**Detecting genomic patterns of ecological adaptation in Galician *Littorina saxatilis* ecotypes through QTL mapping**

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Adaptation to different ecological selection regimes may be impeded by the presence of gene flow, as genetic exchange between populations is expected to break up combinations of adaptive genes and introduce ecologically disadvantageous alleles. The genomic architecture of genes involved in adaptive divergence may play a role in determining the rate and success of ecological adaptation with gene flow. Current sequencing technologies allow the development of high-resolution single nucleotide polymorphism (SNP) markers, enabling comparison of many genomic markers between many sampled individuals at once. These molecular tools can be used to “scan” the genomes of diverging populations to determine the organization and location of regions housing divergent loci, and to find associations between divergent phenotypes and genotypes. Identifying the location and organization of genes involved in divergence with gene flow is key to understanding the role of the genome in shaping adaptive trajectories. The marine snail *Littorina saxatilis* forms distinct ecotypes in different regions of the intertidal zone in the North Atlantic over very short distances, often connected by an intermediate hybrid zone. At sites on the Galician coast of northwestern Spain, two separate ecotypes have evolved different shell morphologies and body sizes to resist predation, UV exposure and dessication on the upper shore, and wave exposure on the lower shore. We are currently using an Illumina Miseq platform to develop SNP markers for QTL mapping F1 hybrid families to simultaneously identify the genes associated with these adaptations, and to better understand how their location and organization within the *L. saxatilis* genome may facilitate divergence despite gene flow.