

**MARKER ASSISTED INTROGRESSION OF *STRIGARESISTANCE*  
INTO FARMER PREFERRED SORGHUM VARIETY (OCHUTI)**

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award of a Masters of Science Plant Breeding and genetics degree,  
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This thesis is my original work and has not been presented for the award of a degree in any other university

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### **Dedication**

I dedicate this research to God without whom I would not have done it, my family and friends from whom I derived encouragement that I needed, and to all those to whom sorghum is a staple food and their sole source of income.

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## Abbreviations and acronyms

%	Percentage
AUSNPC	Area Under <i>Striga</i> Number Progressive Curve
ASARECA	Association for Strengthening Agricultural Research in Eastern and Central Africa
BC	Backcross generation
BC-MAS	Backcross-marker assisted selection
BecA	Biosciences eastern and central Africa
bp	Base pairs
BMZ	Federal Ministry for Economic Cooperation and Development
°C	Degree (s) Celsius
cM	Centimorgan
CTAB	Cetyltrimethyl-ammonium bromide
CIMMYT	International Maize and Wheat Improvement Centre
DNA	Deoxyribonucleic acid
dNTP	Nucleotide Tri phosphate
DPW	Dry panicle weight
DTF	Days to flowering
EB	Extraction buffer
EDTA	Ethylene diamine tetra-acetic acid
GCA	Good combining ability
HCL	Hydrochloric acid
HR	Hypersensitive response
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
ILRI	International Livestock Research Institute
IR	Incompatible response
KARI	Kenya Agricultural Research Institute
LGS	Low germination stimulant
LHF	Low haustorial initiation factor
LSD	Least significant difference
M	Molar
MAB	Marker assisted breeding
MAS	Marker assisted selection
masl	metres above sea level
ml	Millilitre
mm	Millimeter
mM	Millimolar
MR	Mechanical resistance
ng	Nanogram
PCR	Polymerase chain reaction
QTL	Quantitative trait locus
RP	Recurrent parent
SSR	Simple sequence repeat
TWG	Thousand weight grain

$\mu\text{g}$   
 $\mu\text{l}$

Microgram  
Microlitre

## ABSTRACT

Sorghum is the second most important cereal crop in East Africa and the 4<sup>th</sup> most important cereal crop worldwide. *Striga* is the key biotic constraint of sorghum and millet in this region with reported yield reductions of up to 100%. Efforts to control *Striga* through agronomic practices such as mechanical weeding, use of cover crops and trap crops, use of chemicals, early planting have proved futile. Breeding for resistance using conventional methods has also been used with limited success. There have been advances in breeding with the utilization of molecular markers tightly linked to *Striga* resistance quantitative trait loci (QTL) in marker assisted selection (MAS). In this study, *Striga* resistance was introgressed from a resistant sorghum variety, N13 into a farmer preferred sorghum variety in Kenya, Ochuti. This was introgressed into two backcross line 11 and 34 of BC<sub>2</sub>F<sub>3</sub> generation. Nine plants were identified having one QTL in BC<sub>2</sub>F<sub>3</sub>, these materials were advanced to BC<sub>3</sub>F<sub>1</sub> through MAS and four plants were identified each having one QTL. The number of plants advanced from one generation into the next was considerably low. This may have been the reason why there were fewer plants being identified with the *Striga* resistance. On station trials were carried out in Alupe and Kibos which are the hot spots for *Striga* in Kenya. Area under Striga Number progressive Count (AUSNPC) was used as a measure of resistance. The backcross genotypes gave lower *Striga* scores as compared to the susceptible check Ochuti. Line 34 however performed better than line 11. Yield was negatively correlated with AUSNPC. This correlation however was of -0.4 to -0.5. Of interest were factors such as stand count, host damage rate, plant height and plant tillering which varied significantly between the genotypes and the locations.

# CHAPTER 1

## INTRODUCTION

### 1.1 Background study

Sorghum (*Sorghum bicolor* (L) Moench) is the fourth most important cereal worldwide (FAOSTAT DATA, 2008) and together with maize and pearl millet form the most important dry land cereals for the semi-arid tropics.

Sorghum is grown in almost all administrative provinces in Kenya. This is because of its important role in people's diets, (Mutegiet *al* 2010). The area under sorghum production has increased rapidly from 122368Ha in 2005 to 225782 in 2010, (FAOSTAT DATA, 2010). The trend is shown in the table below

**Table 1.1: The production of sorghum in Kenya and the area produced**

Year	Area under production(Ha)	Production quantity(T)	Seed produced(T)
2005	122368	149656	3000
2006	163865	131188	3111
2007	155550	147365	3000
2008	104041	54316	3000
2009	173172	99000	3000
2010	225782	164066	3000

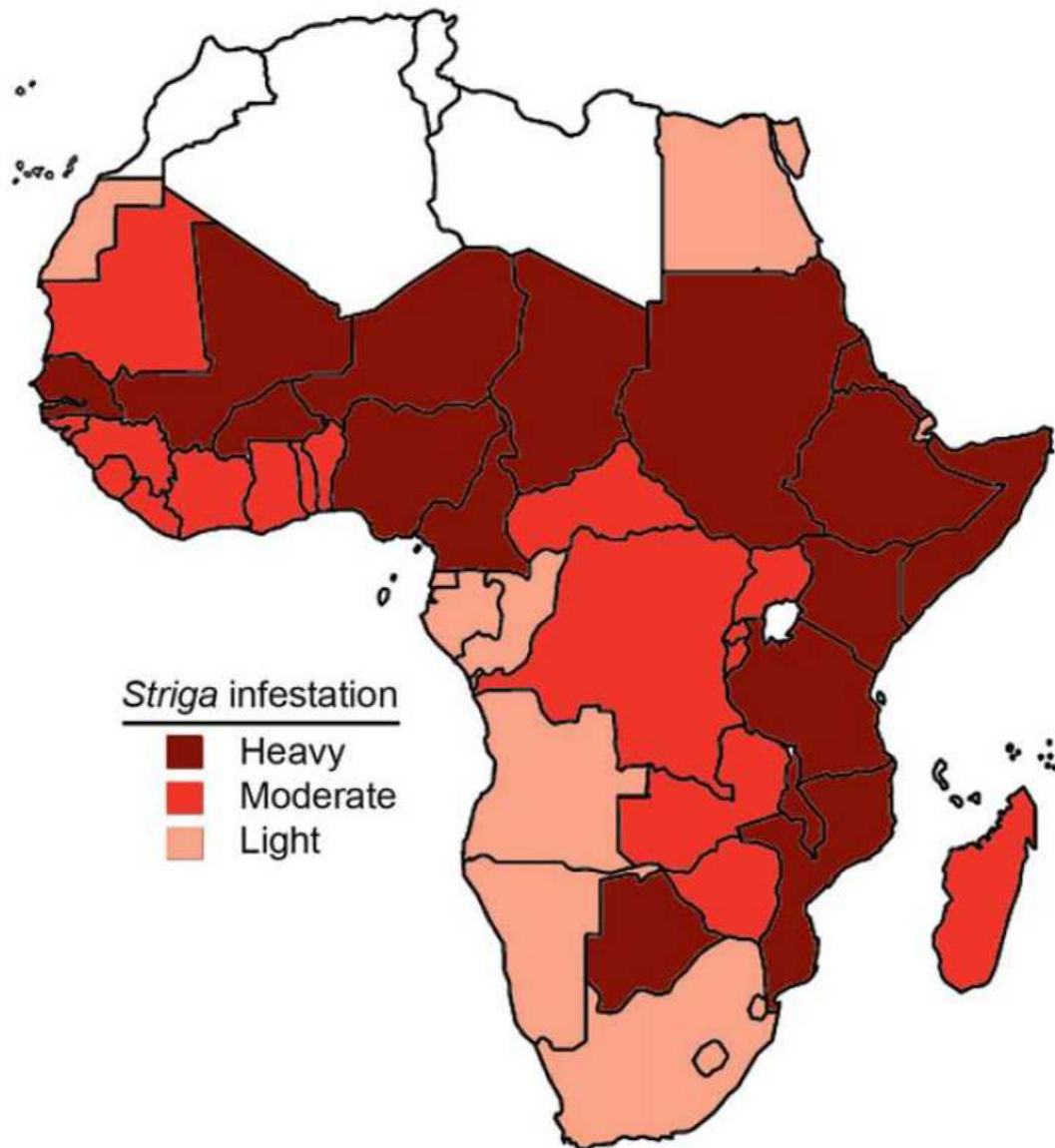
Mann *et al* (1983) hypothesized that the origin and early domestication of sorghum took place in the north eastern Africa approximately 5000 years ago. Primitive domesticated sorghum must have differed from their wild relatives in several morphological and physiological characters such as robustness, glume size, rigidity, grain size and shape. This must have led to its domestication and spread in areas around east and central Africa. The subspecies of cultivated sorghum (*s. bicolor*) are bicolor, guinea, caudatum, kafir and durra (Harlan and de Wet, 1972).

Sorghum provides an important component to the diets of many people in the world in form of unleavened bread, boiled porridge or gruel, malted beverages and specialty foods such as popped grain and beer. Sweet sorghum is used to make syrup. The crop is also used for building material, fencing, and fodder for animals or for brooms (House, 1985 Doggert, 1988). The stalk and foliage is also used as livestock feed either as green chop, hay silage or pasture (House, 1985).

The production constraints to sorghum include *Striga hermonthica* (Del.) Benth, stalk borers, shoot fly, soil water deficits, rust, smut, anthracnose and bacterial streak. However, in Kenya the most important constraints are *Striga* and soil water deficiencies (Wortmann *et al.* 2007). Parasitic weed *Striga hermonthica* (Del.) Benth and *Striga asiatica* (L) Kuntze are major biotic constraints to cereal production in general and sorghum production in particular. This is so especially in marginal areas in semi arid areas where continuous cropping caused by increased population pressure has led to widespread soil infertility (Ejeta and Butler, 1993)

*Striga* is an obligate parasite and presents a particular threat to crop production since most of its damage occurs underground, before the parasitic plant emerges and is therefore out of reach of most control measures. Furthermore, each *Striga* plant produces a large number of minute seeds which remain viable in the soil for many years (Bebawiet *et al.*, 1984). Annually, around 100 million people lose half their crop production to *Striga* (Gresselet *et al.*, 2002) and total yield losses occur in infested farmers' field especially during drought periods. Often, mechanical or chemical control options are too expensive

or ineffective against the *Striga* weed and farmers whose land is infested abandon fields or change crop to overcome the hazard (Ejeta *et al.*, 2004). Overall, in the 1980s, *Striga* threatened African grain production in an area of 44 million ha (Sauerborn, 1991) out of a total area of 79 million hectares dedicated to cereal production, (FAOSTAT DATA 2004, data for 1988). This *Striga* infested area has increased to 57 million ha over the years.



**Figure 1.1; Shows the extent of *Striga* infestation in Africa. Adopted from Ejeta (2007)**

There is need therefore to control *Striga* in the infested areas and prevent its spread to uninfested fields. One control strategy is the development and utilization of *Striga* resistant varieties. The use of resistant varieties will lead to reduction of labor and time spent on weeding, reduction in cost for herbicide spraying and in the preservation of environment. Ochuti is a farmer preferred sorghum variety in Kenya. This is because of its high yielding capacity and dark colored grain. However, its yields are depressed by *Striga*. In assessing resistance in field trials, data is collected on *Striga* development traits and also on the host plant reactions. A good measure of resistance is the Area under *Striga* Number Progressive Curve (AUSNPC). This is the summation of the progressive *Striga* counts per a given area or plot. These counts are taken on a fortnight basis from the 6<sup>th</sup> week to the 14<sup>th</sup> week in Sorghum. AUSNPC is calculated from the formula;

$$AUSNPC = \sum_{i=0}^{n-1} \left[ \frac{Y_i + Y_{(i+1)}}{2} \right] (t_{(i+1)} - t_i)$$

Where n=number of *Striga* assessment dates

$Y_i$ =count at the  $i$ th assessment dates

$T_i$ = days after planting to *Striga* emergence minus 1

$Y_0=0$

Data taken on *Striga* flowering plants and capsule formation gives a measure of the reproductive success of the *Striga* plants. The other traits used in assessing resistance include; yield parameters, host plant reaction, days to host plant flowering and host plant height. A negative correlation between these traits and AUSNPC is basically expected as *Striga* causes stunting in plant severely affected and reduces yield. Host plant reaction is a qualitative measure and is categorized into classes. These are class 1-5, with class 1 as

the resistant plant and class 5, the susceptible plant. Damage taken on the host includes leaf chlorosis, leaf and stem firing symptoms, poor panicle development and stunting.



## 1.2 Problem statement

*Striga hermonthica* is a serious parasitic weed. Of the *Striga* species, it is the largest plant and most robust. *S. hermonthica* is a parasite of food crops such as rice, maize, sorghum, finger millet and cowpea (Mohamed *et al.*, 2001).

*Striga* thrives in poor, degraded, infertile soils. Such is the condition of soils in most areas in Africa due to poor agronomic practices and management (Ejeta, 2007). Over 100M people lose over 50% crop to *Striga* worldwide. Losses in the African savanna region have been estimated to about \$7 billion. In West Africa alone 40M Ha are heavily infested while 70M Ha have moderate infestation (Berneret *et al.*, 1995).

The *Striga* problem in Africa is increasing due to the seed practices in the region. Normally, subsistence farmers' plant superior seed saved from the previous crop because quality improved sorghum seed is lacking in the region. Furthermore, most farmers practice seed aid where seed is shared from one farmer to the next. *Striga* is mainly spread through seed and therefore sharing seed increases the spread and area of coverage of *Striga*. Another problem is the increased population pressure which leads to intensification of farming and therefore practices such as rotation and laying the land fallow are not adhered anymore. Consequently, there is a tendency of farmers to continue planting mono-crops of major cereals which in most cases support *Striga* and hence increase its spread, (Berneret *et al.* 1997 and Ejeta, 2007).

### **1.3 Justification**

The bulk of sorghum production in Kenya is Western and Nyanza administrative provinces. These provinces are heavily infested with the *Striga* weed. The farmer preferred varieties grown in these regions such as Ochuti, Seredo, Wagita are susceptible to *Striga* attack.

The markers associated with *Striga* resistance have been identified by International Crop Research Institute for Semi AridTropics (ICRISAT). Five genomic regions associated with *Striga* resistance from resistant line N13 have been identified across a range of ten field trials in Mali and Kenya. This has been done using two mapping populations. (Hausmann *et al.*, 2004). The Quantitative Trait Loci (QTL) have been identified on linkage group 1, 2, 5 and 6. Each of these QTL explains between 12 and 30 % of total phenotypic variation observed for *Striga* resistance. Because this variation is quantitative, the resistance conferred is expected to be broad and durable.

This project was aimed at introducing *Striga* resistance to a farmer preferred variety in Kenya, Ochuti. This is done so that the productivity of sorghum in *Striga* prevalent areas may be increased even further.

## **1.4 Objectives**

### **1.4.1 General objective**

To enhance sorghum productivity in Kenya by introgression of *Striga* resistance QTL into to a farmer preferred variety in Kenya.

### **1.4.2 Specific objectives**

1. To increase the background of Ochuti in BC<sub>3</sub>F<sub>1</sub> and BC<sub>4</sub>F<sub>1</sub> back-crosses
2. To evaluate the performance of *Striga* introgressed BC<sub>3</sub>F<sub>1</sub> and BC<sub>4</sub>F<sub>1</sub> progenies under artificial infestation in *Striga* prone fields

### **Hypothesis**

1. MAS is capable of selecting *Striga* resistance QTL for introgression into farmer preferred variety
2. The advanced back-cross with introgressed *Striga* resistance QTL lines perform better than farmer preferred varieties under *Striga* infestation.

## **CHAPTER 2**

### **LITERATURE REVIEW**

#### **2.1 Sorghum**

##### **2.1.1 Sorghum's origin, uses and morphology**

The highest distribution and variability of sorghum is found in Africa and is therefore believed to be the center of origin (de Wet & Harlan, 1971). Sorghum is widely grown in most regions of Africa and Asia where they account for up to 80% of total area under sorghum production (Dahlberg, 1995). Sorghum is however adapted to a wide range of environments taking an average of 90-140 days to reach maturity. Sorghum does well in environments of reduced moisture which is attributed its long extensive fibrous root system that is able to obtain greater volumes of water from soil as compared to maize (House, 1985)

Sorghum has a wide range of uses. These include; human food where flour from sorghum is used to make gruel, unleavened bread and porridge or as, animal feed where it is either fed to the animals as hay, green chop, silage or pasture. The sorghum stem is used as fencing or building material, the remains after harvesting are used as fuel. Other uses of sorghum are such as making beer, specialty sorghum such as pop sorghum and sweet sorghum which are perched and eaten.

Sorghum has a wide variation in grain color, hardness and shape that allow it to be used for different ways (House, 1985).

Sorghum is divided into five races based on grain and glume morphology. These races are, Dura, bicolor, Kafir, Caudatum, Guiney. Sorghum root is extensive and has a lot of hairs, twice what maize has. It has primary roots also known as embryonic roots and

secondary roots, the secondary roots branch from the primary roots. The roots can support up to the third crop growing from the adventitious buds of the parent stem, (House,1985).

The stems of sorghum can grow up to 4metres in length while the width varying, highest being 4cm at the stem base and it narrows towards the upper end of the plant. It has a series of nodes and internodes. Leaves develop from the nodes in alternating positions. Different types of sorghum have different types of leaf morphology. Variation includes the angle of attachment to the stem (vertical-near horizontal), length, and the width of the leaves e.t.c. The flag leaf is usually the shortest. It takes thirty days after planting with six to seven leaves for sorghum to attain maturity (House,1985).

The inflorescence of sorghum is known as a panicle. It is large and pyramidal in shape. The raceme bears the spikelet, one being sessile, and the other pedicellate and a terminal spikelet having two pedicellatespikelets. The flower color undergoes changes from green at flowering to cream, buff, yellow, red, brown, purple to near black at grain maturity. The glumes can be thin and papery, thin and brittle or hard and tough depending on the species. The glume may enclose the seed or the seed may protrude from it. The flower has two pistils and three stamens. The pistils are short and attached to the ovary. The anthers are long and threadlike filaments (House, 1985).

### **2.1.2 Constraints in sorghum production**

The biotic production constraints to sorghum production include *Striga*, stalk borers, shoot fly, rust, smut, anthracnose and bacterial streak. The abiotic production constraint is mainly soil water deficits.However, in Kenya the most important constraints are *Striga* and soil water deficiencies (Wortmannet *al.*, 2007).

Several control methods have been used to solve the *Striga* menace, some are as indicated in Table 2.1 below.

**Table 2.1: Alternative control strategies used in *Striga* management. (Table adopted from Haussmann *et al.*, 2006).**

TYPE OF METHOD	CATEGORY	
	Reduction of soil seed bank	Reduction of <i>Striga</i> seed production
Cultural	Traps crops; soybean, cotton, sunflower, groundnut.	Resistant crops
	Cash crops, susceptible hosts.	High plant density
	Organic manure to promote biological soil suppressiveness	Delayed planting
Physical	resistant crops.	
	Deep ploughing	Transplanting mixed cropping (cereals and legumes)
Chemical	Soil solarisation	Weeding (manual or mechanical)
	Fertilization: N and P to promote biological soil suppressiveness.	Fertilizer application
	Soil fumigation: methyl bromide.	Herbicides: 2,4-D, paraqual glyphosate
	Germination stimulants, ethylene, strigol.	Anti transpirants.
Biological	Soil inundation with microbes that destroy <i>Striga</i> seeds.	Use of fungi such as <i>Fusarium</i> spp and <i>Smicrinyx</i> spp.

## 2.2 Striga

### 2.2.1 *Striga* species and its damage in Africa

For the effective control of *Striga*, there is need to understand its morphology, environmental interactions and host-parasite interactions. In the last fifty to sixty years, considerable efforts have gone to the study of *Striga* biology and host parasite interactions. This understanding is important in order to come up with control measures suitable to the different hosts of *Striga* parasite (Ejeta, 2007).

*Striga* belongs to the family *Scrophulariaceae* (*Orobanchaceae*), of root parasites and they are the most specialized in the group. *Orobanchaceae* family members are divided into either holo-parasite which lack chlorophyll hence total parasitism or hemi-parasites which have chlorophyll. *Striga* species are neither holo-parasites nor hemi-parasites as it falls into holo-parasites as a non-emergent seedling and a hemi-parasite when it is an emergent plant, hence attack is severe the *Striga* weed emerges (Mohamed *et al.*, 2001).

The *Striga* plant is parasitic hence it does not produce exclusive vegetative stems. This is due the fact that it does not depend entirely on photosynthesis for energy production but also on its host plant.

Each *Striga* stem produces an inflorescence and at a high rate of production. Depending on the species, *Striga* weed can be out crossing or selfing types, *Striga hermonthica* is an out crosser (Mohamed *et al.*, 2001) *Striga* species vary in their requirements for optimum soil temperature, for germination, water and soil types.

According to (Mohamed *et al.*, 2001), the following features can be used to distinguish between different *Striga* species, the growth duration taken which can either be annual or perennial. Most agronomically important species are annuals. Perennials mostly attack

perennial grasses, however the damage caused is insignificant. The shape of the stem which can be either terete stems which are round in cross section, obtusely square stems which are square with blunt corners or winged stems which are square and acutely angled. The indumentums which includes the surface features and trichomes e.g. the trichomes can be glandular, hispid (stiff hairs), pubescent (long soft hairs) or ciliate (long stiff hairs).

