GENETICS OF WITCHWEED (*STRIGA HERMONTHICA* (DEL.) BENTH) RESISTANCE IN SORGHUM (*SORGHUM BICOLOR* (L.) MOENCH)

BY

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MSc/Agric/1965/10-11

A THESIS SUBMITED TO THE SCHOOL OF POSTGRADUATE STUDIES,

AHMADU BELLO UNIVERSITY, ZARIA

IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE AWARD

OF A

MASTER DEGREE IN PLANT BREEDING.

DEPARTMENT OF PLANT SCIENCE,

FACULTY OF AGRICULTURE

AHMADU BELLO UNIVERSITY, ZARIA

NIGERIA

JUNE, 2014

DECLARATION

I declare that the work in this Thesis entitled GENETICS OF WITCHWEED (*Striga hermonthica* (Del.) Benth) RESISTANCE IN SORGHUM (*Sorghum bicolor* (L) Moench) has been performed by me in the Department of Plant Science. The information derived from the literature has been duly acknowledged in the text and a list of references provided. No part of this Thesis was previously presented for another degree or diploma at this or any other University.

CHUKWU, CHINENYE ---------- ----------
Signature Date

CERTIFICATION

This project thesis entitled GENETICS OF WITCHWEED (*Striga hermonthica* (Del.) Benth) IN SORGHUM (*Sorghum bicolor* (L) Moench) by Chinenye CHUKWU, meets the regulations governing the award of the degree of Master of Science of Ahmadu Bello University, Zaria and is approved for its contribution to knowledge and literary presentation.

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DEDICATION

This thesis is dedicated to God Almighty who by his grace sustained and enabled me to complete the work successfully.

ACKNOWLEDGEMENTS

I am grateful to God who in his infinite mercy, made this research work a success.

My profound gratitude goes to Professor Mary Y. Yeye, the chairman of my supervisory committee whose meaningful contribution, guidance and assistance brought this thesis to this shape and form. I also wish to extend my appreciation to Professor D.A. Aba and Dr U.S. Abdullahi for sparing their time to serve on the supervisory committee and for their guidance and constructive criticism throughout the course of the work. I thank the following people: Prof. M. F. Ishiyaku; Head, Department of Plant Science, all my lecturers and all other staff of Plant Science Department, for their assistance.

My heartfelt thanks go to my parents Mr. and Mrs. F.A. Chukwu, my brothers and sisters for their moral, physical and financial support. In fact this accomplishment would have not been possible without their support. I also thank all my friends and colleagues for their assistance, advice and encouragements.

Finally, I acknowledge the assistance of the technical team of Sorghum Unit, Institute of Agricultural Research, Samaru and all other people who have contributed to the success of this thesis, I say thank you all.

ABSTRACT

Study on the genetics of witchweed (*Striga hermonthica* (Del.) Benth*)* resistance in sorghum (*Sorghum bicolor* (L) Moench) was conducted in a randomised complete block design experiment at the Institute for Agricultural Research Samaru, (Northern Guinea Savanna 11^0 11' N: 7^0 38' E, 686m) Zaria, Kaduna state, Nigeria. Five sorghum varieties: two *Striga* resistant varieties (ICSR94405 and ICSR94407) and three susceptible varieties, (SAMSORG40, SAMSORG14 and SAMSORG17) were used for the study. The study was undertaken to determine the variability for resistance to *Striga* and other agronomic traits in sorghum, to determine inheritance of resistance to *Striga* in sorghum, gene action involved in the inheritance of *Striga* resistance in sorghum, and to determine genetic advance for *Striga* resistance and other agronomic traits in sorghum. The resistant varieties used as male parents were crossed to the susceptible parents which were the females and F_1, F_2 and backcross populations were generated. The six populations: P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2 were evaluated at IAR Samaru *Striga* sick plot in 2012. The result revealed highly significant difference among the genotypes for the traits studied. The result showed that additive gene action is more important for the inheritance of *Striga* resistance in sorghum. Inheritance of resistance to *Striga* in the F_2 populations involving the male parent: ICSR94407 is controlled by two dominant genes which are complementary, while in F_2 populations involving ICSR94405; it is controlled in part by genes at two or more loci. Also high heritability and genetic advance were observed for almost all the traits studied, indicating; positive response, repeatable and transmitability of these traits in selection.

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LIST OF ABBREVIATIONS

AATF	African Agricultural Technology Foundation
ANOVA	Analysis of variance
APHIS	Animal and Plant Health Inspection Service
BC_1P_1	First backcross to parent one
BC_1P_2	First backcross to parent two
CDFA	California Department of Food and Agriculture
CV	Coefficient of Variation
F_1	First filial generation
F_2	Second filial generation
FAO	Food and Agriculture Organization
GA	Genetic Advance
GMA	Generation Mean Analysis
GP	Germination Percentage
GW	Grain Weight
GY/Plt	Grain yield per plant
HD	Days to 50% Heading
IAR	Institute for Agricultural Research
ICRISAT	International Crop Research Institute for the Semi-Arid Tropics
IITA	International Institute of Tropical Agriculture
ITIS	Integrated Taxonomic Information System
MGD	Maximum Germination Distance
MT	metric tons
P_1	Parent one
P_2	Parent two

PaL	Panicle Length
PH	Plant Height
RCBD	Randomized Complete Block Design
SAS	Statistical Analysis System
SC	*Striga* count per plant
SDS	*Striga* damage score
SSA	Sub-Saharan Africa
USDA	United State Department of Agriculture

CHAPTER ONE

INTRODUCTION

Sorghum (*Sorghum bicolor* (L.) Moench) is a major cereal in the semi-arid tropics of sub-Saharan Africa. It belongs to the family Poaceae, and probably originated from south of the Sahara in Africa. It is an important world crop, used for food, fodder, production of alcoholic and non-alcoholic beverages, as well as biofuels. Some varieties are drought and heat tolerant, and are especially important in arid regions, where the grain is staple or one of the staples for the poor and rural people. It is the "fifth most important cereal crop grown in the world after rice, maize, wheat and barley" (Kuhlman *et al*., 2010). Nigeria's annual production of sorghum was 6.8 million metric tons in 2011 (FAO, 2012) and 6.9 million metric tons in 2012 (FAO, 2013).

However, sorghum production is affected by both biotic and abiotic constraints. One of the major biotic constraints to sorghum production in sub-Sahara Africa is the parasitic flowering weeds of the genus *Striga*. This seriously limits cereal production in sub-Saharan Africa. Two out of three fields cropped with cereals are estimated to be infested by *Striga spp* (Lagoke *et al*., 1991). Beside withdrawal of water, nutrient and assimilates, *S. hermonthica* damages its host by inducing enzyme and plant hormone changes, disrupting host-water relationships and carbon fixation (Press *et al*. 1996). Problem with *S. hermonthica* are most severe in degraded environments, with low rainfall, and under subsistence farming systems with few options for external inputs (Rodenburg *et al.*, 2005). The species affecting cereal crops, especially sorghum includes *Striga hermonthica, S. asiathica, and S. forbesi. Striga,* especially *S.*

hermonthica has marked influence in growth and allometry of its host plant (Musselman, 1987; Parker, 1991).

Grain losses of sorghum due to *Striga hermonthica* are difficult to estimate, however, Doggett (1988) reported 59% estimated loss, Ramaiah (1987) reported 10-35% loss and an African regional scale average loss of between 5 and 15% (Riches and Parker, 1995). Heavy infestations by these notorious hemi parasites have caused farms to be abandoned and at times, migrations of farming communities (Lagoke *et al*., 1991). *Striga* has infested over 40% of arable land in sub-Saharan Africa (SSA) (Lagoke *et al.* 1991) and caused yield losses of up to 100% (Hassan *et al.* 1994). In Nigeria, *Striga* is infesting about 6.5 million hectares (out of 9.32million ha under sorghum), causing an estimated 35% yield loss (amounting to about 3.3million MT of sorghum yield loss annually (Obilana, 2011a). It is imperative that *Striga* populations be controlled so that they remain below the economic threshold.

The recommended control methods of *Striga* infestation include heavy application of nitrogen fertilizer, the use of trap crops and chemical stimulants to abort seed germination, hoeing and hand pulling, herbicide application and the use of resistant or tolerant crop varieties. None of these methods is effective on its own and most farmers have not accepted the methods to a great extent due to technological and socio-economic reasons. Chemical control of *Striga* is expensive and cannot be afforded by resource-poor farmers (Lagoke *et al.*, 1991).

However, Mabasa (1996) indicated that resistant cultivars offer an economically feasible and culturally sustainable technology for smallholder farmers since they can be

grown under conditions of erratic rainfall and low soil fertility and do not require additional cost and inputs. *Striga*-resistant cultivars should be a major component of integrated *Striga* control packages, since they effectively reduce *Striga* emergence, and enhance the efficiency of other control measures. Inadequate information on the genetics of *Striga* resistance and the difficulty of evaluating the trait in segregating progenies has limited the transfer of resistance into varieties better adapted to target areas (Vasudeva, 1985: Ejeta *et al*., 1992).

The knowledge of inheritance of resistance to *Striga*, variance components and genotypic performance will therefore be useful in developing *Striga* resistant cultivars or genotypes.

There is therefore a need for solutions to the menace that would ensure satisfactory increase in grain yield without requiring additional investment (Gbehounou and Adango 2003; Rodenburg *et al*., 2005). Thus, this study was undertaken with the following objectives.

1.1 General objective of the study:

The general objective of this study is to study the genetics of *Striga* resistance in some sorghum varieties.

Specific objectives**:**

1. To determine variability for resistance to *Striga* and other agronomic traits in sorghum
2. To determine the mode of inheritance of *Striga* resistance in sorghum
3. To determine the gene action involved in the inheritance of *Striga* resistance.
4. To identify new segregants that are resistant to *Striga* and can be promoted for further improvement

5. To determine genetic advance for *Striga* resistance and other agronomic traits in sorghum.

CHAPTER TWO

LITERATURE REVIEW

2.1 *Striga* Plant

Striga, commonly known as witch weed, is a genus with 28 species of parasitic plants that occur naturally in parts of Africa, Asia, and Australia (Kamal *et al.,* 2001). Witchweeds are characterized by bright-green stems and leaves and small, brightly coloured flower. Furthermore, they are obligate parasites of roots and therefore require a living host for survival (Sand *et al.*, 1990). The genus is classified in the family Orobanchaceae (Nelson *et al.,* 1999), although older classifications place it in the Scrophulariaceae (ITIS, 2007). Most species of *Striga* are not pathogens that affect human agriculture. However 11 species are considered important parasites on agricultural crops particularly those planted by subsistence farmers (Nickrent *et al.,* 2004). Most commonly affected crops are corn, sorghum, and sugarcane (Sand *et al.,* 1990). Three species cause the most damage: *Striga asiatica*, *S. gesnerioides*, and *S. hermonthica*. *Striga* seeds are very tiny; some are 0.30mm long and 0.15mm wide. Depending on the species and the environmental conditions for plant development, one *Striga* plant may produce 40,000 to 90,000 seeds (Ejeta *et al*., 1997). The seed can remain dormant but viable in the soil for 15-20 years (Ramaiah *et al.*, 1983). The organ of parasitism, the haustorium forms a morphological and physiological bridge between *Striga* seedling and host roots. Numerous *Striga* plants may penetrate and attach to a single individual host plant (Ejeta *et al.*, 1997).

2.1.1 Economic importance of *Striga*

Parasitizing important economic plants, witchweed is one of the most destructive pathogens in Africa (Agrions, 2005). In fact, witchweed affects 40% of Africa's arable savanna region, resulting in up to $13 billion loss every year. *Striga* affects 40 million hectares of crops in sub-Saharan Africa alone (AATF, 2005). Witchweed infestation is so bad in parts of Africa that some farmers have to relocate farms every few years. Furthermore, the majority of crops in Africa are grown by subsistence farmers who cannot afford expensive witchweed control, and therefore suffer many losses as a result of this pathogen.

In Nigeria, sorghum (*Sorghum bicolor* (L.) Moench) which accounts for 34% of total cereal production (Akintayo and Sedgo, 2001) is one of the major cereals severely affected by *Striga* infestation than in other West African countries, with about 80% (8.7 million ha) of land cropped to sorghum infested by this weed (Gressel *et al*., 2004). In a recent survey conducted in northeastern Nigeria, Dugje *et al*., (2006) reported that out of 266 farmers' sorghum fields sampled, 94% were infested with *S. hermonthica*. Obilana, 2011 reported that *Striga* is infesting about 6.5 million ha (out of 9.32million ha of sorghum area), causing an estimated 35% yield loss (amounting to about 3.3million MT of sorghum yield loss, annually).

Corn, sorghum, and sugarcane crops affected by witchweed in the United States have an estimated value of well over $20 billion (Sand *et al.*, 1990). Furthermore, witchweed is capable of wiping out an entire crop (Johnson, 2005). In fact, it is so prolific that in 1957 the US Congress allocated money in an attempt to eradicate witchweed. Thus, the Animal and Plant Health Inspection Service (APHIS) of the U.S. Department of Agriculture established a research station and control methods. Through infestation

mapping, quarantine, and control activities such as contaminated seed destruction, the acreage parasitized by witchweed has been reduced by 99% since its discovery in the United States (USDA, 200**3)**. APHIS even offered cash rewards for those who identified and reported the weed, and encourages landowners to check their own fields (USDA, 200**3).**

2.1.2 Mode of parasitism of *Striga*

The mode of parasitism is generally the same in all obligate root parasites. They are propagated by seeds that remain dormant in the soil until stimulated to germinate by exudates from the root of a host crop (Parker *et al.*, 1977; Worsham, 1987). Vasudeva *et al.* (1987) recognized three mechanisms in the host-parasite interactions:

(i) Those governing the adaptation of *Striga* to a parasitic mode of life (adaptation mechanism of parasite)

(ii) Those governing the ability of the parasite to recognize a particular host species (mechanism of host specificity)

(iii) Those by which the host resists the parasite (mechanism of resistance).

The first two mechanisms are located in the parasite, while the third is located in the host. All the three different stages of the mechanism are expressed at different stages of the life cycle of the *Striga.* Nickrent and Musselman (1979) also recognized the following five processes in the life cycle of *Striga.*

- Seed germination
- Haustoria initiation
- Host tissue penetration (up to the establishment of vascular connection)
- Physiological compatibility and Parasite growth and maturation.

