will join the International Max Planck Research School for Genome Science (IMPRS-GS), which provides a vibrant environment for PhD students.

Your Qualifications:

MSc degree in Biology, Bioinformatics or in other relevant fields such as Mathematics or Breeding Science. We expect bioinformatic and statistical skills to handle population genetics/genomics, quantitative genetics, RNAseq and ATACseq data and to integrate such multi-omics data. A willingness to get involved in data generation (wet lab) is a plus.

Application:

Please apply until **February 10, 2023** through the online portal of the IMPRS-GS: https://application.imprs-gs.uni-goettingen.de/public/

References:

[1] https://droseu.net/
[2] Kapun M, et al. Genomic Analysis of European Drosophila melanogaster Populations Reveals Longitudinal Structure, Continent-Wide Selection, and Previously Unknown DNA Viruses. *Mol Biol Evol*. 2020;37:2661–78.
http://dx.doi.org/10.1093/molbev/msaa120
[3] Kapun M, et al. Drosophila Evolution over Space and Time (DEST): A New Population Genomics Resource. *Mol Biol Evol*. 2021;38:5782–805.
http://dx.doi.org/10.1093/molbev/msab259