

Genetic diversity of *Avicennia schaueriana* and *A. germinans* along the Brazilian coast: population structure, migration and admixture

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Abstract

Conservation biology, as others “crisis disciplines”, has expanded its repertoire of techniques and tools to provide multidisciplinary information to support conservation decisions. The development of molecular biology, for instance, has made possible the establishment of conservation genetics as an important branch of this discipline. In this context, our main objective is to better understand the processes that shape the genetic diversity of *Avicennia schaueriana*, an American Atlantic restricted mangrove species, and *A. germinans*, whose distribution approximately coincides with the western mangrove forests distribution. We developed specific polymorphic microsatellite markers for each species, 10 and 14, respectively, and sampled 515 individuals from the entire distribution of mangrove forests in Brazil, covering more than 4800km of coastline. After performing frequentist and bayesian analyses, we observed that the genetic diversity of the 11 sample locales of *A. schaueriana* is structured in five gene pools (populations, in a broad sense) which do not necessarily correspond to geographically close localities. We also found a high rate of migrants and admixed individuals, as expected by the mangrove trees’ water-based dispersal, showing the connectivity among these groups despite the geographic distances among localities. Using similar approaches, we analyzed four samples of *A. germinans* from the northern Brazilian coast, which include two geographically close locales but with different tide influence. We found a high level of inbreeding but also some admixed individuals and migrants, and a substantial population structure including between the two physically close samples. These results highlight the role of the tide as an important factor that shapes the genetic diversity of *A. germinans*. We found no evidence of ongoing hybridization between *A. schaueriana* and *A. germinans*. We are currently using other genetic molecular markers to deepen the knowledge about evolutionary factors of *Avicennia* and, then, support long-term future management and conservation efforts.

Keywords

black mangrove, population genetics, SSR