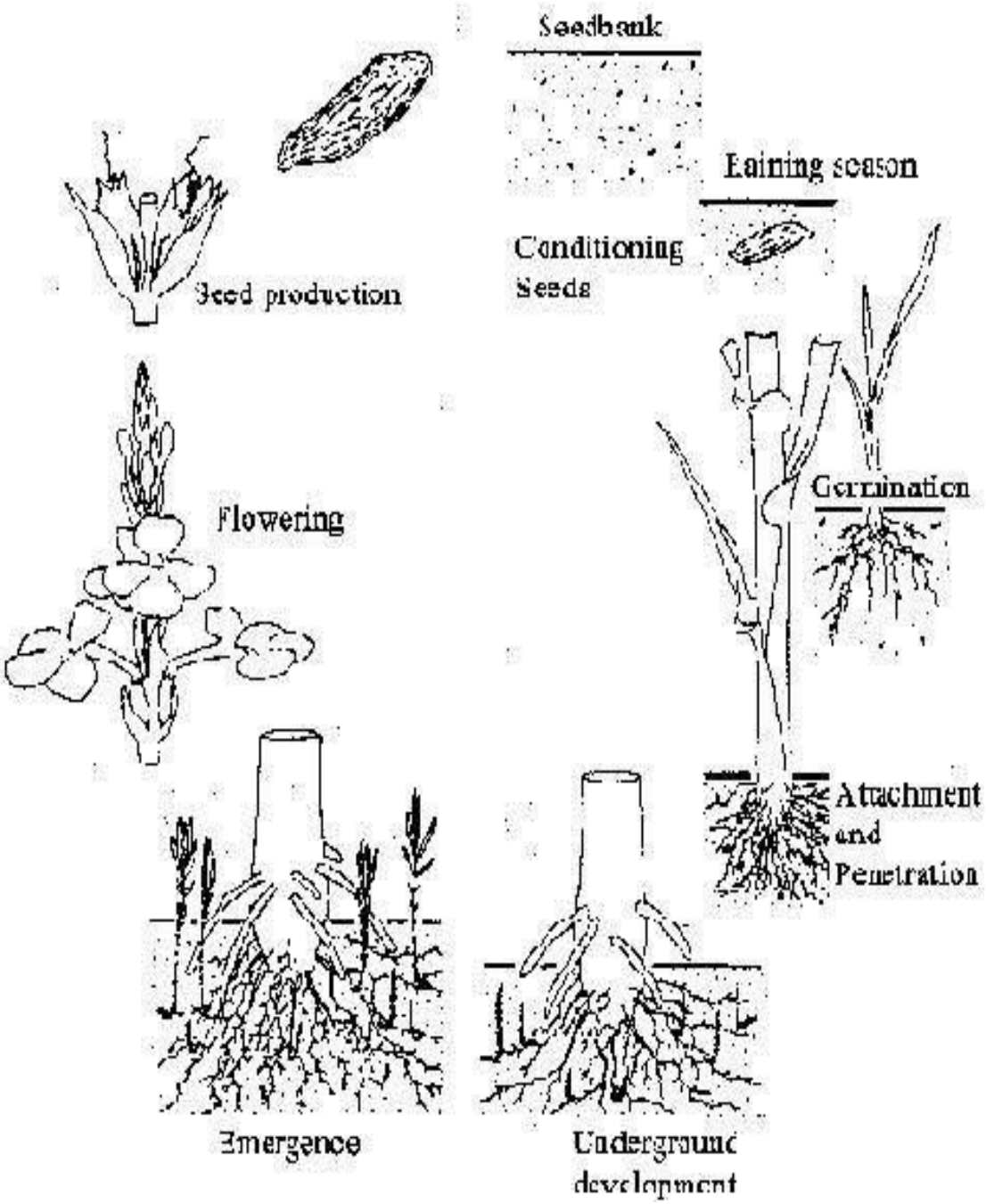


Figure 1. *Striga* life-cycle. (Courtesy Carolina Lis)

2.1.3 Effects of *Striga* on sorghum

Witchweed parasitizes sorghum and it is capable of significantly reducing yields, in some cases wiping out the entire crop (Sand *et al.*, 1990).

Host plant symptoms such as stunting, wilting, and chlorosis are similar to those seen from severe drought damage, nutrient deficiency and vascular disease (Sand *et al.*, 1990). The commonest symptom in the field as well as in the screen house is inter-veinal chlorosis. The *Striga* plant may or may not emerge above the soil level before the appearance of chlorosis or any other external symptom. Obilana (1979) observed in sorghum that the symptoms usually appear before *Striga* emerges from the ground. Both *S. hermonthica* and *S. asiatica* have been reported to cause stunting of the shoots, reduction of vigour, and failure of panicle formation in sorghum.

Pieterse (1985) attributed the effects of *Striga* on sorghum to the diversion of host's photosynthates, mineral salts, and water to the parasite. Tidiane (1983) had observed that carbohydrates, especially sucrose and other soluble sugars, were the main organic compounds withdrawn from the host. These physiological modifications reduced *Striga* photosynthetic capacity and predisposed the host plant to water stress. Each *Striga* plant is capable of producing up to 500,000 seeds, which may remain viable in the soil for over 10 years (USDA, 2003). Its seeds germinate in the presence of host root exudates and develop haustoria which penetrate host root cells (Sand *et al.*, 1990). Host root exudate contains strigolactones, signaling molecules that trigger *Striga* seed germination (Matusova *et al.*, 2005). A bell-like swell forms where the parasite root attaches to the root of the host. The pathogen colonizes underground where it may spend 4-7 weeks before emergence, when it rapidly flowers and produces seeds. Witchweed seeds spread easily by wind, water, and soil via animal vectors (Johnson,

2005). The chief means of dispersal, however, is through human interaction, by means of machinery, tools, and clothing (USDA, 2003).

2.1.4 Mechanism of host response to *Striga*

The defenses of host plants against a potential parasite may be either avoidance or resistance mechanisms. Avoidance reduces the chance of contact between the prospective host tissue and the parasite, whereas resistance operates when host tissue and the parasite come into contact (Parlevliet, 1977).

Early maturity or tolerance of conditions which adversely affect parasite development, such as extremes of temperature or humidity, are examples of an avoidance mechanism. They are genetically determined and may be very useful in breeding for disease and pest control. Ekeleme *et al.,* (2011) and Lagoke *et al*. (1991) reported that late planting of sorghum reduced number of emerged *Striga* plants twice the total found when planting was done earlier. Parker and Riches (1993) and Dugje *et al.,* (2008) also reported that late planting of maize reduced number of emerged *Striga* plants. Gbèhounou *et al*. (2004) and Dugje *et al*., (2008) attributed higher infestation of *S. hermonthica* in early plantings to the ability of the host to produce more stimulants which encouraged *Striga* seed germination and haustoria attachment. When planting is delayed *Striga* seeds are unable to germinate and seedlings fail to attach to host root systems due to unfavourable low soil temperatures during the middle of the rainy season (Hoffmann *et al*., 1997; Odhiambo and Ariga, 2004). Crop root exudates may also be leached following heavy showers, which would reduce *Striga* germination later in the season (Gbèhounou *et al*., 2004). Lower *Striga* counts in varieties with short growth cycles were reported by Oswald and Ransom (2004) in maize and by Dugje *et al*. (2003) in millet. Ransom and Odhiambo (1995) attributed low *Striga* population in

small stature and early maturing maize genotypes to the production of less extensive root systems which provided fewer sites for *Striga* parasitism. The early maturing sorghum varieties may have escaped *Striga* parasitism and supported less *Striga* emergence from the combined effect of reduced stimulant production and unfavourable soil environment for *Striga* seed germination and haustorium attachment later in the season. In a similar study, S. gesnerioides infestation has also been reported to reduce root nodulation and the root and shoot dry weight of cowpea varieties especially in the late planted trials (Alonge *et al.*, 2004).

Oswald and Ransome (2001) and Ransome, (1999) reported that a short growing cycle (escape mechanism), root architecture (fewer roots in the upper soil layer), early growth and vigour and physiological resistance to the phytotoxic effects caused by *Striga* parasitism are some of the factors that determine the level of resistance/tolerance in maize. They reported that maize varieties with a short cycle supported low *Striga* densities due to rapid shoot and root development, which leaves less time for *Striga* to attach itself. Although short –cycle maize varieties appear to be a good choice for *Striga* infested area; their limited yield potential might not satisfy farmers' need. Singh and Emechebe (1991) cautioned that the benefit of late sowing in reducing *Striga* infestation can be negated by yield losses resulting from moisture stress toward crop maturity. Parker (1991) suggested that the use of resistant varieties is probably the most appropriate way for subsistence farmers to control *S hermonthica.* Doggett (1970) and Ramaiah (1987) suggested that three resistance mechanisms to *Striga* were possibly operating in host species and this might be caused by one or more of the following factors:

(i) Low or no *Striga* germination stimulant production

(ii) Mechanical barriers to parasite's ingress (anti-haustorial factors)

(iv) Antibiosis

2.1.5 Germination stimulant production

Freshly produced but mature *Striga* seeds are effectively dormant. They required a period of after-ripening under dry conditions to lower seed moisture content and break their dormancy (Mohamed, *et al.,* 1998), and will only germinate after the after-ripened seeds are conditioned by exposure to warm moist conditions for several days, followed by chemical stimulation (Doggett, 1988). Stimulation of the seeds to germinate initiates the potential host-parasite relationship. It also introduces the first opportunity for host resistance against *Striga.* Root of many host and non-host plants exude a variety of compounds that are effective as germination stimulants, but they are often present at very low levels so that their isolation and identification are difficult (Ejeta *et al.,* 1993). However, strigol (from cotton, maize, sorghum and millet roots), sorgoleone and sorgolactone (from sorghum roots) are some of the compounds that have been identified (Ejeta *et al.,* 1993). Sorgolactones are the most common and important in terms of controlling *Striga* germination by sorghum in the field (Siame *et al.,* 1993). A fourth water-soluble compound with a quantitative biosynthetic pathway has also been isolated from sorghum but has not yet been identified (Hess *et al.,* 1992; Vogler *et al* 1996). *Striga* germination is a multi-factorial phenomenon modulated by an orderly sequence of events that reflects adaptations to the environment and to the parasitic habit (Babiker *et al.,* 2001). The diverse nature of germination stimulants suggests that they may elicit the production of a common molecule, or act as a signalling mechanism that triggers germination. Babiker *et al.* (1994) observed that *Striga* seed germination was

positively correlated with ethylene production. They observed that *Striga* seed germination and ethylene production also increased with strigol concentration.

Sorghum genotypes differ by as much as a billion fold in the amount of stimulant they produce (Ejeta *et al.,* 1993). This variation is responsible in part for the resistance against *Striga* found in some sorghum cultivars (Hess *et al.,* 1992). A host plant that produces low amounts of stimulants will cause fewer *Striga* seeds to germinate, and thus will be subject to less infestation. Conversely, high stimulant producers will cause a greater number of *Striga* seeds to germinate resulting in serious infestation in the absence of other resistance mechanisms (Doggett, 1988). Hess *et al.* (1992) reported that low stimulant production is sufficient to confer field resistance to *Striga*, independent of other mechanisms. However, not all *Striga*-resistant sorghum genotypes are low producers of the stimulant (Ejeta *et al.,* 2000). Coefficients of correlation between maximum germination distance (MGD) and *Striga* resistance under field conditions are generally positive but vary among genetic materials and test locations (Haussmann *et al.,* 2000b). Furthermore, it was also illustrated that the few *Striga* parasites that emerged on resistant cultivars can cause serious yield reductions (Gurney *et al.,* 1999). These are some of the reasons why multiple mechanisms of resistance are a necessity in a single cultivar, to cater for the shortfalls of other mechanisms. Thus, *in vitro* germination distance cannot be used as an indirect selection trait for total field resistance to *Striga,* since the relationship between the two is dependent on genotype and test locations.

2.1.6 Environmental requirement of *Striga*

Temperatures ranging from 30-35°C in a moist environment are ideal for *Striga* germination (Johnson, 2005). *Striga* will not germinate in temperatures below 20°C. Agricultural land with light soil and low nitrogen levels tend to favour the development of witchweed (CDFA, 2007). Still, witchweed has demonstrated a wide tolerance for soil type provided soil temperatures are favorably high. Seeds have been shown to survive in frozen soil, with temperatures as low as -15°C, attesting to their aptitude as overwintering structures. Soil temperature, air temperature, photoperiod, soil type, and soil nutrient and moisture levels do not greatly deter the development of witchweed (Johnson, 2005).

2.1.7 *Striga* management

Management of witchweed is difficult because the majority of its life cycle takes place below ground. If it is not detected before emergence, it is too late to reduce crop loss (Johnson, 2005). To prevent witchweed from spreading, growers should plant uncontaminated seeds and clean soil and plant debris off machinery, shoes, clothing, and tools before entering fields (Johnson, 2005; CDFA, 2007). If there is few witchweed, hand weeding before seeds are produced is an option. If there is a lot, then more intense management strategies need to be used.

Striga has been controlled through the use of several management strategies, including quarantines imposed on affected areas, control of movement of farm machinery and equipment between infected and non-infected areas, herbicide application, and imposed "suicidal germination." For the latter, in fields not yet planted to host crops, *Striga* seeds present in the soil are induced to germinate by injecting ethylene gas which mimics the natural physiological response tied to host recognition. Because no host

roots are available, the seedlings die. Unfortunately, each *Striga* plant can produce tens of thousands of tiny seeds and these can remain dormant in the soil for many years (Mourik, 2007). Thus, such treatments do not remove all seeds from the soil. Moreover, this method is expensive and not generally available to many farmers in developing nations of Africa and Asia.

Another method called trap cropping involves planting a species in an infested field that will induce the *Striga* seeds to germinate, but will not support attachment of the parasite. This method has been used in sorghum plantations by planting *Celosia argentea* (*Striga* "chaser") between the sorghum (Olupot, 2003). Planting silverleaf (*Desmodium uncinatum*) has worked in maize crops (Radford, 2003). Cotton, sunflower, linseed, and witchweed resistant maize are also effective trap crops.

Increasing nitrogen levels in the soil, growing tolerant varieties, and trap-cropping, planting crops that are susceptible but are harvested before witchweed seed is produced, can also be used to reduce *Striga* effect (Radford, 2003). Coating maize seeds with fungi or an herbicide also appear to be promising approach. Some crop cultivars, especially corn, are resistant to herbicides that kill witchweed when the haustoria attaches to the crop (AATF, 2005). STRIGAWAY® maize has been shown to reduce the seed bank of *Striga* by 30% in two seasons (AATF, 2005).

Use of resistant cultivars: Resistance against *Striga* is defined as the capacity of a plant to support fewer emerged *Striga* plants and to yield more grain than a susceptible plant when grown under infestation. In contrast, tolerant genotypes are those which germinate and support as many *Striga* plant as do susceptible genotypes without showing a concomitant reduction in yield (Ejeta *et al.*, 1991). Immune genotypes do not allow parasitic attachment of witchweeds on their roots. Cereals that are immune to

Striga have not yet been identified. Tolerant cultivars are not desirable because their cultivation results in continued growth of the *Striga* seed bank. *Striga* resistant cultivar can offer an economically feasible and culturally sustainable technology under small holder farmer conditions (Ejeta *et al.,* 1991; Mabasa, 1996). This ensues from the recognition that crop resistance is environmentally benign, requires no additional inputs and it is potentially durable. *Striga* can then be controlled by an integrated approach involving resistant cultivars and cultural practices such as use of *Striga*-free planting material, weeding, cereal-legume and cereal-cotton rotation, intercropping and other input-based farming practices. Such an approach should offer an effective and broad scale method of combating *Striga* and also prevent build-up of new strains of *Striga* to levels that can overcome the resistance of new variety. The beneficial effects of a herbicide and/or supplementary nitrogen on resistant or tolerant sorghum genotypes in *S. hermonthica* infested field has already been demonstrated (Ejeta *et al.,* 1993).

2.1.8 Source of *Striga* resistance among cereals

Variation in the reaction of cereals to *Striga* has been observed. Sorghum is the only cereal that exhibits multiple levels of resistance because this crop originated from Africa and it co-evolved with *Striga* parasites for at least 1000 years compared to maize (Obilana and Ramaiah, 1992; Lane *et al.,* 1995). In sorghum, resistance results from one or a combination of the several recognized mechanisms that influence the development of parasitism (Ejeta *et al.,* 1993; Ejeta *et al.,* 2000; Mohamed *et al.,* 2001a). A host plant showing more than one of these mechanisms is more desirable as it is most likely to offer a broad-based and durable control of *Striga*. Multiple mechanisms of *Striga* resistance have not been identified in maize and this might be expected for a crop that was not exposed to *Striga* long enough during its evolutionary

course since it was domesticated in Mexico under *Striga* free conditions (Ramaiah, 1987; Bennetzen *et al.,* 2000). International Institute of Tropical Agriculture (IITA) researchers started selection of maize genotype that support a reduced number of *Striga* plants in the early 1990s (Menkir *et al.*, 2002). Considerable progress has been made as excellent source of resistance were obtained from *Zea diploparents*, African landrace and elite tropical germplasm. Intensive screening of these sources of germplasm yielded open pollinated varieties, inbred lines and hybrids with high levels of resistance to *S. hermonthica* (Menkir *et al.*, 2002).