Leaf lobbing and dentations where in most species leaves are unlobbed and in few species venation extends to the tip of the leaf. The inflorescence types, they differ in different species by the length of the inflorescence, the flower compactness, the size of the bract and its shape, whether opposite or alternate flower. The calyx which can be equal or sub-equal. Corolla color and tube bend, the color of the corolla can be white, red (most common), salmon, orange, or yellow. The most distinguishing feature in *S. hermonthica* is its ability to produce fragrance (Musselman *et al.*, 1986). And lastly, host range and host specificity, this study has not yet been conducted conclusively as it is impossible to determine the different species attacked by single *S. Hermonthica* specie. However *S. gesnerioides* is known to strictly attack dicots. The host range of *S. hermonthica* is however narrow and most of the host are of agronomic importance and hence the concern.

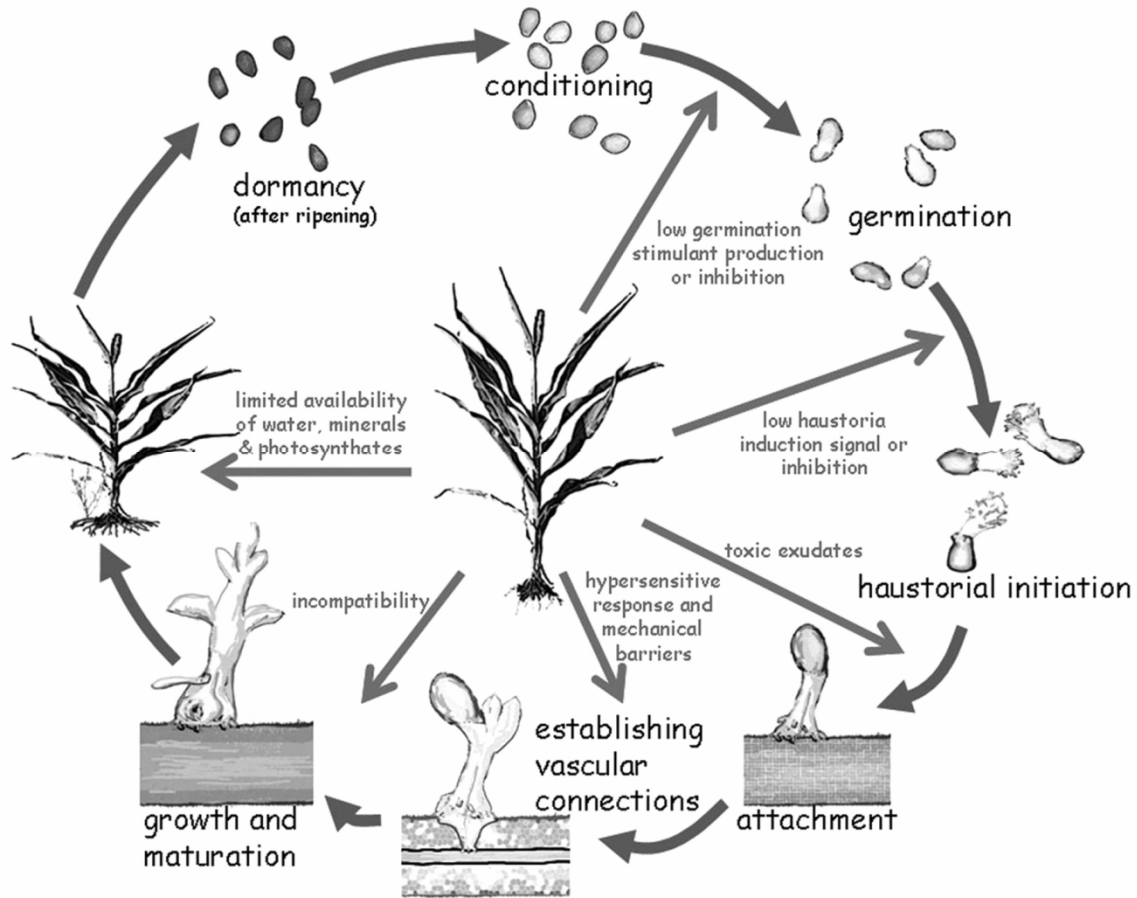
The *striga* species has about forty species, ten of which are parasitic and endemic to Africa. *S. hermonthica* is well adapted to the climatic conditions in sub-Saharan Africa and invades crops with its bewitching effects (Mohamed, 2001, Ejeta, 2007 and Kamal and Lynton, 2008). *S. hermonthica* is the largest among agronomically important *Striga* species and the most destructive. It is adapted to the Sahelian Africa from Senegal to



Ethiopia while the southern limits reached are Congo and Tanzania. *S.hermonthica* is adapted to the Nile Delta region and Yemen. There are reports of the presence of *S. hermonthica* in Angola, Namibia, Nile delta and Yemen. (Mohamed *et al.*, 2001).It is an obligate out breeder. *S.hermonthica* has different strains within the hermonthica species which are specific to different crops it attacks. For instance, the strain of *S.hermonthica* attacking millet is not the same strain which attacks sorghum. Variation observed is mainly on the floral types and corolla coloration. It is closely related to *S.aspera* and *S.gracilima* hence these form a species cluster(Musselman *et al.*, 1986).

### **2.2.2.Biology of *S. hermonthica*; life cycle**

*S. hermonthica* seeds require long term drying and storage to overcome dormancy. This is also known as the ripening period. After ripening, the seeds will imbibe water, swell and break dormancy. They need a stimulus from the host plant in order to germinate, if this stimulus is absent, *S. hermonthica* seeds are capable of reverting to dormancy by loosing the water in the seed(Ejeta, 2007). The process of coming in contact with the chemical stimulant from the host plant is known as seed conditioning. The seed will therefore use its limited resources to grow a haustorium, as shown in figure 2.1 below. It is very important for the seed to be in close contact with the host plant for the haustorium to establish contact and start on parasitism. Haustorial initiation and formation also requires a chemical stimulant form the host plant(Ejeta, 2007).



**Figure 2.1 showing *S. hermonthica* life cycle in relation to its host and the different mechanisms of resistance. Adopted from (Ejeta, 2007).**

Attachment takes place immediately contact is established by a hemicellulose based adhesive. This fixes the parasite to its host. After fixation the process of penetration follows, this is the development of a tubercle which penetrates through the plant cells and connects to the plant conducting tissues to acquire nutrients. Then cotyledonous *S. hermonthica* leaves emerge from the seed coat after successful contact has been made. The plant eventually mature after six weeks, flowers then develops seed capsules two weeks after pollination (Ejeta, 2007).

### **2.2.3 Striga hosts and damage**

The striga spp parasitizes on cereals e.g. maize, sorghum, proso millet, upland rice and legume such as cowpea. It leads up to 100% yield loss in cereals rendering production futile and with increased infestation leads to farmers abandoning farms and moving to less infested areas (Berneret *al.*, 1995). The *S. hermonthica* problem is associated with population growth, with increased population pressure, food demand increases hence land use intensifies. Land use will therefore tend towards monocropping which replaces traditional farming practices such as rotation, intercropping, and laying land fallow for periods of time. *S. hermonthica* flourishes in monocrops especially those of cereals. Change of taste and preference is also a problem as most people in Africa prefer growing maize and sorghum to other crops. These are usually grown in single stands and this intensifies the *S. hermonthica* problem. (Berneret *al.*, 1995).

### **2.2.4 Sources and types of resistance and their utilization**

According to Doggett (1988) and Ejetaet *al.*, (1992) a genotype resistant to *S. hermonthica* is that which when grown under conditions of *S. hermonthica* infestation supports significantly fewer *S. hermonthica* plants and has a higher yield than a susceptible cultivar while a tolerant genotype shows smaller yield reduction than a susceptible plant under the same level of infestation.

*S. hermonthica* weed is an obligate hemi-parasite and survive only in the presence of a suitable host. *S. hermonthica* seeds will therefore germinate due to a stimulus produced

by the host plant. Different plants produce different kinds of stimuli e.g. cowpea produces alectrol, maize and proso millet produce sorgolactones.

After germination, *S. hermonthica* forms a haustorium which attaches to the host's roots to allow acquisition of water and nutrients from the host. This is the beginning of the parasitism process (Ejeta, 2007). The weed therefore grows and matures forming flowers within 6 weeks and thereafter produce seeds.

According to (Ejeta *et al.*, 2000), there are four different mechanisms of host plant resistance. These are low germination stimulant (LGS) production, low production of haustorial initiation factor (LHF), hypersensitive response (HR), and incompatible response (IR) to parasitic invasion of host genotypes. LGS genotypes of sorghum were found to produce low levels of chemicals which initiate the germination of the conditioned *S. hermonthica* seeds. Lines have been identified which produce low levels of stimulus and these are found to be resistant compared to lines producing higher levels of stimulus (Ramaiah, 1987). The LHF genotypes lead to reduction of *S. hermonthica* seed bank due to the fact that the *S. hermonthica* seeds will germinate but lack stimulus leading to haustorial formation hence they do not attach to the host and will eventually die (Ejeta, 2007). (Mohamed *et al.*, 2003) screened a number of sorghum lines and identified lines which responded with HR to *S. hermonthica*. These lines showed localized necrosis to the point of attachment of the *S. hermonthica* haustorium hence no further penetration and attachment. Resistance based on IR shows responses similar to HR differing by necrosis whereby there is no necrosis at the point of attachment. However,

the *S. hermonthica* plant will not grow past the point of one leaf or two as they show stunted growth, wither and die (Grenieret *et al.*, 2001).

### **2.2.5 The search and utilization of mechanical resistance**

The other type of resistance identified and widely used in this project is mechanical resistance (MR.).

In the event to search for MR QTL, a cross was made between two parents N13 xE36-1. N13 is an Indian durra which is known to have mechanical resistance to *S. hermonthica* although the mechanism is not very well understood. E36-1 is a guinea/caudatum hybrid originating from Ethiopia and is known to possess drought tolerance through the stay green mechanism. The resulting crosses were advanced to F<sub>3.5</sub> population. These were used in generating genetic maps which were used to identify the QTL governing MR, (Hausmann *et al.*, 2004, Grenieret *et al.*, 2007).

QTL identification was done using Composite Interval Mapping. Data generated from four locations: Kibos and Alupe in Kenya and Somanko and Cinzani in Mali over two years were used. Eleven and nine QTL were detected from data sets one and two explaining 77% and 60% genetic variance. Five QTL were common in these two data sets and were stable hence these were selected. One QTL each were located in chromosome A, B and I and two QTL were located on chromosome J. Hence these were selected as the QTL governing MR (Hausmann *et al.*, 2004, Grenieret *et al.*, 2007).

MR has been widely utilized to develop farmer preferred sorghum varieties in different countries; Kenya, Eritrea, Sudan, and Mali, (Grenieret *et al.*, 2007). Over two hundred lines were developed from all the countries containing one, two, and three QTL.

The screening for resistance under any of the characterized resistance mechanism can be done both in the field and in the laboratory,(Hausmann *et al.*, 2000). Laboratory screening involves the use of agar-gel assay (Hess *et al.*, 1992), paper roll assay (Ejeta, 2000) and *in vitro* growth system (Ejeta *et al.*, 1992).

Field screening if done should ensure the field is heterogeneous, appropriate layout is used, field inoculation with *S. hermonthica* seeds done uniformly, inclusion of susceptible and resistant checks, appropriate experimental design is used and there is the use of selection indices combining *S. hermonthica* counts, *S. hermonthica* vigor and grain yield or host plant damage score (Hausmann *et al.*, 2000).

A very important measure of resistance is the area under Striga number progressive curve (AUSNPC).

$$ASNPC = \sum_{i=0}^{n-1} \left[ \frac{Y_i + Y_{(i+1)}}{2} \right] (t_{(i+1)} - t_i)$$

AUSNPC is a summation of *S. hermonthica* counts throughout the growing season. It provides a more appropriate measure of *S. hermonthica* infestation over that season, (Hausmann *et al.*, 2000 and Omany *et al.*, 1999)

### **2.2.6 The use of markers in plant breeding**

Marker assisted backcrossing (MAB) use is increasing with time due to the following advantages; molecular markers are unaffected by prevailing environmental conditions, they are detectable at all stages of plant growth, they shorten the time for breeding and they are very abundant. Conventional plant breeding however is time consuming, traits are affected by the prevailing environmental conditions and gene interactions hence gene expression is limited and the process of phenotyping is very expensive, Marker Assisted

Selection (MAS) saves a lot of time since one can select the genotypes to be advanced without waiting for them to reach a stage suitable for an often tedious and difficult phenotypic test. Also one can limit field evaluation only to plants with a very high probability of having the desired genotype. (Francia *et al.*, 2005).

SSR markers linked to the *S. hermonthica* resistance QTL increases the speed of selection for *S. hermonthica* resistance in the backcross progenies. Selection is done when plants are at seedling stage and only selected plants are advanced to the next stage hence eliminating need to wait for plants to reach suitable stage in order to perform rigorous and often tedious phenotypic tests. This greatly saves on time for breeding, (Hausmann *et al.*, 2004).

Backcrossing involves the introgression of one or a few genes from a donor plant into the background of a susceptible plant of an elite variety and recovery of the susceptible parents' genome. MAB is a plant improvement scheme using DNA tests in selection of individuals to take to the next generation (Semagnet *et al.*, 2006b).

The success of MAB is dependent on the distance between the marker and the target gene as the probability of recombination decreases with decreased distance, the number of target genes to be transferred, the type of markers used and the number of individuals which can be analyzed within a given time frame, (Francia *et al.*, 2006; Semagnet *et al.*, 2006a).

MAS has been successfully applied in maize to breed for yield, (Francia *et al.*, 2005). Crosses were made between an exotic donor line and an elite recipient line. A few backcrosses were made with foreground and background selection with only one generation of selfing. Then the lines were crossed to a tester, and then selected for good

combining ability (GCA). The QTL for increased yields were identified and mapped and are now being used in breeding schemes, (Francia *et al.*, 2005).

In rice a Thousand Weight Grain (TWG) QTL has been identified on chromosome six, it causes the increase in yield per hybrid plant by 10-15%. MAS is used in the introgression of this QTL into elite rice cultivars, (Francia *et al.*, 2005).

In sorghum the QTL for drought tolerance have been identified and it has been used successfully in breeding programs. These are the stay green QTL, they are 3 QTL and they allow the plant to remain green to help tolerate post flowering drought, (Ngugi *et al.*, 2010)

There are five QTL on linkage groups LG01, LG02, LG06, and two on LG05. These were identified on resistant parent N13 across 10 environments in Mali and Kenya. (Hausmann *et al.*, 2004). These QTL expressed 76.6% to 78.6% genetic variance and were also of high repeatability. The QTL are flanked by SSR markers. These QTL render mechanical resistance to the resistant parent N13.

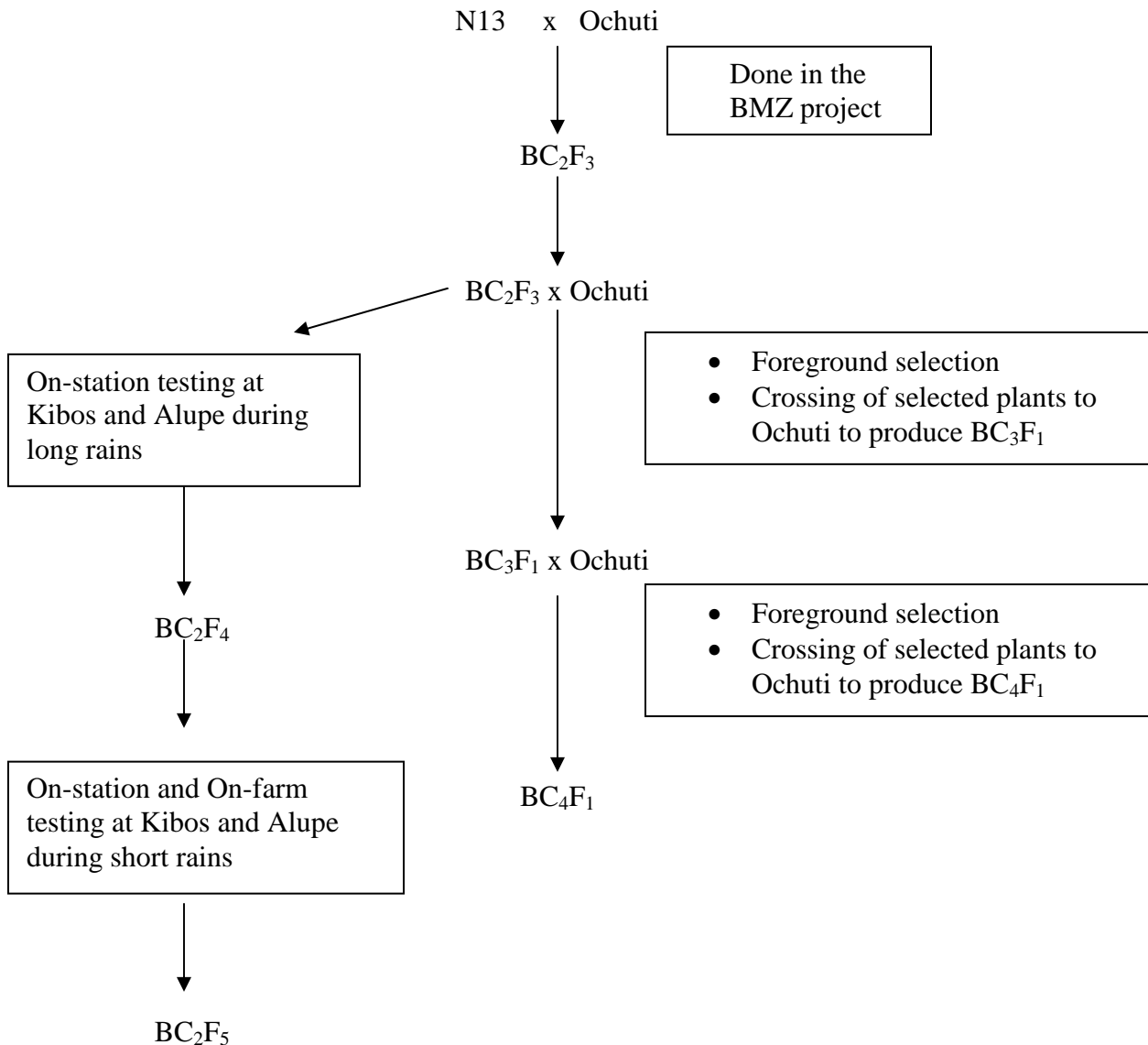


## CHAPTER 3

### MATERIALS AND METHODS

#### 3.1 Laboratory work

The initial crosses were made in a previous BMZ project and seeds were acquired at BC<sub>2</sub>F<sub>3</sub> generation. The work included backcrossing at the greenhouse and sampling. The project scheme is as shown in figure 3.1 below.



**Fig 3.1:** Scheme showing the introgression of *Striga* resistance QTL in various backcrosses

### 3.1.1 Generating backcrosses for genotyping

The initial crosses were made between a farmer preferred variety Ochuti and a donor line N13 from ICRISAT germplasm and advanced the resulting populations to BC<sub>2</sub>F<sub>3</sub>. This was done by the Federal Ministry for Economic Cooperation and Development (BMZ) project which was aimed at introgressing *S. hermonthica* resistance to the farmer preferred variety in Kenya, Ochuti. From BC<sub>2</sub>F<sub>3</sub> generation consisting of two lines namely 11 and 34 with twenty seven and forty five seeds respectively.

The seeds were sown in 25litre pots in the greenhouse at Upper Kabete campus, University of Nairobi. About one hundred seeds of farmer preferred Ochuti variety were sown concurrently. After fourteen days, leaves were harvested and placed in eppendorff tubes containing 96% ethanol. The leaves were then taken to ILRI BecA hub for DNA extraction and analysis. Two months after sowing the plants were bagged, each head separately. Emasculation of the BC<sub>2</sub>F<sub>3</sub> lines was done once the flowers opening had reached about half the panicle. Sorghum anthers were carefully removed in order not to destroy the stigma, the plants were then bagged overnight and pollination was done early the next morning with pollen collected from the Ochuti plants. The date of pollination was indicated on the bags and the bags pinned firmly on the plant. Tillers from these plants were selfed by bagging the panicles once they flowers start opening.

Foreground analysis was done for these backcross plants targeting the *S. hermonthica*QTL. After attaining physiological maturity, these plants were harvested each cross separately, threshed and Stored each in a labeled bag in a refrigerator in the laboratory at the University of Nairobi, Upper Kabete Campus. After fourteen days, again the leaves of BC<sub>3</sub>F<sub>1</sub> were harvested as before in the BC<sub>2</sub>F<sub>3</sub> generation and foreground selection performed to select *S. hermonthica* resistance QTL. As in BC<sub>2</sub>F<sub>3</sub>, the selected

BC<sub>3</sub>F<sub>1</sub> were backcrossed to Ochuti, with Ochuti being the male parent. BC<sub>4</sub>F<sub>1</sub> were subsequently stored in the refrigerator in the laboratory at -20°C.

In the field, plants were sampled at fourteen days old, leaves were placed in eppendorf tubes and labeled. These were then transported to BecA ILRI hub for DNA extraction and further analysis.

