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Analysis of the population genetic structure of *Tabebuia ochracea* applied to conservation

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Tabebuia ochracea is a common Bignoniaceae of the Brazilian savannah, plant formation currently threatened by agricultural expansion. The analysis of the genetic structure of T. ochracea populations will help to understand how diversity is organized within the Cerrado Biome, supporting conservation actions. We sampled 24 populations of T. ochracea throughout the Brazilian savanna and obtained genetic data from three intergenic spacers of chloroplast DNA (cpDNA) and the region ITS from nuclear ribosomal DNA. To test the hypothesis of population differentiation, we performed an AMOVA and estimated the Fsr index. Population structure was accessed using Bayesian clustering implemented in the software BAPS v6.0. The analysis of molecular variance showed significant genetic differentiation among populations de T. ochracea for both cpDNA ($F_{ST} = 0.742$; p < 0.001) and nuclear ITS ($F_{ST} = 0.544$; p <0.001). In general, populations from Parque Estadual da Lagoa do Cajueiro (PLC) and Parque Estadual da Mata Seca (PMS), both found in the Minas Gerais state, had the highest rates of differentiation. Bayesian clustering showed an optimal partition of 4 clusters for both ITS and cpDNA, but with no clear geographical pattern. For ITS, almost all populations were clustered together in one group (cluster I), but individuals from populations Araguaia and São Sebastião from Northest, Serra da Canastra from Southeast and Pandeiros from Central-West were grouped in cluster II. Chloroplast genome showed higher admixture, with most populations grouped in cluster III, but with admixture with the clusters I and IV. Populations from PLC and PMS formed a different cluster for both ITS (cluster IV) and chloroplast (cluster II). The high population structure detected in PLC and PMS calls attention to the need to increase conservation efforts in the northern of Minas, contrary to the promotion of agricultural expansion currently observed.

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