

**Breeding Maize (*Zea mays* L.) for Resistance to *Striga asiatica* and *S. hermonthica*, and compatibility to *Fusarium oxysporum* f.sp. *strigae* in
Tanzania**

By

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THESIS ABSTRACT

Maize (*Zea mays* L., 2n=2x=20), is the third most important staple food crop after wheat (*Triticum aestivum* L.) and rice (*Oryza sativa* L.) globally. Maize has multiple uses, including for food, feed, and as a source of raw material for starch, oil, and beverage industries. In Tanzania, maize is the main staple food crop with an average consumption of about 73 kg/person/year. However, maize production and productivity in the country are hindered by biotic and abiotic stresses, and socio-economic constraints. *Striga* is one of the main biotic constraints, causing yield losses of 18 to 100% in Tanzania. *Striga asiatica* and *S. hermonthica* are the dominant spp. across the country, causing substantial yield losses on maize, sorghum, millet, and upland rice. Various *Striga* control options have been recommended and deployed, including cultural, chemical and biological control methods, and host resistance. However, no single management option is effective in controlling *Striga* infestations. An integrated *Striga* management approach is proposed for maize production, based on host resistance, combined with the fungal biocontrol agent of *Striga*, namely *Fusarium oxysporum* f. sp. *strigae* (*FOS*) and farmer-compatible agronomic practices. This approach would be effective, economic, and environmentally friendly. Therefore, the overall aim of this study was to develop maize genotypes resistant to *S. asiatica* and *S. hermonthica*, and compatible with *FOS* in Tanzania.

The specific objectives of this study were to: (i) assess maize production constraints, traits preference and current *Striga* control options in western Tanzania for farmers consultation and to guide breeding; (ii) characterise maize genotypes for resistance to *S. asiatica* and *S. hermonthica* and compatibility with *FOS* in Tanzania; (iii) determine the genetic diversity of maize genotypes with different levels of resistance to *S. asiatica* and *S. hermonthica* based on phenotypic data and simple sequence repeats markers to select desirable and complementary parents for breeding and (iv) assess newly developed hybrids of maize genotypes for yield and yield components, *Striga* resistance and *FOS* compatibility, and to select experimental hybrids for future breeding.

In the first study a participatory rural appraisal (PRA) exercise was conducted across four districts, eight wards and 16 villages in western Tanzania, involving 324 farmers. Data on major maize production constraints were collected using a semi-structured questionnaire with 166 farmers, focus group discussions with 158 farmers and field observations following transect walks. The results indicated that drought (reported by 97.2% respondents), *Striga* infestation (93.1%), field insect pests (90.1%), storage insects (72.7%) and lack of capital (55.6%) were the major limiting factors for maize production in the study areas. Further, about 59% and 45% of the interviewed farmers used *Striga*-susceptible improved varieties and

farmer-saved maize seed, respectively. Therefore, the development and deployment of improved maize genotypes with *Striga* resistance and farmers' preferred traits and *FOS* compatibility should be welcomed by the farmers.

In the second study, 56 genetically diverse maize genotypes were screened for resistance to *S. hermonthica* (*Sh*) and *S. asiatica* (*Sa*), and *FOS* compatibility. The experiment was laid out using a split-plot design; *FOS* was the main plot, and maize genotypes were the sub-plot treatments with three replications. Data on crop growth, grain yield, and *Striga* parameters were collected. Inoculation of maize seeds with *FOS* significantly ($P<0.001$) reduced both *Sh* and *Sa* infestations. This suggests that the test genotypes possess sufficient genetic variability from which selection of maize genotypes resistant to *Sh* and *Sa* could be made. Compared to untreated controls, *FOS* inoculated maize evaluated in *Sh*, and *Sa* infested soils increased grain yield by 5.2% and 3.4%, respectively. *FOS* significantly suppressed the number of emerged *Sa* and *Sh* plants, which should reduce their populations in the long term. Overall, 23 maize genotypes were selected as the best parental materials for developing *Striga* resistant cultivars in Tanzania.

In the third study, a set of 51 maize genotypes were assessed using phenotypic traits and *Sa* and *Sh* resistance parameters under controlled conditions. The test genotypes were further profiled using 10 diagnostic simple sequence repeat (SSR) markers to complement the phenotyping data. Significant ($P<0.05$) genotypic variation was recorded among the test genotypes for key agronomic traits and resistance to *Striga* spp. There was marked genetic variation, and resistant genotypes could be selected for *Striga* resistance breeding. The selected SSR markers were highly polymorphic. The mean polymorphism information content (PIC) value was 0.73, ranging from 0.41 to 0.92, suggesting high allelic diversity among the assessed maize genotypes. The analysis of molecular variance (AMOVA) revealed that within genotypes, among genotypes, and population variances accounted for 66.8%, 32.6%, and 0.6% of the total genotypic variation. Cluster analysis based on morphological and molecular markers grouped the genotypes into three main groups, irrespective of their geographic origin. SSR markers showed maize genotypes TZA2263 and JL08, TZA4320 and JL12, TZA4205 and JL20, TZA1780 and JL05, TZA2761 and JL01, TZA604 and JL18, TZA4010 and JL12 were the most genetically divergent pairs. These are valuable sources of genetic variation for *Striga* resistance breeding in Tanzania.

To achieve the last objective, 20 parental genotypes involving nine female parents selected for their *FOS* compatibility, adaptability, and farmer preferred traits, and 11 male parents possessing *Striga* resistance, were crossed using a North Carolina design II. The 99

experimental hybrids and three checks were field evaluated, with and without *FOS* treatment, at three *Striga*-infested sites in western Tanzania using a 9 x 12 α -lattice design with two replications. Data on agro-morphological traits of maize and *Striga* parameters were collected and analysed. Both the general combining ability (GCA) and specific combining ability (SCA) had significant ($P < 0.05$) effects on the assessed maize agronomic traits and *Striga* parameters, with and without *FOS* treatment, except for the *Striga* damage rating on eight and 10 weeks after planting under *FOS* treatment. This identified the importance of both additive and non-additive gene action. However, additive gene action was more important than non-additive gene action. Hybrid x location interaction effects were significant ($P < 0.01$) for days to 50% anthesis, days to 50% silking, grain yield, *Striga* emergence count at eight, and 10 weeks after planting with and without *FOS* treatment, and *Striga* damage rating at eight and 10 weeks after planting without *FOS* inoculation. *FOS*-treated progenies had fewer emerged *Striga* plants than untreated controls, confirming the efficacy of *FOS* in controlling *Striga*. Parental genotypes SITUKA M1, TZA4010, TZA4016, TZA4203, JL01, JL05, JL13, and JL17 showed negative GCA effects for all *Striga* parameters and relatively positive GCA effects for grain yield in a desirable direction. Maize hybrids TZA4010xJL13, TZA4010xJL05, TZA1780xJL18 were selected for their desirable grain yield and *Striga* resistance, while the progenies TZA2263xJL13 and TZA4203xJL18 were selected for *Striga* resistance. The new hybrids are recommended for *Striga* resistance breeding in Tanzania or similar agro-ecologies.

Overall, this study documented the present maize production constraints, trait preferences, and *Striga* management practices among smallholder farmers` in western Tanzania. In addition, the study identified new maize genotypes with farmers` preferred traits, superior agronomic performance, *Striga* resistance and *FOS* compatibility that can be used either in maize breeding programs or recommended for commercial production in Tanzania.

DECLARATION

I, John Lobulu, declare that

1. The research reported in this thesis, except where otherwise indicated, is my original research.
2. This thesis has not been submitted for any degree or examination at any other university.
3. This thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons.
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Signed:



.....
John Lobulu

As the candidate's supervisors, we agree to the submission of this thesis:



.....
Prof. Hussein Shimelis (Supervisor)



.....
Prof. Mark Laing (Co-Supervisor)

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DEDICATION

This thesis is dedicated to my parents, Lobulu Loatha (late) and Ngoondiyoi Samaito, for their sacrifice to send me to school. My wife, Stella A. Meeng`ieng`a and our daughters: Naserian, Naatha and Nanyori.

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LIST OF ABBREVIATIONS AND ACRONYMS

ACCI	African Centre for Crop Improvement
AD	Anthesis date
AFLP	Amplified fragment length polymorphism
AGB	Above ground biomass
AGRA	Alliance for a Green Revolution in Africa
AMOVA	Analysis of molecular variance
ANOVA	Analysis of variance
ASI	Anthesis-silking interval
CGIAR	Consultative Group on International Agricultural Research
CTAB	Cetyl-tetramethyl ammonium bromide
CV	Coefficient of variation
CIMMYT	International Maize and Wheat Improvement Centre
DES _a	Number of days taken for the first <i>S. asiatica</i> plant to emerge above the ground
DES _h	Number of days taken for <i>S. hermonthica</i> plant to emerge above the ground
DF	Degrees of freedom
DNA	Deoxyribonucleic acid
DM	Days to maturity
FAO	Food and Agriculture Organisation of the United Nations
FAW	Fall armyworm
FGDs	Focus group discussions
EH	Ear height
Env	Environment
F1	Filial generation one
FOS	<i>Fusarium oxysporum</i> f.sp. <i>strigae</i>
GCA	General combining ability
GPS	Geographical positioning system
GYD	Grain yield
GCA _f	General combining ability of females
GCA _m	General combining ability of males
H ²	Broad-sense heritability
h ²	Narrow-sense heritability
HKWT	Hundred kernel weight
HT _{Sa}	Height for <i>S. asiatica</i> plants
HT _{Sh}	Height for <i>S. hermonthica</i> plants
IBPGR	International Board for Plant Genetic Resources
IITA	International Institute of Tropical Agriculture
IR Maize	Imazapyr resistant maize
LSD	Least significance difference
MSV	Maize streak virus
NCD II	North Carolina Design II
NPGRC	National Plant Genetic Resources Centre
OPV	Open pollinated variety
PCA	Principal component analysis
PCR	Polymerase chain reaction
PH	Plant height

PIC	Polymorphic information content
PRA	Participatory rural appraisal
RAPD	Random amplified polymorphism DNA
RFLP	Restricted fragment length polymorphism
<i>Sa</i>	<i>Striga asiatica</i>
SCA	Specific combining ability
SD	Silking date
SDR8	<i>Striga</i> damage ratings at eight weeks after planting
SDR10	<i>Striga</i> damage ratings at ten weeks after planting
SEC8	<i>Striga</i> emergence count at eight weeks after planting
SEC10	<i>Striga</i> emergence count at ten weeks after planting
SED	Standard error of the mean difference
SSA	Sub-Saharan Africa
SSR	Simple sequence repeats
<i>Sh</i>	<i>Striga hermonthica</i>
SN	Number of <i>Striga</i> plants
SNP	Single nucleotide polymorphisms
SPSS	Statistical package for the social sciences
SV	<i>Striga</i> vigour
UPGMA	Unweighted pair group method with arithmetic mean
TARI	Tanzania Agricultural Research Institute
VAM	Vascular arbuscular mycorrhizal
WAP	Weeks after planting
δ^2_A	Additive variance
δ^2_D	Dominance variance
δ^2_{EW}	Environmental variance
δ^2_g	Genotypic variance
δ^2_{GCA}	Additive variance of females and males
δ^2_{GCAF}	Additive variance of females
δ^2_{GCAM}	Additive variance of males
δ^2_{SCA}	Additive variance for female and male interaction
δ^2_P	Total phenotypic variance

Background of the study

Maize is an important crop globally. It has multiple uses, including for human food, animal feed, and as a source of industrial raw materials such as in the starch industry (Verheye, 2010; Prasanna, 2012; Ranum *et al.*, 2014). Worldwide, over 1.148 billion tons of maize is produced annually from an estimated area of 197.2 million hectares (FAOSTAT, 2019). Half (50.1%) of the global maize production comes from continental America, followed by Asia (31.4%) and Europe (11.1%). In contrast, Africa contributes about 7.4% of the world's total maize production. The eastern and southern African sub-regions account for two-thirds of the maize produced in Africa (Verheye, 2010; FAOSTAT, 2019). Tanzania produces over 5.65 million tons from an estimated 3.43 million hectares, accounting for 0.49% of the global maize production (FAOSTAT, 2019).

Typically, white maize contains 72% starch, 10% protein and 4% fat, and it supplies energy with a value of 365 Kcal/100 g (Ranum *et al.*, 2014). Maize is a major food for more than 1.2 billion people across sub-Saharan Africa (SSA), South Asia, and Latin America (Ritte *et al.*, 2017). The average per capita consumption of maize in SSA ranges between 19 to 119.7 kg/person/year, with the highest consumption recorded in Lesotho at 119.7 kg/person/year (Ranum *et al.*, 2014). In Tanzania, the average maize consumption is about 73 kg/person/year (CIMMYT, 2014). Despite the importance of maize in SSA, including Tanzania, the current productivity is low and stagnant (<1.8 tons/ha) compared to the global average yield of about 6 tons/ha (FAOSTAT, 2019). The low productivity of maize is attributable to many constraints, including biotic, abiotic and socio-economic factors (Shiferaw *et al.*, 2011; Cairns *et al.*, 2013; Shayanowako *et al.*, 2017; Lobulu *et al.*, 2019). The crucial constraints to maize production and productivity in Tanzania are briefly described below.

Constraints to maize production

Biotic stresses (e.g., *Striga* infestation, insect pests and diseases) and abiotic stresses (e.g., recurrent drought, heat, and poor soil fertility) and socio-economic constraints (e.g., lack of financial capital, high costs of production inputs and inadequate labour) are the major impediments to maize productivity in western Tanzania (Lobulu *et al.*, 2019). Among the biotic constraints, *Striga* infestation is the most crucial problem, causing grain yield loss of 18 -100% in SSA, including Tanzania. The magnitude of losses depends on the extent of the infestation, susceptibility of the variety, soil fertility level, and prevailing climatic conditions (Watson *et al.*, 2007; Teka, 2014; Lobulu *et al.*, 2019). Therefore, the present study focused on developing an integrated *Striga* management package to improve maize productivity in Tanzania.

***Striga* infestation**

Striga spp. belonging to the family Orobanchaceae, are popularly known as witchweeds due to the intensity of crop damage that they caused. *Striga* are persistent weeds of grain crops in SSA and Asia (Satish *et al.*, 2011; Lobulu *et al.*, 2021). The genus comprises 43 spp. worldwide, of which 11 spp. are considered parasitic to field crops (Ejeta, 2007b; Lobulu *et al.*, 2019). Among the spp., *Striga hermonthica* (Del.) Benth, *S. asiatica* (L.) Kuntze, *S. forbesii* (Benth.), *S. aspera* (Willd.) Benth., and *S. densiflora* (Benth.) Benth. cause significant losses to cereal crops including maize, sorghum (*Sorghum bicolor* (L.) Moench), pearl millet (*Pennisetum glaucum* (L.) R. Br.), rice (*Oryza sativa* L.) and finger millet (*Eleusine coracana* L.) (Ejeta, 2007a; Parker, 2009; Timko *et al.*, 2012; Spallek *et al.*, 2013). Among the cereal crops, maize is exceptionally badly affected by *Striga* infestations (Badu-Apraku, 2007; Badu-Apraku *et al.*, 2020; Lobulu *et al.*, 2021), particularly under drought and sub-optimal soil nitrogen conditions (Ejeta, 2007a; Badu-Apraku and Akinwale, 2011; Menkir *et al.*, 2012). Millions of hectares of crop fields in Africa are infested by *Striga* spp, affecting over 300 million resource-poor farmers engaged in cereal and legume crop production (Ejeta, 2007b; Nzioki *et al.*, 2016; Yacoubou *et al.*, 2021). *Striga* is widely distributed in Tanzania (Mrema *et al.*, 2017; Lobulu *et al.*, 2021). Thus far, there is no single effective method to control *Striga* due to its reproductive biology, habitat colonisation, and interaction with other biophysical factors.

***Striga* control options**

Various *Striga* control methods have been developed and promoted, either in isolation or combined. These include cultural practices, e.g., hoeing, hand pulling, sowing clean seed, manure application, crop rotation and intercropping maize with legumes (Babiker, 2007). In addition, chemicals including herbicides (Ransom and Odhiambo, 1995), fumigants (e.g., methyl bromide) (Massawe *et al.*, 2002), and germination stimulants (e.g., ethylene) have been used to control *Striga*. Herbicides are useful in preventing the build-up of *Striga* seeds in the soil but may not prevent crop losses occurring prior to the emergence of *Striga* plants. They are largely inaccessible and unaffordable for resource-poor farmers. Herbicides may also have residual effects in the soil, and they are not safe for beneficial insects (Kanampiu *et al.*, 2003).

Despite a range of *Striga* control techniques being recommended, effective management measures of the parasite have not been achieved. Most of the practices are either uneconomical, labour intensive and time-consuming for the farmers. Therefore, there is a need to devise a novel, cost-effective, sustainable, and ecosystem friendly *Striga* control option that can be integrated into existing farming practices, ensuring widespread adoption for maize production by small-scale farmers.

Research focus

Effective control of the *Striga* requires a combination of several control options (Tesso *et al.*, 2007; Sibhatu, 2016; Lobulu *et al.*, 2019). Resistant varieties should be a fundamental component in all integrated methods (Tesso and Ejeta, 2011; Yacoubou *et al.*, 2021). *Striga* resistance genes should be incorporated into locally adapted and productive cultivars that meet the local farmers' needs and trait requirements (Lobulu *et al.*, 2019; Yacoubou *et al.*, 2021). However, the levels of partial *Striga* resistance attained in maize is insufficient to withstand high levels of *Striga* infestation. Thus, for effective *Striga* control, the existing *Striga* partial resistance should be supplemented with a biocontrol agent of *Striga* (Elzein *et al.*, 2006). Pathogenic isolates of *Fusarium oxysporum* f. sp. *strigae* (*FOS*) can be used as biocontrol agents against *S. asiatica* and *S. hermonthica* infestation in maize and sorghum (Venne *et al.*, 2009; Shayanowako *et al.*, 2020; Lobulu *et al.*, 2021).

Therefore, the present study was focused on devising an integrated *Striga* control package with host resistance at the centre, supplemented by a mycoherbicide (*FOS*), in addition to farmer-friendly practices for easy adoption and sustainability. To achieve this, there was a need to identify and document farmers' maize production constraints, current *Striga* control practices, and maize trait preferences of farmers (Lobulu *et al.*, 2019). Breeding maize for *Striga* resistance and *FOS* compatibility depends on accessing sources of *Striga* resistance genes in local and exotic maize germplasm sources (Lobulu *et al.*, 2021). Adequate phenotypic and genotypic characterization of diverse genetic resources would allow for the selection of farmers preferred and complementary parental lines for breeding. In addition, understanding the gene action controlling *Striga* resistance and *FOS* compatibility through concurrent analysis will enable breeders to apply appropriate breeding methods and to select desirable parents and crosses to enhance genetic gain.

The overall aim of the study

The overall aim of this study was to contribute to food security through the development of maize genotypes resistant to *S. asiatica* and *S. hermonthica* that are highly compatible with *FOS*, and which carry farmer preferred traits, in western Tanzania.

The specific objectives

The specific objectives of the study were:

- i. To assess maize production constraints, trait preferences and current *Striga* control options in western Tanzania by formally consulting farmers.
- ii. To characterize maize genotypes for resistance to *S. asiatica* and *S. hermonthica*, and compatibility with *FOS* in Tanzania.

- iii. To determine the genetic diversity of maize genotypes with different levels of resistance to *S. asiatica* and *S. hermonthica* based on phenotypic data and simple sequence repeats (SSR) markers to select desirable and complementary parents for breeding.
- iv. To evaluate hybrids performance and combining ability of selected maize genotypes for farmer-preferred traits, grain yield and yield components, *Striga* resistance and FOS compatibility.

Research hypotheses

The hypotheses of the study were:

- i. Farmers in western Tanzania have varied maize production challenges, trait and variety preferences and perceptions to guide breeding and variety development.
- ii. Significant genetic variation exists among locally adapted maize genotypes that can be selected for *S. asiatica* and *S. hermonthica* resistance, and compatibility with FOS.
- iii. The genotypes to be used in the study are genetically different from each other regarding *Striga* resistance and FOS compatibility when subjected to phenotypic and SSR analysis.
- iv. The selected parents and their crosses exhibit different levels and magnitude of combining ability effects for yield and yield components when evaluated under *S. asiatica* and *S. hermonthica* infestation, with and without FOS.

Outline of the thesis

This thesis consists of a comprehensive review of the literature, four research chapters, and a concluding overview of the research (Table 0.1). The thesis follows a dominant format prescribed by the University of KwaZulu-Natal. The chapters are presented as discrete, interrelated papers and are compiled into a composite thesis, following the study's specific objectives. For this reason, there is some inevitable repetition of references and some information between chapters. The style of referencing is according to the Crop Science Journal, except for Chapters 2 and 3 which were already published elsewhere, as indicated in Table 0.1.

Table 0.1. Outline of Thesis

Chapter	Title	Publication status
-	Introduction to Thesis	-
1	Review of the Literature	-
2	Maize production constraints, traits preference and current <i>Striga</i> control options in western Tanzania: farmers consultation and implications for breeding	Acta Agriculturae Scandinavica, Section B — Soil & Plant Science http://doi.10.1080/09064710.2019.1652680
3	Characterization of maize genotypes (<i>Zea mays</i> L.) for resistance to <i>Striga asiatica</i> and <i>S. hermonthica</i> and compatibility with <i>Fusarium oxysporum</i> f. sp. <i>strigae</i> (FOS) in Tanzania	Agronomy 2021 , 11, 1004. https://doi.org/10.3390/agronomy11051004
4	Genetic diversity of maize genotypes with differential resistance to <i>Striga asiatica</i> and <i>S. hermonthica</i> based on phenotypic and simple sequence repeats markers	Under review in Maydica Journal Manuscript_My dica_2202-7254-1-RV.docx
5	Progeny testing of maize (<i>Zea mays</i> L.) genotypes for yield and yield components, <i>Striga</i> resistance and <i>Fusarium oxysporum</i> f.sp. <i>strigae</i> compatibility	Under review in the journal of Plant Breeding Manuscript ID is PLBR-22-OA-084
6	An overview of the research findings	-

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CHAPTER ONE: A Review of the Literature

Abstract

The present yield of maize (*Zea mays* L.) in western Tanzania is low (<1.5 t/ha) compared with the potential yield of the crop, which is up to 6 t/ha. The low yield in the region is attributable to a multitude of factors, including biotic, abiotic, and socio-economic constraints. *Striga* parasitism is one of the main biotic constraints, causing yield losses of 18 to 100% in Tanzania. The dominant *Striga* spp. present in the country are *Striga asiatica*, *S. hermonthica* and *S. forbesii*. The first two spp. are widely distributed across the country, inflicting yield losses on maize, sorghum, millet, and upland rice. No single management option has been found to be effective in controlling *Striga* infestations globally. An integrated *Striga* management approach, led by host resistance breeding, combined with biocontrol agents such as *Fusarium oxysporum* f. sp. *strigae* (*FOS*) and farmer-compatible cultural practices could provide an economic and effective control program. However, this strategy has yet to be explored in Tanzania for the control of *Striga* affecting maize production. The objective of this chapter is to provide background information on the major maize production constraints in Tanzania, current *Striga* control options, *Striga* resistance breeding, and the development of novel germplasm with resistance to *Striga* and compatibility with *FOS*. In addition, the review discusses combining ability effects and gene action controlling *Striga* resistance and *FOS* compatibility in maize. This review will guide the development of *Striga* resistant genotypes and integrated *Striga* control options to boost the productivity of maize in Tanzania or similar agro-ecologies.