Kling *et al.* (2000) reported that a high level of resistance in a fixed line can be used readily in any breeding programme. Such resistant genotype can be used as parents in hybrids or synthetics, or to introgress resistance into locally adapted germplasm. It is also interesting to note that maize varieties developed for *S. hermonthica* resistance in West Africa have been found to provide useful levels of resistance in many lowland environments throughout sub-Sahara Africa, under both *S. hermontica and S. asistica* infestation (Kling *et al.,* 2000). For instance, researchers in Malawi found good levels of resistance against *S. asiatica* in maize genotype that had been identified by IITA to be resistant to *S. hermonthica* in West Africa (Kabambe *et al.*, 2000). The important thing to be noted here is that resistance for a particular variety will be upheld if it is grown within its region of adaptation.

2.2 Breeding for Durable Resistance to *Striga* in Sorghum

Progress from past efforts in breeding witchweed resistance in crops has been limited. Reasons for slow progress vary from complexity of the resistance trait to lack of

research support and appropriate screening techniques and selection strategies (Ejeta *et al.,* 2001). However, resistant sorghum cultivars that have been developed so far have shown good level of resistance mainly based on low stimulant production (Ejeta *et at.*, 2000). Nevertheless, crop cultivars with durable resistance to *Striga* have not yet been identified (Ejeta *et al.,* 2001). Over the years, resistance has not been long-term or applicable over a wide geographical area. One of the main causes of failure of resistance is that breeding efforts have not been taking good account of both the interspecific variability among *Striga* species, and intraspecific variation for virulence. Thus, witchweed populations have an extraordinary elasticity and capacity to adapt to new host species through the gradual build-up of new "biological forms" (Koyama, 2000). The reported variability of witchweeds implies that using single resistance genes to manage infestations is inadequate. Stacking of resistance genes may be essential to manage witchweeds effectively.

Various researchers have suggested a diversity of breeding strategies that could lead to the development of long-term polygenic resistance to witchweeds (Ejeta *et al.,* 1992; Ejeta and Butler, 1993; Haussman *et al.,* 2000a). If sources of resistance have been identified, they can be incorporated for agronomic performance. Alternatively, the resistance gene in these sources can be incorporated for agronomic performance. Alternatively, the resistance genes in these sources can be obtained by pyramiding resistance genes. Crop genotypes that possess multiple genes for *Striga* resistance, based on distinct mechanisms, are likely to have genetic resistance that is durable across several environmental conditions as well as across ecological variants of the parasite. It has also been emphasized that breeding programmes should target sources of resistance at different areas and understand the nature of resistance required (Koyama, 2000). Suggested breeding methods include: early generation selection for

individual resistance mechanisms; use of recurrent selection procedures to develop breeding populations with multiple sources of resistance; lines with different resistance mechanisms are combined to form hybrids or synthetics, to increase durability of resistance and the use of marker-assisted selection techniques for the development of broad-based, quantitative resistance to witchweeds under field conditions (Haussman *et al.,* 2000b).

Progress has been made in breeding for single gene *Striga* resistance mechanisms in sorghum. The mechanisms have been extensively exploited. Diverse sorghum genotypes with little or no stimulant production capacity have been identified. A number of improved sorghum varieties with *Striga* resistance due to low germination stimulant production have been developed (Ejeta *et al.,* 2001). Screening of landraces and improved sorghum lines using different bioassays has shown that host variants with low germination stimulant production, hypersensitive response, and incompatible response are rare. Rather, a greater preponderance of genetic variation for these traits has been found among wild and related species of sorghum (Ejeta *et al.,* 2001). Introgression of these genes for low germination stimulant production, hypersensitive response, and incompatible response into elite sorghum cultivars is still to be accomplished.

It is generally not possible to select single plants for witchweed resistance in the field, as there are no appropriate techniques. Selection for resistance is therefore usually deferred until true breeding progenies are available (Haussman *et al.,* 2000a). This means that large numbers of progeny have to be advanced before *Striga* resistance is assessed, a time- and cost-intensive procedure. On the other hand, screening for individual resistance mechanisms in the laboratory could result in a loss of valuable

materials possessing resistance mechanisms other than those evaluated. One strategy could be to use laboratory assays for individual resistance mechanisms as an initial screening of a large number of breeding materials, followed by field screening. This would offer the possibility of identifying resistance source with multiple resistance mechanisms (Haussman *et al.*, 2000a). All prospective resistant cultivars should be evaluated at various locations with different *Striga* populations or host-specific races (Ramaiah, 1997; Koyama, 2000).

2.3 Heritability and Genetics of Resistance to *Striga* in Sorghum

The heritability of a character measures the extent to which it is transmitted from one generation to the next. Thus it is a valuable tool when used in conjunction with other parameters in predicting the magnitude of genetic gain that follows selection for the character (Katata *et al.*, 1976a). Sorghum resistant to *S. hermonthica* in Africa have been reported (Doggett, 1965; Ejeta and Jain, 1982; Kambal 1979; Ramaiah, 1987), but resistance in some cultivars does not hold up across geographical regions. The variable performance of a given host cultivar under *Striga* infestation in different areas may be due to the existence of intraspecific physiological variants of the parasite (Bebawi, 1981; King and Zummo, 1977; Parker and Reid, 1979). Published reports on the genetics of resistance to *Striga* spp. in sorghum are few. Saunders (1933) reported that resistance to *S. asiatica* was recessive in two sorghum crosses and partially dominant in the third. Kulkarni and Shinde (1985) found field tolerance to the same species to be governed by non-additive gene action. Obilana (1984), defining resistance to *S. hermonthica* as "low total number of *Striga* per sorghum plant", reported high (0.78) broad sense heritability of this trait. He also found gene action to be non-additive with

over-dominance of susceptibility and estimated that two to five genes control reaction to the weed. More recently, Ramaiah et al. (1990) established that low *Striga* stimulant production in sorghum genotypes, Framida, 555, and SRN4846 is inherited as a single recessive gene. Progress on inheritance studies and breeding for resistance to *Striga* have been limited by variability in performance across geographical regions, lack of uniformity of field infestations and difficulty in evaluating individual segregating progenies for resistance when parasitism occurs below ground. The lack of a suitable laboratory assay that can predict field performance has also hampered progress.

CHAPTER THREE

MATERIALS AND METHODS

3.1 Description of the Study Site

The research was conducted at Institute for Agricultural Research (IAR) Farm, Samaru (11^0 11' N: 7^0 38' E, 686m) in Northern Guinea Savanna of Nigeria in 2011/2012.

3.2 Description of the Plant Materials

The materials that were used in this study comprised three IAR sorghum varieties: SAMSORG14, SAMSORG17 and SAMSORG40; and two *Striga* resistant varieties from ICRISAT India: ICSR94405 and ICSR94407. The descriptions of these varieties are presented in Table 3.1. The IAR sorghum varieties were obtained from the Institute for Agricultural Research (IAR) Cereal Research Program. These varieties were chosen because they are most commonly grown cultivars by the farmers within the sorghum production zone.

Table 3. 1 Morphological description and origin of sorghum genotypes used in the study

Cultivars	Origin	Description
ICSR 94405 P_1	ICRISAT	Medium height plant (140cm-200cm), with slim stem. Well exerted and compacted small panicle. Single seed per spikelet, which is relatively small, round and cream in colour. The plant matures early (90-100 days). Resistant to *Striga*
ICSR 94407 P_2	ICRISAT	Short plant (120cm-170cm), with slim stem. Well exerted and compacted small panicle. Single seed per spikelet, which is relatively small, round and cream in colour. The plant matures early (95-105 days). Resistant to *Striga*.
SAMSORG14 (KSV8) P_3	IAR	Tall plant (210cm – 280cm). Panicle is fairly long, elliptical and semi compact, containing single seed in each spikelet. Seed is round, big and white. Plant matures medium (within 125-135 days). Susceptible to *Striga*
SAMSORG17 (SK5912) P_4	IAR	Medium height plant (140cm-190cm), with short internodes and many leaves. Medium to large compact panicle, bearing single seed per spikelet throughout its length. Seed is yellow, relatively large and round. The plant matures late (about 150 days). Susceptible to *Striga*
SAMSORG40 (ICSV400) P_5	ICRISAT	Short plant (120cm-170cm), with slim stem. Well exerted small panicle. Single seed per spikelet which is relatively small, round and cream in colour. The plant matures early (100-110 days). Susceptible to *Striga*.

IAR: Institute for Agricultural Research, Samaru

ICRISAT: International Crop Research Institute for the Semi-Arid Tropics

3.3 Development of Genetic Populations

3.3.1 The F_1 hybrids

In 2011 growing season, the parent seeds were sown in order to make crosses between *Striga* resistant varieties (males) and the IAR varieties (females) using factorial mating design. The IAR varieties that were used flowered at variable periods: SAMSORG14, 100 days, SAMSORG17, 110 to 120 days, and SAMSORG40, 80 days; while the *Striga* resistant varieties: ICSR94405 flowers at 70 days and ICSR94407, at 75 days. Staggered sowing of the genotypes was adopted in order to synchronize the flowering and subsequent pollination. There were four plots, designated June plot, and July plots. June plot consist of two plots; SAMSOG17 was sown first on one plot, while SAMSORG14 was sown ten days later on the second plot. The July plots were also two; ICR94405, ICR94407 and SMSORG 40 were sown on the same day on one plot; and five days later ICSR94405 and ICSR94407 were sown again on the second plot. All genotypes were sown in plots consisting of 10 rows of 5meters long, with spacing of 75cm between rows and 30cm between plants. All the agronomic practices which include thinning, weeding, fertilizer application and earthen up were observed. In the June plot, SAMSORG14 and SAMSORG17 used as female were hand pollinated with ICSR94405 and ICSR94407 as male. In the July plots SMSORG40 used as female was hand pollinated with ICSR94405 and ICSR94407 as male and all the genotypes were also selfed. Hand emasculation was also done to remove the anthers in order to prevent self-fertilization. The seeds were hand harvested and seeds from each cross and the selfed parents were threshed separately and kept in clearly labelled bags.

The crosses generated were as follows**:**

Cross 2 SAMSORG14 (P_3) x ICSR94405 (P_1)

Cross 1 SAMSORG17 (P_4) x ICSR94405 (P_1)

Cross 3 SAMSORG40 (P_5) x ICSR94405 (P_1)

Cross 5 SAMSORG14 (P_3) x ICSR94407 (P_2)

Cross 4 SAMSORG17 (P_4) x ICSR94407 (P_2)

Cross 6 SAMSORG40 (P_5) x ICSR94407 (P_2)

3.3.2 The F_2 Populations

In 2012 dry season (January to June), the F_1 hybrids developed from crosses in 2011, together with their parental lines were sown in the IAR Samaru irrigation field. All the recommended agronomic practices were observed. At heading, the F_1 panicles in every cross were covered with paper bag to ensure complete selfing. Seeds from the selfed plants in each cross were harvested threshed and kept in clearly labelled bags as F_2 s.

3.3.3 The Backcross.

From the same plots that were used to produce F_2s seeds, before anthesis, the F_1 plant's heads were covered with paper bags to collect pollen. However, the parental lines were emasculated at anthesis. Then the F_1 of each cross was backcrossed to their respective parents to generate BC_1P_1, BC_1P_2, BC_1P_3, BC_1P_4 and BC_1P_5 (given twelve backcross populations); and this was done by hand pollination. At maturity, seeds developed from the plants were harvested and kept in labelled bags as backcross seeds.

3.3.4 Evaluation of Genetic Populations

The parentals, F_1s, F_2s and backcross populations (which were twenty nine genotypes) were sown in 2012 planting season at the IAR Samaru *Striga* sick plot.

The experiment was carried out using Randomized Complete Block Design (RCBD), with three replications. There were six treatments representing plant populations by a given cross: P_1, P_2, F_1, F_2, BCP_1 and BCP_2. Plot size for non-segregating populations (P_1, P_2, and F_1) was 2 rows of 4m length and 75cm apart. And that of the segregating populations (F_2, BCP_1 and BCP_2) was 5 rows of 4m length and 75cm apart. The intra-row spacing was 30cm in every plot. The plots were inoculated with *Striga* during sowing by putting 10ml of *Striga* mixed with fine sand in the hole where the sorghum seeds were sown. Recommended agronomic practices were observed.

3.4 Data Collection.

Data were collected on the following;

- Germination percentage: percentage of plants that germinated after two weeks of sowing.
- Days to 50% heading – days taken from sowing to when 50% of the plants in a plot had completed heading.
- Plant height – distance in centimeter from soil surface to tip of panicle at maturity.
- Panicle length – the distance in centimeter between inflorescence base to its tip.
- Panicle weight – the weight in grams of un-threshed single panicle
- Grain yield per plant – Grains separated from the panicle of each plant were weighed and the weight of the grains recorded and expressed in grams.

- 1000 grain weight – the weight in grams of 1000 randomly selected grains from individual plant.
- *Striga* count per plant at 12 weeks after sowing - the number of *Striga* that emerged on each plant at 12 weeks after sowing was recorded.

Striga damage score – crop syndrome rating which reflect the damage caused to the host plant in reaction to *Striga* infestation was recorded. This was done using a scale of 0 to 9 rating (Sinebo and Drennan 2001). Plants with score 0 to 4 were considered to be resistant, while those with score 5 to 9 were susceptible to *Striga*. The assessment considers chlorosis, blotching, scorching, and stunting, where 0 indicates no symptom developed and 9 indicates the highest intensity of symptoms as shown below:

0 No chlorosis or other symptoms: normal sorghum growth.

1 Chlorosis or other symptoms just visible at about 1%; normal plant growth.

2 Leaf blotching and scorching on about 10% of leaves with purplish-brown necrotic spots; almost normal plant growth. No stunting.

3 Moderate leaf blotching and scorching on about 20% of leaves with some purplish-brown necrotic spots mild stunting.

4 Leaf scorching on about 30% of leaves with some purplish-brown necrotic spots with some stunting.

5 Leaf scorching on about 40% of leaves with some gray-brown necrotic spots with some stunting.

6 Leaf scorching on about 50% of leaves with mostly gray necrotic spots with some stunting.

7 Leaf scorching on about 60% of leaves with severe gray necrotic spots and leaf wilting and rolling with definite stunting.

8 Leaf scorching on about 70% of leaves with definite gray necrotic spots, conspicuous stunting and leaf wilting. Death of host plant.

9 Complete scorching of all (100%); death of host plant (Carl *et al.*, 2001).

3.5 Statistical Analysis

The data was subjected to analysis of variance using generalized linear model procedure of SAS package (SAS, 2009). Analysis of variance (ANOVA) model for RCBD is $y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}$ and i = 1…..a, j = 1…..b

Where:

$y_{ij} =$ An observation in treatment i and block j

$\mu =$ The overall mean

$\alpha_i =$ The effect of treatment

$\beta_j =$ The effect of block j

$e_{ij} =$ Random error with mean 0 and variance σ^2

$a =$ The number of treatments; b = the number of blocks

Table 3. 2 ANOVA Table for RCBD in one year and one location.

