# EVALUATION OF MAIZE GENOTYPES FOR RESISTANCE TO THE MAIZE CHLOROTIC MOTTLE VIRUS IN KENYA

By

## JALAL ELDEEN CHOL ATEM
## (BSc. AGRICULTURAL SCIENCES (HONORS) IN AGRONOMY, UNIVERSITY OF DALANJ)

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## DEPARTMENT OF PLANT SCIENCE AND CROP PROTECTION
## FACULTY OF AGRICULTURE

## UNIVERSITY OF NAIROBI

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# DECLARATION

This MSc. research thesis is my original work and has not been presented for a degree award in this or any other university.
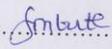
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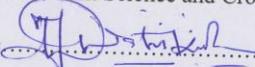The thesis is submitted for examination with our approval as University supervisors.

**Dr. Felister M. Nzuve**

Department of Plant Science and Crop Protection, University of Nairobi

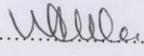Signature.....fnbute....................Date .......2/8/2018...........................

**Dr. Douglas W. Miano**

Department of Plant Science and Crop Protection, University of Nairobi

Signature..........................Date.....03/08/2018..............

**Dr. Anne Wangai**

Kenya Agricultural and Livestock Research Organization – (KALRO)

Signature.....................Date ..0.3/08/2018.........................

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**ABSTRACT**

Maize (*Zea mays L*) is one of world most important crop, after wheat and rice, and it is a source of human diet in east Africa where more than 90% of Kenya's population depend on maize for food. Maize lethal necrosis (MLN) disease which is caused by the synergistic interaction of *Maize chlorotic mottle virus* (MCMV) and *Sugarcane mosaic virus* (SCMV) is a real threat to maize production with yield losses of 100% in years with severe outbreaks. Use of host resistance offers a feasible approach in the management of the MLN and its causal viruses. This study aimed to a) identify sources of resistance to MCMV among assembled germplasm and b) to determine the genetics of resistance to the MCMV. Field and greenhouse experiments were carried out at the University of Nairobi Field station. In the greenhouse, 45 maize genotypes grown in a completely randomized design in two replications were screened for their response to MCMV under artificial inoculation. The 42 genotypes were selected based on their genetic background. The disease severity, percentage disease incidence and others agronomic data such as plant height, days to 50% flowering and days to 50% silking were collected. The MCMV severity was assessed using a scale of 1 to 5 where 1 = No MCMV symptom and 5 = Very severe symptom/complete plant death. All the collected data were subjected to analysis of variance (ANOVA) using Genstat statistical analysis software 15th Edition. The genotypes mean were separated using Fishers protected least significant differences (LSD) at 5% level of significant. The study showed highly significant differences among disease parameters namely area under disease progress curve (AUDPC), final disease score (FNDC), MCMV % incidence and weekly disease severity scores. This study identified some lines with high level of MCMV resistance, particularly among the genotypes which originated from KALRO and CIMMYT, namely MU5, MU26, MU37, MU39, MU41, MU48, MU52, KT92, KT99, KT87, KT86, KT91,

KT94, KT101and KT103. In addition, among the landraces, L/105, L/FM108, L/FM110, L/FM112, L/FM118, L/FM120 and L/FM122 were superior for MCMV resistance. To determine the inheritance of MCMV resistance, $F_2$ seeds derived from $F_1$ crosses through selfing were planted in the screen house for two seasons. A population consisting of 250 plants was established and chi square test was done to test the goodness of fit of observed segregation. Observations in the $F_2$ seeds population were genetically grouped into either resistant (R) and/or Susceptible (S) responses. The segregation data from the $F_2$ families followed the genetic ratios of 9:7, 13:3, and 15:1, which conformed to the presence of dominant epistasis or completely dominant gene effects. This suggested that two non-allelic genes could be involved in conditioning the MCMV resistance among the maize genotypes studied. These genotypes could be used as donors to introgress the MCMV resistance into adapted maize germplasm backgrounds to combat further yield declines.