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Dorothy's Dilemma and the Unification of Plant Population Biology

Jonathan Silvertown

A consensus has existed for many years that a greater synthesis should be possible between population ecology and population genetics, but the synthesis is still to emerge. At the British Ecological Society symposium entitled Genes in Ecology, held in Norwich, UK, in April this year, the organizers attempted to encourage synthesis by teaming an ecologist with a geneticist in every presentation. In fact, rather than bridging it, this bold device emphasized the gap that still separates genetics and ecology. Disappointingly few of the contributors reflected at all on why the gap exists. Specifically in plant population biology, there is a dilemma that few interested in a synthesis of ecology and genetics have yet confronted.

Synthesis between plant genetics, physiology and ecology was one of the goals of the recently concluded interdisciplinary study of the genus Plantago in The Netherlands, and it is now a central objective of the European Network in Population Biology. If the synthesis is still elusive, this is not because of any lack of desire on the part of plant population ecologists to take an evolutionary view. Some have suggested that the problem will be solved when we can identify and track genotypes more easily and they look forward to the fruits of molecular and other techniques that will make this possible. These methods will certainly yield a huge quantity of new information, but will they lead to a qualitative advance over what we already know from the use of less-sophisticated genetic markers? The barrier between population genetics and population ecology may be mainly conceptual, not technological.

For any synthesis to occur between two disciplines they must share a common set of core variables. The components of fitness (fecundity and survival) are demographic variables, so on the face of it the conditions do exist for the merger of population genetics with population ecology, but population ecologists who census individuals and geneticists who census alleles still seem to be having trouble finding common ground. A large part of the problem arises from a fundamental difference in the relative importance that population genetics and plant population ecology accord to population structure.

Key genetic concepts such as the founder effect, genetic drift, genetic differentiation, gene flow, shifting balance, allopatic speciation, neighbour area, effective population size and the hierarchical organization of genetic diversity all assume that populations have spatial structure or are organized into metapopulations. Metapopulations, or networks of populations linked by migration, are a familiar concept in population genetics and animal ecology, but plant population ecologists usually ignore this kind of spatial structure, though it is everywhere we (don't) look. At present, plant population ecology has a limited vision, bounded by the population edge. Most plant population studies concentrate on a small
Instead, we need to survey potential colonization sites in the areas around existing local populations and watch for new populations to show up. Potential colonization sites have to be identified experimentally by the addition of seeds to likely areas, and colonization rates measured as a function of distance from seed source by creating artificial sites. Population extinction rates need to be measured by monitoring large numbers of natural or artificial local populations. One of the very few such studies to date showed that local populations of semelparous perennials in a sand-dune system in The Netherlands had high extinction rates. These experiments and observations would provide parameters of population structure and population projection models that could be used to determine extinction rates for local populations. In fact, because forest trees require canopy gaps for successful recruitment and because these colonization sites are easily identified and counted, tree populations are highly suited to a metapopulation approach. A recent ecological study of the metapopulation dynamics of the neotropical pioneer tree Cecropia obtusifolia in Mexico is a good example. This was not a genetic study, but rates of seed dispersal measured between old and new sites could easily be used to estimate gene flow between local populations. Of course, other genetic parameters could also be measured various explicit spatial structures elucidated by such an ecological study.

**References**


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**The yellow brick road**

To anyone seeking directions to the rainbow’s end, the reply ‘If I was going there, I wouldn’t start from here’ may seem singularly unhelpful, but we cannot hope to find the all-important tail of the seed-dispersal curve by starting at the seed source.