BREEDING VALUES OF SELECTED CASSAVA GENOTYPES AND UTILITY OF DNA MARKERS LINKED TO CMD2 LOCI

BY

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ABSTRACT

Selection of parental material in cassava breeding is mainly based on the performance per se with limited effort on progeny derived breeding values in the national program in Uganda. Besides, cassava is highly heterozygous, making a conventional breeding approach long (7-8 years) and phenotypying imprecise. Therefore, the main objectives of this study were to (1) determine the breeding values of nine parental materials for resistance to cassava mosaic disease (CMD), above ground biomass and root yield and (2) validate known molecular markers linked to the CMD2 resistance locus for use in marker assisted breeding of resistance to CMD.

Field based studies were used to evaluate 9 parental materials comprising of 4 susceptible (Bamunanika, Kakwale, Nyaraboke and Bao) and 5 resistant (NASE10, NASE12, 95lSE-00036, TME5 and TME14) cultivars. Of the 5 resistant parents, 2 have monogenic inheritance while the other 3 possess recessive polygcnic action as the sources of resistance genes to CMD. Seed setting potential was also evaluated and differed among families. The average open pollinated seed (OPS) yield varied from 215 to 2,500 seeds per clone. The highest OPS were produced from families of Bamunanika, Nyaraboke, SEl95-00036 and TME5 parentage. However, these OPS exhibited the lowest seed viability (< 40%).

In contrast, families from Bao, NASElO and TME14 parentage had OPS with high viability but low seed set. Good field survival was exhibited by all OPS (>70%) except those from the NASE12 parentage. The general combining ability (GCA) of each parent was estimated from poly-cross progeny. The estimates of the general combining ability of each parent for reaction to CMD showed that two of the susceptible cultivars Kakwale, Bao and one resistant cultivar NASE12 were good combiners for CMD resistance. The susceptible cultivars Kakwale and Bao, and resistant cultivars 95lSE-00036, TME5 and TME14 were identified as good general combiners for fresh root yield. All susceptible parents were good combiners for fresh foliage yield. In contrast, cultivars Bamunanika, Nyaraboke, NASE10 and NASE12 were poor combiners for yield while TMES and TME14 were poor general combiners for fresh foliage yield. The fidelity of three markers developed at CIAT in selection of the *CMD2* gene was also tested with the view of deploying them in introgression of CMD resistance into selected local cultivars. The three markers, namely, RMEI , a sequence characterized amplified region-SCAR, and two simple sequence repeat (SSR) markers, NS158 and SSRY28, were evaluated by PCR amplification of genomic DNA of the resistant and susceptible cassava cultivars mentioned above.

The preliminary findings indicated absence of polymorphism among the parental materials used for all the markers. This implies that the current molecular markers are not informative across cassava subpopuJations outside the mapping populations. Screening and validation of single nucleotide polymorphisms (SNPs) and more SSR markers for polymorphism and saturation of cassava genetic map with more markers is proposed. This study generated important information for breeders io use in making decisions on selection of potential parents for genetic improvement and also confirms the limitation in the utility of molecular markers for selection in different subpopulations. The populations generated in this study would be useful for further genetic and molecular analyses including possibility of gene pyramiding for resistance to CMD.