Genetic structure of the CITES-listed rosewood species *Dalbergia oliveri* from Indochina: implications for conservation

Hoa Thi Tran1, Patrick Van Damme 2,3

1. Institute of Agricultural Genetics, Pham Van Dong Road, Hanoi, Vietnam
2. Ghent University, Coupure Links 653, B 9000 Gent, Belgium
3. Faculty of Tropical AgriSciences, Czech University of Life Sciences Prague, Kamycka 129, Prague 6 – Suchdol, 165 21, Czech Republic

Abstract

Forest genetic resources are threatened by a broad array of factors such as climate change, environmental pollution, habitat destruction and pest attacks. In developing countries, over-exploitation and the introduction of exotic species are often mentioned as decisive factors for the destruction of tropical forests. The capacity of forest trees to cope with these threats and to persist in spatially and temporarily heterogeneous environments depends on their adaptive potential, which is determined by genetic diversity. This is why conservation strategies for forest trees should be based on an evolutionary approach and focus on the maintenance of within-species genetic diversity.

High rates of deforestation and logging lead to local extinctions and have left a high number of tropical tree species threatened, among these the CITES-listed timber species *Dalbergia oliveri*. The aim of this study was to investigate genetic diversity in natural populations of *D. oliveri* in order to guide management plans for effective conservation of both natural populations and genetic resources for future breeding programs of the species.

We collected seeds, leaf or cambium samples from 16 populations of *D. oliveri* across the entire distribution of area in Vietnam and genotyped them with 28 microsatellite markers (in 8 multiplex-sets). We found evidence that the species reproduces clonally by root suckers, and is capable of self-pollination at rates around 20-30%. The level of genetic diversity was moderate (He=0.53) with high levels of diversity found in Chu Mom Ray National Park/mountain area (covering the combined Laos and Cambodia areas), and low diversity in the more peripheral populations in Laos and Vietnam. Genetic differentiation among populations was high (Gst=0.34), and strongly correlated to geographic distance between populations. Genetic clustering analysis showed a clear division of populations into five geographically defined groups. We recommend that (1) conservation plans should aim at conserving many different populations in order to maintain as much as possible the current genetic variation and (2) populations should be sufficiently large to minimize inbreeding and take into account the possible occurrence of clones.

*Keyword:* conservation genetics, Dalbergia species, threatened species, tropical trees, CITES, timber species