

Project Title: Improving and deploying markers for biotic traits

Targeted Subprogram: Sub-Program 3 (Trait Capture for Crop Improvement)

Principal Investigator: Dr Chiedozi Egesi, National Root Crops Research Institute (NRCRI) Umudike.

Co-PI: Dr Emmanuel Okogbenin, National Root Crops Research Institute (NRCRI) Umudike.

Collaborating Scientists and Institutions

1. Dr Joseph Onyeka, National Root Crops Research Institute (NRCRI), Umudike, Nigeria;
2. Mrs Elizabeth Parkes, Crop Research Institute (CRI), Kumasi, Ghana
3. Dr Geoffrey Mkamilo, National Root and Tuber Program, ARI-Naliendele, Tanzania
4. Dr. M. Fregene, DDPSC, USA

Executive Summary

The genetics of cassava is the least understood of major staple crops in the world. This is largely due in part to its heterozygous nature which makes it difficult to develop appropriate stocks for classical genetic studies. The first genetic map of cassava was published in 1997 using first generation of markers including RFLPs, AFLPs, RAPDs and isozymes. This map was further developed by anchoring SSR markers, which are randomly distributed on the map. The map has been utilized in QTL mapping studies in cassava for various traits including resistance to pests and diseases, yield, morphological and quality traits. While QTLs have been detected for several traits, majority of the markers have yet to be applied in breeding programs due to poor association with traits in MAS schemes. Only markers associated with the CMD2 gene and CGM have so far been deployed in breeding programs. Results of MAS conducted so far for CMD2 gene was 68% efficient, while validation studies for markers linked to the CGM resistance was good in East Africa, but response to the CGM for the markers in West Africa was relatively moderate or tolerant to the pest. The lack of strongly linked markers to economic traits of importance necessitated the need for development of over 800 SSR markers for further mapping of the genomic regions controlling traits of interest. While success has been made in improving map saturation, recent efforts indicate that efficient fine mapping has not been successfully attained using SSR markers. To improve MAS for CMD2 gene, SCAR markers (at 4 cM to the gene) were developed which is now routinely used in breeding programmes. However, the need to accelerate the application of more markers in breeding programmes, means that more efficient marker systems are necessary to efficiently tag genes for MAS schemes. Current initiatives to develop SNPs for cassava in a GCP funded project and another by the BMGF provides a new vista and array of immense opportunities to identify markers closely linked to new sources of CMD resistance and other biotic constraints. This proposal therefore seeks to develop new mapping populations for QTL mapping for new sources of CMD resistance, and validation studies of the detected QTLs using available SNP markers developed from other GCP and BMGF projects.