IMPROVING SORGHUM CULTIVARS FOR RESISTANCE TO SPOTTED STEM BORER (*Chilo partellus,* SWINHOE) AND GRAIN YIELD

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DECLARATION

I declare that this thesis is my original work and has not been presented for any award of degree in any other University.

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Signature…………………………… Date 5/2/2018……………

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DEDICATION

To God Almighty first, my parents: Mr. Morris Lado and Mrs. Adelinda Ajua for believing in me and for their encouragement through the length of this course. I also dedicate it to my wife Helen Dominic for her relentless reminders that I am a father of our son Ruben Jimmy and daughters Suzan Jimmy, Ester Jimmy; and to the rest of the Lou family.

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LIST OF ABBREVIATIONS/ACRONYMS

ASARECA	Association for Strengthening Agricultural Research in East and Central Africa
CIMMYT	International Maize & Wheat Improvement Center
EA	East Africa
ECA	Eastern and Central Africa
ECARSAM	East and Central Africa Regional Sorghum and Millet Network
EPZ	Export Processing Zone
FAO	Food and Agriculture Organization of the United Nations
FAOSTAT	Food and Agriculture Organization Statistics
GOK	Government of Kenya
ICIPE	International Centre of Insect Physiology and Ecology
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
KARI	Kenyan Agricultural Research Institute
KALRO	Kenyan Agricultural and Livestock Research Organization
MoA	Ministry of Agriculture
MOARD	Ministry of Agriculture and Rural Development
PROTA	Plant Resources of Tropical Africa

ABSTRACT

The objectives of this study were to (a) determine inheritance of resistance to *Chilo partellus* and other agronomic traits in sorghum and (b) Estimate the genetic variations, heritability and expected genetic advance for agronomic traits in selected sorghum varieties. The study was carried out in two different agro-ecologies of Kenya; Kenyan Agricultural and Livestock Research Organization (KALRO) / International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Kiboko and the University of Nairobi, College of Agriculture and Veterinary Sciences (CAVS), Kabete Field Station during the 2015 short rains season. North Carolina II mating design was used where three male parents were crossed with each of the ten females to generate 30 F_2 progenies. The 30 F_2 families together with the 13 parents and 6 checks were sown in a 7 x 7 alpha-lattice design with two replications in each location. Ten plants from the 2 middle rows were tagged and artificially infested with five first instar larvae of *C. partellus* per plant using a camel hair brush. The remaining two side-rows served as non-infested control and were used to estimate the genetic variations, heritability and associations among stem borer resistance and agronomic traits in sorghum parents. Analysis of variance was computed for the traits studied using Genstat computer programme 15th edition. The Results revealed variation for resistant parameters with parents IS 1044, ICSV 700 and IS 2055 emerging as the best parents with less damage. General and specific combining ability were calculated for F_2 progenies with respect to sorghum stem borer resistance and agronomic traits using PROC GLM procedures in SAS computer package, version 9.3. GCA and SCA effects were significant ($P \leq 0.05$) for deadheart, number of exit holes, stem tunnelling damages, days to 50% flowering, number of fertile tillers and grain yield suggesting that additive and non-additive gene effects controlled resistance to *C. partellus*. Female lines KARI Mtama-1, Gadam el-Hamam, Macia, Tegemeo, Hugurtay and males IS 1044 and ICSV 700 exhibited high negative GCA effects for the damage traits indicating their good general combining abilities for resistance to *C. partellus*. Female lines Sila, IESV 23011DL, IESV 23008 DL, Gadam, Tegemeo and ICSV 700 demonstrated desirable GCA effects for grain yield. The mean sum of squares due to genotypes revealed significant differences ($P \leq 0.05$) for all the 8 traits studied in both locations. High to moderate estimates of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were recorded for plant height, days to 50% flowering, number of tillers, panicle length, width and weight and grain yield which presents considerable variability and offers scope for genetic improvement through selection. Number of productive tillers and 100 seed mass had high GCV estimates with high heritability.

CHAPTER ONE

INTRODUCTION

1.1 Background information

Sorghum (*Sorghum bicolor* L. Moench) is one of the most important food and fodder crops of dry land agriculture (Rohrbach *et al.,* 2002). It is a staple food crop for millions of poor people living in the Semi-Arid Tropics (SAT) of Africa and Asia (Ashok Kumar *et al.,* 2011). In Africa, sorghum is ranked the second highly produced cereal after maize (Gerda and Christopher, 2007). It is essential in diets of poor people in the SAT where droughts frequently cause crop failures. Sorghum provides food security to many of the world's poorest, most food-insecure agro-ecological zones (FAO and ICRISAT, 1996). Reducing household's food insecurity and poverty relief has been the primary objective of technology development strategies in Sub-Sahara Africa and development of resilient crops like sorghum, millets, and cowpeas is one of the strategies (Shiferaw *et al*., 2014).

Unlike other cereals such as maize and wheat, sorghum is able to grow with less water, and is well adapted to growing in arid and semi-arid regions of the world (Mamoudou *et al.,* 2006). It is mostly grown under rainfed conditions, with a small percentage produced under irrigation (PROTA. 2006). Sorghum is produced at both subsistence and commercial levels. Planting is by direct seed sowing or through nurseries and trans-planting and ratooning is also practiced in some areas. Many types and colours of sorghum grain are used to produce different types of foods and beverages around the world. Generally, the crop is consumed as whole grain or processed as flour to prepare traditional meals. Unfermented bread such as *Chapatii* and *Roti* are commonly found in India, whereas *Tortillas* is found in Central America and Mexico (Dewald and Thomson, 1983). Fermented breads such as *Injera* are found in Ethiopia and Eritrea while *Dosa* and *Kisra* are popular in India and Sudan (Dewald and Thomson, 1983). Stiff porridges known as *ugali, karo and mato* made from sorghum are found across Africa, India and Central America while thin porridges like *uji/odi, akasa* and *koko* are found in Eastern and Western Africa. Low tax to favour locally grown cereals has significantly aided the development of sorghum lager brewing in East African countries such as Uganda and Kenya (Mackintosh and Higgins, 2004). Various types of alcoholic beverages and sour/ opaque beers derived from sorghum are available in markets around the world (Rooney and Waniska, 2000).

Sorghum yields in Semi-arid areas are low due to use of low inputs, the lack of improved high yielding varieties resistant to key biotic and abiotic stresses (Muui *et al*., 2013). This situation has led many farmers to grow maize in unsuitable areas leading to frequent crop failures and increased food insecurity. Better sorghum varieties could be used if their potential was demonstrated and seed made accessible. Sorghum has the potential to improve food security in SAT because it is uniquely drought resistant and can withstand extended periods of high temperatures (Wilson and Ritchie, 2001). The resilience of sorghum is derived from its C_4 photosynthetic nature, extensive root system, waxy leaf and ability to cease growth in periods of drought (Sanchez *et al.,* 2002).

1.2 Significance of sorghum in Eastern Africa

Sorghum is a staple food crop for many low-income families in Eastern Africa (Orr, 2003). Generally, sorghum is grown by resource-poor small-scale farmers mainly for home consumption (Ibeawuchi, 2007). Sorghum is believed to have originated in Ethiopia and the surrounding countries, around 4000-3000 BC (Dillion and Sharma, 2007). In eastern Africa, sorghum offers a safety margin for both human and livestock and is also the principal staple in countries such as Eritrea, Ethiopia, Sudan and South Sudan. In Kenya, Tanzania, Uganda and South Sudan, it is an important crop in alcoholic beverages industry, and an essential feed crop for livestock in Kenya and Uganda (Abdalla, 2016).

Sorghum in South Sudan is the primary crop cultivated with a wide range of local landraces (Zozimo, 2015). It constitutes the main staple food throughout the country, except for the Western, Central and Eastern Equatoria, where the local diet is centered on maize flour mainly imported from Uganda and Cassava from the green belt. Not only does sorghum have the potential to make South Sudan food secure, but also to make the country a fundamental actor in the US$80 billion a year universal cereals industry (Zozimo, 2015). In Kenya, sorghum produced in Eastern, Nyanza, Western, Rift Valley, and Coast regions which account for about 42.5, 40.5, 8.5, 6.6 and 1.5 per cent respectively of Kenya's total sorghum (Figure 1.1). Collectively, the regions produce 99.6% of the country's sorghum (MoA-ERA, 2012). The crop has a large germplasm base that allows for great opportunities for its sustainable production (Huang, 2004). The crop was relegated to a lower place when maize became the favoured and staple food crop having been introduced from Europe. However, due to the need to mitigate impacts of climate change and to stabilize food security and enhance nutrition in the region, there is renewed interest in promoting the crop.

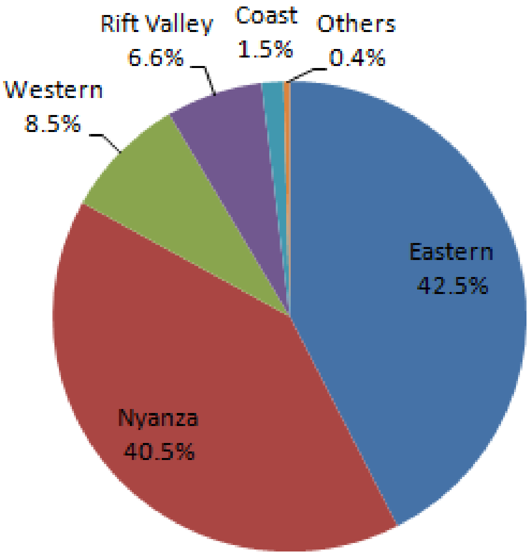

Figure 1.1: Share of Total Sorghum Production by Province-Kenya, 2012 (Source: MoA-ERA, 2012)

1.3 Constraints in sorghum crop production

Low sorghum productivity in East Africa is mainly due to abiotic and biotic stresses. The major abiotic factors include drought, high temperature and low soil fertility. The main biotic stress factors include striga parasitic weed, insect pests and diseases (Olembo *et al.*, 2010). Important diseases of sorghum are Anthracnose (*Colletotrichum graminicola*), Downy mildew (*Peronosclerospora sorgi),* Leaf blight (*Exserohilum turcicum*), Grey leaf spot (*Cercospora sorghi*) and covered smut (*Sphacelotheca sorghi*). Sorghum diseases have been reported to be responsible for more than 500 kg ha^{-1} annual grain yield losses in East Africa (Ngugi *et al.*, 2002). Important arthropods that cause economic damage are: Diptera (*Cecidomyiidae*, *Muscidae*) and Lepidoptera (*Crambidae*, *Pyralidae* and *Noctuidae*) cause most damage (Dhillion *et al*., 2005). Sorghum as a native crop to Africa has developed with indigenous insect pests and it is probably the reason that some genotypes are tolerant/ resistant to these insect pests (Muturi *et al.*, 2012). The insect pests cause an estimated loss of over 1 billion US$ annually worldwide (Sharma *et al.*, 2005).

1. 3.1 Economic importance of stem borers

The species, spotted stem borer (*Chilo partellus*), the African stalk borer (*Busseola fusca*), and the pink stem borer (*Sesamia calamistis*) and sugar cane borer (*Eldana saccharina*) are predominant in East Africa (Mailafiya *et al.,* 2009). Spotted stem borer is the most economically significant foliage insect pest of sorghum in East Africa and causes grain yield loss between 15% - 80% depending on sorghum variety, phenological stage and agro ecology (De Groote, 2002; Karaya *et al*., 2009). About 80% loss in sorghum grain yield due to *C. partellus* has been reported in Kenya when infestation was done on 20 days old crop, whereas comparable infestations revealed non-significant damage when 60 days old plants were infested (Seshu *et al.,* 1989). A surveys carried out in Kenya by Dwumfour (1990) reported that, stem borer species diversity was highest (15 species) in Busia and lowest (5 species) in Machakos district. *C. partellus* was the most dominant among cereal crops and wild grasses species in Machakos and Suba districts, while *Busseola fusca* and *C. partellus* were equally dominant in Busia district (Dwumfour *et al.,* 1990).

1.4 Problem statement and justification

As one of the most important food crops in East Africa, sorghum is mainly grown by resource-poor farmers (Ibeawuchi, 2007). It is an underutilized crop species that could play an important role in food and nutrition security and income generation in Africa. There is a growing demand in East Africa for sorghum mainly in the brewing industry and for breakfast and weaning cereals. Nonetheless the amount produced by farmers is too low to meet the demand (Gerda *et al.,* 2007).

Sorghum production in East Africa and Africa at large remains characterized by low productivity and extensive, low-input cultivation (ECARSAM, 2005). One reason for the yield gap is that farmers mostly use traditional varieties and management practices. In

Ethiopia, Kenya and Uganda less than 5% of sorghum farmers grow improved varieties in contrast to maize (Djurfeldt, 2015). Sources of crop losses vary significantly among countries. In Ethiopia, the largest producer of sorghum in eastern Africa, an estimated 35% of crop loss is associated to pests and diseases. This indicates that improved crop management and new varieties with increase resistance to pests and diseases can significantly increase sorghum yields (Wortmann *et al.,* 2009).

Stem borers are serious insect pests of sorghum in eastern African (Sharma, 1993) seriously reducing grain yield with severe consequences on food security. Losses of up to 85% due to stem borer have been in East Africa (Reddy *et al.,* 1988). Several strategies for managing sorghum-stem borers are intended to protect avoid or mitigate the destructive effect of the borers on crops but each option has its limitations. For instance, chemical control methods which are most effective are expensive to most resource-poor farmers and pose risks to farmer's health, livestock and the environment (Kumar *et al*., 2006). The effectiveness of pesticides is also limited especially when the caterpillars are feeding inside the stems (Kfir *et al.,* 2002). Biological control measures are efficient, cost-effective and environmentally harmless but are inadequate in maintaining the pest populations below the economic injury levels (Mailafiya *et al.,* 2009). Cultural control measures are easy to use and involve no cost, however, they have a confined way of application, may not be appropriate to large scale farms and they have difficulty in the timing (Kfir *et al.*, 2002). Host plant resistance is thus a better option for protecting plants against insect pests and forms an important part of integrated pest management (Hallauer *et al.,* 2010). It renders natural control without environmental concerns (Morais and Pinhero, 2012). Efforts are on-going in East Africa to identify sources of resistance to stem borers in cereal crops (Singh *et al.,* 2011). It is crucial to transfer genes conferring borer resistance to the adapted farmer preferred cultivars for ease of adoption. Future breeding should focus on high yielding stem borer resistant cultivars. This study was carried out to understand the nature of gene action, and the components that contribute to resistance or susceptibility to *C. partellus*, grain yield and yield components.

1.5 Objectives

1.5.1 Overall objective

This study aimed to generate high grain yielding sorghum cultivars which are resistant to stem borer (*C. partellus*) thus assist in addressing the sorghum – stem borer problems facing resource poor farmers, and improve their food security and livelihood.

1.5.2 Specific objectives:

1. To determine inheritance of resistance to stem borer and other agronomic traits in sorghum.
2. To estimate the genetic variability, heritability and expected genetic advance as well as association among agronomic traits in selected sorghum varieties.

1.5.3 Null hypotheses

1. Stem borer and agronomic traits in sorghum are not genetically controlled.
2. There is no genetic variability and low heritability in the selected sorghum parents for the selected traits.

CHAPTER TWO
LITERATURE REVIEW

2.1 Introduction

2.1.1 Importance of sorghum in East Africa

Sorghum, *Sorghum bicolor* (L.) Moench is the second most important cereal crop after maize in Africa and the most important crop in Semi-arid tropics (Adhrikari *et al.,* 2015). It is a staple food crop for many low-income households in East Africa. Sorghum is utilized as a source of human food and animal feed, apart from raw materials for the production of alcoholic beverages and bio-energy (Dahlberg *et al*., 2011). Sorghum consumption can improve human health due to its low cholesterol and high antioxidant phenolic content (Taylor *et al*., 2006). It has an additional advantage of being essentially gluten-free and has been confirmed to be safe for people with celiac diseases (Ciacci *et al*., 2007). Like maize, sorghum (hard and floury endosperm and large fat-rich germ), can be processed using dry and wet milling machineries (Taylor *et al*., 2003). The growing demand for sorghum is reflected in the increasing area under production in East Africa over the last 5 years. Reports indicate that the demands of the brewing industry have placed pressure on sorghum supplies in East Africa (FAOSTAT, 2012). The unique biology of sorghum permits the crop to conserve water resources while producing high yields of biomass and grain on marginal land, making it an ideal crop choice for the dry lands of East Africa (Howell, 2011).

2.1.2 Sorghum production and productivity

In Africa, sorghum is mainly grown by small scale, resource-poor farmers operating at the margins of subsistence (Muui *et al.,* 2013). The area under sorghum production in Eastern and Central Africa increased significantly from early 1970s to 2010 with marginal increase of 18% in productivity from 800 kg ha^{-1} to 940 kg ha^{-1} (Omoro *et al*., 2013) compared to yields >5000 kgha^{-1} usually obtained from experimental plots in this region (ICRISAT, unpublished reports). Production in East Africa and Africa at large is described as low productivity, extensive and low-input cultivation (ECARSAM, 2005). Increased production and productivity are requirements for commercialization leading to continuous contribution to improved livelihoods and economic growth (Mgonja *et al.*, 2006).

2.1.3 Production constraints

Sorghum cultivation in East Africa is affected by both biotic and abiotic factors (Muui *et al.*, 2013). Economically important biotic constraints include foliar and panicle diseases, witch weed (*Striga species*), stem borer and shoot fly (Worlmann *et al.*, 2006). Studies by Doggett (1978) and Guiragossian (1986) listed the constraints of sorghum production in eastern Africa. Although these production constraints cause significant grain yield loss, the relative importance varied from region one to another, within and among countries. For instance shoot fly was reported to cause significant grain losses in Uganda and Ethiopia, but was of less importance in Mozambique (Wortmann *et al.*, 2006). Majority of the sorghum fungal diseases reported worldwide occur in eastern Africa and usually invade susceptible cultivars (Guiragossian, 1986; Hulluka and Esele, 1992; King and Mukuru, 1994). Important abiotic constraints influencing productivity include drought, soil fertility and erratic rainfall. Drought stress at growing stage severely affects plant establishment, whereas at flowering or grain-filling stages it may lead to reduced grain yield or complete crop failure (Tumwesigye and Musiitwa, 2002). Low soil fertility, coupled with poor management practices, lead to low yields in the region (NRC, 1996).

