

Genomic basis of rapid and recurrent evolution in threespine stickleback

Date 17th Dec (Fri.)

Time 16:00 (UTC+8)

Venue 3N01 & Zoom



You can also email us to require the Zoom link
(check SBS website → NEWS & EVENTS)

Threespine stickleback have repeatedly adapted to fresh water from marine progenitors. Genomic studies have found that this repeated adaptation is due to the repeated selection of ancient freshwater alleles circulating in marine populations as standing genetic variation. In our study we used replicate whole lake experiments in Alaska (spanning > 10 years) that were seeded with marine stickleback to elucidate the speed and extent of adaptation to fresh water, allowing us to study the process of rapid adaptation as a time-series. Genotypic and phenotypic changes were observed within 5 years, facilitated by available standing genetic variation and linkage between adaptive regions. Genomic regions that rapidly increased in frequency in the experimental lakes were highly concordant with putative freshwater adaptive alleles observed in natural populations and could be predicted by age of the loci, underlying recombination rate and overlap with known mapped traits.



Dr Kerry Reid is an Research Assistant Professor in the area of Ecology and Biodiversity at HKU. She completed her PhD at the University of Pretoria focused on comparative phylogeography of temperate marine fauna. She then did a postdoc at University of California (Santa Cruz) focused on using genetic and genomics tools to address questions on the conservation and management of depleted fish stocks. After this, she did a Postdoc at Stony Brook University focused on addressing the underlying genomic features that facilitate rapid adaptation using a fish model system. She joined HKU in September 2021.

All are welcome!