

**PhD Thesis Title: Resistance to the Spotted Stem Borer and African Maize Stem Borer in
Tropical Maize**

By: MUNYIRI SHELMITH WANJA

SUMMARY

In sub-Saharan Africa (SSA), maize (*Zea mays* L.) is the staple food for about 50% of the population. Lepidoptera stem borers pose major threats to sustained food sufficiency in SSA where they cause annual yield losses of 15% and particularly Kenya where they cause loss estimated at 13.5%. The potential to manage insect pests using host-plant resistance exists, but has not been adequately exploited. The goal of this study was to determine the resistance levels in tropical maize to the African stem borer (*Busseola fusca* Fuller) and the spotted stem borer (*Chilo partellus* Swinhoe) to support breeding efforts for improved maize productivity in SSA. Specific objectives were; i) Determine the diversity for resistance to stem borers in tropical maize; ii) Investigate the mechanisms of resistance in CIMMYT tropical maize inbred lines and iii) Map the quantitative trait loci (QTL) associated with maize *Chilo partellus* stem borer resistance using a CIMMYT tropical maize breeding population. Two hundred and ninety five (295) genotypes which included 120 inbred lines, 75 landraces, 100 hybrids and open pollinated varieties (OPVs) were evaluated for two seasons at the Kenya Agricultural Research Institute (KARI)-Kiboko and KARI-Embu field stations. Data were recorded on leaf damage, number of stem borer exit holes, stem tunnel length (cm), stem lodging and grain yield. A selection index was computed using the main resistance traits leaf damage, number of borer exit holes and cumulative tunnel length to categorize genotypes into resistant and susceptible categories. Evaluations for mechanisms of resistance were carried out for two seasons at KARI-Kiboko on 120 maize inbred lines. Data were recorded on leaf toughness, stem penetrometer resistance, trichome density and pith sugar content. To map the QTL for stem borer resistance, a population of 203 F2:3 individuals were developed between 2009 and 2011. Field evaluations were carried out at six sites, three for each of the two stem borer species. Data were recorded on leaf damage on a 1-9 scale, number of stem borer exit holes and cumulative tunnel length as putative stem borer resistance traits. The mapping population was genotyped with 152 single nucleotide polymorphism (SNPs) molecular markers. Phenotypic data was subjected to ANOVA using PROC GLM of SAS 2007 and means separated using Fisher's protected LSD ($P < 0.05$).

Variability for resistance to maize stem borers was identified in all the genotypes evaluated. The highly resistant landraces against *C. partellus* were GUAT1050, GUAT280, GUAT1093, GUAT1082, GUAT1014, CHIS114 and GUAN34. Highly resistant commercial hybrids and OPVs to *C. partellus* were DH01, PH1, PH3253 and ECA-STRIGOFF-VL 102-#-#, while, KDV1-3-#, EEQPM-8-EA-3-#, DKC8053 and PH4 were resistant to *B. fusca*. Open pollinated varieties KDV1-1-# and KDV1-2-# were highly resistant to both stem borer species. Inbred lines CKSBL10025, CKSBL10027 and CKSBL10026 were highly resistant to both borer species; CKSBL0039 and CKSBL10014 were highly resistant to *C. partellus* while CKSBL10008 and CKSBL10005 were highly resistant to *B. fusca*. Trichome density was the best mechanism of resistance in discriminating genotypes into resistant and susceptible categories, followed by leaf toughness and stem sugar content in that order. Mechanisms of resistance were found to be germplasm-specific. Number of stem borer exit holes and cumulative tunnel length were the most important traits in assessing resistance. A linkage map that spanned 1248.01 cM on 10 chromosomes with an average 8.21cM was constructed. Several QTL for putative resistance traits were detected on chromosomes 1, 2, 3, 4, 5, 6, 7 and 9 based on data from both individual sites and the different stem borer species. In the combined *B. fusca* sites analysis, one QTL for stem tunnelling was revealed on chromosome 4 (LOD 2.86) while in the *C. partellus* combined sites, one QTL for reduced tunnelling (LOD 2.81) and another QTL for reduced number of exit holes was revealed on chromosome 5 (LOD 2.53). Individual sites analyses revealed five QTL for reduced stem tunnelling, three for number of exit holes and two for leaf damage. The phenotypic variances explained by each QTL ranged from 6 to 10% suggesting a need to validate these QTL using a larger population. Germplasm identified as highly resistant to maize stem borers are recommended as novel sources of resistance for use in resistance breeding in SSA. Information on resistant commercial hybrids and OPVs should be disseminated to farmers in the relevant ecologies for adoption to curb grain yield losses. Trichome density, leaf toughness and stem sugar content could be adopted as satisfactory indicators of resistance mechanisms and used for pyramiding of resistance genes for high and durable resistance. Overall, this study identified new sources of resistance to maize stem borers in tropical germplasm that can be used as new varieties and/or used as sources of resistance in breeding.