Limited access to improved seed and efficient technology is another constraint affecting sorghum production in East Africa. Majority of sorghum farmers are smallholders with limited resources, hence are unable to purchase the necessary inputs such as quality seed, fertilizer and pesticides (Gordon, 2000)

2.2 Geographical distribution of stem borers

The geographical distribution of most injurious stem borers in sorghum is altitude- dependent (Kfir, 1997). Maes (1998) listed 21 economically important lepidopteran stem borers of cultivated grasses in Africa. *C. partellus, C. sacchariphagus Chilo Orichalcociliellus, E. saccharina, B. fusca* and *Sesamia calamitis* are reported as important and widely distributed stem borers of maize and sorghum. Two of them; *C. partellus* and *C. sacchariphagus* are introduced species. *Chilo partellus* is an Asian species (Bleszynsky, 1970) that invaded Africa sometimes before 1930 when it was first observed in Malawi (Tams, 1932). However, it was not reported in Tanzania until some 20 years later (Duerden, 1953). It has since established in Ethiopia, Sudan, Somalia, Kenya, Tanzania, Uganda, Mozambique, South Africa, Swaziland, Lesotho, Zambia, Zimbabwe, Botswana and Malawi (CABI, 1989; Harris, 1990; Ingram, 1983). Overholt *et al*. (2000) predicted the subsequent distribution of *C. partellus* in Africa based on the climate at locations where it was known to occur and then generalizing to other locations with similar climate. Several factors affect stem borers population dynamics which include; location and stability, host availability, mating location, success of oviposition, larvae establishment and survival, temperature and altitude (Mailafiaya *et al.*, 2011). *C. partellus* reportedly occurs below 1500 m a.s.l., while *B. fusca* is found at elevations greater than 1500m a.s.l (Kfir *et al.*, 2002). Distribution of *C. partellus* in low- and mid-altitude areas is attributed to favourable abiotic factors, mainly temperatures and humidity (Reddy, 1988 and Zhou, 2001). However, Kfir (1997), Zhou *et al.* (2001) and Ong'amo *et al.* (2006) have reported its extended distribution into higher elevations. In Kenya, *C. partellus* diapauses for several months in the dry season (Kfir *et al*., 2002). But a population without a resting period was reported from the Coastal Province of Kenya and Uganda (Kfir, 1997). In periods between cropping seasons, in the coastal province of Kenya, some stem borers diapause in maize stubble, whereas others remain active feeding on wild grasses such as wild sorghum (Kfir *et al.,* 2002).

2.3 Biology and spread of stem borer

The first information about the life cycle and the economics of *Chilo partellus* was reported by Swinhoe in the 1900's (Kfir, 1997). *C. partellus* undergoes complete metamorphosis involving changes from egg, larval, pupal and adult stages. The borer goes through 1, 2 or more generations per annum, depending on the site and the availability of host ranges (Muhammad and Underwood, 2004). In warm low-altitude areas with enough hosts to maintain larval populations, *C. partellus* breeds throughout the year. The borer starts diapause in the larval stage, at higher altitudes or during dry seasons (Kfir *et al.,* 2002). Female spotted stem borer moths lay eggs beneath the host leaf near the midrib in 3 – 5 rows and in groups of 50 – 100. These eggs are flattened, ovoid and about 8 mm long. Hatching takes place after 7 – 10 days. A few days after hatching, early larval instars move upwards on plants and into the whorl to feed on leaf surfaces. The late-larval instars bore into the stalk of the host plant. In older plants, the instar feed on the panicle. The larvae of spotted stem borer have a cream coloration, with dark spots on the dorsal surface and a brown head capsule. When mature the larvae measure about 25 millimetres long. These larvae can be differentiated from *B. fusca* and *Sesamia calamistis* larvae by the presence of circular hooks on their prolegs. In *C. partellus*, the hooks are arranged in complete circles, whereas in *B. fusca* the hooks are arranged in curved shapes. The larval period takes about 28 – 35 days. Pupation occurs in seven to ten days in small chamber in the stem of the host plant. Preceding pupation completely grown up larvae cut exit holes to allow the adult moth emerge from the plant (Kfir *et al.*, 2007). *B. fusca* and *C. partellus* are polyphagous. They feed on several plants including maize *(Zea may*), sorghum (*Sorghum bicolor*), rice (*Oryza sativa*); sugarcane

(*Saccharum officinarum*) and several millets such as pearl millet (*Pennisetum glaucum*); various grasses including sudan grass (*Sorghum vulgare sudanense),* napier grass (*Pennisetum purpureum*) and *Sorghum arundinaceum* (Devs.) (Moolman, 2014; Matama *et al.,* 2008). The adult moths of stem borer have a wing span of 20 – 30 mm. The male are smaller and darker than the females. The fore wings of males are pale brown while those of females are paler with the hind wings almost white (Kfir, 1997).

2.4 Sorghum Stem borer damage and symptoms

Wild host plants play an important role in the ecology of gramineous stem borer species. Fodder crops namely Napier grass (*Pennisetum purpureum*) and Sudan grass (*Sorghum sudanense*) worsen significantly more oviposition than sorghum (*Sorghum bicolor*). Nevertheless, the survival of larvae on napier grass is poor (Khan *et al.*, 2011). In sorghum, stem borer larvae feed on the leaf whorls as they move into the stem where they are protected from insecticides and natural enemies (Muhammed *et al.*, 2009). Larval feeding on the leaves reduces plant vigour, photosynthetic efficiency and grain filling (Tende *et al.*, 2005). The caterpillar entry at the apical meristem results in dying of 2 – 3 central leaves, called "deadheart" which may lead to delayed maturity due to tillering (Kishiore *et al.*, 2007). The third-instar larvae leave the whorl leaves and drill into stem base and cause extensive stem tunnels through the vascular system as they feed thereby reducing the biological processes of nutrients and assimilate (Odiyi, 2007). Additionally, stem tunneling reduces grain filling, weakens the stems and may cause lodging and tendency to infection by stalk rot diseases (Buntin, 2009). Prior to pupation, the full-grown larvae cut exit holes in the stem to enables the emerging moths to escape. Yield reduction due to stem damage depends on pest population density and physiological stage of the crop at infestation (Kfir *et al.*, 2002).

2.5 Management of stem borer

Several strategic approaches for stem borers' management have potential to alleviate the destructive effect of these pests. However, each option has its own limitations. Chemical controls are more effective though they are expensive to most small scale farmers and pose risks to humans, livestock and the environment. Biological control measures are efficient, economical and environmentally harmless but are insufficient to manage the pest populations below economic injury level (Mailafiya, 2009). The cultural control methods are economical and considered the first line of defense against pests which includes practices such as destruction of crop remains, crop rotation, intercropping, tillage methods and manipulation of planting dates (Van *et al.,* 1998). Though cultural management seems promising, most African farmers have not adopted them due to lack of capacities by the farmers especially in areas where farming societies lacked support of proper extension service (Harris and Nwanze, 1989). Host plant resistance (HPR) can provide a basis on which to build an integrated control system and will be most effective when used complemented by chemical, biological and cultural methods. A resistant crop variety confers an integral and the best economic control method of certain pests (Sharma *et al.,* 1992). The use of HPR is lagging behind due to the polygenic nature of resistance to insect pests, inadequate understanding of its inheritance, lack of durable resistance sources and the high cost linked to plant breeding (Hallauer, 2010). Nonetheless, understanding of stem borers activities and their association with their hosts is essential for the development of effective management strategies.

2.6 Mechanisms of stem borer resistance in sorghum

Webster, (1975) broke down plant resistance to insect damage into three broad mechanisms: Antibiosis, antixenosis and tolerance.

2.6.1 Antibiosis

Antibiosis refers to a resistance in which biology of the insect is affected so that pest abundance and later damage is reduced compared to that which would have occurred if the insect was feeding on susceptible crop varieties (Teetes *et al.,* 2009). It is expressed as larval and pupal mortality, reduced larval and pupal weights, extended larval and pupal development and decreased fertility (Kumar *et al.,* 2006). Antibiosis components operate in leaf and stem tissues (Dhillon *et al.,* 2006). According to Kumar *et al*. (2007), Sorghum genotypes namely ICSV 705, ICSV 714, IS 1044, IS 2205 and IS 18573 have demonstrated antibiosis to *C. partellus* in terms of decreased larval survival, growth and feeding. Traits associated with resistance to cereal stem borers include high tannin, total phenols, low sugar, high amino acids and high silica content (Padhi, 2004).

2.6.2 Antixenosis (non-preference)

Antixenosis is a plant resistance mechanism in which pests may occur on host plants without changing them or suffering decreases in vigor. Presence of antifeedants such as glycosides, alkaloids, terpenoids contribute to antixenosis mechanism of stem borer resistance in sorghum (Sharma, 2008). Chemical substances in the leaf surface (Benz aldehyde, p-OH benzoate, and -CN-ion metabolites) defend sorghum against dehydration, disease and insect feeding and movement (Kishore *et al.,* 2007). Ligular and trichome hairs interfere with stem borers movement, feeding and oviposition (Muhammad *et al.,* 2009). Increased leaf thickness, fiber and epidermal cell wall toughness hinder feeding by stem borer larvae in maize (Bergvinson *et al.,* 2002).

2.6.3 Tolerance

Reese *et al.* (1994) described tolerance as a situation where the plant is able to harbour a population of insect pests which would harm a susceptible variety without loss of yield/quality. Sorghum tolerance to *C. partellus* damage has been cited in sorghum line IS 2205 after establishing grain yield loss (Dhillon and Sharma, 2012). Studies carried out by ICRISAT - Patancheru, showed that less than 20% plants with deadhearts also exhibited good recovery resistance (Sharma and Nwanze *et al.*, 1997). Sorghum tillering following stem borer damage and in reaction to shoot flies is an element of tolerance (Kishore *et al.*, 2007). Factors of tolerance include changes in photosynthate partitioning, vigour, compensatory development in infested plants, rapid lesion curing, and tissue mechanical defence (Dhillon *et al.*, 2006).

2.7 Gene action for stem borer resistance

Information on gene action for traits controlling resistance to stem borer is useful in development of an appropriate breeding scheme to develop stem borer resistant cultivars (Muturi *et al.*, 2012). Effective breeding for sorghum-stem borer resistance requires proper understanding of gene action involved in the inheritance of the trait (Pathak and Olela, 1983). The genetic components involving quantitative or polygenic traits may be classified as additive, dominance and epistasis effects (Falconer, 1996). The additive effects presents the percentage of a trait that can be inherited from parent to the offspring and it describes the level of resemblance amongst progenies and their parents. Non-additive genetic effects are non-transmissible to the progeny and denote all types of differences that may not be described by the additive model and may include dominance and epistasis (Falconer *et al.*, 1996). Given the preceding, it is vital to demonstrate the nature of inheritance of resistance to stem borer so that appropriate breeding approaches are devised. Most studies of resistance to stem borer in sorghum show both significant GCA and SCA effects suggesting that additive and non-additive gene action are significant in controlling the resistance (Udaykumar *et al.*, 2013). Additive, dominance, and epistatic effects have also been reported by Murenga (2015) which partially clarifies why breeding for stem borer resistance has been difficult. Andre *et al.* (2003) reported additive and dominance effects to influence the manifestation of resistance to *C. partellus* which compromises heritability especially when the non-additive component is predominant. Previous genetic studies have indicated that at least 10 genes are involved in resistance and that gene action is primarily additive (Singh *et al.,* 2012). Significant genotype by environment interactions (G x E) for leaf damage, exit holes and stem tunnels against *C. partellus* and *B. fusca* has been mentioned in different maize backgrounds (Karaya 2009 and Beyene *et al.,* 2011). This observation explains why relatively few cultivars are reported to be resistant to both borers in sorghum and maize. Highly significant genotype by environment interactions results to different ranking of genotypes in diverse environments (Muturi *et al.,* 2012).

Sorghum tolerance to shoot insect pests is generally reported to be controlled by additive gene action (Dhillon *et al.,* 2006). Singh (2011) and Karaya *et al.*, 2009 reported that stem borer resistance is controlled by additive gene effects. In maize, polygenic traits mainly leaf feeding, deadheart, exit holes and stem tunneling damages are considered when selecting for *C. partellus* resistance (Tefera *et al.,* 2011). Crossing among stem borer lines with good combining ability for different stem borer resistance mechanisms would reduce damage in sorghum (Aruna and Padmaja, 2009). Sorghum leaf damage was reported to be controlled by dominance gene action (Sharma *et al.,* 2007). Singh and Verma, (1988) observed that GCA effect (additive gene action) controlled leaf damage, and specific combining ability (SCA) effects (non-additive gene action) were important for sorghum stem damage. Additive gene action has been reported to control exit holes and stem tunneling in maize against *C. partellus* and *B. fusca* (Karaya *et al.,* 2009). Singh (1988) observed additive gene effects to be dominant for deadheart and leaf injury resistance in sorghum.

2.8 Methods of screening sorghum germplasm for resistance to stem borers

Effective screening of sorghum lines for selection requires vigorous plants. Plants subjected to different stress conditions like drought, salinity, heat and low soil fertility may obscure expression of resistance or plants may be "escapes" thereby reducing heritability for insect resistance traits in sorghum (Taneja *et al.*, 1984). Heterosis and different maturity groups may also determine screening procedure for comparison. Utilization of local resistant and susceptible checks will aid in determining the threshold of comparison of sorghum test genotypes (Jotwani *et al*., 1978; Sharma *et al*., 1992).

There are two techniques of infestation with stem borers i.e. natural and artificial. Natural infestation is the use of hotspot locations where the pest pressure is high and frequently coincides with the critical phase of plant growth. Homogeneity in the distribution of the infestation is challenging due to lack of unchanging pest populations across season, and the chance of test genotypes being "escapes" or over infested (Nwanze, 1991). A protocol for artificial infestation in sorghum genotypes in the field with first instar larvae of *C. partellus* for resistance screening was developed at ICRISAT (Taneja and Leuschner, 1985). Through artificial infestation uniformity is accomplished since each test genotype is infested with at least 5 larvae or neonates or egg masses at the whorl stage 2 weeks after sowing. Infestation may be accomplished manually using camel hair brushes or through the bazooka applicator for large-scale experiments (Tefera *et al.,* 2010). Nonetheless, the larvae colonies applied especially the first instar-larvae and egg masses should be vigorous and survive to cause feeding damage to the test genotypes under field conditions. Infestation should be carried out in the late afternoon or mid-morning to limit desiccation of larvae. Uniformity for the number of larvae per plant used for infestation is most critical in separating the test genotypes.

Factors like plant vigour, plant age, temperature and relative humidity may influence the observations on the test genotypes (Tefera *et al.*, 2010).

2.9 Selection indices

These are multivariate techniques that combine data of various traits of agronomic interest with the genetic properties of a population. While using selection indices, numerical values are weighted and serve as an additional hypothetical character resulting from a grouping of various traits of interest (Mutinda, 2013). Selection for *C. partellus* resistance based on single parameters is thus difficult as sorghum genotype resistant to one form of damage may be susceptible to another (Ajala *et al.,* 1993). Sorghum resistance to stem borer damage is based on leaf injury, deadhearts, exit holes, cumulative tunnel length, effect of the survival and development of the insect and recovery resistance (Mahla *et al.,* 2007). Suitable indices help breeders in simultaneous selection for resistance in addition to grain yield performance. Several examples in the use of selection indices with improvements in stem borer resistance and grain yield in sorghum have been stated in literature (Ajala *et al.,* 2010).

2.10 Breeding methods for sorghum improvement

2.10.1 Conventional breeding methods

Breeding is a process of changing characteristics over a number of generations by applying selection pressure on the population. Limited work has been done in developing insect resistance and high yielding sorghum varieties for cultivation by the farmers. This is because of lack of knowledge on inheritance of the morphological traits associated with insect resistance, agronomic traits and grain yield (Sharma *et al*., 2005; Riyazaddin *et al*., 2015). Traditional breeding methods like germplasm evaluation and enhancement, pedigree selection, backcrossing and recurrent selection remain integral in the development of insect resistant cultivars with major resistance genes (Huang *et al*., 2013). In these methods, sorghum breeders look for genetic variability with regard to insect resistance which is then incorporated into the breeding lines, leading to the development of resistant commercial cultivars or hybrids. Most breeding approaches are centred on generation of segregating populations followed by selection (Walker, 2006). Because sorghum is a self-pollinated crop, during selection, the population is continuously allowed to self-pollinate to produce homozygous pure lines.

2.10.2 Biotechnology techniques

In contrast to conventional breeding approaches that takes five to ten generations to transfer a trait within a species into high yielding, locally adapted cultivars, the non-conventional techniques such as marker assisted selection (MAS) offer fast introgression of the resistance genes and ultimately gene pyramiding in high yielding varieties or hybrids (Aruna *et al*., 2011; Chu *et al*., 2011). Resistance in sorghum should be combined with other desirable traits such as grain yield and good quality grain to establish an integrated pest management system (Satish *et al*., 2009; Srinivas *et al*., 2009). Several insecticidal genes from *Bacillus thuringiensis* (Bt) strain have been used in insect control through biotechnology techniques. *Bacillus thuringiensis* genes that are presently utilized expressed significant effectiveness against Lepidoptera. Most of the sorghum insect pests are Lepidoptera insects, hence, Bt genes used in maize and soya bean crops could be applied to control Lepidoptera insects in transgenic sorghum plants. Girijashankar *et al*. (2005) developed transgenic sorghum plants showing a synthetic *cry1Ac* gene under a wound-induced promoter mpiC1. The Bt transgenic plants showed some resistance against spotted stem borer (*C. partellus*) larvae.

2.11 Mating Design

Mating design refers to schematic cross between groups of strains of plants made to generate progenies in plant breeding. Mating designs were developed to study quantitative traits

(Singh *et al*., 2004) and are necessary for successful plant breeding schemes (Khan *et al*., 2009). So far, six mating designs have been developed as follows; Bi-parental progenies, Top cross, Polycross, Diallel (I, II, III and IV), Line x tester design and North Carolina design (I, II and III). The choice of a mating design is determined by the objective of study, time, space and other biological factors or limitations. With the help of these designs, various genetic components of variation were established (Hallauer *et al*., 2010; Acquaah, 2012).

2.11.1 North Carolina II design (NCD II)

Hallauer (2007) recommended NCD II as a preferable mating design which can make use of a large number of parents leading to fewer crosses than a diallel mating design. It has been used in plant breeding for selection of testcross performance (Qu *et al.,* 2012). This design is a factorial experiment that measures the effect of male and female and their interaction (Comstock and Robinson *et al.,* 1952). According to Hallauer *et al.* (1988), male and female main effects and male x female interaction effects in NCD II design are equivalent to the GCA and the SCA effects in a diallel. The main difference between NCD II and diallel is that there are two independent estimates for the GCA effects in the NCD II, which is an advantage of NCD II over the diallel. The two independent GCA estimates allows determination of maternal effects and computation of heritability based on male and female variance, which is free from maternal effects. An additional advantage of the NCD II design is that mating parents in sets can enhance the sample size to be tested (Hallauer *et al.,* 1988). The design is a two way ANOVA in which the variation may be partitioned into variations between males (m) and females (f) and their interactions.

2.12 Estimates of combining ability

Combining ability is the parents' ability to produce superior progenies when combined with another parent (Haron *et al*., 2006). An estimate of combining ability is the measure of value of genotypes, based on the performance of their progenies that have been produced in a definite mating system (Allard *et al.,* 1960). Combining ability estimates enable predicting the performance of genotypes that may be populations, inbred lines or varieties. The performance of a hybrid is associated to the combining ability (GCA) and specific combining ability (SCA) of the inbred lines involved in the cross. The concept of GCA and SCA was introduced by Sprague and Tatum (1942) and its mathematical modelling was established by Griffing (1956). Combining ability estimates provide a useful guide to selecting parents for breeding programmes. Plant breeders have used measurements of GCA and SCA effects to trace heterotic natures among breeding populations and pools.

