

**DISTRIBUTION OF CASSAVA BACTERIAL BLIGHT AND REACTION OF ELITE  
CASSAVA GENOTYPES TO THE DISEASE IN KENYA**

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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

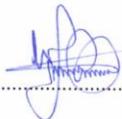
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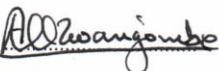
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## ABSTRACT

Cassava bacterial blight (CBB) is the most important bacterial disease of cassava. It is caused by *Xanthomonas axonopodis* pv. *manihotis*. Distribution of this disease within Kenya has not been evaluated for over twenty years. Cassava breeding programs within the country have also not incorporated resistance against CBB in the production of suitable genotypes for farmers. The aim of this study was therefore to establish the distribution of the disease within the country, and to evaluate elite cassava genotypes for their reaction to infection by the disease. A survey was carried out in all cassava growing regions of the country and leaf samples showing CBB symptoms collected. The bacterium was isolated from the leaf samples and analyzed using biochemical and physiological tests in the laboratory to ascertain the identity of the pathogen. PCR was carried out to further detect and affirm the presence of the bacteria in the collected leaf samples. Seven elite cassava genotypes; TME 7, TME 14, TME204, MM96/2480, MM95/0183, Ebwanatareka 1 and Ebwanatareka 2 were inoculated with five isolates obtained from the survey to evaluate their reaction to infection by CBB. Symptoms were observed over a period of 35 days at intervals of seven days. The bacteria extracted from the leaf samples conformed to all the biochemical and physiological tests specific to *Xanthomonas axonopodis* pv. *manihotis* and to *Xanthomads* in general. On PCR amplification, primer set RB1/RB2 which targeted the TAL effectors was used. The amplifications occurred at 500 base pairs as expected. Out of the 21 counties surveyed, the disease was present in 15 counties. The disease prevalence was highest in Kwale County at 100% while the lowest prevalence was recorded in Bomet Baringo, Tharakanithi, Kiambu, Kitui and Machakos at 0%. Kilifi County recorded the highest incidence at 64% while Makueni had the lowest at 8%. All the genotypes had area under disease progress curve (AUDPC) values that were higher than 52.2 which rendered them susceptible. TME7 and

TME14 exhibited a relatively slow reaction to infection compared to the other genotypes in terms of severity of symptoms within the first week post inoculation, indicating resistance mechanisms through delayed symptom development. Susceptibility of all the genotypes to the disease is an indicator that resistance to CBB is not incorporated in most breeding programs. This study reports the presence of CBB in majority of the cassava growing counties in Kenya except in Bomet, Baringo, Kiambu, Tharakanithi, Machakos and Kitui counties. The findings of this study confirm the presence of CBB in the coast region for the first time. The coast region was considered CBB free in previous studies. This study also reports the susceptibility of the elite cassava genotypes tested to CBB. The findings of this study should be used for the enforcement of quarantine measures to prevent further spread of the disease across the cassava growing regions which do not have the disease. In addition, breeding programs should incorporate CBB resistance in the development of new genotypes.