



Effect of selective logging on genetic diversity and gene flow in *Cariniana legalis* sampled from a cacao agroforestry system

J.B. Leal, R.P. Santos and F.A. Gaiotto

Departamento de Ciências Biológicas, Centro de Biotecnologia e Genética,
Universidade Estadual de Santa Cruz, Ilhéus, BA, Brasil

Corresponding author: F.A. Gaiotto

E-mail: gaiotto@uesc.br

Genet. Mol. Res. 13 (1): 626-635 (2014)

Received January 10, 2013

Accepted July 17, 2013

Published January 28, 2014

DOI <http://dx.doi.org/10.4238/2014.January.28.8>

ABSTRACT. The fragments of the Atlantic Forest of southern Bahia have a long history of intense logging and selective cutting. Some tree species, such as jequitibá rosa (*Cariniana legalis*), have experienced a reduction in their populations with respect to both area and density. To evaluate the possible effects of selective logging on genetic diversity, gene flow, and spatial genetic structure, 51 *C. legalis* individuals were sampled, representing the total remaining population from the cacao agroforestry system. A total of 120 alleles were observed from the 11 microsatellite loci analyzed. The average observed heterozygosity (0.486) was less than the expected heterozygosity (0.721), indicating a loss of genetic diversity in this population. A high fixation index ($F_{IS} = 0.325$) was found, which is possibly due to a reduction in population size, resulting in increased mating among relatives. The maximum (1055 m) and minimum (0.095 m) distances traveled by pollen or seeds were inferred based on paternity tests. We found 36.84% of unique parents among all sampled seedlings. The progenitors of the remaining seedlings (63.16%) were most likely out of the sampled area. Positive and significant spatial genetic structure was identified in this

population among classes 10 to 30 m away with an average coancestry coefficient between pairs of individuals of 0.12. These results suggest that the agroforestry system of cacao cultivation is contributing to maintaining levels of diversity and gene flow in the studied population, thus minimizing the effects of selective logging.

Key words: Spatial genetic structure; Microsatellites; Atlantic Forest; Jequitibá rosa; *Cariniana legalis*