2.12.1 General combining ability (GCA)

GCA is the average performance of a genotype in a series of hybrid combinations (Sprague and Tatum, 1942) and is due to the activity of genes which are mainly additive in their effects as well as additive by additive interactions (Griffing *et al.,* 1956). GCA evaluation is used in early screening of segregating populations in a breeding program, enabling lines with poor GCA to be discarded. High GCA estimates imply higher heritability and less error effects. It may also lead to less gene interactions and higher accomplishment (Allard *et al.,* 1960). Hybridization among stem borer lines with good combining ability for various resistance mechanisms would reduce damage in sorghum (Aruna and Padmaja, 2009). Singh and Verma (1988) reported predominance of GCA effects for leaf damage, however SCA effects (non-additive genetic effect) was important for stem borer resistance in sorghum.

2.12.2 Specific combining ability (SCA)

Specific combining ability the performance of a combination of a specific inbred line in a particular cross (Sprague *et al.,* 1942). It is considered as interaction of loci with dominance and epistatic effects (non-additive effects) of the genes and so suggests the value of particular hybrid combinations. A high SCA indicates a large effect of non-additive gene action (Fasahat and Payvandy, 2016). In addition, SCA estimates can be used to determine heterotic relations among different genotypes. According to Hallauer and Miranda (1988), any new elite germplasm introduced into a breeding program should be tested for GCA and SCA estimates, since these are related to and dependent on a particular set of materials under evaluation (inbreds or populations).

2.13 Broad sense heritability, genetic variability and genetic advance

Heritability refers to the proportion of variability among individuals in a given population due to genetic variation (Singh *et al.,* 2003). Two types of heritability can be estimated, namely;

- Broad sense heritability (H^2) as the ratio of total genetic variance to the phenotypic variance ($H^2 = V_G/V_P$). The total genetic variance is made up of additive, dominance and epistatic variances, where dominance involves intra-locus effects and epistasis involves interactions among loci (Singh, 2003).
- Narrow sense heritability (h^2) refers to the ratio of additive genetic variance to total phenotypic variance ($h^2 = V_A/V_P$) (Singh, 2003)

The desired variability can successfully be employed by various breeding techniques. Heritability especially narrow sense is important for plant breeders as effectiveness of selection depends on the additive genetic components in relations to total variance (Falconer *et al.,* 1996). H^2 is more important in plant and animal selection programs, because response to selection depends on additive gene effects. Besides, resemblance between relatives is driven commonly by additive genetic effects (Hill, 2008) when individuals have different alleles at loci that contribute to measurable variation in performance.

Heritability may be decreased by using either inbred lines (thus decreasing variance G) or those reared in very diverse environments (thus increasing variance G). Due to such variances, different populations of a species might have different heritabilities for even the same character. Practical knowledge of mechanisms of resistance of the genetic attributes involved helps in formulating a breeding strategy for their improvement. The transmissibility of polygenic traits such as plant height, panicle length, 100 seed mass and grain yield per plant depends on the extent of their heritability (Firouzian, 2003).

Genetic variability for yield related traits is vital for developing high yielding varieties in sorghum (Tester and Langridge, 2010). Phenotypic variability in a particular environment can be easily evaluated. The phenotypic variation is separated into genetic and environmental variances for perfect understanding of the nature of variation. Genotypic coefficient of variation (GCV) measures the variability of any trait due to genetic factors and the magnitude of the environmental influence on any character is determined by the extent of the differences between the GCV and phenotypic coefficients of variation (PCV) (Akinwale *et al*., 2011).

CHAPTER THREE

INHERITANCE OF RESISTANCE TO SPOTTED STEM BORER (*Chilo partellus*) AND YIELD TRAITS IN SELECTED SORGHUM PARENTS

3.1 Introduction

Sorghum [*Sorghum bicolor* (L) Moench] is an essential crop for farmers in semi-arid and arid areas for its resilience to low moisture, high temperatures and less fertile soils compared to other cereal crops. It is a major cereal crop and a staple food for more than 500 million people, mostly in sub-Saharan Africa and Asia (National Research Council, 1996). The spotted stem borer [*Chilo partellus* (Swinhoe)] a species which was incidentally introduced to Africa from Asia (Tams *et al*., 1932), is one of the most important lepidopteran stem borer pests of sorghum and maize in Eastern and Southern Africa (De Groote and Dorsch, 2003).

Cultural, biological and chemical control methods have been employed, but are either ineffective or costly to small scale farmers. Cultural methods reduce the pest population but do not effectively manage the pest (Hill,1983). Biological control is costly, labour intensive and profits are made in long-term (Zhang *et al*., 2007). Chemical insecticides though effective, are uneconomical on small farm holdings and are rarely available on time (Abate *et al*., 2000). In addition, chemical insecticides have harmful effects on the environment as they are health hazards to humans and may be harmful to beneficial insects (Edwards, 2013). Plant resistance is an important component for controlling this pest under subsistence farming conditions (Sharma, 2008). Host plant resistance to insects is the effect of heritable plant trait that result in a plant being relatively less damaged than the plant without these traits (Beck, 1965). Stem borer research in East Africa has been mainly geared towards cultural and biological control methods and lately in maize on genetic engineering using *Bacillus thuringiensis* (Bt) *cry 1Ac* gene against *Chilo partellus* (Mailafiya *et al*., 2009).

Breeding to improve sorghum local landraces for resistance to *C. partellus* and *B. fusca* has been limited partially owing to inadequate understanding of the genetics of resistance (Karaya *et al.,* 2009) and there is inadequate literature concerning inheritance and resistance mechanisms to *C. partellus* in East Africa (Muturi *et al.,* 2012). Sources of sorghum-stem borer resistance have been reported but the levels differ from low to moderate hence the need to enhance the levels and broaden the basis of resistance through screening more germplasm (Singh *et al.,* 2011). Selective breeding based on inheritance studies has contributed to crop improvement. Breeding for resistance to stem borer in sorghum is challenging because it is a quantitative trait and involves polygenes with low heritability (Sandoya *et al.,* 2010; Muturi *et al*., 2012 and Murenga *et al*., 2015). Hence, for effective management of stem borers by host plant resistance, effective breeding methods should be incorporated for better application of new and existing sources of resistance. Better understanding of the genetic basis of the resistant traits among the parents used may contribute towards the development of effective breeding against *C. partellus*.

Before undertaking any crossing program, it is essential to understand the breeding value of the parents. Hallauer and Miranda (1988) advised that any new elite germplasm introduced into a breeding program should be tested for GCA and SCA estimates, since these are related to and are dependent on a particular set of materials under evaluation (inbreds or populations). GCA is the result of additive gene effects, while the SCA is the result of non-allelic interaction (Jinks, 1954). Estimates of combining ability are useful to predict the relative performance of different lines in hybrid combinations (Kenga *et al*., 2004).

The information on the nature and magnitude of gene action is essential in understanding the genetic potential of a population in determining the appropriate parent lines and designing the breeding strategy to be adopted in a given population (Liberatore *et al.,* 2013). Therefore, the study was undertakaen at determining the nature of inheritance of stem borer resistance and yield traits in selected sorghum parents adapted in eastern Africa.

3.2 Materials and Methods

3.2.1 Planting material

The experimental material used in the study comprised of three sorghum lines with resistance to stem borer sourced from the International Research Institute for Semi-Arid Tropics (ICRISAT) which were used as male parents and 10 agronomically superior farmer preferred females susceptible to stem borer (Table 3.1). North Carolina Mating Design (NCD II) was used where the three male parents were crossed to each of the ten female parents to generate 30 F_1 progenies.

Crossing was carried out at KALRO – Kiboko during the 2013 short rainy season. Where each of the ten female parents was crossed with each of the three donor parents following NCD II mating design. The emasculation was done using the plastic bag technique. The crossing block was stagger planted to aid in the nicking of male and female parents. The F_1s were planted together with their parents to identify true crosses using morphological traits. The harvested seed from the true crosses was bulked per cross and advanced to F_2.

Table 3.1 List of 18 sorghum lines used in this study

Parent	Entry	Origin
Females		
1	Gadam el-Hamam	Sudan
2	Hariray	Eritrea
3	Hugurtay	Eritrea
4	IESV 23008 DL	ICRISAT-Nairobi
5	IESV 23010 DL	ICRISAT-Nairobi
6	IESV 23011 DL	ICRISAT-Nairobi
7	KARI Mtama-1	Kenya
8	Macia	ICRISAT-Zimbabwe
9	Sila	Seed Co. Zimbabwe
10	Tegemeo	Uganda
Males		
11	ICSV 700	ICRISAT-India
12	IS 1044	ICRISAT-India
13	IS 2205	ICRISAT-India
Checks		
14	IS 8193	Kenya
15	ICSB 464	ICRISAT-India
16	ICSV 745	ICRISAT-India
17	Kiboko local-2	ICRISAT-Nairobi
18	Seredo	Uganda

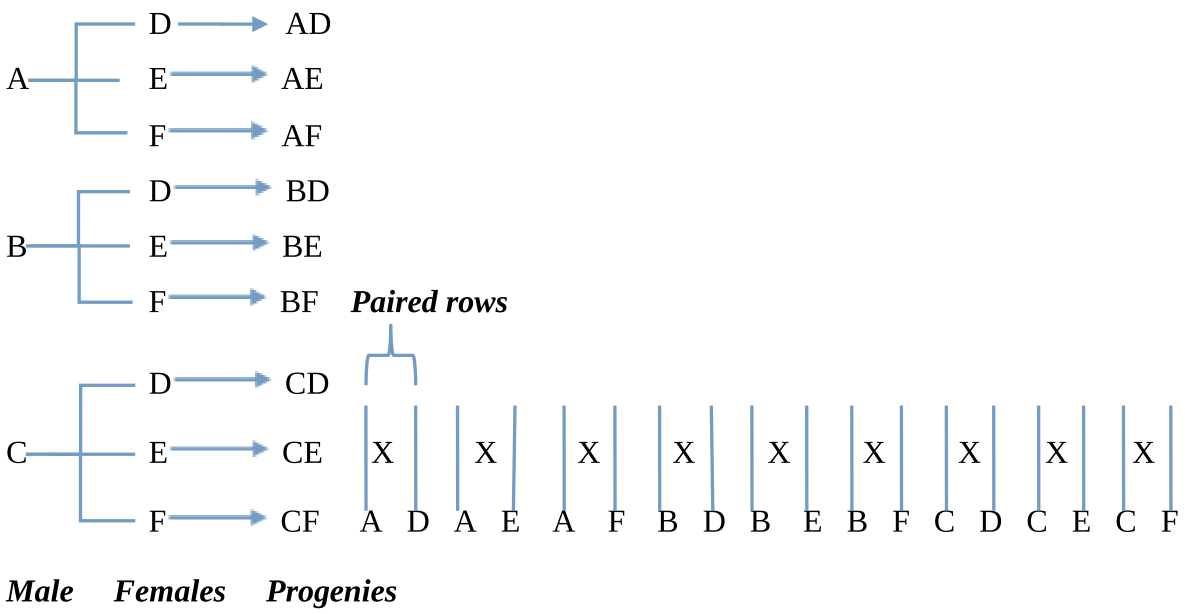

Figure 3.1: North Carolina Design II (Factorial design with paired rows)

3.2.2 Experimental sites

Experiments were carried out at two different locations, Kenya Agricultural and Livestock Research Organization (KALRO)/ICRISAT- Kiboko and at the University of Nairobi, Faculty of Agriculture field station, Kabete during the short rainy season in 2015. KALRO/ICRISAT - Kiboko (2^0 20'S $37^0$45'E, 960m a.s.l) is located in the dry lowland agro-ecological zone of eastern Kenya and experiences an average minimum and maximum daily temperature of 16.6^0 to 29.4^0C respectively with February and October being the hottest months (Franzel *et al.*, 1999). The location has an average annual precipitation of approximately 604 mm. The soils are well drained with a soil pH of about 7.9 (Jaetzold *et al*., 1982).

The University of Nairobi, Kabete field station lies at latitude 1^0 15'S and longitude 36^0 44'E and at an altitude of about 1940m above sea level (Muturi *et al.*, 2012). The area experiences a bimodal rainfall with average annual precipitation of 1000 mm. The long rains occur from March/ April to May/ June and the short rains from October through December with average minimum and maximum daily temperature of 16^0C to 23^0C, respectively (Franzel *et al.*, 1999). Nyandat *et al.* (1970) described the site as having dark reddish brown clay and overlying dark red clay, well drained soils with top soil pH range of 5.2 - 7.2 and sub soil pH range of 5.2 - 7.7.

3.2.3 Weather data during the experiment period

The average seasonal temperatures were 31.8^0C and 14.5^0C at Kiboko and Kabete, respectively. Amount of rainfall was 465.2 mm at Kiboko while at Kabete was 944.5mm. The relative humidity (RH) at Kiboko and Kabete was around 84% and 58% respectively. The weather data were obtained from KARLO-Kiboko and Kabete meteorological stations (Table 3.2).

Table 3.2: Average daily temperature, Relative humidity and Rainfall recorded at Kiboko and Kabete in 2015 – 2016

Month	Average Temperature (^{0}C)	Relative Humidity (RH)%	Rainfall (mm)
		KIBOKO	
November	31.4	81.5	155.0
December	30.9	87.1	160.5
January	31.8	86.1	65.7
February	32.9	82.6	84.0
Mean	31.8	84.3	116.3
Total			**465.2**
		KABETE	
November	14.9	64.5	478.3
December	14.7	61.7	177.7
January	15.1	61.0	98.4
February	14.2	55.0	100.3
March	13.6	48.0	89.8
Mean	14.5	58.0	188.9
Total			**944.5**

3.2.4 Experimental design and field operations

The 30 F_2 families together with 13 parents and six checks were sown in alpha-lattice trial design, consisting of seven plots in seven blocks in each replication with two replications in each location. Each plot comprised of 4 rows with inter-row spacing of 75 cm and intra-row spacing of 25 cm. Between replicates, a 1.5m route was left to allow for easy movement during data collection and agronomic management. Two seeds were sown per hill and later thinned to one plant per hill. The plots were fertilized with a basal application of diammonium phosphate (DAP) as a source of Phosphorous and Nitrogen at recommended rate of 60kg P_2O_5/ha and 40kg N/ha respectively. Top dressing was carried out with CAN at the rate of (60kg N/ha) as recommended for each location. The trial was rain-fed with supplementary irrigation depending on need at both locations. The fields were kept free of weeds by hand weeding throughout the growth period. Bird damage was prevented by scaring.

3.2.4.1 Artificial infestation with *C. partellus*

First instar neonates of *C. partellus* used in this study were obtained from KALRO, Katumani stem borer insect pests mass rearing facility. At 30 days after sowing, 10 healthy plants selected randomly from the 2 middle rows were tagged and artificially infested in a controlled and uniform manner with five to seven larvae per plant using a camel hair brush. To prevent dying of larvae in the water held in leaf whorls, sorghum seedling whorls were tapped gently before infestation. Infestation for both locations was carried out late in the evening, when the temperatures were low to avoid larval mortality.

3.2.4.2 Data collection

All stem borer damage data were collected from tagged plants. Data on leaf damage were taken at two and four weeks after artificial inoculation. The tagged ten plants in the two middle rows were carefully monitored and data were collected systematically from plant as follows:

i. Data on leaf feeding was recorded by visual rating score two weeks after infestation on a scale of 1-9 where, 1 = highly resistant and 9 = plants dying as described by Beyene *et al.* (2011) (Table 3.3).

Table 3.3. Scale for scoring stem borer foliar damage in sorghum

Score	Visual ratings of plant damage	Reaction to resistance
1	Few pin holes	Highly resistant
2	Few shot holes on a few leaves	Resistant
3	Several shot holes on leaves (<50%)	Resistant
4	Several shot holes on leaves (>50%)	Moderately resistant
5	Elongated lesions (>2cm long) on a few leaves	Moderately resistant
6	Elongated lesions on several leaves	Susceptible
7	Several leaves with long lesions with leaf tattering	Susceptible
8	Several leaves with long lesions	Highly susceptible
9	Plant dying due to death of growing points (deadhearts)	Extensively sensitive

Source: Adapted and modified from CIMMYT (1989).

ii. Observations on deadheart were recorded at 2 and 4 weeks after infestation. Deadheart incidence was taken by expressing the number of plants showing deadhearts as a percentage of the total number of plants sampled.

iii. At harvest, all the sampled plants were cut from the base and leaf sheaths removed and the number of exit holes on the stem were counted.

iv. The main culms of the plants infested with *C. partellus* were dissected from the base to the apex, number of larvae recovered alive and dead were recorded and the cumulative tunnel length measured in centimetres to determine the nature and the magnitude of the stem injury to the different plant parts.

Resistant/susceptible traits namely; leaf damage, deadheart, number of exit holes and stem tunnelling were used to express the response of the sorghum genotypes to *C. partellus*. A selection index based on the four damage parameters considered was computed by adding the ratios between the genotypic values and the trait mean and divided by 4 (number of damage parameters considered) Tedele *et al.*, (2011).

Data were also taken on the following agronomic traits namely; plant stand after thinning; number of days to 50% flowering; plant height (cm); panicle length and width (cm); plant stand at harvest; dry panicle weight (g); number of harvested tillers; grain weight (g); 100 seed mass (g) and sugar brix (%) at harvest.

1. Plant stand after thinning was recorded from the two middle rows.
2. Days to 50% flowering was recorded as the number of days from planting to anthesis of 50% of the plants in the 2 central rows.
3. Plant height of the marked plants was measured and recorded from the base of the plant to the tip of the panicle at grain filling stage.
4. The number of productive tillers was recorded per plant from the 2 middle rows.

5. Panicle length was measured in centimetres as the mean length of the panicle measured on a sample of 10 heads from the base to the tip of the head.
6. Dry panicle weight was measured as the dry weight of all harvested panicle.
7. Brix is a measure of the soluble solids in the sorghum juice (Nibouche and Tebere, 2008). The cane was crushed and squeezed by hand and the juice dispensed on the sample area of a refractometer. The sample dip area was cleaned using methylated spirit to avoid sample contamination.
8. Hundred seed mass was measured on 100 seeds in each sample and weight expressed in grams.
9. Grain yield was measured using an electronic balance from each of the tagged ten plants after harvesting sun drying and threshing.

3.2.5 Statistical analysis

3.2.5.1 General analysis of variance

Data on percentages was arcsin transformed whereas that of counts was log transformed before analysis of variance (Kishore *et al*., 2007). Percentages of plants showing leaf damage were calculated by expressing the number of plants with pinholes damage as a percentage of the total number of plants studied.

The general analysis of variance to determine differences between genotypes was performed for individual experiments as well as for combined environments, considering genotypes as fixed and environment as random effects for all traits. This was carried out according to Gomez and Gomez (1984) using Genstat 15th edition computer software (Payne *et al*., 2015). The treatment means were compared using protected Fisher’s least significant difference test at $P \leq 0.05$.

3.2.5.2 Combining ability estimates

Combining ability analysis was performed by estimating General and specific combining ability effects and variance according to the factorial model by Comstock and Robinson (1948) as follows:

$$Y_{hijk} = \mu + \alpha_i + ß_j + (\alpha ß)_{ij} + R_h + {}_{hijk} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (3.1)$$

Where:

Y_{hijk} = the observation of the Kth full-sib progeny in a plot in h-replication of the ith paternal parent and the jth maternal parent; μ = the general mean; α_i = the effect of the ith male parent; $ß_j$ = the effect of the jth female parent; $(\alpha ß)_{ij}$ = the interaction of the paternal and maternal genotypes; R_h + the effect of hth replication and $\mathcal{E}_{hijk}$ = the environment effect and remainder of the genetic effect between full-sibs on the same plot.