### **3.1.2 DNA extraction and genotyping**

#### **3.1.2.1 DNA extraction**

The harvested leaves from BC<sub>2</sub>F<sub>3</sub>, BC<sub>3</sub>F<sub>1</sub> and BC<sub>2</sub>F<sub>4</sub> (sampled from the field in Alupe and Kibos) generation were then placed in well labeled eppendorf tubes containing 90% alcohol and were immediately placed in cooler box containing ice at -4°C, transported to ILRI BecA laboratory and stored at -80°C.

Sampling was done for each leaf individually and DNA extracted using the Cetyltrimethyl Ammonium Bromide (CTAB) mini-prep method as developed by Mace *et al.* (2004). Adding two steel beads in each of the wells of a Geno Grinder 2000 (SpexCertiPrep, USA) plate with leaf samples, the plates were placed in a bucket with liquid nitrogen in order to make the leaf material brittle to grind. 450µl Preheated (65°C) Extraction Buffer (EB) (3% (w/v) CTAB, 1.4M NaCl, 0.2 % (v/v) β-Mercapto-ethanol and 20 mM EDTA) was added to the leaf samples and ground using the Genogrinder. Incubation of the macerated substances was done for 15 minutes at 65°C with occasional mixing. 450µl Chloroform: isoamylalcohol (24:1) was added to each sample and mixed by inversion in order to perform solvent extraction. Then the tubes were centrifuged at 12000 rpm for 10 minutes at 24°C and the upper portion transferred into fresh tubes (about 400µl). 0.7 volumes of cold iso-propanol (stored at -20°C) was added and inverted

once to mix and the tubes were centrifuged after 20-30 minutes at 12000rpm for 15 minutes, this is done in order to precipitate the crude DNA pellet. Decanting of the supernatant was done and the pellet air dried for 30 minutes. 200µl low salt TE buffer (1mM Tris and 0.1mM EDTA [PH 8]) with 3µl RNase A (10mg/ml) was added to each sample and incubated at 37°C in a water bath to remove the RNA. A second solvent extraction was done by adding 200 µl chloroform: isoamylalcohol (24:1) to each tube and inverting twice to mix and centrifuged. The aqueous layer was then transferred into fresh tubes. DNA was purified by adding 315µl ethanol and 1/10 volume of 3M sodium acetate solution (PH 5.2) to each sample and then the samples were placed in -20°C for 5 minutes for the DNA to precipitate. The tubes were then centrifuged at 12000rpm for 5 minutes and the supernatant decanted. 200µl of 70% ethanol was added and centrifuged at 3500 rpm for 5 minutes. This process is done so as to wash the DNA pellet. DNA pellet was air-dried for one hour. The pellet was then re-suspended in 100µl very low salt TE [10mM Tris, 1mM EDTA (PH 8)] buffer and stored at 4°C.

### 3.1.2.2 Polymerase Chain Reaction

A set of 11 foreground SSR markers were used for flanking these QTL were used in foreground screening to identify plants containing these QTL. These are shown in the table 3.1 below,

**Table 3.1 Markers used in foreground screening.**

Sample File	Marker	Dye	Allele 1	Allele 2	Repeat type
n13	Xtxp302	Vic	237	0	(TGT)8
Ochuti	Xtxp302	Vic	196	0	(TGT)8
n13	Xtxp145	Pet	243	0	(AG)22
Ochuti	Xtxp145	Pet	213	0	(AG)22
n13	Xtxp304	Fam	304	0	(TCT)42
Ochuti	Xtxp304	Fam	212	0	(TCT)42
n13	Xtxp 57	Pet	242	0	(GT)21
Ochuti	Xtxp 57	Pet	249	0	(GT)22
n13	Xtxp225	Ned	164	188	(CT)9(CA)8CCC(CA)6
Ochuti	Xtxp225	Ned	168	0	(CT)9(CA)8CCC(CA)6
n13	Xtxp208	Fam	260	0	(GGA)8
Ochuti	Xtxp208	Fam	257	0	(GGA)8
n13	Xtxp303	Ned	150	0	(GT)13
Ochuti	Xtxp303	Ned	152	0	(GT)13
n13	Xtxp50	Ned	297	0	(CT)13(CA)9
Ochuti	Xtxp50	Ned	295	0	(CT)13(CA)9
n13	Xtxp201	Vic	183	0	(GA)36
Ochuti	Xtxp201	Vic	188	0	(GA)36
n13	Xtxp15	Fam	217	0	(TC)16
Ochuti	Xtxp15	Fam	219	0	(TC)16
n13	Xtxp 65	Vic	130	0	(ACC)4+(CCA)3CG(CT)8
Ochuti	Xtxp 65	Vic	132	0	(ACC)4+(CCA)3CG(CT)8

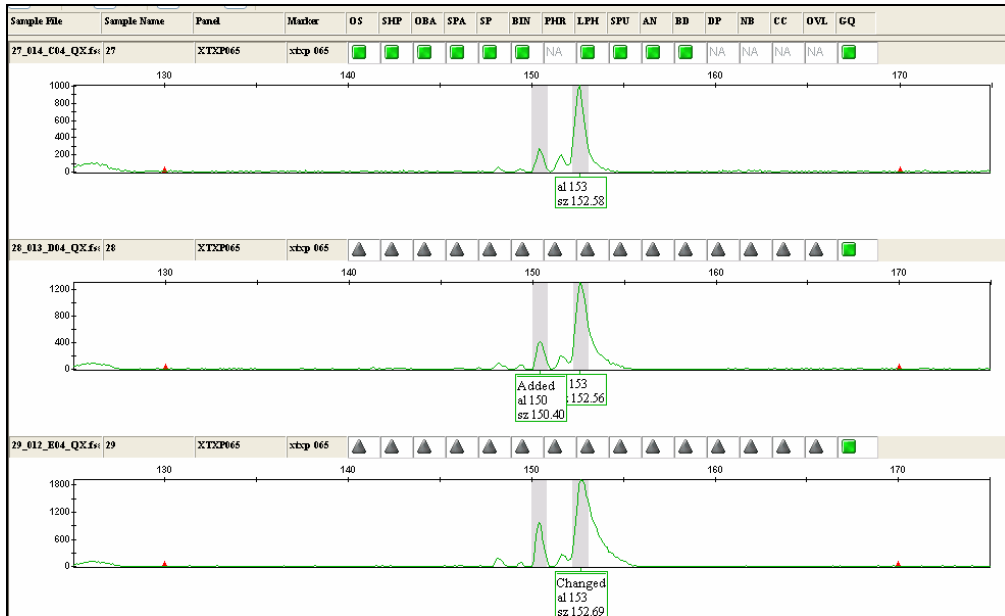
The markers used flank the QTL that confer resistance to *S. hermonthica* in N13 sorghum variety. M13 forward primers were labeled with fluorescent dyes; FAM, NED, VIC and PET (PE-Applied Biosystems.) since the amplicons were to be separated using a capillary electrophoresis.

The PCR components for a 10 µl reaction were: 2 mM MgCl<sub>2</sub>, 0.20 µM reverse primer, 0.04 µM forward primer, 0.04 mM of each of the four dNTPs and 0.2 U AmpliTaq Gold DNA polymerase (AmpliTaq® with GeneAmp® Taq DNA polymerase:

Applied Biosystems), 30 ng template DNA and top up to 10 µl reaction volume, double distilled water was added. Temperature cycling was carried out using the GeneAmp PCR systems 9600 (PE-Applied Biosystems) with the following protocol: 15 min at 94°C, 40 cycles of 1 min at 94°C, 1 min at 50°C and 2 min at 72°C, with a final extension of 20 min at 72°C. The PCR products were run on 2% (w/v) agarose gel electrophoresis to check the amplifications and the PCR segment quality. The numbers of BC<sub>2</sub>F<sub>3</sub> genotyped were 150 plants and those of BC<sub>3</sub>F<sub>1</sub> genotyped were 600 plants.

### **3.1.2.3 Capillary electrophoresis**

Genotyping was carried out by capillary electrophoresis using the ABI PRISM 3730 (Applied Biosystems), a fluorescent based capillary detection system that uses polymer as the separation matrix. The loaded PCR products for capillary electrophoresis were mixed with 7.84 µl formamide (PE-Applied biosystems) and 0.16 µl GeneScan Liz 500 internal molecular weight size standard (orange) (Applied Biosystems). The DNA fragments were denatured at 95°C for 3 min and then size fractionated using capillary electrophoresis. This system has automated sample loading and rapid electrophoresis.



**Figure 3.2: Electropherograms showing alleles of markers flanking marker XTXP 303.**

### 3.2 Field work

The experiment to determine Striga resistance of generated BC lines was done in Alupe KARI station and Kibos CIMMYT station in Kenya during the long and short rain seasons. The information on climatic and edaphic factors and when this was done is given in Table 3.2 below.

**Table 3.2: Climatic and edaphic factors of the trial plots and the seasons under which the trials were run.**

<b>Parameters</b>	<b>Kibos long rains(Apr-Sep)</b>	<b>Kibos short rains(Oct-Dec)</b>	<b>Alupe long rains(Apr-Sep)</b>	<b>Alupe short rains(Oct-Dec)</b>
Temperature	29 <sup>0</sup> C	30 <sup>0</sup> C	30 <sup>0</sup> C	30 <sup>0</sup> C
Rainfall	2000mm	1100mm	1850mm	1500mm
Planting dates	May 2010	October 2010	May 2010	October 2010
Altitude	1,214		1,189	
Latitude	00 <sup>0</sup> 04' S		00 <sup>0</sup> 29' N	
Longitude	34 <sup>0</sup> 48' E		34 <sup>0</sup> 08' E	
Soil type	Retroentricplanosols; loams	Sandy	Orthicferrosol, partly petroferic phase with orthicacrisols	
Plot size (M)	5 by 3		5 by 3	

### **3.2.1 On-station field experiment**

Randomized Complete Block Design was used with three replicates for the first season and four replicates for the second season. N13 and Ochuti were used as control and planted together with the backcross lines. Spacing used was 75 by 20 per plant with blocks of sizes 5M by 3M. Plants per line were twenty one. At planting, the hills were infested with one tablespoonfull of *S. hermonthica* inoculum which contains about 3000*S. hermonthica* seeds. The genotypes were sown including both parental lines, BC<sub>2</sub>F<sub>4</sub>, line 11(genotypes H1, H2 and H3) and BC<sub>2</sub>F<sub>4</sub>, line 34 (genotypes H1, H2, H3, H4



and H5). Data collected include seedling vigor, stand after thinning, dates to flowering, plant height, *S. hermonthica* seed counts which were done fortnightly from the 6<sup>th</sup> week to the 12<sup>th</sup> week, number of *S. hermonthica* flowering plants and forming seeds, number of plants logged, number of tillers, plant height, dry panicle weight, grain weight, and 100 seed weight.

This data was collected from the three mid rows and the border rows avoided in order eliminating the border row effect. At harvesting the sorghum heads were cut and those harvested from mid rows taken to the labs for grain traits analysis. The seeds were bulked per row and the different rows not mixed.



**Plate1: panicle heads of the backcross genotypes and N13**



**Plate 2: Harvesting of the sorghum panicle heads**  
**Plate 3: Harvested panicles heads ready for threshing**

## CHAPTER 4

### RESULTS AND DISCUSSION

#### 4.1 RESULTS

##### 4.1.1 DNA quality and quantity checks

The quantity of the DNA extracted from the samples ranged from 2ng/ $\mu$ l to 1032ng/ $\mu$ l with most of their 260/280 ratio ranging from 1.7 to 2.2. Some samples however showed a higher or much lower value than this such as samples A5 and A6 as shown in table 3.2.

This may be due to contamination of the DNA samples.

**Table 4.1: DNA quantity from BC<sub>2</sub>F<sub>4</sub> generation sampled from Kibos and Alupe Research sub-stations of KARI (Oct 2010-March 2011)**

KIBOS SAMPLES		ALUPE SAMPLES	
Sample ID	260/280	Sample ID	260/280
K1	1.96	A1	1.95
K2	2.12	A2	1.71
K3	2.01	A3	1.85
K4	1.94	A4	1.58
K5	2.11	A5	1.65
K6	2.19	A6	1.67
K7	2.04	A7	1.95
K8	2.18	A8	1.89
K9	1.89	A9	1.63
K10	1.8	A10	1.54
K11	2.1	A11	1.92
K12	2.01	A12	1.94
K13	2.02	A13	1.88
K14	1.09	A14	1.74
K15	2.14	A15	1.91
K16	2	A16	1.96
K17	2.16	A17	1.67
K18	2.06	A18	1.97
K19	2.19	A19	1.97
K20	3.1	A20	1.97
K21	1.85	A21	1.72
K22	1.64	A22	1.88
K23	1.57	A23	1.97
K24	2.16	A24	1.91
K25	2.2	A25	1.95
K26	2.2	A26	1.94
K27	1.87	A27	1.97

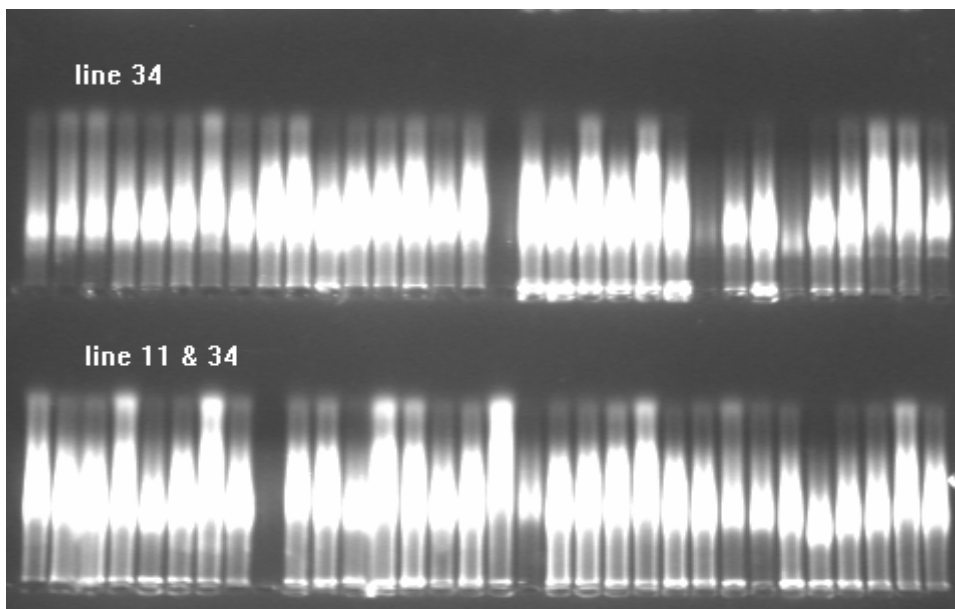
Table 4.1 continued

K28	1.51	A28	1.74
K29	2	A29	1.57
K30	1.89	A30	1.98
K31	2.41	A31	1.99
K32	1.51	A32	1.95
K33	2.26	A33	1.75
K34	2.38	A34	1.89
K35	2.55	A35	1.6
K36	2.46	A36	1.78
K37	2.2	A37	1.95
K38	1.61	A38	1.87
K39	2.05	A39	1.86
K40	2.8	A40	1.91
K41	1.99	A41	1.84
K42	2.13	A42	1.94
K43	1.07	A43	1.95
K44	2.72	A44	1.97
K45	1.11	A45	1.96
K46	2.3	A46	1.94
K47	2.71	A47	1.95
K48	2.03	A48	1.83
K49	2.01	A49	1.84
K50	2.01	A50	1.86
K51	1.98	A51	1.73
K52	1.86	A52	1.65
K53	1.83	A53	1.92
K54	1.8	A54	1.82
K55	1.71	A55	1.85
K56	2.07	A56	1.84
K57	1.48		
K58	1.95		
K59	1.61		
K60	1.92		
K61	1.37		
K62	1.96		
K63	1.98		
K64	1.89		
K65	1.97		
K66	2.02		
K67	1.97		
K68	1.97		
K69	1.62		
K70	1.9		
K71	1.96		
K72	1.93		
K73	1.96		
K74	1.93		
K78	1.97		

Table 4.1 continued

K79	1.95	
K80	1.96	
K81	1.97	
K82	1.51	
K83	1.95	
K84	1.73	

The quality of the DNA was high as indicated by the gel image below. The bright thick bands show high quantity of DNA.



0.8% gel image for DNA samples, 110V, run for 30 minutes.

**Figure 4.1 showing gel images for the DNA samples from line 34 and 11.**

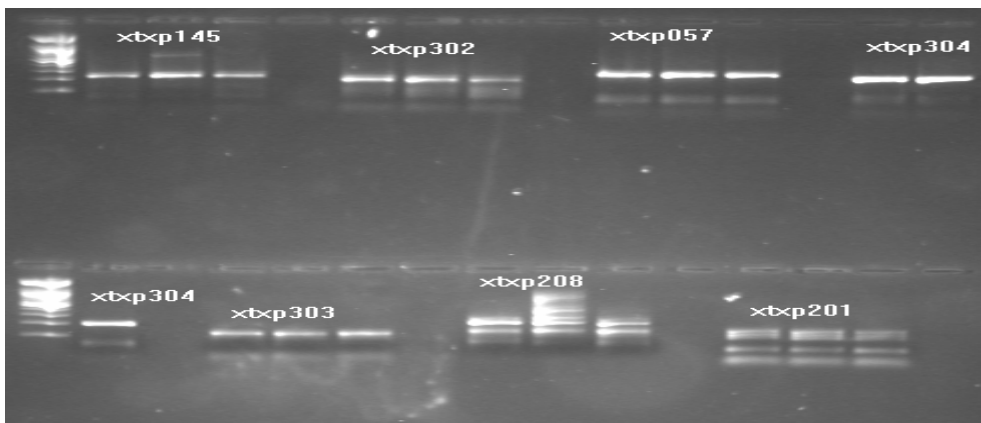
#### 4.1.2 Foreground analysis

Foreground selection was conducted on BC<sub>2</sub>F<sub>3</sub> and BC<sub>3</sub>F<sub>1</sub> populations to detect the presence of the *S. hermonthica* QTL in the backcross population. Eleven SSR markers used for as indicated in the table 4.2.

**Table 4.2: SSR markers flanking five *S. hermonthica* resistance QTL used in the foreground selection in BC<sub>2</sub>F<sub>3</sub> and BC<sub>3</sub>F<sub>1</sub> generations**

MARKER	CHOMOSOME	LINKAGE GROUP
Xtxp208 Xtxp302	A	1
Xtxp303 Xtxp65	J	5
Xtxp201 Xtxp50 Xtxp304	B	2
Xtxp145 Xtxp57	I	6
Xtxp15 Xtxp225	J	5

Gel images run for sampled PCR products indicated that the PCR worked and gave sharp bands as shown the figure 3.4.



2% gel image for 8 SSR markers, 110V, run for 30 minutes

**Figure 4.2 showing the gel images for PCR products from eight different markers**

#### 4.1.2.1 Foreground Screening For BC<sub>2</sub>F<sub>3</sub>

Out of 60 plants which were genotyped, nine had *S. hermonthica* resistance QTL J and B in heterozygous state, where both alleles for the donor and the recipient parents were in one locus.

