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Ms Namusoke during the collection of ANT diseased samples.

Identification and validation of codominant molecular markers for selection of anthracnose disease resistance in common bean

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Abstract

Common bean landrace G2333, of Mesoamerican origin, offers broad resistance to Colletotrichum lindemuthianum. The cultivar is pyramided with three genes Co-42, Co-5 and Co 7. Of these resistant genes, Co-42 has been found to offer the broadest resistance. However, the National legumes breeding program lacks informative and easily assayable markers for Marker assisted selection of Co-42 gene. The aim of this study was to identify and validate easily assayable polymerase chain reaction (PCR)-based co-dominant molecular markers for selection of the Co-42gene. The sequence of CoK-4 gene, earlier on found to be part of the Co-42 gene locus was used as a reference and was blasted in the Phaseolus gene database to obtain markers close to the gene in a range of + or - 400kbp. Markers were amplified by PCR using primers obtained from database or designed with primer 3 software. Phenotypic segregation of disease resistance in a segregating population was necessary to associate the disease phenotype and the presence of the identified marker alleles. This was done in F2 populations derived from crosses of G2333 with two susceptible commercial Andean cultivars NABE 13 and NABE 14 with respect to Colletotrichum lindemuthinum pathotype, race 7, identified from the study. Results of the polymorphism test indicated that out of 20 identified markers, only two markers, namely BMB 588 and BM 211, behaved co-dominantly. Phenotypic segregation of resistance to susceptibility revealed that duplicate genes controlled disease resistance. Segregation analysis of these two markers tested in the F2 populations revealed that BM 211 marker did not segregate with disease resistance and could not be used for MAS. However, BMB 588 marker co segregated with disease resistance with co-dominance of two alleles of 200bp and 400bp. The segregation of BMB 588

marker fitted the expected segregation ratio of 1:2:1 and showed potential for use in marker-assisted selection of the Co-42gene during bean anthracnose resistance breeding.

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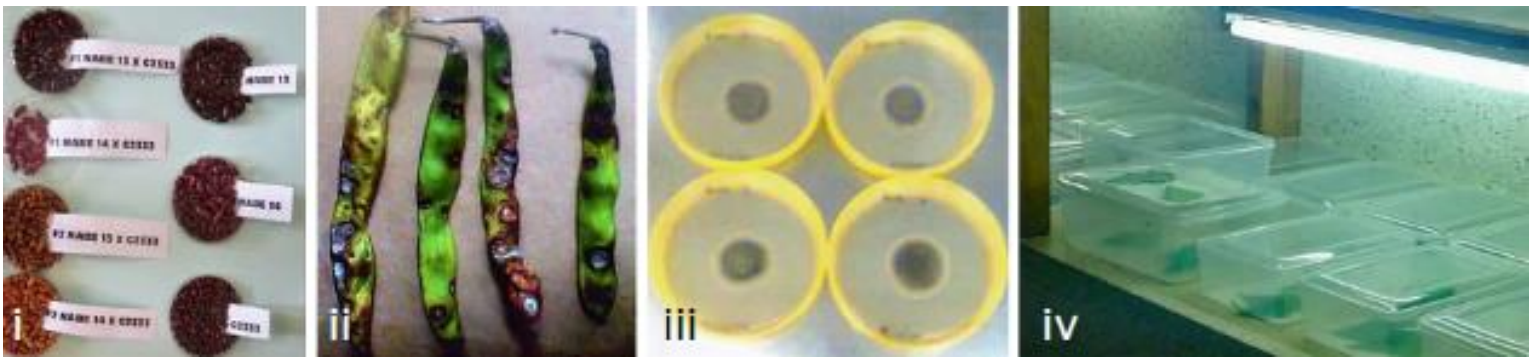

Bean varieties used to develop the populations to test markers; diseased pods collected (ii); C. lindemuthianum cultured in the lab (iii); the detached leaf method used to test the pathogenicity of the isolates by artificial infection (iv).