

Molecular population genetics of inducible defense genes in *Populus tremula*

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Akademisk avhandling

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Abstract

Plant-herbivore interactions are among the most common of ecological interactions. It is therefore not surprising that plants have evolved multiple mechanisms to defend themselves, using both constitutive chemical and physical barriers and by induced responses which are only expressed after herbivory has occurred. Herbivores, on the other hand, respond to these plant defenses by evolving counter-adaptations which makes defenses less effective or even useless. Adaptation can occur at different geographical scales, with varying coevolutionary interactions across a spatially heterogeneous landscape. By looking at the underlying genes responsible for these defensive traits and herbivore related phenotypic traits, it is possible to investigate the coevolutionary history of these plant-herbivore interactions. Here I use molecular population genetic tools to investigate the evolutionary history of several inducible defense genes in European Aspen (*Populus tremula*) in Sweden. Two genes, belonging to the Polyphenol oxidase gene-family (*PPO1* and *PPO2*), show skewness in their site frequency spectrum together with patterns of diversity and divergence from an outgroup which correspond to signatures of adaptive evolution (Paper II). 71 single nucleotide polymorphisms (SNPs) from seven inducible defense genes (*PPO1-PPO3*, *TI2-TI5*) show elevated levels of population differentiation compared to control genes (genes not involved in plant defense), and 10 of these defense SNPs show strong signatures of natural selection (Paper III). These 71 defense SNPs also divide a sample of Swedish *P. tremula* trees into three distinct geographical groups, corresponding to a Southern, Central and Northern cluster, a pattern that is not present in control SNPs (Paper III). The same geographical pattern, with a distinct Northern cluster, is also observed in several phenotypic traits related to herbivory in our common garden in Sävar (Paper IV). These phenotypic traits show patterns of apparent local maladaptation of the herbivore community to the host population which could indicate the presence of "information coevolution" between plants and herbivores (Paper IV). 15 unique defense SNPs also show significant associations to eight phenotypic traits but the causal effects of these SNP associations may be confounded by the geographic structure found in both the underlying genes and in the phenotypic traits. The co-occurrence of population structure in both defense genes and herbivore community traits may be the result from historical events during the post-glacial recolonization of Sweden.

Keywords

Populus, herbivore defense, adaptation, population genetics, population structure, association mapping, complex traits

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