**Table 4.3: Foreground analysis of BC<sub>2</sub>F<sub>3</sub>, lines 34 and 11**

Sample name	chromosome A		chromosome J1		chromosome B			Chromosome I		Chromosome J	
	xtxp208(GGA)8	xtxp302(TGT)8	xtxp303(GT)13	xtxp65(ACC)4+(CCA)3CG(CT)8	xtxp201(GA)36	xtxp50(CT)13(CA)9	xtxp304(m13)(TC)42	xtxp145(m13)(AG)22	xtxp57(m13)(GT)21	xtxp15(TC)16	xtxp199(CC)
34.p1	R(257)	(197)236	x	X	R(188)	D(316)	x	x	X	(217)219	R(199)
34.p2	R(257)	(197)236	x	X	R(188)	D(316)	x	x	X	(217)219	R(199)
34.p3	R(257)	R(197)	x	X	R(188)	D(316)	x	x	X	(217)219	R(199)
34.p4	R(257)	(197)236	x	X	R(188)	D(316)	x	x	X	R(219)	R(199)
34.p5	R(257)	(197)236	x	X	R(188)	D(316)	x	x	X	(217)219	R(199)
34.p6	R(257)	(197)236	x	X	R(188)	D(316)	R(213)	R(232)	X	(217)219	R(199)
34.p7	R(257)	R(197)	x	X	R(188)	X	(213)323	R(232)	X	(217)219	R(199)
34.p8	R(257)	R(197)	x	X	R(188)	D(316)	R(213)	R(232)	X	(217)219	R(199)
34.p9	R(257)	R(197)	x	X	R(188)	X	R(213)	R(232)	X	R(219)	x
34.p10	R(257)	(197)236	x	X	R(188)	D(316)	R(213)	R(232)	X	(217)219	R(199)
34.p11	R(257)	(197)236	R(150)	X	X	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p12	R(257)	(197)236	R(150)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p13	R(257)	R(197)	R(150)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p14	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p15	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	R(219)	R(199)
34.p16	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	x
34.p17	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p18	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p19	R(257)	(197)236	D(152)	(150)153	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p20	R(257)	(197)236	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(199)
34.p21	R(257)	R(197)	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	(18)
34.p22	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p23	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p24	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	(18)
34.p25	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	R(219)	R(199)
34.p26	R(257)	(197)236	D(152)	R(153)	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p27	R(257)	(197)236	D(152)	R(153)	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(199)
34.p28	R(257)	R(197)	D(152)	(150)153	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p29	R(257)	R(197)	D(152)	R(153)	R(188)	R(314)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p30	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p31	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(199)
34.p32	R(257)	(197)236	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(199)

34.p33	R(257)	(197)236	D(152)	(150)153	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
34.p34	R(257)	(197)236	D(152)	X	R(188)	R(314)	R(213)	R(232)	R(266)	(217)219	R(
34.p35	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
34.p36	R(257)	R(197)	D(152)	X	R(188)	D(316)	x	x	R(266)	(217)219	R(
34.p37	R(257)	(197)236	D(152)	X	R(188)	D(316)	(213)323	R(232)	R(266)	(217)219	R(
34.p38	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
34.p39	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	(18
34.p40	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
34.p41	R(257)	(197)236	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(
34.p42	R(257)	(197)236	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(
34.p43	R(257)	R(197)	D(152)	R(153)	R(188)	D(316)	(213)323	R(232)	X	(217)219	R(
34.p44	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
34.p45	R(257)	R(197)	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(
11.p1	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
11.p2	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
11.p3	R(257)	(197)236	D(152)	(150)153	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
11.p4	R(257)	R(197)	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(
11.p5	R(257)	(197)236	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(
11.p6	R(257)	R(197)	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(
11.p7	R(257)	R(197)	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(
11.p8	R(257)	R(197)	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	R(
11.p9	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
11.p10	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	(18
11.p11	R(257)	(197)236	D(152)	R(153)	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
11.p12	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
11.p13	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	R(
11.p14	R(257)	(197)236	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)219	x
11.p15	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)219	x

Key

R	Homozygous for the recipient parent allele
D	Homozygous for the donor parent allele
H	Heterozygote
X	no allele

**Table 4.4: Nine selected plants of the BC<sub>2</sub>F<sub>3</sub> generation having the *S. hermonthica* resistance QTL**

	chromosome A		chromosome J1		chromosome B			Chromosome I		Chromosome J2	
Sample name	xtxp208(GGA)8	xtxp302(TGT)8	xtxp303(GT)13	xtxp65(ACC)4+(CCA)3CG(CT)8	xtxp201(GA)36	xtxp50(CT)13(CA)9	xtxp304(m13)(TC)T42	xtxp145(m13)(AG)22	xtxp57(m13)(GT)21	xtxp15(TC)16	xtxp225(m13)(CT)9(CA)8CCC(CA)6
34.p19	R(257)	(197)236	D(152)	(150)153	R(188)	D(316)	R(213)	R(232)	R(266)	(217)231	R(187)
34.p21	R(257)	R(197)	D(152)	X	R(188)	X	R(213)	R(232)	R(266)	(217)233	(183)187
34.p24	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)236	(183)187
34.p33	R(257)	(197)236	D(152)	(150)153	R(188)	D(316)	R(213)	R(232)	R(266)	(217)235	R(187)
34.p37	R(257)	(197)236	D(152)	X	R(188)	D(316)	(213)323	R(232)	R(266)	(217)239	R(187)
34.p39	R(257)	(197)236	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)241	(183)187
34.p43	R(257)	R(197)	D(152)	R(153)	R(188)	D(316)	(213)323	R(232)	x	(217)245	R(187)
11.p3	R(257)	(197)236	D(152)	(150)153	R(188)	D(316)	R(213)	R(232)	R(266)	(217)250	R(187)
11.p10	R(257)	R(197)	D(152)	X	R(188)	D(316)	R(213)	R(232)	R(266)	(217)257	(183)187

**Key**

- R** Homozygous for the recipient parent allele
- D** Homozygous for the donor parent allele
- H** Heterozygote
- X** no allele

The results show that, plants 34.p19, 34.p33 and 11.p10 have QTL J1 introgressed. This is indicated by the markers XTXP 30 containing the donor allele and XTXP 65 containing both the donor and recipient parent alleles (heterozygote). Plants 34.p21, 34.p24, 34.p39 and 11.p10 have QTL J2 introgressed as indicated by the flanking markers XTXP 15 and XTXP 225. These are in heterozygous state. Plants 34.p37 and 34.p43 have QTL B. however the QTL has two markers, XTXP 304 and XTXP 50. The plants lack in marker XTXP 201.



#### 4.1.2.2 Foreground Screening for BC<sub>3</sub>F<sub>1</sub>

The total number of plant samples genotyped was 187. Of these only 4 were found to have QTL J in heterozygous state in 3 plants and homozygous state in 1 plant as shown in the Table 4.4.

**Table 4.5: Foreground analysis of BC<sub>3</sub>F<sub>1</sub> generation for the *S. hermonthica* resistance QTL**

Sample name	chromosome A		chromosome J		chromosome B			Chromosome I		Chromosome J	
	txp208(GGA)8	302(TGT)8	txp303(GT)13	txp65(ACC)4+(CCA)3CG(CT)8	txp201(GA)36	txp50(CT)13(CA)9	txp304(m13)(TCT)42	txp145(m13)(AG)22	txp57(m13)(GT)21	txp15(TC)16	txp225(m13)(CT)9(CA)8CC(CA)6
11.P10S77	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P10S78	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P10S79	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P10S80	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P13S87	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P13S88	R(257)	R(197)	X	X	X	X	x	x	x	x	x
11.P13S89	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P13S90	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P15S10	R(257)	X	D(152)	R(153)	X	D(316)	R(231)	x	x	x	R(187)
11.P15S11	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P15S4	R(257)	X	D(152)	R(153)	X	D(316)	R(231)	x	x	x	R(187)
11.P15S5	X	X	X	X	X	X	R(231)	x	x	x	R(187)
11.P15S6	R(257)	X	D(152)	X	X	D(316)	R(231)	x	266	x	R(187)
11.P15S7	R(257)	X	D(152)	X	X	X	x	x	x	x	x
11.P15S8	R(257)	X	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P15S9	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P17S66	R(257)	R(197)	D(152)	R(153)	X	D(316)	x	R(232)	266	x	R(187)
11.P17S67	R(257)	X	X	R(153)	X	D(316)	x	x	266	x	x
11.P17S68	X	R(197)	D(152)	X	X	D(316)	x	x	266	x	x
11.P17S69	X	X	X	R(153)	X	D(316)	x	x	266	x	R(187)
11.P17S70	R(257)	X	D(152)	R(153)	X	D(316)	x	R(232)	266	x	R(187)
11.P17S71	R(257)	R(197)	X	R(153)	X	D(316)	x	x	266	x	R(187)
11.P17S72	R(257)	X	D(152)	R(153)	X	D(316)	x	R(232)	266	x	R(187)
11.P17S73	R(257)	R(197)	X	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P17S74	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P17S75	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	x
11.P17S76	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P21S51	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P21S52	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P21S53	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P21S54	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P21S55	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)

11.P21S56	R(257)	(197)236	X	D(150)	X	X	x	x	x	x	x
11.P21S57	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
11.P21S58	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P21S59	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P21S60	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P21S61	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P21S62	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P21S63	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P21S64	R(257)	X	D(152)	X	X	X	R(231)	x	x	x	x
11.P21S65	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	x
11.P23S81	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
11.P23S82	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P23S83	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P23S84	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P23S85	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P23S86	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P26S31	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S32	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S33	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S34	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S35	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S36	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S37	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P26S38	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S39	R(257)	R(197)	X	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P26S40	R(257)	X	X	D(150)	X	X	x	x	x	x	x
11.P26S41	X	R(197)	X	X	X	X	x	R(232)	x	x	R(187)
11.P26S42	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S43	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S44	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S45	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P26S46	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P26S47	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P26S48	X	(197)236	X	R(153)	X	X	x	R(232)	x	x	x
11.P26S49	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P26S50	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P2S14	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	x	x	R(187)
11.P2S15	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	x	x	R(187)
11.P2S16	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P2S17	X	X	X	X	X	X	x	x	x	x	x
11.P2S18	R(257)	(197)236	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P2S19	X	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P2S20	X	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P2S21	X	(197)236	X	X	X	X	x	x	x	x	183(187)
11.P2S22	R(257)	X	X	R(153)	X	D(316)	x	x	x	x	R(187)
11.P2S23	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P2S24	R(257)	R(197)	D(152)	150	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P2S25	R(257)	R(197)	D(152)	R(153)	X	D(316)	x	x	266	x	R(187)
11.P2S26	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P2S27	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)

11.P2S28	R(257)	R(197)	D(152)	X	X	R(314)	R(231)	R(232)	266	x	R(187)
11.P2S29	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P2S30	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P36S1	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P36S2	R(257)	R(197)	D(152)	(150)153	X	X	R(231)	x	266	x	R(187)
11.P36S3	X	X	D(152)	X	X	R(314)	x	x	x	x	R(187)
11.P36S95	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P36S96	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
11.P36S97	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P36S98	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P36S99	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P3S142	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S143	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S144	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S145	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	x
11.P3S146	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	x	x	R(187)
11.P3S147	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	x	x	R(187)
11.P3S148	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	x
11.P3S149	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	x	x	R(187)
11.P3S150	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	x	x	R(187)
11.P3S151	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	x	x	R(187)
11.P3S152	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P3S153	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S154	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P3S155	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S156	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S157	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S158	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P3S159	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P3S160	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S161	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S162	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P3S163	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P3S164	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
11.P3S165	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
11.P3S166	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S167	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P3S168	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S169	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	x	x	R(187)
11.P3S170	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S171	R(257)	R(197)	D(152)	R(153)	X	X	R(231)	R(232)	266	x	R(187)
11.P3S172	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S173	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
11.P3S174	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
11.P3S175	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P3S176	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P5S12	R(257)	X	D(152)	R(153)	X	X	x	x	x	x	R(187)
11.P5S13	X	X	D(152)	X	X	X	x	x	x	x	183(187)
11.P7S100	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
11.P7S101	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)





34.P17S80	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P17S81	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	x
34.P17S82	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P17S83	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
34.P17S84	R(257)	R(197)	D(152)	X	X	R(314)	R(231)	x	266	x	R(187)
34.P17S85	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	x
34.P17S86	R(257)	R(197)	D(152)	R(153)	X	R(314)	x	x	266	x	R(187)
34.P17S87	R(257)	R(197)	D(152)	X	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P17S88	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P17S89	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
34.P17S90	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
34.P17S91	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
34.P17S92	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
34.P17S97	R(257)	R(197)	D(152)	(150)153	X	D(316)	R(231)	x	266	x	R(187)
34.P17S98	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	x
34.P17S99	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P27S32	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
34.P27S33	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P27S34	R(257)	R(197)	D(152)	(150)153	X	D(316)	R(231)	R(232)	266	x	x
34.P27S35	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	x	x	x
34.P27S36	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	x	x	R(187)
34.P27S37	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P28S13	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P28S14	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P28S15	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P28S16	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
34.P28S17	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
34.P28S18	R(257)	R(197)	D(152)	X	X	R(314)	R(231)	x	266	x	R(187)
34.P28S19	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
34.P28S20	R(257)	R(197)	D(152)	X	X	R(314)	R(231)	x	x	x	R(187)
34.P2S22	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P2S23	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P2S24	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P2S25	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
34.P2S26	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P2S27	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
34.P2S91	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P30S21	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P30S88	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P30S89	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
34.P30S90	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P35S1	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	x	266	x	R(187)
34.P35S2	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P35S3	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P35S4	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
34.P35S5	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P35S6	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P35S7	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
34.P35S8	R(257)	R(197)	X	R(153)	X	D(316)	R(231)	x	266	x	R(187)

34.P42S28	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	266	x	R(187)
34.P42S29	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P42S30	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
34.P42S31	R(257)	R(197)	D(152)	R(153)	X	D(316)	R(231)	R(232)	x	x	R(187)
34.P44S10	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)
34.P44S11	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	R(232)	266	x	R(187)
34.P44S12	R(257)	R(197)	D(152)	R(153)	X	R(314)	R(231)	x	266	x	R(187)

Key

R	Homozygous for the recipient parent allele
D	Homozygous for the donor parent allele
H	Heterozygote
X	no allele

**Table 4.6: Selected plants having 1 *S. hermonthica* resistance QTL**

Sample name	chromosome A		chromosome J1		chromosome B			Chromosome I		Chromosome
	xtxp208(G GA)8	xtxp302(T GT)8	xtxp303(G T)13	xtxp65(ACC)4+(CCA)3CG(CT)8	xtxp201(GA)36	xtxp50(CT)13(CA)9	xtxp304(m13)(TCT)42	xtxp145(m13)(AG)22	xtxp57(m13)(GT)21	xtxp15(TC)16
11.P36S2	R(257)	R(197)	D(152)	(150)153	x	X	R(231)	x	266	x
11.P2S24	R(257)	R(197)	D(152)	D(150)	x	D(316)	R(231)	R(232)	266	x
34.P27S34	R(257)	R(197)	D(152)	(150)153	x	D(316)	R(231)	R(232)	266	x
34.P17S97	R(257)	R(197)	D(152)	(150)153	x	D(316)	R(231)	x	266	x

Key

R	Homozygous for the recipient parent allele
D	Homozygous for the donor parent allele
H	Heterozygote
X	no allele

The results show that, plants 11.P36S2, 34.P27S34 and 34P17S97 have *S. hermonthica* resistance QTL J1, this is as indicated by the flanking markers XTXP 303 and XTXP 65. XTXP 303 has the donor parent allele in homozygous state while XTXP 65 has both the donor parent allele and the recipient parent allele. This is the heterozygous state. Plant 11.P2S24 has QTL J1 introgressed. Both the flanking markers alleles are of the donor parent allele.

#### 4.1.2.3 Foreground screening for on station samples from Alupe and Kibos

A total of 81 samples from Kibos and 50 samples from Alupe were analyzed. This included both Ochuti and N13 as the checks. None of these had any of the QTL introgressed.

#### 4.1.3 Evaluation of advanced backcrosses (BC<sub>2</sub>F<sub>4</sub>) under *Striga* infestation in the fields at Alupe and Kibos

##### 4.1.3.1 Evaluation of *Striga* resistance at Alupe field station in Busia

###### a) Season 1 (May 2010-Sept 2010)

During season 1, the experiment in Alupe to show agronomic traits related to *Striga* was evaluated. These traits were such as height, days to flowering, seedling vigor and others.

Table 4.7 gives the performance of the BC lines at the end of the season.

**Table 4.7: Table of means showing agronomic traits for Alupe season 1 (May 2010-Sep 2010)**

Variety	stand after thinning	seedling vigor	number of tillers	days to flowering	plant height (cm)	dry panicle weight (Gms)	grain weight (Gms)	100 seed weight	Yield (Gms/M <sup>2</sup> )
N13	20 <sub>a</sub>	4.83 <sub>b</sub>	4 <sub>a</sub>	108.7 <sub>a</sub>	140 <sub>a</sub>	360 <sub>a</sub>	269 <sub>a</sub>	29.4 <sub>a</sub>	30.7 <sub>a</sub>
Ochuti	81 <sub>d</sub>	3.67 <sub>ab</sub>	5.33 <sub>ab</sub>	97.7 <sub>a</sub>	235 <sub>b</sub>	1106 <sub>ab</sub>	891 <sub>ab</sub>	36.3 <sub>a</sub>	101.8 <sub>ab</sub>
S4/L11/H1	80.7 <sub>d</sub>	3.83 <sub>ab</sub>	7 <sub>ab</sub>	83.7 <sub>a</sub>	238.3 <sub>b</sub>	1010 <sub>a</sub>	806 <sub>ab</sub>	43.9 <sub>a</sub>	92.2 <sub>ab</sub>
S4/L11/H2	56.7 <sub>bc</sub>	3.67 <sub>ab</sub>	12.33 <sub>ab</sub>	94.3 <sub>a</sub>	238.3 <sub>b</sub>	1118 <sub>ab</sub>	943 <sub>ab</sub>	39.4 <sub>a</sub>	107.8 <sub>ab</sub>
S4/L11/H3	51.3 <sub>bc</sub>	3.33 <sub>ab</sub>	13 <sub>b</sub>	91.3 <sub>a</sub>	240 <sub>b</sub>	1220 <sub>ab</sub>	924 <sub>ab</sub>	41.7 <sub>a</sub>	105.6 <sub>ab</sub>
S4/L34/H1	83 <sub>d</sub>	2.83 <sub>a</sub>	7.67 <sub>ab</sub>	88 <sub>a</sub>	251.7 <sub>b</sub>	1375 <sub>b</sub>	1141 <sub>b</sub>	41.6 <sub>a</sub>	130.4 <sub>b</sub>
S4/L34/H2	68.7 <sub>cd</sub>	3.33 <sub>ab</sub>	4.67 <sub>ab</sub>	92.7 <sub>a</sub>	258.3 <sub>b</sub>	1138 <sub>ab</sub>	925 <sub>ab</sub>	38.4 <sub>a</sub>	105.7 <sub>ab</sub>
S4/L34/H3	39.3 <sub>ab</sub>	4 <sub>ab</sub>	8.67 <sub>ab</sub>	99.7 <sub>a</sub>	241.7 <sub>b</sub>	814 <sub>a</sub>	684 <sub>ab</sub>	47.5 <sub>a</sub>	78.2 <sub>ab</sub>
S4/L34/H4	26.7 <sub>a</sub>	3.67 <sub>ab</sub>	10 <sub>ab</sub>	94.3 <sub>a</sub>	236.7 <sub>b</sub>	1109 <sub>ab</sub>	905 <sub>ab</sub>	38.2 <sub>a</sub>	103.4 <sub>ab</sub>
S4/L34/H5	51 <sub>bc</sub>	3 <sub>a</sub>	6.67 <sub>ab</sub>	88.3 <sub>a</sub>	253.3 <sub>b</sub>	1336 <sub>b</sub>	1207 <sub>b</sub>	43.3 <sub>a</sub>	137.9 <sub>b</sub>
<b>Grand mean</b>	55.8	3.6	7.93	93.3	233.3	1061	869	40	99.4
<b>S.E</b>	5.78	0.5	2.26	7.95	13.23	242.3	224.4	8.47	25.65
<b>LSD</b>	12.15	1	4.75	16.71	27.79	509.1	471.5	17.78	53.89
<b>C.V reps</b>	2.3	7.6	5.7	3.7	2.2	3.2	2.6	1.1	2.6

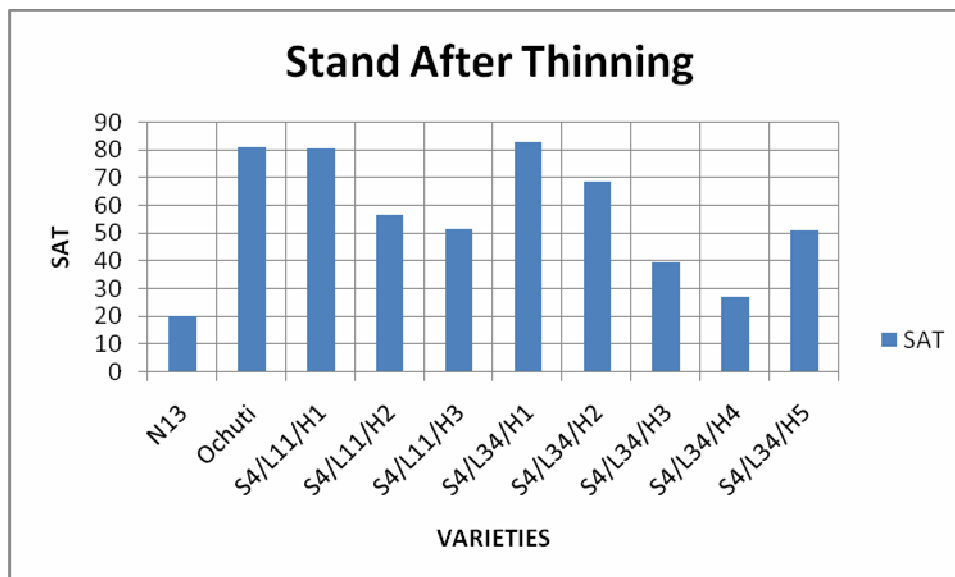


<b>M.S</b>	50.16	0.3	7.66	94.89	262.5	75560	88083	107.5	986.9
<b>P value</b>	<.001	0	0.01	0.201	<.001	0.038	0.028	0.716	0.038

- *The means in the same column followed by the same subscript letters are not statistically significant according to Boniferroni test t  $p \leq 5\%$ .*

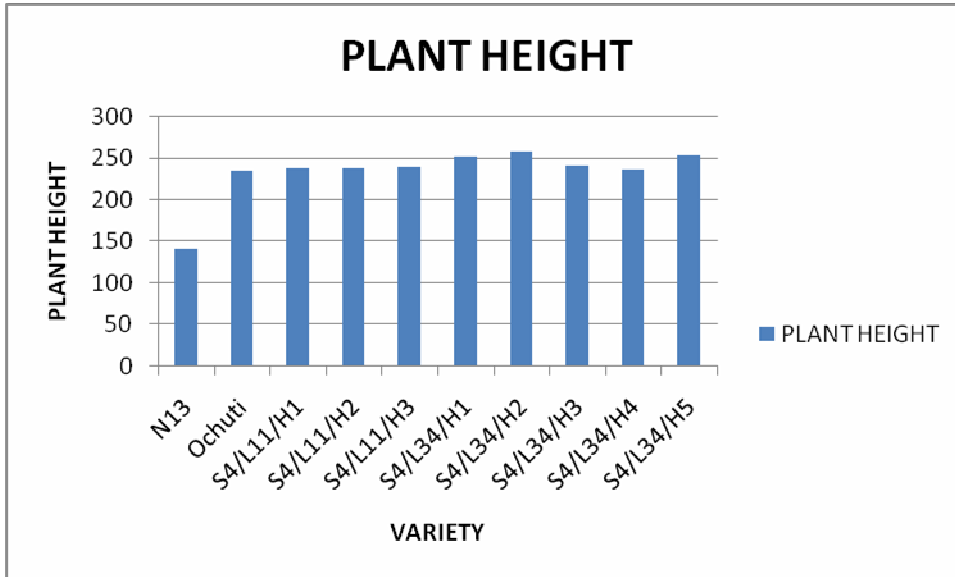
The results show that at  $p \leq 5\%$  stand after thinning and plant height gave significant differences within the varieties. The other traits however showed no difference with at  $P \leq 5\%$ . The stand count of the BC<sub>2</sub>F<sub>4</sub>genotypes varied significantly. Height is an important parameter in assessing *S. hermonthica*resistance as susceptible plants tends to be shorter or dwarfed. Table 4.2 shows that the plants varied in their height significantly.