The SAS computer package, version 9.3 was used with effect of genotype considered as fixed effects whereas the environments were considered as random effects. The GCA effects of all the 13 lines and SCA effects of the 30 crosses were determined. Test for significance of GCA and SCA effects were executed by computing the standard error for females, males and their interactions. Narrow sense heritability (h^2) was estimated following the formula by Dhillon *et al*. (2006) as;

$$h^2 = \frac{V_{gca}}{V_{gca} + V_{sca} + V_E}\ x\ 100 \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (3.2)$$

Where, V_{gca} = variance of general combining ability, V_{sca} = specific combining ability variance and V_E = Error variance.

To estimate the GCA and SCA effects, a general linear model (GLM) procedure was used in SAS software. Relative significance of GCA and SCA was calculated according to Baker (1978) ratio.

$$\text{Baker ratio} = \frac{2MS_{GCA}}{2MS_{GCA}+MS_{SCA}} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(3.3)}$$

Where; $2MS_{GCA}$ is the component of variance for females and males GCA and MS_{SCA} is the variance components of SCA.

3.2.5.3 Pearson’s correlation coefficient

Pearson’s correlation coefficients were computed to determine relationship between stem borer damage and morphological traits using the formula suggested by Miller *et al.* (1958) as follows:

$$r = \frac{cov.x_1x_2}{(var.x_1)(cov.x_2)} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (3.4)$$

Where, r = correlation coefficient; $cov.x_1x_2$ = covariance between traits x_1x_2; $var.x_1$ = variance of trait x_1 and $cov.x_2$ = variance of trait x_2 to calculate simple linear correlation coefficients.

3.3 Results

3.3.1 Variance for the parental lines at Kiboko and Kabete.

Analysis of variance at individual location revealed significant ($P \leq 0.05$) differences among the parents for most of the traits studied except for number of productive tillers which suggested that the genotypes were genetically divergent (Table 3.4). The genotype x environment interaction was significant ($P \leq 0.05$) for all the traits observed implying that the genotypes responded differently for traits in both locations. Further analysis was therefore confined to individual location basis (Table 3.4).

Table 3.4. ANOVA of parents and checks at Kiboko, Kabete and across sites

Source	df	LD%	DH%	EH	ST%	DF	PH (cm)	NT/P	PL(cm)	PW (cm)	DPW	SM (g)	SB%	GY (t ha^{-1})
KIBOKO														
Rep	1	1.3	0.0	90.6	297.6	7.1	186.8	0.0	2.2	0.2	48.2	0.8	0.3	0.0
Gen	17	1.2*	0.0**	149.4**	210.0**	85.0**	3676.6**	0.29ns	17.8**	1.8*	368.2**	0.4**	35.9**	1.2**
Error	17	2.0	0.0	7.6	19.0	9.1	229.2	0.0	16.2	1.8	329.6	0.2	3.3	1.2
KABETE														
Rep	1	0.0	0.0	8.9	69.4	0.0	16.2	0.0	3.5	0.1	0.1	0.5	22.4	0.3
Gen	17	0.2*	0.1**	48.3**	70.8**	14.6*	1304.3**	2.3**	68.8**	20.0*	20.0**	0.7**	24.3**	3.5**
Error	17	0.1	0.0	2.3	12.4	11.0	30.6	0.1	1.9	0.8	0.8	0.3	3.4	0.2
ACROSS SITES														
Rep	1	0. 5	0.0	78.1	327.3	3.6	45.8	0.0	5.6	0.0	176.9	0.4	8.8	0.1
Gen	17	1.0*	0.1**	177.4**	248.2**	52.5**	3729.3**	1.3**	57.8**	21.6**	1398.7**	0.6*	46.5**	1. 4*
Env	1	14.5**	0.3**	1643.6**	6375.0**	2175.8**	4312.1**	36.7**	136.4**	185.3**	32664.0**	11.2*	305.9**	44.2**
G x E	17	0.9*	0.0**	20.4**	32.6*	47.1**	1551.6**	1.3**	28.7**	9.3**	1699.0**	0.3**	13.7**	3.3**
Error	35	0.5	0.0	5.4	16.4	9.9	130.7	0.1	8. 8	1.3	190.7	0.2	3.7	0.7

df = degrees of freedom, LD = leaf damage, DH = deadhearts, EH = exit holes, ST = stem tunneling, DF = days to 50% flowering, PH = plant height, NT/P = number of productive tillers, PL (cm) = panicle length, DPW = dry panicle weight, SM = 100 seed mass, GY (t ha^{-1}) = grain yield, Rep = replication, Env = environment, Gen = genotype, G x E = genotype x environment interaction and *, **, = significant levels at P≤0.05 and P≤0.001.

3.3.2 Relative susceptibility of different sorghum parental lines to *C. partellus* damage at KALRO Kiboko.

Susceptibility parameters mainly leaf feeding, deadhearts, exit holes, stem tunnelling damage, all varied significantly (P≤0.05) among genotypes and selection was based on the four damage parameters (Table 3.5). Leaf damage was highest in IS 8193 at 49%, a susceptible line with an index of 1.2. The lowest score of 17% for leaf damage was recorded in IS 1044 followed by ICSV 700 (0.90) with indices of 0.8 and 0.5 respectively. Low dead heart damage of 0% was recorded in parents IS ICSV 700, IS 2205 and Kiboko local-2 with indices of 0.4, 0.7 and 1.0 respectively. Female parental lines Hariray and Hugurtay exhibited the highest dead heart damage of 30% as compared to the susceptible checks Kiboko local 2, IS 8193, Seredo, ICSV 745 and ICSB 464 which showed damages of less than 20%. The highest number of exit holes per plant was 36.4 in IS 8193 which was also the susceptible check with an index of 1.3, while the lowest was 8.3 in IS 1044 which was a resistant parental line with an index of 0.8. The cumulative stem tunnel damage per plant was low in genotypes IS 1044, ICSV 700 (<25cm) as compared to Gadam, Hariray, Tegemeo, IESV 23010, Seredo, that suffered more stem tunneling greater than 50cm. Stem tunneling was shortest in IS 1044 (22.5cm) and longest in Seredo at 61.8cm which was susceptible with an index of 1.2. The selection index categorized the genotypes into 16.7% resistant (≤0.7), 22.2% moderately resistant (0.8 - 0.9), 44.4% moderately susceptible (1.0 - 1.1) and 16.7% as susceptible (≥1.2) (Table 3.5). Some susceptible checks were better than the parental lines and it is notable that some female parents succumbed to *C. partellus* damage clearly more than the susceptible check.

3.3.2.1 Agronomic and morphological traits

Plant height, days to 50% flowering, number of productive tillers, panicle length, panicle width, dry panicle weight, hundred seed weight and total grain yield varied significantly

($P \leq 0.05$) among the parental lines (Table 3.5). The tallest genotype ICSV 700 was 264.1 cm tall while the shortest Macia reached a height of 107.6 cm. Days to 50% flowering ranged from 51 to 70 days in IS 1044 and ICSV 700 respectively. Genotypes that produced harvestable tillers were ICSB 464 and Hariray with ICSB 464 producing the highest number of productive tillers (3). The shortest panicle length (7.1 cm) and the longest (22.9 cm) were recorded in the genotypes Hugurtay and ICSB 464 respectively. Grain weight ranged from 0.9 t ha^{-1}. in Hugurtay to 4.4 t ha^{-1} in Sila with an average of 2.7 t ha^{-1} (Table 3.5). The highest hundred seed mass of 2.6 g was recorded in IS 2205.

Table 3.5. Response of 18 parental lines and checks to *C. partellus* damage at KALRO-Kiboko.

	Stem borer damage traits						Agronomic and morphological traits								
Genotypes	**LD%**	**DH%**	**EH**	**ST (cm)**	**RSI**	**Category**	**PH (cm)**	**DF**	**NT/P**	**PL (cm)**	**PW (cm)**	**DPW (cm)**	**SM (g)**	**SB%**	**GY (t ha^{-1})**
ICSV 700	19	0	12.4	24.2	0.4	R	264.1	70	1	17.7	7.2	62.9	2.0	15.8	3.9
IS 1044	17	10	8.3	22.5	0.5	R	203.7	51	1	22.2	7.9	69.2	2.1	11.6	3.0
IS 2205	38	0	15.7	34.6	0.7	R	184.1	62	1	15.6	5.8	33.4	2.7	7.6	2.9
ICSB 464	38	20	12.8	28.9	1.8	MR	134.8	65	3	22.9	6.0	63.8	1.7	19.4	3.7
Sila	25	20	20.1	36	1.9	MR	189.0	55	1	21.8	7.2	74.6	1.9	15.1	4.4
Hugurtay	25	30	17	34.8	1.9	MR	124.5	55	1	7.1	3.6	10.2	1.9	13.9	0.9
ICSV 745	27	20	24.4	38.4	1.9	MR	145.9	63	1	19.6	5.2	63.5	1.6	8.5	2.4
IESV 23008 DL	25	20	23.2	45.5	1.0	MS	147.9	55	1	22.5	7.7	63.3	2.3	18.6	3.2
Macia	38	20	20.6	33.5	1.0	MS	107.6	67	1	20.9	6.7	58.6	1.7	9.6	2.6
Kiboko local 2	43	0	34.9	44.1	1.0	MS	221.1	57	1	16.8	5.8	34.9	2.5	16.8	2.1
Tegemeo	42	10	23.5	54.3	1.0	MS	152.7	62	1	19.4	8.0	72.1	2.3	18.4	3.1
IESV 23011 DL	35	20	26	40.6	1.0	MS	145.7	64	1	22.7	6.9	58.8	1.5	5.5	1.6
IESV 23010 DL	38	10	25.7	60.5	1.0	MS	153.9	55	1	20.2	7.2	73.9	2.6	16.5	2.0
Gadam el Hamam	36	10	35.6	57.5	1.1	MS	164.1	56	1	21.0	6.8	62.5	1.9	7.0	2.2
Hariray	28	30	22.5	50.3	1.1	MS	200.2	53	2	14.3	4.7	28.9	1.6	13.1	3.2
KARI Mtama 1	43	20	32.5	53.2	1.2	S	166.6	61	0	20.6	8.5	77.0	2.5	16.0	2.5
Seredo	36	20	33.6	61.8	1.2	S	162.5	56	0	22.0	6.6	60.9	2.2	12.5	2.2
IS 8193	49	20	36.4	42.8	1.3	S	130.1	65	1	16.3	5.1	51.0	1.7	11.4	1.8
Grand mean	33.4	15.6	23.6	42.4			166.6	59.6	1.1	19.1	6.5	56.6	2.0	13.2	2.7
SE±	0.99*	0.1**	2.8**	4.4**			15.1**	3.0**	0.0	4.0*	1.4*	18.2**	1.39ns	1.7**	1.1**
LSD $_{(0.05)}$	2.1	0,1	5.3	9.2			31.9	6.4	0.1	8.5	2.9	58.3	0.9	3.4	2.3
CV%	29.7	33.6	12	10.4			8.7	5.1	3.9	20.8	20.9	31.6	18.8	12.3	27.4

LD = leaf damage, DH = number of deadhearts, EH = exit holes, ST (cm) = stem tunnelling, RSI = rank selection index, PH (cm) = plant height, DF = days to 50% flowering, NT/P = number of productive tillers per plant, PL (cm) = panicle length, DPW (g) = Dry panicle width, SM = 100 seed mass (g), GY(t ha^{-1}) = grain yield, R = resistant, MS = moderately resistant, MS = moderately susceptible, S = susceptible, SE ± = standard errors of difference of means and CV% = coefficient of variation, *****, ** = significant, highly significant difference (P<0.05) respectively.

3.3.3 Damage caused by *C. partellus* infestation on parental lines at Kabete, Kenya.

The analysis of variance indicated significant ($P \leq 0.05$) differences in leaf damage, deadheart formation, cumulative stem tunneling, exit holes, number of larvae alive/dead and sugar brix among the genotypes tested (Table 3.6). Genotypes with low percent leaf damage were IESV 23010 DL (13), IESV 23008 DL (18), IESV 23011 DL (21) and Tegemeo (22). Leaf damage was highest in KARI Mtama -1 at 33% which is moderately susceptible with an index of 1.1. Resistant parent IS 2205 suffered no deadheart damage. Susceptible checks Kiboko local -2 (40%), ICSB 464 (50%) and Seredo (50%) showed higher deadheart damage. Hugurtay which was categorized as susceptible exhibited the highest deadheart damage of (80%). Genotypes with fewer number of exit holes per stem were IS 1044 (4.4), ICSB 464 (7.5), ICSV 700 (8.9), and IS 2205 (9.0). Susceptible checks IS 8193 (24.3), Kiboko local-2 (18.8) and Seredo (16.7) recorded highest number of exit holes (Table 3.6). Stem tunneling was low in IS 1044 (15.5cm) and ICSV 700 (16.7cm) (Table 3.6). Highest stem tunneling damage was observed in Seredo (42.3cm), Tegemeo (29.0cm), Hariray (27.5cm) and Gadam (27.1cm).

3.3.3.1 Agronomic traits among parental lines evaluated at Kabete-Kenya.

Grain yield and all agronomic traits were significantly different ($P \leq 0.05$) among the genotypes examined (Table 3.6). Plant height differed significantly among the genotypes with trial mean of 153.6 cm as shown in Table 3.6 and 44.4% of the genotypes attained above average plant height. The tallest genotype IS 2205 attained a height 191.9 cm while the shortest, Macia attained a height of 114.4cm. Days to 50% flowering ranged from 66 to 76 for Sila and ICSB 464, respectively. The longest (32.9cm) and shortest (9.8cm) panicles were recorded on genotypes IESV 23010 DL and Hugurtay, respectively. Grain weight ranged from 0.6 t ha^{-1} in Hugurtay to 6.9 t ha^{-1} in IS 8193 with an average of 4.3 t ha^{-1}. The highest 100 seed mass was recorded in Seredo (3.5g), Hugurtay (3.2g), Sila (3.1g) and ICSV 745

(3.1g). Despite the fact that IS 8193 was used as a susceptible check, it yielded two times more than the resistant check IS 2205.

Table 3.6. Response of parental lines and checks to *C. partellus* damage at Kabete.

	Stem borer traits						Agronomic and morphological traits								
Genotype	**LD%**	**DH%**	**EH**	**ST (cm)**	**RSI**	**Category**	**PH (cm)**	**DF**	**NT/P**	**PL (cm)**	**PW (cm)**	**DPW (g)**	**SM (g)**	**SB%**	**GY (t/ha)**
IS 1044	28	10	4.4	15.5	0.6	R	139.2	70	3	18.3	6.7	90.9	2.5	6.8	3.1
IS 2205	27	0.0	9.0	19.4	0.7	R	191.9	74	2	16.5	7.5	80.8	2.3	5.3	3.7
ICSV 700	23	20	8.9	16.7	0.7	R	153.6	71	2	17.4	5.9	89.2	2.9	11.0	3.1
Sila	27	10	10.9	22.6	0.9	MR	121.2	66	2	20.4	9.3	64.0	3.1	8.9	3.0
Tegemeo	22	10	12.4	29.0	0.9	MR	136.3	68	1	20.2	10.1	98.5	2.8	9.0	4.8
Macia	25	30	10.7	22.1	0.9	MR	114.3	67	2	26.5	12.5	158.5	2.6	3.4	6.3
IESV 23011 DL	21	30	13.9	21.5	1.0	MS	173.0	69	2	29.9	15.2	73.8	2.0	13.3	3.2
Gadam el Hamam	25	10	15.3	27.1	1.0	MS	150.9	69	2	21.6	9.0	132.5	2.7	6.1	5.3
ICSB 464	24	50	7.5	18.4	1.0	MS	134.5	76	1	20.5	8.4	79.5	3.0	13.7	3.0
ICSV 745	26	30	14.1	22.5	1.0	MS	165.3	68	1	22.6	8.1	112.9	3.1	5.4	5.5
IESV 23008 DL	18	30	15.4	22.6	1.0	MS	175.6	74	3	31.9	14.0	74.1	2.0	14.8	3.4
IESV 23010 DL	13	40	16.1	23.2	1.0	MS	179.2	71	4	32.9	12.7	74.7	1.7	16.1	3.1
KARI Mtama 1	33	30	15.1	21.6	1.1	MS	129.1	73	2	24.1	12.6	119.1	2.4	8.8	5.1
IS 8193	23	40	24.3	22.2	1.2	S	159.8	69	4	20.8	8.6	190.1	2.4	8.2	6.9
Kiboko local 2	25	40	18.8	25.6	1.2	S	188.9	72	2	26.1	12.9	77.7	2.8	8.9	4.4
Hariray	27	60	12.1	27.5	1.3	S	190.2	73	2	15.6	5.8	67.5	2.6	7.1	2.9
Hugurtay	25	80	9.4	19.2	1.3	S	119.6	69	5	9.8	4.1	68.4	3.2	9.1	0.6
Seredo	26	50	16.7	42.3	1.5	S	143	71	3	22.4	11.8	141.7	3.5	7.5	6.1
Grand mean	24	0.3	13.1	23.3			153.6	70.6	2.3	22.1	9.7	100.1	2.6	9.1	4.0
SE±	0.2*	0.1**	1.5**	3.5**			5.5**	3.3*	0.4**	1.4**	1.9**	7.9**	0.6*	0.5**	1.9**
LSD $_{(0.05)}$	0.5	0.2	3.2	7.3			11.6	7.0	0.7	2.9	1.9	22.7	1.2	4.5	1.0
CV%	9.2	28.9	11.2	15.1			3.6	4.7	15.3	6.2	9	10.8	20.7	23.4	11.2

LD= leaf damage, DH = number of deadhearts, EH = number of exit holes, ST = stem tunnelling (cm), RSI = rank selection index, PH = plant height, DF = days to 50% flowering, NT/P = productive tillers per plant, PL (cm) = panicle length, PW (cm) = panicle weight, DPW (g) = dry panicle width, SM = 100 seed mass, GY(t ha^{-1}) = grain yield, R= resistant, MR = moderately resistant, MS = moderately susceptible, S = susceptible, SE± = standard errors of difference of means, LSD = least significant difference, CV% = coefficient of variation and *, ** = significance levels at P≤0.05 and P≤0.001 respectively.

3.3.4 Combining ability for *C. partellus* damage and agronomic traits

Analysis of variance for combining ability and estimates of GCA, SCA variance for borer damage traits are shown in Table 3.8. The mean squares due to GCA males and females were significant ($P \leq 0.05$) for deadheart, leaf damage, stem tunnelling and exit holes. Significant SCA mean squares were noted on dead hearts, exit holes and stem tunnelling. Baker's ratio estimates for leaf feeding, deadheart, exit holes and stem tunnel damages ranged between 46 - 64%. The narrow sense heritability ranged between 71 to 80%.

Table 3.7 Combined analysis of variance for general (GCA) and specific (SCA) combining ability for stem borer resistance and agronomic traits in sorghum.

