

Reduced genetic diversity in endemic Brazilian *Lymania* spp (Bromeliaceae) populations and implications for conservation

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ABSTRACT. We analyzed the genetic diversity of populations of two sympatric species of *Lymania* (Bromeliaceae), both endemic to the Atlantic rainforest of southern Bahia (Brazil). *Lymania azurea* has a restricted occurrence, while *Lymania smithii* has a wider distribution. Our aim was to provide genetic data to contribute to the design of more efficient conservation strategies for these bromeliads, possibly justifying inclusion in the official Brazilian list of Endangered Species. Up to now, *L. azurea* has been classified by the Brazilian Ministry of the Environment as "data deficient". We sampled four populations of *L. azurea* throughout its distribution area in southern Bahia and two populations of *L. smithii* in the same region. Genotyping was performed with 48 random amplified polymorphic DNA markers. Based on the

Jaccard genetic similarity index, *L. smithii* has greater diversity than *L. azurea*. An analysis of molecular variation showed greater genetic variance within than between populations for both species. *L. azurea* was found to have 20% inbreeding, probably due to population fragmentation, with *L. smithii* showing only 10%. When we analyzed pairs of populations of *L. azurea* within a conservation unit, we found low population structure ($\Phi_{ST} = 0.098$), apparently due to a large degree of gene flow between them. In disturbed areas, we found a higher Φ_{ST} (0.372). We found low genetic variability for *L. azurea*, probably as a consequence of habitat fragmentation, supporting the need for its inclusion in the Brazilian list of endangered flora.

Key words: Endangered species; Tropical forest; Genetic structure; Dominant marker; Fragmentation