Source of variation	Df	MS	EMS
Replication	$r-1$		
Genotype	$g-1$	M_2	$\sigma^2 + r\sigma_g^2$
Error	$(r-1)(g-1)$	M_1	σ^2

Where;

r = number of replications, g = number of genotype

3.5.1 Coefficient of variation

The coefficient of variation was calculated to measure the relative variability of given populations. Variance estimates have units attached to them. A common application of variance is the test to find out if one biological sample is more variable for one trait than for another. The coefficient of variation facilitates the comparison because it is unit free. The coefficient of variation (CV) is calculated as:

CV = $(S/\overline{X}) \times 100$

Where S = Standard deviation, and $\overline{X}$ = mean

3.5.2 Joint Scaling Test

The model described by Cavalli (1952) was used to estimate the parameters of the model viz., m (mean), a (additive) and d (dominance), and to test the goodness of fit of the model.

$$\overline{p}_1 = m - a$$

$$\overline{p}_2 = m + a$$

$$\overline{F}_1 = m + d$$

$$\overline{F}_2 = m + 1/2(d)$$

$$\overline{BCP}_1 = m - (1/2)a + (1/2)d$$

$$\overline{BCP}_2 = m + (1/2)a + (1/2)d$$

Where; m = mean

a = value of additive gene effects

d = value of dominance gene effects

3.5.3 Generation Mean Analysis (GMA)

To estimate mode of gene interaction, the generation mean analysis (GMA) was conducted to measure genetic parameters following the procedure described by Kang (1994). Generation mean was calculated for six generations on an individual plant basis. To determine the mode of gene action governing inheritance of resistance to *Striga* in sorghum, Gamble's (1962) notations were used as:

$$Y = m + \alpha a + \beta d + \alpha 2aa + 2\alpha\beta ad + \beta 2dd.$$

Where Y = the observed generation mean; m = mean; a = additive gene effects; d = dominance gene effects; aa = additive x additive epistatic gene effects; ad = additive x dominance epistatic gene effects; dd = dominance x dominance epistatic gene effects. α and β represent the coefficients for the genetic effects for the particular generation being estimated (Hayman, 1958; Mather and Jinks, 1982).

Means of six generations *viz.*, P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 were used to estimate six parameters by following the equation given by Hayman (1958).

$m = F_2$

$d = BC_1P_1 - BC_1P_2$

$h = 2BC_1P_1 + 2BC_1P_2 + F_1 - 4F_2 - ½\ P_1 - ½\ P_2$

$i = 2BC_1P_1 + 2BC_1P_2 - (1/2\ P_1) + ½\ P_2$

$j = BC_1P_1 - BC_1P_2 - (1/2\ P_1) + ½\ P_2$

$l = P_1 - P_2 + ½\ F_1 + 4F_2 - 4BC_1P_1 - 4BC_1P_2$

The variances of the estimates of gene effects were obtained as follows.

$Vm = VF_2$

$V(d) = VBC_1P_1 + BC_1P_2$

$V(h) = 4(BC_1P_1 + BC_1P_2) + VF_1 + 16VF_2 + ½\ (VP_1 + VP_2)$

$V(i) = 4 (BC_1P_1 + BC_1P_2) + 16V F_2$

$V(j) = VBC_1P_1 + VBC_1P_2 + ¼ (VBC_1P_1 + VP_2)$

$V(l) = VP_1 + VP_2 + 4VF_1 + 16(VF_2 + VBC_1P_1 + VBC_1P_2)$

Where, Vm, V(d), V(h), V(i), V(j) and V(l) were variances of m, d, h, i, j and l, respectively. VP_1, VP_2, VF_1, VF_2, VBC_1P_1 and VBC_1P_2 were variances of the mean of these estimates that provided standard errors for testing the significance of corresponding estimates.

The significance of the above parameters is tested with the help of 't'. To test the significance of the estimates, the 't' values were calculated for each component by dividing the gene effect of respective components by their standard error (SE) as given below.

$$t(m) = \frac{m}{SE(m)} \qquad t(d) = \frac{d}{SE(d)} \qquad t(h) = \frac{h}{SE(h)}$$

$$t(i) = \frac{i}{SE(i)} \qquad t(j) = \frac{j}{SE(j)} \qquad t(l) = \frac{1}{SE(1)}$$

The calculated' values were compared with table 't' value at 5 and 1 percent level of significance, respectively at pooled degrees of freedom.

The information about gene effects is very important. Generation mean analysis is a simple but useful technique for estimating these genetic effects, and nature of epistasis is helpful in deciding breeding procedures to be adopted for the improvement of quantitative characters like yield.

3.5.4 Chi-square Test

A chi-square test was conducted to test the goodness of fit of the F_2 population of the six crosses involving the resistant and susceptible parents, into the following segregation ratios: 3:1, 9:7, and 13:3 using the formula by (Little and Hill, 1978)

$$\chi^2 = \sum \frac{(O-E)^2}{E} \text{ At (n-1) df.}$$

Where, χ^2 = chi-square value, O = Observed value, E = Expected value, n = Number of classes, df = Degrees of freedom and $\sum$ = summation.

Deviations were taken as non-significant wherever the calculated χ^2 value is less than the table value at 5% level of significance and the ratio presumed was taken as showing good fit.

3.5.5 Heritability

Broad sense and narrow sense heritability estimates were obtained using the variance component methods. The F_2 variances were used to compute the broad sense heritability according to Burton (1951) as given below:

$$H_{(B)} = \frac{VF_2 - VF_1}{VF_2}$$

Where VF_1 and VF_2 are the variances of F_1 and F_2 generations

$H_{(B)}$ = broad sense heritability

The narrow sense heritability estimates was computed using the formulae described by Warner (1952).

$$H_{(N)} = \frac{2\sigma^2 F_2 - (\sigma^2 BC_1P_1 + \sigma^2 BC_1P_2)}{\sigma^2 F_2}$$

Where $H_{(N)}$ = narrow sense heritability, $\sigma^2 F_2, \sigma^2 BC_1P_1$ and $\sigma^2 BC_1P_2$ are the variances of the F_2, BC_1P_1 and BC_1P_2 generations.

$$\sigma^2 F_2 = \tfrac{1}{2} A + \tfrac{1}{4} D + E$$

$$\sigma^2 BC_1P_1 + \sigma^2 BC_1P_2 = \tfrac{1}{2} A + \tfrac{1}{2} D + E$$

$2\sigma^2 F_2 - \sigma^2 BC_1P_1 - \sigma^2 BC_1P_2 = A + \tfrac{1}{2} D + 2E - (\tfrac{1}{2} A + \tfrac{1}{2} D + 2E) = \tfrac{1}{2} A$

A = additive variance

D = dominance variance

E = environmental variance

BC_1P_1 = backcross to parent P_1

BC_1P_2 = backcross to parent P_2

F_2 = second filial generation

Additive genetic variance (or simply additive variance) is the variance of breeding values and is the primary cause of resemblance between relatives. Hence *V*A is the primary determinant of the observable genetic properties of the population, and of the response of the population to selection. Further, *V*A is the only component that the researcher can most readily estimate from observations made on the population. Consequently, it is common to partition genetic variance into two – additive versus all other kinds of variance. This ratio, *V*A/*V*P, gives what is called the heritability of a trait, an estimate that is of practical importance in plant breeding.

$$\sigma_A^2 = (\sigma_{F2}^2) - (\sigma_{BC1}^2 - \sigma_{BC2}^2)$$

Dominance Genetic Variance (σ_D^2)**:** Variance due to heterozygotes not being exact midpoints of homozygote parents. So that, $\sigma_G^2 = \sigma_A^2 + \sigma_D^2$

Dominance variance (σ_D^2) is considered to be any genetic variation that cannot be explained by average allelic differences, or additive genetic variance (σ_A^2). For example, if a trait is affected by multiple loci then any epistatic interactions between the loci will appear as variance not associated with additive variance. Thus, dominance genetic variance, involves deviation due to interactions between alternative alleles at a specific locus

$$\sigma_D^2 = \sigma_G^2 - \sigma_A^2$$

3.5.6 Genetic Advance (GA)

Genetic Advance (GA) was calculated in accordance with the method illustrated by Allard (1960) as: GA or $G_s = K * \sigma^2_A * h^2_{(n)}$

Where, K is the standardized selection differential, at 10 % selection intensity, K = 1.755

σ^2_A is additive variance and h^2 is narrow sense heritability estimate.

CHAPTER FOUR

RESULTS

4.1 Analysis of Variance

The analysis of variance showed significant differences among the genotypes ($P < 0.01$) for all the traits measured. However, Mean squares for replication were not significant for all the traits measured (Table 4.1).

Table 4. 1 Mean square for eight agronomic traits of sorghum grown in Samaru in 2012

Source of variation	**Df**	**GP**	**HD**	**PH**	**GY/Plt**	**1000GW**	**PaL**	**SDS**	**SC**
Rep	2	15.53	0.84	0.56	0.42	1.45	0.54	0.92	0.05
Genotype	28	233.78**	113.03**	1813.85**	331.73**	55.51**	40.35**	27.26**	3.69**
Error	56	14.03	0.63	0.59	0.18	4.92	0.63	0.41	0.05

** Highly significant at 1 percent level of significant, GP: Germination percentage, HD: Days to 50% heading, PH: Plant height, GY/Plt: Grain yield per plant, 1000GW: 1000 grain weight, PaL: Panicle length, SDS: *Striga* damage score, SC: *Striga* count per plant

4.2 Means, Ranges and Coefficient of variation

The performances of various generations of the six crosses involving two *Striga* resistant parents and three IAR released varieties are presented in Table 4.2 below.

Plant height.

As presented in Table 4.2.1. For the cross SAMSORG14 x ICSR94405, the resistant parent, ICSR94405 had a mean height of 170.20cm and a range between 145cm and 200cm. SAMSORG14 had a mean of 200.70cm with a range between 157cm and 260cm. The F_1 hybrid had a mean of 188.47cm with a range between 180 and 263cm. The F_1 mean was a bit higher than the mid-parent (185.45). There were high level of segregation among the F_2 population with the range of the F_2 being outside the parental range (139 – 304) couple with the CV of 28.36% and mean height of 210.11cm. Mean Plant height for the backcrosses, BCP_1 and BCP_2 were 173.94 and 207.29, respectively.

In the second cross: SAMSORG17 x ICSR94405, SAMSORG17 had a mean plant height of 180.00cm. The F_1 generation from this cross had a mean plant height of 179.87cm, higher than the mid-parental value (175.10cm). F_2 population had a range from 136cm to 231cm with mean of 184.81cm and CV of 15.95%. The $BCP_1$and BCP_2 had mean values of 170.50cm and 184.56cm, respectively.

In the cross between SAMSORG40 x ICSR94405, SAMSORG40 had a mean plant height of 156.33cm, with the range of 137cm -167cm. The F_1 mean was 167.00cm higher than the mid-parental mean (163.26cm), and the F_2 ranges from 130cm - 210cm with mean plant height of 170.67cm and CV of 12.93%. The BCP_1 and BCP_2 had mean values of 160.50cm and 161.56cm, respectively.

In crosses involving ICSR94407 as the resistant parent, ICSR94407 had a mean plant height of 155.73cm.The F_1 hybrid of SAMSORG14 x ICSR94407 had a mean height of 180.5cm. The F_2 population had a mean height of 204.64cm with a range of (135-281cm) and CV of 23.42%. Mean Plant height for the backcrosses BCP_1 and BCP_2 were 160.31cm and 217.82cm, respectively.

In the second cross: SAMSORG17 x ICSR94407, the F_1 hybrids had a mean plant height of 170.13cm, the F_2 population had a range from 127cm to 225cm with mean of 166.68cm and CV of 12.67%. The $BCP_1$and BCP_2 had mean values of 157.08cm and 176.59cm, respectively.

In SAMSORG40 x ICSR94407, the mean height of the F_1s was 157.57cm, similar to the mid parent mean (156.03cm). The F_2 had a mean height of 170.67cm with a range of 130cm to 210cm and CV of 14.82%. The $BCP_1$and BCP_2 had mean height of 157.08cm and 176.59cm, respectively.

Panicle length.

As shown in Table 4.2.1. In all the crosses, the mean panicle lengths of the susceptible parents are higher than that of the resistant parent. The mean panicle length for the susceptible parents varied from 27.77cm for SAMSORG40 to 30.35cm for SAMSORG14. Those of the resistant parents were 20.96 and 22.82 for ICSR94405 and ICSR94407, respectively. Mean Panicle length of the F_1 hybrids in the first cross (SAMSORG14 x ICSR94405) was 34.25cm, higher than the mid parent mean (25.66cm). The F_2 population had mean panicle length of 33.76cm, range from 24cm to 40cm and CV of 13.01%. The backcrosses, BCP_1 and BCP_2 had mean panicle length of 25.98cm and 29.04cm, respectively.

In SAMSORG17 x ICSR94405, the F_1 had mean panicle length of 27.02cm; the F_2 had mean panicle length of 24.15cm, range from 19cm to 39cm and CV of 15.84%. BCP_1 and BCP_2 had mean panicle length of 23.09cm and 31.32cm, respectively.

F_1 (SAMSORG40 x ICSR94405) recorded mean panicle length of 25.59cm; the F_2 had mean panicle length of 26.12cm, range of 19cm-31cm and CV of 10.98%. The BCP_1 and BCP_2 population recorded mean panicle length of 22.69cm and 27.98cm, respectively.

For the crosses involving ICSR94407, the resistant parent ICSR94407 had mean panicle length of 22.82cm. The F_1 (SAMSORG14 x ICSR94407) recorded mean panicle length of 34.19cm a bit higher than the mid parent mean (26.59cm). The F_2 had mean panicle length of 31.10cm, range of 25cm-44cm and CV of 14.68%. BCP_1 and BCP_2 had mean panicle length of 23.99cm and 31.34cm, respectively.

In the cross between SAMSORG17 and ICSR94407, the F_1 had mean panicle length of 28.42. The F_2 had mean of 27.28cm, range of 22cm-38cm and CV of 18.35%. BCP_1 and BCP_2 had mean value of 23.23cm and 29.75cm, respectively.

In SAMSORG40 x ICSR94407, the F_1 had mean panicle length value of 26.43cm. F_2 population had mean panicle length of 23.92cm, range of 19cm-36cm and CV of 14.48%. The BCP_1 and BCP_2 recorded mean panicle length of 24.63cm and 27.21cm, respectively.

Panicle weight.

As presented in Table 4.2.1. Mean values for panicle weight varied from 82.62g (SAMSORG40) to 118.09g (SAMSORG17), then 76.43g and 81.90g for ICSR94405 and ICSR94407 respectively. In the six crosses, the mean values for the F_1 hybrids varied from 80.77g (SAMSORG40 x ICSR94405) to 107.23g (SAMSORG17 x ICSR94407). The F_2 population had a wide range of segregation. The mean panicle weight for the F_2 population in

the six crosses varied from 83.35g (SAMSORG40 x ICSR94405) to 121.31g (SAMSORG17 x ICSR94407), the CV range from 18.67% (SAMSORG17 x ICSR94407) to 40.74% (SAMSORG14 x ICSR94405). Mean panicle weight for BC_1P_1 varied from 78.32g [ICSR94407 x (SAMSORG40 x ICSR94407)] to 85.92g [ICSR94407 x (SAMSORG17 x ICSR94407)] and that of BC_1P_1 varies from 80.19g [SAMSORG40 x (SAMSORG40 x ICSR94405)] to 120.26g [SAMSORG17 x (SAMSORG17 x ICSR94407)].

