



# Intravarietal polymorphisms reveal possible common ancestor of native *Schinus terebinthifolius* Raddi populations in Brazil

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**ABSTRACT.** *Schinus terebinthifolius* Raddi is a perennial native from Atlantic forest. It is of high ecological plasticity and is used in traditional medicine. Based on promising reports concerning its bioactivity, it was included as a species of great interest for distribution through the National Health System. A number of agronomic studies to guide its crop production are therefore underway. This study examined diversity and phylogenetic relationships among native *S. terebinthifolius* populations from different Brazilian ecosystems: Cerrado; sandbanks; dense rainforest; and deciduous forest. The intergenic regions rpl20-5'rps12, trnH-psbA, and trnS-trnG were sequenced from cpDNA and aligned using BLASTn. There

were few fragments for comparison in GenBank and so only region trnS-trnG was informative. There were variations among and within populations with intravarietal polymorphisms and three distinct haplotypes (HpSM, HpDDO, HpNE), once populations from NE (sandbanks and rainforest) clustered together. Sequences from HpSM, HpNE, and HpDDO returned greater similarity to haplotypes A (AY928398.1), B (AY928399.1), and C (AY928400.1), respectively. A network, built by median-joining among native haplotypes and 10 available on GenBank, revealed HpSM as the origin of all other haplogroups. HpDDO showed the most mutations and was closely related to haplogroups from Argentina. While this could indicate hybridization, we believe that the polymorphisms resulted from adaptation to events such as deforestation, fire, rising temperature, and seasonal drought during the transition from Atlantic forest to Cerrado. While more detailed phylogeographical studies are needed, these results indicate eligible groups for distinct climates as an important step for pre-breeding programs before field propagation.

**Key words:** Brazilian peppertree; *Schinus terebinthifolius*; Medicinal plant; Haplotypes; Population genetics