Source of variation	df	LD%	DH%	EH	ST (cm)
Rep	1	0.90	0.00	88.9	983.03
Env	1	3. 80*	1.26**	1642.10**	10511.28**
GCA_m	2	1.10*	0.07*	62.30*	360.58*
GCA_f	9	0.60**	0.06**	54.20**	47.82*
SCA	18	0.30	0.03**	18.90*	74.25*
Env x Male	2	0.70	0.02	18.90	27.20
Env x Female	9	1.30**	0.04**	12.00	33.00
Env x Male x Female	18	0.40	0.27**	6.25	30.13
Error	58	0.40	0.01	9.87	60.66
		Proportional contribution to total variance (%)			
Males		15.9	10.2	13.1	29.0
Females		39.3	43.6	51.2	17.3
Females x Males		44.8	46.3	35.7	53.7
Baker's Ratio		0.55	0.54	0.64	0.46
		Narrow sense heritability (%)			
		71	76	80	75

df = degrees of freedom, LD = leaf damage, DH = deadhearts, EH = exit holes, ST = stem tunnelling and * = significant ($p \leq 0.05$), ** = highly significant ($P \leq 0.01$), Rep = replication, Env = environment, GCA_f = general combining ability for females, GCA_m = general combining ability for males, SCA = specific combining ability.

3.3.4.1 Agronomic traits

Analysis of variance for combining ability for agronomic traits is presented in Table 3.9. Mean squares due to GCA females were significant ($P \leq 0.05$) for all the eight traits studied. Mean squares GCA males were significant for plant height, fertile tillers, panicle length and width and dry panicle weight. SCA mean squares were significant ($P \leq 0.05$) for days to 50% flowering, number of tillers, panicle weight, seed mass and grain yield. The greatest proportional contribution to total variance from females was recorded in plant height and panicle weight. The Proportional contribution to total variance was greatest from males in plant height. Baker's ratio ranged between 0.49 in grain yield, 100 seed mass and days to 50% flowering to 0.85% in panicle length while heritability in narrow sense values ranged between 61 to 88% in grain yield and panicle length respectively.

Table 3.8: Combined analysis of variance for GCA and SCA for agronomic traits.

Source of variation	df	PH (cm)	DF	NT/P	PL(cm)	PW(cm)	DPW(g)	SM(g)	GY(t/ha)
Rep	2	92.20	1.80	0.10	0.40	2.20	514.10	0.30	0.10
Env	1	58525.30**	3203.30**	92.80**	13.6	73.80**	12499.10**	12.80*	8.70*
GCA$_m$	2	8552.90**	52. 10	3.20**	32.30*	6.20*	873.60*	1.40	0.70
GCA$_f$	9	1718.90*	96.80*	1.70**	96.30**	16.80**	1686.50**	0.40*	2.80*
SCA	18	1201.5	56.40*	0.50*	8.80	2.80	901.50**	0.40*	1.50*
Env x Male	2	127.00	116.50*	2.60*	0.20	5.10	1055.80	0.10	1.40*
Env x Female	9	670.60	72.80*	1.80*	23.60*	18.50**	701.90*	0.50*	1.60*
Env x Male x Female	18	824.40	27.10	0.40*	4.70	2.00	906.10	0.26*	1.60
Residual	58	634.04	28.00	0.20	8.30	1.70	244.60	0.23	0.70
				Proportional contribution to total variance (%)					
Males		31.6	5.2	20.6	5.9	5.9	5.3	22.3	2.5
Females		28.5	43.8	49.6	79.6	70.6	45.7	27.2	46.9
Males x Females		39.9	51.0	29.8	14.5	23.5	49.0	50.5	50.6
Baker's ratio		0.60	0.49	0.70	0.85	0.76	0.51	0.49	0.49
					Narrow Sense Heritability (%)				
		85	64	86	88	84	69	74	61

df = degree of freedom, PH (cm) = plant height, DF = days to 50% flowering, NT/P = number of tillers per plant, PL (cm) = panicle length, PW (cm) = panicle width, DPW (g) = dry panicle weight, SM (g) = hundred seed mass and GY (t ha^{-1}) = grain yield, Rep = replication, Env = environment, GCA$_f$ = general combining ability for females, GCA$_m$ = general combining ability for males, SCA = specific combining ability, * = significant ($P \leq 0.05$) and ** = significant ($P \leq 0.01$).

3.3.5 General combining ability effects of the parents in reaction to *Chilo partellus* damage and agronomic traits.

3.3.5.1 Stem borer damage

The GCA effects for leaf damage, deadheart, exit holes and cumulative stalk tunnels are shown in Table 3.10. The GCA effects varied among the parents. The female parents Hugurtay and IESV 23011 DL had significant (P≤0.05) negative desirable GCA effects for all the borer traits (Table 3.10). Among the male parents, IS 1044 exhibited significant (P≤0.05) negative GCA effects for all damage parameters. The significant (P≤0.05) negative GCA effects for leaf damage was observed in IESV 23010 DL (-0.31) and ICSV 700 (-0.34). Significant (P≤0.01) negative estimates of GCA effects were detected in Macia (-0.12) and ICSV 700 (-0.04) for deadheart. Female parents Hariray (-2.9), KARI Mtama -1 (-1.58), Macia (-1.40) and Sila (-3.65) had significant (P≤0.01) negative GCA for number of exit holes while parent Hariray (-2.69) and ICSV 700 (-0.08) expressed desirable significant (P≤0.05) GCA effects for stem tunnel length. Using the susceptible parameters (leaf damage, deadheart, number of exit holes and stem tunneling) as the measure for resistance, parent Hugurtay, IS 1044 and IESV 23011 DL presented the best GCA values. Genotypes Hariray, IESV 23010 DL and IS 2205 exhibited significant undesirable positive GCA effects to either leaf damage, deadheart, stem tunnels and number of exit holes. Furthermore, IESV 23010 DL showed positive significant (P≤0.05 and 0.001) undesirable GCA effects to deadhearts, exit holes and stem tunneling.

3.3.5.2 Agronomic traits

Significant (P≤0.01) positive GCA effects for plant height were recorded in Hariray (24.0) and Macia (19.9) among females and ICSV 700, among males (Table 3.10). Negative significant (P≤0.01) GCA effects for days to 50% flowering among female lines were recorded on Hugurtay (-4.9), IESV 23010 DL (-3.9) and Hariray (-2.8) and IS 1044 (-2.9) among the males while significant (P≤0.05) positive GCA effects were recorded in Tegemeo (4.08) and Macia (3.16) among the females and ICSV 700 (2.62) among the males. High positive significant (P≤0.01) GCA effects for the number of fertile tillers were observed in Gadam (0.4), Hariray (0.37), IESV 23010 DL (0.28), Tegemeo (0.27) and IS 1044 (0.31). Two female parents IESV 23011 DL (0.33) and KARI Mtama-1 (0.53) showed significant (P≤0.01) positive GCA effects for 100 seed mass whereas Hariray (-0.2), Tegemeo (-0.3) and IS 2205 (-0.2) displayed significant (P≤0.01) negative GCA effects. Parental lines IESV 23008 DL (1.0), IESV 23011 DL (0.9) and Sila (0.38) expressed favourable and significant GCA effects for grain yield (Table 3.10).

Table 3.9: General combining ability (GCA) effects of females and males for *Chilo partellus* damage and agronomic traits

Parents	LD%	DH%	EH	ST (cm)	NLA	PH (cm)	DF	NT/P	SM (g)	GY (t ha^{-1})
Females										
Gadam	-0.16	0.01	-0.67	-2.83	-0.31	-10.21	-1.18	0.4**	-0.07	0.25
Hariray	0.45**	0.01	-2.9**	-2.69*	-1.0**	24.0**	-2.76**	0.37**	-0.2**	-0.45*
Hugurtay	-0.13*	-0.13**	-3.10**	-3.82*	-0.36	-5.74	-4.90**	0.15	-0.07	-1.4**
IESV 23008 DL	-0.10	-0.02	-0.99	-2.48	0.12	-1.50	1.16	-0.21*	0.03	1.0**
IESV 23010 DL	-0.31*	0.06*	3.68**	4.25*	0.20	-27.7**	-3.93**	0.28**	-0.10	-0.18
IESV 23011 DL	-0.26*	-0.01*	-3.01**	-0.31*	-0.27	-0.41	-1.74	0.18*	0.33**	0. 9**
KARI Mtama-1	-0.06	-0.03	-1.58**	-0.04	0.30	-4.37	0.24	-0.6**	0.53**	-0.4*
Macia	-0.08	-0.12**	-1.40*	1.80	0.35	19.94**	3.16*	-0.5**	-0.08	-0.34*
Sila	-0.19	-0.07	-3.65**	-2.92	0.94**	-4.76	2.41	0.01	-0.03	0.38*
Tegemeo	-0.06	-0.03	0.26	-1.76	-0.50*	9.96	4.08*	0.27**	-0.3**	0.21
Males										
ICSV 700	-0.34**	-0.04**	0.10	-0.08*	0.34*	15.12**	2.62*	-0.25**	0.07	0.18
IS 1044	-0.3**	-0.04*	-1.55**	-3.2**	-0.4**	-4.00	-2.9**	0.31**	0.13	0.01
IS 2205	-0.04	0.01	1.44**	3.3**	0.09	-11.12**	0.24	-0.06	-0.2**	-0.18*

LD% = leaf damage, DH% = deadhearts, EH = exit holes, ST (cm) = stem tunnelling, NLA = number of larvae alive, PH = plant height, DF = days to 50% flowering, NT/P = number of productive tillers per plant, SM = hundred seed mass, GY (t ha^{-1}) = grain yield, * = significant ($P \leq 0.05$), ** = significant ($P \leq 0.01$).

3.3.6 Estimates of specific combining ability (SCA) effects for reaction to stem borer and agronomic traits.

Results on specific combining ability for the different stem borer damage and agronomic traits are given in Table 3.11. In general, most of the SCA estimates were negative. Crosses Hugurtay X ICSV 700 (-0.62), Gadam x IS 1044 (-0.14), IESV 23011 DL X IS 1044 (-4.7) and Hariray X ICSV 700 (-9.16) expressed the highest significant ($P \leq 0.05$) negative SCA effects for leaf damage, deadheart, exit holes and stem tunnels respectively. Considering the number of larvae recovered alive, significant ($P \leq 0.05$ – ≤ 0.01) SCA values of -0.57, -0.62 and -0.75 were observed in crosses IESV 23008 DL X IS 2205, IESV 23010 DL X IS 2205 and IESV 23011 DL X IS 1044. Among the 30 crosses under study, the four combinations namely, IESV 23010 DL X IS 1044 (26.0), IESV 23011 DL X IS 1044 (23.9), Tegemeo x IS 2205 (19.28) and KARI Mtama 1 X IS 2205 (17.4) recorded high positive ($P \leq 0.01$) SCA effects for plant height while cross IESV 23011 DL X IS 2205 (-36.7) displayed high significant negative SCA effects followed by IESV 23010 DL X IS 2205 (-34.4) and Hariray X IS 1044 (-24.2). Six crosses viz., Hugurtay X ICSV 700 (-6.70), Gadam X IS 2205 (-6.33), Macia X IS 1044 (-5.56), IESV 23008 DL X IS 2205 (-4.41), Sila X IS 2205 (-3.59) and KARI Mtama -1 X IS 1044 (-3.64) exhibited significant ($P \leq 0.01$) negative SCA effects for 50% days to flowering (Table 3.11). Significant ($P \leq 0.01$) positive SCA effects were observed in Gadam X IS 2205 (0.67), KARI Mtama -1 X IS 1044 (0.51) and Hugurtay X ICSV 700 (0.35) for 100 seed mass. Gadam X IS 1044 (0.62), IESV 23011 DLX ICSV 700 (0.53), Sila X IS 2205 (0.51). Hugurtay X ICSV 700 was best cross for leaf damage, deadheart, and exit holes, stem tunneling, number of tillers, 100 seed mass and grain yield based on the significance desirable SCA effects recorded in the traits. Crosses Gadam X IS 1044 (0.62), IESV 23011 DL X ICSV 700 (0.53), Hugurtay X ICSV 700 (0.51), Sila x IS 2205 (0.51), and

Hugutay X IS 1044 (0.50) exhibited significant ($P \leq 0.01$) positive SCA effects for grain yield (Table 3.11).

Table 3.10: Specific combining ability (SCA) estimates from female x male analysis for various stem borer and agronomic traits.

ENTRY	LD%	DH%	EH	ST(cm)	NLA	PH(cm)	DF	NT/P	SM(g)	GY(t ha^{-1})
Gadam X ICSV 700	0.41*	-0.01	-1.40	-3.72	-0.45	1.47	2.80	-0.07	0.10	-0.25
Gadam X IS 1044	0.02	-0.14**	-0.17	1.80	0.30	-15.07*	3.53*	-0.15	-0.8**	0.62**
Gadam X IS 2205	-0.44*	0.14**	1.57	1.93	0.15	13.6	-6.33**	0.22	0.67**	-0.37
Hariray X ICSV 700	0.07	0.09**	-1.57	-9.16**	-0.04	11.21	0.38	0.00	0.00	-0.28
Hariray X IS 1044	0.31	0.04	2.50**	10.19**	-0.11	-24.20**	-0.14	0.26*	-0.19	0.04
Hariray X IS 2205	-0.38*	-0.13**	-0.93	-1.03	0.14	12.99	-0.24	-0.26*	0.19	0.24
Hugurtay X ICSV 700	-0.62**	-0.07*	-3.6**	-4.53*	0.03	11.37	-6.70**	0.27*	0.35**	0.51**
Hugurtay X IS 1044	0.51**	0.05	5.27	3.29	0.01	-5.32	5.03**	0.08	-0.17	0.50**
Hugurtay X IS 2205	0.11	0.03	-1.72*	1.24	-0.04	-6.05	1.68	-0.35**	-0.18	-1.0**
IESV 23008 DL X ICSV 700	0.15	-0.04	1.00	-2.45	0.10	-2.54	2.22	-0.50**	-0.18	-0.22
IESV 23008 DL X IS 1044	-0.12	-0.05	-1.82*	-1.20	0.48	5.4	2.19	0.44**	-0.02	0.25
IESV 23008 DL X IS 2205	-0.03	0.09**	-2.82**	3.65	-0.57*	-2.86	-4.41**	0.06	0.19	-0.03
IESV 23010 DL X ICSV 700	-0.31	-0.07*	0.78	-0.33	-0.03	8.43	0.05	-0.32**	0.03	0.23
IESV 23010 DL X IS 1044	0.40*	0.07*	-0.25	0.42	0.65*	26.01**	1.78	-0.33**	0.22	-0.21
IESV 23010 DL X IS 2205	-0.09	0.00	-0.53	-0.75	-0.62*	-34.4**	-1.83	0.65**	-0.25	-0.02
IESV 23011 DL X ICSV 700	0.21	-0.01	1.97**	3.61	0.60*	12.69	-0.62	0.12	-0.25	0.53**
IESV 23011 DL X IS 1044	-0.40*	0.09**	-4.7**	-3.19	-0.75**	23.98**	0.36	-0.02	0.14	-0.43*
IESV 23011 DL X IS 2205	-0.19	-0.08**	2.68**	-0.42	0.15	-36.7**	0.26	-0.10	0.12	-0.11
KARI Mtama-1 X ICSV 700	-0.17	-0.01	-0.06	2.97	0.27	-11.62	0.88	-0.21	-0.15	0.12

Table 3.10: Specific combining ability (SCA) estimates from female x male analysis for various stem borer and agronomic traits.

ENTRY	LD%	DH%	EH	ST(cm)	NLA	PH(cm)	DF	NT/P	SM(g)	GY(t ha^{-1})
KARI Mtama-1 X IS 1044	-0.16	-0.08**	-0.16	0.61	0.05	-5.76	-3.64**	-0.27*	0.51**	-0.34
KARI Mtama-1 X IS 2205	0.33	-0.06*	0.23	-3.58	-0.32	17.39**	2.76	0.48**	-0.36*	0.23
Macia X ICSV 700	-0.02	0.00	1.53	3.13	-0.78**	-6.08	2.97	0.19	-0.04	-0.18
Macia X IS 1044	-0.06	-0.06	-0.97	-7.43*	-0.45	1.98	-5.56**	0.23*	0.23	-0.17
Macia X IS 2205	0.08	0.05	-0.56	4.30	1.23**	4.1	2.59	-0.42**	-0.19	0.35
Sila X IS 1044	-0.43*	-0.08**	-0.56	-0.67	-0.69**	-7.17	-2.06	-0.08	-0.03	-0.21
Sila X ICSV 700	0.34	0.10**	0.74	-1.94	0.63*	-5.48	-1.53	-0.02	0.21	-0.30
Sila X IS 2205	-0.09*	-0.02**	-0.18*	-1.27*	0.06	-12.65	-3.59**	0.10	-0.17	0.51**
Tegemeo X ICSV 700	-0.07	0.01	0.57	-7.89**	-0.34	-19.43**	-0.45	0.54**	-0.06	-0.16
Tegemeo X IS 1044	-0.06	0.00	-2.9**	-3.82	0.52	0.16	-1.48	-0.17	0.08	-0.04
Tegemeo X IS 2205	0.13	-0.01	2.26**	-4.07	-0.18	19.28**	1.93	-0.37**	-0.02	0.20

LD% = leaf damage, DH% = deadheart, EH = exit holes, ST (cm) = stem tunnelling, NLA = number of larvae alive, PH (cm) = plant height, DF = days to 50% flowering, NT/P = productive tillers per plant, SM = 100 seed mass, GY (t ha^{-1}) = grain yield, * = significant ($P \leq 0.05$), ** = significant ($P \leq 0.01$) and *** = ($P \leq 0.001$).

3.3.7 Association between *C. partellus* damage parameters, agronomic and morphological traits

The results of correlation between *C. partellus* damage and agronomic traits are presented in Table 3.12. Leaf damage was significant (P≤0.05) and positively associated with deadheart (r =0.2), exit holes (r=0.5), stem tunnels (r=0.4) and number of live larvae (r=0.4). Deadhearts were significantly (P≤0.001) and positively correlated with days to 50% flowering (r =0.3) and with number of productive tillers (r=0.6) and 100 seed mass (r=0.3). Positive and highly significant (P≤0.05) correlations between sugar brix with exit holes (r=0.3), stem tunneling (r=0.5) and number of larvae recovered alive (r=0.4). Number of tillers (r=0.3), panicle length (r=0.4), panicle diameter (r=0.5), dry panicle weight (r=0.8) and 100 seed mass (r=0.3) were significant (P≤0.05) and positively correlated to grain yield (Table 3.12). Grain yield was negatively correlated with exit hole (r=-0.2), stem tunnelling (r=-0.3) and number of larvae recovered alive (r=-0.5). Panicle diameter was significant and positively correlated with panicle length (r=0.8). Deadhearts were highly significant and negatively associated with plant height (r=-0.5). Negative and significant (P≤0.05) correlations were noted between seed mass and exit holes (r=-0.5). Highly significant (P≤0.001) negative relationships were observed between days to 50% flowering with number of exit holes (r=-0.3), stem tunnelling (r=-0.5) and the number of live larvae (r=-0.3).

Table 3.11: Correlation among damage parameters, agronomic and morphological trait in sorghum across sites.

