

Underlying processes governing genetic differentiation in the Western Ghats

During the last three years, supported by IPGRI and CIFOR, Prof. Bawa and coworkers, have addressed *in situ* conservation issues for bamboo and sandal in Southern India. These two important forest resources are closely interrelated with the economy of the Karnataka State as well as the livelihood of rural artisans.

This collaborative endeavor among the University of Massachusetts at Boston, the Ashoka Trust for Research in Ecology and the Environment (ATREE) and the University of Agricultural Sciences in Bangalore has produced spatially explicit information on the distribution of intraspecific genetic variability. It has also contributed to an in-depth understanding of the underlying processes that govern the genetic differentiation of the populations of these two species in the Western

Ghats of India. Thus the work provides new information for designing conservation strategies for the two species.

Since last update, the project has conducted additional studies on assessment of the conservation status of bamboo and sandal genetic resources in the Western Ghats, and the genetic basis of seed abortion in *Dalbergia sissoo*, which is one of the most important social forestry species in South India. (See related box)

THREATS TO SANDAL GENETIC RESOURCES IN KARNATAKA STATE

Sandal genetic resources are threatened by a variety of activities such as systematic logging, poaching and major changes in land use. The trees have a long history of being harvested with increasing intensity in the latter half of this century when timber export began in large scale. Between 1952 and 1973, the average annual extraction of sandal in the State of Karnataka was approximately 2300 tonnes, while in the period 1975-1996 the quantity extracted was curtailed to 1000 tonnes per year. Despite this reduction, the revenue realized from sandal in the last two decades underwent an extraordinary increase, from annual revenues of about 2 crores (in 1980-1981), up to 14 crores (in 1994-1996). Extraction of sandal by factories in Karnataka showed a gradual decline from nearly 900 tonnes/year

to less than 400 tonnes/year between 1980 and 1988 indicating perhaps the dwindling resource status of the trees: most of the extraction is in fact exerted on natural populations. The large-scale tree poaching further aggravates this pressure. Between 1980 and 1998, about 100 to 500 tonnes of sandal have been recovered annually from poaching. The loss of natural populations due to poaching alone is substantial and the above mentioned figure is likely to represent an underestimate of the actual figure. Effective measures to prevent the losses are therefore necessary to safeguard the natural populations of sandal as well as employment opportunities for traditional craftsmen.

Besides extensive harvesting and poaching, poor information is available on the distribution and genetic diversity of sandal populations in India. This research programme examined 13 sandal populations over the four southern States of India (Kerala, Tamilnadu, Karnataka and Andhra Pradesh) with the aim to identify hot-spots of genetic variability for *in situ* conservation. Population genetic variability was assessed using allozyme analysis involving six loci.

The observed heterozygosity over all populations and over all loci was 29.8 per cent, which is comparable with the estimates reported earlier for other tropical trees. The observed

GENETIC BASIS OF SEED ABORTION IN *Dalbergia sissoo*

Seed abortion in multi-ovulated species, especially those dispersed by wind and animals, is a widespread phenomenon. The abortion is mostly independent of the resource and pollen limitation and cannot be attributed to developmental lethal genes. Scientists hypothesize that the consistent patterns of intra-fruit seed abortion could be related to sibling competition among the developing seeds and that the extent of this competition might be a function of the genetic dissimilarity among the sibs developing in the fruit. The prediction has been tested in *Dalbergia sissoo*, a wind dispersed tropical tree. In most cases, only one (and in rare cases two or three) of the four-five ovules in a flower develops to maturity. Researchers compared the genetic similarity among pairs of seeds developing within a pod with a) random pairs from the pool of all seeds, b) random pairs from single seeded pods, c) random pairs from two seeded pods using both RAPDs and isozymes in five trees. Results of this study showed that the pairs of seeds developed within a pod are genetically more similar than any random pairs of seeds in a tree. Thus the formation of two seeded pods appear to be associated with increased genetic relatedness among the developing seeds. In other words, seed abortion in multiple seed fruits could be a consequence of rivalry among genetically unrelated sibs.

Photo Kamel Bawa



Forest-dwellers, settlement in India

heterozygosity was positively correlated with the density of sandal populations sampled, suggesting that gene flow and mating opportunities might be constrained in small fragmented populations or in populations with sparse distribution of trees. Populations from southern Karnataka (Savandurga, Siddarabeta and Devarayandurga), which are in the core of the geographical distribution of sandal, showed the highest observed heterozygosity (39.1 %) as compared to that from northern Karnataka (33.5%), Tamilnadu (30.0%), Andhra Pradesh (23.33%) and Kerala (29.4%).

