

Genetic structure and assembling of core collection of tropical forage *Calopogonium mucunoides*

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A large *C. mucunoides* germplasm collection that comprises more than 200 accessions is available at the EMBRAPA Cerrados. However, the genetic diversity of the germplasm collection has not been evaluated in detail. The application of genomic tools such as microsatellite markers include long-term germplasm conservation and have been used to demonstrate that accessions or cultivars are true to standard types, to help ensure proper population maintenance, to determine the degree of relatedness among individuals or groups of accessions and to clarify the genetic structure or the partitioning of genetic variation among individuals, accessions, populations and species. This work presents the molecular genetic variation found in 195 *C. mucunoides* accessions from the Embrapa Cerrados germplasm collection and also, an assembled core collection for this species using microsatellite loci. STRUCTURE software was used to generate a Bayesian inference of the population structure. A cluster analysis was performed using the neighbor-joining (NJ) method. The reliability of the generated dendrogram was also tested by bootstrap analysis using the BooD program with 1,000 iterations. Finally, we assembled a core collection that represented the entire genetic diversity explored in the study using CoreFinder software. The algorithm for extracting the core collection was obtained heuristically by solving the (NP-complete) Set-Covering problem. Among the 17 microsatellite loci analysed, 93 alleles were identified. The number of alleles ranged from 3 to 8, with an average of 5.5 alleles per locus. STRUCTURE analysis coupled with the computation of Evanno ΔK statistics suggested a primary partition of 195 *C. mucunoides* accessions into 6 clusters ($K = 6$), with only a few admixed accessions. The clustering showed a particular assignment of the accessions from Venezuela with one of Bolivia, as well as a genetic relationship among the accessions from Brazil, Colombia and Panama. Furthermore, there was a close relationship between the accessions from Peru and Mexico, as well as the formation of the isolated cluster of accessions from Indonesia. The genetic relationships among the *C. mucunoides* accessions reflected their geographic distribution with exceptions of some accessions of unknown origin. A geographical origin was an important parameter for genetic differentiation among clusters. A core collection for *C. mucunoides* was assembled to capture the allelic diversity found in this study. The complete allelic diversity was represented by only 15 accessions. The core collection was represented by accessions from Colombia, Brazil, Peru, Panama, Mexico, Indonesia and Venezuela. This result can be justified by mixed reproduction system of *C. mucunoides* with a predominance of autogamy. This factor can contribute to higher proportions of homozygous accessions or crosses between close relatives within natural conditions. These results should be useful for exploiting the genetic resources of *C. mucunoides* and could influence future conservation efforts and breeding programs. Financial Support: FAPESP and CNPq.