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PUBLICATIONS

Phenotypic screening and molecular characterization of cassava mosaic disease resistance in Côte d'Ivoire cassava germplasm

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ABSTRACT

Cassava is the staple food crop for hundreds of millions of people in Africa. In Côte d'Ivoire, it is a main source of calories for over 26 million people. However, cassava mosaic disease (CMD), caused by cassava mosaic geminiviruses (CMGs) threaten its production. The development, adoption, and use of CMD resistant varieties remain a key CMD management strategy. Therefore, 610 accessions from the Côte d'Ivoire national cassava germplasm maintained by Centre National de Recherche Agronomique (CNRA) research stations in the cities of Man and Bouaké were characterized to assess their resistance to CMD. We found 72 accessions which were symptomless at both sites. Thirty five out of these 72 accessions were infected by African cassava mosaic virus (ACMV) without any CMD symptoms and 37 were virus free. None of the 72 symptomless accessions were infected by East African cassava mosaic Cameroon virus (EACMCMV). The remaining 538 accessions were CMD infected and displayed clear CMD symptoms. The promising 72 accessions (10 locals and 62 improved) were then tested for the presence of resistance genes, CMD1, CMD2 or CMD3. Except for 2 accessions for which no resistance gene was found, the remaining 70 accessions contained one or more resistance genes. Genotyping of the 69 symptomless accessions revealed that 56 were unique genotypes and 13 were potential duplicates. Accessions were structured in three groups with the variabilities at the individual's level. These findings reveal the existence of potential tolerant/resistant cassava accessions in CNRA's germplasm, which can contribute to CMD control and the increase of cassava production in Côte d'Ivoire.