Of interest are the yield parameters. These include grain weight and panicle weight. The difference between Ochuti did not differ significantly from the backcross progenies in yield. However, the difference observed between N13 all other genotypes is significant. N13 yielded poorly. The difference between N13 and the other genotypes is shown by LSD test at 5% but the variation among the genotypes is not significant at  $P \leq 5\%$ .



**Figure 4.3 showing stand after thinning (stand count) for the different sorghum varieties.**

The stand counts of the plants differed significantly among all the genotypes with the highest variation being observed between N13 with S4/L34/H1, Ochuti and S11/L11/H1. From figure 4.1, we can see the highest mean stand count is from S4/L34/H1 with 83 plants, while the lowest mean stand is from N13 with a count of 20 plants. The grand mean is 55.8 plants per plot. The count in the different varieties are highly varied



**Figure 4.4 Plant height of the parental checks and their BC<sub>2</sub>F<sub>4</sub>**

N13 is a usually a shorter plant. Ochuti on the other hand is a tall variety. Variation is however observed between Ochuti and the backcross lines, some e.g. S4/L34/H2 are taller than Ochuti.

**Table 4.8: Area Under *Striga* Number Progressive Curve (AUNSPC) value, striga capsule formation and striga flowering for Alupe season 1 (May 2010-Sep2010)**

Variety	AUSNP1	AUSNP2	AUSNP3	AUSNP4	AUSNPC	<i>Striga</i> plants forming capsules	<i>Striga</i> flowering
N13	0 <sub>a</sub>	0 <sub>a</sub>	26 <sub>a</sub>	166 <sub>a</sub>	191 <sub>a</sub>	0 <sub>a</sub>	0 <sub>a</sub>
Ochuti	82 <sub>a</sub>	317 <sub>a</sub>	1118 <sub>a</sub>	2854 <sub>ab</sub>	4370 <sub>ab</sub>	3.33 <sub>a</sub>	7 <sub>a</sub>
S4/L11/H1	161 <sub>a</sub>	597 <sub>a</sub>	2459 <sub>b</sub>	5644 <sub>b</sub>	8862 <sub>b</sub>	6 <sub>a</sub>	12.67 <sub>a</sub>
S4/L11/H2	142 <sub>a</sub>	560 <sub>a</sub>	1472 <sub>ab</sub>	3703 <sub>ab</sub>	5878 <sub>ab</sub>	7.33 <sub>a</sub>	10.33 <sub>a</sub>
S4/L11/H3	105 <sub>a</sub>	516 <sub>a</sub>	1717 <sub>ab</sub>	4580 <sub>b</sub>	6918 <sub>ab</sub>	4.33 <sub>a</sub>	7.67 <sub>a</sub>
S4/L34/H1	147 <sub>a</sub>	681 <sub>a</sub>	2154 <sub>b</sub>	5376 <sub>b</sub>	8358 <sub>b</sub>	5.33 <sub>a</sub>	10.33 <sub>a</sub>
S4/L34/H2	82 <sub>a</sub>	322 <sub>a</sub>	1713 <sub>ab</sub>	6027 <sub>b</sub>	8143 <sub>b</sub>	4.67 <sub>a</sub>	7.67 <sub>a</sub>
S4/L34/H3	47 <sub>a</sub>	107 <sub>a</sub>	572 <sub>ab</sub>	2030 <sub>ab</sub>	2756 <sub>ab</sub>	5 <sub>a</sub>	6 <sub>a</sub>
S4/L34/H4	68 <sub>a</sub>	247 <sub>a</sub>	1078 <sub>ab</sub>	3225 <sub>ab</sub>	4618 <sub>ab</sub>	5.67 <sub>a</sub>	6 <sub>a</sub>
S4/L34/H5	96 <sub>a</sub>	434 <sub>a</sub>	1489 <sub>ab</sub>	3773 <sub>ab</sub>	5791 <sub>ab</sub>	7.33 <sub>a</sub>	11.33 <sub>a</sub>
<b>Grand mean</b>	93	378	1380	3738	5589	4.9	7.9
<b>S.E</b>	1.11	1.286	0.665	0.457	0.5	2.89	4.206
<b>LSD</b>	116.7	392.6	1085.4	2301.8	3656.1	6.071	8.836
<b>C.V reps</b>	3.6	5.1	3.8	3.2	2.8	12.2	9.1
<b>M.S</b>	1.85	2.48	0.663	0.3136	0.3757	12.53	26.53
<b>P value</b>	0.008	0.002	<.001	<.001	<.001	0.421	0.233

- *The means in the same column followed by the same subscript letters are not statistically significant according to Boniferroni test  $t p \leq 5\%$ .*

From the results, AUSNPC value differed significantly in all varieties. By the 5<sup>th</sup> count, indicated as AUSNPC, the backcross lines had more emerged *S. hermonthica* plants than the resistant Check N13. Some genotypes however had fewer emerged *S. hermonthica* plants than the susceptible parent, Ochuti. The best line scored in this experiment is S4/L34/H3. Under the given area, it had fewer *S. hermonthica* plants emerged as compared to Ochuti and the other backcross lines.

## Season 2; Oct 2010- March 2011 for Alupe field station

The results indicate that there was no significant difference in most of the traits measured this season. The P value of these traits was not significant at 5% indicating no significant variation within the genotypes. There was variation in days to flowering ( $p \leq 5\%$ ). The highest mean observed is from S4/L34/H5 with 109.75 while the lowest mean was 85.75 days from N13. The grand mean is 104.75.

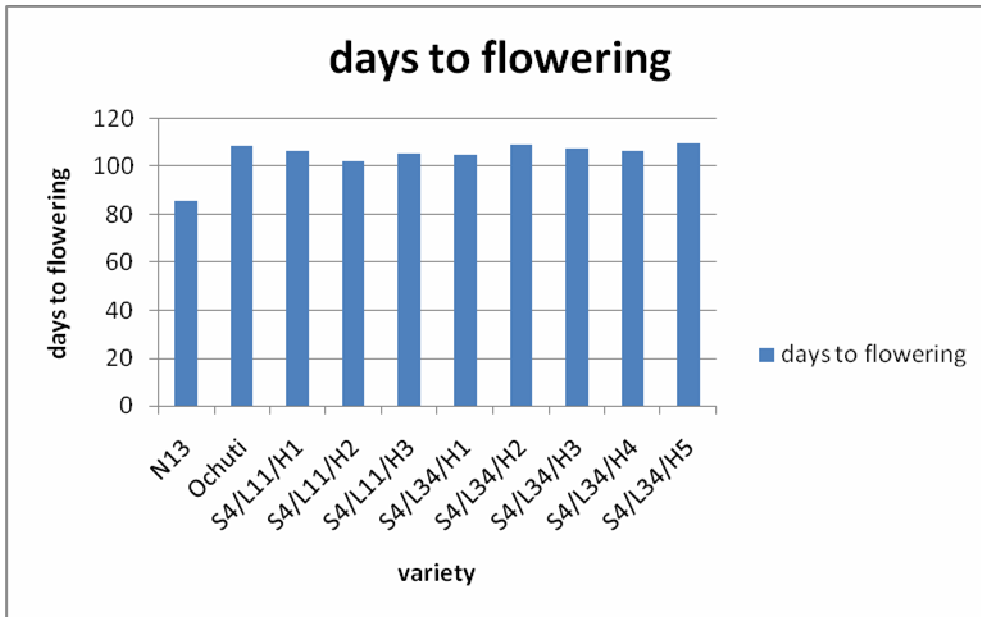
**Table 4.9: Agronomic traits for Alupe Season 2 (Oct 2010-March 2011)**

Variety	stand after thinning	seedling vigor	number of tillers	plan height (cm)	days to flowering	number of plants logged	dry panicle weight (Kgs)	grain weight (Kgs)	100 seed weight	Yield (Kgs/M <sup>2</sup> )	Host damage rate
N13	90.25 <sub>a</sub>	3.75 <sub>a</sub>	36.75 <sub>a</sub>	115 <sub>a</sub>	85.75 <sub>a</sub>	11.8 <sub>a</sub>	0.3 <sub>a</sub>	0.15 <sub>a</sub>	2.9 <sub>a</sub>	1.31 <sub>a</sub>	1.75 <sub>a</sub>
Ochuti	83.75 <sub>a</sub>	3 <sub>a</sub>	47.75 <sub>a</sub>	155 <sub>a</sub>	108.5 <sub>cde</sub>	19.2 <sub>a</sub>	0.7 <sub>a</sub>	0.45 <sub>a</sub>	2.5 <sub>a</sub>	3.94 <sub>a</sub>	3 <sub>b</sub>
S4/L11/H1	92.5 <sub>a</sub>	3 <sub>a</sub>	43.25 <sub>a</sub>	160 <sub>a</sub>	106.5 <sub>cde</sub>	18.2 <sub>a</sub>	0.7 <sub>a</sub>	0.45 <sub>a</sub>	2.175 <sub>a</sub>	3.94 <sub>a</sub>	2.25 <sub>ab</sub>
S4/L11/H2	95.75 <sub>a</sub>	2.5 <sub>a</sub>	60.25 <sub>a</sub>	152.5 <sub>a</sub>	102.5 <sub>b</sub>	19 <sub>a</sub>	0.525 <sub>a</sub>	0.325 <sub>a</sub>	2.425 <sub>a</sub>	2.84 <sub>a</sub>	1.875 <sub>a</sub>
S4/L11/H3	95.5 <sub>a</sub>	2.75 <sub>a</sub>	56.5 <sub>a</sub>	127.5 <sub>a</sub>	105.5 <sub>bcd</sub>	20 <sub>a</sub>	0.3 <sub>a</sub>	0.188 <sub>a</sub>	2.25 <sub>a</sub>	1.64 <sub>a</sub>	2.375 <sub>ab</sub>
S4/L34/H1	100.5 <sub>a</sub>	2.75 <sub>a</sub>	53.5 <sub>a</sub>	153.8 <sub>a</sub>	105.25 <sub>bc</sub>	24.8 <sub>a</sub>	0.9 <sub>a</sub>	0.575 <sub>a</sub>	2.425 <sub>a</sub>	5.03 <sub>a</sub>	2.5 <sub>ab</sub>
S4/L34/H2	92.25 <sub>a</sub>	2 <sub>a</sub>	59.25 <sub>a</sub>	153.8 <sub>a</sub>	109.25 <sub>de</sub>	22.8 <sub>a</sub>	0.7 <sub>a</sub>	0.425 <sub>a</sub>	2.325 <sub>a</sub>	3.72 <sub>a</sub>	2.625 <sub>ab</sub>
S4/L34/H3	95.5 <sub>a</sub>	2.5 <sub>a</sub>	46.5 <sub>a</sub>	142.5 <sub>a</sub>	107.75 <sub>cde</sub>	24 <sub>a</sub>	0.625 <sub>a</sub>	0.338 <sub>a</sub>	2.525 <sub>a</sub>	2.95 <sub>a</sub>	2.5 <sub>ab</sub>
S4/L34/H4	88 <sub>a</sub>	2.75 <sub>a</sub>	55.25 <sub>a</sub>	156.2 <sub>a</sub>	106.75 <sub>cde</sub>	17 <sub>a</sub>	0.5 <sub>a</sub>	0.312 <sub>a</sub>	2.4 <sub>a</sub>	2.73 <sub>a</sub>	2.25 <sub>ab</sub>
S4/L34/H5	96.25 <sub>a</sub>	2.75 <sub>a</sub>	47.5 <sub>a</sub>	158.8 <sub>a</sub>	109.75 <sub>e</sub>	24.2 <sub>a</sub>	0.625 <sub>a</sub>	0.425 <sub>a</sub>	2.525 <sub>a</sub>	3.72 <sub>a</sub>	2 <sub>ab</sub>
<b>Grand mean</b>	93	2.77	50.6	147.5	104.8	20.1	0.588	0.36	2.445	3.18	2.312
<b>S.E</b>	17.9	0.732	8.44	12.41	1.036	5.42	0.3119	0.1424	0.258	1.806	0.304
<b>LSD</b>	12.34	1.062	17.32	25.45	2.126	11.12	0.64	0.4235	0.53	3.706	0.624
<b>C.V reps</b>	6.4	15.1	15.7	6.7	0.5	14.1	20.9	23.8	4.7	27.2	4.5
<b>M.S</b>	152.2	0.536	142.5	307.8	2.148	58.74	0.0665	0.0406	0.133	6.525	0.185
<b>P value</b>	0.785	0.199	0.165	0.016	<.001	0.393	0.617	0.571	0.353	0.64	0.012

- *The means in the same column followed by the same subscript letters are not statistically significant according to Boniferroni test  $t p \leq 5\%$ .*

Severity is an ordinal data set. It was taken in a range from 1-5, 1 indicating resistance while 5 indicates susceptibility. From Table 4.4 above, the LSD test at 5% shows the

genotypes differed in host damage rate. Ochuti gave a score of 3 indicating it is fairly tolerant to *S. hermonthica* attack. The backcross genotypes performed better than Ochuti indicating that they have higher *S. hermonthica* resistance than Ochuti. Furthermore, the backcross genotypes scored less than the parental check N13. This is an indication that their resistance is an intermediate between Ochuti and N13 as would be expected.



**Figure 4.5 showing the days to flowering of the backcross genotypes and their parental lines**

The results show, N13 flowered and reached maturity earlier than Ochuti. N13 took an average of 85 days to flower. The backcross lines and Ochuti had slight variations in flowering. In assessing recovery, the days to flowering is a good indicator of difference between the backcross lines and the farmer preferred variety. From this we can see that the recovery is good. This is because of the little variation observed between Ochuti and the backcross progenies.

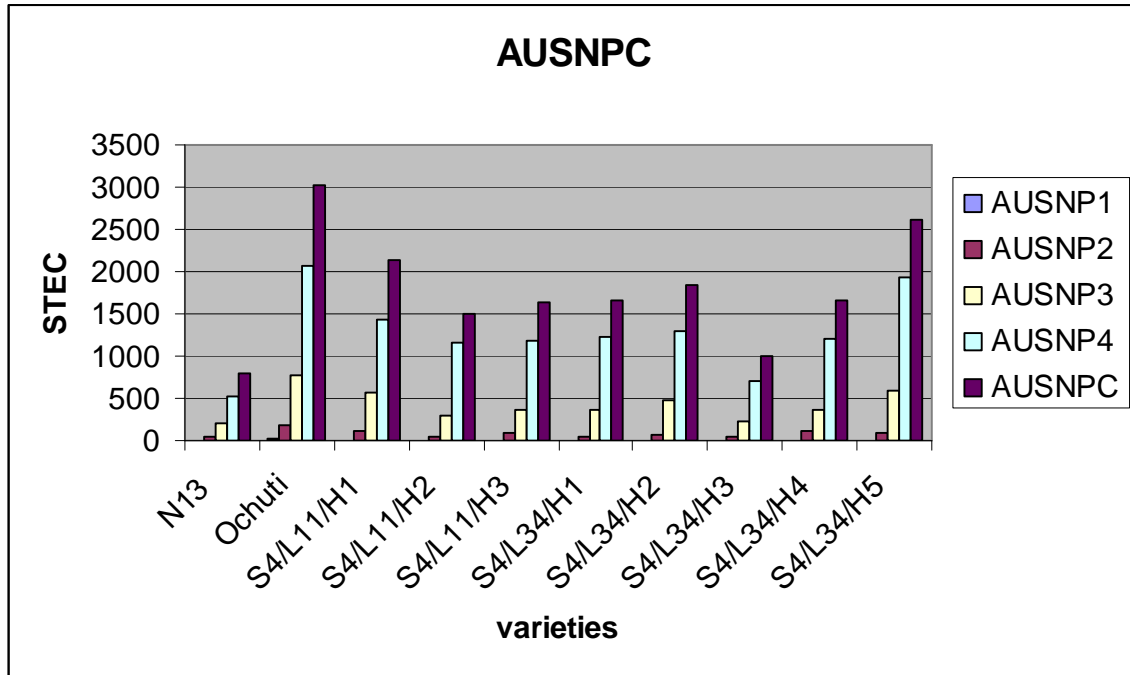
**Table 4.10: Area under *Striga* Number Progressive Curve (AUSNPC) value for Alupe season 2 (Oct 2010-March 2011)**

Variety	AUSNP1	AUSNP2	AUSNP3	AUSNP4	AUSNPC	<i>Strigacapsule</i> formation	<i>Striga</i> flowering
N13	5.2 <sub>a</sub>	51 <sub>a</sub>	214 <sub>a</sub>	528 <sub>a</sub>	798 <sub>a</sub>	7.8 <sub>a</sub>	10.75 <sub>a</sub>
Ochuti	15.8 <sub>a</sub>	177 <sub>a</sub>	768 <sub>a</sub>	2063 <sub>a</sub>	3024 <sub>a</sub>	21.2 <sub>a</sub>	42 <sub>a</sub>
S4/L11/H1	7 <sub>a</sub>	117 <sub>a</sub>	567 <sub>a</sub>	1440 <sub>a</sub>	2132 <sub>a</sub>	13.5 <sub>a</sub>	17.5 <sub>a</sub>
S4/L11/H2	0 <sub>a</sub>	46 <sub>a</sub>	294 <sub>a</sub>	1169 <sub>a</sub>	1508 <sub>a</sub>	7.5 <sub>a</sub>	13.75 <sub>a</sub>
S4/L11/H3	3.5 <sub>a</sub>	82 <sub>a</sub>	362 <sub>a</sub>	1186 <sub>a</sub>	1634 <sub>a</sub>	10.8 <sub>a</sub>	17 <sub>a</sub>
S4/L34/H1	5.2 <sub>a</sub>	54 <sub>a</sub>	369 <sub>a</sub>	1234 <sub>a</sub>	1662 <sub>a</sub>	14.2 <sub>a</sub>	6 <sub>a</sub>
S4/L34/H2	1.8 <sub>a</sub>	65 <sub>a</sub>	472 <sub>a</sub>	1298 <sub>a</sub>	1838 <sub>a</sub>	10 <sub>a</sub>	15.25 <sub>a</sub>
S4/L34/H3	8.8 <sub>a</sub>	56 <sub>a</sub>	228 <sub>a</sub>	705 <sub>a</sub>	998 <sub>a</sub>	8.2 <sub>a</sub>	9.5 <sub>a</sub>
S4/L34/H4	8.8 <sub>a</sub>	107 <sub>a</sub>	359 <sub>a</sub>	1195 <sub>a</sub>	1670 <sub>a</sub>	9.8 <sub>a</sub>	14 <sub>a</sub>
S4/L34/H5	10.5 <sub>a</sub>	89 <sub>a</sub>	588 <sub>a</sub>	1934 <sub>a</sub>	2622 <sub>a</sub>	18 <sub>a</sub>	20 <sub>a</sub>
<b>Grand mean</b>	6.7	84	422	1275	1788	12.1	16.6
<b>S.E</b>	0.935	1.084	11.72	0.74	0.775	0.767	0.784
<b>LSD</b>	13.93	177.7	739.1	1922.3	2807.1	18.62	30.05
<b>C.V reps</b>	32.4	15.1	8.3	4	4.4	23.2	24.7
<b>M.S</b>	1.747	2.35	1.744	1.094	1.201	1.176	1.229
<b>P value</b>	0.445	0.936	0.936	0.808	0.856	0.653	0.505

- *The means in the same column followed by the same subscript letters are not statistically significant according to Boniferroni test  $t p \leq 5\%$ .*

There was no significant difference between the varieties in their AUSNPC. This is as indicated by  $P \leq 0.05$ . Ochuti however supported the largest number of *S. hermonthica* plants per given area. The backcross genotypes had fewer *S. hermonthica* plants as compared to their susceptible check Ochuti; this is an indication that the backcross generations had the *S. hermonthica* resistance QTL. Genotype S4/L34/H3 which had the lowest number of *S. hermonthica* plants supported. S2/L34/H1 had the lowest number of plants forming capsules. This again demonstrates that the *S. hermonthica* resistance QTL

was conferring resistance under field conditions. This is important as it leads to the reduction of the *S. hermonthica* seed bank in the soil.



**Figure 4.6 Progressive *Striga* counts for the test varieties.**

N13 had the least count being the resistant check and Ochuti, the susceptible check had the highest count. The best performer for the backcross line is S4/L34/H3. AUSNPC is the final count. The progression from count one to five is rapid as compared to the backcross genotypes.

#### 4.1.3.2 Evaluation of *Striga* resistance at Kibos field station in Kisumu

##### Kibos season 1; May 2010-Sep 2010

The results show that, genotypes S4/L34/H3 and S4/L34/H4 had lower amounts of *S. hermonthica* plants growing per given plot compared to Ochuti, though not statistically significant.

