

Pollen Dispersal in Tree Populations with Different Spatial Aggregation Patterns

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Assessment of real-time landscape-scale pollen flow is a central topic in evolutionary and conservation biology of tree species [1]. Using an individual-based model fitted to experimental data, we explore in this work the effect of varied spatial aggregation patterns of woodlands on within-population pollen dispersal parameters. We consider a bivariate exponential power function to describe the potential pollen dispersal kernel for individual trees [2]:

$$p(x, y) = \frac{b}{2\pi a^2 \Gamma\left(\frac{2}{b}\right)} \exp\left(-\left(\frac{\sqrt{x^2 + y^2}}{a}\right)^b\right), \quad (1)$$

where $p(x, y)$ denotes the probability per unit area of pollen dispersal to a point at a distance $\sqrt{x^2 + y^2}$, Γ is the gamma function, a is the scale parameter for distance, and b is the shape parameter. Using a recently developed maximum likelihood procedure [3], we fitted this function to paternity-analysis data of an isolated *Pinus sylvestris* L. population.

Then we will generate a wide set of (200 ha, 10,000 trees) populations with different aggregation patterns via a Poisson-cluster spatial point process [4], defined by (ρ, σ) , where ρ is the clump density, and σ is the

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variance of a radially symmetric Gaussian distribution defining point dispersal around each clump. After simulating isotropous pollen dispersal from individual trees within each population using (1), we will compare the effect of aggregation on effective dispersal by computing the average effective pollination distance, the average effective number of pollinating males for single mothers, and the self-fertilization rate for each (ρ, σ) pair.

References

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