

Genetics of adaptation in **sticklebacks**: the roles of pleiotropy and linkage

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Science Building A222

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Despite much recent progress, relatively little is still known about the specific genetic and molecular changes that underlie adaptation to new environments. Stickleback fish have been at the forefront of research to uncover the genetic and molecular architecture of adaptation and speciation. A wealth of quantitative trait locus (QTL) mapping studies in sticklebacks has provided insight into the distribution of effect sizes during adaptation and has also revealed that several regions of the genome contain more loci than expected for traits involved in adaptation. Some of these QTL clusters overlap with genomic regions under divergent selection between marine and freshwater populations.

In order to disentangle the relationships between genotype, phenotype and fitness in these genomic “hotspots”, we are focusing on a 16kb region of marine-freshwater divergence encompassing the Ectodysplasin (Eda) gene on chromosome IV. The Eda gene has been shown to contribute to variation in three phenotypes (lateral plate number, lateral line pattern, schooling behavior) that differ between marine and freshwater sticklebacks. However, it is unknown whether the effects of Eda on these phenotypes are due to pleiotropic effects of a single mutation, or linkage of multiple mutations. To distinguish between linkage and pleiotropy, we conducted association mapping across this 16kb region in a freshwater population in Lake Washington (Seattle, USA), where both the marine and freshwater haplotypes are present. Surprisingly, we find extensive recombination has occurred across this haplotype in Lake Washington, and that the effects of Eda on multiple phenotypes are due to pleiotropy.