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## Three-year PhD fellowship

### *Developmental phenotypic plasticity in water striders*

**Where:** The Khila lab at the Institute of Functional Genomics, École Normale Supérieure de Lyon, UMR CNRS 5242, Lyon, France

<http://igfl.ens-lyon.fr/>

<http://igfl.ens-lyon.fr/equipes/a.-khila-developmental-genomics-and-evolution>

**Starting date:** October 1<sup>st</sup>, 2021 or slightly after

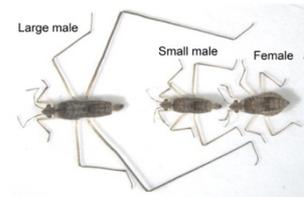
**Deadline for applications:** June 30<sup>th</sup>, 2021 (Only short-listed candidates will be notified).

**Project title: Molecular origin of extreme growth variation with focus on DNA methylation**

**Background:** Growth variation under environmental influence is widespread in nature, yet our understanding of the underlying molecular mechanisms remains limited. This process, known as developmental phenotypic plasticity, provides an invaluable opportunity to understand the genotype-phenotype relationship and the impact of the environment on this relationship.

**Hypothesis:** Variation in nutritional input causes extreme growth variation through changes in DNA methylation states and transcriptional regulation. This hypothesis is supported by preliminary data.

**Model system:** We test this hypothesis in the water strider *Microvelia longipes* (Image). The males have longer legs than females, but also extreme variation in hind-leg length between males (Image). Our recent work showed that males use their hind legs as weapons during contests, and that long-legged males have significantly higher chance to dominate egg-laying sites and access females ([Toubiana and Khila, Proc B. 2019](#)). We recently identified the gene *BMP11* as a primary regulator of scaling relationships between the body and the hind-legs in a male-specific manner ([Toubiana et al. PLoS Biology, 2021](#)). We also built the resources required for this project, including a high-quality genome and transcriptomes ([Toubiana, Armisen et al. BMC Biology 2021](#)), isogenic lines and lab populations (easy to keep), DNA methylation datasets, as well as various developmental genetics tools ([Toubiana et al. PLoS Biology, 2021](#)).



**Project:** The successful PhD candidate will collaborate with a team of postdocs and lab technicians studying how variation in nutritional input causes extreme growth variation through changes in epigenetic states and transcriptional regulation. The objectives are:

- Build the genome-wide methylome of this species (using Bisulfite sequencing and isogenic lines)
- Determine the fraction of DNA methylation sites that responds to nutritional treatment
- Determine the genes whose expression profiles correlate with changes in nutritional treatment and changes in DNA methylation states.
- Functionally test (by RNAi or Crispr-Cas) a small selection of the loci identified above.

**Mandatory requirement:** Master's degree (or equivalent).

**Concepts:** Epigenetics, genetic variation, nutritional manipulation, developmental genetics

**Expertise we seek:** DNA methylation analyses, Bioinformatics, Statistics, Programming in R

**Skills:** Good English (written and spoken), motivation, creativity, curiosity, good work ethics, teamwork, and good inter-personal relationship with colleagues. Knowledge in evolutionary biology, epigenetics or development is a plus.

**How to apply:** By email to [abderrahman.khila@ens-lyon.fr](mailto:abderrahman.khila@ens-lyon.fr) with a **motivation letter** explaining why you are interested by this position and how you think you are qualified, your **CV** and names and e-mail addresses of **two or three referees** who can write letters of reference on your behalf.