TRAITS	LD%	DH%	EH	ST (cm)	NLA	DF	PH (cm)	NT/P	PL (cm)	PW (cm)	DPW (g)	SM (g)	GY (tha)	SB%
LD%	-													
DH%	0.2*	-												
EH	0.5**	-0.3**	-											
ST (cm)	0.4**	-0.4**	0.7**	-										
LA	0.4**	-0.3**	0.6**	0.7**	-									
DF	0.0	0.3**	-0.3**	-0.5**	-0.3**	-								
PH (cm)	0.1	-0.5**	0.1	0. 2*	0.2**	-0.2	-							
NT/P	-0.3**	0.6**	-0.3*	-0.6**	-0.5*	0.4**	-0.4**	-						
PL (cm)	-0.2*	-0.1	0.0	-0.1	0.1**	0.2	0.0	0.0	-					
PW (cm)	-0.3**	0.1	-0.2	-0.3**	-0.1	0.3**	0.0	0.1*	0.8**	-				
DPW (g)	-0.2**	0.1	-0.2	-0.3**	-0.1**	0.3**	-0.2**	0.4**	0.4**	0.5**	-			
SM (g)	-0.3**	0.3**	-0.3*	-0.4**	-0.2	0.3**	-0.1	0.3**	0.2*	0.4**	0.3**	-		
GY (t ha $^{-1}$)	-0.2	0.0	0.2	-0.3**	-0.0**	0.3**	-0.1	0.3**	0.4**	0.5**	0.8**	0.3**	-	
SB%	-0.3	-0.3**	0.3*	0.5**	0.4**	-0.3**	0.3**	-0.4**	0.0	-0.2*	-0.3**	-0.3**	-0.2*	-

LD% = leaf damage, DH% = deadheart, EH = exit holes, ST (cm) = stem tunnelling, NLA = larvae recovered alive, DF = days to 50% flowering, PH (cm) = plant height, NT/P = number of fertile tillers per plant, PL (cm) = panicle length, PW (cm) = panicle width, DPW (g) = dry panicle weight, SM (g) = 100 seed mass, GY (t ha^{-1}) = grain yield and SB% = sugar brix, * = significant ($P \leq 0.05$) and ** = highly significance ($P \leq 0.01$).

3.4 Discussion

3.4.1 Site effect on sorghum-stem borer damage and agronomic traits across sites

The study revealed that there were differences among the genotypes across the two locations for all resistance and agronomic traits studied. The separation of genotypes, environment and their interactions provided a better understanding of the different patterns among parental lines and their response to *C. partellus* infestation across environments. Genotype x environment interactions presented significant ($P<0.05$) differences for all the traits studied indicating that genotypes reacted differently for these traits at the two sites.

The male parents IS 1044, ICSV 700 and IS 2205 maintained their resistance across the two environments while all females and the checks were moderately resistant, moderately susceptible or susceptible to *C. partellus* at both sites. Higher means were recorded for leaf feeding, deadheart, number of exit holes and cumulative stem tunnelling at Kiboko than at Kabete. The fact that borer damage was significantly lower at Kabete than at Kiboko could be attributed to the lower temperatures and heavy rainfall at high altitude test site which is an unfavourable environment for survival of *C. partellus.* In contrast, relatively high temperatures and lower precipitation at Kiboko favoured the development and fecundity of *C. partellus.* The most suitable conditions for development and fecundity of *C. partellus* have been reported as 26^0C – 30^0C temperature and 60% - 80% relative humidity levels (Choudhary, 2011). In this present study, abiotic factors varied significantly across locations. Through correlation studies, Agrawal and House (1972) found that there was a joint influence of rainfall, relative humidity and mean minimum temperature on the stem borer infestation. Kasimoto and Dyck (1976) reported that low temperature was the limiting factor for survival and distribution of insect pests.

3.4.2 Mechanism of resistance to stem borer damage in the selected sorghum parents across sites.

Based on the three approaches that plant breeders use to develop resistant cultivars namely; antibiosis, antixenosis and “tolerance” or “recovery resistance”, defense mechanism responsible for this resistance were established. The resistance mechanism was primarily tolerance as some genotypes supported high leaf feeding, deadheart and stems damages and produced substantial grain yield.

Tillering in sorghum serves as a component of recovery resistance (Bruns and Horrocks, 1984) thus was used as a measure of tolerance by counting the number of productive tillers. Genotypes IS 1044, IESV 23008 DL, IESV 23010 DL, IESV 23011 DL, Kiboko local-2 and IS 8193 showed recovery resistance through tillering. The sorghum genotypes resistant to stem borer had significantly less deadhearts than the susceptible lines. The present results also showed a positive association between deadheart damage and tillering. Rana *et al.* (1985) reported that sorghum varieties with high recovery resistance compensate for grain yield loss under insect pests infestation.

Antibiosis against larval feeding offers stimulating possibilities of exerting biotic pressure against stem borer and causes low larval survival on resistant varieties (Soto and Galin, 1974). Antibiosis mechanism measured in terms of reduced leaf and stem damage was observed on parent ICSV 700, IS 1044 and IS 2205. A number of studies on antixenosis and antibiosis to *C. partellus* in sorghum have been reported by Kumer (2006) and Singh (2011). Previously, parent IS 2205 was reported to be resistant based on antixenosis to *C. partellus* in India (Sharma *et al.,* 2007).

On the other hand, great magnitude of *C. partellus* damage to sorghum could have been due to the brix level in the plant. Generally, genotypes with low to moderate stem sugar content fell into the resistant and moderately resistant categories. The most resistant sorghum genotypes namely, IS 2205 and IS 1044 had low stem sugar content (<10%). IESV 23011 DL, ICSB 464, and IESV 23010 DL which ranged between moderately susceptible to susceptible had the highest sugar contents (>15%). It is probable that sugar content played a key role in plant resistance to *C. partellus*. Several variations were observed where some genotypes with low sugar levels were moderately susceptible. There is no clear cut trend for all entries, suggesting that resistance and susceptibility was genotype-specific for a few lines tested. It may be deduced that since there are different types of sugars, some specific types of sugars could have acted as anti-feedants while others might have promoted feeding. However, this result agrees with previous reports by Arabjafari and Jalali (2007) that generally, susceptible maize varieties contained significantly higher percentages of stem sugars than in resistant varieties. Munyiri (2013) also found that low sugar contents are associated with resistance to *C. partellus* in maize.

3.4.3 Proportional contribution of females, males and their interaction to total variance

A females x males interaction analysis of sorghum lines with 10 females and 3 donor parents for stem borer resistance were carried out to obtain the proportional contribution of females, males and females x males to the total variance for different sorghum stem borer and agronomic traits (Table 3.8 and 3.9). The results revealed that the contribution of maternal and paternal interaction (female x male) exhibited higher estimates for leaf damage, deadheart and stem tunneling for damage traits and plant height, days to 50% flowering, panicle weight, 100 seed mass and grain yield for yield and yield contributing traits. This indicated superiority of maternal and paternal interaction effects for these traits. These findings are partly in agreement with the results by Sharma *et al*., 2007 and Kenga *et al*. (2004) in sorghum. Sarker *et al*. (2002) and Shams *et al.* (2010) reported similar observation in maize and rice, respectively.

3.4.4 Narrow sense heritability and Baker's ratio

Narrow sense heritability (h^2) is estimated by additive genetic effects, thus it is an essential criteria in selection of the elite genetic materials from segregating population (Dhillon *et al*., 2006). Narrow sense heritability estimates were categorized as low (<30%), moderate (30 – 50%) and high (50% and above) by Bhateria *et al*. (2006). This present study generally presented higher h^2 estimates for stem borer damage and agronomic traits studied. This suggested high heritability of these traits across locations and predominant role of additive genetic effects which indicates that these traits can be improve faster through selection. These observations were similar to earlier published results (Elangovan *et al*., 2014).

The closer Baker ratio to 1 indicates influence of additive genes over non-additive effects (Baker, 1978). For self-pollinated crops such as sorghum, a character with high Baker's ratio implies that the genes governing that trait can be fixed by the breeder in later generations when non-additive genes have been minimized. The estimate of Baker's ratio suggested that deadhearts, stem tunneling, days to 50% flowering, panicle weight, 100 seed mass and grain yield were controlled by both additive and non-additive genes since GCA: SCA was almost 1:1. Selecting resistant parents based on both high desirable GCA and SCA effects for the traits could be effective in improving cultivars for *C. partellus resistance.* Both additive and non-additive gene effects have been identified by researchers as important in controlling stem borer resistance and agronomic traits (Huang *et al*., 2013; Muturi *et al.*, 2012). Another study by Pathak (1990) found both additive and non-additive gene action to be crucial for inheritance of stem borer resistance but additive type gene action was predominant.

3.4.5 General and specific combining ability

In this present study, the significant difference of mean squares among males, females and males x females interaction for stem borer resistance and agronomic traits demonstrated their suitability for combining ability studies. The results showed that mean squares for GCA_m were larger than the GCA_f for resistant parameters, plant height, number of harvestable tillers and 100 seed mass suggesting greater diversity between the male parents. SCA effects were significant but less important than GCA effects for deadheart, number of exit holes, stem tunnel length, days to 50% flowering, number of productive tillers, panicle weight, 100 seed mass and grain yield suggesting that dominant effects played a role in inheritance of these traits although to a lesser extent. Rana *et al.* (1984) and Murenga *et al.* (2014) reported similar results on inheritance of stem borer resistance in sorghum and maize, respectively. Sharma *et al*. (2007) reported that inheritance of resistance to leaf damage, deadheart, number of exit holes and stem tunnelling were governed by additive gene action. Previous studies on stem borer resistance and grain yield in maize reported similar observations (Udaykumar *et al.,* 2013; Beyene *et al.,* 2011).

In this study, the desirable parental lines expressed negative GCA effects for the damage traits and positive GCA effects for grain yield and other agronomic traits. In addition genotypes which had negative GCA for days to flowering are preferred because they mature early and escape from drought and insect damage. Correlation analysis revealed that leaf feeding, number of exit holes and cumulative stem tunneling were negatively associated with days to 50% flowering suggesting that early maturing plants eluded stem damage due to the relatively short growth period. This study found male parents IS 1044, and female IESV 23011 DL as superior and desirable for the borer resistance and yield related traits studied. Thus, they can be classified as good general combiners for borer damage traits, grain yield and yield components. Parents IESV 23008 DL exhibited significant positive GCA effects for grain yield and positive GCA effects for damage traits making it not suitable for stem borer resistance. Female parent Hugurtay and Hariray with highly significant and negative GCA effects for stem borer traits but negative GCA effect for grain yield could be used in sorghum breeding to develop cultivars with resistance to *C. partellus.* There was a disaccord among GCA for resistance traits and GCA for grain yield. Karaya *et al*. (2009) also reported that good combiners for grain yield were not always good for stem borer resistance. The influence of additive gene action over non-additive effects was noted for borer damage and plant height, number of productive tillers, panicle length and width, and 100 seed mass. This result is consistent with that of Ajala (1993) and Karaya *et al. (*2009).

Utility of a particular cross in exploiting heterosis is estimated by the SCA effects of component lines. Several crosses manifested significant negative SCA for *C. partellus* resistance and a highly significant positive SCA effects for grain yield and yield related traits. In this study, the SCA effects were lower than GCA effects, probably showing that the SCA effects were less significant, a result also reported by Ojulong *et al.* (1995) in maize. Crosses Hugurtay x ICSV 700 and Sila x IS 2205 could be considered as the best cross combination for borer resistance, yield and yield related traits. Previous study by Vacaro *et al.* (2002) also showed that maize inbred lines with high GCA led to hybrids lines with high SCA effects for grain yield. Parents with significant negative GCA values for *C. partellus* produced high number of crosses with significant negative SCA values. The conclusion that can be drawn from these findings is that crosses involving parent IS 1044 were desirable for damage traits while ICSV 700 exhibited desirable characters for stem tunnels.

There was a positive correlation between leaf damage and number of exit holes, stem tunnel length and number of larvae alive implying that leaf damage would indicate stem damage and presence of living larvae inside the stem. Stem tunnelling affects nutrient and water uptake and leaf damage reduces the photosynthetic area while exit holes may weaken the stems (Tefere *et al*., 2010) which may result in susceptibility to lodging and other plant deformities leading to grain yield losses as demonstrated by the negative relationship of number of exit holes and stem tunnelling with grain yield. The positive significant association between days to 50% flowering and grain yield but negatively correlated to stem tunnelling, as well as the strong negative association between cumulative stem tunnels and grain yield, implied that late maturing plants exhibited more yield and reduced stem tunnelling. This suggested that reduced stem tunnels is an important parameter to select for high grain yield. The results from the current study partially agree with the findings of Ajala *et al.* (2010), Akinwale *et al.* (2011) and Mailafiya *et al*. (2011) who found significant positive correlation between leaf damage and stem tunnelling. Similar observations were also reported earlier by Ajala and Saxena (1994) and Odiyi (2007) in *C. partellus* in maize.

CHAPTER FOUR

GENETIC VARIABILITY, HERITABILITY, GENETIC ADVANCE AND TRAIT CORRELATIONS IN SELECTED SORGHUM (*Sorghum bicolor* [L.] Moench) VARIETIES

4.1 Introduction

Sorghum grain yields in Africa and Asia are generally low (0.95 – 1.17 t ha^{-1}) compared to 3.63 t ha^{-1} reported in USA and Europe. (FAOSTAT, 2011). The grain of sorghum is a major factor in the daily menu of millions of people while the stover is used to feed livestock (De Vries and Toenniessen, 2001). Being a native crop of Africa, tremendous diversity exists in East Africa (Ngugi *et al.,* 2012). However, the existence of variation alone in the population is not adequate for improving suitable traits unless the genetic variability is well understood. Yield is an essential and complex trait and is a function of several component traits (Churchill *et al*., 2004). In the mixed structure of a plant, most of the traits are interrelated (Loveless and Hamrick, 1984). Selection for yield indirectly through its components rather than directly is more valuable to realize their mutual association (Grafius, 1964).

Genetic improvement in crop yield depends on quality and magnitude of genetic variability, heritability and genetic advance in the population as well as the nature of association between yield and its components. This enables simultaneous selection for many traits associated with yield (Nyadanu and Dikera, 2014). Sorghum in general possesses a wide range of genetic variability (Sharma *et al.,* 2006) that provides options from which selections are made for improvement and possible hybridization. Binodh *et al.* (2008) reported that information on trait association in crops is essential for effective selection in crop improvement. The phenotype of a plant is the result of interaction of a large number of factors and final yield is the sum of effects of several component factors (Biradar *et.al.,* 1996). Correlation coefficients assist in deciding the direction of selection and number of traits to be looked at in improving grain yield.

Heritability of a trait is important in determining its response to selection. Estimates of heritability assist breeders to allocate resources necessary to effectively select for desired traits and to achieve maximum genetic gain with little time and resources (Smalley *et al.,* 2004). Estimates of heritability with genetic advance are more dependable and important than individual consideration of the parameters (Nwangburuk, 2012). When more traits are involved in correlation study, it becomes hard to determine the traits that really contribute to yield due to the existence of some amount of mutuality. According to Tah (2011) the extent of variability is measured by GCV and PCV which provide information about relative amount of variation in different traits studied. The present study was done to estimate the genetic variations, heritability and expected genetic advance in the selected sorghum varieties for effective selection.

4.2 Materials and Methods

4.2.1 Experimental Sites

The study was carried out during the 2015 short rain season at Kenyan Agricultural and Livestock Research Organization (KALRO) - Kiboko and at the University of Nairobi Kabete Campus field stations. Kiboko station lies at altitude 960m above sea level with average annual rainfall of 604mm and average maximum and minimum temperature of 16.6 and 29.4^{0}C respectively. The University of Nairobi, Kabete campus Field Station lies at an altitude of 1820 m above sea level with an average annual rainfall of 1000 mm and average maximum and minimum temperature of 16 and 23^{0}C, respectively. The data for rainfall and temperature of the locations were obtained from the respective meteorological stations.

4.2.2 Experimental germplasm

The seed of 15 sorghum genotypes were obtained from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). The details of the varieties are presented in Table .4.1.

Table 4.1: Colour and head type of the 15 sorghum genotypes

Genotype	Grain colour	Head type
Gadam	Chalky white	Semi-compact
Hariray	Brown	Loose
Hugurtay	Brown	Compact
IESV 23008 DL	Creamy white	Semi-compact
IESV 23010 DL	Creamy white	Semi-compact
IESV 23011 DL	Creamy white	Semi-compact
KARI Mtama-1	Creamy white	Semi-compact
Macia	Creamy white	Semi-compact
Sila	Creamy white	Semi-compact
Tegemeo	Creamy white	Semi-compact
Seredo	Brown	Semi-compact
Kiboko local-2	Red	Loose
ICSV 700	Creamy white	Compact
IS 1044	Creamy white	Compact
IS 2205	Creamy white	Compact

4.2.3 Experimental design and layout

The experimental design and treatments are as described in Chapter 3. Data for the 15 genotypes were pooled from the main field and analyzed in a randomized complete block design (RCBD) with two replications at both sites.

4.2.4 Data collection

Data were recorded on 10 randomly selected plants from the two side-rows at each plot for plant height (cm), days to 50% flowering, number of productive tillers, panicle length (cm), panicle width (cm), dry panicle weight (g), hundred seed mass (g), sugar brix (%) and total grain yield (t ha^{-1}). These have been described in section 3.2.4.2.

4.2.5 Statistical analysis

Data collected for each quantitative trait were subjected to analysis of variance. Treatment means were compared using Fisher's protected least significant differences at $p \leq 0.05$.

4.2.5.1 Estimation of variance components

The genotypic, environmental and phenotypic variances were computed according to the formula by Singh and Chaudhury (1985) as follows:

- Genotypic variance (σ^2g) = $\frac{MS_G - MS_E}{r} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (4.1)$

- Phenotypic variance (σ^2p) = $\sigma^2 g + \frac{\sigma^2 e}{r} \ldots . (4.3)$

Where,

MS_G = mean squares due to genotype, MS_E = mean squares of error (environmental variance), r = the number of replications, S = number of seasons, σ^2e = random error variance, σ^2g = genotypic variance and σ^2p = phenotypic variance.

Based on the ANOVA, the phenotypic (PCV) and genotypic (GCV) coefficient of variation (individual and combined analysis) were estimated using the formula by Burton (1952) as follows:

$$\mathrm{GCV} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} X\ 100\% \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (4.5)$$

$$\mathrm{PCV} = \frac{\sqrt{\sigma^2 p}}{\bar{x}} X\ 100\% \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (4.6)$$

Where; $\bar{x}$ = phenotypic trait population mean. GCA and PCV values were considered as low (0 – 10%), moderate (10 – 20%) and high (≥20%) as suggested by Burton and Devane (1953).

Broad sense heritability (H^2) was expressed as the percentage of the ratio of the genotypic variance (σ^2g) to the phenotypic variance (σ^2p) according to Allard (1960) as:

Broad sense heritability from individual analysis of variance;

$$(H^2) = \frac{\sigma^2 \mathrm{g}}{\sigma^2 \mathrm{p}} X100 \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (4.7)$$

Where; S, r and *l* are a number of seasons, replications and locations, respectively. Heritability estimates were categorized as low (0 – 30%), moderate (30 – 60%), high (≥60%) as suggested by Johnson *et al*. (1955).

