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Molecular genetic tools to infer the origin of forest plants and wood

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Abstract Most forest tree species exhibit high levels of genetic diversity that can be used to trace the origin of living plants or their products such as timber and processed wood. Recent progress to isolate DNA not only from living tissue but also from wood and wood products offers new opportunities to test the declared origin of material such as seedlings for plantation establishment or timber. However, since most forest tree populations are weakly differentiated, the identification of genetic markers to differentiate among spatially isolated populations is often difficult and time consuming. Two important fields of “forensic” applications are described: Molecular tools are applied to test the declared origin of forest reproductive material used for plantation establishment and of internationally traded timber and wood products. These applications are illustrated taking examples from Germany, where mechanisms have been developed to improve the control of the trade with forest seeds and seedlings, and from the trade with wood of the important Southeast Asian tree family Dipterocarpaceae. Prospects and limitations of the use of molecular genetic methods to conclude on the origin of forest plants, wood, and wood products are discussed.

Keywords DNA marker · Genetic fingerprint · Forensic application · Forest reproductive material · Tropical timber · Dipterocarpaceae

Introduction: genetic variation of forest trees

Genetic variation within most forest tree species is high in comparison to other organisms. Comprehensive reviews of isozyme variation revealed that forest trees are among the most genetically diverse groups of organisms (Hamrick and Godt 1996). Longevity, efficient gene flow mechanisms, and dominance of outcrossing are life history traits promoting the maintenance of high diversity within forest tree species (Austerlitz et al. 2000). Most studies on genetic variation patterns within tree species were primarily motivated by attempts to improve our understanding of biodiversity at the intraspecific level or the evolutionary dynamics within “natural” plant species or populations in an early stage of domestication. Main applications of marker-based diversity studies have been in molecular tree improvement (e.g., Krutovsky and Neale 2005) and conservation of forest genetic resources (e.g., Finkeldey and Ziehe 2004).

The focus of this review is on the use of the rapidly growing “genomic resources” of forest tree species in the context of forensic applications. Specifically, the knowledge of diversity patterns can be used to clarify the origin of populations, single plants, logs, or even processed wood. Forensic applications imply that optimum material for DNA extraction, for example young leaves, may not be available for investigation (Finkeldey et al. 2007a). Thus, DNA extraction from wood and other “difficult” plant tissue is briefly reviewed as a prerequisite for the development of molecular methods to clarify the origin of plant material.

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