



P1156: Application of the Axiom 3K SNP Genotyping Array in Cassava Breeding and Genetics

Use of high-throughput SNP genotyping platforms improves technical quality and traceability control in breeding programs and germplasm management. We had previously reported the development of a 3,417 SNP array for *Manihot esculenta*, as part of a five-species 50K SNP Axiom genotyping array for cashew, coffee, araucaria, eucalypts and cassava (Grattapaglia et al. 2017). SNPs were selected from variants identified in resequenced genomes of 52 worldwide cassava accessions publicly available from Phytozome. A subset of 160,000 SNPs was initially screened from 26 million variants for optimal array design, targeting 16 South American wild and cultivated cassava and 4 *M. glaziovii* accessions. A list of 3,417 high-quality SNPs distributed throughout 18 chromosomes and scaffolds of the v6.1 AM560-2 genome assembly was sent to final design. In this work, this SNP array was used for pedigree reconstruction of open pollinated progeny and to characterize 447 accessions of the Embrapa Cerrados cassava germplasm collection. Maximum-likelihood parentage analysis determined the correct parents for 91 progeny individuals. For only 35 of them these matched the expected parents from pedigree records, clearly showing the advantage of using SNP data to guarantee the correct pedigree and thus the estimates of heritability and genetic gain thereof. Multi-locus identity analysis revealed a large number of duplicated accessions, such that only 204 of the 447 accessions in the collection were actually unique. Discriminant analysis of principal components and fastStructure indicated the collection was composed of six clusters. A naïve genome-wide estimate of linkage disequilibrium (LD) r^2 of 0.019 was significantly reduced when corrected for population structure and relatedness going to r^2_{VS} of 0.005, decaying to < 0.2 within *c.* 75 kb. These results offered a first simple glimpse at the huge impact that the integration of SNP data can cause in cassava breeding and genebank management. Given the very high data quality and plummeting costs of array genotyping especially in a multi-species format, we anticipate its routine adoption to accelerate breeding via genomic selection.

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