Estimation of expected genetic advance (GA); Genetic Advance as % of mean (GAM) for both individual and combined analysis was expressed under selection in broad sense, assuming selection intensity of 5% and calculated using the formula adopted from Johnson *et al.*, 1955 and Allard, 1960 as follows:

$$\mathrm{GA} = \mathrm{K}\ x\ \sigma\ x\ \mathrm{H}^2 \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (4.8)$$

$$\mathrm{GAM} = \frac{GA}{\bar{x}}\ x100 \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (4.9)$$

Where; GA = expected genetic advance, k = the standard selection differential which has the value of 2.063 at 5% selection intensity as defined by Lush (1949), σ^2g = genotypic variance, σ^2p = phenotypic variance and $\bar{x}$ = grand mean. The range of GAM (%) were categorised as low (0 – 10%), moderate (10 – 20%) and high (20% and above) as suggested by Johnson *et al*. (1955).

4.2.5.2 Correlation coefficient

Simple linear correlation coefficient (Pearson, 1986) was performed to understand the relationship among the agronomic traits studied. The correlation coefficient was derived as below;

$$r = \frac{cov_1.x_1x_2}{(var.x_1)(cov.x_2)} \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots. (4.10)$$

Where:

r = correlation coefficient

cov.x_1x_2 = covariance between traits x_1 and x_2

var.x_1= variance of trait x_1

var.x_2= variance of trait x_2 to calculate simple linear correlation coefficients.

4.3 Results

4.3.1 Variances for grain yield and its components at individual and combined cross locations.

The results revealed that the genotypes presented significant ($P<0.05$) differences for all characters examined at individual and across sites. Mean squares due to genotypes, environment and genotype by environment interaction were highly significant at $P\leq0.05$ for all the traits except in seed weight. Hence, analysis of variance was confined to individual location (Table 4.2).

Table 4.2: ANOVA for vareities evaluated at Kiboko, Kabete and across locations

SOURCE	df	PH (cm)	DF (cm)	NT/P	PL (cm)	PW (cm)	DPW (g)	SM (g)	GY (t ha^{-1})
KIBOKO									
Replication	1	13.88	1.89	0.15	3.33	0.35	86.27	0.03	0.05
Genotype	12	5169.08	94.07	0.57	34.61	1.85	533.56	0.53	1.49
Error	12	50.83	4.14	0.07	2.97	0.50	37.88	0.07	0.04
SE±		7.13**	2.03**	0.27**	1.72**	0.71*	6.16**	0.27**	0.20**
LSD		15.53	4.43	0.58	3.75	1.54	13.41	0.58	0.44
CV %		4.1	3.50	28.80	9.10	10.50	11.70	11.10	6.6
KABETE									
Replication	1	179.42	0.62	0.02	7.76	0.11	165.51	0.24	0.50
Genotypes	12	1388.05	55.37	1.50	92.01	26.34	1711.89	0.43	1.49
Error	12	25.51	2.70	0.31	1.60	0.39	76.98	0.11	0.21
SE±		5.05**	1.64**	0.56*	1.27**	0.62**	8.77**	0.33*	0.45**
LSD		11.00	3.58	1.22	2.76	1.35	19.12	0.72	0.99
CV %		3.30	2.50	25.30	5.70	6.20	9.80	13.00	11.7
ACROSS LOCATIONS									
Replication	1	146.56	0.17	0.14	0.46	0.42	6.40	0.05	0.12
Genotype	12	4512.15**	109.53**	1.20**	102.58**	14.25**	1089.90**	0.60**	1.48**
Environment	1	4801.92**	2056.33**	21.58**	145.22**	138.62**	17317.06**	0.31*	8.28**
G x E	12	2044.98**	39.91**	0.88**	24.04**	13.95**	1155.56**	0.36ns	1.49**
Error	25	38.51	3.37	0.19	2.62	0.43	64.95	0.10	0.14
Means		164.60	64.90	1.60	20.70	8.40	71.00	2.50	3.50
CV %		4.00	2.80	27.50	7.80	7.80	11.40	12.40	10.50

df = degrees of freedom, PH (cm) = plant height, DF = days to 50% flowering, NT/P = number of productive tillers per plant, PL (cm) = panicle length, PW (cm) = panicle width, DPW (g) = dry panicle weight, SM (g) = hundred seed mass, GY (t ha^{-1}) = grain yield, SE ± = standard error of difference of means, LSD = least significant difference of means (5% level), G x E = genotype by environment interactions, CV % = coefficients of variation, *, **= significance levels at $P \leq 0.05$ and $P \leq 0.001$ respectively.

4.3.2 Estimates of mean, genotypic, phenotypic and environmental variance at two locations

Table 4.3 shows the genotypic (σ^2g), phenotypic (σ^2p) and environmental (σ^2e) variances for Kiboko and Kabete locations. The average means for the traits evaluated varied from 1.0 in number of productive tillers to 176.3 cm for plant height at Kiboko and from 2.2 for number of tillers to 157.1 cm for plant height at Kabete (Table 4.3). Values of genotypic variances ranged from 0.2 (hundred seed mass) to 2284.8 (plant height) at Kiboko and from 0.2 (hundred seed weight) to 897.3 (dry panicle weight) at Kabete location (Table 4.3). Similarly, phenotypic variances ranged from 0.2 (hundred seed mass) to 2306.7 (plant height) at Kiboko and 0.3 (100 seed mass) to 250.9 (dry panicle weight) at Kabete location. Environmental variances in Kiboko ranged from 0.0 in grain yield to 43.9 in plant height. At Kabete site, the range for environmental variances ranged from 0.1 in hundred seed mass to 67.9 in dry panicle weight (Table 4.3).

Table 4.3: Estimate of genotypic, phenotypic and environmental variance for eight traits evaluated at Kiboko and Kabete.

	Mean		**σ^2g**		**σ^2p**		**σ^2e**	
TRAITS	Kiboko	Kabete	Kiboko	Kabete	Kiboko	Kabete	Kiboko	Kabete
PH (cm)	176.3	157.1	2284.8	688.9	2306.7	702.0	43.9	26.1
DF	58.7	71.5	38.7	24.1	40.6	25.3	3.7	2.5
NT/P	1.0	2.2	0.3	0.5	0.3	0.7	0.1	0.3
PL (cm)	19.0	22.6	17.0	39.6	18.4	40.3	2.7	1.4
PW (cm)	6.6	10.4	0.9	12.2	1.1	12.4	0.5	0.3
DPW (g)	52.5	92.0	233.8	897.3	250.9	931.2	34.2	67.9
SM (g)	2.4	2.7	0.2	0.2	0.2	0.3	0.1	0.1
GY (t ha^{-1})	3.0	4.1	0.7	1.0	0.7	1.1	0.0	0.2

σ^2e = environmental variance, σ^2g = genotypic variance, σ^2p = phenotypic variance, PH = plant height, DF = days to 50% flowering, NT/T = number of productive tillers, PL = panicle length, PW = panicle width, DPW = dry panicle weight, SM = 100 seed mass, GY = grain yield.

4.3.3 Genotypic and phenotypic coefficient of variations, broad sense heritability and genetic advance as per cent of mean

Genetic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), broad sense heritability (H^2) and genetic advance as per cent of mean (GAM) estimates are presented in Table 4.4. The highest GCV and PCV values were recorded for number of productive tillers (57.9 at Kiboko; 33.6% at Kabete) and (61.1 at Kiboko; 37.2% at Kabete) respectively, followed by dry panicle weight (29.1 at Kiboko; 33.2% at Kabete) and (30.2 at Kiboko; 33.8% at Kabete) repectively (Table 4.4). The broad sense heritability (H^2) estimates were high at Kiboko and Kabete for plant height (99.0, 98.1), days to 50% flowering (95.4, 95.1), number of tillers (89.8, 79.7), panicle length (92.6, 98.3), panicle width (79.3, 98.6), panicle weight (93.2, 96.4), hundred seed mass (86.1, 81.1), and grain yield (97.1, 91.3). The expected genetic advance as % of mean ranged from 11.3 – 58.0% in number of productive tillers and dry panicle weight at Kiboko and from 13.8 – 68.9% for number of tillers and panicle width at Kabete respectively (Table 4.4).

Table 4.4: Genotypic and phenotypic Coefficients of variations; heritability and genetic advance (as % of population mean) for eight traits of sorghum at Kiboko and Kabete

	Kiboko		Kabete		Kiboko	Kabete	Kiboko	Kabete
TRAIT	**GCV%**	**PCV%**	**GCV%**	**PCV%**	**H%**		**GAM%**	
PH (cm)	27.1	27.2	16.7	16.9	99.0	98.1	55.7	34.1
DF	10.6	10.9	6.9	7.0	95.4	95.1	21.3	13.8
NT/P	57.9	61.1	33.2	37.2	89.8	79.7	11.3	61.2
PL (cm)	21.7	22.6	27.9	28.1	92.6	98.3	43.1	57.0
PW (cm)	14.1	15.9	33.6	33.8	79.3	98.6	26.0	68.9
DPW (cm)	29.1	30.2	32.6	33.2	93.2	96.4	58.0	65.9
SM (g)	18.6	20.0	17.3	19.2	86.1	81.1	35.6	32.2
GY (t ha^{-1})	27.0	27.3	24.7	25.8	97.1	91.3	54.8	48.6

GCV% = genotypic coefficient of variation, PCV% = phenotypic coefficient of variation, H^2 %= broad sense heritability, GAM = genetic advance as % of mean, PH (cm) = plant height, DF = days to 50% flowering, NT/P = number of harvestable tillers, PL (cm) = panicle length (cm), PW (cm) = panicle width (cm), DPW (g) = dry panicle weight, SM (g) = 100 seed mass and GY (t ha^{-1}) = grain yield.

4.3.4 Correlation among traits

Phenotypic correlation coefficients between pairs of trait are presented in Table 4.5. Grain yield displayed significant (P≤0.05 and P≤0.01) positive association with days to 50% flowering (r=0.53), number of productive tillers (r=0.32), panicle length (r=0.35), panicle width (r=0.47), dry panicle weight (r=0.80), and hundred seed weight (r=0.43). Significant (P≤0.01) positive correlations were observed between days to 50% flowering (r=0.64), number of productive tillers (r=0.40), panicle length (r=0.48) and panicle width (r=0.59) with dry panicle weight. Significant (P≤0.01) positive associations were observed between panicle width with days to 50% flowering (r=0.61), number of tillers (r=0.38), and panicle length (r=0.77). Panicle length was highly significant (P≤0.01) and positively related to days to 50% flowering (r=0.48). Highly significant (P≤0.01) positive association was recorded between number of productive tillers and days to 50% flowering (r=0.37). There were negative significant (P≤0.05) relationships between number of productive tillers (r=0.28), dry panicle width (r=0.30) with plant height (Table 4.5).

Table 4.5: Phenotypic Correlation among traits

TRAIT	PH (cm)	DF	NT/P	PL (cm)	PW (cm)	DPW (g)	SM (g)	GY (t ha^{-1})
PH (cm)	-							
DF	0.03	-						
NT/P	-0.28*	0.37*	-					
PL (cm)	-0.12	0.48**	0.19	-				
PW (cm)	-0.15	0.61**	0.38**	0.77**	-			
DPW (g)	-0.30*	0.64**	0.40**	0.48**	0.59**	-		
SM (g)	-0.22	0.1	0.16	-0.24	-0.03	0.27*	-	
GY (t ha^{-1})	-0.19	0.53**	0.32*	0.35*	0.47**	0.80**	0.43**	-

PH (cm) = plant height, DF = days to fifty per cent flowering, NT/P = number of harvestable tillers per plant, PL (cm) = panicle Length, PW (cm) = panicle width, DPW (g) = dry panicle weight, SM (g) = 100 seed mass (g), GY (t ha^{-1}) = grain yield, *, ** = significance levels at P≤0.05 and P≤0.01 respectively.

4.4 Discussion

There are differences among the genotypes for all the traits studied at individual and across environments. This implies that the genotypes performed differently due to their genetic constitutions. The GXE interaction effects were significant for all the traits suggesting their instability across sites and thus, do not portray genetic relationships since GXE interaction reduces the rates of genetic improvement. The differences found for traits in the environment component indicated that the environmental factors such as rainfall, temperature and relative humidity in the two locations were different. This significant interaction effects affected the performance of the genotypes leading to the differences in performance among the sorghum varieties across the two sites. Thus, it is important to evaluate sorghum genotypes at individual locations to ensure their stability for use as reliable genetic materials for crop improvement in a particular environment. These observations agree with those of Omogui *et al*. (2006), and Mangoel *et al.*, (2011) who reported that these traits may possibly be under both genetic and environmental influence. Significant effects due to genotype by environment interaction have been reported for different characters in sorghum (Ezzat *et al.*, 2010). Highly significant differences presented for all traits studied implied the existence of high genetic variability among the selected materials, hence their potential for use in sorghum improvement. Grain yield, which is the primary concern in most breeding programs, demonstrated a wide range of variation. The presence of such range of variations of the traits indicated the presence of large amount of genetic variation among the varieties (Amare *et al.,* 2015).

The phenotypic variation was separated into genotypic and environmental variances for perfect understanding of the pattern of variation are presented in Table 4.3 for different individual locations. The results for phenotypic variance were slightly greater than that of genotypic variance at both locations suggesting that environmental variance had influenced on the expression of the traits. The results for genetic variability also showed that plant height and panicle weight displayed the highest phenotypic variance. In addition, the traits expressed higher σ^2p and σ^2g values than the σ^2e values indicating that most of the traits are due to genetic factor. Hence, they can be exploited in breeding programs. This finding is in agreement with observations of other researchers on several quantitative traits in sorghum genotypes (Abu-Gasim and Kambal, 1985; Abraha *et al.*, 2015).

High values recorded for genotypic and phenotypic variance for plant height and dry panicle weight is in agreement with the results reported in sorghum by Can and Yoshida. (1999). Deshmukh (1986) suggested that PCV and GCV values lower than 10% are regarded as low whereas values more than 20% are considered to be high and between 10 and 20% to be moderate. PCV values were slightly higher than the GCV for all the traits suggesting presence of little environmental influence for their expression. Similarly, the closer GCV and PCV estimates for most of the traits under consideration, suggest low environmental impact for these traits and hence high heritability. Therefore, improvement of these traits through selection is possible. The high GCV recorded for most of the characters studied alone is not enough to determine the extent of the advance to be expected through selection. According to Burton (1952), estimates of GCV together with heritability would offer better scope for advance through selection. High values of PCV and GCV were found for most traits indicates that the genotypes have broad base genetic background and good potential that will respond positively to selection. Murray *et al*. (2009) found similar results while studying environmental effect on yield components of sorghum. Similarly, Ghosh *et al*. (2014) reported high PCV and GCV values for maize grain yield and other traits and Iftekharuddeula *et al.* (2001) reported moderate genotypic and phenotypic coefficients of variation for plant height, days to maturity and panicle length in nineteen rice hybrids. The minor differences observed between GCV and PCV for panicle length, dry panicle weight and overall grain yield imply the presence of adequate genetic variability for traits which may enhance selection (Yadav, 2000).

Broad sense heritability (H^2) combined with genetic advance as % of mean GAM is a more reliable indicator for selections of traits (Ubi *et al.,* 2001). Broad sense heritability was classified by Dobholkar *et al.* (1992) as low (5 – 10%), medium (10 – 30%) and high (> 30%). High heritability and GAM indicate additive gene effect. This was observed for all the traits under study at both sites except for GAM in number of tillers at Kiboko. This is an indication that most probably that heritability is due to genetic factor and selection could be effective in early generations for this traits and the possibility of improving sorghum grain yield through direct selection for grain yield and its components. Sharma *et al.* (2006) reported high broad sense heritability of 90% for biological yield per plant and Chavan *et al.* (2010) for grain yield. Likewise, Mahagan *et al.* (2011) also reported high values GAM for dry panicle weight and grain yield. Several researchers like Arunkumar (2004); Shegro *et al.* (2013), have also made similar observations. Ali *et al.,* (2002) observed that high heritability may not always associate with high genetic advance as % of mean. Thus, heritability should be considered in association with genetic advance to predict the effect of selecting superior crops varieties.

Grain yield is a complex trait and depends on other agronomic traits in crop improvement programmes. Therefore, associations of different agronomic traits with each other and their relationship to yield are important. The positive relationship recorded between grain yield with panicle length, panicle width, panicle weight and 100 seed mass is justifiable as increasing panicle length and width through selection may lead to proportional increase in grain yield. The positive and significant association among panicle length, width and weight suggested that selection for any one of these yield contributing traits will contribute positively to the other traits, thereby finally enhancing the grain yield. These traits could be considered as important traits for improving grain yield. The results corroborated with the findings of Abdel-Fatah *et al*. (2013) who observed significant and positive correlations between panicle lengths, panicle width and total grain yield. Thus, selection for these traits can simultaneously improve potential grain yield and gather the desirable genes. Similar outcomes were reported by Matthews (2005) for panicle weight, Bohra *et al.* (1986) for panicle length. Previous workers Aba and Zaria (2000) and Kambel and Webster, 1966 have described grain yield as a function of seed mass and panicle weight.

CHARTER FIVE

GENERAL DISCUSSIONS, CONCLUSIONS AND RECOMMENDATIONS

5.1 General Discussions

The overall objective of this study was to generate high yielding sorghum which are cultivars resistant to spotted stem borer, thus assist in solving the sorghum-stem borer constraints facing resource poor farmers, and improve their food security and livelihood. The results demonstrated the existence of genetic variability for stem borer resistance, grain yield and yield components among the 18 sorghum genotypes across the two locations. The nature of resistance to stem borer is polygenic and partially dominant over susceptibility (Panthak and Olela, 1983; Rana *et al*., 1984). Multiple traits mainly leaf damage, deadheart, stem tunneling damages are considered when selecting for stem borer resistance in sorghum and maize (Tadele *et al*., 2011).

The study also revealed that inheritance for resistance to *C. partellus* is predominantly governed by additive genetic effects. However, both additive and non-additive genes were important for controlling deadheart, stem tunnels, earliness, dry panicle weight, 100 seed mass and grain yield as demonstrated by the Baker's ratio. Inheritance of resistance to leaf damage, number of deadhearts, stem tunneling damage and number of exit holes has been reported to be governed by additive type of gene action (Nour and Ali 1998). Both additive and non-additive (dominant) gene effects have been described in the literature for grain yield and its components for several crops (Muturi *et al*., 2012, Sanghera *et al*., 2012; Schnable *et al*., 2013).

The results of estimated genetic variability, heritability and genetic advance for grain yield and yield contributing traits demonstrated differences among the genotypes for all the character measured at each location. The PCV was higher than the GCV for all the traits which indicated that all traits were highly influenced by environment. But the variations between them were of lower extent. High estimates of GCV and PCV were found for plant height, panicle length and dry panicle weight suggesting that the phenotypic expression of the traits is more influenced by genetic factors than the environment. The high heritability coupled with high genetic advance recorded for all the traits at each location, indicates the prevalence of additive gene effects which are less affected by environment hence the possibility of their improvement through selection. Similar results have been made in sorghum by several researchers like Deepalakshmi (2007); Najeeb *et al*. (2009); Chavan *et al*. (2010); Shegro *et al.* (2013).

