# Rates of *de novo* mutations in sticklebacks

**Date: 18 April 2023 (Tue)**

**Time: 2 PM**

**Venue: 6N11 & Zoom**



## About the speaker:

Chaowei (Charlene) ZHANG is a PhD student in the Merilä Lab. She is interested in fish population genomics, especially understanding how fish genomes evolve in populations differing in their demographies.



## Abstract:

Mutation, the genetic change occurring during cell division, is vital as the ultimate source of genetic variability. Mutation rates ($\mu$) are generally low, but they vary enormously among species but less is known about variation among populations. $\mu$ is an important scaling parameter for demographic and phylogenetic inference, and allows one to understand at what rate new genetic diversity is generated. However, except for well-established model organisms, accurate estimates of $\mu$ are available for a very limited number of organisms from the wild. This is true also in the case of emerging ecological and evolutionary biology model, the nine-spined stickleback (*Pungitius pungitius*). In this PhD project, I have been estimating $\mu$ in 480 stickleback individuals from 4 pond and 4 marine populations with the aid of several 2- and 3-generational family pedigrees, deep (>50×) whole genome re-sequencing and a high-quality reference genome. The $\mu$ was significantly higher in pond than in marine populations. This result fits the predictions of the "drift-barrier hypothesis" which posits that the capacity of natural selection removing deleterious mutations is less constrained by genetic drift in the large than small populations leading elevated mutation rates in small populations. My PhD project aims to uncover how $\mu$ varies among ecotypes, how the parental age and sex influences $\mu$, and how $\mu$ and recombination rate together shape the localised genetic diversity among genomes.