

MATING PATTERNS OF CANOPY TREES IN THE NEW AND OLD WORLD TROPICS

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In the last two decades, surveys of floral morphology of rain forest canopy trees revealed that the majority of trees are hermaphroditic (Bawa *et al.* 1985). However, crossing experiments on hermaphroditic trees implicate low levels of inbreeding since many trees have partial or complete self-incompatibility systems (Bawa *et al.* 1985). Recently, the use of genetic markers in studies of population reproductive patterns has allowed us to quantify actual levels of inbreeding vs. outcrossing, and to examine the structuring of genetic diversity within and among populations. For example, allozyme surveys of Panamanian trees indicate mid to high levels of outcrossing; populations occurring at low densities had on average lower genetic variation and more self-fertilization than trees at higher densities (Murawski & Hamrick 1991).

We used allozyme markers to study mating patterns and genetic diversity of Central American and Sri Lankan rain forest canopy trees. Treetop samples were collected using sling shot, shotgun or rifle in Central America, and local tree-climbers in Sri Lanka. Fresh leaf or seed samples were frozen in liquid nitrogen, or lyophilized prior to shipment to the University of Massachusetts for electrophoretic analysis.

In general, we found evidence for high levels of genetic variation, a combination of outcrossing and mixed mating strategies, and extensive gene flow. Locally endemic populations of Sri Lankan dipterocarps in the genus *Stemonoporus* were exceptionally high in genetic diversity compared with Central American tree populations from this study and from previous studies (Hamrick & Loveless 1989). This high diversity might be explained in part by high local population

densities, high outcrossing rates, and a lack of severe population bottlenecks in the past. In addition, many *Stemonoporus* species occupy ecological islands (e.g., isolated hilltops) and their habitats persisted in situ during the last glaciation. This contrasts with the relatively more continuous habitats covering long distances in Central America that presumably were reinvaded from centers of diversity in Amazonia following the Pleistocene.

By taking a mixture of approaches, we are beginning to understand the importance of different evolutionary forces in structuring the genetic variation of rain forest trees. Although our studies involve neo- and paleotropical species, much more information would be needed to make an intercontinental comparison. For now, we suggest it would be more fruitful to compare reproductive differences between canopy and understory trees, and species with different life history strategies.

LITERATURE CITED

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