Keywords: Combining ability, *Fusarium oxysporum* f.sp. *strigae*, maize breeding, *Striga* infestation, *Striga* resistance

1.1 Introduction

Maize is an important crop globally. World-wide, over 1.148 billion tons of maize is produced annually from an estimated area of 197.2 million hectares (FAOSTAT, 2019). The American continent accounts for about 50.1% of the global maize production, followed by Asia (31.4%) and Europe (11.1%). Africa contributes about 7.4% of the world's total maize production. The eastern and southern Africa sub-regions account for two-thirds of the maize produced in Africa (Verheye, 2010; FAOSTAT, 2019). Tanzania produces over 5.65 million tons from an estimated area of 3.43 million hectares, accounting for 0.49% of the global maize production (FAOSTAT, 2019).

Maize has multiple uses including for human food, animal feed and as a source of industrial raw materials such as starch (Verheye, 2010; Prasanna, 2012; Ranum *et al.*, 2014). Typically, white maize contains 72% starch, 10% protein and 4% fat, and it supplies energy with a value of 365 Kcal/100 g. Maize serves as staple food for more than 1.2 billion people across sub-Saharan Africa (SSA), South Asia, and Latin America (Ritte *et al.*, 2017). The average per capita consumption of maize in SSA ranges between 19 to 119.7 kg/person/year, with the highest consumption being recorded in Lesotho at 119.7 kg/person/year (Ranum *et al.*, 2014). In Tanzania, the average maize consumption is about 73 kg/person/year, indicating the vital contribution of maize production for food security, and the economies of local and regional markets (CIMMYT, 2014).

Despite the socio-economic importance of maize in SSA, the present productivity is low and stagnant (<1.8 tons/ha). The global average yield of maize is about 6 tons/ha (FAOSTAT, 2019). The low productivity of maize in SSA is attributable to diverse biotic stresses (*Striga* infestation, use of low yielding varieties, diseases, stalk borers and storage insect pests), abiotic stresses (low soil fertility, drought and heat stress) (Shiferaw *et al.*, 2011; Cairns *et al.*, 2013), and several socio-economic constraints (lack of financial capital, inadequate use of inputs and shortage of labour (Mbwaga and Massawe, 2002; Lobulu *et al.*, 2019).

1.2 Threat of *Striga* spp. in crop production systems in SSA

Parasitic plants belonging to the family Orobanchaceae are among the most serious constraints limiting cereal crop production in SSA. The parasitic weed of the genus, *Striga*, comprises of over 40 spp. worldwide, of which 11 spp. attack major food and industrial crops globally (Ejeta, 2007b). *Striga hermonthica* (Del.) Benth, *S. asiatica* (L.) Kuntze, *S. gesnerioides* (Willd.) Vatke, *S. forbesii* (Benth.) and *S. aspera* (Willd.) Benth. are the dominant spp. inflicting economic yield loss or crop failure in SSA (Timko *et al.*, 2012; Gebretsadik *et al.*, 2013). All these spp., except *S. gesnerioides*, parasitizes cereal (monocots) crops (e.g., maize, sorghum, pearl millet, sugarcane, and upland rice). *Striga gesnerioides* parasitizes

dicots (e.g., cowpea, tobacco, and sweet potato) and wild relatives (Babiker, 2007; Parker, 2012). *Striga* spp. infest about 100 million hectares of crop lands in Africa (Ejeta, 2007b; Tesso and Ejeta, 2011; Mrema *et al.*, 2017b). Consequently, these weeds affect the livelihoods of over 300 million peoples in SSA (Ejeta, 2007b; Nzioki *et al.*, 2016; Yacoubou *et al.*, 2021).

Grain yield losses due to *Striga* damage in SSA range from 20 to 100%, depending on the susceptibility of the host, cultural practices, prevailing weather and soil conditions, and the degree of infestation (Amusan *et al.*, 2008). More than 10 million tons of grain are lost annually due to *Striga* damage in the region (Watson *et al.*, 2007). On a monetary basis, the annual economic losses due to *Striga* are estimated at USD 7 billion in SSA (Ejeta, 2007b; Badu-Apraku and Akinwale, 2011). In Ethiopia, Mali and Nigeria, the annual losses are estimated at USD 75 million, USD 87 million and USD 1.2 billion, respectively (AATF, 2011). In East Africa, about 1.2 million tons of cereal grains are lost annually (MacOpiyo *et al.*, 2009), translating to an economic loss estimated at USD 335 million annually (Khan *et al.*, 2011).

Of all the cereal crops affected by *Striga*, maize is the most susceptible (Badu-Apraku, 2007), particularly under drought and sub-optimal soil nitrogen conditions, which are common in SSA (Ejeta, 2007a; Badu-Apraku and Akinwale, 2011; Menkir *et al.*, 2012b). More than one million hectares of maize, i.e., approximately 80% of the total maize cultivated in southern Africa are affected by *S. asiatica* (De Groote *et al.*, 2008). In Sudan, over 500,000 ha of crop lands under rainfed cultivation are heavily infested by *S. hermonthica*, resulting in yield losses of 70 to 100%. Severe *Striga* infestation can result in a total crop failure (Babiker, 2007). Socio-economic constraints, including limited access to production inputs, a lack of understanding of *Striga* management options, and inadequate extension services, contribute to a high level of infestation. Furthermore, most of the current methods for *Striga* control are inappropriate for small-scale farmers to adopt. The biggest problem is that there have been no successful programs to breed for *Striga*-resistant maize varieties adapted to the affected agro-ecologies in Tanzania.

1.3 Extent of *Striga* problem in Tanzania

Striga spp. are widely found in Tanzania with variable levels of infestation. The following cereal growing regions have high *Striga* densities: Mwanza, Mara, and Shinyanga (Lake zone) (Khan, 2011); Tabora and parts of Kigoma (Western zone); Dodoma and Singida (Central zone); and Morogoro in the Eastern zone (Mbwaga and Obilana, 1993; Mbwaga, 1996; MacOpiyo *et al.*, 2009; Mrema *et al.*, 2017a). Infestations extend to the Ruvuma region in the south, the Iringa and Mbeya regions in the Southern Highlands, and along the coastal regions of Tanga, Pwani, Lindi, and Mtwara (MacOpiyo *et al.*, 2009; Khan, 2011). The

predominant *Striga* spp. are *S. asiatica*, *S. hermonthica* and *S. forbesii*, infesting maize, sorghum, finger millet, upland rice, and sugarcane (MacOpiyo *et al.*, 2009; Rodenburg *et al.*, 2015). In most cases, farmers abandon heavily infested fields because they no longer produce a viable crop (Ejeta, 2007a; Atera *et al.*, 2011).

Grain yield losses of 18 to 90% has been reported in Tanzania due to *Striga* infestation (Mbwaga, 1996; Massawe *et al.*, 2002). This depends on the variety grown, *Striga* seed density, soil fertility status, and climatic conditions (Mbwaga and Massawe, 2002; Lobulu *et al.*, 2019). Socio-economic constraints, inadequate extension services, monocropping and reduced fallows intensify *Striga* severity (Lobulu *et al.*, 2019). Losses due to *Striga* damage on maize are severe, amounting to a monetary value of about USD 173 million per year (Khan, 2011). Other cereals that incur significant losses due to the *Striga* parasitism in Tanzania include rice (with a loss of 232,913 tons per year) and sorghum (192,975 tons) (MacOpiyo *et al.*, 2009). Crop losses drive the resource-poor farmers into extreme poverty. It is estimated that in heavily infested areas, rural poverty can encompass 70% of the population (Khan, 2011). This necessitates a concerted drive to develop effective and affordable *Striga* control options that are compatible with farmer operations, to ensure high levels of adoption. Use of *Striga* resistant improved varieties and cultural practices have been reported to control *Striga* infestations (Badu-Apraku *et al.*, 2004; Akaogu *et al.*, 2019; Lobulu *et al.*, 2019). The development of an effective *Striga* control package requires an understanding of the intricate *Striga*-host parasitic interactions.

1.4 *Striga* biology and host interaction

Striga parasites produce large quantities of tiny seeds that can remain viable in the soil for 20 years or more (Gurney *et al.*, 2003; Gurney *et al.*, 2006). One *Striga* plant can produce up to 500,000 tiny, dust-like seeds, which mature at different times (Berner *et al.*, 1994; Yoneyama *et al.*, 2010). The vast numbers of seeds produced increase the chances that some of the *Striga* seeds will find a suitable host (Ejeta, 2007b). *Striga* seed germinates only in response to chemical cues (strigolactones) produced by both host and non-host plant spp. (Siame *et al.*, 1993; Bouwmeester *et al.*, 2007a). Strigol is among the sesquiterpenes responsible for triggering *Striga* seed germination in cereals (Siame *et al.*, 1993). Before germination, *Striga* seeds must go through, maturation process or pre-conditioning in a warm, moist environment for several days after which they respond to chemical germination stimulants (Siame *et al.*, 1993; Ejeta, 2007a).

Another feature of *Striga* seeds is that not all seeds are pre-conditioned simultaneously for germination (Khan *et al.*, 2005). In each cropping season, some of the seeds germinate, some revert to dormancy, and some remain unconditioned in the soil. The next generation of seed

are then deposited in the soil, continuously enriching the soil seed bank (Ejeta, 2007b). When environmental conditions are wet but unsuitable for seed germination, *Striga* seeds possess the capacity to become "wet-dormant," which is an ability to revert to a dormant state, which is reversible after desiccation (Mohamed *et al.*, 1998). After *Striga* germination, haustorial initiation occurs in response to specific xenononins produced by the potential host (Keyes *et al.*, 2000; Gurney *et al.*, 2003). These secondary metabolites are responsible for directing the *Striga* radicle to the host roots, and are different from the exudates that initiate *Striga* germination (Albrecht *et al.*, 1999).

The haustorium is an organ of attachment and acts as a physiological bridge between the host and the parasite (Babiker *et al.*, 1993). This enables the weed to form a complicated mode of parasitism, with vascular connections to the host occurring below the ground. The haustorium attaches, penetrates the host root, and establishes a connection with the host xylem just after germination to support *Striga* growth and survival (Babiker *et al.*, 1993). Following attachment, the parasite remains subterranean for six to eight weeks, siphoning off water, organic nutrients, and mineral solutes from the host xylem and phloem (Babiker *et al.*, 1993; Gurney *et al.*, 1999). During this period, the parasite is completely dependent on its host and is at its most damaging, exerting phytotoxic effects, which impair photosynthesis within days of attachment to its hosts (Gurney *et al.*, 1999; Joel, 2000; Gurney *et al.*, 2002). The effects of *Striga* damage on crops include stunted growth, wilting, yellowing, and scorching of leaves, reduced yields, and death of affected plants. The parasite exerts its greatest damage on the crop before its emergence above ground (Sibhatu, 2016).

Photosynthesis is reduced by up to 47% in maize and 62% in sorghum due to *S. asiatica* infestation (Press *et al.*, 1987; Gurney *et al.*, 2002). *Striga* spp. can only survive for 3 to 7 days after germination, after which it will die if there is no established connection to the host plant (Babiker, 2007). Even though *Striga* spp. have green biomass, their photosynthetic apparatus is inefficient, making them dependent on their host for most of their nutrition (Parker, 2012). According to Watson *et al.* (2007), *Striga* photosynthesizes about 20% of their needs after emerging from the soil, which is insufficient to sustain their survival. Therefore, successful parasitism is a series of interactive processes between the host and parasite, conditioned by a large number of genetic and physiological events, each of which is influenced by an array of environmental factors (Ejeta, 2007a).

Understanding the parasite biology, its interaction with host plants, and the physical environments afford the breeders the opportunity to develop *Striga* resistant/tolerant maize varieties. From an ecological point of view, management of host plant resistance and the biophysical environment would be key components of an integrated *Striga* control package.

However, there are no *Striga* resistant maize varieties in Tanzania or elsewhere in SSA. Using locally adapted, *Striga*-resistant maize germplasm could lead to *Striga* control options that would be economically viable, socially acceptable, and environmentally friendly. They would increase maize yields, productivity and profitability in the maize producing areas of Tanzania.

1.5 *Striga* management in maize production

Various *Striga* control methods have been developed and deployed, either in isolation or combined. These include cultural practices, chemical control and *Striga* host resistance (Babiker, 2007). The development of an integrated *Striga* control program requires a thorough knowledge of each control method for effective deployment. These approaches are briefly described below.

1.5.1 Cultural practices

Several cultural control measures have been suggested to manage *Striga* infections. These control options are based on four main principles: (1) reducing the *Striga* soil seed bank; (2) minimizing *Striga* seed production; (3) preventing the spread of *Striga* seed from infested to non-infested fields; (4) and improving soil fertility (Khan *et al.*, 2014). Cultural control options include sowing clean seeds that are not contaminated with *Striga* seeds, rotating cereals with trap crops that induce suicidal germination of *Striga* seeds, and intercropping cereals with leguminous plants (Ransom, 2000; Babiker, 2007). Other cultural techniques include: use of green manures (e.g., *Crotalaria ochroleuca* G. (Sunhemp), *Mimosa invisa* L. (Colla) (Kayeke *et al.*, 2007), and hoeing and hand pulling of emerged *Striga* plants (Babiker, 2007).

In recent years, a push-pull technology has been promoted by the CGIAR system. This technology is based on intercropping maize with a forage legume, such as *Desmodium uncinatum* Jacq., and planting of Napier grass (*Pennisetum purpureum* Schumach) as a border crop (Khan *et al.*, 2011; Khan *et al.*, 2014). The push-pull technology controls stem borer and *Striga* infestation simultaneously, while improving soil fertility through nitrogen fixation and increasing soil organic matter (Khan *et al.*, 2014). *Desmodium* repels stem borer moths (push) while Napier grass attracts them (pull). In addition, *Desmodium* leads to suicidal germination of *Striga* seed through the production of germination stimulants but is not susceptible to the parasite (Khan *et al.*, 2002). Soil fertility improvement is one of the important components of an integrated *Striga* control approach because the degree of *Striga* infestation is strongly correlated with low soil nitrogen and phosphorus content. Organic and inorganic fertilizers can reduce the impact of *Striga* on cereal hosts (Jamil *et al.*, 2014; Gebremariam and Assefa, 2015).

Under mineral nutrient deficiency, host plants release strigolactones to attract endophytic vascular arbuscular mycorrhizal (VAM) fungi to colonize the roots of the maize plants to enhance nitrogen and phosphorus uptake by the VAM mycelia in the rhizosphere (Bouwmeester *et al.*, 2007b). Unfortunately, parasitic plants also use these signalling molecules (strigolactones) to detect the presence of a suitable host and subsequently induce *Striga* seed germination (Jamil *et al.*, 2012). However, in the presence of high levels of inorganic fertilizers, plants do not generate much strigolactones because they do not need the VAM fungi as much. Thus, increasing nitrogen and phosphorus availability lowers the production of *Striga* germination stimulants (exudation of strigolactones) from host roots, hence, inhibiting *Striga* germination and subsequent attachment (Jamil *et al.*, 2014). Therefore, commercial farmers who use inorganic fertilizers usually experience less problems with *Striga*.

Despite all the availability of a variety of cultural control techniques, effective control of *Striga* has not been fully realised with this approach. This is because the practices are either uneconomical, labour intensive, impractical, or are not compatible with other farm operations (Ejeta, 2007a; Sibhatu, 2016).

1.5.2 Chemical control

Various chemicals including herbicides, fumigants (e.g., methyl bromide), and germination stimulants (e.g., ethylene) have been reported to be effective in controlling *Striga*. Fumigation of soils with methyl bromide gas at a rate of 500 kg/ha was reported to be effective at killing all viable *Striga* seeds in the soil (Massawe *et al.*, 2002). However, methyl bromide has been banned globally (UNEP, 1999). Ethylene promotes suicidal germination, whereas application of post-emergence herbicides such as 2,4-D prevent weed reproduction (Ransom and Odhiambo, 1995). The use of imazapyr-resistant maize (IR maize) and applying the herbicide to the seed has resulted in a significant increase in maize yields where *Striga* infestations are prevalent (Kanampiu *et al.*, 2003; Makumbi *et al.*, 2015). Seeds of IR maize variety are coated with the imidazolinone herbicide (imazapyr) and sold under the name StrigAway® in Kenya. However, IR maize technology has several disadvantages. Firstly, it is toxic to all other crops that do not have resistance to imazapyr, hence, it is not suitable in a mixed cropping system (Teka, 2014). Secondly, farmers need to purchase coated seed annually since the IR maize is susceptible to *Striga* without imazapyr treatment (Khan *et al.*, 2014). Thirdly, IR maize coated with imazapyr can shed the imazapyr dust, and therefore they cannot be stored with non-resistant seeds, and this creates a major problem for seed companies, agro-dealerships, and farmers (de Vries, pers. comm.). Herbicides are useful in preventing the build-up of *Striga* seeds in the soil but may not prevent the damage prior to *Striga* emergence, and they have residual effects in the soil (Kanampiu *et al.*, 2003).

The physiological association between *Striga* and its host plants makes it difficult to apply conventional weed control practices, including herbicides. Furthermore, small-scale farmers' have limited access to chemical control options due to their high costs, inaccessibility in rural areas, and limited knowledge about their application, rendering this control option non-viable for these farmers. Therefore, there is a need to devise a cost-effective, sustainable, and ecosystem friendly *Striga* control option that can be integrated into existing farming practices, ensuring widespread adoption.

1.5.3 Host plant resistance

The use of resistant varieties to control *Striga* is considered the most economic and environmentally sustainable option available to resource poor-farmers (Badu-Apraku *et al.*, 2004; Teka, 2014; Akaogu *et al.*, 2019). *Striga* resistance refers to the ability of the host roots to avoid stimulating *Striga* seed germination, or to stimulate *Striga* germination but to prevent attachment of the seedlings to its roots, or to kill the seedlings when they attached to the roots. *Striga* tolerance refers to the ability of the host plant to withstand the effects of the parasitic plants that are attached, regardless of their number, with little or no yield loss (Kim, 1994; Badu-Apraku *et al.*, 2013). *Striga* resistant genotypes can reduce both new *Striga* seed production and reduce the *Striga* seed bank in infested soils in successive seasons (Akaogu *et al.*, 2019; Lobulu *et al.*, 2021; Yacoubou *et al.*, 2021).

Deployment of resistant germplasm with complete or partial resistance, or an immunity response, has been effective (Rodenburg and Bastiaans, 2011). There is little information on *Striga* resistance levels in landraces of maize in Africa (Babiker, 2007), although some landraces expressing tolerance have been identified (Kim *et al.*, 1999; Midega *et al.*, 2016). Maize is native to South America and was introduced into Africa in the 16th Century (McCann, 2001; Shepherd *et al.*, 2010; Oppong *et al.*, 2014), unlike sorghum, which is a native cereal in Africa. Sorghum has co-evolved with *Striga*, endowing it with a greater range of resistance and tolerance than maize (Rich and Ejeta, 2008; Hearne, 2009). However, *S. hermonthica* resistance genes have been identified in wild maize spp. that can inhibit the pre-emergence and post-emergence stages of the *Striga* life cycle, as does sorghum (Rich and Ejeta, 2008; Menkir *et al.*, 2012a; Akaogu *et al.*, 2019).

The International Institute of Tropical Agriculture (IITA) has developed some maize genotypes with *Striga* resistance genes (Menkir *et al.*, 2012a; Akaogu *et al.*, 2019). These genotypes may be a useful source of resistance genes for breeding programs in SSA, including Tanzania.

Striga resistance in maize occurs at two stages: (1) Pre-attachment resistance against *Striga* spp. which is expressed in various ways: low stimulation of *Striga* seed germination, identified in *Zea diploperennis* (Iltis, Doebley & Guzmàn) (Amusan *et al.*, 2008), and an open-pollinated maize variety (KSTP 94) grown in Kenya (Midega *et al.*, 2016), low haustorial induction detected from *Tripsacum dactyloides* (L.) (Gurney *et al.*, 2003), avoidance through unique root architecture (e.g. formation of fewer thin branches) (Amusan *et al.*, 2008), or escape through early maturity (Oswald and Ransom, 2004); (2) Post-attachment *Striga* resistance is expressed through incompatibility responses, identified from both *Z. diploperennis* and *Z. dactyloides* (Lane *et al.*, 1997; Gurney *et al.*, 2003; Amusan *et al.*, 2008). These mechanisms result in physiological or biochemical barriers that prevent *Striga* haustoria from connecting to the host xylem (Van Dam and Bouwmeester, 2016).

However, the levels of *Striga* resistance attained so far in maize may have been underestimated and underexploited previously due to the extremely high *Striga* infection pressures in hot spots, which overrides partial resistance responses that would be effective under low to medium infestation levels (Hearne, 2009). Thus, the addition of a biological control agent to suppress *Striga* has been suggested to supplement such partial resistance for effective control of the parasite (Elzein and Kroschel, 2006; Venne *et al.*, 2009; Shayanowako *et al.*, 2018b; Lobulu *et al.*, 2021).

1.5.4 Biological control

Biological control agents or bioherbicides are one way of managing root parasitic weeds. Biocontrol has been defined as the deliberate use of living organisms to suppress, reduce, or eradicate a pest population (Boyetchko, 1999). The method is more environmentally friendly than chemical control practices and has no residual effect on the soil (Abbasher *et al.*, 1998; Zimmermann *et al.*, 2016). The presence of mycoherbicides surrounding the rhizosphere retards the efficacy of *Striga* parasitism on the host plant (Beed *et al.*, 2007; Lobulu *et al.*, 2021) and may stimulate plant growth (Gebretsadik *et al.*, 2013; Mrema *et al.*, 2017b). Gebretsadik *et al.* (2013) and Mrema *et al.* (2017b) reported a significant reduction in days to flowering and maturity for sorghum plants grown from seeds coated with *Fusarium oxysporum* f. sp. *strigae* (FOS) compared to the untreated controls. The pathogenic isolates of FOS can suppress both *S. asiatica* and *S. hermonthica* in maize and sorghum (Beed *et al.*, 2007; Venne *et al.*, 2009; Shayanowako *et al.*, 2020). Three isolates of FOS, namely, "Foxy-2", "PSM 197" and "M12-4A", were reported to be highly virulent and host-specific to the two *Striga* spp. hence, they were classified into a new *forma specialis* (f. sp.) referred to as f. sp. *strigae* (Ciotola *et al.*, 1995; Elzein and Kroschel, 2006). The isolates infect *Striga* spp. and are non-pathogenic to maize, sorghum, pearl millet, rice, cotton, groundnut, cowpea, and okra (Beed *et al.*, 2007; Zimmermann *et al.*, 2016). FOS strains are endophytic and colonize the

root system of cereal hosts. They can infect *Striga* spp. at all growth stages, including seeds, germlings, seedlings and flowering plants, thus hindering parasite growth and development. This results in enhanced crop growth, seed set and grain yields, and a reduced *Striga* seedbank (Elzein *et al.*, 2006; Beed *et al.*, 2007). *FOS* strains infect *Striga* by clogging the xylem and phloem vessels and causing wilting symptoms (Elzein *et al.*, 2010; Ndambi *et al.*, 2011).

FOS works better when combined with *Striga*-resistant genotypes and other control measures (Gebretsadik *et al.*, 2013). The synergistic effects of *Striga*-resistant maize genotypes and *FOS* compatibility can reduce *Striga* emergence by over 90% (Venne *et al.*, 2009). Gebretsadik *et al.* (2013) reported that a reduction of up to 92% of *Striga* infections was measured when *FOS* was combined with *Striga* resistant sorghum varieties. Beed *et al.* (2007) reported that the use of *FOS* reduced *S. hermonthica* emergence by 98% and increasing sorghum yield by 26%. Field studies conducted in West Africa confirmed the efficacy of *FOS* against *S. hermonthica*. In contrast, in a study in Kenya *FOS* did not show any suppressive effect against *Striga* (Avedi *et al.*, 2014). The low efficacy of *FOS* in Kenya was attributed to the strain of the fungus being used losing its pathogenicity, or incompatible environmental conditions, including the conditions of the soil, precipitation and temperatures (Gerbore *et al.*, 2014).