**Table 4.11: Area under *Striga* Number Progressive Curve for Kibos season 1 (May 2010-Sep2010)**

Variety	AUSNP1	AUSNP2	AUSNP3	AUSNP4	AUSNPC	<i>Striga</i> plants forming capsules	<i>Striga</i> plants flowering
N13	0 <sub>a</sub>	4.7 <sub>a</sub>	4.7 <sub>a</sub>	30 <sub>a</sub>	40 <sub>a</sub>	2 <sub>a</sub>	2 <sub>a</sub>
Ochuti	0 <sub>a</sub>	7 <sub>a</sub>	63 <sub>a</sub>	180 <sub>a</sub>	250 <sub>a</sub>	16.7 <sub>a</sub>	18.7 <sub>a</sub>
S4/L11/H1	0 <sub>a</sub>	9.3 <sub>a</sub>	79.3 <sub>a</sub>	257 <sub>a</sub>	345 <sub>a</sub>	29.3 <sub>a</sub>	28 <sub>a</sub>
S4/L11/H2	0 <sub>a</sub>	2.3 <sub>a</sub>	60.7 <sub>a</sub>	231 <sub>a</sub>	294 <sub>a</sub>	22.7 <sub>a</sub>	22.3 <sub>a</sub>
S4/L11/H3	0 <sub>a</sub>	4.7 <sub>a</sub>	116.7 <sub>a</sub>	327 <sub>a</sub>	448 <sub>a</sub>	30 <sub>a</sub>	30 <sub>a</sub>
S4/L34/H1	0 <sub>a</sub>	18.7 <sub>a</sub>	84 <sub>a</sub>	273 <sub>a</sub>	376 <sub>a</sub>	32.3 <sub>a</sub>	31.3 <sub>a</sub>
S4/L34/H2	0 <sub>a</sub>	16.3 <sub>a</sub>	102.7 <sub>a</sub>	289 <sub>a</sub>	408 <sub>a</sub>	31.3 <sub>a</sub>	30.3 <sub>a</sub>
S4/L34/H3	0 <sub>a</sub>	9.3 <sub>a</sub>	44.3 <sub>ab</sub>	121 <sub>a</sub>	175 <sub>a</sub>	14.3 <sub>a</sub>	14 <sub>a</sub>
S4/L34/H4	0 <sub>a</sub>	7 <sub>a</sub>	42 <sub>ab</sub>	128 <sub>a</sub>	177 <sub>a</sub>	14.7 <sub>a</sub>	15 <sub>a</sub>
S4/L34/H5	0 <sub>a</sub>	14 <sub>a</sub>	58.3 <sub>a</sub>	168 <sub>a</sub>	240 <sub>a</sub>	20.7 <sub>a</sub>	20 <sub>a</sub>
<b>Grand mean</b>	0	9.3	65.6	200	275	21.4	21.2
<b>S.E</b>	0	1.337	0.734	0.818	0.814	9.81	9.62
<b>LSD</b>	0	20.05	64	180	238.5	20.61	20.22
<b>C.V reps</b>	0	26	3	3	3.9	4.2	5.4
<b>M.S</b>	0	2.682	0.808	1.005	0.995	144.3	138.9
<b>P value</b>	0	0.955	0.004	0.041	0.027	0.106	0.124

- *the means in the same column followed by the same subscript letters are not statistically significant according to Boniferroni test  $t p \leq 5\%$*
- *The means are transformed by taking their natural logs*



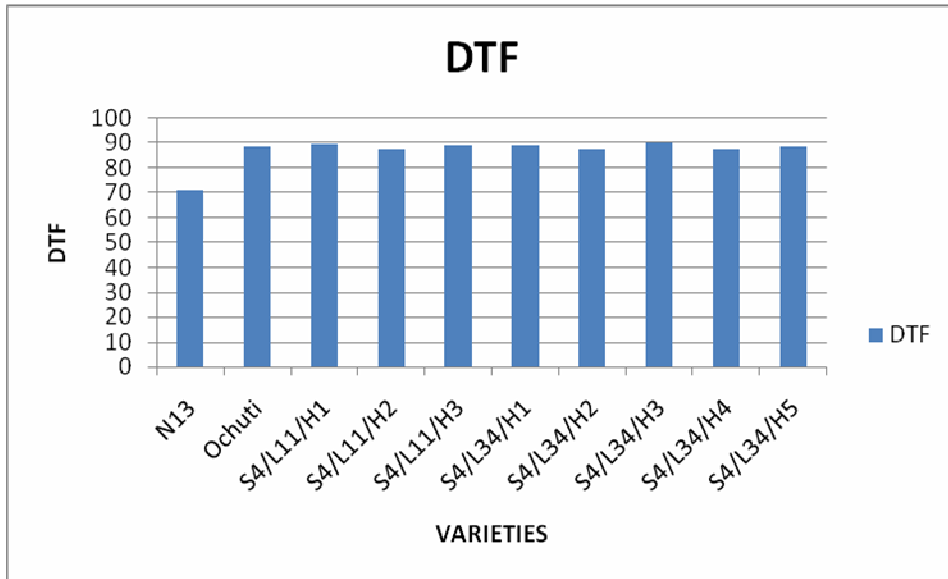
**Table 4.12: Agronomic traits for Kibos season 1 (May 2010-Sep2010)**

Variety	stand after thinning	seedling vigor	number of tillers	days to flowering	plant height (cm)	dry panicle weight (gms)	100 seed weight	grain weight (Kgs)	yield (Kgs/M <sup>2</sup> )
N13	16 <sub>a</sub>	2 <sub>a</sub>	14	71 <sub>a</sub>	112.9 <sub>a</sub>	12.2 <sub>a</sub>	2.26 <sub>a</sub>	0.961 <sub>a</sub>	0 <sub>a</sub>
Ochuti	36.67 <sub>b</sub>	1 <sub>a</sub>	50.7	88.67 <sub>b</sub>	208.5 <sub>b</sub>	63 <sub>b</sub>	2.151 <sub>a</sub>	0.95 <sub>a</sub>	0.109 <sub>a</sub>
S4/L11/H1	34.33 <sub>b</sub>	1 <sub>a</sub>	43.3	89.67 <sub>b</sub>	210.3 <sub>ab</sub>	58.5 <sub>b</sub>	2.291 <sub>a</sub>	1.3 <sub>a</sub>	0.149 <sub>a</sub>
S4/L11/H2	36.67 <sub>b</sub>	1 <sub>a</sub>	42.3	87.67 <sub>b</sub>	204.4 <sub>ab</sub>	59.5 <sub>b</sub>	2.359 <sub>a</sub>	1.05 <sub>a</sub>	0.12 <sub>a</sub>
S4/L11/H3	31.33 <sub>b</sub>	1.333 <sub>a</sub>	41.7	89.33 <sub>b</sub>	195.7 <sub>ab</sub>	49.6 <sub>ab</sub>	2.163 <sub>a</sub>	0.8 <sub>a</sub>	0.091 <sub>a</sub>
S4/L34/H1	36 <sub>b</sub>	1.333 <sub>a</sub>	40	89 <sub>b</sub>	215.1 <sub>ab</sub>	64.1 <sub>b</sub>	2.154 <sub>a</sub>	1.05 <sub>a</sub>	0.12 <sub>a</sub>
S4/L34/H2	33.67 <sub>b</sub>	1.333 <sub>a</sub>	37.7	87.67 <sub>b</sub>	218.1 <sub>ab</sub>	69.8 <sub>b</sub>	2.494 <sub>a</sub>	0.967 <sub>a</sub>	0.111 <sub>a</sub>
S4/L34/H3	38.33 <sub>b</sub>	1 <sub>a</sub>	31.3	90 <sub>b</sub>	217.6 <sub>ab</sub>	62.9 <sub>b</sub>	2.032 <sub>a</sub>	1.167 <sub>a</sub>	0.133 <sub>a</sub>
S4/L34/H4	29.33 <sub>b</sub>	1 <sub>a</sub>	27.7	87.67 <sub>b</sub>	204 <sub>ab</sub>	47 <sub>ab</sub>	2.394 <sub>a</sub>	0.55 <sub>a</sub>	0.063 <sub>a</sub>
S4/L34/H5	31 <sub>b</sub>	1 <sub>a</sub>	22.7	88.67 <sub>b</sub>	197.9 <sub>ab</sub>	65.4 <sub>b</sub>	2.303 <sub>a</sub>	0.817 <sub>a</sub>	0.093 <sub>a</sub>
<b>Grand mean</b>	32.33	1.2	35.1	86.93	198.4	55.2	2.26	0.961	0.099
<b>S.E</b>	3.172	0.2722	7.73	2.54	16.55	9.88	0.239	0.396	0.043
<b>LSD</b>	6.663	0.5718	16.23	5.336	34.77	20.75	0.506	0.840	0.091
<b>C.V reps</b>	8.7	0	10.7	0.2	10.8	9.2	9	23.000	22.900
<b>M.S</b>	15.09	0.1111	89.56	9.678	410.8	146.4	0.085	0.235	0.003
<b>P value</b>	<.001	0.03	0.005	<.001	<.001	<.001	0.652	0.750	0.118

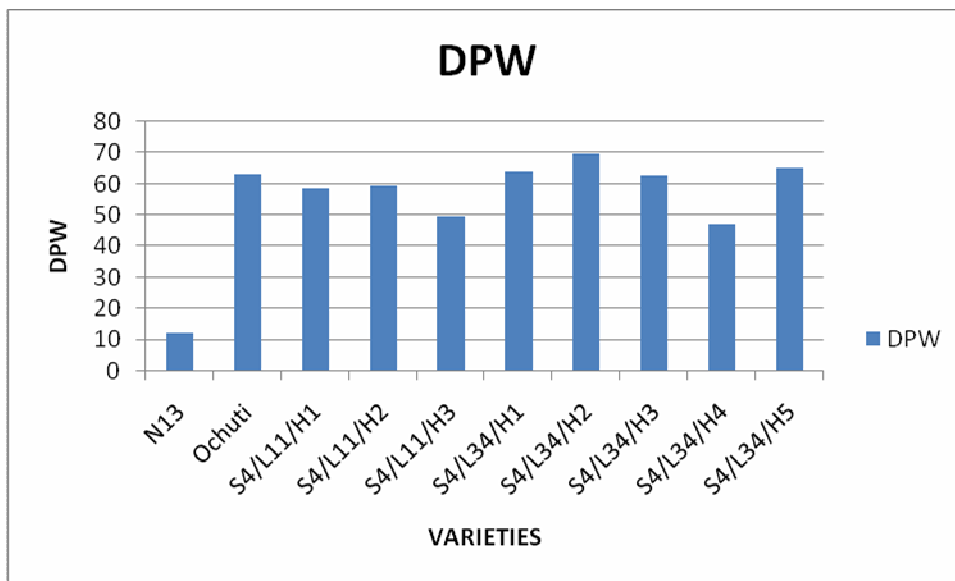
- *the means in the same column followed by the same subscript letters are not statistically significant according to Boniferroni test  $t p \leq 5\%$*

From the results, there was no significant difference between the genotypes in traits such as seedling vigor, *S. hermonthica* plants flowering and forming capsules and %100 seed weight. It appears in the backcross generations the *S. hermonthica* resistance QTL may have not been incorporated or may have been masked by the environment. However, the stand count for N13 seemed different from all other genotypes with a mean of 16 which is statistically different from means from the other genotypes. Other traits such as dry panicle weight, days to flowering, plant height and days to flowering, N13 is significantly different from all other varieties.

From this data, stand count, days to flowering plant height and panicle weight show a statistical significance at 95% level. This indicates difference within the varieties for these traits.



**Figure 4.7 Days to 50% flowering of the different genotypes and their parental checks**



**Figure 4.8 Dry panicle weight of the different genotypes and their parental checks**

The results show that, there was a lot of variation between the genotypes in dry panicle weight. N13 gave the least weight with a mean of 12.2gms, the highest weight was from S2/L34/H2 with a mean weight of 69.8gms.

### Season 2; Oct 2010- March 2010 for Kibos field station

The results show that the height of the genotypes varied. N13 being a shorter plant, had a height of 150cm. The variation in height between Ochuti and the backcross genotypes was very little and was not significant as per the Boniferroni test.

**Table 4.13: Agronomic traits for Kibos season 2 (Oct 2010-March 2011)**

Variety	stand after thinning	seedling vigor	number of tillers/ plot	days to flowering	plant height (cm)	number of plants logged	dry panicle weight (gms)	grain weight (gms)	% 100 seed weight	Host damage rate	Yield(Kgs/m <sup>2</sup> )
N13	63 <sub>a</sub>	1.414 <sub>a</sub>	273.8 <sub>b</sub>	70.75 <sub>a</sub>	150 <sub>a</sub>	2.75 <sub>a</sub>	1.31 <sub>a</sub>	0.975 <sub>a</sub>	2.742 <sub>a</sub>	1.573 <sub>a</sub>	0.124 <sub>a</sub>
Ochuti	62.5 <sub>a</sub>	1.104 <sub>a</sub>	139.5 <sub>ab</sub>	90.25 <sub>b</sub>	222.5 <sub>b</sub>	6 <sub>a</sub>	2.94 <sub>a</sub>	2.275 <sub>a</sub>	2.625 <sub>a</sub>	1.494 <sub>a</sub>	0.29 <sub>a</sub>
S4/L11/H1	62.5 <sub>a</sub>	1.104 <sub>a</sub>	143.8 <sub>ab</sub>	88.25 <sub>b</sub>	235 <sub>b</sub>	8 <sub>a</sub>	2.96 <sub>a</sub>	2.2 <sub>a</sub>	2.51 <sub>a</sub>	1.414 <sub>a</sub>	0.28 <sub>a</sub>
S4/L11/H2	63 <sub>a</sub>	1.104 <sub>a</sub>	81.2 <sub>a</sub>	88.5 <sub>b</sub>	225 <sub>b</sub>	6 <sub>a</sub>	2.49 <sub>a</sub>	1.75 <sub>a</sub>	2.525 <sub>a</sub>	1.653 <sub>a</sub>	0.223 <sub>a</sub>
S4/L11/H3	63 <sub>a</sub>	1.104 <sub>a</sub>	94 <sub>a</sub>	86.5 <sub>b</sub>	220 <sub>b</sub>	5 <sub>a</sub>	2.69 <sub>a</sub>	2 <sub>a</sub>	2.41 <sub>a</sub>	1.573 <sub>a</sub>	0.225 <sub>a</sub>
S4/L34/H1	62.25 <sub>a</sub>	1.207 <sub>a</sub>	119 <sub>ab</sub>	90 <sub>b</sub>	238.8 <sub>b</sub>	7.25 <sub>a</sub>	2.44 <sub>a</sub>	1.821 <sub>a</sub>	2.52 <sub>a</sub>	1.414 <sub>a</sub>	0.231 <sub>a</sub>
S4/L34/H2	63 <sub>a</sub>	1.104 <sub>a</sub>	97.8 <sub>a</sub>	87.5 <sub>b</sub>	237.5 <sub>b</sub>	5.5 <sub>a</sub>	2.7 <sub>a</sub>	2.05 <sub>a</sub>	2.458 <sub>a</sub>	1.573 <sub>a</sub>	0.261 <sub>a</sub>
S4/L34/H3	63 <sub>a</sub>	1 <sub>a</sub>	69.2 <sub>a</sub>	87 <sub>b</sub>	213.8 <sub>b</sub>	6.25 <sub>a</sub>	2.69 <sub>a</sub>	2.062 <sub>a</sub>	2.487 <sub>a</sub>	1.653 <sub>a</sub>	0.263 <sub>a</sub>
S4/L34/H4	63 <sub>a</sub>	1 <sub>a</sub>	115.2 <sub>ab</sub>	85.75 <sub>b</sub>	220 <sub>b</sub>	4.75 <sub>a</sub>	2.89 <sub>a</sub>	1.975 <sub>a</sub>	2.52 <sub>a</sub>	1.653 <sub>a</sub>	0.252 <sub>a</sub>
S4/L34/H5	62.25 <sub>a</sub>	1.104 <sub>a</sub>	80.2 <sub>a</sub>	88.75 <sub>b</sub>	230 <sub>b</sub>	6.75 <sub>a</sub>	2.51 <sub>a</sub>	1.925 <sub>a</sub>	2.31 <sub>a</sub>	1.573 <sub>a</sub>	0.245 <sub>a</sub>
<b>Grand mean</b>	62.75	1.124	121	86.33	219	5.83	2.56	1.902	2.51	1.56	1.557
<b>S.E</b>	0.471	0.117	45.7	2.661	11.95	0.38	0.475	0.3585	0.122	0.1	0.046
<b>LSD</b>	0.967	0.24	93.8	5.459	24.53	4.67	0.974	0.7355	0.251	0.2	0.094
<b>C.V reps</b>	0.8	7.4	11	0.7	2.3	11.5	9.6	8.6	2	5.1	8.6
<b>M.S</b>	0.4444	0.027	4181	14.16	285.7	0.29	0.4505	0.257	0.03	0.02	0.004
<b>P value</b>	0.464	0.076	0.007	<.001	<.001	0.42	0.077	0.073	0.114	0.14	0.073

- *the means in the same column followed by the same subscript letters are not statistically significant according to Boniferroni test t p ≤ 5%*

N13 took considerably fewer days to flower as compared to the other genotypes. This is because it is an early maturing variety. The other trait of interest was the number of tillers/plot is. This was highest in N13. Tillering is more in N13 because of its poor adaptability to Kenya sorghum growing environments. The main shoots die off then the plants form secondary shoots which form the main plant. This was from attack by shoot flies.

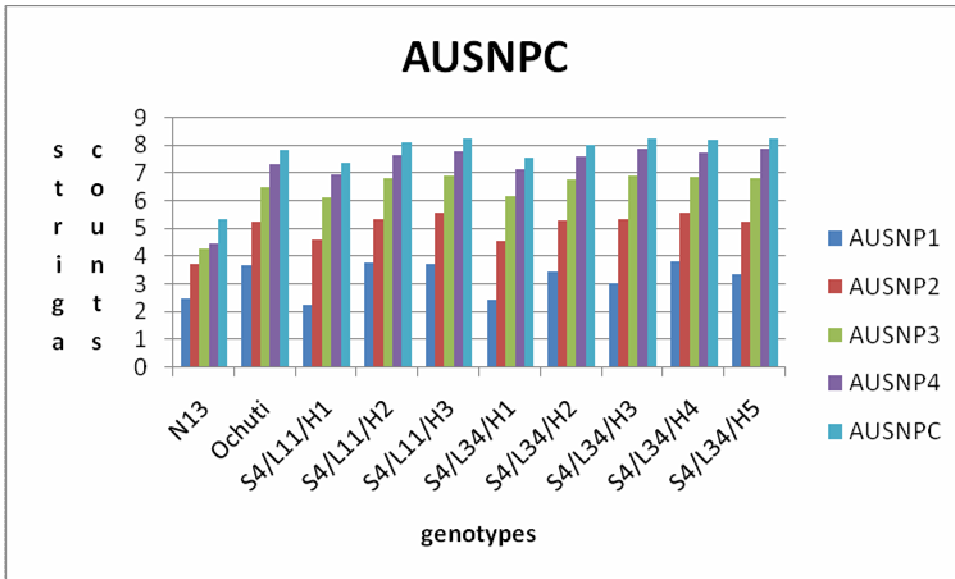
**Table 4.14: Area Under *Striga* Progressive Curve for Kibos season 2 (Oct 2010-March 2011)**

<b>Variety</b>	<b>AUSNP1</b>	<b>AUSNP2</b>	<b>AUSNP3</b>	<b>AUSNP4</b>	<b>AUSNPC</b>	<b><i>Striga</i> capsule formation</b>	<b><i>Striga</i> flowering</b>
N13	2.49 <sub>a</sub>	3.72 <sub>a</sub>	4.27 <sub>a</sub>	4.49 <sub>a</sub>	5.35 <sub>a</sub>	12.75 <sub>a</sub>	17 <sub>a</sub>
Ochuti	3.71 <sub>a</sub>	5.28 <sub>a</sub>	6.5 <sub>b</sub>	7.34 <sub>b</sub>	7.83 <sub>a</sub>	80.75 <sub>a</sub>	116 <sub>a</sub>
S4/L11/H1	2.24 <sub>a</sub>	4.63 <sub>a</sub>	6.15 <sub>ab</sub>	6.96 <sub>b</sub>	7.4 <sub>a</sub>	55.5 <sub>a</sub>	88.5 <sub>a</sub>
S4/L11/H2	3.77 <sub>a</sub>	5.37 <sub>a</sub>	6.81 <sub>b</sub>	7.66 <sub>b</sub>	8.1 <sub>a</sub>	108.75 <sub>a</sub>	157.2 <sub>a</sub>
S4/L11/H3	3.72 <sub>a</sub>	5.57 <sub>a</sub>	6.92 <sub>b</sub>	7.81 <sub>b</sub>	8.24 <sub>a</sub>	11.25 <sub>a</sub>	168.8 <sub>a</sub>
S4/L34/H1	2.43 <sub>a</sub>	4.57 <sub>a</sub>	6.2 <sub>ab</sub>	7.14 <sub>b</sub>	7.55 <sub>a</sub>	61.5 <sub>a</sub>	100.5 <sub>a</sub>
S4/L34/H2	3.48 <sub>a</sub>	5.3 <sub>a</sub>	6.77 <sub>b</sub>	7.61 <sub>b</sub>	8.05 <sub>a</sub>	81.25 <sub>a</sub>	147.2 <sub>a</sub>
S4/L34/H3	3.03 <sub>a</sub>	5.37 <sub>a</sub>	6.93 <sub>b</sub>	7.89 <sub>b</sub>	8.28 <sub>a</sub>	99.75 <sub>a</sub>	157.2 <sub>a</sub>
S4/L34/H4	3.84 <sub>a</sub>	5.57 <sub>a</sub>	6.88 <sub>b</sub>	7.75 <sub>b</sub>	8.2 <sub>a</sub>	122.75 <sub>a</sub>	167.8 <sub>a</sub>
S4/L34/H5	3.36 <sub>a</sub>	5.26 <sub>a</sub>	6.82 <sub>b</sub>	7.89 <sub>b</sub>	8.25 <sub>a</sub>	108 <sub>a</sub>	169.2 <sub>a</sub>
<b>Grand mean</b>	3.21	5.06	6.42	7.25	7.73	84.7	129
<b>S.E</b>	0.835	0.604	0.604	0.596	0.574	0.623	0.597
<b>LSD</b>	1.713	1.239	1.17	1.223	1.177	75.93	106.4
<b>C.V reps</b>	6.9	4.1	4.1	4.1	3.6	6.3	6
<b>M.S</b>	1.394	0.7297	0.73	0.71	0.658	0.776	0.7137
<b>Pvalue</b>	0.398	0.099	0.099	<.001	<.001	0.001	<.001

- *the means in the same column followed by the same subscript letters are not statistically significant according to Boniferroni test  $t p \leq 5\%$*
- *The means are transformed by taking their natural logs*

The results show that the AUSNPC of the genotypes had significant difference. This was especially so for the fourth progressive count labelled as AUSNPC4 and the final count

(AUSNPC). Some of the backcross genotypes showed a higher number of *S. hermonthica* plants supported per a given area than the susceptible check Ochuti. However S4/L11/H1 and S4/L34/H1 had fewer number of supported *S. hermonthica* plants, this is good indication of the incorporation of the *S. hermonthica* resistance QTL.



