



Seminar/Talk

Using hybrid zones to understand the links between genotype, phenotype and selection

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Outlier scans facilitate the identification of loci potentially affected by divergent selection between ecotypes or incipient species. However, these approaches have various shortcomings; the strength and nature of selection acting on outliers is often unclear, and functional roles and locations in the genome are commonly unknown. After performing outlier scans in our study organism, the marine snail *Littorina saxatilis*, we now use data from hybrid zones to fill some of these gaps. *L. saxatilis* contains two distinct ecotypes, adapted to wave-exposed vs. high-predation habitats and showing partial reproductive isolation. To gain insight into the genomic basis of divergence, we have phenotyped hundreds of snails sampled across a hybrid zone on the Swedish west coast and sequenced 40,000 genomic markers. We have identified loci with steep allele frequency clines across the habitat transition, which often correspond to outliers from earlier work, supporting the role of divergent selection. However, we also show that clines for some loci do not coincide with the habitat transition and may reveal other axes of divergent selection. Using a genetic map, we demonstrate that divergent selection is pervasive across the genome. Currently we are using an admixture mapping approach to establish the link between selected loci and phenotypes.

A particularly useful aspect of the *L. saxatilis* system is that divergent ecotypes have evolved repeatedly in multiple geographical locations. A key question is to what extent the genetic basis of divergence – i.e. the set of loci under divergent selection – is the same across such instances of parallel divergence. Answering this question is hindered by the fact that local signatures of selection, detected e.g. in outlier scans, may be modified by genetic drift, potentially leading to an underestimation of the number of selected loci shared among locations. I will discuss potential future work that takes the effects of genetic drift into account, combining simulation approaches and analyses of *L. saxatilis* whole-genome resequencing data.

Wednesday, May 17, 2017 09:45am - 10:45am

Mondi Seminar Room 3, Central Building



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