Elzein and Kroschel (2006) examined the host ranges of *FOS* using three *Striga* spp. and 25 non-target plant spp. belonging to nine families. The results showed that the *FOS* that they used was highly virulent against *S. hermonthica* and *S. asiatica*. However, this *FOS* strain was avirulent against *S. gesnerioides* and did not colonize non-target plant spp.. Another study reported disease symptoms in the crops in the Solanaceae family due to *FOS* infection (Zarafi *et al.*, 2015). However, other crops that are commonly intercropped with cereal crops were found to be immune to *FOS*. Intercropping, crop rotation and relay cropping systems can boost *Striga* control, while using *FOS*. Reportedly, *FOS* strains grow well in the soil and colonizes the rhizosphere of both compatible and non-target genotypes, enhancing their growth relative to growth in plots that were not inoculated with *FOS* (Elzein and Kroschel, 2006; Mrema *et al.*, 2017b; Lobulu *et al.*, 2021). Therefore, there is a need to select maize genotypes for *FOS* compatibility while breeding for *Striga* resistance to utilise the multiple benefits of both systems by smallholder farmers. The use of *Striga*-resistant genotypes, combined with a biological control agent and farmers' compatible agronomic practices could be used to create an effective integrated *Striga* control package.

1.5.5 Integrated *Striga* management

Several control methods have been attempted but none of them has been effective when deployed independently (Tesso *et al.*, 2007). The extraordinary numbers of seeds produced by *Striga* spp. and their prolonged viability, coupled with underground host damage before the parasite emerges above the ground, makes *Striga* control difficult through conventional methods (Sibhatu, 2016; Lobulu *et al.*, 2019). For effective control of the parasite, a combination of several control options has been proposed (Tesso *et al.*, 2007; Sibhatu, 2016). Tesso *et al.* (2007) reported the effectiveness of the combined use of host plant resistance, crop rotation, trap cropping and intercropping in reducing *S. hermonthica* infestation in West Africa. This reduced the weed by 35 to 45%, thereby increasing maize yield by 76 to 100%. For effective control of *Striga*, resistant varieties should serve as fundamental component in all integrated methods (Tesso and Ejeta, 2011; Yacoubou *et al.*, 2021). This can only be achieved if resistance is incorporated into locally adapted and productive cultivars that meet the local farmers quality trait requirements (Yacoubou *et al.*, 2021).

The use of pathogenic isolates of *FOS* in controlling both *S. asiatica* and *S. hermonthica* infestation in maize and sorghum has allowed agricultural researchers to devise an effective, sustainable, and environmentally friendly *Striga* control package (Abbasher *et al.*, 1998; Ciotola *et al.*, 2000; Elzein and Kroschel, 2004; Venne *et al.*, 2009). Thus, the present study focused on devising an integrated *Striga* control package considering host resistance as the main criteria, supplemented by a mycoherbicide (*FOS*) and farmer-friendly practices.

1.6 Integrating resistance breeding and biocontrol for *Striga* management

1.6.1 Identification of maize genotypes with resistance to *Striga* and *FOS* compatibility

A successful breeding program depends not only on the available genetic variation within the germplasm resources (Yan *et al.*, 2016; Al-Naggar *et al.*, 2020), but also on the economic benefits of such variation for cultivar development and market opportunity. Genetically distant genotypes from distinct sources, incorporating farmer preferred traits have been assessed for *S. asiatica* and *S. hermonthica* resistance, and their compatibility with *FOS* (Lobulu *et al.*, 2021). This work led to participatory breeding, generating breeding populations of maize. The next goal was to analyse the modes of gene action of host resistance in controlling *Striga* resistance and *FOS* compatibility in Tanzania.

1.6.2 Combining ability and gene action conditioning *Striga* resistance and *FOS* compatibility in maize

The extent and type of genetic variability are of major importance in a breeding program. The degree of genetic variability determines selection response, while the type of variability helps

the breeder to determine the most appropriate breeding method (Badu-Apraku, 2007). General combining ability (GCA) and specific combining ability (SCA) effects are discerned using genetic mating designs (Christie and Shattuck, 1992). There are many mating designs, and the choice of the design depends on the nature of the parents and the breeding goals (Fasahat *et al.*, 2016; Amegbor *et al.*, 2020). The North Carolina Design II (NCD II) is a robust mating design that was selected for the present study because more parents can be included than in a diallel design, with fewer crosses required. The design provides valuable genetic information about the parents and progenies (Hallauer *et al.*, 2010). NCD II helps to identify appropriate parents and families from crosses that can be advanced in a breeding program. NCD II (Comstock and Robinson, 1948) estimates variance components in addition to the GCA and SCA effects. The main effects of male and female parents used in NCD II correspond to the GCA effect, while the female x male interaction refers to the SCA effect (Cach *et al.*, 2006; Fasahat *et al.*, 2016).

Various studies have reported the GCA and SCA effects associated with *Striga* resistance in maize. For instance, Kim (1994) and Badu-Apraku (2007) reported that additive gene action was more important in normal-endosperm maize inbreds against *Striga* damage, while non-additive gene action was more important in suppressing *Striga* emergence. A larger proportion of GCA sum of squares over SCA has been reported against *Striga* damage and for low number of emerged *Striga* plants at 8 and 10 weeks after planting (WAP) in early-maturing, normal-endosperm maize inbreds (Gethi and Smith, 2004; Ifie *et al.*, 2015). A larger proportion of SCA sum of squares over GCA against *Striga* damage and low number of emerged *Striga* plants at 8 and 10 WAP were reported by Badu-Apraku *et al.* (2016), who indicated that non-additive gene action played a major role in the inheritance of *Striga* resistance. *Striga* damage rating of host plants were used as a tolerance index, while *Striga* emergence count (number of emerged *Striga* plants) and yield performance were used as indices of resistance (Badu-Apraku, 2007).

1.6.3 Genetic variability assessment for *Striga* resistance and FOS compatibility in maize using phenotypic traits and SSR markers

Genetic diversity studies can be carried out using phenotypic or molecular markers. Phenotyping is the foremost step in identifying and categorizing germplasm for breeding purposes (Govindaraj *et al.*, 2015). Although phenotypic evaluations are limited by the effect of environment on trait expression, it offers an unparalleled means of identifying genotype variation (Twumasi *et al.*, 2017; Al-Naggar *et al.*, 2020). Accurate phenotyping provides crucial information to describe genetic resources for ideotype breeding (Ignjatovic-Micic *et al.*, 2015). Maize genotypes are usually assessed using phenotypic traits based on standard descriptors such as those developed by the International Maize and Wheat Improvement

Center and the/ International Board for Plant Genetic Resources (CIMMYT and IBPGR, 1991). The key phenotypic traits include days to flowering, days to maturity, anthesis-silking interval, plant height, ear height, 100 seed weight, grain yield and *Striga* parameters such as the number of *Striga* plants emerged, and *Striga* plant height and vigour. For efficient germplasm characterization, phenotyping is often complimented with DNA-based molecular markers.

Molecular markers may be effective in elucidating the genetic variability among genotypes (Smith and Smith, 1992; Maniruzzaman *et al.*, 2018). Genetic diversity analyses have been done using several DNA markers (Senior *et al.*, 1998; Legesse *et al.*, 2007; André *et al.*, 2015; Kumari *et al.*, 2018). Simple sequence repeat (SSR) or microsatellites are frequently used because of their high polymorphism, detection of multi-allelic variation, co-dominance, reproducibility, ease of detection by polymerase chain reaction (PCR), relative abundance with a uniform coverage within the maize genome, and their requirement of a small amount of DNA (Powell *et al.*, 1996; Saxena *et al.*, 2010; Xu *et al.*, 2013; Maniruzzaman *et al.*, 2018). SSR markers have been widely used in maize genetic diversity studies to define potential heterotic groups for parental selection (Surender *et al.*, 2014; Vega-Alvarez *et al.*, 2017; Shayanowako *et al.*, 2018a).

Maize landraces are locally adapted and often harbour useful and novel genes for multiple stress tolerance and for resistance to pests and diseases (Warburton *et al.*, 2008; Shimelis and Laing, 2012; Midega *et al.*, 2016). Hence, it is imperative to exploit the genetic variability present among landraces and other locally adapted improved maize populations for breeding new varieties (Cholastova *et al.*, 2011). Landraces have a long agricultural history, are genetically diverse and have usually co-evolved with parasitic weeds, insect pests and diseases under the prevailing agroecology (Midega *et al.*, 2016). Therefore, the information on genetic diversity and genetic relationships among maize genotypes could enable breeders to identify genetically unique parents, new sources of *Striga* resistance and to develop farmer-preferred, locally adapted, and promising maize varieties in Tanzania. This would also support germplasm conservation units in the country.

1.6.4 Farmers` trait preferences, perceptions, and participatory variety development under *Striga* environment

Demand-led breeding requires consulting the end-users and key stakeholders during cultivar development and variety release. Farmers` perceptions and trait preferences are dynamic and regionally specific. The knowledge derived through participatory rural appraisal (PRA) would bring original and insightful objectives in breeding maize for *Striga* management in Tanzania. Engaging farmers at the beginning of the breeding ensures that their perceptions

about the traits they prefer in a variety, and the management of the crop, are used for breeding goals and variety selection criteria (Efisue *et al.*, 2008). Thus, the development of the *Striga* control package requires understanding the farming system, current *Striga* control options, farmers' preferred traits, and other socio-economic requirements for easy adoption and sustainability of the proposed technology package.

Incorporating farmers' opinions in breeding various crops ensures variety adoption. This is becoming increasingly popular and effective in terms of developing the suitable varieties and technologies to farmers in a reciprocal engagement (Efisue *et al.*, 2008; Mrema *et al.*, 2017a). For example, a PRA study conducted in Nigeria involving 42 rural communities enabled farmers to understand that there were two types of *Striga* damage, i.e., underground and above ground damage, with more damage being caused by underground *Striga* activity (Emechebe *et al.*, 2004). The same study enabled farmers to identify *Striga* distribution and ultimately the location of suitable sites for field trials. In another PRA study conducted in Kenya, farmers described the sharing of farming tools as one means of *Striga* spread across the community (Nambafu *et al.*, 2014). Farmers involvement in plant breeding programs is vital for the release, acceptance, and adoption of the developed varieties (Grüneberg *et al.*, 2009). PRA studies also reveal crucial traits that may not have been recognized by breeders themselves, when developing new cultivars (Danial *et al.*, 2007). Lobulu *et al.* (2019) identified and documented farmers' maize production constraints, perceptions, dominant farming systems and varietal preferences in western Tanzania. This information is essential to developing *Striga* resistant lines, as an indispensable component in the development of an integrated *Striga* control package.

1.7 Conclusions

No single management option has been found effective to control *Striga* infestations across locations and time. An integrated *Striga* management approach with host resistance as the foundation technology offers the best possibility for minimizing the impact of *Striga* in Africa. The use of *Striga* resistant maize genotypes that are compatible with *FOS*, combined with practical cultural practices, should reduce *Striga* damage. The present chapter documented the major maize production constraints, current *Striga* control options, *Striga* resistance breeding, germplasm assessment with resistance to *Striga* and compatibility with *FOS*. In addition, the review discussed combining ability effects and gene action controlling *Striga* resistance and *FOS* compatibility in maize. The literature presented in this chapter will guide the development and deployment of *Striga* resistant genotypes and an integrated *Striga* control package to boost the productivity of maize in Tanzania and similar agro-ecologies in SSA.

1.8 References

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CHAPTER TWO: Maize production constraints, traits preference and current *Striga* control options in western Tanzania: farmers consultation and implications for breeding

Abstract

Striga spp. severely affect maize yields in Tanzania causing yield losses varying from 20% to 100%. The use of *Striga* resistant varieties is an economical and environmentally friendly option that can be easily adopted by smallholder farmers. Uptake of newly developed varieties would be high if the breeding process is inclusive and consultative to farmer preferred traits and preferences. The aim of this study was to identify farmers' maize production constraints, current *Striga* control options, trait preference and perceptions among smallholder farmers in western Tanzania. Surveys were conducted in four districts, namely Igunga, Shinyanga rural, Urambo and Uyui during the 2017/2018 cropping season. Data were collected from 324 farmers using a semi-structured questionnaire (166), focus group discussions (158) and field observations. The major maize production constraints reported by farmers were; drought (97.2%), *Striga* infestation (93.1%), and insect pests in field (90.1%) and in stores (72.7%). The main *Striga* control options described by farmers across the studied districts were: hoe weeding, uprooting, manure application and crop rotation in descending order. Only 59% of the farmers used the seed of improved maize varieties of either hybrids or open-pollinated varieties (OPV) which are *Striga* susceptible, and the remaining used home saved seed. A breeding programme aiming at improving maize varieties for *Striga* resistance, including farmers' preferred traits, should be designed, and executed to control *Striga* infestations thus improving maize production, productivity, and profitability in western Tanzania.

Keywords: *Striga* infestation, *Striga* dispersal, trait preference, maize breeding, western Tanzania

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2.1 Introduction

Worldwide, maize is the third most important staple food crop after wheat and rice (Awika 2011) and it is ranked first in terms of total production (Awika 2011; FAOSTAT 2016). Tanzania has the second largest area planted to maize in Africa after Nigeria (CIMMYT 2014). In year 2016, Tanzania produced about 5.9 million tons of maize from an estimated area of 4.04 million hectares (FAOSTAT 2016). Maize is grown in nearly all agro-ecological zones, accounting for 31% of the total food production, and constitutes more than 75% of the cereal consumption in the country (Magehema et al. 2014). The per capita consumption of maize is about 73 kg/person/year, providing 60% of dietary calories and more than 35 percent of utilizable protein (CIMMYT 2014). Despite the role of maize in the country, its productivity is still very low with average yields between 1.0 and 1.5 t/ha compared to its potential yield of four to five t/ha (Bisanda et al. 1998; Mbwaga and Massawe 2002; Barreiro-Hurle 2012).

The low productivity of maize is attributed to various factors including, abiotic and biotic stresses; and their interactions and socio-economic constraints. Abiotic factors include poor soil fertility, drought and heat stresses (Shiferaw et al. 2011; Cairns et al. 2013). Biotic factors include *Striga* weed infestations, use of low yielding germplasm, diseases, stalk borers and storage pests (Mbwaga and Massawe 2002). Among the biotic stresses, *Striga* spp. belonging to the family Orobanchaceae, are one of the most serious constraints to major crops in sub-Saharan Africa (SSA). The genus comprises of 43 spp. worldwide, of which 11 spp. are considered parasitic to agricultural crops (Ejeta 2007b). Among the spp., *Striga hermonthica* (Del.) Benth., *S. asiatica* (L.) Kuntze, *S. forbesii* (Benth.), *S. aspera* (Willd.) Benth., and *S. densiflora* (Benth.) Benth. cause immense losses in cereal crops (Ejeta 2007a; Parker 2009; Timko et al. 2012). Among all the cereals, maize is exceptionally susceptible to *Striga* infestations especially under drought and suboptimal soil nitrogen conditions, which are common in marginal maize production areas of SSA (Ejeta 2007a; Badu-Apraku and Akinwale 2011; Menkir et al. 2012).

Cereal yield losses due to *Striga* in SSA range from 20 to 100% depending on *Striga* seed density, cultivar grown, soil fertility status and climatic conditions (Massawe et al. 2002; Teka 2014). More than 10 million tons of cereal grains are lost annually due to *Striga* damage in the SSA region (Watson et al. 2007). Studies done by MacOpiyo et al. (2009), estimated cereal production losses in Tanzania due to *Striga* to be over 890,000 tons, maize incurring losses of 464,599 tons (52%), followed by rice (232,913) and sorghum (192,975) from a total area of 963,532 hectares.

Striga control is more difficult compared to that of other weeds due to its biology. The weed is highly prolific producing large quantities of very small seeds that can remain viable in the

soil for 20 years or more (Gurney et al. 2003; Gurney et al. 2006). A single plant can produce up to 500,000 tiny dust-like seeds, which mature at different times (Yoneyama et al. 2010). The large number of parasitic seeds produced increases the chance that some *Striga* seeds will find a suitable host (Ejeta 2007b). Under the smallholder farming system, the available cultural control practices like hand-hoe weeding and uprooting are laborious and time consuming hence expensive and are seldom effective as severe damage occurs even before germination (Massawe et al. 2002; Sibhatu 2016). Chemical control like the use of methyl bromide gas, ethylene and post emergence herbicides like 2,4-D are very expensive and not accessible by farmers in low-input agricultural production systems. Use of host plant resistance combined with sound cultural practices is essential for enhancing crop yields. However, development and deployment of *Striga* resistant maize cultivars is yet to be explored in Tanzania. This requires in-depth understanding of farmers' trait preferences, production challenges, farming systems, current *Striga* control options and socio-economic requirements to be able to breed elite *Striga* resistant varieties.

Participatory rural appraisal (PRA) is a multidisciplinary tool useful to understand farmers' knowledge, experiences, challenges, preferences and their needs (Chambers 1992; Mrema et al. 2017). Farmers' perceptions and trait preferences are dynamic and region-specific and are not static, and the knowledge derived through PRA would bring insightful gains in breeding maize for *Striga* management in Tanzania. Farmers' involvement in plant breeding programs is vital for the release, acceptance, and adoption of the developed varieties (Grüneberg et al. 2009). This helps in revealing a number of crucial traits that would not have been considered by breeders themselves in developing new cultivars (Danial et al. 2007). There is a lack of current information on maize production constraints, farmers' traits preference, their perceptions and current *Striga* control strategies in western Tanzania. Therefore, the objective of this study was to assess farmers' maize production constraints, *Striga* control measures and farmer's preferred traits in *Striga* infested areas of western Tanzania. Such information is vital for developing effective and environmentally friendly *Striga* control measures for improved maize productivity and food security of maize farming communities in western Tanzania.

2.2 Materials and methods

2.2.1 Description of study sites

The study was conducted in Tabora (Igunga, Uyui and Urambo districts) and Shinyanga (Shinyanga rural district) regions of Tanzania (Figure 2.1). The study districts in the two regions were selected due to their high infestation and the distribution of *S. asiatica* and *S. hermonthica*. In addition, the locations represent major maize production regions and *Striga* hot-spot areas where either *S. asiatica* or *S. hermonthica* dominates. Also, co-parasitism

exists between *S. asiatica* and *S. hermonthica* in the same field infesting the same host (maize) in Igunga district. Tabora region receives a unimodal and erratic rainfall, with a mean of 880 mm per year that falls in the period between November and April with a short dry spell of two to three weeks in between January and February. The districts are further characterized by long dry seasons of about five to six months with temperatures ranging from 14.6°C in June to 32.5°C in October and a mean daily temperature of 23°C. Soils are predominantly sandy to loamy. Shinyanga rural district has a well-drained clay loamy soil with low fertility and a growing season running from November to April.

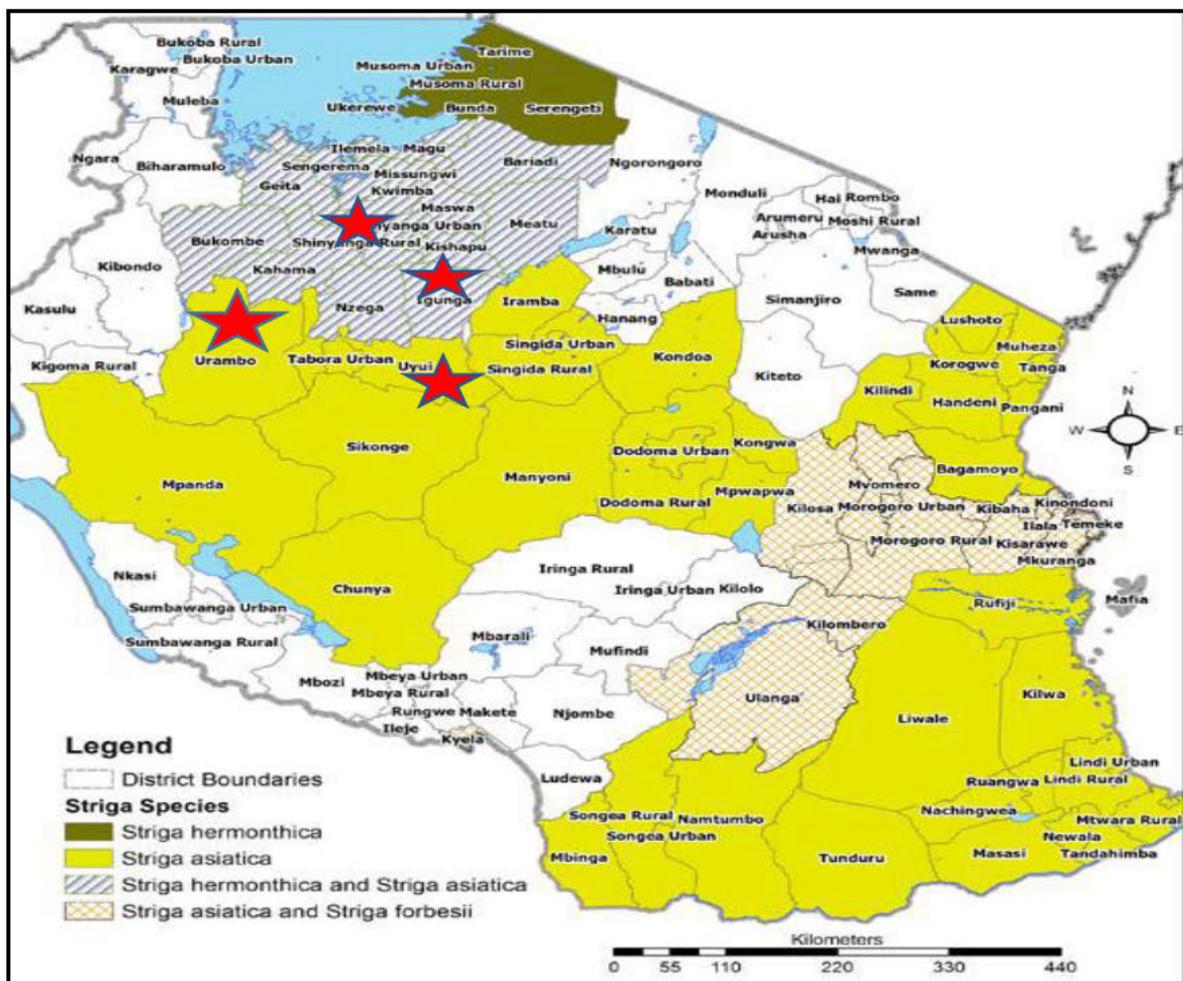


Figure 2.1. *Striga* distribution in Tanzania (adapted from MacOpiyo et al. 2009) and the location of the four study districts marked with a red star.

2.2.2 Sampling procedures

Purposive sampling was employed to increase the probability of including appropriate sites and samples targeting *Striga* hotspots. The details of the study locations' geographical positioning systems (GPS) are presented in Table 2.1. In each district, two wards were selected; and in each ward two villages were selected, thus a total of 16 villages were sampled. In each village, at least 10 farmers were interviewed individually or as a group. A total of 324 farmers were interviewed, out of which 166 were for structured survey using semi-

structured questionnaire, and 158 were for focus group discussions (FGDs) across the study districts. FGDs were conducted in each district using checklists developed to guide discussions. Sixteen FGDs were conducted across the four districts with each group comprising of at least eight participants. The FGDs composed of farmers, community leaders, extension agents and key informants.