**Figure 4.9: Area Under *Striga* Number Progressive Curve (AUSNPC) for Kibos field station, planting season 2 (Oct 2010- March 2011)**

#### 4.1.4. Combined seasonal analysis for the two locations; Alupe and Kibos field stations

##### 4.1.4.1. Season; May 2010- Sep 2010

**Table 4.15; mean sums of squares showing the combined seasonal ANOVA data for Kibos and Alupe for Season 1(May 2010-Sep2010)**

Source	d.f	AUSNP3	AUSNP4	AUSNPC	Days to Flowering	Number of Tillers	Stand count	Plant Height	Panicle weight
Env	1	25904196***	187690907***	423456727***	721.1***	11097.6***	8283.8***	18253.3***	15183105**
Rep(Env)	2	260460	3243139	5257252	56.1	63.95	32.6	2864.2***	4404
Genotype	9	832510***	5288622***	12006937***	33.0	227.73***	1117.2***	6163.9***	137773**
Genotype*Env	9	722581**	4400746***	10168740***	211.3***	169.16**	541.3***	140.8	114903*
Error	36	200880	905772	2281020	52.3	48.61	32.63	336.6	44115

- *\*indicates P value 95%, \*\*indicates P value 99% and \*\*\*indicates P value 99.9%*

The results show that the two environmental factors of the locations; Kibos and Alupe are very different from each other. This is indicated by the level of significance (99.9). The sums of squares for the genotypic effect of AUSNPC3, AUSNPC4 and AUSNPC are large than the sums of squares of the G\*E effect. This is an indication that the variation contributed by the genotypes is higher as compared to the interaction effect. This therefore shows the stability of these traits as they are not largely influenced by the environment. With respect to plant height, the G\*E was not significant. The genotype also showed considerable variation for the traits being measured at P value  $\leq$  99% and 99.9%

The genotypes varied significantly for all but one of the traits indicated in Table 4.15 above.

**Table 4.16; Correlations for combined seasonal data for Alupe and Kibos season 1; May-Oct 2010**

	AUSNP1	AUSNP2	AUSNP3	AUSNP4	AUSNPC
100 seed weight	0.7042*	0.7108*	0.7661*	0.7923*	0.793*
days to flowering	-0.0882	-0.1199	-0.1481	-0.096	-0.113
dry panicle weight (gms)	0.7801*	0.8141*	0.8395*	0.8505*	0.8602*
grain weight (Kgs)	-0.4899*	-0.4865*	-0.5193*	-0.5423*	-0.5416*
number of tillers	-0.5689*	-0.5606*	-0.6076*	-0.6431*	-0.6387*
plant height (cm)	0.4445*	0.4748*	0.5223*	0.5693*	0.5586*
seedling vigor	0.486*	0.461*	0.4968*	0.5289*	0.5248*
stand after thinning	0.7102*	0.7212*	0.7448*	0.7378*	0.7522*
<i>Striga</i> capsule formation	-0.4035*	-0.415*	-0.4458*	-0.4748*	-0.4706*
<i>Striga</i> flowering	-0.2411	-0.2507	-0.2827	-0.3306	-0.3167
yield (Kgs/M2)	-0.4899*	-0.4865*	-0.5193*	-0.5423*	-0.5416*

- \*indicates P value 99%, \*\*indicates P value 99.9% one tailed

The results showed that the days to flowering, grain weight, number of tillers, *S. hermonthica* capsule formation, *S. hermonthica* flowering and yield are negatively correlated with the *S. hermonthica* counts. These traits are negatively affected by the amount of *S. hermonthica* in the fields. As the amount of *S. hermonthica* increases, these factors decrease.

#### 4.1.4.2 Season 2; Oct 2010-March 2011

**Table 4.17; mean sums of squares of combined seasonal ANOVA data for Kibos and Alupe for Season 2 (Oct 2010-March 2011)**

Source	d.f	AUSNPC4	Host damage rate	Days to Flowering	Number of Tillers	Seedling Vigor Score	Striga Capsule Formation	Grain Weight
Env	1	6.0238**	0.3781	6789.613***	100041***	43.5125***	79.476***	47.355***
Rep(Env)	2	0.0203	0.1781	5.979	1877	1.3125**	0.4341	0.0776
Genotype	9	3.2019**	0.3017	308.668***	5863**	0.9181**	2.0574*	0.397*
genotype*Env	9	1.6041	0.5795**	15.89	8328***	0.2069	2.1888*	0.1941
Error	36	0.9021	0.1869	8.153	2162	0.3477	0.9762	0.1711

- *\*indicates P value 95%, \*\*indicates P value 99% and \*\*\*indicates P value 99.9%*

From the results, there was a significant difference among the genotypes in the host damage rate, number of tillers formed and *S. hermonthica* capsule formation with respect to G\*E. The days to flowering, seedling vigor score and AUSNPC4 were however more stable with no significant variation due to the G\*E interaction. This is true for AUSNPC, days to flowering, seedling vigor score and grain weight. The genotypic partition of variance is larger than the G\*E partition as indicated in Table 4.17 above. This indicates stability of the genotypes as most of the observed variation is due to the genotypic variance. The genotypes differed significantly in all of the traits indicated except in host damage rate.

The results indicate that the correlation between the *S. hermonthica* counts and host damage rate is 99% significant. The damage increases as the counts increase with the highest value being observed at the fifth *S. hermonthica* count indicated as AUSNPC. The correlation between *S. hermonthica* counts and logging is negative with the highest value at AUSNPC1. This count is a summation of the counts at 6 and 8 weeks. Therefore



the plants are weaker and could not stand *S. hermonthica* attack. Logging reduces as more counts are taken. Other factors such seedling vigor, 100 seed weight, number of tillers per plot, days to flowering and yield are also negatively correlated with the *S. hermonthica* counts.

**Table 4.18; Correlation for combined seasonal data for Alupe and Kibos season 2; Oct 2010-Mar 2011**

	AUSNP1	AUSNP2	AUSNP3	AUSNP4	AUSNPC
grain weight	0.372**	0.362*	0.368**	0.313*	0.341*
number of plants logged	-0.434**	-0.316*	-0.212	-0.128	-0.176
panicle weight	0.350*	0.336*	0.344*	0.290*	0.317*
<i>Striga</i> capsule formation	0.539**	0.687**	0.778**	0.769**	0.779**
<i>Striga</i> flowering	0.517**	0.666**	0.759**	0.753**	0.761**
Seedlingvigorscore	-0.352*	-0.374**	-0.372**	-0.330*	-0.354*
Yield	-0.348*	-0.325*	-0.289*	-0.240	-0.269
days to flowering	-0.326	-0.227	-0.148	-0.059	-0.104
number of tillers/plot	0.071	-0.091	-0.166	-0.235	-0.204
plant height (cm)	0.311	0.319	0.364**	0.328	0.345
Host damage rate	0.384**	0.418**	0.444**	0.431**	0.443**
stand after thinning	-0.373**	-0.303*	-0.281	-0.208	-0.244
100 seed weight	0.039	-0.103	-0.165	-0.215	-0.192

- \*indicates *P* value 99%, \*\*indicates *P* value 99.9% one tailed

There is a strong positive correlation between *S. hermonthica* capsule formation and *S. hermonthica* flowering with AUSNPC, this is as shown in table 4.13. This indicates that with higher *S. hermonthica* counts, the rate of reproductive success will be very high as more *S. hermonthica* plants tend to flower and hence form capsules. Host damage rates are also partially positively correlated with AUSNPC. This is as shown by the figure on table 4.18. This is expected as higher infestation lead to even higher damage on the host plant.

#### 4.1.5 Principle Component analysis based on combined seasonal data

##### 4.1.5.1 Principle components for season 1 data; May 2010-Oct 2010

In season 1, the principle components 1 and 2 had a total variation of 97.92% and 1.22% respectively. The variation in PC1 was majorly from AUSNP (counts data) with the largest variation being from AUSNPC with 0.80744 and dry panicle weight (0.112). The other agronomic traits gave little contribution towards PC1 with the lowest variation contribution being from yield ( $\text{kgm}^{-2}$ ) giving 0.00001.

PC2 variation was majorly from yield ( $\text{kgm}^{-2}$ ) giving 0.93696 and the dry panicle weight contributing negatively with -0.3299. The other factors gave little contribution to variation ranging from 0.001-0.01. This contribution is either positive or negative.

**Table 4.19; Principle component analysis for combined season 1 data**

	PC1	PC2
100seedweight	0.00369	-0.01526
AUSNP1	0.0132	-0.0087
AUSNP2	0.05573	-0.00775
AUSNP3	0.20427	0.05261
AUSNP4	0.53424	0.04743
AUSNPC	0.80744	0.08358
Daystoflowering	-0.0002	-0.00584
Drypanicleweight (gm)	0.11235	-0.3299
Grainweight(Kg)	-0.00006	0.00082
Numberofillers	-0.00254	0.01925
Plantheightcm	0.0043	0.01265
Seedlingvigor	0.00017	-0.00154
Standafterthinning	0.0034	0.00352
<i>Strigacapsuleformation</i>	-0.0014	0.01259
<i>Strigaflowering</i>	-0.00088	0.01255
Yield Kg/M2	-0.00001	0.00009
Yield Kg/ha	-0.07033	0.93696
Variance proportion	97.92%	1.22%

#### 4.1.5.2 Principle components for season 2 data; Oct 2010-Mar 2011

The proportion of variance contributed by PC1 was higher than PC2. PC1 gave 98.83% of the total variation while PC2 gave 1.16%. Looking at loading from PC1, the highest variation was attributed to Yield (kg/ha) giving a loading of -0.99963. The AUSNP counts data also contributed highly with positive factors towards PC1. The other agronomic factors gave low contributions towards variability with 100 seed weight and seedling vigor score giving no contribution to the total variation. This is as shown in table 4.20 below.

**Table 4.20; Principle component analysis for combined season 2 data**

PC ANALYSIS		
	1	2
100seedweight(gm)	0	-0.00002
AUSNP1	0.00048	0.00906
AUSNP2	0.00212	0.05739
AUSNP3	0.00661	0.22221
AUSNP4	0.01334	0.52827
AUSNPC	0.02254	0.81692
Grain weight	0.00001	0.00005
Number of plants logged	-0.00002	-0.00001
Panicle weight	0.00001	0.00005
<i>Striga</i> capsule formation	0.00002	0.00043
<i>Striga</i> flowering	0.00003	0.00043
Seedling vigor score	0	-0.00004
Yield kg/m <sup>2</sup>	-0.00003	-0.00001
Yield kg/ha	-0.99963	0.02706
Daysto50%flowering	-0.0003	0.00025
Standafterthinning	-0.0004	-0.00079
Plantheight(cm)	0.00067	0.00467
Numberofillers/plot	0.00091	-0.00792
Variance proportion	98.83%	1.16%

AUSNP traits were also the factors giving a large percent of variation towards PC2 with the highest contribution being from AUSNPC (0.8169) and AUSNP4 (0.53). The lowest contribution was from yield (kgm<sup>-2</sup>) and the number of plants logged giving -0.000.

## 4.2 DISCUSSION

A MAB scheme aims at transferring a gene/several genes a QTL of specific advantage from a donor plant to a recessive plant which in most cases is an elite variety but lacking in certain attribute of agronomic importance. It is however of importance to regain the recessive plants' genome wholly with exception of the target allele from the donor plant, (Semagnet *al.*, 2006b, Babuet *al.*, 2002).

The most important factors to consider therefore in a MAB scheme are; the number of target genes, the genetic distance between the target gene and the flanking markers and the number of genotypes to be handled in every generation, (Babuet *al.*, 2002).

From the BMZ project the initial crosses were made and the lines were advanced to BC<sub>2</sub>F<sub>3</sub> generation using the MAB scheme. However there is limited information on both the phenotypic and genotypic data of these materials.

The number of targeted QTL was five, these were on chromosomes A, B, I, and two on chromosome J. Each of these markers was flanked by two markers except the QTL on chromosome B which had three markers. The markers used were found to be polymorphic. This allowed selection as identification of plants having QTL was enabled.

According to Visscher *et al.*,(1996), two markers flanking a QTL can be used in foreground screening if the inter-marker distance does not exceed 20centimorgans (cM).

If the inter-marker distance is higher than 20cM then more markers should be used. This is due to the increased chances of cross over and hence recombination. In this study the inter-marker distance varied from 10-45cM. The makers used were however few hence chances of loss of the QTL due to recombination were very high.

From the sixty eight genotyped individuals of BC<sub>2</sub>F<sub>3</sub>, nine samples were selected each having a single introgression QTL. These were the materials received from BMZ project. From the cross BC<sub>2</sub>F<sub>3</sub> x Ochuti, four plants were selected each having single introgression QTL. The QTL captured was on chromosome J.

QTL B had three markers, two flanking markers and one mid marker. As observed, some plants had two out of the expected three markers. This therefore may indicate partial introgression of the QTL B.

The observed low number of captured QTL may be due to the low numbers of progeny acquired after advancing the generation by backcrossing. De Villiers and Semagn., 2009 reported on the number of progeny required to capture a given number of QTL e.g. to capture three QTL, ninety progenies or successful crosses should be made. However in this study the number of successful crosses varied from ten to thirty, this is sufficient to capture one to two QTL.

From the field work, a total of eighteen traits were evaluated over two seasons; long and short rains. The fields used were Kibos and Alupe. These have been identified as hot spots for the *S. hermonthica* weed in Kenya, (Hausmann *et al.*, 2004). To assess a plants' resistance to the *S. hermonthica* weed, selection is based on the assessment of the plant/ host damage, the number of emerged *S. hermonthica* plants, the yield of the plant under *S. hermonthica* infested conditions and the agronomic characteristics of the host. Hausmann *et al.*, (2000) listed these traits as useful in assessing resistance to *S. hermonthica* in sorghum. A total of ten genotypes were evaluated. This included two parental checks. This is important as it offers a comparison among the genotypes.

The AUSNPC is an important measure of resistance to *S. hermonthica*. A resistant genotype is expected to support fewer if any *S. hermonthica* plants. AUSNPC gives a summation of all the *S. hermonthica* plants emerging per plot over the entire season. It therefore is a good measure of comparing the performance of genotypes in the field with respect to the number of *Striga* plants supported over a given season. Haussmann *et al.*, (2000) derived the formula from Shanner and Finney., (1977) area under disease progressive curve (AUDPC).

The backcross genotypes gave lower *S. hermonthica* counts than Ochuti but higher than N13. This is an indication of the backcross genotypes being more resistant to *S. hermonthica* than Ochuti. It also shows the backcross genotypes had the *S. hermonthica* resistance QTL introgressed. The number of *S. hermonthica* resistance QTL introgressed was however low, one QTL. They therefore did not perform as the resistant check N13 which has five *S. hermonthica* resistance QTL. According to (Grenier *et al.*, 2007) each of the *S. hermonthica* resistance QTL explains a given amount of phenotypic variation observed. This was from an experiment done in Kenya and Mali using two sets of RIP which were derived from a cross between N13 and E36-1. Table 4.16 below shows the percent phenotypic variation explained by each of the *S. hermonthica* resistance QTL.

**Table 4.21: The percent phenotypic variance explained by a single QTL**

Set	LG01-185	LG02-65	LG06-90	LG05-5	LG05-70
1	24	17	30	19	15
2	21	22	15	12	29

Table adopted from Grenier *et al.*, 2007

Therefore with only one QTL introgressed, the percent phenotypic variance observed is lower.

Among the backcross genotypes, S4/L34/H3 performed well giving lower *S. hermonthica* counts than the other backcross genotypes in most of the growing seasons. In assessing resistance to the *S. hermonthica* weed, Omanyia *et al.*, (1999) used AUSNPC as a selection factor. He recommended its use in assessing *S. hermonthica* resistance among genotypes.

*S. hermonthica* weed suppresses yields in sorghum. It can lead up to 100% yield loss, (Berneret *et al.*, 1995). This was not so in this study. The backcross genotypes yielded desirably. This is a good indication of resistance to *S. hermonthica*. Ochuti, the susceptible check also yielded well out yielding the backcross genotypes and N13 in some trials. N13 yielded poorly in all the trials. N13 is an Indian durra. It is not adapted to the growing conditions in Kenya; this explains its low yields. Ochuti on the other hand has been characterized as tolerant to *S. hermonthica* (Ndung'u, 2009). This was from a survey conducted in Nyanza and Western administrative provinces in Kenya. From his findings he stated that Ochuti is also a landrace grown by farmers in Kenya over a long time and farmers characterized it as tolerant to *S. hermonthica* because despite the *S. hermonthica* problem, Ochuti yields are still desirable.

Host damage rate was also assessed. This was done on a scale of 1-5, 1 indicating resistance while 5 indicated susceptible. The damage caused on the plant included stunting, leaf chlorosis, wilting, leaf and stem firing. In her review paper, Haussmann *et al.*, (2000) advised the use of 1-9 severity classes, 1 indicating resistance while 9 indicates susceptible. Classes 1-5 were used as it eases the process of scoring and eliminates the confusion caused by having many intermediate classes. N13 was scored under the class 1 indicating resistance to *S. hermonthica*. The backcross genotypes scored a range of

classes from 1.5-2.6. This indicates resistant and fairly resistant. Ochuti scored under class 3. This indicates tolerance to *S. hermonthica* attack. Gethi and Smith., (2004) used host damage rating to select among the single crosses of hybrid maize for resistance to both *S. hermonthica* and *S. asiatica*. They however recommended the use of host damage rating with *S. hermonthica* emergence counts (STEC) and *S. hermonthica* vigor rating (SVR) as the use of only one factor will not be efficient.

The number of *S. hermonthica* flowering plants and forming capsules is important. This helps in assessing the reproductive success of the *S. hermonthica* plants and hence the number of seeds going back to the soil. From this study, the number of *S. hermonthica* plants flowering and hence forming capsules were observed to decline from the last *S. hermonthica* count. This is an indication that the *S. hermonthica* plants die off before they reach the reproductive stage. This is important observation as the numbers of seeds added to the soil are lower and hence leading to the reduction of the *S. hermonthica* weed seed bank.

The agronomic traits that were evaluated were; days to 50% flowering of the sorghum plants, dry panicle weight, 100 seed weight, plant height, plant tillering, seedling vigor and stand count. From the first season data (May2010-Oct2010), correlating the *S. hermonthica* counts data to the days to 50% flowering, grain weight *S. hermonthica* capsule formation, *S. hermonthica* flowering and plant tillering gave negative indices. On the other hand, 100 seed weight, dry panicle weight, plant height, seedling vigor and stand count were positively correlated to the *S. hermonthica* counts data. In the second season (Oct 2010-Mar2011), grain weight, *S. hermonthica* capsule formation and *S. hermonthica* flowering were positively correlated to the *S. hermonthica* counts data.



Yield was negatively correlated to the *S. hermonthica* counts data. This was highly significant P value 99%. The correlation index was however low  $\leq 0.5$ . Olakojo and Olaoye, (2011) reported the same findings while working on *S. asiatica* infestation on maize in Nigeria. They concluded that these traits are controlled by different genes and therefore one trait cannot be used to select for another.

Host damage rate was positively correlated to the *S. hermonthica* counts data with a low index but of high significance ratio of P value 99.9. This indicates that the damage observed on the host increases with increasing number of *S. hermonthica* counts. This is in agreement with Gethi and Smith, (2004) reported findings in maize. They reported that *S. hermonthica* counts and host damage rates were positively correlated with low index. They therefore suggested the use of one trait to select for the other.

