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**RESISTANCE TO THE AFRICAN AND SPOTTED STEM BORERS  
IN SORGHUM IN KENYA**

**By**

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## ABSTRACT

Sorghum (*Sorghum bicolor*, L. Moench) is a key cereal crop to over 500 million people in semi arid tropics. Sorghum production in subsistence farming is low and ranges between 0.5– 0.8 t/ha compared to potential yields of 10 t/ha. Diseases, drought, insect pests and parasitic striga weeds are the most important causes of the low grain yield. Lepidopteran stem borers mainly *Busseola fusca* Fuller (Noctuidae) and *Chilo partellus* Swinhoe (Crambidae) are among the economically important insect pests of sorghum and maize in East Africa. Stem borers cause grain yield losses ranging between 15 % - 80% through leaf feeding, deadheart formation, exit holes and stem tunnelling damage. Considering multiple stem borer damage traits is useful since resistance to stem borers is quantitatively inherited thus selecting for resistance based on a single parameter would not be effective. Cultural strategies, biological control, as well as chemical pesticide application have been employed, but are either ineffective or uneconomical for resource constrained farmers. Host plant resistance is an economically viable strategy for stem borer management in cereal production. Sources of resistance to stem borers have been reported and the levels vary from low to moderate. Therefore, it is important to identify sorghum genotypes with higher levels of resistance and with different mechanisms of resistance to diversify the bases of resistance to these pests. In Kenya, little research attention has been accorded to indigenous economically important stem borers like *B. fusca* in cereals. The reason for chilo is because the pest is highly invasive and persistent and has expanded its distribution to areas where it had not been reported earlier. The objectives of this study were to (1) Identify sources of resistance to *B. fusca* and *C. partellus* in sorghum; (2) Establish the mode of inheritance of resistance traits to *B. fusca* and *C. partellus* in sorghum and (3) Map quantitative trait loci associated with resistance traits to *B. fusca* and *C. partellus* in sorghum.

The first study was conducted in two separate experiments in different agroecologies in Kenya. Evaluation of sorghum genotypes for resistance to *B. fusca* was conducted in the University of Nairobi, Kabete campus field station. Experiments to identify sorghum genotypes resistant to *C. partellus* were conducted at the Kenya Agricultural Research Institute (KARI), Kiboko. The reason for conducting these studies in these locations was that the pests causes epidemics on sorghum in these areas. The experiments were carried out in 2010 during long and short rain seasons. Seven East African commercial sorghum cultivars and twenty introduced cultivars from

India were evaluated in this study. Test material was sown in  $\alpha$ -lattice design, consisting of nine plots in three blocks, replicated twice. Rows were 2 m long and 0.75 m apart, and the spacing between plants within rows was 0.25 m. First instar neonates of *B. fusca* and *C. partellus* were obtained from the International Centre of Insect Physiology and Ecology (ICIPE), Nairobi. At 30 days after sowing, five plants in each row were tagged and artificially infested with five larvae/plant using a camel hairbrush. Data collected on percentages was arcsin transformed while that of counts was log transformed before analysis of variance. Data was subjected to Genstat statistical software version 14 for analysis of variance. Treatment means were compared using protected Fishers' least significant difference test at  $P = 0.05$ . Selection index was calculated based on leaf damage, deadheart, stem tunneling and exit holes by adding the ratios between the values for each genotype and the overall mean for each parameter, and dividing by 4 (number of damage parameters considered). Pearson's correlation coefficients were computed to determine association between morphological characteristics with traits measuring plant reaction to *B. fusca* and *C. partellus* infestation. Susceptibility parameters leaf damage, deadheart incidence, stem tunneling and exit holes were employed to define the reaction of the sorghum genotypes to *B. fusca* and *C. partellus*. Sorghum genotypes namely ICSB 467, ICSA 473, Macia, ICSB 464 and ICSA 472 with cross resistance to *B. fusca* and *C. partellus* based on leaf damage, deadheart, stem tunneling and exit holes following artificial infestation with stem borer neonates were identified. The mechanism of this resistance to *B. fusca* and *C. partellus* was mainly tolerance since numerous genotypes produced substantial grain yield after supporting high leaf damage, deadheart, exit holes and stem tunnelling damages. Bloomy sorghum genotypes with highly glossy and non-vigorous seedlings suffered lower damage compared to the bloomless, non-glossy but highly vigorous plants. Highly vigorous sorghum genotypes tended to have higher total grain yields than those with low vigor perhaps because the whorls of the less vigorous genotypes provided a better environment for the stem borer larvae. Seedling vigor and trichome density could be used as morphological markers to select for sorghum resistance to both borers. The resistant sorghum genotypes can be used to increase the levels of resistance to SB in high yielding but susceptible genotypes.