Table 2.1. Location of the study sites in western Tanzania

District	Ward	(geographic coordinate)	Village	Altitude (m.a.s.l)
Igunga	Mbutu	(4.238°S; 33.899°E)	Mbutu; Mwang'halanga	1038
	Nanga	(4.257°S; 33.609°E)	Bulyang'ombe; Igogo	1141
Shinyanga Rural	Samuye	(3.783°S; 33.350°E)	Ibingo; Isela	1077
	Mwalukwa	(3.490°S; 33.361°E)	Mwalukwa; Bulambila	1046
Urambo	Kapilula	(5.088°S; 32.113°E)	Kapilula; Urassa A	1107
	Usoke	(5.087°S; 32.325°E)	Usoke; Usongelani	1139
Uyui	Isikizya	(4.892°S; 33.105°E)	Ilalwansimba; Ibushi	1236
	Magiri	(4.936°S; 33.057°E)	Magiri; Mayombo	1228

Note; m.a.s.l – meters above sea level

2.2.3 Data collection and analysis

A semi-structured, open and closed-ended questionnaire was prepared, pre-tested and administered to farmers through interviews during the 2017/2018 cropping season. The interviewees provided information on: household descriptions, farm size, farming system, maize production constraints, maize preferred traits, current *Striga* control options, modes of *Striga* seed dispersal, farmers' source of maize seed and important crops grown. Transect walk across each village and in selected farm fields was done to appraise *Striga* severity and validate data generated from individuals' interviews. Other PRA tools used to gather information included FGDs, absolute and pairwise ranking. FGDs allowed for joint identification and prioritization of farmers' traits preference and constraints. Farmers' maize preferred traits and perceived constraints were listed and ranked using a pair-wise matrix technique (Ceccarelli, 2012). The values of 1 and 0 were assigned to the most and least preferred trait, respectively. The same applied for the constraints facing maize production. Finally, the scores were counted, and traits were ranked based on relative values in a particular location. Mean score values were used to rank maize production constraints and farmers' trait preference across sites. The research team comprised of six multidisciplinary members, including two agricultural research officers (breeders), two research assistants, one agricultural extension officer from District Agricultural and Irrigation Office and one ward agricultural extension officer. Other participants were farmers and village leaders, who participated in either personal interviews or FGD.

Quantitative and qualitative data collected through the questionnaire were coded and subjected to statistical analyses using the Statistical Package for Social Sciences version 24 (SPSS, 2016) computer software. Cross-tabulation were computed, and descriptive statistics were generated to summarize data from the questionnaires and FGDs. To make statistical inferences, Pearson Chi-square test procedure were computed to analyse relationships between maize growing sites and variables.

2.3 Results

2.3.1 Demographic profile and socio-economic aspects of the interviewed farmers

A summary for the demographic profile and socio-economic aspects of the interviewed farmers is presented in Table 2.2. Out of the 166 interviewees, 65% were males and 35% were females. Gender parity was however not significantly different. The results indicated that age of the respondents differed significantly among the studied districts ($X^2=18.312$, $P=0.005$). Most of the respondents (44%) were within the age range of 18 to 36 years followed by age range of 37 to 55 (36%). This imply that, the bulk of youth were engaged in agriculture across the study area with Igunga taking the lead (70%). Sources of income across the study districts were significantly different ($X^2=24.66$; $P=0.016$). Crop production (99%) was the main source of income, followed by livestock rearing. Igunga (51%) and Shinyanga (46%) had high proportion of farmers engaged in cattle and small ruminants rearing. Livestock kept were mainly indigenous cattle (38%), goat and sheep (30%) and chicken (29%). Education level was not significantly different ($P<0.05$). A large number of the respondents had attained primary school education (73%) with very few others achieving ordinary level secondary school certificate (8%). On the other hand, 1% of the respondents had attained tertiary education while 18% did not attain formal education. Household demographics indicated that more than half of the families (52%) in the study area comprised of five to eight people and only 7% of the households had a family size of more than 13 individuals. On the other hand, 24% of the households had a family size of not more than four individuals while 18% comprised of nine to 12 members. Farm sizes differed significantly across the study sites ($X^2 = 19.258$, $P=0.023$). Fifty-three percent of the households in the surveyed areas owned more than five acres of agricultural land. And about 25% of the respondents owned between two to three acres.

Table 2.2. Demographic profile and socio-economic activities of the interviewed maize farmers in western Tanzania during the 2017/18 cropping season

Variable	Category	Districts				Mean	DF	χ^2	P-value
		Urambo	Uyui	Igunga	Shinyanga rural				
Gender	Male	67	51	70	71	65	3	4.664	0.198
	Female	33	49	30	29	35			
Age (years)	18 to 36	31.1	32.6	70.3	43.9	44.5	6	18.316	0.005
	37 to 55	40.0	41.9	27.0	36.6	36.4			
	≥56	28.9	25.6	2.7	19.5	19.2			
Education level	Illiterate	7	19	24	24	18	9	0.141	13.502
	Primary	89	65	73	63	73			
	Secondary	4	14	3	10	8			
Source of income	Tertiary	0	2	0	2	1	12	24.664	0.016
	Crop production	100	98	100	100	99			
	Cattle rearing	20	32	51	46	38			
	Small ruminants	7	16	51	44	30			
	Poultry	22	21	27	44	29			
Family size in number	Shop	7	5	0	2	3	9	9.828	0.365
	≤4	24	21	14	37	24			
	5 to 8	58	58	51	39	52			
	9 to 12	13	14	24	20	18			
Farm size in acres	≥13	4	7	11	5	7	9	19.258	0.023
	1 to 1.5	11	7	0	7	6			
	2 to 3	31	37	19	12	25			
	3.5 to 5	11	7	16	29	16			
	>5	47	49	65	51	53			

Note; DF - Degrees of freedom; χ^2 – Chi-square

2.3.2 Commonly grown crops and cropping system in the surveyed areas

Maize, groundnuts, rice, and sweet potato ranked in descending order of importance in the study sites (Table 2.3). Results of Chi-square test for independence revealed that crops grown by farmers differed significantly across the study areas ($\chi^2=122.684$; $P=0.000$). In addition, 20% and 12% of the respondents in Urambo and Uyui districts, respectively depended on tobacco as a cash crop. On the other hand, about 49% and 17% of the households in Igunga and Shinyanga rural, respectively depended on cotton as a cash crop. The rest of other crops serve a dual purpose, as cash and subsistence crops, but mainly subsistence given that most farmers hold small farms meant to grow crops to be consumed by the family. Sole cropping, intercropping and crop rotation were the dominant cropping systems practiced by farmers across the studied districts (Figure 2.2). About 84% of the farmers planted maize as a sole crop, while 21% intercropped maize with other crops. Crops commonly intercropped with maize were groundnuts, green gram, common beans, and

cowpea. About 4% of the respondents practiced crop rotation across the study sites with an exception of Igunga districts

Table 2.3. Commonly grown crops across the study sites in western Tanzania.

Crop	Name of the district				Mean	Rank	DF	χ^2	P- value
	Urambo	Uyui	Igunga	Shinyanga rural					
Maize	100	100	100	100	100	1			
Groundnuts	62.22	37.21	8.11	39.02	36.64	2			
Rice	26.67	13.95	18.92	34.15	23.42	3			
Sweet potato	8.89	11.63	16.22	31.71	17.11	4			
Cotton	0.00	0.00	48.65	17.07	16.43	5	27	122.684	0.000
Green gram	0.00	2.33	35.14	12.20	12.41	6			
Tobacco	20.00	11.63	0.00	0.00	7.91	7			
Sorghum	0.00	0.00	18.92	17.07	9.00	8			
Common bean	2.22	4.65	0.00	2.44	2.33	9			
Cowpea	0.00	4.65	0.00	2.44	1.77	10			

Note; DF - Degrees of freedom; χ^2 – Chi-square; crops with lower ranks are highly preferred, high ranks less preferred

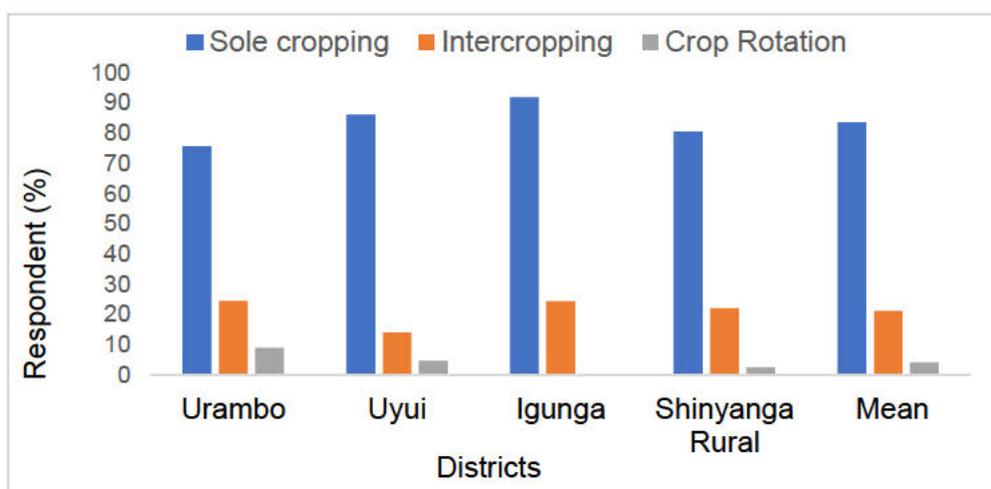


Figure 2.2. Maize cropping systems practiced in the study district in western Tanzania

2.3.3 Farmers` perceived maize production constraints

The major maize production constraints described by farmers` in the study districts are presented in Table 2.4. Among the 10 maize production challenges reported by farmers across the study sites; drought (97.2%) was ranked the most important constraint, followed by *Striga* infestation (93.1%) and field insects (90.1%) especially stalk borers (*Chilo partellus* (Swinhoe)), *Busseola fusca* (Fuller) and fall armyworm (FAW) (*Spodoptera frugiperda*) (JE Smith. Other maize productions constraints reported by farmers were; storage insects, especially grain borers (72.7%), lack of financial capital (55.6%), maize streak virus (MSV) (36.9%), poor soil fertility (30.6%), termites (24.3%) shortage of labour (14.2%), and fake

seed (8.9%). Chi-square test analysis revealed that MSV differed significantly across sites ($\chi^2=13.92$; $P=0.043$). Additionally, poor soil fertility differed significantly across the studied districts ($\chi^2=8.7$; $P=0.034$). During FGDs, some constraints emerged like timely delivery of fertilizer, inadequate extension services and high prices of inputs but did not earn scores during pairwise ranking.

Table 2.4. Farmers` perceived maize production constraints across the study districts in western Tanzania during the 2017/18 cropping season

Constraint	Category	Urambo	Uyui	Igunga	Shinyanga rural	Mean	DF	Overall rank	χ^2	P-value
Drought	Yes	91.11	97.67	100.00	100.00	97.20	3	1	7.812	0.050
	No	8.89	2.33	0.00	0.00	2.80				
<i>Striga</i> infestation	Yes	95.56	97.67	86.49	92.68	93.10	3	2	4.500	0.212
	No	4.44	2.33	13.51	7.32	6.90				
Stalk borers	Yes	86.67	83.72	97.30	92.68	90.09	3	3	4.842	0.184
	No	13.33	16.28	2.70	7.32	9.91				
Grain borers	Yes	64.44	74.42	81.08	70.73	72.67	3	4	2.957	0.398
	No	35.56	25.58	18.92	29.27	27.33				
Lack of capital	Yes	44.44	65.12	56.76	56.10	55.60	3	5	3.865	0.276
	No	55.56	34.88	43.24	43.90	44.40				
Maize Streak Virus (MSV)	Yes	44.44	41.86	27.03	34.15	36.87	3	6	13.923	0.043
	No	55.56	58.14	72.97	65.85	63.13				
Poor soil fertility	Yes	31.11	44.19	32.43	14.63	30.59	3	7	8.702	0.034
	No	68.89	55.81	67.57	85.37	69.41				
Termites	Yes	26.67	16.28	29.73	24.39	24.27	3	8	2.243	0.523
	No	73.33	83.72	70.27	75.61	75.73				
Shortage of Labour	Yes	17.78	9.30	2.70	26.83	14.15	3	9	10.533	0.015
	No	82.22	90.70	97.30	73.17	85.85				
Fake seed	Yes	6.67	2.33	21.62	4.88	8.87	3	10	4.599	0.054
	No	93.33	97.67	78.38	95.12	91.13				

DF – Degrees of freedom; χ^2 – Chi-square; constraints with lower ranks are the most yield limiting ones, high ranks less limiting factors

2.3.4 Farmers` preferred traits of maize varieties

The criteria used by farmers in the selection of maize varieties across the study sites were listed, compared on one to one basis according to pairwise matrix, are presented in Table 2.5. Chi-square test analysis revealed that farmer preferred traits differed significantly across sites ($\chi^2=46.62$; $P=0.011$). Ranking of mean scores across sites in order of importance revealed that drought tolerance, *Striga* resistance, grain yield, resistance to field insects, and earliness were the most desirable maize traits preferred by respondents. Other important traits that ranked fifth, sixth and seventh were resistance to diseases, large kernels, good poundability, good taste in roasting and tolerance to storage pests.

Table 2.5. Pair-wise ranking of farmers` maize preferred traits across the study sites in western Tanzania during the 2017/18 cropping season

Maize traits	Districts/scores				Mean scores	Rank
	Urambo	Uyui	Igunga	Shinyanga rural		
Drought tolerance	23	11	13	16	16	1
Striga resistance	11	12	14	12	12	2
Grain yield	4	6	5	8	6	3
Resistance to field insect pests	6	0	3	8	4	4
Earliness	3	2	2	9	4	4
Resistance to disease	3	0	0	4	2	5
Large kernels	0	0	0	3	1	6
Good poundability	0	2	0	0	1	6
Sweet when roasting	0	2	0	0	1	6
Tolerance to storage pests	0	0	0	1	0	7
Overall mean score					5	
DF					27	
χ^2					46.62	
P-value					0.011	

DF - Degrees of freedom; χ^2 – Chi-square, traits with lower ranks are highly preferred, high ranks are less preferred

2.3.5 Maize varieties grown, sources of maize seed for planting and use of other inputs

A list of maize cultivars grown across the four surveyed districts was recorded using their local names and is presented in Table 2.6. Farmers reported both maize landraces and improved varieties that had been grown across the study districts. Some of the landraces reported were grown in a particular district, while others have been grown in more than one district. For instance, Katumbili, have been reported across the four surveyed districts, while Gembe, Bunane and Katumani were reported in three districts out of four. The farmers' varieties have been maintained by the farmers from season to season through selection and bulking. About 45% of the interviewed farmers across the districts used own saved seeds selected from previous harvests for planting (Figure 2.3). Urambo district was the leading in seed recycling (66.7%) and Uyui being the least (23%) (Figure 2.3). Some of the described landraces were obsolete varieties that have been released in the 1970s like ilonga (released as Ilonga Composite White) and ukiliguru (released as Ukiliguru Composite A). These landraces and some of the OPVs like Kilima and Situka have been grown for quite a long time due to their good characteristics. This includes adaptability to environmental stresses, grain quality and earliness. There was a significant difference among respondents on maize varieties grown ($\chi^2=12.675$; $P=0.048$) (Table 2.7). On average, more than 30% of the interviewed farmers grow local maize varieties and about 60% of the interviewed farmers

grow improved maize varieties. Furthermore, more than 10% of the respondents grow both improved and local varieties concurrently. Landraces were grown mainly for home consumption while improved varieties are for the market; though small quantities may be consumed. The predominant sources of maize seeds across the studied districts were stockists and farmer saved seed (Figure 2.3). On average, 45% of the interviewed farmers use home saved seed for planting while 60% obtain maize seeds for planting from stockists. Uyui (72%) and Shinyanga rural (66%) were the leading districts with a higher proportion of farmers purchasing maize seeds from stockists (Figure 2.3). Other sources of maize seed described by the farmers include; market (5%), neighbour (3%), cooperative (1%) and research institute.

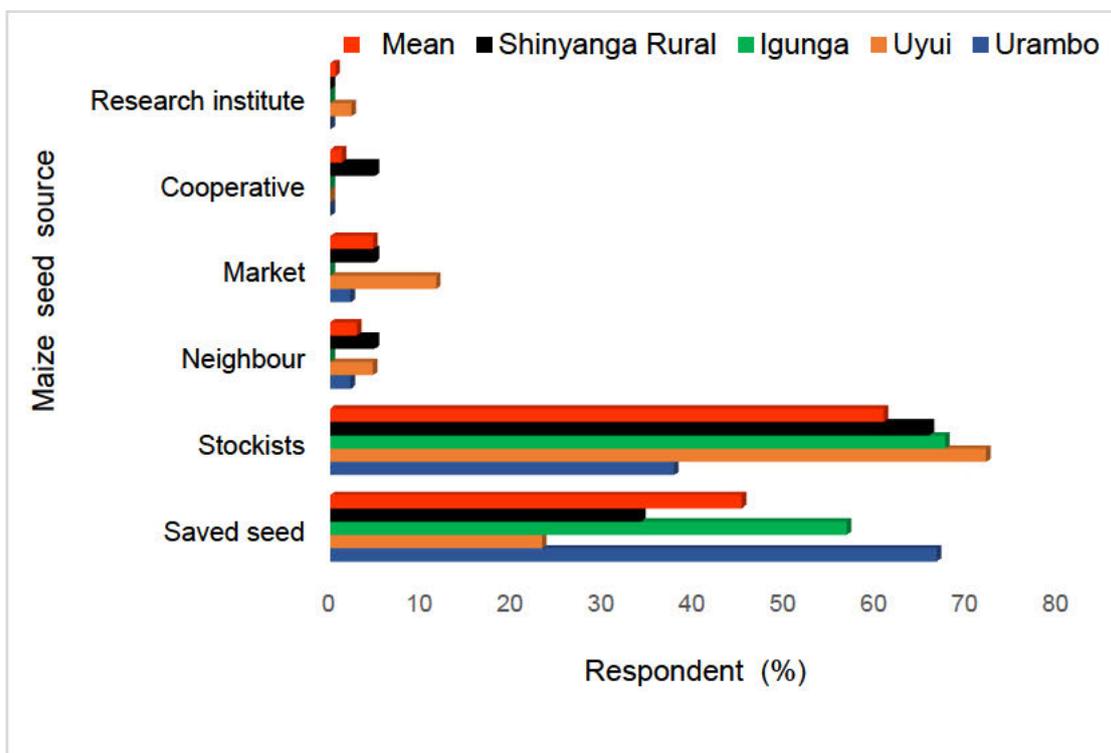


Figure 2.3. Farmers` source of maize seed for planting in western Tanzania

Table 2.6. Farmers' trait preferences in maize varieties grown across the study districts in western Tanzania

District	Variety name	Agro - morphological characteristics	
		Preferred traits	Non-preferred traits
Igunga	Yanga, Katumbili, Gembe	Tolerance to storage pests, lodging tolerance	Late maturity, low grain yield
	Kabelegete, Ndala saba	Early maturity, drought tolerance, sweet when roasted	<i>Striga</i> susceptible, drought susceptible, non-uniform
	Seedco 513, Pannar, Situka	Drought tolerance, early maturity	Susceptible to termites, susceptible to storage insects, Poor milling quality, <i>Striga</i> susceptible
Shinyanga rural	Gembe, Katumbili, Yanga	Tolerance to storage pests, drought tolerance	Late maturing, low grain yield, susceptible to storage insects
	Bunane, Kilima, Situka	Sweet when roasted, early maturity, hard kernels	<i>Striga</i> susceptible, susceptible to diseases, low yield,
	Seedco, Pannar 4M -19	Early maturity, drought tolerance, lodging tolerance	Poor milling quality, high fertilizer rates, less kernel weight
Urambo	Katumbili, Ilonga, Bunane	Tolerance to storage pests, big cobs, heavy flour	Non-uniform, drought susceptible
	Ukiliguru, Katumani	Early maturity, good milling quality, heavy flour	<i>Striga</i> susceptible, low grain yield, drought susceptible
	Nyati, Pundamilia, Seedco Lubango	Drought tolerance, early maturing, uniformity High grain yield, drought tolerance	Poor milling quality, need high fertilizer rates, <i>Striga</i> susceptible, susceptible to storage insects
Uyui	Pioneer, Lubango	High grain yield, drought tolerance, uniformity	Poor germination, susceptible to storage insects
	Pannar 4M - 19, DKC 8053	Early maturity, drought tolerance, large kernels	<i>Striga</i> susceptible, not good when roasted, poor milling quality
	Katumbili, Gembe, Situka	High grain yield, drought tolerance, big cobs	<i>Striga</i> susceptible, late maturity, non-uniform,
	Katumani, Ukiriguru, Ilonga	Early maturity, heavy flour, good milling quality Sweet when roasted, less fertilizer use	Low grain yield, non-uniform

2.3.6 Use of other farm inputs

The use of various inputs for crop production across the study districts is presented in Table 2.7. Chi-square test analysis revealed significant differences among respondents for the use of fertilizers in the study sites ($\chi^2=140.559$; $P=0.000$). About 49% of the interviewed farmers used inorganic fertilizers across the study districts. Urambo (93%) and Uyui (86.1%) districts were the main users of inorganic fertilizers than other districts. About 37% and 11% of the farmers in Shinyanga rural and Igunga respectively used animal manure for crop production. There were significant differences in sources of labour used across the four districts ($\chi^2=19.385$; $P=0.004$) (Table 2.7). About 80% and 38.4% were family and hired labour for crop production respectively. Less than 10% of the respondents used community labour across the study sites. With community labour, society members during the season organize themselves and work for one family per day while that family providing food and drinks for the society labour in that day. The following morning is the turn for another household. This practice is common among the Sukuma society in Shinyanga and Tabora regions. The use of agrochemicals in crop production across the study districts was not significant ($\chi^2=0.591$; $P=0.899$). More than 96% of the interviewed farmers applied neither herbicides nor insecticides.

Table 2.7. Farmers` use of various production inputs for crop production in the study area during the 2017/18 cropping season

Input	Type/source	Districts				Mean	DF	χ^2	P-value
		Urambo	Uyui	Igunga	Shinyanga rural				
Fertilizer	Inorganic	93.33	86.05	13.51	2.44	48.83	6	140.559	0.000
	Organic	0.00	0.00	10.81	36.59	11.85			
	Both	2.22	6.98	0.00	0.00	2.30			
Variety	Local	46.67	16.28	29.73	29.27	30.49	6	12.675	0.048
	Improved	40.00	72.09	59.46	65.85	59.35			
	Both	13.33	11.63	10.81	4.88	10.16			
Chemicals	Yes	2.22	4.65	2.70	2.44	3.00	3	0.591	0.899
	No	97.78	93.02	97.30	97.56	96.41			
Labour	Family labour	82.22	79.07	75.68	75.61	78.14	6	19.385	0.004
	Hired labour	40.00	46.51	37.84	29.27	38.40			
	Communal labour	2.22	0.00	8.11	24.39	8.68			

DF - Degrees of freedom; χ^2 – Chi-square

2.3.7 Effects of *Striga* infestation, dispersal mechanisms and current control strategies

The farmers described several effects of *Striga* infestation on maize crop and these are presented in Table 2.8. Chi-square test analysis revealed no significant difference among *Striga* infestation effects on maize across the studied districts ($\chi^2=16.734$; $P=0.16$). The most commonly reported effects of *Striga* weed infestation on maize were stunted growth (93%), wilting (58%), yellowing (52%) and withering or complete death of the plants (7%). Farmers' appraisal of maize grain yield reduction due to *Striga* infestation ranged between 20 to 100% and are presented in Figure 2.4. During FGDs, farmers reported *Striga* as most damaging at the pre-flowering stage of maize growth especially under low moisture caused by low and erratic rainfall. There was no significant difference among the agents responsible for *Striga* dispersal across the surveyed districts ($\chi^2=17.456$; $P=0.133$) (Table 2.9). The most reported factors responsible for *Striga* seed dispersal in the surveyed areas were; wind (39%), animals (27%), water (26%) and sharing of farming tools (9%). In addition, about 35% of the respondents described that *Striga* seeds are always there in the soil. More than 59% of the respondents used hand-hoe weeding to reduce the impact of *Striga* infestation across the study districts (Figure 2.5). Igunga (73%), Urambo (67%) and Uyui (60%) were the main users of hand weeding practices. Other main *Striga* control options used across the surveyed districts include; uprooting (53%), manure application (42%) and crop rotation (30%) (Figure 2.5).