## CHAPTER 5

### CONCLUSION AND RECOMMENDATIONS

#### 5.1 Conclusion

This study was designed to improve a farmer preferred sorghum variety in Kenya, Ochuti. The aim of the study was to transfer *S. hermonthica* resistance QTL from a resistant donor variety N13 into Ochuti through marker assisted introgression and evaluate the *S. hermonthica* resistant backcross progenies in *S. hermonthica* prevalent areas in Kenya.

The use of marker assisted selection was an advantage to the study as it shortened the amount of time taken to develop the *S. hermonthica* resistant backcross material. Selection was done of the material containing the *S. hermonthica* resistant QTL after every cross was made. Only the progeny containing the resistant QTL were advanced to the next generation. This saved on time, space and resources.

The materials were evaluated in the field at backcross two. A MAS generated genotype can be evaluated in the field as early as backcross two because performing background selection fastens recovery of the elite parent background. At backcross two, the background of the elite parent is recovered up to 99% hence eliminating the need to perform multiple successive backcrosses to recover the elite parents' background.

Out of sixty BC2S2 plant genotyped, nine plants were identified to contain at least one QTL each. From the genotyping results of one hundred and eighty seven BC3F1 plants, four plants were identified to contain one QTL each.

The results from the field analysis indicated that the backcross genotypes performed well. They gave very good yield under *S. hermonthica* pressure. They also gave lower AUSNPC as compared to the susceptible parent Ochuti. Lastly, they gave lower scores

when assessed from host damage rates for striga. These low scores indicate resistance to the *S. hermonthica* weed.

The generated backcross genotypes are of high value. These genotypes have been selected to go into another project designed by ASARECA. Seed increase is to be done for *S. hermonthica* resistant genotypes generated in Kenya, Sudan, Eritrea and Rwanda. These will then undergo multi environmental tests in these countries after which the seed will be officially released. However, the seed need further evaluation for the presence of QTL as moving from one generation to another due to recombination, some QTL are lost.

## **5.2 Recommendations**

- i. Further work should be done on the striga tolerant materials generated from this project. For example incorporating the material generated in integrated pest control program in order to overcome the striga menace.
- ii. With marker assisted backcross, in order to prevent losses of QTL occasioned by subsequent backcrossing, I recommend that selection of plants with a good elite parent background and containing resistance QTL be done at backcross generation 2 or 3. This should then be later used in pyramiding schemes in order to come up with elite material having an increased number of QTL.
- iii. There is also a high variation of Striga spp. in the soil. The *S. hermonthica* weed could therefore adapt and overcome the type of resistance option being used leading to increased infestation. A single QTL therefore is not sufficient to offer complete resistance to the striga weed. I recommend the use of more than two QTL for better resistance or tolerance to the striga weed.

- iv. Genotypes developed in breeding schemes with good characteristics should be used in breeding programs as parental materials to produce elite varieties with combined number of desired traits instead of starting from scratch repeatedly.

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## Appendices

Appendix 1: Table showing analysis of variance for Alupe season 1

100 seed weight						
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	

replication stratum	2	4	2	0.02	
replication.*Units* stratum identity	9	659.3	73.3	0.68	0.716
Residual	18	1934.8	107.5		
Total	29	2598.1			

Days to flowering					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	242.07	121.03	1.28	
replication.*Units* stratum identity	9	1333.47	148.16	1.56	0.201
Residual	18	1707.93	94.89		
Total	29	3283.47			

Dry panicle weight (gms)					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	22550	11275	0.13	
replication.*Units* stratum identity	9	2266608	251845	2.86	0.028
Residual	18	1585493	88083		
Total	29	3874651			

Number of tillers					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	4.067	2.033	0.27	
replication.*Units* stratum identity	9	255.867	28.43	3.71	0.009
Residual	18	137.933	7.663		
Total	29	397.867			

Plant height (cm)					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	541.7	270.8	1.03	
replication.*Units* stratum identity	9	30750	3416.7	13.02	<.001
Residual	18	4725	262.5		

Total	29	36016.7			
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Seedling vigor					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	1.5167	0.7583	2.35	
replication.*Units* stratum identity	9	8.5083	0.9454	2.93	0.025
Residual	18	5.8167	0.3231		
Total	29	15.8417			

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Stand after thinning					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	33.07	16.53	0.33	
replication.*Units* stratum identity	9	13812.17	1534.69	30.59	<.001
Residual	18	902.93	50.16		
Total	29	14748.17			

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<i>Striga</i> flowering					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	10.4	5.2	0.2	
replication.*Units* stratum identity	9	350.7	38.97	1.47	0.233
Residual	18	477.6	26.53		
Total	29	838.7			

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<i>Striga</i> capsule formation					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	7.2	3.6	0.29	
replication.*Units* stratum identity	9	122.03	13.56	1.08	0.421
Residual	18	225.47	12.53		
Total	29	354.7			

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Yield

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	138	69	0.07	
replication.*Units* stratum					
identity	9	23499.8	2611.1	2.65	0.038
Residual	18	17764.3	986.9		
Total	29	41402.1			

AUSNP1					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	0.375	0.188	0.1	
replication.*Units* stratum					
variety	9	62.235	6.915	3.74	0.008
Residual	18	33.293	1.85		
Total	29	95.904			

AUSNP2					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	1.279	0.64	0.26	
replication.*Units* stratum					
variety	9	111.534	12.393	5	0.002
Residual	18	44.64	2.48		
Total	29	157.454			

AUSNP3					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	1.2868	0.6434	0.97	
replication.*Units* stratum					
variety	9	52.9288	5.881	8.87	<.001
Residual	18	11.9336	0.663		
Total	29	66.1492			

AUSNP4					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.

replication stratum	2	1.2543	0.6271	2		
replication.*Units* stratum						
variety	9	33.1707	3.6856	11.75	<.001	
Residual	18	5.6454	0.3136			
Total	29	40.0704				

AUSNP						
Source of variation	d.f.	s.s.	m.s.	v.r.	F	pr.
replication stratum	2	1.0208	0.5104	1.36		
replication.*Units* stratum						
variety	9	38.3112	4.2568	11.33	<.001	
Residual	18	6.7634	0.3757			
Total	29	46.0954				

Appendix 2: Table showing analysis of variance for Alupe season 3

<i>Striga</i> Flowering						
Source of variation	d.f.	s.s.	m.s.	v.r.	F	pr.
rep stratum	3	9.326	3.109	2.53		
rep.*Units* stratum						
identity	9	10.451	1.161	0.94	0.505	
Residual	27	33.196	1.229			
Total	39	52.973				

<i>Striga</i> Capsule Formation						
Source of variation	d.f.	s.s.	m.s.	v.r.	F	pr.
rep stratum	3	6.906	2.302	1.96		
rep.*Units* stratum						
identity	9	8.046	0.894	0.76	0.653	
Residual	27	31.761	1.176			
Total	39	46.714				

Panicle Weight						
Source of variation	d.f.	s.s.	m.s.	v.r.	F	pr.

rep stratum	3	0.24178	0.08059	1.21	
rep.*Units* stratum identity	9	0.48032	0.05337	0.8	0.617
Residual	27	1.79502	0.06648		
Total	39	2.51713			

Grain Weight					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	0.14368	0.04789	1.18	
rep.*Units* stratum identity	9	0.31381	0.03487	0.86	0.571
Residual	27	1.09511	0.04056		
Total	39	1.5526			

Yield (Kgs/M2)					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	22.562	7.521	1.15	
rep.*Units* stratum identity	9	45.502	5.056	0.77	0.64
Residual	27	176.166	6.525		
Total	39	244.23			

Severity					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	0.3187	0.1062	0.57	
rep.*Units* stratum identity	9	5.0312	0.559	3.02	0.012
Residual	27	4.9937	0.185		
Total	39	10.3438			

100 seed weight					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	0.393	0.131	0.98	
rep.*Units* stratum Identity	9	1.404	0.156	1.17	0.353
Residual	27	3.602	0.1334		

Total	39	5.399			
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Days to 50% flowering					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	8.5	2.833	1.32	
rep.*Units* stratum					
Identity	9	1769	196.556	91.5	<.001
Residual	27	58	2.148		
Total	39	1835.5			

Number of plants lodged					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	240.6	80.2	1.37	
rep.*Units* stratum					
Identity	9	583.1	64.79	1.1	0.393
Residual	27	1585.9	58.74		
Total	39	2409.6			

Number of tillers/plant					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	1900.1	633.4	4.45	
rep.*Units* stratum					
Identity	9	2052.6	228.1	1.6	0.165
Residual	27	3846.4	142.5		
Total	39	7799.1			

AUSNP					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	2.791	0.93	0.77	
rep.*Units* stratum					
VARIETIES	9	5.493	0.61	0.51	0.856
Residual	27	32.42	1.201		
Total	39	40.703			

AUSNP1					
Source of	d.f.	s.s.	m.s.	v.r.	F pr.

variation					
rep stratum	3	5.016	1.672	0.96	
rep.*Units* stratum					
VARIETIES	9	16.134	1.793	1.03	0.445
Residual	27	47.158	1.747		
Total	39	68.309			

AUSNP2					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	9.14	3.047	1.3	
rep.*Units* stratum					
VARIETIES	9	7.979	0.887	0.38	0.936
Residual	27	63.441	2.35		
Total	39	80.559			

AUSNP3					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	6.048	2.016	1.16	
rep.*Units* stratum					
VARIETIES	9	5.926	0.658	0.38	0.936
Residual	27	47.094	1.744		
Total	39	59.069			

AUSNP4					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	2.158	0.719	0.66	
rep.*Units* stratum					
VARIETIES	9	5.633	0.626	0.57	0.808
Residual	27	29.535	1.094		
Total	39	37.325			

Appendix 3: Table showing analysis of variance for Kibos season 1



Yield (Kgs/M2)					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	0.010286	0.005143	1.84	
replication.*Units* stratum identity	9	0.047814	0.005313	1.9	0.118
Residual	18	0.050318	0.002795		
Total	29	0.108418			

Grain weight(Kgs)					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	0.9737	0.4869	2.07	
replication.*Units* stratum identity	8	1.1667	0.1458	0.62	0.75
Residual	16	3.765	0.2353		
Total	26	5.8067			

<i>Striga</i> capsule formation					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	15.8	7.9	0.05	
replication.*Units* stratum identity	9	2553.9	283.8	1.97	0.106
Residual	18	2597.5	144.3		
Total	29	5167.2			

Striga flowering					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	26.5	13.2	0.1	
replication.*Units* stratum identity	9	2333.5	259.3	1.87	0.124
Residual	18	2500.2	138.9		
Total	29	4860.2			

Stand after thinning					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	157.07	78.53	5.2	
replication.*Units* stratum					

identity	9	1114	123.78	8.2	<.001
Residual	18	271.6	15.09		
Total	29	1542.67			

#### Seedling vigor

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	0	0	0	
replication.*Units* stratum					
identity	9	2.8	0.3111	2.8	0.03
Residual	18	2	0.1111		
Total	29	4.8			

#### Plant height(cm)

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	9194.6	4597.3	11.19	
replication.*Units* stratum					
identity	9	25992.9	2888.1	7.03	<.001
Residual	18	7393.8	410.8		
Total	29	42581.3			

#### Number of tillers

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	281.27	140.63	1.57	
replication.*Units* stratum					
identity	9	3316.13	368.46	4.11	0.005
Residual	18	1612.07	89.56		
Total	29	5209.47			

#### Dry panicle weight (gms)

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	515.4	257.7	1.76	
replication.*Units* stratum					
identity	9	7476	830.7	5.68	<.001
Residual	18	2634.7	146.4		
Total	29	10626.2			

Days to flowering					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	0.467	0.233	0.02	
replication.*Units* stratum identity	9	865.2	96.133	9.93	<.001
Residual	18	174.2	9.678		
Total	29	1039.867			

100 seed weight					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	0.75246	0.37623	4.41	
replication.*Units* stratum identity	8	0.50961	0.0637	0.75	0.652
Residual	16	1.36592	0.08537		
Total	26	2.62799			

AUSNP					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	0.8349	0.4175	0.42	
replication.*Units* stratum VARIETIES	9	25.7292	2.8588	2.87	0.027
Residual	18	17.9045	0.9947		
Total	29	44.4687			

AUSNP1					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
replication stratum	2	0	0		
replication.*Units* stratum VARIETIES	9	0	0		
Residual	18	0	0		
Total	29	0			

AUSNP2					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.

replication stratum	2	3.25	1.625	0.61		
replication.*Units* stratum						
VARIETIES	9	7.852	0.872	0.33	0.955	
Residual	18	48.277	2.682			
Total	29	59.378				

AUSNP3						
Source of variation	d.f.	s.s.	m.s.	v.r.	F	pr.
replication stratum	2	0.2614	0.1307	0.16		
replication.*Units* stratum						
VARIETIES	9	31.2851	3.4761	4.3	0.004	
Residual	18	14.5456	0.8081			
Total	29	46.0922				

AUSNP4						
Source of variation	d.f.	s.s.	m.s.	v.r.	F	pr.
replication stratum	2	0.444	0.222	0.22		
replication.*Units* stratum						
VARIETIES	9	23.48	2.609	2.6	0.041	
Residual	18	18.088	1.005			
Total	29	42.013				

Appendix 4: Table showing analysis of variance for Kibos season 2

Yield(Kgs/m <sup>2</sup> )						
Source of variation	d.f.	s.s.	m.s.	v.r.	F	pr.
rep stratum	3	0.012889	0.004296	1.03		
rep.*Units* stratum						
identity	9	0.076693	0.008521	2.04	0.073	
Residual	27	0.112613	0.004171			
Total	39	0.202195				

Seedling Vigor Score						
Source of variation	d.f.	s.s.	m.s.	v.r.	F	pr.

rep stratum	3	0.20589	0.06863	2.51	
rep.*Units* stratum identity	9	0.49756	0.05528	2.02	0.076
Residual	27	0.73776	0.02732		
Total	39	1.44121			

SVR					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	0.19194	0.06398	3.35	
rep.*Units* stratum identity	9	0.29296	0.03255	1.71	0.136
Residual	27	0.5152	0.01908		
Total	39	1.0001			

<i>Striga</i> Flowering					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	2.1428	0.7143	1	
rep.*Units* stratum identity	9	33.4143	3.7127	5.2	<.001
Residual	27	19.2686	0.7137		
Total	39	54.8257			

<i>Striga</i> Capsule Formation					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	1.9834	0.6611	0.85	
rep.*Units* stratum identity	9	30.1698	3.3522	4.32	0.001
Residual	27	20.9533	0.776		
Total	39	53.1064			

Number of Plants Logged					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	1.2857	0.4286	1.5	
rep.*Units* stratum identity	9	2.7498	0.3055	1.07	0.416
Residual	27	7.7236	0.2861		

Total	39	11.759			
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Panicle weight(Kg)					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	1.8072	0.6024	1.34	
rep.*Units* stratum identity	9	8.1706	0.9078	2.01	0.077
Residual	27	12.1647	0.4505		
Total	39	22.1424			

Grain weight					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	0.7942	0.2647	1.03	
rep.*Units* stratum identity	9	4.726	0.5251	2.04	0.073
Residual	27	6.9395	0.257		
Total	39	12.4597			

100 seed weight(gms)					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	0.07561	0.0252	0.85	
rep.*Units* stratum identity	9	0.48385	0.05376	1.8	0.114
Residual	27	0.80502	0.02982		
Total	39	1.36448			

Stand after thinning					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	7.5	2.5	5.62	
rep.*Units* stratum identity	9	4	0.4444	1	0.464
Residual	27	12	0.4444		
Total	39	23.5			

Severity					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.

rep stratum	3	1.9	0.6333	3.35	
rep.*Units* stratum identity	9	2.9	0.3222	1.71	0.136
Residual	27	5.1	0.1889		
Total	39	9.9			

Plant height(cm)					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	772.5	257.5	0.9	
rep.*Units* stratum identity	9	23790	2643.3	9.25	<.001
Residual	27	7715	285.7		
Total	39	32277.5			

Number of tillers/plant					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	5312	1771	0.42	
rep.*Units* stratum identity	9	125665	13963	3.34	0.007
Residual	27	112882	4181		
Total	39	243859			

Days to 50% flowering					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	10.47	3.49	0.25	
rep.*Units* stratum identity	9	1152.02	128	9.04	<.001
Residual	27	382.27	14.16		
Total	39	1544.77			

<b>AUSNP</b>					
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	2.3366	0.7789	1.18	
rep.*Units* stratum VARIETIES	9	28.4207	3.1579	4.8	<.001
Residual	27	17.772	0.6582		

Total	39	48.5292				
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#### AUSNP1

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	1.451	0.484	0.35	
rep.*Units* stratum					
VARIETIES	9	13.751	1.528	1.1	0.398
Residual	27	37.646	1.394		
Total	39	52.848			

#### AUSNP2

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	1.315	0.4383	0.6	
rep.*Units* stratum					
VARIETIES	9	12.3625	1.3736	1.88	0.099
Residual	27	19.7023	0.7297		
Total	39	33.3798			

#### AUSNP3

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	1.9504	0.6501	1	
rep.*Units* stratum					
VARIETIES	9	23.5387	2.6154	4.02	0.002
Residual	27	17.5702	0.6507		
Total	39	43.0593			

#### AUSNP4

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
rep stratum	3	2.7069	0.9023	1.27	
rep.*Units* stratum					
VARIETIES	9	37.6206	4.1801	5.88	<.001
Residual	27	19.1793	0.7103		



Total 39 59.5068

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Appendix 5: Table showing the nanodrop reading for the first filial generation

Sample ID	ng/ul	A260	A280	260/280	260/230
1	251.91	5.038	3.07	1.64	1.28
2	318.54	6.371	3.715	1.71	1.19
3	715.57	14.311	7.573	1.89	1.62
4	222.52	4.45	2.545	1.75	1.36
5	327.04	6.541	3.537	1.85	1.63
6	384.56	7.691	4.228	1.82	1.42
7	134.77	2.695	1.523	1.77	1.15
8	204.42	4.088	2.353	1.74	1.35
9	355.7	7.114	3.781	1.88	1.63
10	405.59	8.112	4.876	1.66	1.42
11	338.35	6.767	3.635	1.86	1.6
12	286.53	5.731	3.324	1.72	1.34
13	297.32	5.946	3.495	1.7	1.33
13	280.26	5.605	3.073	1.82	1.33
14	222.01	4.44	2.368	1.88	1.96
15	440.78	8.816	4.598	1.92	1.81
16	126.1	2.522	1.454	1.73	1.47
17	239	4.78	3.036	1.57	1.16
18	546.83	10.937	6.158	1.78	1.85
19	146.26	2.925	1.541	1.9	2.03
20	243.28	4.866	2.534	1.92	1.92
21	800.42	16.008	8.088	1.98	1.88
22	347.97	6.959	3.837	1.81	1.87
23	435.14	8.703	4.72	1.84	1.52
24	298.73	5.975	3.424	1.75	1.22
25	248	4.96	2.948	1.68	1.4
26	264.46	5.289	3.034	1.74	1.14
27	2.73	0.055	0.067	0.82	2.09
28	249.78	4.996	2.778	1.8	1.3
29	174.91	3.498	2.016	1.74	1.1
30	264.71	5.294	2.7	1.96	2.25
31	245.24	4.905	2.726	1.8	1.3
32	305.39	6.108	3.187	1.92	1.85
33	127.92	2.558	1.485	1.72	1.15
34	112.49	2.25	1.27	1.77	1.25
35	160.38	3.208	1.795	1.79	1.21
36	69.5	1.39	0.843	1.65	0.95
37	90.54	1.811	1.04	1.74	1.25
38	109.4	2.188	1.401	1.56	0.68
39	80	1.6	1.115	1.43	0.57
40	72.36	1.447	0.81	1.79	1.37
41	456.17	9.123	4.683	1.95	1.65
42	548.87	10.977	6.358	1.73	1.62
43	-233.37	-4.667	-1.594	2.93	NaN

43	619.92	12.398	6.125	2.02	2.25
44	438.51	8.77	4.604	1.9	1.74
45	318.29	6.366	4.268	1.49	0.9
45	269.03	5.381	3.106	1.73	1.38
46	397.77	7.955	4.362	1.82	1.41
47	106.8	2.136	1.137	1.88	1.24
48	299.66	5.993	3.139	1.91	2.08
49	114.89	2.298	1.407	1.63	1.09
50	62.84	1.257	0.755	1.66	1.03
51	43.61	0.872	0.467	1.87	1.62
52	129.34	2.587	2.093	1.24	0.96
53	130.31	2.606	1.432	1.82	1.62
54	121.19	2.424	1.44	1.68	0.96
55	161.69	3.234	1.842	1.76	1.25
56	199.61	3.992	2.279	1.75	1.23
57	279.45	5.589	3.022	1.85	1.52
58	165.2	3.304	1.912	1.73	1.18
59	583.83	11.677	5.955	1.96	1.98
60	212.02	4.24	2.29	1.85	1.42
61	150.47	3.009	1.62	1.86	1.75
62	287.11	5.742	3.212	1.79	1.27
63	149.3	2.986	1.71	1.75	1.23
64	248.94	4.979	2.67	1.86	1.51
65	613.11	12.262	6.178	1.98	1.88
66	304.67	6.093	3.272	1.86	1.52
67	399.69	7.994	4.182	1.91	1.72
68	324.17	6.483	3.735	1.74	1.14
69	213.36	4.267	2.385	1.79	1.18
70	371.25	7.425	3.951	1.88	1.59
71	253.23	5.065	2.861	1.77	1.16
72	203.71	4.074	2.302	1.77	1.13

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