Table 4. 2 Range, mean and CV of plant height, panicle length and panicle weight of the parents, F2 and backcross populations of six sorghum crosses evaluated under *Striga* infestation at IAR Samaru *Striga* sick plot in 2012

Generation/cross	Plant height (cm)			Panicle length (cm)			Panicle weight/plant (g)		
	Range	Mean	CV	Range	Mean	CV	Range	Mean	CV
SAMSORG14 x ICSR94405									
ICSR94405	145-200	170.20	10.89	19-27	20.96	8.69	50-108	76.43	10.25
SAMSORG14	157-260	200.70	10.98	25-36	30.35	9.22	60-120	113.03	12.96
F_1	180 – 263	188.47	11.29	28-44	34.25	11.48	88-112	100.52	16.44
F_2	139 -304	210.11	28.36	24-40	33.76	13.01	78-126	103.19	40.74
BC_1P_1	130 -220	173.94	28.32	20-34	25.98	10.3	45-111	87.40	40.87
BC_1P_3	143 – 242	207.29	16.47	25-37	29.04	11.63	48-124	118.64	28.52
SAMSORG17 x ICSR94405									
ICSR94405	145 – 200	170.20	10.89	19-27	20.96	8.69	50-108	76.43	10.25
SAMSORG17	140 -190	180.00	8.26	22-36	29.07	8.04	79-129	118.09	10.91
F_1	150 – 246	179.87	10.60	25-31	27.02	6.21	71-125	100.75	15.28
F_2	136 – 231	184.81	15.95	19-39	24.15	15.84	42-131	105.21	25.48
BC_1P_1	120 – 221	170.50	13.89	18-31	23.09	11.99	44-108	79.56	22.66
BC_1P_4	130 – 218	184.56	13.73	21-38	31.32	12.97	63-112	110.45	23.72

Table 4.2 Continued

Generation/cross	Plant height (cm)			Panicle length (cm)			Panicle weight/plant (g)		
	Range	Mean	CV	Range	Mean	CV	Range	Mean	CV
SAMSORG40 x ICSR94405									
ICSR94405	145 – 200	170.20	10.89	19-27	20.96	8.69	50-108	76.43	10.25
SAMSORG40	137 – 167	156.33	6.62	24-32	27.77	7.14	57-111	82.62	12.26
F_1	155 – 180	167.00	4.20	21-29	25.59	8.82	61-117	80.77	15.51
F_2	130 – 210	170.67	12.93	19-31	26.12	10.98	36-123	83.35	23.89
BC_1P_1	121 -231	160.50	14.11	19-29	22.69	9.82	35-117	79.31	20.33
BC_1P_5	127 – 208	161.56	12.63	21-32	27.98	10.10	33-102	80.19	21.92
SAMSORG14 x ICSR94407									
ICSR94407	140 – 170	155.73	6.11	20-27	22.82	8.97	60-95	81.90	10.25
SAMSORG14	157 – 260	200.70	10.98	25-36	30.35	9.22	60-120	113.03	12.96
F_1	167 – 221	180.50	13.58	25-40	34.19	11.65	84-130	102.30	13.74
F_2	135 – 281	204.64	23.42	25-44	31.1	14.68	53-134	119.95	35.66
BC_1P_2	120 – 231	160.31	22.91	19-30	23.99	11.82	30-115	82.85	33.41
BC_1P_3	155 – 271	217.82	11.75	22-39	31.34	11.42	87-124	112.26	16.68

Table 4.2 Continued

Generation/cross	Plant height (cm)			Panicle length (cm)			Panicle weight/plant (g)		
	Range	Mean	CV	Range	Mean	CV	Range	Mean	CV
SAMSORG17 x ICSR94407									
ICSR94407	140 -170	155.73	6.11	20-27	22.82	8.97	60-95	81.90	10.25
SAMSORG17	140 -190	180.00	8.26	22-36	29.07	8.04	79-129	118.09	10.91
F_1	150 – 180	170.13	8.48	22-34	28.42	10.82	86-133	107.23	11.94
F_2	127 – 215	166.68	12.67	22-38	27.28	18.35	57-135	121.31	18.67
BC_1P_2	136 – 190	157.08	6.48	19-29	23.23	14.14	58-109	85.92	15.46
BC_1P_4	147 – 209	176 59	8.52	26-34	29.75	16.29	61-115	120.15	14.42
SAMSORG40 x ICSR94407									
ICSR94407	140 – 170	155.73	6.11	20-27	22.82	8.97	60-95	81.90	10.25
SAMSORG40	137 – 167	156.33	6.62	24-32	27.77	7.14	57-111	82.62	12.26
F_1	140 – 167	157.57	5.19	20-30	26.43	10.32	60-104	84.84	11.64
F_2	130 – 210	170.67	14.82	19-36	23.92	14.48	42-114	88.80	20.71
BC_1P_2	122 – 195	160.21	10.98	21-32	24.63	12.11	46-103	78.32	18.74
BC_1P_5	125 – 185	161.94	10.67	24-34	27.21	11.90	49-96	80.10	18.57

Grain yield

As shown in table 4.2.1, mean values for grain yield per plant, ranges from 75.73g (SAMSORG40) to 110.93g (SAMSORG17) and 67.97g (ICSR94405) to 78.33cm (ICSR94407). The F_1 means ranges from 73.40g (SAMSORG40 x ICSR94405) to 96.10g (SAMSORG17 x ICSR94407) in all the crosses. F_2 means for grain yield per plant ranges from 77.84g (SAMSORG40 x ICSR94407) to 117.29g (SAMSORG17 x ICSR94407). The CV varied from 12.74% (SAMSORG40 x ICSR94407) to 28.55% (SAMSORG14 x ICSR94405). There were high ranges of segregation among the F_2 populations as shown in the CV. Mean grain yield per plant for BCP_1 in all the crosses varied from 73.65g [ICSR94405 x (SAMSORG17 x ICSR94407)] to 84.73g [ICSR94407 x (SAMSORG14 x ICSR94407)], while that of BCP_2 varied from 76.44g [SAMSORG40 x (SAMSORG40 x ICSR94407)] to 110.33g [SAMSORG17 x (SAMSORG17 x ICSR94407)].

Grain weight (1000)

SAMSORG14, SMSORG17 and SAMSORG40 had mean values of 34.04g, 39.35g and 27.71g with range of 30g - 36g, 38g – 42g and 27g -30g and CV of 6.64%, 3.29% and 6.12%, respectively, while the resistant parents had mean values of 22.48g and 21.83g with range of 20 – 27g and 20g - 24g and CV of 7.62% and 5.54% for ICSR94405 and ICSR94407 respectively. In the cross between SAMSORG14 and ICSR94405 the F_1 means was 30.62g, with the range of 30g -34g and CV of 4.28%. The F_2 had a mean of 28.14g, with range of 20g – 30g and CV of 13.47. Mean, range and CV for BCP_1 in the same cross were: 25.71g, 23g-29g and 9.77%, respectively and BCP_2 had mean, range and CV of 38.01g, 35g – 41g and 11.41%, respectively.

For the second cross; SAMSORG17 x ICSR94405, the F_1 had the mean 1000 grain weight of 32.03g, with range of 29g – 36g and CV of 8.06%. The F2 recorded mean 1000 grain weight of 30.31g, range of 21g – 37g and CV of 13.74%. BCP1 mean was 22.67g with CV of 12.67% and range of 21g- 26g, while BCP_2 of the same cross had mean of 34.45g, CV of 10.10% and range of 20g – 38g. Cross between SAMSORG40 and ICSR94405 had F_1 mean, range, and CV values for the trait to be 27.68g, 26g – 32g and 8.85%, respectively and the F_2 mean was 25.67g, with the range of 25g-37g and CV of 15.96%. Also the BCP_1 mean, range and CV of the trait were 24.99g, 22g-29g and 10.74%, respectively. BCP_2 of the same cross had mean, range and CV of 26.35g, 24g – 32g and 12.61%, respectively.

Cross of SAMSORG14 and ICSR94407 had F_1 mean, range and CV values for 1000 grain weight to be 29.01g, 32g – 35g and 9.62%. The F_2 mean was 29.34g, with range of 27g – 38g and CV of 16.45%. BCP_1 had mean, range and CV of 25.66g, 26g-31g and 11.17%, respectively and BCP_2 of the same cross had mean, range and CV of 30.69g, 29g – 34g and 13.16%, respectively.

For SAMSORG17 X ICSR94407 cross, the F_1 mean was 31.28g with the range of 31g – 34g and CV of 2.24%. The F_2 had mean, range and CV of 26.35g, 23g – 29g and 10.02%, respectively. BCP_1 mean for the trait was 22.70g with CV of 9.37% and range of 21g - 27g and BCP_2 of the same cross had mean of 35.35g, CV of 6.54% and range of 28g – 39g.

SAMSORG40 x ICSR94407 had F_1 mean, ranges and CV values for the same trait to be 26.96g, 26g – 30g and 5.83%. The F_2 mean was 24.67g, with range of 22g – 29g and CV of 10.18%. BCP_1 mean was 25.97g with CV of 8.53% and range of 23g-30g and BCP_2 of the same cross had mean of 30.02g, CV of 9.54 and range of 26g – 33g.

Striga count.

In the six crosses, ICSR94405 and ICSR94407 were resistant, with mean *Striga* count value: 0.03 for ICSR94405 (only one *Striga* emerged) and 0 for ICSR94407 (no *Striga* emergence). Meanwhile SAMSORG14 and SAMSORG40 were susceptible to *Striga,* with mean *Sriga* count value of 3.13 and 4.53 and the range of 2-6 and 2-7 respectively. SAMSORG17 was tolerant with mean *Striga* count of 1.13, range of 0 – 4 and CV of 6.51%. The F_1 of the cross between SAMSORG14 and ICSR94405 had a mean *Striga* count value of 0.97, range of 0-3 and CV of 9.12%. The F_2 had a mean of 1.18, range of 0-5 and CV of 24.20%. BCP_1 of the same cross had mean value of 0.39, range of 0-4 and CV of 16.34%, while the BCP_2 had mean of 2.05, range of 0-5 and CV of 13.40%.

In the cross between SAMSORG17 x ICSR94405, the F_1 had mean *Striga* count value of 0.70, range of 0-3 and CV of 11.34%. The F_2 had a mean of 1.03 and range of 0-5 and CV of 24.10%. BCP_1 of the same cross had mean value of 0.62, range of 0-3 and CV of 16.23%., while the BCP_2 had mean *Striga* count of 1.13, range of 0-4 and CV of 12.56%.

The cross of SAMSORG40 x ICSR94405 had F_1 mean *Striga* count value of 1.06, with the range of 0-3 and CV of 9.42%. The F_2 had a mean of 1.17 with the range of 0-5 and CV of 18.73%. BCP_1 of the same cross had mean value of 0.30, with range of 0-4 and CV of 12.33%, while the BCP_2 had mean of 3.75, range of 0-5 and CV of 10.62%.

In the cross between SAMSORG14 x ICSR94407, the F_1 had mean *Striga* count value of 0.90 with range of 0-3 and CV of 10.44%. The F_2 had a mean of 1.25, with range of 0-4 and CV of 25.11%. BCP_1 of the same cross had mean value of 0.36, with range of 0-3 and CV of 15.30%, while the BCP_2 had mean of 1.92, range of 0-5 and CV of 16.18%.

The cross of SAMSORG17 x ICSR94407 had F_1 mean *Striga* count value of 0.63, with the range of 0-3 and CV of 11.71%. The F_2 had a mean of 0.99, range of 0-5 and CV of 21.33%. BCP_1 of the same cross had mean value of 0.60, with range of 0-3 and CV of 16.61% while the BCP_2 had mean of 1.12, with range of 0-4 and CV of 14.21%.

Finally, in the cross between SAMSORG40 x ICSR94407, the F_1 had mean *Striga* count value of 1.00, with range of 0-3 and CV of 9.50%. The F_2 had a mean of 1.16 with range of 0-5 and CV of 19.43%. BCP_1 of the same cross had mean value of 0.29, range of 0-4 and CV of 13.94%, while the BCP_2 had mean of 3.01, range of 0-5 and CV of 11.41%.

Table 4.2. 1 Range, mean and CV of grain yield/ plant, 1000 grain weight and Striga count of the parents, F1, F2 and backcross populations of six sorghum crosses evaluated under Striga infestation at IAR Samaru Striga sick plot in 2012

	Grain yield/plant (g)			**1000 Grain weight (g)**			***Striga* count/plt**		
Generation/crosses	**Range**	**Mean**	**CV**	**Range**	**Mean**	**CV**	**Range**	**Mean**	**CV**
SAMSORG14 x ICSR94405									
ICSR94405	45 – 100	70.97	11.85	20-27	22.48	7.62	0-1	0.03	-
SAMSORG14	54 – 111	102.1	9.34	30-36	34.04	6.64	2-6	3.13	6.51
F_1	78 – 101	91.47	10.39	30-34	30.62	4.28	0-3	0.97	9.12
F_2	65 – 113	94.77	28.55	20-30	28.14	13.47	0-5	1.18	24.20
BC_1P_1	40 – 107	78.75	27.55	23-29	25.71	9.77	0-4	0.39	16.34
BC_1P_3	42 – 118	108.78	17.90	35-41	38.01	11.41	0-5	2.05	13.40
SAMSORG17 x ICSR94405									
ICSR94405	45 – 100	70.97	11.85	20-27	22.48	7.62	0-1	0.03	-
SAMSORG17	68 – 120	110.93	8.94	38-42	39.35	3.29	0-4	1.13	6.56
F_1	62 – 114	93.80	11.04	29-36	32.03	8.06	0-3	0.70	11.34
F_2	37 – 120	97.36	14.96	21-37	30.31	13.74	0-5	1.03	24.10
BC_1P_1	36 – 94	73.65	12.07	21-26	22.67	12.67	0-3	0.62	16.23
BC_1P_4	43 – 122	112.13	13.97	20-38	34.45	10.10	0-4	1.13	12.56

Table 4.2.1 Continued.

Generation/cross	Grain yield/plant (g)			1000 Grain yield (g)			*Striga* count/plt		
	Range	**Mean**	**CV**	**Range**	**Mean**	**CV**	**Range**	**Mean**	**CV**
SAMSORG40 x ICSR94405									
ICSR94405	45 – 100	70.97	8.85	20-27	22.48	7.62	0-1	0.03	-
SAMSORG40	50 – 105	75.73	6.67	27-30	27.71	6.12	2-7	4.53	7.30
F_1	55 – 107	73.40	4.31	26-32	27.68	8.85	0-3	1.06	9.42
F_2	31 – 117	78.59	14.83	25-37	25.67	15.96	0-5	1.17	18.73
BC_1P_1	37 – 92	69.49	12.47	22-29	24.99	10.74	0-4	0.30	12.33
BC_1P_5	43-107	75.85	13.11	24-32	26.35	12.61	0-5	3.75	10.62
SAMSORG14 x ICSR94407									
ICSR94407	53 – 82	78.33	5.55	20-24	23.83	5.54	0	0.00	-
SAMSORG14	54 – 111	102.10	9.34	30-36	34.04	6.64	2-6	3.13	6.51
F_1	80 – 124	91.40	4.23	32-35	29.01	9.62	0-3	0.90	10.44
F_2	49 -128	108.93	23.24	27-38	29.34	16.45	0-4	1.25	25.11
BC_1P_2	27 – 110	84.73	22.89	26-31	25.66	11.17	0-3	0.36	15.30
BC_1P_3	80 – 118	99.82	11.67	29-34	30.69	13.16	0-5	2.92	16.18

Table 4.2.1 Continued.

