The genomic signatures of adaptive evolution in *Populus*

Jing Wang

Akademisk avhandling

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Fakultetsopponent: Professor, Barbara Mable,
Institute of Biodiversity, Animal Health & Comparative Medicine, University of Glasgow, UK.
Title
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Abstract
Understanding the genetic basis of adaptive evolution, and how natural selection has shaped patterns of polymorphism and divergence within and between species are enduring goals of evolutionary genetics. In this thesis, I used whole genome re-sequencing data to characterize the genomic signatures of natural selection along different evolutionary timescales in three *Populus* species: *Populus tremula, P. tremuloides* and *P. trichocarpa*. First, our study shows multiple lines of evidence suggesting that natural selection, due to both positive and purifying selection, has widely shaped patterns of nucleotide polymorphism at linked neutral sites in all three species. Differences in effective population sizes and rates of recombination largely explain the disparate magnitudes and signatures of linked selection that we observe among species. Second, we characterize the evolution of genomic divergence patterns between two recently diverged aspen species: *P. tremula* and *P. tremuloides*. Our findings indicate that the two species diverged ~2.2–3.1 million years ago, coinciding with the severing of the Bering land bridge and the onset of dramatic climatic oscillations during the Pleistocene. We further explore different mechanisms that may explain the heterogeneity of genomic divergence, and find that variation in linked selection and recombination likely plays a key role in generating the heterogeneous genomic landscape of differentiation between the two aspen species. Third, we link whole-genome polymorphic data with local environmental variables and phenotypic variation in an adaptive trait to investigate the genomic basis of local adaptation in *P. tremula* along a latitudinal gradient across Sweden. We find that a majority of single nucleotide polymorphisms (SNPs) (>90%) identified as being involved in local adaptation are tightly clustered in a single genomic region on chromosome 10. The signatures of selection at this region are more consistent with soft rather than hard selective sweeps, where multiple adaptive haplotypes derived from standing genetic variation sweep through the populations simultaneously, and where different haplotypes rise to high frequency in different latitudinal regions. In summary, this thesis uses phylogenetic comparative approaches to elucidate how various evolutionary forces have shaped genome-wide patterns of sequence evolution in *Populus*.

Keywords: *Populus*, adaptive evolution, natural selection, genomic diversity and divergence, recombination, Next-generation sequencing (NGS), local adaptation