Development of a cassava core collection based on single nucleotide polymorphism markers

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ABSTRACT. Single nucleotide polymorphism (SNP) markers were used in the largest cassava (Manihot esculenta Crantz) germplasm collection from Brazil to develop core collections based on the maximization strategy. Subsets with 61, 64, 84, 128, 256, and 384 cassava accessions were selected and named PoHEU, MST64, PoRAN, MST128, MST256, and MST384, respectively. All the 798 alleles identified by 402 SNP markers in the entire collection were captured in all core collections. Only small alterations in the diversity parameters were observed for the different core collections compared with the complete collection. Because of the optimal adjustment of the validation parameters representative of the complete collection, the absence of genotypes with high genetic similarity and the maximization of the genetic distances between accessions of the PoHEU core collection, which contained 4.7% of the accessions of the complete collection, maximized the genetic conservation of this important cassava collection. Furthermore, the development of this core collection will allow concentrated efforts toward future characterization and agronomic evaluation of accessions to maximize the diversity and genetic gains in
cassava breeding programs.

**Key words:** Breeding; Genetic diversity; Germplasm; Core subset; *Manihot esculenta* Crantz; Molecular markers