Table 2.8. Farmers' description of noticeable *Striga* symptoms in maize fields across the study districts in western Tanzania during 2017/18 growing season

<i>Striga</i> symptoms	Districts				Mean	DF	χ^2	P-value
	Urambo	Uyui	Igunga	Shinyanga Rural				
Stunted growth	86.67	90.70	97.30	97.56	93.06			
Wilting of plants	75.56	58.14	40.54	56.10	57.58			
Yellowing of plants	37.78	48.84	62.16	60.98	52.44	12	16.734	0.160
Withering of plants	15.56	6.98	5.41	0.00	6.98			
Red flowered plants	2.22	2.33	0.00	0.00	1.14			

DF – Degrees of freedom; χ^2 – Chi-square

Table 2.9. Farmers` perceived mechanisms of *Striga* seed dispersal in study sites in western Tanzania during the 2017/18 cropping season

Dispersal mechanisms	Districts				Mean	DF	χ^2	P-value
	Urambo	Uyui	Igunga	Shinyanga rural				
Wind	44.44	41.86	37.84	31.71	38.96	12	17.456	0.133
Stay in the soil	28.89	34.88	24.32	53.66	35.44			
Animals	17.78	41.86	21.62	26.83	27.02			
Water (runoff)	31.11	25.58	29.73	19.51	26.48			
Sharing of farming tools	4.44	4.65	8.11	19.51	9.18			

DF – Degrees of freedom; χ^2 – Chi-square

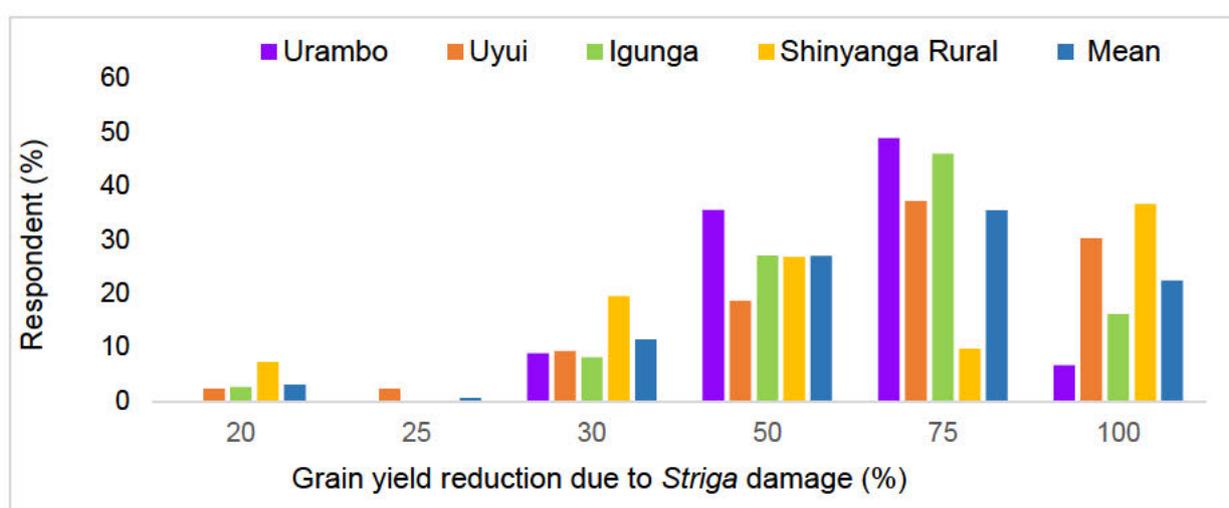


Figure 2.4. Farmers` assessment of maize grain yield reduction due *Striga* damage in the surveyed areas of western Tanzania

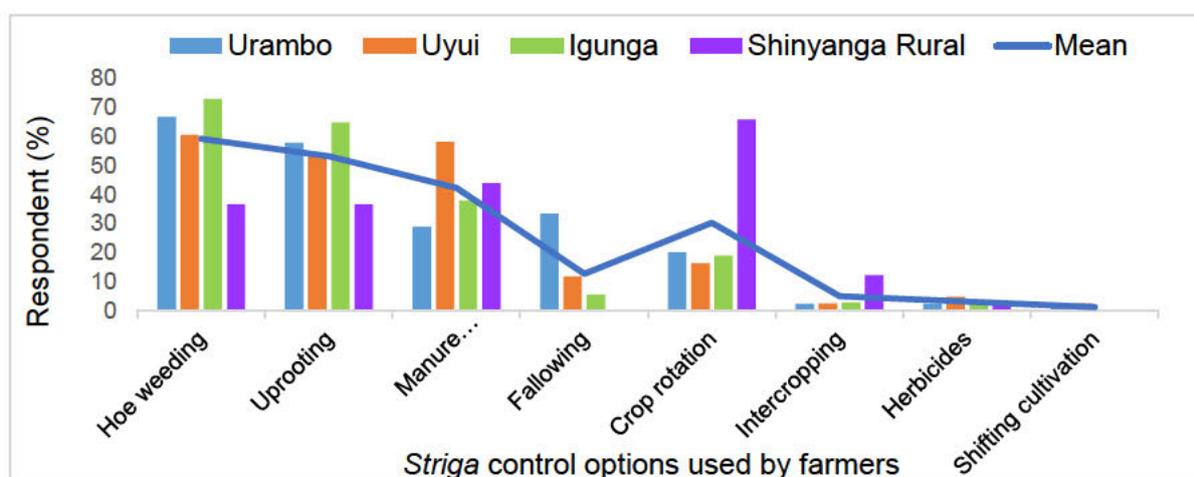


Figure 2.5. Farmers` current *Striga* control strategies in maize

2.4 Discussion

Striga infestation was the second most limiting factor of maize production after drought as described by respondent farmers across the study districts (Table 2.4). This was not surprising because in Tanzania, the western zone, central zone and some parts of lake zone are characterized by semi-arid conditions with poor soil fertility, low and erratic rainfall (Morris et al. 2001; Yanda et al. 2015). Low moisture and suboptimal soil nitrogen aggravate the spread of *Striga* infestation in marginal production areas (Ejeta 2007a; Badu-Apraku and Akinwale 2011), and maize is greatly affected under these conditions (Badu-Apraku 2007; Bua and Nowamani 2014). Sole cropping was the predominant cropping system across the surveyed districts (Figure 2.2). Discussion with farmers during transect walks, revealed that, *Striga* damage was more severe in sole maize cropping than maize intercropped with legumes. Continuous cultivation of maize or other cereal crops in the same piece of land without proper soil amendment strategies intensify *Striga* infestation (Spallek et al. 2013; Mrema et al. 2017; Tippe et al. 2017). Furthermore, monocropping contribute to the build-up of pests and diseases, poor soil fertility, and consequently grain yield reduction (Mrema et al. 2017).

In this study, farmers reported grain yield losses due to high *Striga* infestation that ranged between 20 to 100%, resulting in abandoning of maize production fields heavily infested with *Striga* (Figure 2.4). Similar results have been reported before in maize and sorghum studies in Tanzania (Mbwaga 1996; Massawe et al. 2002) and in Nigeria (Emechebe et al. 2004). In the current study, farmers were able to describe various agents responsible for *Striga* seed dissemination from infested field's to uninfested ones (Table 2.9). Animals migrating or grazing on crop residues could disseminate *Striga* seeds through their hooves or dung (Nambafu et al. 2014). In addition, use of contaminated maize seeds harvested from infested fields may accelerate the *Striga* problem. Use of contaminated seed is a common practice across the study districts as more than 45% of the interviewed farmers use maize seed harvested from the previous crop for planting (Figure 2.3). These results corroborate with the findings of Berner et al. (1994) and Emechebe et al. (2004) who found that *Striga* seeds were mostly disseminated through contaminated host crop seeds and cattle. In addition, wind, sharing of farming tools especially during main farming operations and water (runoff) during the rainy season were among the factors raised by farmers to be responsible for *Striga* seed dissemination in the study areas. These results are in agreement with those reported by Nambafu et al. (2014), when studying farmers' knowledge, attitude and practices used to control *Striga* in western Kenya. Earlier studies conducted elsewhere reported the same to be the factors exacerbating *Striga* infestation and its spread (Berner et al. 1994; AATF 2006; Hearne, 2009; Mrema et al. 2017). Furthermore, during FGDs, it was noted that, many farmers were not aware of the biology of *Striga*. Thus, after hoe weeding or hand picking, they gathered the weed remains and placed it

at the boarder of the field. By doing this, farmers unknowingly spread *Striga* seeds to uninfested fields.

In an attempt to combat *Striga* menace in the study districts, different control options were employed (Figure 2.5). The most widely used control options across the study districts were hand-hoe weeding, uprooting, manure application, crop rotation and fallowing. Other control options that were rarely used across the study sites include intercropping, herbicides application and shifting cultivation. Earlier studies conducted elsewhere, described use of some or all of these practices against *Striga* infestation (Emechebe et al. 2004; Hearne, 2009; Nambafu et al. 2014). Hand-hoe weeding which was the main control option across the studied districts has no immediate effect on protecting maize crop from *Striga* damage since much of the crop damage leading to grain yield losses occurs before *Striga* emerges above the ground (Massawe et al. 2002; Emechebe et al. 2004; Nambafu et al. 2014). However, hand-hoe weeding, and uprooting plays an important role in reducing *Striga* soil seed bank especially when done early before flowering and seed set of the parasite (Emechebe et al. 2004; Nambafu et al. 2014).

Farmers understood that *Striga* is associated with low and declining soil fertility. The application of animal manure in *Striga* infested farms improves soil fertility: thus hindering *Striga* seed conditioning and subsequent germination when in proximity with the host/pseudo host. These results are in line with earlier findings that, application of organic and/or inorganic fertilizers reduce *Striga* infestation in cereal crops (Gacheru and Rao 2001; Riches 2003; Emechebe et al. 2004). Additionally, manure supplies nutrients to the plant throughout the plant life cycle as compared to inorganic fertilizers which are prone to leaching (Riches 2003). In addition, intercropping as a *Striga* control option was practiced with only few households (21%) across the study sites with main users coming from Igunga and Urambo. Maize was mainly intercropped with groundnuts, cowpea and green gram in the study areas. Other reasons for intercropping apart from *Striga* control was more food or cash, maximize labour use and crop diversification (Katinila et al. 1998). Furthermore, the nitrogen rich residues/mulch from the legumes, protect the soil surface, suppress weeds, contribute to soil organic matter and improve soil fertility (Punyalue et al. 2018). Most of these control practices are labour intensive thus, it may not be a viable option for families with few members or with large production areas unless they could afford hired labour (Nambafu et al. 2014). The number of individuals per household indicated a good availability of labour for farming activities. For smallholder farmers, the family is the main source of labour (Mendola 2007). Even in the present study, more than 78% of the work force was coming from the family (Table 2.7). Thus, the larger the family size the greater the labour force available for farming activities and *vice versa* (Table 2.2). Furthermore, lack of capital and limited access to credit facilities hinder farmers' ability to hire labour, buy production inputs such

as fertilizer, improved seed and pesticides (Tippe et al. 2017). Earlier studies concluded that, for effective control of *Striga*, any control technology should not require further resources for implementation (Emechebe et al. 2004). Generally, no single *Striga* control option is applicable under all circumstances, rather each has its own merits and demerits (AATF 2006; Sibhatu 2016). Some management practices are best suited to agroecology while others are more readily adopted by better resource endowed families (AATF 2006), as described in the current study, where crop rotation was mainly localized in Urambo and Uyui districts.

2.5 Conclusions

For effective control of *Striga*, development and deployment of *Striga* resistance maize genotypes with farmers preferred traits, combined with farmers current control practices could form an affordable integrated *Striga* package. This should involve the use of uncontaminated seeds, avoiding sharing of farming tools, preventing animals from browsing in *Striga* infested farms, hand weeding and uprooting of *Striga* should be done at an appropriate time. Since there are no efficient seed delivery in the study area, community seed production should be initiated to provide farmers with affordable and appropriate seed. Furthermore, proper use of crop rotation, intercropping and fallowing is expected to reduce *Striga* infestation levels and the resulting damage accordingly. *Striga* residues from hoe weeding and hand picking should be burned off immediately after the operations to prevent infestation in uninfested areas. Short-term fallowing combined with leguminous (cover crops) such *Mucuna pruriens*, *Desmodium uncinatum* and *Dolichos lablab* could reduce *Striga* infestation and the associated damage tremendously. Cover crops suppress *Striga* through shading effect and soil fertility improvement through atmospheric nitrogen fixation. Furthermore, awareness creation to farmers, local agricultural extension agents on *Striga* biology, its life cycle, fecundity, seed longevity and spreading mechanism, would help stakeholders understand the dynamics of the weed, hence consider *Striga* as a threat that need special attention and management practices.

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CHAPTER THREE: Characterization of maize genotypes for resistance to *Striga asiatica*, *S. hermonthica* and compatibility with *Fusarium oxysporum* f.sp. *strigae* (FOS) in Tanzania

Abstract

Striga spp. cause significant yield loss in maize varying from 20 to 100%. The aim of the present study was to screen and identify maize genotypes with partial resistance to *S. hermonthica* (*Sh*), *S. asiatica* (*Sa*) and compatible with *Fusarium oxysporum* f. sp. *strigae* (*FOS*), a biocontrol agent. Fifty-six maize genotypes were evaluated for resistance to *Sh* and *Sa*, and *FOS* compatibility. Results showed that *FOS*-treatment significantly ($P<0.001$) enhanced *Striga* management compared to the untreated control under both *Sh* and *Sa* infestations. The mean grain yield was reduced by 19.13% in *FOS*-untreated genotypes compared with a loss of 13.94% in the same genotypes treated with *FOS* under *Sh* infestation. Likewise, under *Sa* infestation, *FOS*-treated genotypes had a mean grain yield reduction of 18% while untreated genotypes had a mean loss of 21.4% compared to the control treatment. Overall, based on *Striga* emergence count, *Striga* host damage rating, grain yield and *FOS* compatibility, under *Sh* and *Sa* infestations, 23 maize genotypes carrying farmer preferred traits were identified. The genotypes are useful genetic materials in the development of *Striga* resistant cultivars in Tanzania and related agro-ecologies.

Keywords: Host resistance; maize; *Fusarium oxysporum* f.sp. *strigae*; *Striga*; breeding; Tanzania

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3.1 Introduction

Witchweeds (*Striga* spp.), belonging to the family Orobanchaceae, are persistent weeds of grain crops in sub-Saharan Africa (SSA) and parts of Asia [1]. The obligate root hemiparasitic weed causes yield losses of 20 to 100%, depending on *Striga* seed density, cultivar susceptibility, soil fertility status and climatic conditions [2-4]. The genus comprises of more than 40 spp. worldwide, of which 11 spp. are considered parasitic on agricultural crops [5]. Of these, *Striga asiatica* (L.) Kuntze, *S. hermonthica* (Del.) Benth, *S. gesnerioides* (Willd.) Vatke, *S. forbesii* (Benth.) and *S. aspera* cause devastating yield and quality losses to staple food crops in SSA [6,7]. *Striga asiatica*, *S. hermonthica*, *S. forbesii* and *S. aspera* parasitize cereal crops, while *S. gesnerioides* parasitize legumes, including wild and cultivated spp. [6,8]. *Striga* spp. inflict severe yield losses in maize (*Zea mays* L.), sorghum (*Sorghum bicolor* (L.) Moench), pearl millet (*Pennisetum glaucum* (L.) R. Br.), rice (*Oryza sativa* L.), finger millet (*Eleusine coracana* L.) and cowpea (*Vigna unguiculata* L. Walp) [6,9].

Striga spp. affect about 100 million hectares of farmland cultivated by resource poor farmers in Africa. Consequently, it affects the livelihoods of over 300 million people who depends on the above major grain crops [5,10]. The most important cereal crop in Africa, maize, is exceptionally susceptible to *Striga* infestations. Low soil moisture caused by uneven and erratic rainfall, suboptimal soil nitrogen conditions and a lack of production inputs are common in marginal maize production areas of SSA, and these factors exacerbate the severity of losses [9,11,12]. An estimated 10 million tons of cereal grains are lost annually due to *Striga* damage in the SSA [13], which is worth an estimated 7 billion USD in SSA [5,11]. In East Africa, monetary losses due to *Striga* damage was estimated at 335 million USD per year [14]. In Tanzania alone, monetary losses due to *Striga* damage are estimated to be 173 million USD [14]. Resource poor farmers are the most severely affected community in SSA, and *Striga*-induced losses increase the occurrence of food insecurity and abject poverty. This situation calls for a sustainable *Striga* control strategy that is compatible with current agronomic practices in the existing agro-ecosystem.

Conventional weed control strategies do not work well against *Striga* spp. because of its biology and the intimate physiological relationship it has with the host [15]. The weed produces large quantities of fine seeds that can remain viable in the soil for 20 years or more [16,17]. A single plant can produce up to 500,000 tiny, dust-like seeds, which mature at different times [18,19]. The effectiveness of *Striga* seed dispersal mechanisms, which include migrating or grazing animals, wind, runoff during the rainy season and contaminated seeds, aggravate the situation [20-22]. Thus, every year some seeds germinate, some revert to dormancy and some remain in the soil unconditioned, while more seeds are added from the current generation of plants,

endlessly enriching the soil seed bank [5]. After germination, haustorial initiation occurs in response to specific chemical stimulants produced by a potential host [16,23]. The haustorium attaches, penetrates the host root and establishes a connection with the host xylem just after germination to support *Striga* growth and survival [24]. Following attachment, the parasite remains subterranean for six to eight weeks, siphoning off water, nutrients and inorganic solutes from the host xylem and/or phloem [24,25]. This is the most damaging stage, where *Striga* spp. exert a phytotoxic effect and impair photosynthesis within days of their attachment to the roots of hosts [25-27].

Under the smallholder farming system, the current control practices used include hand-hoe weeding and uprooting of *Striga* plants. However, these practices are laborious and time-consuming, and are seldom effective against *Striga* because the most severe damage leading to yield loss occurs before the *Striga* plants emerge above the ground [28,29]. A range of cultural practices such as manure application, rotating cereal crops with legumes, the use of trap crops that induce abortive germination of *Striga* seeds, shifting cultivation and long fallowing, are useful in reducing *Striga* damage and improving soil fertility [22,30,31]. However, they are not feasible for most smallholder farmers in SSA due to their need to use all agricultural lands intensively. Manure application remains the best *Striga* control option for smallholder farmers, but its application is limited by a limited supply of manure.

Chemical *Striga* control approaches includes the use of methyl bromide, application of inorganic soil amendments such as fertilizers, ethylene and post-emergence herbicides such as 2,4-D. Use of ethylene to promote suicidal germination followed by application of post emergence herbicide such as 2,4-D to prevent weed reproduction has been widely and successfully used in the USA to control *S. asiatica* in maize production [32]. Fumigation of soils with methyl bromide was reported to be effective in killing *Striga* seeds in the soil [28]. Post-emergence herbicides are useful in preventing the build-up of *Striga* seeds in the soil but may not prevent damage prior to emergence [33]. However, these options are expensive and are not accessible to most smallholder farmers who operate in low-input agricultural production systems.

A relatively recent innovation has been the use of imazapyr applications to seeds of imazapyr-resistant maize (IR maize). This has resulted in significant increases in maize yields under *S. hermonthica* infestation [33-35]. However, the IR maize technology has one main drawback in that imazapyr is toxic to most other crops grown in Africa, hence it is not suitable in mixed cropping systems, which are common in SSA [4,36].

Therefore, control measures are needed that minimize the impact of *Striga* on crop losses, reduce the *Striga* seed banks in the soil, prevent new seed production and reduce the spread of *Striga* to uninfested fields [37]. Host resistance, combined with compatible agronomic practices, may solve some of the problems. Resistant cultivars can reduce both new *Striga* seed production as well as the *Striga* seed bank in infested soils in successive seasons [10,38].

Use of resistant varieties to control *Striga* spp. is considered to be the most effective, economical and environmentally viable option for resource poor farmers [4,39]. *Striga* resistance refers to the ability of the host root to stimulate *Striga* seed germination but at the same time to prevent attachment of the *Striga* seedlings to its roots, or to kill the seedlings which attach to the roots. Tolerance refers to the ability of the host plant to withstand the effects of the parasitic plants that are already attached, regardless of their number with little yield loss [40,41]. Various studies have revealed that genes conferring resistance to *S. hermonthica* can be stacked in maize and these can intervene at several points in the pre-emergence stages of the *Striga* life cycle [38,42,43]. A significant breakthrough was attained by the International Institute of Tropical Agriculture (IITA) in developing maize genotypes with *S. hermonthica* resistance [38,43]. These genotypes could serve as a valuable genetic resource for *Striga* resistance breeding programs in SSA, including Tanzania.

Striga resistance in maize is expressed in several ways, including low stimulation of *Striga* seed germination [16,44,45], low haustorial induction [16], avoidance through root architecture (fewer thin branches) [46], escape by early maturity [47], host resistance to *Striga* attachment [46], and failure to support attached parasites (incompatibility) [16,46,48]. However, the levels of *Striga* host resistance that have been attained so far in maize are not adequate to counteract high levels of *Striga* infestation. The current *Striga* resistant/tolerant genotypes allow for the flowering and seed set of *Striga* plants, thus enriching the *Striga* seedbank in the soil [49-51]. Thus, the use of *Striga* resistant genotypes combined with a biological control agent and farmers' current agronomic practices may constitute a substantially more effective *Striga* control strategy.

Biological control denotes the deliberate use of living organisms to suppress, reduce, or eradicate a pest population [52]. The technique is less expensive and more environmentally friendly than chemical control options [53,54]. Prior research has shown that the presence of mycoherbicides in the rhizosphere of susceptible crops reduces the levels of *Striga* parasitism on the host plant [10,55,56]. Pathogenic isolates of *Fusarium oxysporum* Schlecht. Emend. Snyder & Hans f.sp. *strigae* (*FOS*) are reported to be efficient in controlling *S. asiatica* and *S. hermonthica* infestation in maize and sorghum [7,57]. The biocontrol agent is most effective when combined with *Striga* resistant genotypes and other control measures [7,10]. It is reported

that the integrated effects of *Striga*-resistant maize genotypes and *FOS* reduced *Striga* emergence by over 90% [57]. Gebretsadik [7] reported up to a 92% reduction in *Striga* emergence counts when a *FOS* treatment was applied to *Striga* resistant sorghum varieties. Beed [55] reported a reduction of *S. hermonthica* emergence by 98% and an increase in sorghum yield by 26% following *FOS* application. *FOS* can endophytically colonize the root system of the maize host, and from this base, can attack *Striga* spp. at all growth stages including seeds, seedlings and flowering shoots. Thus affecting the target prior to seed set and crop yield loss, thereby reducing the *Striga* seedbank [55,58]. Fungi are preferred to other microorganisms as bio-herbicides because they are usually host-specific, attacking only *Striga* spp. [15,59,60]. Also, fungi are highly aggressive, easy to mass produce and are diverse in terms of number of strains available [7,61]. *FOS* compatible genotypes support no or few *Striga* plants and produce relatively high yields under *Striga* infestation. Thus, the use of host plant resistance combined with *FOS* and sound cultural practices is a viable strategy for enhancing crop yields in *Striga* infested fields. The development of host plant resistance through breeding is a fundamental component of a sustainable integrated *Striga* management strategy to minimize yield losses in farmers' fields. A successful maize breeding program depends mainly on the available genetic variation within the germplasm resources [62,63]. Therefore, the aims of the present study were to screen genetically diverse maize genotypes with farmer preferred traits from a range of distinct sources and identify genotypes resistant to *S.asiatica* and *S. hermonthica*, and compatible with *FOS*, aiming to develop an integrated *Striga* control measures in Tanzania.

