

**Genetic diversity of mocū cotton (*Gossypium hirsutum* race *marie galante*) from the North-East of Brazil: implications for conservation.**

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Mocu cotton (*Gossypium hirsutum* race *marie galante*) is a potential source of valuable alleles for breeding programs, mainly due to its great adaptability to semi arid conditions. With the aim of quantifying mocu cotton genetic variability, 187 plants collected in the North-East of Brazil were evaluated using 12 microsatellite markers. A total of 63 alleles were amplified, ranging from three to eight polymorphic alleles per locus. Total genetic diversity was high (0.52), and when measured on a per state basis, was of 0.37 on average. The population showed a low level of heterozygosity ( $HO=0.16$ ), reflecting a high level of endogamy ( $FIS=0.69$ ). Phylogenetic analysis using the neighbour-joining method revealed that plants sampled in different states tended to cluster according to their geographic origin, except for those collected in the states of Paraíba and Rio Grande do Norte which grouped together. Plants from the state of Piauí formed two groups, one with an apparent allelic contribution from *G. barbadense*, while the second group of plants was closer to those from the states of Paraíba and Rio Grande do Norte. Despite the high genetic diversity that was observed in the remaining populations, urgent conservation efforts should be undertaken due to the high level of endogamy and accelerated extinction process that characterizes these populations. Such efforts should focus on the collection and *ex situ* maintenance of representative genetic diversity.

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