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NEWS AND VIEWS

PERSPECTIVE

New interpretations of fine-scale spatial genetic structure

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Abstract

Recent methodological advances permit refined inferences of evolutionary processes from the fine-scale spatial genetic structure of plant populations. In this issue of *Molecular Ecology*, Born *et al*. (2008) exploit the full power of these methods by examining effects of ancient and recent landscape histories in an African rainforest tree species. The authors first detected admixture of distinct gene pools that may have formed in Pleistocene forest refuges. Then, comparing across six study populations in Gabon, the authors found similar patterns of fine-scale spatial genetic structure despite natural and anthropogenic variation in population density. The latter results suggest that enhanced gene dispersal may compensate for low population densities in fragmented landscapes.

Keywords: assignment methods, forest history, Gabon, spatial genetic structure, tropical tree

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Limited dispersal in plants can generate clusters of closely related individuals, which manifests as fine-scale spatial genetic structure (SGS). SGS develops at landscape levels over ecological timescales (a few generations) and may be represented as a regression of kinship over the logarithm of distance (kinship–distance curve). Development of SGS is the first stage in Wright's (1943) model of isolation by distance (IBD) for continuous populations. The recently developed *Sp* statistic, which quantifies the strength of SGS, can be used to compare SGS among populations and species (Vekemans & Hardy 2004). Recent meta-analyses have shown that species with self-compatibility, low population densities or poorly dispersed seeds tend to exhibit strong SGS (Vekemans, Hardy 2004; Hardy *et al*. 2006). Born *et al*. (2008) are among the first researchers to examine intraspecific landscape patterns of SGS variation. Their primary objective was to examine the effect of landscape history on SGS and gene dispersal in the African rainforest tree *Aucoumea klaineana* Pierre (Burseraceae).

Fig. 1 Seasonal fires maintain a forest-savannah mosaic in lowland Gabon. Photo credit: C. Born.

Aucoumea klaineana is a member of a tropical tree family known for its fragrant resins, which include frankincense, myrrh and copal, and it is the most economically important timber species in Gabon. *Aucoumea klaineana* is a predominantly bee-pollinated, wind-dispersed species that colonizes savannah and, in the absence of fire, persists as a long-lived member of established rain forest (Figs 1 and 2). The authors sampled *A. klaineana* along > 10-km transects through six continuous forests in Gabon, including one site (Mounana) that had experienced intensive slash and burn agriculture ending about 15 years ago. The sampled trees (approximately 100 per site) were genotyped at 10 microsatellite loci.

Kinship–distance curves are appropriate to characterize SGS resulting from an isolation-by-distance process, but SGS patterns can also arise from genetic discontinuities, hybridization, or spatial clines in allele frequencies. An original aspect of the paper is that Bayesian clustering methods are first applied to detect discrete population substructure, which helps in correctly interpreting kinship–distance curves.

The cluster analyses showed that one transect (Boumango) spanned two distinct gene pools, which may have been formed in forest refuges. In her dissertation research, Born (2007) showed that gene pools with high genetic diversity were centred on moist upper elevation sites, while dryer lowland populations of *A. klaineana* harboured less genetic variation except in zones of admixture. The moist upper elevation sites were likely to have been forested during the last glacial

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Fig. 2 *Aucoumea klaineana* (sapling in foreground) is among the first rainforest tree species to colonize savannah in Gabon. Photo credit: C. Born.

maximum and through dry phases of the mid-Holocene. While genetic admixture produced a distinct SGS pattern in Boumango, the extent of SGS (*Sp* statistic) did not differ from other sites.

The authors found no significant differences in the intensity of SGS across sites. Since SGS is largely the product of effective population density (D_e) and mean gene dispersal distances (σ_g), the authors suggest that a similar SGS in the low-density populations may result from enhanced gene dispersal. This is an intriguing idea. Long-distance pollen dispersal has been reported among scattered trees in tropical forest and pasture landscapes (Dick *et al*. 2008). By reducing aerial obstruction, deforestation can also enhance seed dispersal of wind-dispersed tree species (Bacles *et al*. 2006).

The SGS-based estimates of mean gene dispersal for *A. klaineana* ranged from 210 to 570 m, depending on the estimate of D_e used. These are higher than direct estimates of gene flow for this species (~88 m) and they are higher than direct measures of seed dispersal in other wind-dispersed tropical forest trees (e.g. Jones *et al*. 2005), but they fall within the range of pollen dispersal distances for other predominantly bee-pollinated tree species (Dick *et al*. 2008).

The SGS method offers several advantages for estimating gene dispersal in forest trees. For example, the method does not require seed collections or genotypes of potential pollen donors. Further research is needed to examine the precision of SGS-based gene dispersal estimates, however. Comparing direct estimates of seed and pollen dispersal to the SGS estimates can do this. Such comparisons will also permit testing of new methods used to disentangle the relative contributions of pollen and seed dispersal to SGS (Heuertz *et al*. 2003). The decoupling of seed and pollen-mediated gene dispersal is possible for *A. klaineana* because, like many tropical tree species, it is dioecious and hence the male and female parents can be discerned.

Born and colleagues use SGS analyses to their fullest potential at multiple spatial scales. Further refinement and application of these methods will help to unravel the interplay of ecology and historical contingency in other species and biomes.

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Christopher Dick's research is focused on the biogeographic history and evolutionary processes that underlie the rich diversity of tropical forest trees.

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