3.2 Materials and methods

3.2.1 Germplasm

The study used 56 genetically diverse maize genotypes consisting of 34 landraces acquired from the National Plant Genetic Resources Centre (NPGRC) – Tanzania, 18 improved open-pollinated varieties (OPVs) from the International Institute of Tropical Agriculture (IITA) – Nigeria and four OPVs from Tanzania Agricultural Research Institute (TARI) – Tanzania. The IITA collection included 17 *Striga* resistant genotypes and one *Striga* susceptible genotype, which were used as checks. The details of the studied genotypes are presented in Table 3.1.

Table 3.1. List and source of maize accessions used for the study

S/No	Germplasm code	Name/designation/pedigree	Description	<i>Striga</i> resistance status	Source/origin
1	TZA599	Ipukile	Landrace	Unknown	NPGRG/Tanzania
2	TZA604	Ipukele	Landrace	Unknown	NPGRG/Tanzania
3	TZA615	Mahindi	Landrace	Unknown	NPGRG/Tanzania
4	TZA687	Nyamula	Landrace	Unknown	NPGRG/Tanzania
5	TZA1771	Katumani	Landrace	Unknown	NPGRG/Tanzania
6	TZA1775	Mahindi	Landrace	Unknown	NPGRG/Tanzania
7	TZA1780	Mahindi	Landrace	Unknown	NPGRG/Tanzania
8	TZA1782	Mahindi	Landrace	Unknown	NPGRG/Tanzania
9	TZA1784	Mahindi	Landrace	Unknown	NPGRG/Tanzania
10	TZA2263	Mahindi	Landrace	Unknown	NPGRG/Tanzania
11	TZA2749	Mahindi	Landrace	Unknown	NPGRG/Tanzania
12	TZA2761	Mahindi	Landrace	Unknown	NPGRG/Tanzania
13	TZA2881	Mahindi	Landrace	Unknown	NPGRG/Tanzania
14	TZA3095	Landrace	Landrace	Unknown	NPGRG/Tanzania
15	TZA3181	Uruwinga	Landrace	Unknown	NPGRG/Tanzania
16	TZA3417	Mahindi	Landrace	Unknown	NPGRG/Tanzania
17	TZA3502	Katumbili	Landrace	Unknown	NPGRG/Tanzania
18	TZA3561	Mahindi	Landrace	Unknown	NPGRG/Tanzania
19	TZA3570	Oloman	Landrace	Unknown	NPGRG/Tanzania
20	TZA3614	Magereza	Landrace	Unknown	NPGRG/Tanzania
21	TZA3827	Mahindi	Landrace	Unknown	NPGRG/Tanzania
22	TZA3942	Zimbabwe	Landrace	Unknown	NPGRG/Tanzania
23	TZA3951	Mwarabu	Landrace	Unknown	NPGRG/Tanzania
24	TZA3952	Mwarabu	Landrace	Unknown	NPGRG/Tanzania
25	TZA3964	Amakuria	Landrace	Unknown	NPGRG/Tanzania
26	TZA4000	Nchanana	Landrace	Unknown	NPGRG/Tanzania
27	TZA4010	Kagire	Landrace	Unknown	NPGRG/Tanzania
28	TZA4016	Mahindi	Landrace	Unknown	NPGRG/Tanzania
29	TZA4064	Ya kieneyeji	Landrace	Unknown	NPGRG/Tanzania
30	TZA4078	Mnana	Landrace	Unknown	NPGRG/Tanzania
31	TZA4165	Ibahakazi	Landrace	Unknown	NPGRG/Tanzania
32	TZA4203	Gembe	Landrace	Unknown	NPGRG/Tanzania
33	TZA4205	Katumbili	Landrace	Unknown	NPGRG/Tanzania
34	TZA4320	Mahindi	Landrace	Unknown	NPGRG/Tanzania
35	JL01	DT-STR-Y-SYN14	OPV	Resistant	IITA/Nigeria
36	JL02	DT-STR-Y-SYN15	OPV	Resistant	IITA/Nigeria
37	JL03	DT-STR-W-SYN11	OPV	Resistant	IITA/Nigeria
38	JL04	DT-STR-W-SYN13	OPV	Resistant	IITA/Nigeria
39	JL05	STR-SYN-Y2	OPV	Resistant	IITA/Nigeria
40	JL06	TZB-STR-Susceptible	OPV	Susceptible	IITA/Nigeria
41	JL08	Z.Diplo.BC4C3-W-DTC1	OPV	Resistant	IITA/Nigeria
42	JL09	TZECOMP3DT/white DT-STRR-SYND2	OPV	Resistant	IITA/Nigeria
43	JL11	9022 – 13 Hybrid (Resistant)	OPV	Resistant	IITA/Nigeria
44	JL12	SAMMAZ – 16	OPV	Resistant	IITA/Nigeria
45	JL13	TZECOMP5C7/TZECOM3DT.C2	OPV	Resistant	IITA/Nigeria
46	JL15	1 WDC3SYN *2 white DSTR-SYN-DTC1	OPV	Resistant	IITA/Nigeria
47	JL16	2*TZECOMP3DT/W DSTR/SYN DC2	OPV	Resistant	IITA/Nigeria
48	JL17	TZLCOMP1-WCB*2C W DT-STR-SYNJ-DTC1	OPV	Resistant	IITA/Nigeria
49	JL18	STR-SYN-W1	OPV	Resistant	IITA/Nigeria
50	JL19	DT-STR-W-SYN12	OPV	Resistant	IITA/Nigeria
51	JL20	Z.DIPLO-BC4 -C3-W/ DOGONA-1/Z.DIPLO-BC4-C3-W	OPV	Resistant	IITA/Nigeria
52	JL21	TZCOM 1/ZDP-SYN	OPV	Resistant	IITA/Nigeria
53	JL22	SITUKA M1	OPV	Unknown	TARI/Tanzania
54	JL23	STAHA	OPV	Unknown	TARI/Tanzania
55	JL24	T104	OPV	Unknown	TARI/Tanzania
56	JL25	T105	OPV	Unknown	TARI/Tanzania

S/No – serial number; NPGRG – National Plant Genetic Resources Centre for Tanzania; TARI – Tanzania Agricultural Research Institute; IITA – International Institute of Tropical Agriculture; OPV – Open pollinated variety.

3.2.2 *Striga inoculum*

Striga seeds were collected from maize and sorghum fields infested with either of the two *Striga* spp. or both in the 2016/2017 growing season. The seed of *S. asiatica* was collected at the TARI – Hombolo Research Centre, Dodoma region and the TARI - Tumbi Research Centre, Tabora region, while the seed of *S. hermonthica* was collected in the Mbutu and Igogo wards, Igunga district, Tabora region. *Striga* seeds from both spp. were separately processed, packed, labelled, and stored in the Soil Science Laboratory of TARI - Tumbi for further use.

3.2.3 *Fusarium oxysporum f. sp. strigae (FOS) inoculum*

A virulent strain of *FOS* was used as the biocontrol agent. This was initially isolated from severely diseased *Striga* plants in sorghum fields in north eastern Ethiopia [7]. The host specificity and pathogenicity of the *FOS* isolate to *Striga* spp. were confirmed by Gebretsadik [7]. The Phytomedicine Department of Humboldt University in Berlin, Germany confirmed the taxonomic identification of *FOS*. Pure *FOS* spores are produced and preserved by Plant Health Products (Pty) Ltd., KwaZulu-Natal, South Africa [7]. *FOS* in a dry powder formulation (supplied by Dr M.J. Morris of Plant Health Products (Pty) Ltd) was used to coat the maize seeds before sowing. The *FOS* inoculum was applied to the whole surface of the seed. The specialized hairy structures present at the tip of maize seeds (the pedicel) bind enough *FOS* inoculum to be effective, without the need for a sticker.

3.2.4 Experimental procedure

The experiment was established during the 2017/2018 growing season in a screen house facility at TARI -Tumbi Research Centre situated in the Tabora Municipality, western Tanzania. The centre is located at 5°03'S latitude and 32°41'E longitude with an altitude of 1190 m. The experiment was established using a split-plot design, with a *FOS* treatment being the main plot factor and maize genotypes as the subplot factor. The genotypes were sown in a screenhouse using polyethylene plastic pots (250 mm diameter and 350 mm height) filled with a growing medium consisting of topsoil and sandy soil mixed at a ratio of 6:3. A total of 1680 pots were filled with the growing medium and divided into sets of 336, and two equal sets of 672 pots. The set of 336 pots was not infested with *Striga* seeds nor treated with *FOS* (the untreated, uninoculated control). The first set of 672 pots was infested with 30 mg of one-year old *S. asiatica* (*Sa*) seeds uniformly distributed at a depth of 30 mm in the growing medium. The second set of 672 pots was infested with 30 mg of one-year old *S. hermonthica* (*Sh*) seeds. After 14 days of *Striga* seed preconditioning, maize seeds were sown in the following order: half of the pots (336) assigned either to *Sa* or *Sh* were planted with two seeds of the maize genotypes coated with 26.8 mg of *FOS* powder. The seeds planted in the other 336 pots infested with *Sa* or *Sh* were not inoculated with *FOS*. After emergence, maize plants were thinned to one seedling per pot.

Each experimental plot consisted of two pots, and these were replicated three times for each treatment. The trial was maintained following standard agronomic practices for maize in Tanzania. Weeds other than the two *Striga* spp. were uprooted manually.

3.2.5 Data collection

Data were collected based on maize agronomic characters and *Striga* resistance parameters. The following data were recorded on maize plants: anthesis date (AD) was recorded as the number of days from sowing to when 50% of the plants in a plot shed pollen. Silking date (SD) was recorded as the number of days from planting to when 50% of the plants in a plot produced silks. Anthesis-silking interval (ASI) was determined as the difference between days to 50% silking and 50% anthesis. The days to 75% maturity (DM) were recorded as the number of days from planting to when 75% of the plants reached physiological maturity. Physiological maturity is attained when a black separation layer forms at the pedicel, and grain moisture content is about 35%. This usually occurs after a growing period of 90 to 120 days (early varieties) or 170 to 190 days (late varieties) [64]. Plant height (PH) was measured from the base of the plant (expressed in cm) to the top of the first tassel branch. Ear height (EH) was measured (cm) from the ground level to the node bearing the uppermost ear. Grain yield/plant (GYD) was determined as the weight (g), of the grain from the ears of individual plants after shelling, converted to a constant moisture of 12.5%. Hundred kernel weight (HKWT) was recorded based on a weight (g) of 100 kernels at field moisture content and converted to a constant moisture of 12.5%. The above ground biomass (AGB) was determined by weighing (g/plant) the above ground plant parts which included: leaves, stems, and ears. Individual maize plants were cut at the base of the stem.

The following *Striga* parameters were recorded: *Striga* emergence counts at eight (SEC8) and 10 (SEC10) weeks after planting as the number of emerged *Striga* plants per genotype. A rating of host plant damage was made at eight and 10 weeks after planting, denoted as SDR8 and SDR10, using a scale of 1 to 9 as described by Kim [40]. A scale of 1 = normal maize growth with no visible symptoms and 9 = virtually all area scorched, two-thirds or more reduction in height, most stems collapsing, no useful ear formed, miniature or no tassel, no pollen production, and dead or nearly dead plant.

3.2.6 Data analysis

Maize agronomic and *Striga* parameters were organised in an Excel spreadsheet and subjected to analysis of variance (ANOVA) using the split-plot procedure in Genstat 18^h Edition [65]. Significance tests were carried out at the 5% probability level. Data on the *Striga* emergence counts were square root transformed ($y=\sqrt{x+0.5}$) before analysis to meet normalization

assumptions. Mean separation was performed using Fisher's least significant difference (LSD) test at the 5% probability level. Correlation analysis was conducted separately between *FOS*-treated and untreated maize genotypes under both *Sh* and *Sa* infestation to discern the relationship among maize agronomic traits and *Striga* parameters. Furthermore, maize agronomic data and *Striga* parameters from *FOS*-treated and untreated genotypes were subjected to principal component analysis (PCA) using the mean values of the 56 maize genotypes using the Statistical Package for Social Science Studies (SPSS) Version 24.0 (SPSS, 2017) [66], to group and identify important traits under *Striga* infestation, with and without *FOS* treatment.

3.3 Results

3.3.1 Effects of *FOS* on maize genotypes and *S. hermonthica* parameters

Genotypes exhibited highly significant ($P < 0.001$) differences for all agronomic traits studied under *Sh* infestation, with and without *FOS* treatments (Table 3.2). Furthermore, the test genotypes differed significantly ($P < 0.001$) for all *S. hermonthica* parameters studied. The interaction between maize genotypes and *FOS* was highly significant ($P < 0.01$) for all the maize traits assessed except hundred kernel weight. The interaction between maize genotypes and *FOS* showed highly significant ($P < 0.001$) differences for *S. hermonthica* resistance parameters such as *Sh* emergence count at eight (*Sh*EC8) and 10 weeks after planting (*Sh*EC10), except for the *Sh* damage rating at both *Sh*EC8 and *Sh*EC10.

3.3.2 Mean performance of maize genotypes under *S. hermonthica*, with and without *FOS* treatments

The mean performance of the test genotypes under *Sh* infestation, with and without *FOS* treatments, are summarized in Table 3.3, together with the control (without both *Sh* and *FOS*) are presented in Table 3.4. The mean anthesis-silking interval under *Sh* infestation without *FOS* treatment ranged from 0.33 (genotype TZA4165) to 6.00 days (TZA3952) with an overall mean of 2.16 days. The genotypes anthesis-silking-interval under *Sh* infestation with *FOS* treatment ranged from 1.33 (JL16) to 7.67 days (TZA1782) with a mean of 2.40 days (Table 3.3) and that of the control treatment varied from 1.67 to 7.33 days with a mean of 2.08 days (Table 3.4). The results show an increase of 15% anthesis-silking interval for *FOS*-treated genotypes and 4% for untreated genotypes under *Sh* infestation. The mean grain yield in the control, *FOS*-treated, and untreated genotypes under *Sh* infestation was 93.86, 80.78 and 75.90 g/plant, respectively (Tables 3.3 and 3.4). Grain yield varied from 42.85 g/plant (TZA3181) to 146.64 g/plant (TZA3827) under the control treatment, from 45.59 g/plant (TZA3952) to 128.11 g/plant (TZA3827) in *FOS*-treated genotypes, and from 38.47 g/plant (TZA3964) to 119.60 g/plant (TZA2263) for untreated genotypes under *Sh* infestation. *FOS*-treated genotypes had higher

grain yields than untreated genotypes under *Sh* infestation. The mean value showed a grain yield reduction of 19.13% in untreated genotypes compared to a loss of 13.94% in *FOS*-treated genotypes, relative to the control. Some *FOS*-treated genotypes recorded higher percent yield increases than the control treatment: TZA1782 (19.07%), TZA3181 (14.88%), JL21 (14.73%), JL02 (9.16%), JL25 (10.4%), TZA3417 (11.72%), TZA3964 (12.20%) and TZA604 (9.11%) (Tables 3.4 and 3.5). The mean fresh biomass ranged from 88.30 g/plant (TZA3502) to 354 g/plant (TZA1780) in the control, 72.5 g/plant (TZA3502) to 335 g/plant (TZA4203) in *FOS*-treated genotypes, and 75.80 (TZA3502) to 289.20 g/plant (TZA1780) under *Sh* infestation without *FOS* treatment. The mean fresh biomass was 190.6 g/plant in the control, 152.7 g/plant in *FOS*-treated genotypes and 143.5 g/plant in untreated genotypes under *Sh* infestation. The results show a 24.7% reduction of fresh biomass in *Sh* infested genotypes without *FOS* treatment and 20% loss for *FOS*-treated genotypes compared to the control. The application of *FOS* significantly reduced the number of emerged *Sh* plants compared to the untreated genotypes. Under *Sh* infestation without *FOS* application, the following genotypes had the highest number of emerged *Sh* plants at 10 WAP: TZA4165 (9.37 *Sh* plants), TZA1771 (17.11), TZA4000 (10.99), TZA615 (10.62), JL06 (11.86), and TZA3570 (8.00). When the same genotypes were treated with *FOS*, the mean *Sh* emergence count dropped to 0.87, 5.35, 3.68, 2.19, 6.66 and 2.65, respectively (Table 3.3). Significant percent reductions in the number of emerged *Sh* plants were recorded as 90.72% (TZA4165), 68.73% (TZA1771), 66.52% (TZA4000), 79.38% (TZA615), 43.84% (JL06), and 69.56% (TZA3570), in *FOS*-treated genotypes. Although most of the *FOS*-treated genotypes stimulated fewer *Sh* plants to emerge at both eight and 10 WAP than untreated genotypes, some of the *FOS*-treated genotypes showed an increased number of emerged *Sh* plants compared to the untreated genotypes. The following *FOS*-treated genotypes showed an increase in the number of *Sh* emergence 10 WAP compared to untreated genotypes: TZA3181 (9.32 *Sh* plants), TZA599 (8.79), JL01 (8.69), TZA604 (6.79), TZA1780 (4.5), JL20 (3.46) and JL09 (3.36) (Table 3.3). The *Sh* damage rating score 10 weeks after planting, with and without *FOS* treatment, ranged from 1.00 (TZA4320) to 2.33 (JL25, TZA599, TZA604) and did not differ significantly. The mean *Sh* damage rating score, with and without *FOS* treatment, at 10 weeks after planting was 1.26 and 1.36, respectively. Based on *Sh* emergence count, *FOS* compatibility, grain yield and the presence of farmer preferred traits, the following genotypes were selected for *Striga* breeding purposes; TZA4205, TZA1775, TZA3417, TZA4203, TZA1780, TZA4010, TZA4165, TZA4016, TZA2263, TZA3827, JL24, JL22, JL01, JL05, JL08, JL09, JL13, JL15, JL16, JL17, JL18, JL19 and JL20. These genotypes are denoted in bold face text in Table 3.3.

Table 3.2. Analysis of variance on maize and *Striga* traits recorded from 56 maize genotypes evaluated under *S. hermonthica* infestation with and without FOS treatments in western Tanzania during the 2017/18 growing season

Source of variation	Maize agronomic traits										<i>Striga hermonthica</i> traits			
	DF	AD	SD	ASI	PH	EH	DM	AGB	GYD	HKWT	ShDR8	ShDR10	ShEC8	ShEC10
Replication	2	38.13	94.44	14.68	1626.30	18.20	10.72	10870.50	1892.90	9.73	0.33	0.99	3.26	4.93
FOS	1	24.45ns	0.53ns	17.81ns	1163.60ns	298n.00s	20.57*	10639.50ns	308.50ns	0.24**	0.30*	0.86ns	0.00ns	0.55ns
Error (a)	2	7.22	17.45	10.09	1767.30	143.00	1.07	2750.80	507.90	0.00	0.01	0.18	1.20	1.72
Genotypes	55	129.85***	178.79***	15.67***	8997.10***	10113.90***	310.47***	18793.60***	2752.60***	132.43***	0.63***	0.98***	2.02***	2.68***
FOS x Genotypes	55	8.51***	11.01***	6.87***	1384.30***	897.90***	23.82**	2250.10***	572.90***	0.11ns	0.15ns	0.16ns	0.69***	0.85***
Error (b)	220	3.87	4.52	3.04	397.80	333.30	14.93	885.30	204.90	1.26	0.15	0.17	0.35	0.38
Total	335													

*, **, *** Significant at $P < 0.05$; $P < 0.01$ and $P < 0.001$ probability level respectively; ns – Not significant at $P < 0.05$ probability level; DF - Degrees of freedom; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD – Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; PH – Plant height (cm); EH – Ear height (cm); DM – Days to maturity; AGB – Above ground biomass recorded as the weight (g) of above ground plant parts; GYD – Grain yield/plant (g); HKWT – Weight of 100 kernel (g); ShDR8 – *Striga hermonthica* damage rating recorded eight weeks after sowing; ShDR10 – *Striga hermonthica* damage rating recorded 10 weeks after sowing; ShEC8 - Number of emerged *S. hermonthica* plants (count) recorded eight weeks after sowing; ShEC10 – Number of emerged *S. hermonthica* plants (count) recorded 10 weeks after sowing; FOS = *Fusarium oxysporum* f.sp. *strigae*

Table 3.3. Mean performance for 56 maize genotypes evaluated under *S. hermonthica* infestation with (+) and without (-) FOS during the 2017/18 growing season