The populations from southern Karnataka also had a slight excess of heterozygotes while in the rest of the populations, there was a deficit in heterozygotes. The higher genetic diversity of the populations from the Deccan plateau might be explained by the fact that being located in the core of the distribution range, these populations can easily exchange gene pool with many other populations. Population differentiation statistics indicated a clear separation of the individual populations based on their geographic origin. There appeared to be three major distinct clusters, namely those of a) the Deccan plateau, b) West Coast and Western Ghats, c) Eastern Ghats.

These results are important for the long-term *in situ* conservation of the genetic resources of sandal. First, based on the spatial patterns of distribution of the observed heterozygosity, it appears that populations from the Deccan plateau have the highest priority for conservation, to maintain the existing levels of heterozygosity and the gene pool. Second, due to the geographic correlation found among populations, it is proposed that representative collection of germplasm be made through an appropriate sampling strategy focusing on the populations in the Deccan plateau but also including representatives of other populations from the entire distribution range.

ARE SANDAL GENETIC RESOURCE SUFFICIENTLY PROTECTED IN WILDLIFE SANCTUARIES?

The impact of sandal extraction on the regeneration and genetic parameters of populations in and around Biligiri Rangan Temple Wildlife Sanctuary (Western Ghats) was assessed along a disturbance gradient, comparing the size-class structure and genetic diversity of three populations.

At each site, young unopened leaf tissues from 30 to 40 randomly chosen trees were collected and then processed for isozyme analysis. Four enzyme systems, PGM, GPI, MDH and PGDH

were selected based on the resolution and polymorphism exhibited.

The size class distribution clearly indicated that the proportion of large girth trees decreased gradually from the core to the external zone, indicating a greater level of extraction of mature trees that yield heartwood. Moreover, the core zone harbored a greater proportion of small size class individuals, indicating a greater turnover of population, in comparison with that found in buffer and external zones. The average number of alleles per loci, effective allele number and the Shannon diversity index, based on allele frequencies were found to increase marginally from core to buffer to the population outside the park. All populations showed an excess of heterozygotes, the core population showed 46% excess of heterozygotes compared to 36% found in the outside population.

Compared to the core area, few alleles were selectively affected in the periphery and exterior limits of the sanctuary. These results suggest that excessive harvesting of trees from natural populations is likely to lead to the genetic deterioration of the population itself. The present study provides evidence of the effectiveness of the sanctuary for *in situ* conservation of sandal genetic resources.

GENETIC DIVERSITY OF *Ochlandra scriptoria*, A GREGARIOUS SHRUBBY BAMBOO IN WESTERN GHATS

Ochlandra scriptoria is a gregarious shrubby bamboo with a relatively restricted distribution in the Western Ghats (Kerala, Karnataka and Tamilnadu States). Unlike many other species of bamboo, *O. scriptoria* flowers sporadically each year and does not exhibit monocarpic senescence. The species is extensively harvested and used in mat and basket making. In Karnataka, *O. scriptoria* occurs patchily in the Western Ghats districts of Dakshina Kannada, Madikeri and Chickmagalur. Despite its economic importance, not much is known about the distribution and the density of their populations.

Photo: Kamal Bawa



Timber and non-timber resources in India

Researchers analysed the genetic variability of five populations at Karnataka using allozyme analysis of six enzyme systems (PGM, PGDH, ME, SKDH, MR, PGI). Sampaje in Coorg exhibited the highest genetic diversity among the five population followed by populations at Subramanya, Bhagmandala, Sullia and Makut. No clear genetic differentiation of the populations based on their geographic distribution was noted, as found for *Bambusa arundinaceae* in the same region. Lack of differentiation may be due to the fact that *O. scriptoria*, unlike other species of bamboo, is a sporadically flowering and non-masting bamboo. Such a reproductive behaviour might facilitate gene pool exchange through either pollen or seeds. Principal component analysis of the allozyme data revealed two major clusters, without any clear geographic segregation. This suggests that conservation plans should be based on genetic variability rather than geographical distribution of the populations.

Further information on this project can be requested from:

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PUBLICATIONS PRODUCED ON PROJECT ACTIVITIES

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