

GENETIC DIVERSITY IN FOREST TREE POPULATIONS AND CONSERVATION: ANALYSIS OF NEUTRAL AND ADAPTIVE VARIATION

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Summary

Conservation genetics of forest tree species takes advantage from the availability of molecular markers. Depending on the processes that need to be analysed, molecular markers may provide extremely useful information to monitor processes related to adaptation and migration. Markers must be carefully selected depending on the specific question. Some examples are provided and usefulness of molecular markers in conservation genetics of forest tree species is discussed. Direct analysis of adaptive variation is now possible by analysis of QTNs (Quantitative Trait Nucleotides): this requires that QTNs are known. A perspective on the possibilities for discovering genes involved in adaptive variation in forest trees is provided.

Keywords

Neutral diversity, adaptive diversity, molecular markers, phylogeography, gene discovery

Contribution

The genomics revolution of the last 10 years has improved our understanding of the genetic make up of living organisms. Together with the achievements represented by complete genomic sequences for an increasing number of species, high throughput and parallel approaches are available for the analysis of transcripts, proteins, insertional- and chemically-induced mutants. All this information facilitates the understanding of the function of genes in terms of their relationship to the phenotype. Despite its great relevance, such an understanding could be of little value to population and conservation genetics because it will not elucidate the relationship between genetic variation in gene sequences and phenotypic variation in traits but rather just that between a gene and a mutant phenotype. The relationships between complex trait variation and molecular diversity of genes can be studied based on a genomic approach but the identification of genes responsible for the variation remains a slow and time consuming process, especially in long lived organisms such as forest trees. Work in model plant species such as *Arabidopsis* and rice has however started to unveil an ever increasing number of genes involved in the determination of traits of adaptive significance such as phenology and abiotic stress tolerance/resistance. These progresses will finally allow ecological and conservation genetics to analyse directly variation in genes involved in adaptive processes rather than in neutral markers. Neutral markers will however remain important to make inferences on stochastic processes affecting natural population evolution. Populations may follow two main strategies to react to abiotic stresses originating from climate changes: 1) adapt to the new climatic conditions; 2) migrate to more favourable areas. Some neutral markers (e.g. highly polymorphic microsatellites and organelle markers) are very useful to monitor past and present migration processes. Plants offer excellent models to investigate how gene flow shapes the organization of genetic diversity. Their three genomes

(chloroplast, mitochondrial and nuclear) can have different modes of transmission and will hence experience varying levels of gene flow. Based on a very large data set, [1] demonstrates that mode of inheritance appears to have a major effect on genetic differentiation (G_{ST}). G_{ST} for chloroplast DNA and mitochondrial DNA markers covary narrowly when both genomes are maternally inherited. At the range-wide scale, historical levels of pollen flow are generally at least an order of magnitude larger than levels of seed flow and pollen and seed gene flow vary independently across species [1]. Moreover, [1] show that measures of subdivision that take into account the degree of similarity between haplotypes (N_{ST} or R_{ST}) make better use of the information inherent in haplotype data than standard measures based on allele frequencies only. Neutral organelle markers can be extremely useful for phylogeographic studies [2]. Phylogeographic structure of forest tree species can be influenced by several factors, among which history during the glaciations and in the post-glacial period, life history traits of the species and human impact are assumed to have played a major role. Phylogeography can provide essential background information to disentangle current from past processes and to understand the consequences of crucial events such as colonisation in the life and longevity of plant species [3]. The comprehension of the past dynamics of diversity can be extremely useful to predict the possible future migrations related to the expected climate changes [4]. In conservation and management of genetic resources, phylogeographic studies may help identify key regions deserving priority for conservation [3]. Phylogeographic survey may allow tracing of wood and other plant products, providing tools to combat illegal logging or to label products originating from sustainably managed regions [5]. Finally, the background on seed flow to emerge from phylogeographic surveys can be used to evaluate risks associated with the use of transplastomic plants [2, 6].

Technology is rapidly evolving also in neutral marker analysis, moving from markers such as microsatellites towards SNPs due to cost, efficiency and automation considerations. Due to the different characteristics of the two markers systems in terms of mutation processes and rates, they will both find use in ecological studies.

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