The second study was conducted in two separate locations in Embu and Kiboko to investigate inheritance of resistance traits associated with *B. fusca* and *C. partellus*, respectively in sorghum. The experimental material consisted of sorghum lines with varying levels of resistance to *B.*

*fusca* and *C. partellus* identified in study one above. Classification of the sorghum lines into different resistance categories was based on leaf damage, deadheart, exit holes and stem tunneling in 2010 long and short rain seasons. North Carolina mating design 2 was employed where 15 lines were used as females and 2 as males. Test material was sown in  $\alpha$ -lattice design, consisting of eleven plots in five blocks, replicated twice. Spacing and artificial infestation were carried out as in the first study described above. Genetic analysis was performed using line x tester analysis using Genstat version 14 statistical software. Major finding was that general combining ability and specific combining ability effects were significant indicating that both additive and non-additive gene effects conditioned resistance to both *B. fusca* and *C. partellus*. General combining ability and specific combining ability effects were significant for leaf feeding, deadheart, number of exit holes and stem tunnels damages indicating that additive and non-additive gene effects conditioned resistance to these stem borers. Additive gene action conditioned deadheart formation and leaf feeding damages. Number of stem borer exit holes and stem tunneling damages were controlled largely by additive and non additive gene action. Females ICSA 464, ICSB 474, ICSB 464 and ICSA 472 and male ICSB 473 exhibited high negative GCA effects for leaf damage, deadheart, exit-holes and stem tunneling, implying their good general combining ability for resistance to *B. fusca* and *C. partellus*. These parents could be utilized in development of stem borer resistant sorghum cultivars.

The objective of study three was to map quantitative trait loci (QTLs) associated with resistance traits to *B. fusca* and *C. partellus* in sorghum. The experiments were conducted in three locations namely Kabete, Embu (to phenotype for *B. fusca*) and Kiboko for *C. partellus*. QTLs associated with resistance to *B. fusca* and *C. partellus* were mapped in 243 F<sub>9</sub>:<sub>10</sub> recombinant inbred lines (RILs) derived from a cross between ICSV 745 (S) and PB 15520-1 (R). The 243 RILs along with both parents were imported to Kenya from India and phenotyped in Embu and Kabete for *B. fusca* resistance and in Kiboko for resistance against *C. partellus* in 2011 and 2012 rain seasons. Each experiment was laid out in 24 × 10 alpha-lattice design consisting of twenty seven plots in ten blocks in two replications in plots of 2m length, 0.75m interspacing x 0.25m intraspacing. Data was subjected to analysis of variance using residual maximum likelihood model (ReML) in Genstat Version 14 statistical package. The predicted means for each genotype was estimated with genotypes as fixed and reps as random effects in the analyses. Sorghum linkage maps were

constructed using JoinMap 4.0 software. Composite interval mapping was performed on the data using PLABQTL software, version 1.2. Genetic maps and QTLs were drawn using MapChart program version 2.1. The identified QTLs on sorghum chromosomes 1,3,4,5,6,8,9 and 10 controlling *B. fusca* and *C. partellus* resistance against leaf damage, Deadheart, exit holes and stem tunneling are novel and had not been reported in earlier studies. Findings of the present study are also novel as QTLs governing more than one trait (pleiotropic QTLs) were identified. For example, chromosome 3 controlled stem tunneling and leaf damage; chromosome 4 conditioned deadheart, exit holes and stem tunneling and chromosome 6 conditioned exit holes and leaf damage. This study detected 2 QTLs for bloom waxiness, two for leaf glossiness, four for trichome density, five for leaf toughness and two for seedling vigour. Genomic regions governing trichome density detected on sorghum chromosomes 2, 3 and 6 are novel and have not been reported. Chromosome 9 was observed to possess pleiotropic effects and controlled seedling vigour, leaf toughness and bloom waxiness. The strong positive significant association observed in this study between exit holes and stem tunneling could be attributed to the fact that both damage traits are controlled by chromosomes 2, 4 and 9 and either of the traits can be used to predict the other. The positive significant relationship between deadheart formation and leaf feeding damages could be explained by the fact that chromosome 8 controlled both traits and they are governed by additive type of gene action. The identification of more than one QTL for different traits supports the hypothesis that several genomic regions condition expression of resistance to *B. fusca* and *C. partellus* in sorghum. The information generated in this study can be used in marker-assisted selection and the breeding of both *B. fusca* and *C. partellus* resistant sorghum cultivars. There is need for further studies to identify gene(s) underlying the mapped QTLs. Discovery of high through-put strategies that allow greater power and precision in utilization of QTLs conditioning sorghum resistance to stem borers will enhance sorghum improvement against these insect pests.