Accessions	AD		SD		ASI		PH		EH		GYD		HKWT		AGB		ShEC8		ShEC10		ShDR8		ShDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
TZA599	67.56	68.67	70.00	70.00	2.44	1.33	289.42	303.25	195.50	230.00	72.27	76.88	31.76	32.00	141.70	165.00	7.28	11.65	7.20	15.99	2.00	2.00	2.33	2.33
TZA604	66.11	66.33	70.22	72.67	4.11	6.33	280.75	259.75	189.83	164.50	82.56	95.96	25.01	25.22	179.20	217.50	7.23	13.31	10.87	17.66	1.67	2.00	2.33	2.33
TZA615	66.22	65.33	68.56	67.67	2.33	2.33	289.25	296.25	192.75	183.75	71.45	89.63	20.60	20.45	208.30	230.00	6.72	1.95	10.62	2.19	1.33	1.00	1.67	1.00
TZA687	62.33	61.00	63.56	64.67	1.22	3.67	280.58	285.25	171.58	189.25	86.27	67.57	19.37	18.98	131.00	120.00	2.95	5.93	5.48	8.62	1.33	1.00	1.67	1.67
TZA1771	63.89	64.33	65.67	69.00	1.78	4.67	272.08	270.25	145.92	150.25	71.39	71.16	23.24	23.45	123.30	115.00	12.25	3.68	17.11	5.35	2.00	1.33	2.00	1.67
TZA1775	65.56	65.33	67.33	66.67	1.78	1.33	280.22	283.15	160.33	154.50	88.46	83.67	24.58	24.72	154.20	152.50	4.87	3.32	6.61	5.00	1.00	1.00	1.00	1.00
TZA1780	74.89	75.33	78.00	76.00	3.11	0.67	271.25	328.75	177.33	200.00	87.54	77.64	20.39	20.29	289.20	327.50	6.61	10.74	9.93	14.43	1.00	1.33	1.67	1.67
TZA1782	75.11	72.00	80.56	79.67	5.44	7.67	332.17	341.00	239.33	263.50	49.68	66.45	24.92	25.05	185.80	222.50	9.57	8.14	14.44	10.87	2.67	1.67	2.00	1.67
TZA1784	67.00	67.00	72.44	72.00	5.44	5.00	295.92	313.75	242.25	206.25	45.62	47.16	28.92	29.05	193.30	235.00	2.19	4.28	4.70	5.97	1.00	1.00	1.00	1.00
TZA2263	64.78	64.33	67.33	68.67	2.56	4.33	293.92	294.25	190.58	194.25	119.60	97.93	27.70	27.83	180.00	135.00	2.94	6.28	6.35	8.55	1.00	1.00	1.33	1.33
TZA2749	61.44	61.00	64.00	64.67	2.56	3.67	273.35	313.75	148.08	151.25	85.90	84.38	25.45	25.58	100.00	105.00	3.90	1.42	4.00	1.42	1.33	1.00	1.33	1.00
TZA2761	64.56	64.33	66.33	67.67	1.78	3.33	263.33	291.50	152.17	162.50	85.33	66.36	25.76	25.88	144.20	142.50	3.56	2.65	5.60	2.95	1.00	1.00	1.00	1.00
TZA2881	67.33	66.00	69.78	70.00	2.44	4.00	336.25	336.75	222.17	217.50	68.17	70.15	22.35	22.48	187.50	197.50	5.15	7.48	7.66	11.49	1.67	1.67	1.67	2.00
TZA3095	66.33	65.67	71.33	70.67	5.00	5.00	284.25	316.25	184.42	186.25	75.74	86.81	26.01	26.14	100.00	100.00	5.60	5.44	8.62	7.96	1.00	1.33	1.33	1.33
TZA3181	68.56	67.67	71.11	68.00	2.56	0.33	313.83	270.00	180.17	183.00	56.78	50.34	21.19	21.32	98.30	90.00	1.95	10.08	4.44	13.76	1.00	2.00	1.00	2.00
TZA3417	61.33	62.00	62.22	62.67	0.89	0.67	279.83	299.50	161.17	172.50	70.29	93.96	20.56	20.54	135.80	127.50	3.32	3.23	3.96	3.84	1.00	1.00	1.00	1.00
TZA3502	54.33	53.00	59.56	56.67	5.22	3.67	255.25	260.75	150.25	177.75	59.78	65.92	19.50	18.93	75.80	72.50	0.89	2.82	1.64	3.56	1.00	1.00	1.00	1.00
TZA3561	68.67	64.67	72.44	68.00	3.78	3.33	318.67	347.00	212.25	221.75	50.51	73.10	21.96	22.09	148.30	165.00	5.98	7.33	8.51	10.66	2.00	1.67	2.33	2.33
TZA3570	66.44	66.00	68.33	67.67	1.89	1.67	293.92	282.75	179.72	173.75	64.23	60.85	22.40	22.53	107.50	122.50	8.00	2.65	11.99	3.65	1.33	1.33	2.33	1.67
TZA3614	66.44	65.33	69.33	68.67	2.89	3.33	326.33	354.00	207.17	231.50	84.77	77.15	24.92	25.05	161.70	170.00	5.29	2.65	7.53	2.65	1.33	1.00	1.33	1.00
TZA3827	69.11	68.00	72.67	70.00	3.56	2.00	308.00	335.00	168.50	202.50	91.01	128.11	31.79	31.92	164.20	171.50	2.24	2.71	3.84	4.44	1.00	1.00	1.00	1.00
TZA3942	58.22	58.67	58.67	58.00	0.44	-0.67	246.67	252.50	146.00	138.00	70.33	59.02	27.19	27.04	103.30	80.00	2.74	3.62	4.17	3.96	1.00	1.00	1.00	1.00
TZA3951	63.22	62.33	65.67	65.67	2.44	3.33	303.50	319.00	166.33	179.00	50.20	50.29	31.32	31.45	156.70	185.00	3.32	2.48	4.97	4.44	1.00	1.00	1.00	1.00
TZA3952	64.78	63.00	70.78	67.00	6.00	4.00	313.25	345.75	177.00	179.00	40.53	45.59	29.84	29.97	149.20	157.50	1.16	3.32	3.00	5.00	1.00	1.00	1.00	1.00
TZA3964	65.89	62.33	68.22	66.67	2.33	4.33	330.00	298.00	204.00	182.00	38.47	51.52	32.45	32.72	166.70	150.00	2.10	3.32	4.42	3.96	1.00	1.00	1.00	1.00
TZA4000	62.56	63.67	63.00	65.00	0.44	1.33	291.83	292.50	152.67	146.00	94.48	91.20	26.87	27.00	112.50	122.50	7.64	3.49	10.99	3.68	1.67	1.33	2.00	1.33
TZA4010	58.67	58.00	62.22	62.67	3.56	4.67	307.75	316.25	163.00	160.00	88.01	97.61	30.93	31.07	104.20	137.50	0.89	1.64	0.87	1.93	1.00	1.00	1.00	1.00
TZA4016	65.56	65.33	67.00	67.00	1.44	1.67	266.67	260.00	141.67	140.00	70.72	70.63	21.07	21.21	102.50	97.50	4.76	2.32	4.97	2.95	1.33	1.33	1.67	1.00
TZA4064	65.78	66.00	68.22	70.67	2.44	4.67	331.33	315.00	207.92	188.75	80.47	73.75	34.78	34.88	178.30	185.00	1.93	3.86	2.79	6.10	1.00	1.00	1.00	1.00
TZA4078	64.67	68.67	69.33	72.67	4.67	4.00	310.83	312.50	199.58	203.75	53.98	55.67	27.82	27.95	151.70	135.00	6.67	3.52	6.17	2.95	1.67	1.33	1.67	1.00
TZA4165	67.67	67.67	67.33	68.67	-0.33	1.00	246.17	212.50	145.42	118.75	82.68	81.07	23.25	23.52	102.50	102.50	6.07	0.00	9.37	0.87	1.33	1.00	1.67	1.00
TZA4203	71.00	71.00	73.00	71.67	2.00	0.67	272.67	276.00	164.17	177.50	85.63	91.91	24.41	24.54	270.00	335.00	0.89	0.50	1.93	1.42	1.00	1.00	1.00	1.00
TZA4205	61.78	62.00	62.78	63.00	1.00	1.00	274.17	237.50	129.58	126.75	86.72	77.21	23.85	23.99	151.70	155.00	3.66	4.16	4.97	5.28	1.00	1.00	1.33	1.33
TZA4320	69.67	71.67	74.33	75.67	4.67	4.00	285.92	307.75	182.08	208.75	76.91	77.03	23.25	23.38	221.70	270.00	0.00	0.00	0.00	0.00	1.00	1.00	1.00	1.00
JL01	63.11	63.33	64.22	64.67	1.11	1.33	270.50	251.50	138.08	126.75	79.86	82.88	23.14	22.99	111.70	115.00	3.32	10.94	4.97	13.64	1.33	1.67	1.00	2.00
JL02	61.11	61.33	62.22	62.67	1.11	1.33	265.75	244.75	126.92	112.25	97.64	121.74	22.64	22.54	121.70	105.00	5.79	3.84	8.43	4.70	1.33	1.33	1.33	1.00
JL03	61.78	62.00	62.67	62.67	0.89	0.67	277.50	275.00	137.75	144.75	73.35	101.34	23.43	23.56	135.00	140.00	3.27	1.64	5.66	2.00	1.00	1.00	1.00	1.00
JL04	61.78	62.00	62.56	63.67	0.78	1.67	257.08	257.75	139.08	124.75	48.68	60.41	24.78	24.91	132.50	147.50	0.50	1.70	0.87	2.65	1.00	1.00	1.00	1.00
JL05	61.78	62.00	62.22	62.67	0.44	0.67	237.25	231.75	130.33	117.50	90.31	89.25	21.17	21.30	139.20	172.50	1.42	1.64	1.64	1.93	1.00	1.00	1.00	1.00
JL06	63.56	64.67	64.89	68.67	1.33	4.00	226.25	257.25	124.08	156.25	92.23	93.79	19.01	18.56	102.50	127.50	9.41	5.00	11.86	6.66	2.33	1.33	2.00	1.67
JL08	64.00	64.67	63.78	64.00	-0.22	-0.67	252.33	246.00	141.08	131.25	117.56	117.48	21.69	21.83	164.20	192.50	8.71	7.33	11.02	10.00	2.00	1.33	2.00	1.67
JL09	61.11	61.33	62.00	62.00	0.89	0.67	217.92	216.25	110.00	104.50	88.73	93.36	21.68	21.81	114.20	102.50	0.27	2.19	1.00	3.36	1.00	1.00		

Table 3.3. Continued.

Accessions	AD		SD		ASI		PH		EH		GYD		HKWT		AGB		ShEC8		ShEC10		ShDR8		ShDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
JL21	62.44	63.33	63.89	63.67	1.44	0.33	259.20	252.50	144.08	141.75	63.77	76.42	22.58	22.71	141.70	165.00	2.32	2.65	3.84	3.56	1.00	1.00	1.33	1.00
JL22	53.11	53.33	55.44	55.00	2.33	1.67	233.92	230.75	115.50	117.00	67.06	68.60	23.96	23.80	80.80	82.50	2.95	3.65	3.56	4.59	1.00	1.00	1.00	1.00
JL23	63.33	62.67	65.89	65.00	2.56	2.33	289.33	336.00	155.92	179.25	53.14	86.76	26.62	26.75	130.80	107.50	5.60	3.00	5.76	4.00	1.33	1.00	1.00	1.00
JL24	61.44	60.33	62.89	62.67	1.44	2.33	297.50	257.50	146.75	132.75	95.84	102.01	28.19	28.32	173.30	170.00	4.28	5.15	6.61	5.54	1.00	1.00	1.00	1.33
JL25	63.89	62.33	66.67	66.00	2.78	3.67	215.58	224.75	98.50	98.00	89.95	107.09	27.29	27.41	127.50	112.50	9.00	13.09	11.63	15.45	1.67	2.33	2.33	2.00
Mean	64.23	63.96	66.39	66.36	2.16	2.40	276.47	280.26	158.42	160.02	75.90	80.78	24.37	24.40	143.50	152.70	4.16	4.24	5.93	5.65	1.25	1.19	1.36	1.26
CV%	3.1		3.2		13.9		7.1		11.3		17.5		4.6		18.7		28.5		25.8		32.2		31.8	
P<0.05	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***
LSD	2.95		3.19		2.62		30.29		28.70		21.53		1.68		44.87		0.97		1.02		0.63		0.67	

*** Significant at $P < 0.001$ probability level; CV% - Coefficient of variation; LSD – Least significant difference; AD – Number of days from sowing to when 50% of the plants in a plot shed silks; SD – Number of days from sowing to when 50% of the plants in a plot produce silks; ASI – Anthesis-silking interval; PH – Plant height (cm); EH – Ear height (cm); GYD – Grain yield/plant (g); HKWT – Weight of 100 kernel (g); AGB – Above ground biomass recorded as the weight (g) of above ground plant parts; ShEC8 - Number of emerged *S. hermonthica* plants (count) recorded eight weeks after sowing; ShEC10 - Number of emerged *S. hermonthica* plants (count) recorded 10 weeks after sowing; ShDR8 – *S. hermonthica* damage rating recorded eight weeks after sowing; ShDR10 – *S. hermonthica* damage rating recorded 10 weeks after sowing; Note: bold faced text show selected genotypes.

Table 3.4. Mean performance of maize genotypes without *FOS* or *Striga* infestation

Accessions	AD	SD	ASI	PH	EH	DM	GYP	HKWT	AGB
TZA599	67.56	69.00	1.44	286.67	173.50	127.00	87.28	32.112	162.70
TZA604	71.11	73.89	2.78	291.00	221.08	130.67	87.95	25.35	279.20
TZA615	66.56	67.22	0.67	306.25	140.25	115.89	95.56	20.522	238.30
TZA687	59.33	63.56	4.22	297.08	207.58	113.00	98.47	18.929	142.00
TZA1771	65.89	71.67	5.78	268.08	158.67	126.89	89.89	23.584	235.80
TZA1775	66.89	68.33	1.44	307.97	192.58	121.78	93.24	24.931	229.20
TZA1780	74.22	79.00	4.78	314.50	216.33	135.67	91.52	20.385	354.20
TZA1782	75.44	79.22	3.78	338.42	249.58	123.78	55.89	25.265	280.80
TZA1784	70.67	75.44	4.78	326.17	194.25	131.56	57.66	29.265	308.30
TZA2263	63.44	65.33	1.89	321.92	212.83	118.67	112.80	28.035	295.00
TZA2749	61.78	66.00	4.22	304.95	161.58	122.00	100.63	25.801	145.00
TZA2761	63.56	65.00	1.44	341.58	205.92	121.00	104.21	26.088	249.20
TZA2881	68.33	69.78	1.44	358.25	226.92	119.89	80.61	22.695	210.00
TZA3095	65.33	72.67	7.33	287.25	170.17	117.67	87.85	26.355	145.00
TZA3181	69.56	73.44	3.89	282.83	128.17	117.56	58.85	21.532	133.30
TZA3417	62.00	62.89	0.89	313.58	161.67	108.11	82.95	20.555	138.30
TZA3502	55.33	57.56	2.22	281.50	163.00	110.00	63.05	18.8	88.30
TZA3561	65.67	66.44	0.78	373.17	250.50	116.67	72.43	22.308	228.30
TZA3570	63.78	64.67	0.89	304.92	185.77	113.33	83.72	22.75	157.50
TZA3614	67.44	67.67	0.22	347.58	213.42	118.67	98.33	25.261	236.70
TZA3827	65.44	67.33	1.89	338.00	196.25	117.78	146.64	32.138	184.20
TZA3942	63.22	66.33	3.11	267.17	151.25	125.00	88.77	27.117	133.30
TZA3951	62.22	64.67	2.44	354.75	231.83	127.78	81.03	31.669	201.70
TZA3952	70.11	72.78	2.67	352.25	161.00	119.33	55.72	30.187	176.70
TZA3964	61.89	66.22	4.33	304.00	144.00	122.33	45.92	32.8	186.70
TZA4000	61.56	64.67	3.11	259.33	179.92	109.67	97.08	27.221	132.50
TZA4010	61.33	63.89	2.56	320.25	171.50	119.56	126.60	31.285	149.20
TZA4016	65.89	68.00	2.11	323.17	192.17	120.56	124.10	21.419	125.00
TZA4064	66.11	68.89	2.78	336.83	188.67	123.67	100.82	35.129	213.30
TZA4078	66.67	67.67	1.00	328.33	212.08	109.44	79.29	28.161	174.20
TZA4165	62.00	63.33	1.33	231.42	100.67	114.33	99.45	23.597	145.00
TZA4203	66.00	67.33	1.33	267.92	152.17	128.00	94.25	24.751	309.00
TZA4205	64.78	63.11	-1.67	238.42	120.83	115.11	93.71	24.202	156.70
TZA4320	67.00	69.67	2.67	297.17	213.33	127.67	111.79	23.599	319.20
JL01	58.11	61.89	3.78	256.60	118.08	114.00	83.75	23.057	134.20
JL02	63.78	64.22	0.44	248.25	134.42	121.00	111.52	22.638	141.70
JL03	63.11	64.67	1.56	349.00	159.75	121.44	85.22	23.775	167.50
JL04	62.11	64.22	2.11	302.33	128.83	114.67	79.08	25.126	142.80
JL05	63.78	63.89	0.11	242.25	132.08	116.56	105.70	21.517	141.50
JL06	70.56	74.89	4.33	296.75	191.83	120.00	98.69	18.478	195.00
JL08	64.33	63.78	-0.56	249.58	140.33	120.00	123.19	22.041	184.20
JL09	61.11	61.67	0.56	247.42	124.75	122.78	137.32	22.023	174.20
JL11	61.78	64.67	2.89	308.75	149.67	114.00	95.32	20.036	115.80
JL12	66.22	68.00	1.78	297.42	163.08	116.67	107.28	22.948	184.20
JL13	60.44	61.56	1.11	246.25	162.50	113.78	111.11	18.536	148.30
JL15	62.11	64.33	2.22	272.92	151.92	116.56	85.28	22.291	136.70
JL16	59.00	60.22	1.22	224.92	103.42	116.44	113.04	19.655	179.20
JL17	63.67	64.11	0.44	274.58	151.00	115.67	95.01	22.177	186.70
JL18	61.00	61.89	0.89	217.58	100.75	124.67	104.19	24.174	255.80
JL19	65.44	66.11	0.67	224.08	103.50	113.78	111.49	19.25	176.70
JL20	61.33	63.00	1.67	338.00	134.92	122.22	114.20	23.105	213.30
JL21	62.44	62.89	0.44	262.65	169.33	126.56	66.61	22.925	214.20
JL22	52.11	54.44	2.33	264.17	127.00	111.67	71.97	23.866	120.80
JL23	66.67	68.56	1.89	351.08	173.42	116.33	95.02	26.958	208.30
JL24	64.11	64.89	0.78	278.75	149.50	120.11	132.24	28.526	208.30
JL25	63.22	64.33	1.11	253.33	103.25	126.33	97.03	27.623	180.00
Mean	64.367	66.444	2.077	294.27	166.48	119.56	93.86	24.545	190.6
CV	3.1	3.2	13.9	7.1	11.3	3.3	17.5	4.6	18.7
P<0.05	***	***	***	***	***	***	***	***	***
LSD	2.76	3.04	2.48	28.67	25.26	5.33	20.19	1.55	42.22

*** Significant at $P < 0.001$ probability level; CV% - Coefficient of variation; LSD - Least significant difference; AD - Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI - Anthesis-silking interval; PH - Plant height (cm); EH - Ear height (cm); DM - Days to maturity; GYP - Grain yield/plant (g); HKWT - Weight of 100 kernel (g); AGB - Above ground biomass recorded as the weight (g) of above ground plant parts.

3.3.3 Effects of *FOS* on maize genotypes and *S. asiatica* parameters

The ANOVA revealed highly significant ($P < 0.001$) differences for all maize agronomic traits studied under *Sa* infestation, with and without *FOS* treatment (Table 3.5). *FOS* treatment on maize genotypes significantly ($P < 0.001$) affected the test genotypes and *Sa* resistance traits. The interactions between maize genotypes and *FOS* were highly significant ($P < 0.01$) for all the maize traits studied except for hundred kernel weight. Likewise, the interaction mean squares between maize genotypes and *FOS* exhibited significant ($P < 0.001$) differences for the *Sa* emergence counts at eight and 10 weeks after sowing (Table 3.5).

3.3.4 Mean performance of maize genotypes under *S. asiatica*, with and without *FOS*

Table 3.6 summarizes the mean performance of the maize genotypes evaluated under *Sa* infestation, with and without *FOS* treatment. The mean *Sa* emergence count eight weeks after sowing under *Sa* infestation, with and without *FOS* treatment, ranged from 0.0 *Sa* plants (for the genotype TZA3417) to 45.90 *Sa* plants (TZA4064), and 0.5 (TZA4320) to 45.52 *Sa* plants (TZA599), respectively. The *Sa* emergence count 10 weeks after sowing, with and without *FOS* treatment, ranged from 1.42 *Sa* plants for the genotype TZA3417 to 58.07 plants (TZA4064), and 1.42 (TZA4320) to 59.52 (TZA599). Most of the *FOS*-treated genotypes under *Sa* infestation showed a remarkable reduction in the number of emerged *Sa* plants. Likewise, *Sa* damage rating at eight and 10 weeks after sowing was significantly reduced in *FOS*-treated genotypes relative to untreated counterparts. The following genotypes showed over 50% reduction on the number of emerged *Sa* counts when treated with *FOS* compared to untreated ones under *Sa* infestation, 10 weeks after sowing: TZA3417 (90.7%), TZA3502 (76.65%), TZA1784 (72.5%), TZA4016 (65.4%), TZA3181 (63.44%), JL17 (60.94%), JL22 (57.75%), and TZA2881 (50.25%) (Table 3.6). However, some *FOS*-treated genotypes under *Sa* infestation supported more *Sa* plants than untreated genotypes 10 weeks after planting. Example of these are TZA3952 (12.47), TZA3570 (27.42), TZA3964 (16.91), JL01 (10.45), TZA604 (25.52), TZA4064 (32.54), TZA1782 (24.19), TZA1775 (22.38), and TZA2761 (16.92). These counts can be converted to percentages of *Sa* plants supported: 494.84% (genotype TZA3952), 427.77% (TZA3570), 383.45% (TZA3964), 211.73% (TZA1775), 177.12% (JL01), 157.24% (TZA604), 127.45% (TZA4064), TZA1782 (114.70%) and TZA2761 (107.84%) 10 weeks after planting, under *Sa* infestation with *FOS* treatment. Under *Sa* infestation, *FOS*-treated genotypes had higher grain yields than untreated genotypes (Table 3.6). Mean grain yields in the controls, *FOS*-treated, and untreated genotypes with *Sa* infestation were 93.86, 77.07 and 73.80 g/plant, respectively. On average, *FOS*-treated genotypes under *Sa* infestation suffered a grain yield reduction of 18%, while untreated genotypes had a 21.4% grain yield loss, compared to the control treatment (Tables 3.4 and 3.6). Grain yield performance of some *FOS*-treated genotypes under *Sa* infestation surpassed that of the control treatment, including TZA1780 (31.44%), TZA3181

(28.47%), JL21 (11.48%), TZA1782 (10.27%), TZA604 (8.81%), TZA3964 (6.71%) and TZA4165 (6.04%). Conversely, grain yield for TZA1780 under *Sa* without *FOS* treatment exceeded that of the control treatment by 7.18%. Grain yield for the genotypes JL03 and JL13 under *Sa* infestation with *FOS* treatment are not substantially different from that of the control (Tables 3.4 and 3.6). The mean fresh biomass was 190.6 g/plant in the control, 150.9 g/plant in *FOS*-treated and 143.6 g/plant in untreated genotypes under *Sa* infestation. The mean above ground biomass under *Sa* infestation, with and without *FOS* application, varied from 60 g/plant (TZA3502) to 350 g/plant (TZA1780), and 65 g/plant (TZA3502) to 318.30 g/plant (TZA1780), respectively. The mean plant height was 294.27 cm in the control, 279.56 cm in *FOS*-treated and 272.64 cm in untreated genotypes, respectively. Plant height was reduced by 5% for *FOS*-treated genotypes and 7.4% for untreated genotypes, under *Sa* infestation compared to the control. Based on the number of emerged *Sa* plants, *FOS* compatibility and grain quality characteristics, the following genotypes were selected for *Striga* resistance breeding purposes: TZA4205, TZA1775, TZA3417, TZA4203, TZA1780, TZA4010, TZA4165, TZA4016, TZA2263, TZA3827, JL24, JL22, JL01, JL05, JL08, JL09, JL13, JL15, JL16, JL17, JL18, JL19 and JL20.

