



Seed dispersal and gene flow in red oak: A Bayesian approach integrating genetic and ecological data

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The future of biodiversity will depend on species' capacity to migrate or adapt in response to climate change. Gene flow via seed and pollen is important to both processes, yet has been challenging to estimate in forest trees. I developed a hierarchical Bayesian model that combines ecological and genetic data in order to estimate the scale of seed and pollen movement, and applied it to two populations of red oaks in North Carolina (figure 1). I also tested whether the scale of dispersal varies between sites. All adult trees and sampled seedlings were genotyped at 6 microsatellite loci.



Figure 1. Little genetic differentiation was found between *Quercus rubra*, *Q. falcata*, *Q. velutina*, and *Q. coccinea*; all are treated as one population.

The model estimates a pedigree for all sampled seedlings and dispersal parameters. The probability of the parameters given the data is proportional to the probability (over all seedlings) that a) tree j pollinates tree i and that seed from tree i disperses to the location of seedling k, and b) that trees i and j produce an offspring with the observed genotype given genotyping error rates (figure 2). Dispersal of pollen and seed from outside the mapped area is considered, assuming tree densities outside are similar to those inside.

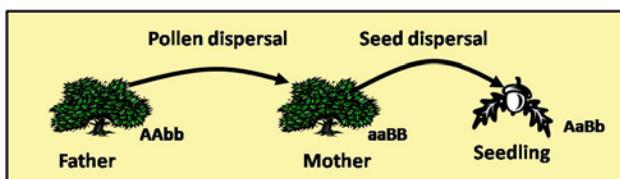


Figure 2. Seed and pollen dispersal

Pollen dispersal was extensive at both sites (mean distances 146 m & 178 m), as expected for a wind-pollinated plant. Seed dispersal was much more restricted at the Appalachian site than the Piedmont site (mean distance 15 m vs. 125 m). This was not due to differences in disperser number, as densities of squirrels were similar at both sites, but may be related to differences in disperser behavior.

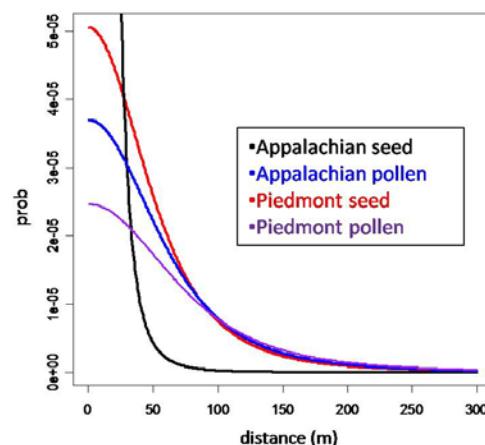


Figure 2. Fitted dispersal kernels

This dispersal model is the first that both accounts for genotyping error and treats dispersal from within and beyond a plot in a fully consistent manner. The results shown here indicate that there can be considerable spatial variation in seed dispersal distance within a species, which may affect tree species ability to respond to climate change by colonizing newly suitable areas.

For more information, see:

- Moran, E.V., & J.S. Clark. In press. Estimating seed and pollen movement in a monoecious plant: a hierarchical Bayesian approach integrating genetic and ecological data. *Molecular Ecology*.
- Moran, E.V., & J.S. Clark. In review. Contrasting patterns of dispersal and gene flow in two populations of red oak. *Molecular Ecology*.