

Sampling Scheme on Genetic Structure of Tree Species in Fragmented Tropical Dry Forest: an Evaluation From Landscape Genetic Simulations¹

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Investigating how genetic variation is distributed across the landscape is fundamental to inform forest conservation and restoration. Detecting spatial genetic discontinuities has value for defining management units, germplasm collection, and target sites for reforestation; however, inappropriate sampling schemes can misidentify patterns of genetic structure. Appropriate sampling is more critical in fragmented landscapes where patterns of genetic diversity and structure might not yet reflect the current landscape structure. Landscape genetic simulations are useful for assessing the uncertainty of sampling schemes and the statistical power of hypothesis testing under varying scenarios. Here, we explore the effects of sampling design, sampling effort, and microsatellite number on the ability to detect patterns of genetic structure in two tropical dry forest tree species. The tropical dry forest is a species-rich ecosystem in México that is experiencing fast fragmentation rates due to habitat conversion to agriculture, expansion of rangeland for livestock, urban development, and overharvesting. The decline of tropical dry forests threatens biodiversity and the livelihood of rural communities that are dependent on forest resources. We used spatially explicit landscape simulations to model gene flow in two species that vary in spatial distribution and life history traits. (*Bursera* spp.: discrete populations, dioicous, and shorter dispersal distances vs. *Acacia* spp.: continuous distribution, monoicous, and larger dispersal distances). Gene flow was modeled under isolation by distance (IBD) to ask the following: Which is the best performing spatial sampling design? Does performance of spatial sampling design vary with sampling effort and the number of microsatellite loci? Results revealed that random sampling was the best performing sampling scheme, irrespective of sampling intensity, while the cluster and the systematic sampling did not perform well for both species. The number of microsatellites affect estimation of IBD, because using a low number of loci ($n = 8$) underestimated IBD. Our study highlights the usefulness of computer simulations for advance planning in empirical landscape genetic studies (Rico, Y. 2017. Using computer simulations to assess sampling effects on spatial genetic structure in forest tree species. *New Forests*. 48: 225–243. DOI: 10.1007/s11056-017-9571-y.).

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