

**RESISTANCE OF COMMON BEAN GENOTYPE TO FOLIAR FUNGAL AND  
BACTERIAL DISEASES**

**BATUMIKE NSHOBOLE RUPHINE**

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FACULTY OF AGRICULTURE  
UNIVERSITY OF NAIROBI**

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## DECLARATION

This thesis is my original work and has not been presented for award of a degree in any other university.

Batumike Nshobole Ruphine..........Date 09/06/2018

The thesis is submitted for examination with our approval as the University supervisors:

Dr. Felister Mbutu Nzuve..........Date 9/6/2018

Department of Plant science and Crop protection

University of Nairobi

Prof. James W. Muthomi..........Date 9/6/2018

Department of Plant science and Crop protection

University of Nairobi

Dr. Reuben Otsyula (PhD)..........Date 16/6/2018

Kenya Agricultural and Livestock Research Organization –Kakamega

## **ABSTRACT**

Foliar diseases have been reported to cause 45 to 100% of grain losses in common bean. However, conventional management strategies are not effective and sustainable to combat the bean yield losses. The use of host plant resistance is a more effective strategy to reduce losses. The objective of this study was to contribute to improved common bean productivity through a) Screening bean germplasm to identify sources of resistance to multiple diseases and b) determination of the genetics of resistance to the common bacterial blight resistance in common bean. To identify sources of resistance to multiple diseases, twenty four common bean lines were evaluated in the field at the Kenya Agricultural and Livestock Research Organization (KALRO)-Kakamega and Lugari during the short rains 2016 and long rains 2017. The trial was laid out in a randomized completed block design replicated three times in a 12 x 2 arrangement within the block. Data was collected on agronomic traits, disease incidence and severity and yield and yield related traits of common bean. The data was subjected to analysis of variance to determine the differences among the traits. Results showed significant variations among genotypes in their reaction to the fungal and bacterial diseases' intensity. Significant differences were also observed among genotypes for the percentage of emergence, days to 50% flowering and days to 75% maturity, number of pod per plant, 100-seed weight and grain yield. All the 24 bean lines evaluated showed moderate resistance to angular leaf spot. The genotypes Red34, KK15, Cal5B, Cal137, GLPX92, Cal6, Red45 and Cal33 were resistant to anthracnose while Red34, KKBC05/32, KK071, GLP2, Ciankui, RWR2245 and Cal6 were resistant to common bacterial blight. The genotypes Cal139A, Red16 and Red13 recorded the highest grain yield. In determining the genetics of resistance to the common bacterial blight, three generations namely F<sub>1</sub>, F<sub>2</sub> and backcrosses were developed from two parents namely VAX3 and MCM2001, resistant

and susceptible respectively to common bacterial blight. Both parents and progenies were planted in the screenhouse at KALRO- Kakamega. The plants were inoculated and assessed for common bacterial blight disease severity/intensity. Chi square test was used to compare the Mendelian segregation ratios and heterosis was also calculated. Parental line VAX3 presented resistant reactions to common bacterial blight, while all the plants from the parental line MCM2001 were susceptible. All the F<sub>1</sub> plants from crosses between VAX3 and MCM2001 were resistant to common bacterial blight. The F<sub>2</sub> populations revealed segregation pattern following a 3:1 genetic ratio for resistance and susceptibility respectively implying that resistance to common bacterial blight was governed by a single dominant gene. The plants generated from the backcross with the resistant parent VAX3 were resistant to common bacterial blight with 1:0 genetic ratios for resistance and susceptibility while the plants generated from backcross with susceptible parent MCM2001 showed 50% of resistance and 50% susceptibility with an expected ratio of 1:1. Thus, the resistant parents VAX3 could be utilized to develop common bean varieties that are resistant to common bacterial blight. The percentage values from mid-parent heterosis had negative values which increased the resistance from about 75 to 80% compared to the resistant parent. The values from better parent heterosis remained constant compared to the resistant parent VAX3. The progeny F<sub>1</sub> increased the resistance to common bacterial blight compared to the resistant parent VAX3. The best performing genotypes for resistance to the multiple diseases could be tested under more diverse environments for release to the farmers to increase bean productivity in Kenya.