Generation/cross	Grain yield/plant (g)			1000 Grain yield (g)			*Striga* count/plt		
	Range	Mean	CV	Range	Mean	CV	Range	Mean	CV
SAMSORG17 x ICSR94407									
ICSR94407	53 – 82	78.33	5.55	20-24	23.83	5.54	0	0.00	-
SAMSORG17	68 – 120	110.93	8.94	38-42	39.35	3.29	0-4	1.13	6.56
F_1	79 -126	96.10	6.23	31-34	31.28	2.24	0-3	0.63	11.71
F_2	53 – 129	117.29	18.91	23-29	26.35	10.02	0-4	0.99	21.33
BC_1P_2	53 – 98	80.63	16.67	21-27	22.70	9.37	0-3	0.60	16.61
BC_1P_4	55 – 106	110.33	10.05	28-39	35.35	6.54	0-4	1.12	14.21
SAMSORG40 x ICSR94407									
ICSR94407	53 – 82	78.33	5.55	20-24	23.83	5.54	0	0.00	-
SAMSORG40	50 – 105	75.73	6.67	27-30	27.71	2.14	2-7	4.53	7.30
F_1	54 – 98	79.87	5.51	26-30	26.96	5.83	0-3	1.00	9.50
F_2	34 – 105	77.84	12.74	22-29	24.67	10.18	0-5	1.16	19.43
BC_1P_2	36 – 99	78.71	11.23	23-30	25.97	8.53	0-4	0.29	13.94
BC_1P_5	32 – 85	76.44	10.56	26-33	30.02	9.54	0-6	3.01	11.41

CV=Coefficient of variation

4.3 Estimates of Gene Effects

The estimates of the genetic effects and their magnitudes for each trait are presented below in Table 4.3.1 – 4.3.9.

Joint scaling tests

First the data were subjected to three parameter model to test the adequacy of additive-dominance model. However the calculated chi-square at 3 degree of freedom was found to be significant for the six crosses and for all the traits studied except *Striga* count which the chi-square test were not significant for the six crosses Table 4.3.1 and 4.3.2.

Table 4.3. 1 Joint scaling test for assessing adequacy of additive-dominance model for plant height, panicle length, panicle weight, and grain yield of six sorghum crosses evaluated in IAR samara *Striga* sick plot in 2012.

Character	**Cross**	**m**	**a**	**d**	**chi-square**
plant height (cm)	P1xP3	221.07**	-89.78**	110.46**	19.77**
	P1xP4	216.22**	-57.71**	-66.05	1374.65**
	P1xP5	153.74**	-9.24**	82.33**	86.35**
	P2xP3	214.70**	-78.21*	103.86**	28.12**
	P2xP4	209.04**	-44.61**	-57.41*	1455.26**
	P2xP5	146.62**	-7.12*	71.77**	83.48**
Panicle length (cm)	P1xP3	32.08**	-16.10**	-2.94**	28.47**
	P1xP4	29.67**	-14.66**	-6.21**	23,12**
	P1xP5	26.67**	12.44**	-14.30**	41.42**
	P2xP3	31.25**	-15.54**	-2.65**	39.60**
	P2xP4	30.20**	-13.47**	-1.05**	20.40**
	P2xP5	24.32**	-20.11**	-12.54**	51.43**
Panicle Weight (g)	P1xP3	84.19**	-13.27**	-1.41	39.30**
	P1xP4	82.43**	-2.83	-51.38**	15.41**
	P1xP5	69.52**	-12.73	-11.66	25.o2**
	P2xP3	65.83**	-17.86*	24.18	84.60**
	P2xP4	67.34**	-10.80**	67.35**	13.11**
	P2xP5	62.56**	-15.85**	4.05	14.04**
Grain yield/plt (g)	P1xP3	90.53**	-13.01**	-4.07	8.08*
	P1xP4	97.91**	-4.28	36.80**	18.00**
	P1xP5	62.26**	-11.79*	-8.16	32.49**
	P2xP3	83.15**	-16.71**	15.80	13.00**
	P2xP4	91.96**	10.22**	55.97**	32.9**
	P2xP5	59.56**	-12.87**	-23.72	63.50**

Table 4.3. 2 Joint scaling test for assessing adequacy of additive-dominance model for 1000 grain weight, *Striga* count and *Striga* damage score of six sorghum crosses evaluated in IAR samara *Striga* sick plot in 2012.

Character	**Cross**	**m**	**a**	**d**	**chi-square**
1000GW(g)	P1xP3	27.31**	-7.54**	2.25*	77.00**
	P1xP4	29.71**	-9.47**	2.87	87.00**
	P1xP5	26.00**	-3.11**	1.77	29.10**
	P2xP3	29.87**	-6.26**	3.49	95.12**
	P2xP4	29.18**	-7.73**	11.26**	51.80**
	P2xP5	23.46**	-3.51*	2.09	82.00**
Striga Count	P1xP3	1.19**	-1.56	-0.22	5.02
	P1xP4	1.09**	-1.32	-0.88	3.84
	P1xP5	1.27**	-1.55	0.47	4.86
	P2xP3	1.51**	-0.87	0.75	4.66
	P2xP4	1.19**	-1.54	-0.98	3.88
	P2xP5	1.73**	-1.58	-0.53	4.35
Striga damage score	P1xP3	2.58**	-3.42**	5.98*	43.01**
	P1xP4	2.07**	-2.19**	5.23	57.00**
	P1xP5	3.01**	-4.30**	4.22*	39.41**
	P2xP3	2.11**	-2.71**	6.10	67.00**
	P2xP4	1.97**	-3.33**	7.02**	84.61**
	P2xP5	2.85**	-2.98**	4.83	32.00**

*Significant at 5% levels of significant, ** significant at 1% level of significant.
m = mean, a = additive effects, d = dominance effects

Six generation mean analysis

Haymen's six parameter model (1958) was followed to estimate gene interaction effects based on mean values of the six generation. The results obtained are tabulated in table 4.3.3 to 4.3.9 and are presented for each character as below.

Plant height

As presented in Table 4.3.3. The six-parameter model showed that additive effects were highly significant ($p < 0.01$) for plant height in three crosses and significant ($p < 0.05$) in two crosses, and non-significant in the cross between SAMSORG17 and ICSR94405. In the cross of SAMSORG14 x ICSR94407 and SAMSORG17 x ICSR94407 additive effects were highly significant and negative. Dominant effects were non-significant in all the crosses. Additive-by-additive epistatics effects were significant ($p < 0.05$) and negative in SAMSORG17 x ICSR94405 and SAMSORG40 x ICSR94407. Additive-by-dominant effects were significant in two crosses (SAMSORG14 x ICSR94405 and SAMSORG17 x ICSR94407). Meanwhile dominant-by-dominant effects were non-significant on plant height in all the crosses.

Panicle length

Additive by additive effects were highly significant in all the crosses for panicle length and they were all negative, except in SAMSORG40 x ICSR94407 Table 4.3.4. Dominant effects were significant in two crosses; SAMSORG17 x ICSR94405 and SAMSORG40 x ICSR94407. Additive by additive effects were significant in two crosses; SAMSORG17 x ICSR94405 and SAMSORG14 x ICSR94407, and highly significant in SAMSORG40 x ICSR94407 cross. Additive by dominant effects were non-significant in all the crosses, while dominant by dominant effects were significant only in SAMSORG40 x ICSR94407 cross.

Panicle weight

As shown in Table 4.3.5. Additive effects were significant in four crosses: SAMSORG40 x ICSR94405, SAMSORG14 x ICSR94407, SAMSORG17 x ICSR94407 and SAMSORG40 x ICSR94407. And were non-significant for two crosses: SAMSORG14 x ICSR94405 and SAMSORG17 x ICSR94405. Additive by additive effects were significant and negative in SAMSORG17 x ICSR94405 and SAMSORG40 x ICSR94407. Additive by dominant effects were significant for SAMSORG14 x ICSR94407. Dominant effects and dominant by dominant effects were non-significant for all the crosses.

Table 4.3. 3 Estimates of gene effects for plant height in a six generation of six sorghum crosses evaluated under *Striga* infestation at the IAR Samaru *Striga* sick plot in 2012.

Crosses	**m**	**a**	**d**	**aa**	**ad**	**dd**
SAMSORG14 x ICSR94405	210.11** ±8.48	49.65** ±12.86	-60.36 ±74.86	-59.96 ±59.66	80.31** ±20.9	82.16 ±115.8
SAMSORG17 x ICSR94405	184.81** ±3.66	10.95 ±6.68	-55.85 ±38.68	-59.12* ±28.02	7.35 ±11.91	51.92 ±62.71
SAMSORG40 x ICSR94405	170.67** ±3.64	±15.63* 6.59	-6.9 ±34.91	-11.07 ±27.75	9.13 ±11.51	-20.76 ±55.26
SAMSORG14 x ICSR94407	204.64** ±6.82	-35.51** ±10.58	87.61 ±56.05	61.71 ±48.45	-8.64 ±15.73	-159.8 ±84.8
SAMSORG17 x ICSR94407	166.68** ±2.05	-19.51** ±3.58	7.38 ±21.53	0.61 ±15.36	-15.87* ±7.33	-16.95 ±34.86
SAMSORG40 x ICSR94407	170.67** ±3.11	12.27* ±4.88	-52.83 ±28.05	-50.36* ±22.2	12.57 ±8.11	37.25 ±43.66

** Highly significant at 1% level of significant, * significant at 5% level of significant.

m = mean; a = additive gene effects; d = dominance gene effects; aa = additive x additive epistatic gene effects; ad = additive x dominance epistatic gene effects; dd = dominance x dominance epistatic gene effects.

Table 4.3. 4 Estimate of gene effects for panicle length in a six generation of six sorghum crosses evaluated at IAR Samaru *Striga* sick plot in 2012.

Crosses	**m**	**a**	**d**	**aa**	**ad**	**dd**
SAMSORG14 x ICSR94405	33.76** ± 0.60	-7.05** ± 1.10	1.32 ± 7.43	-1.01 ± 4.60	-0.63 ± 2.39	-0.68 ± 12.46
SAMSORG17 x ICSR94405	24.15** ± 0.48	-8.23** ± 1.29	14.2* ± 6.50	12.20* ± 4.47	-4.18 ± 2.53	-16.96 ± 11.09
SAMSORG40 x ICSR94405	26.12** ± 0.58	-5.28** ± 0.97	-2.88 ± 5.96	-3.12 ± 4.25	-1.86 ± 1.75	-0.35 ± 9.62
SAMSORG14 x ICSR94407	31.10** ± 0.73	-7.35** ± 1.30	-8.47 ± 8.98	-13.75* ± 5.50	-1.25 ± 2.54	29.32 ± 15.06
SAMSORG17 x ICSR94407	27.28** ± 0.40	-6.52** ± 0.85	-0.67 ± 5.95	-3.15 ± 3.31	-3.40 ± 2.17	5.91 ± 10.28
SAMSORG40 x ICSR94407	23.92** ± 0.46	0.43** ± 0.93	14.16* ± 5.58	14.02** ± 3.70	2.90 ± 1.80	-22.42* ± 9.32

Table 4.3. 5 Estimate of gene action for panicle weight in a six generation of the six sorghum crosses evaluated at IAR *Striga* sick plot in 2012

Crosses	**m**	**a**	**d**	**aa**	**ad**	**dd**
SAMSORG14 x ICSR94405	103.19** ± 5.93	18.77 ± 9.84	-14.07 ± 52.14	-20.71 ± 43.42	42.07** ± 13.81	40.84 ± 80.55
SAMSORG17 x ICSR94405	105.21** ± 2.80	7.88 ± 4.99	-49.60 ± 29.70	-50.75* ± 21.18	2.86 ± 9.23	51.27 ± 48.18
SAMSORG40 x ICSR94405	83.35** ± 2.48	11.13* ± 4.83	-33.50 ± 25.03	-34.40 ± 19.57	3.90 ± 8.58	16.55 ± 40.14
SAMSORG14 x ICSR94407	119.95** ± 4.97	-26.43** ± 7.72	46.39 ± 41.29	44.25 ± 35.31	10.10 ± 11.61	-82.40 ± 62.71
SAMSORG17 x ICSR94407	121.31** ± 1.69	-15.27** ± 3.00	II.99 ± 18.28	-2.04 ± 12.74	-10.37 ± 5.96	24.97 ± 29.81
SAMSORG40 x ICSR94407	88.80** ± 2.47	9.18* ± 3.91	-32.93 ± 22.11	-40.47* ± 17.69	9.55 ± 6.19	9.57 ± 34.35

Grain yield

As presented in Table 4.3.6. Additive effects were significant ($P < 0.05$) in SAMSORG40 x ICSR94405 and SAMSORG40 x ICSR94407 and highly significant ($p < 0.01$) and negative in SAMSORG14 x ICSR94407 and SAMSORG17 x ICSR94407, but non-significant in two crosses: SAMSORG14 x ICSR94405 and SAMSORG17 x ICSR94405. Additive by additive effects were significant and negative in SAMSORG17 x ICSR94405 and SAMSORG40 x ICSR94407. Additive by dominant effects were significant in SAMSORG14 x ICSR94407 cross. Dominant effects and dominant by dominant effects were non-significant in all the crosses.

Grain weight (1000)

Additive effects were highly significant and negative in all the crosses, while dominant effects were highly significant in all the crosses, except SAMSORG17 x ICSR94407 and negative; Table 4.3.7. Additive by additive effects were significant in one cross: SAMSORG17 x ICSR94405. Additive by dominant effects were highly significant in three crosses: SAMSORG14 x ICSR94405, SAMSORG14 x ICSR94407 and SAMSORG40 x ICSR94407. Dominant by dominant effect were significant ($p < 0.05$) in two crosses; SAMSORG14 x ICSR94405 and SAMSORG17 x ICSR94405.

Striga count

For *Striga* count only additive gene effects were significant and negative in all the crosses, while the other gene effects were non-significant; Table 4.3.8.

Striga damage score

As shown in Table 4.3.9; Additive by additive effects were significant and negative in all the crosses. Dominant effects were significant in two crosses; SAMSORG17 x ICSR94405 and SAMSORG17 x ICSR94407. Additive by additive effects were significant in all the crosses. Additive by dominant effects were significant in one cross: SAMSORG40 x ICSR94405; while dominant by dominant effects were highly significant and negative in all the crosses.

Table 4.3. 6 Estimate of gene effects for grain yield in a six generation of six sorghum crosses evaluated at IAR Samaru *Striga* sick plot in 2012.