5.2 Conclusions

Genotypes IS 1044, IS 2205 and ICSV 700 exhibited good stem borer resistance and can be effectively utilized in sorghum improvement programs as resistant donors. Both additive and non-additive genes governed *C. partellus* resistance (deadheart, exit holes and cumulative stem tunneling) and agronomic traits (days to 50% flowering, number of productive tillers, panicle weight 100 seed mass and grain yield). Thus, it is essential to exploit heterosis breeding for *C. partellus*, agronomic traits and grain yield in sorghum. Among the 13 parental lines, male lines IS 1044 and female IESV 23011 DL are good general combiners for *C. partellus* resistance traits, plant height, earliness, number of fertile tillers, 100 seed mass and gran yield since these parental lines showed favourable GCA effects. Utilization of the two lines in hybridization programs will result in generation of sorghum cultivars with high level of resistance to *C. partellus* and desirable agronomic traits. Crosses Hugurtay x ICSV 700 and Sila x 2205 had the desirable SCA effects for *C. partellus* and grain yield. These could be used to develop superior hybrids for grain yield with resistance to *C. partellus.*

This study demonstrated a wide range of genetic variability among the genotypes used for all of the characters tested, thus indicating high potential for use in trait improvement. Moreover, the presence of significant high heritability (H^2) and expected GAM% implied the possibility of improvement of the traits through selection. The correlation analysis revealed that panicle length/ width, panicle weight and 100 seed weight were the most important yield associated components. These traits also demonstrated high H^2 and GAM %. Hence suggesting that panicle weight, panicle length and breadth and hundred seed mass are important yield contributing traits and selection based on these traits would be most effective. Understanding the interaction of these traits among themselves and with the environment is of great use in sorghum yield improvement.

5.3 Recommendations

The following recommendations were made;

i. Genetic improvement of sorghum should be explored through selection for reduction in the leaf feeding damage, number of deadhearts, number of exit holes and cumulative stem tunnelling which are the most effective resistance mechanisms. This can be performed alongside emphasis of the key agronomic traits such as grain yield.

ii. Genetic gain is likely to be accomplished through conventional breeding for these traits since the narrow sense heritability figures were moderately high.

iii. Broad sense heritability couples with GAM% were high for traits evaluated. This indicated that these traits were under control of additive gene effects. Thus, considering these traits for sorghum improvement through selection should lead to quick genetic improvement.

iv. Effective genetic improvement in grain yield would be easier through indirect selection for component traits such as panicle length, panicle width, hundred seed mass and panicle weight which indicated high positive phenotypic correlation coefficients with grain yield.

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APPENDICES

Appendix 1: List of sorghum parents, progenies, and checks evaluated for resistance to *C. partellus* at Kiboko and Kabete, Kenya

S.No	Entry Name	S.No	Entry Name	S.No	Entry Name
1	Gadam X IS 1044	6	IESV 23011 DL X 2205	35	Macia-Parental check
1	Gadam X IS 2205	7	KARI Mtama 1 X IS 1044	36	IS 8193-Parental check
1	Gadam X ICSV700	7	KARI Mtama 1 X IS 2205	37	Sila-Parental check
2	Hariray X IS 1044	7	KARI Mtama 1 X ICSV 700	38	Tegemeo-Parental check
2	Hariray X IS 2205	8	Macia X IS 1044	39	IS 1044-Parental check
2	Hariray ICSV 700	8	Macia X IS 2205	40	IS 2205-Parental check
3	Hugurtay X IS 1044	8	Macia X ICSV 700	41	ICSV 700-Parental check
3	Hugurtay X IS 2205	9	Tegemeo X 1044	42	ICSB 464-Parental check
3	HugurtayX ICSV 700	9	Tegemeo X 2204	43	ICSV 745-Parental check
4	IESV 23008 DL X ICSV 700	9	Tegemeo X ICSV 700	44	Kiboko local 2-local check
4	IESV 23008 DL X IS 1044	10	Sila X IS 1044	45	IESV 23008 DL-Sweet sorghum
4	IESV 23008 DL X IS 2205	10	Sila X IS 2055	46	IS 23010 DL-Sweet sorghum
5	IESV 23010 DL X ICSV 700	10	Sila X ICSV 700	47	IESV23011 DL-Sweet sorghum
5	IESV 23010 DL X IS 1044	31	KARI Mtama 1-Parental check	48	Seredo-Commercial check
5	IESV 23010 DL X 2055	32	Gadam-Parental check	49	SWARNA-Commercial check
6	IESV 23011 DL ICSV 700	33	Hariray-Parental check		
6	IESV 23011 DL IS 1044	34	Hugurtay- Parental check		

Appendix 2: Response of 49 sorghum parents and their progenies to *C. partellus* damage across two sites during 2015 short rain season

Genotypes	LD%	DH%	EH	ST%	NLA	LDD	SB%	PH (cm)	DF	NT/P	PL(cm)	DPW(g)	SM(g)	GY(t)
Gadam	2.9	0.1	26.7	39	1.3	0.7	6.5	164.2	63	1.4	21.2	98	2.2	3.7
Gadam X ICSV 700	3.3	0.1	13.5	26.9	1.8	1.0	9.4	195.7	67	1.8	20.3	76.8	2.7	3.5
Gadam X IS 1044	2.3	0.1	13	29.3	1.8	0.6	9.2	160.1	62	2.3	23.7	109.2	1.9	4.1
Gadam X IS 2205	2.1	0.3	17.8	35.9	2.1	0.4	13.3	181.6	56	2.3	21.5	82	3	3
Hariray	2.7	0.4	16.7	39.5	1.7	0.5	10.1	195.4	62	1.1	15.1	50.3	2.1	3
Hariray X ICSV 700	3.6	0.2	11.1	21.6	1.5	0.7	12.3	239.7	63	1.8	17.6	66.5	2.4	2.7
Hariray X IS 1044	3.2	0.3	13.5	37.9	0.7	0.8	13.2	185.1	57	2.6	11.8	58	2.3	2.9
Hariray X IS 2205	2.8	0.1	13.1	33.1	1.4	0.8	6.8	215.2	60	1.7	14	50.3	2.3	2.9
Hugurtay	2.6	0.5	11.5	23.4	1.3	0.8	11.5	135.7	56	3	12.1	58.8	2.6	2.6
Hugurtay X ICSV 700	2.3	0.2	8.9	25.1	2.2	0.8	9.2	210.1	54	1.8	15.6	63.1	2.9	2.6
Hugurtay X IS 1044	2.8	0.4	16.1	29.8	1.4	0.5	11.2	174.3	60	2.2	15.3	67.2	2.5	2.4
Hugurtay X IS 2205	2.7	0.3	12.1	34.3	1.9	0.4	13.1	166.4	60	1.4	14.4	22.7	2.2	0.7
ICSB 464	3.1	0.4	10.1	26.7	2.1	0.5	16.5	127.9	70	1.1	21.8	73.5	2.3	3.5
ICSV 700	3.1	0.2	10.7	21.6	1.3	1.6	13.3	207.9	70	1.3	17.6	77	2.4	3.7
ICSV 745	2.8	0.2	19	30.5	2.9	0.6	6.9	153.3	64	1.1	21.3	91.7	2.3	3.9
IESV 23008 DL	2.0	0.3	18.6	31.3	2.5	0.9	16.7	162.3	63	1.9	27.3	71.4	2.1	3.3
IESV 23008 DL X ICSV 700	3.1	0.1	15.5	33.5	2.8	1	15	200.4	69	0.7	21.2	90.3	2.5	4.2
IESV 23008 DL X IS 1044	2.2	0.2	14.7	31.6	2.4	0.8	14.3	189.2	64	2.2	23.9	104.8	2.8	4.5
IESV 23008 DL X IS 2205	2.6	0.3	13.1	43	1.8	0.6	14.2	173.9	60	1.5	21.8	73.2	2.6	4
IESV 23010 DL	2.8	0.3	20.8	40.5	2.4	1.2	16.6	164.3	63	2.3	26.1	74.3	2.1	3.1
IESV 23010 DL X ICSV 700	2.5	0.1	20	38.1	2.7	0.8	11.3	185.2	62	1.4	17.7	80	2.6	3.5
IESV 23010 DL X IS 1044	2.5	0.3	17.3	35	2.6	0.7	10.3	183.6	58	1.9	23.1	76.6	2.8	2.9
IESV 23010 DL X IS 2205	2.3	0.2	20	40.3	1.9	0.9	12.1	116.1	58	2.5	19.2	77.7	2	2.9
IESV 23011 DL	2.7	0.4	20.2	28.5	1.1	0.9	9.4	160.3	67	1.7	26.1	63.8	1.7	2.4
IESV 23011 DL X ICSV 700	3.5	0.1	20.5	36.8	3.4	1.3	10.9	217.6	67	1.4	24.8	111	2.8	4.9

Appendix 2: Response of 49 sorghum parents and their progenies to *C. partellus* damage across two sites during 2015 short rain season

Genotypes	LD%	DH%	EH	ST%	NLA	LDD	SB%	PH (cm)	DF	NT/P	PL(cm)	DPW(g)	SM(g)	GY(t)
IESV 23011 DL X IS 1044	2.3	0.3	12.2	26.9	1.3	0.7	10.6	209.7	62	1.8	25.6	96.7	3.2	3.7
IESV 23011 DL X IS 2205	3.1	0.1	22.6	36.1	2.7	0.5	10.2	142	65	1.3	26.5	78	2.8	3.9
IS 1044	2.5	0.1	8.2	24.4	1.8	0.4	9.8	186.1	62	1.7	20.4	78.6	2.4	3.4
IS 2205	3.4	0.1	14.4	27.1	1.5	0.9	6.4	221.7	71	1.2	17.6	65.5	2.1	3.3
IS 8193	3.8	0.2	30.6	32	3.3	0.7	9.8	148.8	67	2.6	18.6	120.9	2.0	5.8
KARI Mtama 1	3.7	0.3	24.7	36.5	2.5	0.9	12.4	147.2	67	0.8	22.1	94.6	2.4	3.8
KARI Mtama 1 X ICSV 700	2.9	0.1	13.9	36.4	3.1	0.5	11.9	188.5	67	0.6	20.0	72.3	3.1	3.2
KARI Mtama 1 X IS 1044	2.2	0.3	12.1	30.9	2.1	0.8	11.6	175.2	57	1.1	22.6	67.6	3.8	2.5
KARI Mtama 1 X IS 2205	3.0	0.1	15.5	33.2	2.3	0.4	9.9	191.2	66	1.5	19.3	72.9	2.6	2.9
Kiboko local 2	3.6	0.2	27.3	35.2	3.1	1.5	12.8	203.2	64	1.5	21.3	54.7	3.4	3.3
Macia	2.4	0.2	14.3	30.2	1.6	0.7	6.5	112.0	64	1.4	20.5	101.3	2.4	4.6
Macia X ICSV 700	3.0	0.0	15.7	38.4	2.1	0.7	12.0	218.3	72	1.1	23.1	74.9	2.5	2.9
Macia X IS 1044	2.3	0.0	11.5	24.7	1.7	0.4	6.7	207.3	58	1.7	23.7	65.9	2.9	2.8
Macia X IS 2205	2.7	0.1	14.9	42.9	3.9	0.6	11.1	202.3	69	0.7	19.5	60.1	2.1	3.1
Seredo	3.3	0.2	23.7	53.9	3.0	0.7	10	149.4	64	1.4	22	98.6	2.8	4.1
Sila	2.7	0.1	14.2	28.5	2.1	0.9	11.1	120.5	62	1.3	19.9	60.9	2.8	3.2
Sila X ICSV 700	3.6	0.2	19.9	38.3	4.1	0.6	10.6	194.2	66	1.4	21.1	52.7	2.8	3.5
Sila X IS 1044	2.2	0.1	17.0	32.6	2.0	0.6	12.6	173.4	60	1.9	20.9	66	2.7	3.4
Sila X IS 2205	3.0	0.1	20.3	38.5	3.3	0.8	9.8	186.1	69	1.7	20.0	104.1	2.2	4.0
Swarna	2.8	0.2	16.5	33.3	2.2	0.8	11.2	178.9	64	1.6	20.4	76.4	2.5	3.4
Tegemeo	3.2	0.1	18.3	41.5	1.2	0.4	13.7	143.8	65	1.1	19.9	84.8	2.6	4.0
Tegemeo X ICSV 700	2.9	0.1	16.4	39.6	1.7	0.6	14.0	195.0	69	2.2	18.6	67.3	2.3	3.5
Tegemeo X IS 1044	2.3	0.2	11.3	24.8	1.8	0.7	9.8	195.5	63	2.1	22.1	78.3	2.5	3.4
Tegemeo X IS 2205	2.8	0.1	19.4	31.0	1.6	0.6	12.4	207.5	69	1.5	19.1	81.2	2.1	3.5
Grand mean	2.8	0.2	16.5	33.3	2.2	0.8	11.2	178.9	64	1.6	20.4	76.4	2.5	3.4
Entry	0.8**	0.1**	3.1**	8.1**	1.0**	0.4**	2.5**	9.8**	4.9**	0.3**	3.2**	19.3**	0.6**	0.9**

Appendix 2: Response of 49 sorghum parents and their progenies to *C. partellus* damage across two sites during 2015 short rain season

Genotypes	**LD%**	**DH%**	**EH**	**ST%**	**NLA**	**LDD**	**SB%**	**PH (cm)**	**DF**	**NT/P**	**PL(cm)**	**DPW(g)**	**SM(g)**	**GY(t)**
Site	0.2**	0.0**	0.6**	1.6**	0.2**	0.1*	0.5**	2.0**	1.0**	0.1**	0.7**	3.9**	0.1**	0.2**
Genotypes X Site	1.2**	0.2**	4.4**	11.5**	1.5**	0.6**ns**	3.6**	13.8**	6.9**	0.5**	4.6**	27.3**	0.8*	1.3**
CV%	20.8	40	13.3	17.3	34.4	38.8	16	7.7	5.4	15	20.4	18.2	16.6	19.3

Appendix 3: Grain yield potential and response of sorghum lines under *Chilo partellus* infested and non-infested conditions during the short rain season (2015) at KALRO-Kiboko, Kenya.

	Grain yield (t ha^{-1})					
	Kiboko		**Kabete**		**Grain yield loss (%)**	
Entry	Response (infested)	Potential (uninfested)	Response (infested)	Potential (uninfested)	**Kiboko**	**Kabete**
Gadam	2.6	3.3	5.3	6.0	20.49	11.67
Gadam X ICSV 700	2.6	3.9	4.0	3.6	33.33	-11.11
Gadam X IS 1044	2.4	4.2	5.8	3.3	42.99	-75.76
Gadam X IS 2205	2.9	5.0	2.8	4.6	41.71	39.13
Hariray	2.8	4.8	2.9	4.8	42.09	39.58
Hariray X ICSV 700	2.8	2.7	2.7	2.7	-5.66	0.00
Hariray X IS 1044	1.7	2.5	3.8	3.1	32.54	-22.58
Hariray X IS 2205	2.6	3.6	3.2	4.6	27.17	30.43
Hugurtay	0.3	1.5	2.8	4.2	79.38	33.33
Hugurtay X ICSV 700	2.2	3.5	2.6	3.8	36.23	31.58
Hugurtay X IS 1044	1.8	4.2	3.0	3.7	56.89	18.92
Hugurtay X IS 2205	0.7	2.9	0.6	3.2	75.95	81.25
ICSB 464	3.6	4.6	3.4	3.2	21.05	-6.25
ICSV 700	4.0	4.1	3.5	4.0	1.72	12.50
ICSV 745	2.1	4.1	5.5	6.4	49.03	14.06
IESV 23008 DL	3.4	5.6	3.4	4.0	38.96	15.00
IESV 23008 DL X ICSV 700	3.7	4.9	4.6	3.9	24.57	-17.95
IESV 23008 DL X IS 1044	4.5	4.7	4.7	5.0	3.74	6.00
IESV 23008 DL X IS 2205	4.1	5.0	4.0	4.1	18.16	2.44
IESV 23010 DL	3.2	4.6	3.5	3.2	30.21	-9.37
IESV 23010 DL X ICSV 700	2.8	5.0	4.0	5.3	44.00	24.53
IESV 23010 DL X IS 1044	3.3	5.4	2.5	3.8	39.39	34.21
IESV 23010 DL X IS 2205	2.4	5.2	3.7	4.2	53.76	11.90
IESV 23011 DL	2.2	4.1	3.2	3.8	45.68	15.79
IESV 23011 DL X ICSV 700	3.8	4.0	6.1	4.1	6.06	-48.78
IESV 23011 DL X IS 1044	4.3	4.3	4.0	3.8	0.58	-5.26
IESV 23011 DL X IS 2205	3.5	5.3	3.6	3.4	33.46	-5.88
IS 1044	3.3	3.6	4.4	3.4	8.33	-29.41
IS 2205	1.6	2.5	3.1	4.3	36.38	27.91
IS 8193	1.8	3.9	3.7	4.6	53.25	19.57
Kari Mtama 1	3.1	3.6	9.8	6.1	14.72	-60.66
Kari Mtama 1 X ICSV 700	3.2	5.5	5.1	3.8	41.34	-34.21
Kari Mtama 1 X IS 1044	3.3	4.9	3.1	4.4	32.52	29.55
Kari Mtama 1 X IS 2205	2.1	4.2	1.7	6.1	49.94	72.13
Kiboko local 2	2.3	3.6	3.6	4.2	35.84	14.29
Macia	3.4	4.7	6.7	4.1	28.27	-63.41
Macia X ICSV 700	3.1	4.0	2.8	5.0	22.89	44.00
Macia X IS 1044	3.5	1.9	2.3	5.4	-81.35	57.41
Macia X IS 2205	1.8	3.0	4.6	6.2	40.40	25.81
Seredo	2.4	3.6	6.1	4.5	34.07	-35.56
Sila	3.9	5.0	3.0	6.3	22.23	52.38
Sila X ICSV 700	4.0	3.9	3.2	4.4	-2.96	27.27
Sila X IS 1044	4.0	5.1	2.8	3.4	21.57	17.65
Sila X IS 2205	2.4	3.7	5.7	6.9	35.22	17.39
Swarna	3.0	4.1	4.1	3.1	27.55	-32.26
Tegemeo	2.9	4.3	4.8	3.1	31.84	-54.84
Tegemeo X ICSV 700	3.5	5.5	3.9	4.1	36.88	4.88

Appendix 3: Grain yield potential and response of sorghum lines under *Chilo partellus* infested and non-infested conditions during the short rain season (2015) at KALRO-Kiboko, Kenya.

	Grain yield (t ha^{-1})					
	Kiboko		**Kabete**			
	Response	Potential	Response	Potential	**Grain yield loss (%)**	
Entry	(infested)	(uninfested)	(infested)	(uninfested)	**Kiboko**	**Kabete**
Tegemeo X IS 1044	3.5	5.2	3.2	6.0	32.30	46.67
Tegemeo X IS 2205	2.7	4.3	4.9	3.5	36.92	-40.00
Grand mean	**2.9**	**4.14**	**3.9**	**4.3**	**29.62**	**6.65**
LSD$_{0.05}$	**1.0****	**0.21****	**1.14****	**2.52****		
CV	**11.3**	**2.5**	**17.4**	**28.9**		

*, **, = significant P≤0.05, significant P≤0.05, LSD = least significant difference and CV = coefficient of variance.