

## NEWS AND COMMENTARY

Plant population biology

# Paternal analysis in a fragmented landscape

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One of the key issues facing evolutionary biology, and indeed any scientific endeavour, is the effectiveness of knowledge transfer from basic science to application. Bittencourt and Sebbenn (2007) present a study that addresses the basic biology of the genetic structure of tree populations and gene flow between them in a manner that will also inform conservation biology and those concerned with genetic management and conservation in a fragmented landscape.

One of the more useful findings presented by Bittencourt and Sebbenn, that seed distribution is more limited than pollen distribution as a means of gene dispersal within and between populations, seems intuitively obvious. However, the implications regarding genetic isolation of forest fragments are not as obvious. Fragmentation of forested landscapes is widespread, and has existed in some areas, such as North America and Europe, for decades or even centuries. In other parts of the world, including Brazil, the locale for their study, such forest fragmentation is taking place now and at a rapid pace. The short-term implications of ongoing forest fragmentation for biodiversity loss are immediately apparent; what is less apparent is the ability of such fragmented forests to recover when landscape management priorities change.

Second growth forests, widespread in the Eastern US, are an example of such recovery. To what extent does the genetic composition of such forests, and the potential biological resource that such variation represents, resemble primary forests? A case has been made that trees may be sufficiently long-lived that remnant forest fragments can effectively serve as genetic reservoirs from which forests can ultimately recover if management priorities allow them to do so (Hamrick, 2004). The same may be true for long-lived understory herbaceous plants, although they may lack the long-distance pollen dispersal of trees in remnant fragments. The genetic interconnectedness of forest fragments, as

demonstrated by Bittencourt and Sebbenn, suggests that pollen flow may be an important contributing force in the maintenance of genetic diversity across a landscape, lending further hope that forest fragments may have scope for recovery under appropriate land management practices.

Difference in magnitude between seed and pollen dispersal also has strong implications for the spatial genetic neighbourhood composition of local populations. Wright (1945) introduced the concept of local genetic neighbourhoods in large populations, and indeed his method of hierarchical F-statistic analysis (Wright, 1965) is a widespread method for assessing their impacts on genetic variation. However, as useful as F-statistics have been, this is an indirect approach that assesses consequences of genetic dynamics in terms of departures from Hardy–Weinberg equilibrium genotype frequencies rather than directly assessing mating and dispersal events. The methods used by Bittencourt and Sebbenn, paternal analysis to articulate mating events and estimation of pairwise relationships to assess dispersal, are examples of more direct genealogical inference methods that are being taken up by population biologists. Their basic work represents a good example of the effectiveness of such direct methods for analysing and interpreting genetic dynamics of natural populations.

In terms of the interplay between basic and applied biology, the main methods used by Bittencourt and Sebbenn, likelihood-based paternal analysis and genealogical inference, have an interesting history. The genetic likelihood approach to paternal analysis, introduced into plant population biology by Meagher (1986) along with a more general statistical framework for genealogical inference (Meagher and Thompson, 1986), was originally derived from statistical approaches to genealogical inference developed in human biology (reviewed in Thompson, 1986) and bears strong similarity to forensic methods of paternal assign-

ment. In addition to its widespread use in the study of genetic dynamics of plant populations, this approach has a widespread application, including genetic management in tree plantations (Burczyk *et al.*, 2002), analysis of potential gene flow from transgenic crops to adjacent feral plant populations (Meagher *et al.*, 2003; Smouse *et al.*, 2007), and, as in Bittencourt and Sebbenn, conservation biology. Thus, paternal analysis has gone full circle from application in human biology, to use in understanding the evolutionary dynamics of natural populations, to new applications in genetic management and conservation.

An ongoing challenge facing evolutionary biology is whether the interest in the products of that science is sufficient to justify societal investment (Meagher, 2007). Studies of the genetic dynamics and dispersal properties of natural populations, even if conducted in the context of basic science, clearly address this challenge. They provide important insight into the evolutionary process that ultimately results in adaptation to new or changing conditions. Moreover, with the growing concern over biodiversity loss, and the concomitant demand for biodiversity assessment and management, such studies are accumulating considerable added value as an important baseline in conservation biology. There has been a growth industry in meta-analysis across related studies to answer broader questions in conservation biology, such as understanding general trends associated with invasiveness or the underlying causes of rarity. Studies that show how results obtained out of basic scientific interest in understanding the evolutionary dynamics of populations can be recast in a conservation context to add value to the whole scientific enterprise.

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