Crosses	**m**	**a**	**d**	**aa**	**ad**	**dd**
SAMSORG14 x ICSR94405	94.77** ± 3.85	10.97 ± 5.66	-33.05 ± 32.90	-34.00 ± 26.72	27.52** ± 8.73	52.90 ± 50.40
SAMSORG17 x ICSR94405	97.36** ± 1.53	4.51 ± 2.85	-23.21 ± 16.68	-23.88* ± 11.83	1.68 ± 5.27	24.19 ± 27.22
SAMSORG40 x ICSR94405	78.59** ± 1.42	6.35* ± 2.76	-19.12 ± 14.29	-19.67 ± 11.18	2.24 ± 4.90	9.49 ± 22.91
SAMSORG14 x ICSR94407	84.73** ± 2.84	-15.09** ± 4.42	26.59 ± 23.64	25.39 ± 20.21	5.77 ± 6.65	-47.28 ± 35.92
SAMSORG17 x ICSR94407	117.29** ± 0.96	-8.70** ± 1.71	6.73 ± 10.43	-1.24 ± 7.27	-5.90 ± 3.40	-14.20 ± 17.01
SAMSORG40 x ICSR94407	77.84** ± 1.41	5.27* ± 2.24	-18.72 ± 12.66	-23.05* ± 10.12	5.47 ± 3.54	5.55 ± 19.67

Table 4.3. 7 Estimate of gene effects for 1000 grain weight in a six generation of the six sorghum crosses evaluated under *Striga* infestation at IAR Samaru *Striga* sick plot in 2012

Crosses	**m**	**a**	**d**	**aa**	**ad**	**dd**
SAMSORG 14 x ICSR94405	28.14** ± 0.22	-12.30** ± 0.21	18.26** ± 1.71	-36.99 ± 18.80	29.41** ± 8.82	114.93* ± 44.57
SAMSORG17 x ICSR94405	30.31** ± 0.53	-8.78** ± 0.09	-11.89** ± 2.51	-109.4** ± 23.06	-8.96 ± 10.16	128.88* ± 60.86
SAMSORG40 x ICSR94405	25.67** ± 0.03	-1.36** ± 0.08	2.73** ± 0.49	-6.99 ± 22.16	-9.23 ± 9.08	11.20 ± 49.53
SAMSORG 14 x ICSR94407	29.34** ± 0.03	-3.03** ± 0.07	8.40** ± 0.50	-33.01 ± 19.90	41.87** ± 8.51	90.08 ± 48.34
SAMSORG17 x ICSR94407	26.35** ± 0.03	-6.65** ± 0.06	-0.60 ± 0.47	32.80 ± 24.25	10.40 ± 10.67	-66.75 ± 59.34
SAMSORG 40 x ICSR94407	24.67** ± 0.03	-4.05** ± 0.09	16.46** ± 0.52	-15.81 ± 20.80	36.15** ± 8.93	-20.43 ± 47.30

Table 4.3. 8 Estimate of gene effect for *Striga* count in a six generation of six sorghum crosses evaluated under *Striga* infestation at IAR Samaru *Striga* sick plot in 2012

Crosses	**m**	**a**	**d**	**aa**	**ad**	**dd**
SAMSORG 14 x ICSR94405	1.18** ± 0.22	-1.66** ± 0.37	0.36 ± 2.17	0.17 ± 1.60	-0.91 ± 0.60	-1.57 ± 3.48
SAMSORG17 x ICSR94405	1.03** ± 0.19	-1.07** ± 0.34	0.61 ± 2.00	0.49 ± 1.44	-0.52 ± 0.57	-2.55 ± 3.25
SAMSORG40 x ICSR94405	1.17** ± 0.21	-1.45** ± 0.35	-0.53 ± 2.12	-0.56 ± 1.56	-0.52 ± 0.56	0.39 ± 3.38
SAMSORG 14 x ICSR94407	1.25** ± 0.19	-0-56** ± 0.34	-0.26 ± 1.94	-0.43 ± 1.43	-0.83 ± 0.50	-0.87 ± 3.11
SAMSORG17 x ICSR94407	0.99** ± 0.18	-1.05** ± 0.34	0.61 ± 1.89	0.55 ± 1.38	-0.48 ± 0.56	-2.64 ± 3.07
SAMSORG 40 x ICSR94407	1.16** ± 0.22	-1.72** ± 0.36	-0.02 ± 2.12	-0.03 ± 0.59	-0.77 ± 0.55	-0.69 ± 3.37

Table 4.3. 9 Estimate of gene effects for *Striga* damage score in a six generation of six sorghum crosses evaluated under *Striga* infestation at IAR Samaru *Striga* sick plot in 2012.

Crosses	**m**	**a**	**d**	**aa**	**ad**	**dd**
SAMSORG14 x ICSR94405	2.10** ± 0.31	-2.60** ± 0.55	5.15 ± 3.10	7.65** ± 2.34	0.10 ± 0.93	-15.51** ± 4.96
SAMSORG17 x ICSR94405	1.60** ± 0.30	-2.62** ± 0.46	6.83* ± 2.63	9.00** ± 2.11	-0.55 ± 0.71	-16.87** ± 4.07
SAMSORG40 x ICSR94405	2.90** ± 0.21	-2.67** ± 0.54	3.16 ± 2.56	7.35** ± 1.92	-1.76* ± 0.87	-11.53** ± 4.29
SAMSORG 14 x ICSR94407	2.47** ± 0.37	-2.53** ± 0.53	5.98 ± 3.18	8.43** ± 2.53	0.32 ± 0.86	-16.65** ± 4.88
SAMSORG17 x ICSR94407	2.30** ± 0.14	-3.15** ± 0.48	5.18* ± 1.94	7.49** ± 1.51	-0.93 ± 0.68	-16.35** ± 33.34
SAMSORG40 x ICSR94407	2.40** ± 0.17	-3.16** ± 0.55	4.47 ± 2.42	7.12** ± 1.79	-0.41 ± 0.84	-14.83** ± 4.14

4.4 Segregation Ratios and Chi-square for *Striga* Damage Score

Table 4.4 shows mean *Striga* damage score, range and segregation in F_2 and backcross populations. Plants with scores of 0 to 4 were considered resistant, while plants with score 5 to 9 were considered susceptible (Sinebo and Drennan, 2001). The female parents had mean damage score of 6.6, 5.3, and 6.4, and range of 5-9, 5-6, and 5-8 for SAMSORG14, SAMSORG17 and SAMSORG40, respectively, while the mean damage score for the male parents were 1.2 and 0.9 with range of 0-3, and 0-2 for ICSR94405 and ICSR94407, respectively. The F_1 populations had the following means: 1.4, 1.1, 1.3, 1.3, 0.8, and 1.0 for SAMSORG14 x ICSR94405, SAMSORG17 x ICSR94405, SAMSORG40 x ICSR94405, SAMSORG14 x ICSR94407, SAMSORG17 x ICSR94407 and SAMSORG40 x ICSR94407, respectively. In the F_2 population the chi-square values at expected segregation ratio 3:1 (resistant: susceptible) are significant in all the crosses. The expected ratio 9:7 is significant in F_2 of three crosses involving the resistant parent: ICSR94405 but not significant in the three crosses involving the resistant parent: ICSR94407. Similarly significant chi-square values were obtained in three crosses involving ICSR94407 at the expected segregation ratio 13:3, while the F_2 of three crosses involving ICSR94405 were not significant.

Table 4. 3 mean *Striga* damage score, range and segregation ratio for *Striga* resistance among parents and their F1, F2 and backcrosses

Cross	Parent and Progeny	Mean SDS and Range	Observed R	Observed S	Total	Expected Ratio	χ^2	df	P(0.05)
P_3 x P_4	P_1 (ICSR94405)	1.2 (0-3)	30	0	30	1:0			
	P_3(SAMSORG14)	6.6 (5-9)	0	30	30	0:1			
	F_1	1.4 (0-4)	30	0	30	1:0			
	F_2	2.1 (0-9)	126	24	150	13:3	0.88	1	0.35^{NS}
	BC_1P_1	1.5 (0-4)	150	0	150	16:0			
	BC_1P_3	2.0 (0-9)	112	38	150	3:1	0.01	1	0.92^{NS}
P_4 x P_1	P_1(ICSR94405)	1.2 (0-3)	30	0	30	1:0			
	P_4(SAMSORG17)	5.3 (5-6)	0	30	30	0:1			
	F_1	1.1 (0-3)	30	0	30	1:0			
	F_2	1.6 (0-7)	130	20	150	13:3	3.13	1	0.08^{NS}
	BC_1P_1	1.3 (0-4)	150	0	150	16:0			
	BC_1P_4	1.6 (0-9)	115	35	150	3:1	0.22	1	0.64^{NS}
P_5 x P_1	P_1 (ICSR94405)	1.2 (0-3)	30	0	30	1:0			
	P_5(SAMSORG40)	6.4 (5-8)	0	30	30	0:1			
	F_1	1.3 (0-4)	30	0	30	1:0			
	F_2	1.5 (0-4)	115	35	150	13:3	1.83	1	0.18^{NS}
	BC_1P_1	2.9 (0-8)	150	0	150	16:0			
	BC_1P_5	2.7 (0-9)	109	41	150	3:1	0.44	1	0.51^{NS}

Table 4.4 continued.

Cross	Parent and Progeny	Mean SDS and Range	Observed R	Observed S	Total	Expected Ratio	χ^2	df	P(0.05)
P_3 x P_2	P_2(ICSR94407)	0.9 (0-2)	30	0	30	1:0			
	P_3(SAMSORG14)	6.6 (5-9)	30	0	30	0:1			
	F_1	1.3 (0-3)	30	0	30	1:0			
	F_2	2.5 (0-9)	93	57	150	9:7	2.19	1	0.14^{NS}
	BC_1P_2	1.4 (0-4)	150	0	150	16:0			
	BC_1P_3	2.4 (0-9)	77	73	150	1:1	0.11	1	0.74^{NS}
P_4 x P_2	P_2 (ICSR94407)	0.9 (0-2)	30	0	30	1:0			
	P_4(SAMSORG17)	5.3 (5-6)	30	0	30	0:1			
	F_1	0.8 (0-2)	30	0	30	1:0			
	F_2	2.3 (0-6)	94	56	150	9:7	2.71	1	0.10^{NS}
	BC_1P_2	1.0 (0-4)	150	0	150	16:0			
	BC_1P4	2.5 (0-9)	75	75	150	1:1	0.00	1	1.00^{NS}
P_5 x P_2	P_2 (ICSR94407)	0.9 (0-2)	30	0	30	1:0			
	P_5(SAMSORG40)	6.4 (5-8)	30	0	30	0:1			
	F_1	1.0 (0-4)	30	0	30	1:0			
	F_2	2.4 (0-8)	95	55	150	9:7	3.27	1	3.27^{NS}
	BC_1P_2	1.2 (0-4)	150	0	150	16:0			
	BC_1P_5	2.2 (0-8)	79	71	150	1:1	0.43	1	0.51^{NS}

** Highly significant at 1% level of significant, * Significant at 5% level of significant, R = resistant
S = susceptible

4.5 Heritability and Genetic advance

Heritability estimates and genetic advance for the traits studied are shown in Table 4.5. Narrow sense heritability estimates were less than broad-sense heritability estimate for all the traits across the crosses.

Plant height.

Narrow sense heritability estimate for plant height in the six crosses ranged from 10% to 77%. Table 4.5. The narrow sense estimates were high in five crosses: SAMSORG14 x ICSR94405 (69%), SAMSORG17 x ICSR94405 (34%), SAMSORG14 x ICSR94407 (73%), SAMSORG17 x ICSR94407 (41%) and SAMSORG40 x ICSR94407 (77%) and low (10%) in one cross SAMSORG40 x ICSR94405. The broad sense heritability estimate for plant height ranged from 51% (SAMSORG17 x ICSR94407) to 91% (SAMSORG14 x ICSR94407). Estimate of genetic advance (GA) ranged from 4.20 - 72.40 in the six crosses.

Panicle length.

As presented in Table 4.5. Broad sense heritability estimates were high in all the crosses, while narrow sense heritability estimates were moderate to high in all the crosses; 48%, 19%, 24%, 48%, 27%, and 55% for SAMSORG14 x ICSR94405, SAMSORG17 x ICSR94405, SAMSORG40 x ICSR94405, SAMSORD14 x ICSR94407, SAMSORG17 x ICSR94407 and SAMSORG40 x ICSR94407, respectively. Genetic advance ranged from 9.20 (SAMSORG14 x ICSR94405) to 18.16 (SAMSORG17 x ICSR94407).

Panicle Weight

The narrow sense heritability estimates for panicle weight were high in almost all the crosses: 53%, 43%, 72%, 35% and 74% for SAMSORG14 x ICSR94405, SAMSORG17 x ICSR94405, SAMSORD14 x ICSR94407, SAMSORG17 x ICSR94407 and SAMSORG40 x ICSR94407, respectively, except in SAMSORG40 x ICSR94405 cross which had a low narrow sense heritability estimate of 8%. Genetic advance ranged from 2.60 - 44.30.

Grain yield

The grain yield per plant, narrow sense heritability estimates in two crosses: SAMSORG40 x ICSR94405 and SAMSORG17 x ICSR94405 were low to moderate (9% and 28%), while in the remaining four crosses, narrow sense heritability estimates were high. Broad sense heritability estimates were high in all the crosses. Genetic advance ranged from 1.5 to 33.4. Table 4.5.

Grain weight (1000)

As presented in Table 4.5. Narrow sense heritability estimates were moderate to high in all the crosses with values of: 32%, 34%, 16%, 42%, 37% and 45% for SAMSORG14 x ICSR94405, SAMSORG17 x ICSR94405, SAMSORG40 x ICSR94405, SAMSORD14 x ICSR94407, SAMSORG17 x ICSR94407 and SAMSORG40 x ICSR94407, respectively, while the broad sense heritability estimates in all the crosses were high. Genetic advance ranges from 5.40 for SAMSORG40 x ICSR94405 to 19.40 for SAMSORG14 x ICSR94405.

Striga count

Narrow sense heritability estimates were lower than broad sense in all the crosses; Table 4.5. The narrow sense heritability estimates ranges from 4% for SAMSORG17 x ICSR94407 to 43% for SAMSORG40 x ICSR94405 cross. Broad sense heritability estimates were high in all the crosses. Genetic advance ranged from 2.0 for SAMSORG14 x ICSR94405 to 4.10 for SAMSORG17 x ICSR94407.

Striga damage score

As shown in Table 4.5. *Striga* damage score showed high broad sense heritability estimates in all the crosses, while narrow sense heritability estimates were moderate to high in all the crosses ranging from 21% for SAMSORG40 x ICSR94405 to 75% for SAMSORG14 x ICSR94407. The genetic advance ranged from 1.0 for SAMSORG40 x ICSR94407 to 3.40 for SAMSORG14 x ICSR94407.

Table 4. 4 Estimate of heritability and genetic advance of 10% selection intensity for PH, PaW, PL, GY, 1000GW, SC and SDS of six sorghum crosses evaluated in IAR Samaru *Striga* sick plot in 2012

Crosses	**PH**	**PL**	**PaW**	**GY**	**1000GW**	**SC**	**SDS**
SAMSORG14 x ICSR94405							
$H_{(B)}$ (%)	82.00	61.00	89.00	90.00	69.00	54.00	72.00
$H_{(N)}$ (%)	69.00	48.00	53.00	73.00	32.00	37.00	33.00
G.A	72.40	9.20	39.20	33.40	19.40	2.00	1.30
SAMSORG17 x ICSR94405							
$H_{(B)}$ (%)	53.00	38.00	50.00	46.00	41.00	43.00	84.00
$H_{(N)}$ (%)	34.00	19.00	43.00	28.00	34.00	32.00	31.00
G.A	15.40	16.40	15.10	5.40	11.50	3.80	1.20
SAMSORG40 x ICSR94405							
$H_{(B)}$ (%)	75.00	56.00	69.00	70.00	61.00	56.00	56.00
$H_{(N)}$ (%)	10.00	24.00	8.00	9.00	16.00	43.00	17.13
G.A	4.20	14.20	2.60	1.50	5.40	2.20	1.10
SAMSORG14 x ICSR94407							
$H_{(B)}$ (%)	91.00	66.00	91.00	91.00	71.00	52.00	84.00
$H_{(N)}$ (%)	73.00	48.00	72.00	72.00	42.00	26.00	75.00
G.A	61.60	11.30	44.30	25.40	15.30	3.60	3.40
SAMSORG17 x ICSR94407							
$H_{(B)}$ (%)	51.00	38.00	41.00	41.00	39.00	43.00	60.00
$H_{(N)}$ (%)	41.00	27.00	35.00	35.00	37.00	4.00	19.32
G.A	10.60	18.60	7.30	4.20	13.20	4.10	2.30
SAMSORG40 x ICSR94407							
$H_{(B)}$ (%)	82.00	60.00	84.00	84.00	54.00	60.00	38.00
$H_{(N)}$ (%)	77.00	55.00	74.00	74.00	45.00	42.00	7.70
G.A	29.80	12.00	22.60	12.90	17.60	3.10	1.00

$H_{(B)}$ = broad sense heritability, $H_{(N)}$ = narrow sense heritability, GA = genetic advance.

