
Evolutionary genomics of adaptation and speciation in a model forest tree

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I will outline evolutionary genomic approaches to the study of adaptive population divergence and speciation in the face of gene flow. Within this talk, I will cover empirical work from different ends of the divergence continuum, ranging from conspecific populations with recent common ancestry to highly divergent species that nevertheless still mate and recombine in hybrid zones. I will introduce our current primary model system for addressing these topics, *Populus alba* and *P. tremula*, two ecologically divergent, hybridizing Eurasian tree species related to *P. trichocarpa*, the first completely sequenced forest tree. Reviewed work from my lab will include both established molecular ecology and “next generation” approaches based on Restriction site Associated DNA (RAD) and whole genome-resequencing. I will close by discussing some open questions in landscape genetics, e.g. the need to consider the genomic landscape of recombination in studies of adaptive evolution.

Landscape genomics of North American conifers

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The long-term interest of my lab is to understand the molecular basis of plant adaptation to the environment in forest tree populations. A rich history of common garden experimentation has show genetic control of adaptive traits and precise patterning of adaptation across heterogeneous environments. Adaptive traits are assumed to be highly polygenetic but the exact underlying genes were unknown. We have used QTL mapping and association studies in loblolly pine (*Pinus taeda* L.) and Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco) to begin to dissect these complex traits to their individual genes. This approach has led to many candidate genes for adaptive traits such as cold-hardiness and water-use efficiency. Next we have conducted candidate gene resequencing (Sanger) to discover SNPs. These studies have been done in a large number of North American and European conifers. Gene and SNP annotations are performed and measures of nucleotide diversity and departures from neutrality are estimated. Finally, large populations of geo-referenced trees are genotyped for SNPs and patterns of demographic and adaptive diversity are estimated.

Detecting local adaptations in aposematic species: a phenotypic-genotypic approach

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In aposematic species (i.e. those that possess a warning colour signal advertising unpalatability), directional selection by predators is expected to result in the fixation of aposematic traits. Hence, variation in the warning signal within an aposematic species is not predicted because of the increased costs of having to ‘educate’ predators about multiple warning signals. However, variation in the warning signals of aposematic prey is commonly found in nature, suggesting the