Genetic diversity assessment of hydrocyanic acid, total carotenoid content, and dry matter content in biofortified cassava using trait-linked SNP markers

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Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

Hierarchical clustering (UPGMA) of cassava genotypes based on genetic dissimilarity (allele-mismatch distance)
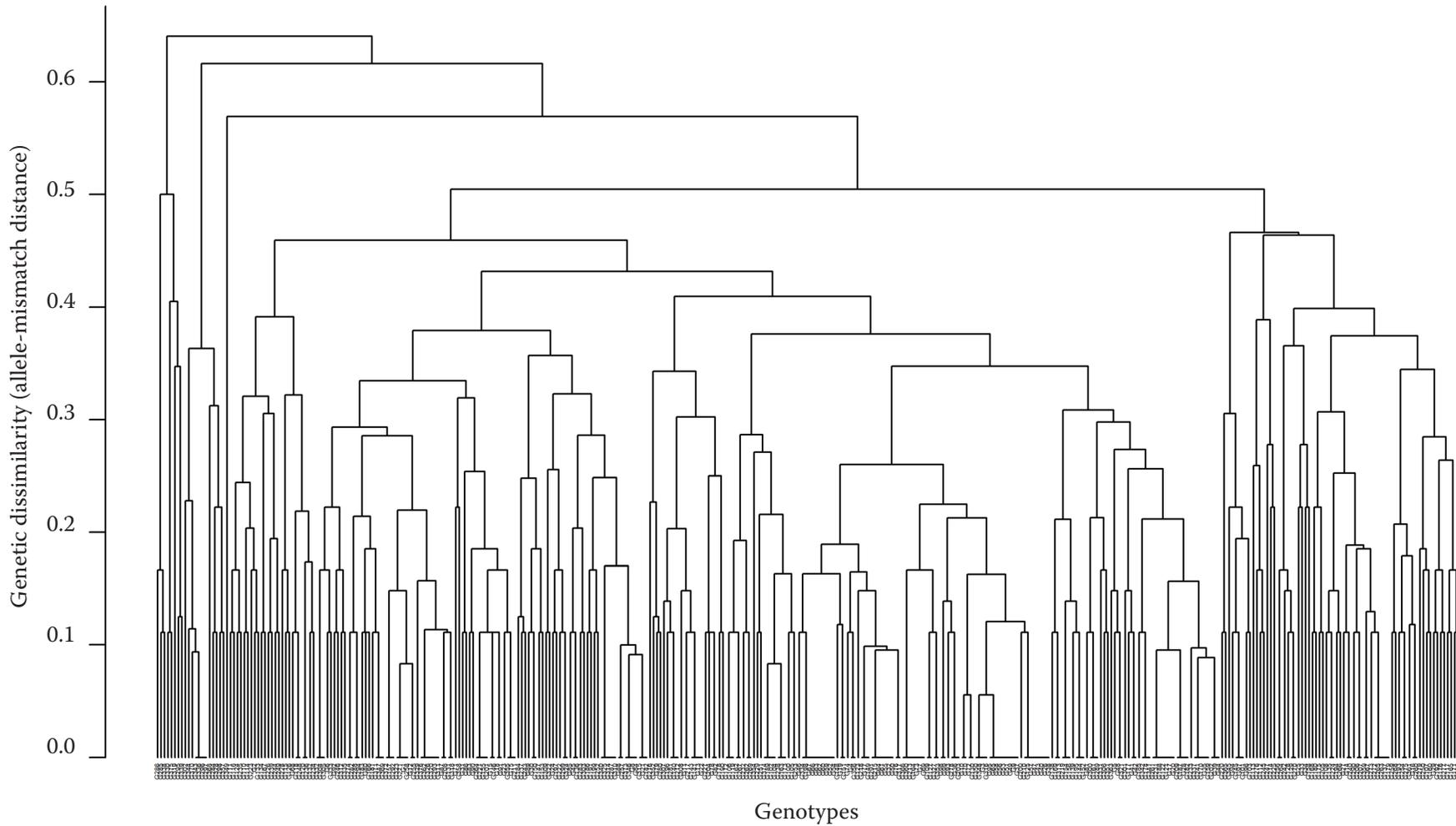

Figure S1. Dendrogram showing clustering of cassava genotypes using unweighted pair group method with arithmetic mean (UPGMA) based on allele-mismatch genetic distance

The *y*-axis represents genetic dissimilarity among genotypes; cluster robustness was evaluated using approximately unbiased (AU) *P*-value obtained from 1 000 bootstrap replicates using pvclust; statistically supported clusters are presented, with detailed cluster assignments in supplementary Table S1