



Diversity and genetic structure among subpopulations of *Gossypium mustelinum* (Malvaceae)

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ABSTRACT. *Gossypium mustelinum* is the only cotton species native to Brazil; it is endemic to the semi-arid region of the northeast. The populations are found near perennial and semi-perennial sources of water, such as ponds or pools in intermittent streams. Problems with *in situ* conservation derive from human interference in its habitat, mainly because of excessive cattle grazing and deforestation. Establishing efficient strategies for *in situ* conservation requires knowledge of the genetic structure of the populations. We evaluated the structure and genetic variability of populations of *G. mustelinum* in the Tocó

and Capivara Rivers (State of Bahia). Two hundred and eighteen mature *G. mustelinum* plants were genotyped with SSR markers. The molecular data were used to estimate the allelic frequencies, the heterozygosity, the F statistics, and the genetic distance among the populations and among individuals. We found high genetic diversity among the populations. The F_{ST} indexes for each population were also high and strongly correlated with physical distance. The high estimated level of endogamy and the low observed heterozygosity are indicative that the populations reproduce mainly by self-fertilization and crosses between related individuals. Consequently, strategies for *in situ* preservation should include at least three occurrence sites of *G. mustelinum* from each population. For *ex situ* conservation, the collections should include as many sites as possible.

Key words: Conservation; Genetic structure; *Gossypium mustelinum*; Microsatellites; Wild cotton