CHAPTER FIVE

DISCUSSION

5.1 Analysis of Variance

In the present study, the mean square values of all the characters studied were highly significant among the genotypes, indicating that there are variations among the genotypes for all the characters.

5.2 Mean, Range and Coefficient of Variation

The susceptible parent (SAMSORG14) had the highest mean plant height value of 200.70cm while resistant parent (ICSR94407) had the lowest mean plant height value of 155.73cm. The mean plant heights for the F_1 hybrid in the entire cross were similar to the mid parental value. This indicated the preponderance of additive gene action for plant height. The height of F_2 plants were distributed over the range of both parents with continuous distribution, suggesting the involvement of more than one gene controlling the inheritance of the trait and it also suggests that gene controlling the trait, are dispersed among the parents. Also from the result, the mean plant heights for the backcrosses (BCP1 and BCP2) skewed towards their respective recurrent parents.

Mean values of the F_1 hybrids in the six crosses, for panicle lengths were similar to their respective susceptible parents. The distributions of the segregating F_2 populations in the crosses imply that the trait is governed by more than one gene. The frequency distribution of the backcrosses skewed towards their respective recurrent parents.

SAMSORG17 had the highest panicle weight, with mean value of 118.09g, while ICSR94405 had the lowest with mean value of 76.43g. Mean value of F_1 hybrids in almost all the crosses were similar to the mid parental value, indicating preponderance

of additive gene for this trait. The F_2 populations segregated outside their parental range, suggesting that the panicle weight genes are dispersed among the parents. BCP_1 and BCP_2 mean distribution skewed towards their respective recurrent parents.

The low mean grain yield value of the resistant varieties were not due to *Striga* effect, rather it was due to the poor agronomic qualities of the varieties. Most of the F_1 means were similar to their mid parental value, indicating preponderance of additive gene effect. The distributions of the segregating F_2 populations in all the crosses imply that grain yield is governed by more than one gene. Quantitative inheritance of grain yield has been reported by Showemimo *et al.,* (2005) in the study of genetics of sorghum cultivars under *Striga* infestation. BCP_1 and BCP_2 frequency distribution skewed towards their respective recurrent parents.

SAMSORG17 had the highest 1000 grain weight while ICSR94405 had the lowest. Most of the F_1 means were similar to the mid parental value, indicating predominance of additive gene effect. The distributions of the segregating F_2 populations in the crosses imply that the trait is governed by more than one gene. The backcrosses mean distribution skewed towards their respective recurrent parents.

The donor parents; ICSR94405 and ICSR94407 were truly *Striga* resistance with mean *Striga* count value of 0.03 and 0.00, respectively. Only one *Striga* emerged on ICSR94405, while on ICSR94407 there was no *Striga* emergence. Also the other three parents (SAMSORG14, SAMSORG17 and SAMSORG40) were susceptible with SAMSORG40 having the highest *Striga* emergence with mean *Striga* count value of 4.53, followed by SAMSORG14 with mean value of 3.13 while SAMSORG17 had fewer *Striga* emergence with mean value of 1.13. The fewer *Striga* emergences observed in SAMSORG17 conforms to result of Showemimo (2005) that SAMSORG17 is a promising genotype with some level of *Striga* resistance. There

were few *Striga* emergences on the F_1 plants from the six crosses. This was in agreement with result from similar investigations with other sorghum genotypes (Vogler *et al.,* 1996; Haussmann *et al.,* 2000a; Greiner., *et al* 2001, Hess *et al.,* 2006). For the F_2 and backcrosses, *Striga* emerged on some plants while some plants had no *Striga.*

5.3 Chi-square Values at Expected Segregation Ratios

In the present study, plants with score of 0 to 4 were considered resistant, while plants with scores of 5 to 9 were considered susceptible. From the result, resistant parents common in different crosses showed consistency in reaction to *Striga* resistance in their F_1. The hybrids for all combinations were resistant with the mean damage score near that of the resistant parent, thus indicating that one or more dominant gene(s) which are complimentary controlled the resistance. In the F_2 population the chi-square values at expected segregation ratio 3:1 (resistant: susceptible) are significant in all the crosses, indicating poor fit of the observed segregation ratios. The expected ratio 9:7 is significant in the F_2 of three crosses, indicating poor fit of the observed segregating ratio, while it is non-significant in SAMSORG14 x ICSR94407, SAMSORG17 x ICSR94407 and SAMSORG40 x ICSR94407, indicating good fit of the observed segregating ratio. The 9:7 indicate complementary gene action or duplicate recessive epistasis where recessive alleles at either of two loci mask the expression of dominant alleles at both loci. Similarly, significant chi-square values were obtained in three crosses at the expected segregation ratio 13:3, indicating poor fit of the observed segregation ratio. While three crosses where not significant, therefore indicating good fit of the observed segregation ratio. Three F_2 populations gave the best fit of 9:7 and

the other three populations gave the best fit of 13:3 ratios. While those F_2 populations that fit into13:3 revealed that resistance is controlled by inhibitory gene interaction where a dominant article at one locus mask the expression of both dominant and recessive alleles at the second locus. The BC_1P_1 populations gave the best fit of 3:1 backcross ratio, while BC_1P_2 fitted into 1:1 ratio.

5.4 Estimate of Gene Effects

The chi-square significance of joint scaling test for the crosses and for almost all the traits studied, indicated the inadequacy of additive-dominance model which in turn indicated the presence of non-allelic interactions also suggesting possible involvement of digenic interaction the traits. However the chi-square test in joint scaling with no statistically significant difference in *Striga* count indicated that the additive-dominance model is adequate to use for the explanation of the trait (Mather and Jinks, 1982).

The six-parameter model showed that mean effects were highly significant in all the crosses for plant height. Additive effects were significant in all the crosses except the cross between SAMSORG17 and ICSR94405; this suggests that additive gene action contributed significantly to the inheritance of this trait. Also additive by additive effects were significant and negative in two crosses (SAMSORG17 x ICSR94405 and SAMSORG40 x ICSR94407) and additive by dominant effects were also significant in two crosses (SAMSORG14 x ICSR94405 and SAMSORG17 x ICSR94407), indicating some kind of epistasis for the trait. Meanwhile dominance and dominance by dominance effects were not significant in all the crosses, indicating that dominance does not contribute significantly to the inheritance of the trait.

The major contribution of the gene effects to the variation was indicated by the relative magnitude of the parameter as related to the overall means (Gamble, 1962). In the six crosses, estimate of the additive genetic effects (fixable effect) for plant height were quite small relative to the overall mean.

Heritability estimates for panicle weight were high in all the crosses except in one cross (SAMSORG40 x ICSR94405) which had a low narrow sense heritability estimate of 8%. However, the high heritability estimate obtained for this trait, indicated that the trait is highly heritable and selection can be done to improve the characters. Similar result was obtained by Ejeta *et al*, (1997).

Panicle length: for this trait, mean effects were highly significant in all the crosses. Additive gene effects were significant in all the crosses, dominance gene effects were significant in two of the crosses, additive by additive gene effects were significant in three crosses, additive by dominant effects were non-significant in all the crosses and dominance by dominance gene effects were significant in one cross (SAMSORG40 x ICSR94407). This indicated that additive gene effects played a prominent role in the genetic control of this trait, meanwhile dominance and epistatic gene effects also contributed significantly to the inheritance of the trait.

Grain yield: mean effects were significant in all the crosses. Additive effects were significant in four crosses, indicating that additive gene effects played a prominent role in the genetic control of these traits. Additive by additive effects were significant and negative in two crosses (SAMSORG17 x ICSR94405 and SAMSORG40 x ICSR94407) and additive by dominant effects were significant in one cross (SAMSORG14 x ICSR94405), indicating the presence of epistatic gene effect for the traits.

1000grain weight: mean effects were significant in all the crosses for this trait. Additive gene effects were significant and negative in all the crosses, dominance gene effects were significant in all the traits except SAMSORG17 x ICSR94407, additive by additive gene effects were significant and negative in one of the crosses (SAMSORG17 x ICSR94405), additive by dominance gene effects were significant in three crosses and dominance by dominance gene effects were significant in two crosses. This indicated that additive, dominance and epistatic gene effects contributed significantly to the inheritance of this trait.

Striga count per plant: mean effects were significant in all the crosses. Additive gene effects were significant in all the crosses, and no other gene effect was significant in any of the cross. This indicated the preponderance of additive gene action for this trait. And since all other gene effects were non-significant, it indicated that dominance and epistatic gene effects do not contribute significantly to the inheritance of this trait.

Striga damage score: mean effects were significant in all the crosses for this trait. Additive gene effects were significant and negative in all the crosses, dominance gene effect were significant in two crosses, additive by additive gene effects were significant in all the crosses, additive by dominance gene effects were significant and negative in one cross (SAMSORG40 x ICSR94405) and dominance by dominance effects were significant in all the crosses. This indicated that additive, dominance and epistatics gene effects contributed significantly to the genetic control of the trait. Moreover, additive and epistasis is more important than dominance to the breeder of self-pollinating species, because dominance will be broken by segregation following hybridization. Also epistasis does not depend on heterozygosity and can therefore permit more gene combinations than dominance.

5.5 Heritability

Narrow sense heritability estimates were less than broad-sense heritability estimate in the six crosses for all the traits. Dabholkar (1992) classified heritability estimate as low (5% to 10%), medium (11% to 30%) and high (> 30%).

Following the classification above, the broad and narrow sense estimates for plant height were high in all the crosses except SAMSORG40 x ICSR94405 cross which had a moderate narrow sense estimate (15%). The high narrow sense heritability observed in almost all the crosses for plant height confirms the presence of additive genetic variability for the trait as observed in the generation means analysis. Similar result was obtained by Showemimo (2005), Obilana, (1984). The high broad sense heritability observed in all the crosses for this trait, indicates that the trait have sufficient genetic variability and that there would be high probability of success in selecting for *Striga* resistance in the early generation using this trait.

Similarly, heritability estimate for panicle length in all the crosses ranged from moderate to high. Broad sense heritability estimates were high in all the crosses while narrow sense heritability estimates were high in three crosses and moderate in three crosses. The high heritability estimate obtained for this trait, indicated that the trait can be heritable, and it also confirms the presence of additive genetic variability for the trait as observed in the generation means analysis.

Heritability estimates for panicle weight and grain yield per plant were high in all the crosses except in one cross (SAMSORG40 x ICSR94405) which had a low narrow sense heritability estimate of 8% and 10% for panicle weight and grain yield respectively. However, the high heritability estimate obtained for these traits, indicated that the traits are highly heritable and selection can be done to improve the charactesr. Similar result was obtained by Ejeta and Butler, (1993), and Ejeta *et al,* (1997).

Meanwhile the low narrow sense heritability obtained may be due to the effect of epistasis.

For 1000 grain weight, high heritability estimates were observed in all the crosses except in SAMSORG40 x ICSR94405 cross which had a moderate heritability estimate of 16%. This also indicated that this trait can be heritable and that selection can easily be made on it for further improvement.

Broad sense heritability estimates were high in all the crosses for *Striga* damage score, while narrow sense heritability estimates were high in three crosses and moderate in three crosses. The high heritability signifies positive response and the ability to transmit this trait through selection. This result is in agreement with that of Showemimo (2005). According to Johnson *et al* (1955), characters with high heritability accompanied with high genetic advance also result in better genetic gain through selection as high heritability will always be associated with genetic advance (Amin *et al.,* 1992). Heritability can also be used to predict gain from selection in breeding.

Genetic advance (GA) of reduction of susceptibility by 2 to 4 number of *Striga* per plant was predicted in the future generation. Thus indicating that in the F_3 generation, there will be fewer number of *Striga* per plant compared to the F_2 generation. This implies that, genetic advance in yield of the future generation is expected to be higher because the fewer the *Striga* the more resistant and the higher the yield. Moreover the high genetic advance observed for most traits indicate better genetic gain through selection.

CHAPTER SIX

SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

The current genetic studies were carried out using five sorghum genotypes, two resistant varieties: ICSR94405 and ICSR94407 and three susceptible varieties: SAMSORG14, SAMSORG17, and SAMSORG40 at Institute for Agricultural Research (IAR), Samaru, in 2011/2012. Population development was carried out in IAR Samaru research field using factorial mating design in 2011 planting season. The F_1 hybrids in each cross were advanced to F2, and were backcrossed to their respective parent to generate BCP_1 and BCP_2 using irrigation at IAR Samaru irrigation site in 2012 before the raining season. Evaluation of the genetic populations (P_1, P_2, F_1, F_2, BCP_1, and BCP_2) was done at the *Striga* sick plot in IAR Samaru research field in 2012 planting season. Variability for resistance to *Striga* and other agronomic traits, Mode of inheritance of *Striga* resistance and the gene action involved in the inheritance of *Striga* resistance in sorghum varieties used in this experiment were studied in the six crosses involving six genetic populations (P_1, P_2, F_1s, F_2s BCP_1, and BCP_2). Plant height, grain yield, panicle weight, panicle length, 1000 grain yield, *Striga* damage score and *Striga* count were the resistance criteria used.

Analysis of variance revealed highly significant difference among the genotypes for all the traits studied viz., germination percentage, days to 50% flowering, plant height, panicle weight, grain yield, 1000 grain weight, panicle length, plant virgour and *Striga* count.

It was confirmed that the two male parents (ICSR94405 and ICSR94407) were truly resistant, though their mean grain yield, plant height, panicle weight, panicle length and 1000 grain weight values were not the highest, due to their poor agronomic qualities when compared to the female parents, but the *Striga* damage score and *Striga* count which are the major resistance criteria, prove them to be resistant to *Striga hermonthica*. From the experiment, SAMSORG17 showed some level of tolerance because it recorded the lowest mean value for *Striga* count and *Striga* damage score among the IAR varieties.

Chi-square test revealed that none of the F_2 populations fitted into 3:1 (resistance: susceptible) segregation ratio, suggesting that resistance is not controlled by one dominant gene, three crosses fit into 9:7 ratio, suggesting that two dominant genes which are complimentary are in control and three crosses fit into 13:3 segregation ratio, revealing that resistance is controlled in part by gene at two or more loci.

Estimates of the six parameters for the various gene effects showed that additive, dominance and epistatic gene effect contributed significantly to the inheritance of the traits studied, with the preponderance of additive gene effects. In the present study, additive and epistasis made major contributions to the inheritance of *Striga* resistance in sorghum genotypes used.

The high heritability estimates and genetic advance obtained in almost all the traits studied, signifies positive response, repeatable and transmitability of these traits in selection, thus, these traits are easily selected and further improved.

In conclusion, the study revealed that *Striga* resistance in sorghum is controlled by a few genes (oligogenic). Thus oligogenic inheritance of pest resistance genes is generally assumed to be more stable than monogenic resistance. All the traits are quantitatively heritable, thus repeatability of result and traits can be easily improved on.

Since host-plant resistance is used as a component in integrated programme for pest control in several crops it is therefore recommended that:

- *Striga* resistance, available in sorghum should be used with appropriate complementary agronomic practices as ideal control package.
- Collaboration among national and international research institutions to establish host-plant resistance program on *Striga* should be encouraged.
- The resistance indicated by the two parents used in this study and the F_2 sergregants could be used as resistance sources to increase and diversify resistance in commercial sorghum cultivars.
- SAMSORG17 is a tolerant variety, and should be improved on.

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