

**APPLYING LANDSCAPE GENETICS TO EVALUATE THE CONSEQUENCES OF FOREST FRAGMENTATION AND AGRICULTURAL INTENSIFICATION ON GENETIC DIVERSITY AND GENETIC STRUCTURE OF UNDERSTORY TREE *SYMPHONIA GLOBULIFERA* (CLUSIACEAE).**

*Andre Sanfiorenzo*<sup>1</sup>, *Lisette Waits*<sup>2</sup> and *Bryan Finegan*<sup>3</sup>

<sup>1</sup> Agriculture Technology, University of Puerto Rico, Utuado, Puerto Rico.

<sup>2</sup> Department of Fish and Wildlife Sciences, University of Idaho, Moscow Idaho 83844-1136, United States

<sup>3</sup> Production and Conservation in Forests Program, Tropical Agricultural Research and Higher Education Center (CATIE), Turrialba 30501, Costa Rica  
Corresponding Author: andre.sanfiorenzo@upr.edu

Forest fragmentation and consequent land cover change are known to have an overall strong negative impact on plant reproduction with different effects on individual plant species. Most studies of the impacts of fragmentation on tropical tree species have focused on canopy tree species, especially those that are valuable for timber, which represent a low fraction of plant species present in tropical forests. Using nine nuclear DNA microsatellite loci, we examined the effects of forest fragmentation and landscape composition on the genetic diversity and structure of understory *Symphonia globulifera* in the wet lowland tropical forests of northeastern Costa Rica. Our study site encompasses the San Juan-La Selva biological corridor and surrounding areas, and within this fragmented landscape we compare genetic diversity and genetic structure across three life stages (adults, saplings, seedlings) using 324 samples per cohort and 9 nuclear DNA microsatellite loci. We predicted lower genetic diversity and increased genetic structure between the younger life stages since these individuals were likely established under current fragmentation conditions and limited movement of seed and pollen will promote greater differentiation between populations. Results followed these expectations with significantly lower numbers of alleles, observed heterozygosity, Shannon's information index, and allelic richness in seedlings compared to adults. Inbreeding, measured by  $F_{IS}$ , exhibited an increasing trend from adults (0.009) to seedlings (0.029). We predicted genetic diversity of seedlings and saplings would be correlated with the percent of forest in the contemporary surrounding landscape while there would be no correlation for adults. Land cover maps for the years 1986, 1996, 2001 and 2011 were used to relate landscape composition with genetic parameters. The amount of forest and pasture surrounding remnant mature forest patches positively correlated with the observed patterns of genetic diversity. Genetic differentiation among adult trees was low (mean pairwise  $G'st = 0.15$ ), probably reflecting larger population sizes and broad gene flow in the past. Genetic differentiation of seedlings was significantly higher (mean pairwise  $G'st = 0.22$ ) probably reflecting smaller population sizes and restricted gene flow in the present. Results from this study provide evidence that forest fragmentation and land use change have significantly reduced genetic diversity, increased inbreeding and reduced gene flow for *S. globulifera* understory populations.