Introgression of genes conferring resistance against angular leaf spot (*Pseudocercospora griseola*) and anthracnose (*Colletotrichum lindemuthianum*) into common bean (*Phaseolus vulgaris* L.) using marker assisted selection.

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MSc in Plant Breeding, University of Hawassa, Ethiopia, 2019.

Abstract

Angular leaf spot (ALS), Anthracnose (ANT) and Common Bacterial Blight (CBB) are important diseases of common bean in Ethiopia that can cause severe yield reduction. This study was conducted to pyramid resistant genes for ALS and ANT diseases into advanced line and to evaluate isolines against ALS, ANT and CBB using marker assisted selection in combination with phenotypic selection. The parent AND277 donor of Phg-1 and Co-14 genes for ALS and ANT respectively and the recipient was KT-ABC001 line with the ALS and CBB resistant genes Phg-2 and CBB QTL respectively. In genotypic selection, SSR and SCAR marker linked to Phg-1, Phg-2, Co-14 and CBB QTL genes were used. Marker assisted backcrossing procedure was adopted; inheritances for resistant genes were characterized by using F2 and backcrosses. The Chi-square values showed no significant differences for ALS and ANT, 0.05 (P<0.78) and = 0.03 (P<0.9) in genotypic and phenotypic selection respectively. The resistance to ALS and ANT was found to be monogenic and the genes involved are dominant. The narrow sense heritability for ALS and ANT were (0.97 & 0.95) implying that selection for ALS and ANT can be done at early stage in a segregating population. High correlation values, for ALS (r = -0.65) and for ANT (r=-0.73) were obtained between phenotypic and molecular data respectively, indicating high reliability for the markers used. Eight gene pyramid groups were developed and evaluated against ALS, ANT and CBB. The gene pyramid group means were significantly different from each other (P<0.01) of which, Phg1+phg2+co14+cbb qtl and Phg 1+co-14+cbb qtl exhibited the lowest mean disease score to all the three pathogens indicating both a high degree and a broad spectrum of resistance. The AMOVA result revealed that there was high variation within population (90%) than between population (10%). The study

identified three isolines with four desirable genes, those plants should be advanced and incorporated to breeding program in order to release variety with resistant to ALS, ANT and CBB pathogens. In general, pyramiding multiple genes for durable resistance using MAS in combination with phenotypic selection is invaluable for breeding program.

Publication

Lema, M. 2019 Introgression of genes conferring resistance against angular leaf spot (*Pseudocercospora griseola*) and anthracnose (*Colletotrichum lindemuthianum*) into common bean (*Phaseolus vulgaris* L.) using marker assisted selection.

Mr Lema making crosses between the parental lines (i); an elongated pod from a successful cross (ii); Mr Lema working in the lab (iii); isolates of the fungus Colletotrichum lindemuthianum (the pathogen responsible for ANT), grown in culture media in the lab to test for disease resistance in breeding populations by artificial inoculation (iv).