Table 3.5. Analysis of variance on maize and *Striga* traits recorded from 56 maize genotypes evaluated under *S. asiatica* (*Sa*) infestation, with and without *FOS* treatments, in western Tanzania during 2017/18 growing season

Source of variation	Maize agronomic traits										<i>Striga asiatica</i>			
	DF	AD	SD	ASI	PH	EH	DM	AGB	GYD	HKWT	SaDR8	SaDR10	SaEC8	SaEC10
Replication	2	49.26	207.48	65.99	2735.00	1898.20	18.33	6783.10	290.50	12.40	1.41	0.91	4.50	5.33
FOS	1	0.00ns	31.79ns	31.43s	1854.10**	0.30ns	61.51ns	19955.60*	2670.30*	0.80*	1.44*	4.30*	0.16ns	0.02ns
Error (a)	2	5.26	3.36	12.59	12.60	1681.90	3.86	429.80	53.60	0.01*	0.047	0.06	1.33	2.15
Genotypes	55	129.81***	173.59***	15.51***	10083.40***	10348.80***	296.16***	23699.40***	2669.20***	133.47***	1.51***	2.29**	9.54***	9.88***
FOS x Genotypes	55	7.914**	14.43***	8.46***	1132.10***	636.10*	29.90***	1689.80***	501.60***	0.02ns	0.33ns	0.38ns	2.30**	2.58***
Error (b)	220	4.45	6.47	3.80	376.70	442.60	13.77	924.50	214.80	1.25	0.31	0.41	1.28	1.25
Total	335													

*, **, *** Significant at $P < 0.05$, $P < 0.01$ and $P < 0.001$ probability level; ns – Not significant at $P < 0.05$ probability level; DF – Degrees of freedom; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD – Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; PH – Plant height (cm); EH – Ear height (cm), DM – Days to maturity; AGB – Above ground biomass recorded as the weight (g) of all plants parts above the ground; GYD – Grain yield/plant (g); HKWT – Weight of 100 kernel (g); SaDR8 – *S. asiatica* damage rating recorded eight weeks after sowing; SaDR10 – *S. asiatica* damage rating recorded 10 weeks after sowing; SaEC8 – Number of emerged *S. asiatica* plants (count) recorded eight weeks after sowing; SaEC10 – Number of emerged *S. asiatica* plants (count) recorded 10 weeks after sowing; *FOS* – *Fusarium oxysporum* f.sp. strigae.

Table 3.6. Mean performance for 56 maize genotypes evaluated under *Striga asiatica* infestation with (+) and without (-) FOS during 2017/2018 growing season

Accessions	AD		SD		ASI		PH		EH		GYD		HKWT		AGB		SaEC8		SaEC10		SaDR8		SaDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
TZA599	70.56	69.00	73.33	72.00	2.78	3.00	265.67	292.50	185.33	220.00	84.20	88.75	32.29	32.39	197.50	217.50	45.52	32.08	59.52	39.32	3.00	2.00	3.33	2.00
TZA604	67.00	69.00	71.67	75.00	4.67	6.00	299.75	302.75	209.50	203.50	87.29	95.70	25.54	25.63	206.70	225.00	11.86	32.59	16.23	41.75	1.67	2.33	2.33	2.00
TZA615	67.44	67.00	70.22	71.33	2.78	4.33	291.58	296.75	203.92	199.75	62.24	62.21	21.30	21.00	188.30	140.00	15.27	26.56	22.40	29.64	2.00	2.00	3.00	2.67
TZA687	59.67	61.00	62.56	63.00	2.89	2.00	273.00	263.00	158.50	170.50	73.26	59.85	19.89	19.52	123.30	135.00	13.04	13.72	17.39	17.27	2.00	2.00	2.33	2.00
TZA1771	63.78	64.00	69.00	67.00	5.22	3.00	254.67	228.00	157.83	157.50	69.57	61.30	23.94	23.87	139.20	147.50	25.63	26.50	31.60	32.53	2.33	2.00	2.67	2.33
TZA1775	64.78	67.67	66.33	68.33	1.56	0.67	274.42	282.75	165.50	173.50	84.47	81.29	25.17	25.27	193.30	190.00	7.13	25.27	10.57	32.95	1.00	1.67	1.00	2.00
TZA1780	72.67	74.00	76.11	77.67	3.44	3.67	289.08	295.75	199.00	204.50	98.09	120.29	20.90	20.84	318.30	350.00	11.65	16.12	16.66	20.42	1.00	1.33	1.67	1.67
TZA1782	75.78	75.33	80.11	77.67	4.33	2.33	326.25	333.25	224.50	226.00	46.42	61.63	25.49	25.59	281.70	260.00	17.27	34.62	21.09	45.28	1.67	2.33	3.00	2.33
TZA1784	67.22	69.00	71.33	72.00	4.11	3.00	316.83	331.00	212.00	222.00	43.30	45.03	29.49	29.59	198.30	235.00	22.87	5.42	31.08	8.55	2.33	1.67	2.33	1.67
TZA2263	65.00	65.00	67.44	65.00	2.44	0.00	304.17	320.00	184.42	199.25	103.32	95.55	28.26	28.36	163.30	185.00	10.02	9.00	14.61	12.00	1.33	1.00	2.00	1.33
TZA2749	62.44	62.67	64.11	63.67	1.67	1.00	283.33	291.50	149.25	167.25	71.48	79.43	26.04	26.14	89.20	92.50	7.66	10.57	12.63	16.54	1.00	1.33	2.00	1.33
TZA2761	61.89	63.00	63.11	62.67	1.22	-0.33	263.58	273.25	169.75	161.25	94.28	96.00	26.31	26.41	185.00	155.00	10.94	25.61	15.69	32.61	1.33	1.67	1.33	2.33
TZA2881	68.22	66.67	72.22	66.67	4.00	0.00	308.33	339.00	210.00	212.50	51.74	60.69	23.15	23.02	198.30	215.00	40.82	25.35	50.25	29.31	3.00	2.33	3.00	1.67
TZA3095	63.89	65.67	68.67	67.33	4.78	1.67	262.42	295.75	156.08	153.25	61.49	67.75	26.58	26.68	121.70	125.00	27.88	21.48	33.61	26.40	2.00	2.00	2.33	2.33
TZA3181	65.33	66.67	69.89	68.33	4.56	1.67	286.27	258.80	171.67	167.00	50.56	74.32	21.76	21.86	88.30	95.00	8.37	3.06	13.04	6.52	1.33	1.00	1.67	1.00
TZA3417	62.78	65.67	62.78	62.33	0.00	-3.33	271.93	278.30	161.42	134.75	65.21	68.65	21.23	20.96	90.00	80.00	10.63	0.00	15.27	1.42	1.67	1.00	1.67	1.00
TZA3502	55.67	53.00	59.00	57.00	3.33	4.00	240.42	273.75	114.92	141.75	49.83	53.23	19.82	19.47	65.00	60.00	4.17	0.87	7.11	1.66	1.00	1.00	1.00	1.00
TZA3561	68.00	68.67	69.56	71.33	1.56	2.67	338.25	324.25	219.25	225.25	48.86	39.18	22.77	22.64	123.30	155.00	28.08	36.14	37.47	48.00	2.33	2.33	3.33	3.00
TZA3570	65.67	65.00	65.89	65.00	0.22	0.00	318.92	326.75	210.83	205.00	68.24	78.29	22.98	23.08	110.00	125.00	4.97	28.85	6.41	33.83	1.00	2.00	1.00	1.67
TZA3614	67.00	67.00	70.78	69.00	3.78	2.00	329.92	351.25	191.25	216.25	71.02	89.44	25.49	25.59	129.20	127.50	21.51	17.81	28.42	21.82	2.33	1.33	2.33	1.33
TZA3827	66.56	69.00	68.44	70.67	1.89	1.67	293.92	281.25	157.42	141.25	68.83	83.08	32.37	32.47	177.50	202.50	28.25	23.19	35.58	27.59	2.33	2.33	3.00	2.67
TZA3942	59.89	55.67	60.00	54.67	0.11	-1.00	233.08	248.25	144.00	140.50	70.56	68.33	27.48	27.58	151.70	125.00	1.42	1.57	3.17	3.96	1.00	1.00	1.00	1.00
TZA3951	62.44	60.00	64.78	63.67	2.33	3.67	308.08	307.75	176.58	166.25	70.37	64.10	31.90	32.00	141.70	165.00	24.95	15.28	29.78	20.00	2.33	2.00	2.33	1.67
TZA3952	64.56	63.00	66.22	66.00	1.67	3.00	313.58	284.75	156.42	153.25	48.12	53.19	30.42	30.52	113.30	85.00	0.87	11.00	2.52	14.99	1.00	1.00	1.00	1.33
TZA3964	61.56	62.00	62.44	62.67	0.89	0.67	293.50	265.50	166.67	161.00	40.91	49.00	32.97	33.07	160.00	125.00	2.64	15.34	4.41	21.32	1.00	1.67	1.33	1.67
TZA4000	61.22	61.67	61.89	61.67	0.67	0.00	290.33	343.50	143.33	166.00	60.54	69.57	27.46	27.56	89.20	87.50	9.00	6.05	12.99	8.51	1.33	1.00	1.67	1.33
TZA4010	61.78	62.67	63.89	65.67	2.11	3.00	300.25	313.75	152.75	169.75	93.37	80.41	31.52	31.62	105.00	130.00	7.45	4.27	13.12	8.52	1.33	1.33	1.67	1.67
TZA4016	63.44	65.00	64.78	66.33	1.33	1.33	283.25	286.25	149.33	160.00	77.35	75.80	21.81	21.75	117.50	112.50	12.75	3.92	17.61	6.10	1.67	1.00	1.00	1.33
TZA4064	66.78	67.00	71.44	67.67	4.67	0.67	341.25	350.75	200.75	209.75	63.86	43.00	35.23	35.48	212.50	202.50	16.31	45.90	25.53	58.07	2.00	3.00	2.67	3.33
TZA4078	62.67	62.00	66.44	66.67	3.78	4.67	312.08	331.25	184.50	207.50	43.87	40.49	28.39	28.49	132.50	147.50	17.55	15.18	22.95	18.67	1.67	1.67	2.33	2.00
TZA4165	62.89	64.00	63.89	65.00	1.00	1.00	243.42	237.75	126.00	126.00	92.49	105.46	23.96	23.86	104.20	87.50	3.84	3.56	6.75	7.66	1.33	1.00	1.00	1.00
TZA4203	65.67	67.67	68.22	73.33	2.56	5.67	256.67	252.50	115.33	155.00	76.99	84.85	24.98	25.08	156.70	145.00	7.64	7.98	11.02	11.99	1.67	1.00	1.33	1.00
TZA4205	61.67	61.67	63.33	64.00	1.67	2.33	245.42	268.75	142.92	163.75	97.56	105.34	24.44	24.54	124.20	117.50	2.42	3.84	4.17	6.75	1.00	1.33	1.00	1.33
TZA4320	70.22	68.67	74.67	71.33	4.44	2.67	293.42	308.75	197.83	197.50	55.40	60.99	23.83	23.93	259.20	317.50	0.50	0.27	1.42	2.00	1.00	1.00	1.00	1.00
JL01	61.56	62.00	63.33	63.33	1.78	1.33	252.08	243.75	129.25	118.75	71.96	65.39	23.43	23.53	120.00	150.00	2.87	11.02	5.90	16.35	2.00	1.00	1.33	1.33
JL02	61.44	61.69	61.56	62.00	0.11	0.33	245.50	248.00	126.75	133.75	84.03	90.19	22.98	23.08	135.80	152.50	15.18	16.87	22.56	21.02	1.67	1.67	2.33	2.00
JL03	61.22	60.33	62.00	59.33	0.78	-1.00	277.17	259.00	166.92	140.25	69.90	80.85	24.01	24.11	98.30	115.00	4.26	4.98	7.53	8.28	1.00	1.33	1.00	1.33
JL04	61.44	61.00	63.89	62.33	2.44	1.33	252.67	256.00	129.67	137.00	45.98	37.99	25.35	25.45	96.70	120.00	3.96	6.27	7.72	10.71	1.00	1.00	1.33	1.33
JL05	62.00	62.00	61.56	62.00	-0.44	0.00	236.08	268.75	117.58	133.25	94.94	94.91	21.96	21.85	130.00	140.00	14.43	5.50	17.48	8.93	1.33	1.00	1.33	1.00
JL06	65.78	66.00	66.67	64.00	0.89	-2.00	244.50	230.50	143.17	118.00	79.86	90.83	19.41	19.09	126.70	115.00	35.99	30.99	43.15	40.40	3.00	2.67	3.33	2.67
JL08	62.78	63.67	63.78	64.67	1.00	1.00	248.17	254.50	139.58	139.75	106.58	129.51	22.44	22.37	130.80	147.50	16.71	20.95	21.63	27.86	2.00	1.67	2.33	2.33
JL09	61.33	62.00	61.11	61.33	-0.22	-0.67	218.25	219.25	113.08	115.25	76.36	74.95	22.25	22.35	90.80	112.50	9.51	12.12	1					

Table 3.7. Continued.

Accessions	AD		SD		ASI		PH		EH		GYD		HKWT		AGB		SaEC8		SaEC10		SaDR8		SaDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
JL20	62.67	64.00	64.00	65.33	1.33	1.33	250.17	268.50	135.08	138.75	84.33	84.08	23.33	23.43	135.00	160.00	6.38	13.03	10.94	17.66	1.00	1.33	1.33	1.67
JL21	63.22	65.67	64.00	65.33	0.78	-0.33	275.00	293.00	162.83	152.50	58.28	74.26	23.15	23.25	147.50	152.50	6.07	4.17	8.52	7.53	1.00	1.00	1.00	1.00
JL22	51.56	52.00	53.67	53.67	2.11	1.67	252.25	252.75	128.67	114.50	70.42	68.84	24.24	24.34	116.70	135.00	20.56	8.26	26.91	11.37	2.00	1.33	2.33	1.33
JL23	64.00	64.00	67.89	68.33	3.89	4.33	316.17	341.00	162.92	186.25	86.22	72.47	27.19	27.28	144.20	182.50	22.26	17.32	27.66	21.65	2.00	1.33	2.33	2.00
JL24	61.56	62.00	62.56	63.67	1.00	1.67	260.50	274.00	138.17	137.00	90.64	90.71	28.75	28.85	186.70	230.00	9.72	10.63	14.25	13.64	1.33	1.00	1.33	1.00
JL25	61.56	62.00	64.33	66.33	2.78	4.33	213.75	218.75	105.67	108.50	91.57	97.78	27.85	27.95	150.80	192.50	25.73	25.72	32.61	33.68	2.33	2.00	3.00	2.00
Mean	63.81	64.09	65.84	65.65	2.03	1.57	272.64	279.56	156.50	160.59	73.79	77.07	24.91	24.93	143.60	150.90	13.76	14.30	18.69	18.92	1.63	1.49	1.87	1.64
CV%	3.30		3.90		25.60		6.90		13.10		18.20		4.50		19.00		31.80		26.90		35.40		36.60	
P<0.05	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***
LSD	3.22		4.09		3.03		29.32		33.86		21.98		1.68		45.68		1.82		1.81		0.88		1.03	

*** Significant at $P < 0.001$ probability level; CV% - Coefficient of variation; LSD - Least significant difference; AD - Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI - Anthesis-silking interval; PH - Plant height (cm); EH - Ear height (cm); GYD - Grain yield/plant (g); HKWT - Weight of 100 kernel (g); AGB - Above ground biomass recorded as the weight (g) of all plants parts above the ground, SaEC8 - Number of emerged *S. asiatica* plants (count) recorded eight weeks after sowing, SaEC10 - Number of emerged *S. asiatica* plants (count) recorded 10 weeks after sowing; SaDR8 - *S. asiatica* damage rating recorded eight weeks after sowing; SaDR10 - *S. asiatica* damage rating recorded 10 weeks after sowing; Note: bold faced text show selected genotypes

3.3.5 Association between maize agronomic traits and *Striga* parameters assessed under *S. hermonthica* infestation, with and without FOS

Coefficients of correlation explaining the degree of association for the studied traits among 56 maize genotypes evaluated under *Sh* infestation, with and without FOS, are summarized in Table 3.7. For FOS-treated genotypes, grain yield exhibited significant ($P<0.05$) and negative correlation with the anthesis-silking interval ($r=-0.17$) and ear height ($r=-0.19$). Above ground biomass was significantly ($P<0.01$) correlated with days to 50% anthesis ($r=0.54$), days to 50% silking ($r=0.51$) and days to maturity ($r=0.66$). In addition, days to 50% anthesis had significant ($P<0.05$) correlations for all *Sh* parameters studied under FOS treatment. Likewise, the anthesis-silking-interval showed significant ($P<0.05$) correlations with *Sh* emergence counts at eight ($r=0.20$) and 10 weeks after sowing ($r=0.18$). *Striga* traits like *Sh*EC8, *Sh*EC10, *Sh*DR8 and *Sh*DR10 were significant ($P<0.05$) and positively correlated among each other under *Sh* infestation with FOS treatment. Furthermore, under *Sh* infestation without FOS treatment, grain yield was significantly ($P<0.05$) and negatively correlated with hundred kernel weight ($r=-0.17$), days to 50% silking ($r=-0.22$), anthesis-silking interval ($r=-0.35$) and plant height ($r=-0.24$). Additionally, days to 50% anthesis exhibited significant ($P<0.01$) correlations with days to 50% silking ($r=0.93$), ear height ($r=0.95$) and days to maturity ($r=0.48$). Moreover, days to 50% anthesis showed significant ($P<0.05$) correlations with *Sh* emergence counts at eight weeks ($r=0.18$) and ten weeks ($r=0.25$). Days to 50% anthesis was significantly ($P<0.05$) correlated with *Sh* damage ratings at eight ($r=0.19$) and 10 ($r=0.20$) weeks after sowing. All *Striga* parameters under *Sh* infestation without FOS treatments are highly correlated.

3.3.6 Association between maize agronomic traits and *Striga* parameters assessed under *S. asiatica* infestation, with and without FOS treatment

Pearson correlation coefficients describing the relationship of the studied traits among 56 maize genotypes assessed under *Sa* infestation, with and without FOS treatments, are summarized in Table 3.8. Grain yield showed significant ($P<0.01$) and negative correlations with plant height ($r=-0.23$), ear height ($r=-0.20$) and hundred kernel weight ($r=-0.22$) under FOS treatment. Furthermore, grain yield exhibited a significant ($P<0.01$) positive correlation with days to maturity ($r=0.23$). For FOS-treated genotypes, hundred kernel weight was significantly ($P<0.01$) correlated with plant height ($r=0.38$), ear height ($r=0.3$) and above ground biomass ($r=0.23$). Also, hundred kernel weight had significant ($P<0.05$) correlations with *Sa* emergence counts at eight ($r=0.19$) and 10 ($r=0.21$) weeks after sowing. Hundred kernel weight was significantly ($P<0.05$) correlated with *Sa* damage rating at eight ($r=0.18$) and 10 ($r=0.17$) weeks after sowing. Likewise, above ground biomass, exhibited significant ($P<0.01$) correlations with days to maturity ($r=0.74$), days to 50% silking ($r=0.52$), days to 50% anthesis ($r=0.49$), and *Sa* emergence counts eight ($r=0.25$), and 10 ($r=0.23$) weeks after sowing. Above ground biomass

had significant ($P<0.05$) correlations with *Sa* damage ratings at eight ($r=0.23$) and 10 ($r=0.18$) weeks after sowing. Under *FOS* treatment, all the *Sa* parameters exhibited strong and significant ($P<0.05$) correlations among each other ($r>0.7$) Table 3.8. When genotypes were infested with *Sa* without *FOS* treatment, grain yield showed significant ($P<0.01$) and negative correlations with days to 50% silking ($r=-0.23$), anthesis-silking interval (-0.26), plant height ($r=-0.31$) and ear height ($r=-0.29$). Furthermore, above-ground biomass exhibited significant ($P<0.05$) correlations with days to maturity ($r=0.73$), ear height ($r=0.52$), days to 50% silking ($r=0.51$) and days to 50% anthesis ($r=0.54$). In addition, above-ground biomass without *FOS* treatment revealed significant ($P<0.05$) correlations with *Sa* emergence count 10 ($r=0.16$) weeks after sowing and the *Sa* damage rating 10 ($r=0.18$) weeks after sowing. Furthermore, for untreated maize genotypes, days to 50% anthesis had significant ($P<0.05$) correlations with *Sa* emergence counts eight ($r=0.18$) and 10 ($r=0.18$) weeks after sowing. Days to 50% anthesis also showed significant correlations with *Sa* damage ratings eight ($r=0.16$) and ten ($r=0.26$) weeks after sowing without *FOS* treatment.

Table 3.8. Pearson correlation coefficient (r) for maize agronomic traits recorded among 56 maize accessions under *S. hermonthica* with FOS (above diagonal) and without FOS treatment (below diagonal)

	AD	SD	ASI	PH	EH	DM	GYD	AGB	HKWT	ShEC8	ShEC10	ShDR8	ShDR10
AD	1	0.85**	-0.10	0.25**	0.44**	0.47**	-0.07	0.54**	0.09	0.19*	0.21**	0.17*	0.22**
SD	0.93**	1	0.45**	0.45**	0.58**	0.47**	-0.15	0.51**	0.21**	0.27**	0.28**	0.22**	0.26**
ASI	0.29**	0.63**	1	0.31**	0.34**	0.09	-0.17*	0.04	0.24**	0.20*	0.18*	0.13	0.12
PH	0.35**	0.36**	0.21**	1	0.83**	0.12	-0.08	0.31**	0.38**	0.06	0.08	0.04	0.07
EH	0.95**	0.53**	0.32**	0.77**	1	0.22**	-0.19*	0.41**	0.32**	0.14	0.17*	0.14	0.21**
DM	0.48**	0.45**	0.16*	0.07	0.22**	1	0.08	0.66**	0.23**	0.13	0.15	0.08	0.10
GYD	-0.10	-0.22**	-0.35**	-0.24**	-0.24**	0.01	1	0.11	-0.12	-0.02	-0.01	0.05	-0.02
AGB	0.46**	0.40**	0.08	0.29**	0.40**	0.58**	0.07	1	0.15*	0.00	0.02	0.00	0.05
HKWT	0.09	0.17*	0.23**	0.43**	0.38**	0.20*	-0.17*	0.17*	1	0.01	-0.01	-0.01	-0.10
ShEC8	0.18*	0.11	-0.09	0.00	0.05	0.05	0.02	-0.01	-0.09	1	0.97**	0.70**	0.73**
ShEC10	0.25**	0.16*	-0.10	0.04	0.10	0.08	0.08	0.04	-0.10	0.92**	1	0.68**	0.75**
ShDR8	0.19*	0.15*	0.00	0.09	0.15*	0.10	-0.03	0.01	-0.07	0.69**	0.60**	1	0.71**
ShDR10	0.20**	0.14	-0.05	0.00	0.07	0.10	0.07	0.01	-0.12	0.71**	0.72**	0.65**	1

*, **, *** Significant at $P < 0.05$; $P < 0.01$ and $P < 0.001$ probability level, respectively; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD – Number of days from sowing to when 50% of the plants in a plot produce si k; ASI – Anthesis-silking interval; PH – Plant height (cm); EH – Ear height (cm); DM – Days to maturity; FOS- *Fusarium oxysporium* f.sp. *strigae*; GYD – Grain yield/plant (g); AGB – Above ground biomass recorded as the weight (g) of above ground plant parts; HKWT – Weight of 100 kernel (g); ShEC8 – Number of emerged *S. hermonthica* plants (count) recorded eight weeks after sowing; ShEC10 – Number of emerged *S. hermonthica* plants (count) recorded ten weeks after sowing; ShDR8 – *S. hermonthica* damage rating recorded eight weeks after sowing; ShDR10 – *S. hermonthica* damage rating recorded ten weeks after sowing.

Table 3.9. Pearson correlation coefficient (r) for maize agronomic traits recorded among 56 maize accessions under *Striga asiatica* with FOS (above diagonal) and without FOS treatment (below diagonal).

	AD	SD	ASI	PH	EH	DM	GYD	AGB	HKWT	SaEC8	SaEC10	SaDR8	SaDR10
AD	1	0.85**	0.01	0.344**	0.47**	0.50**	0.07	0.49**	0.06	0.29**	0.30**	0.18*	0.20*
SD	0.89**	1	0.53**	0.351**	0.51**	0.56**	0.02	0.52**	0.12	0.30**	0.31**	0.23**	0.26**
ASI	0.21**	0.64**	1	0.12	0.22**	0.26**	-0.08	0.21**	0.14	0.11	0.10	0.14	0.18*
PH	0.40**	0.45**	0.28**	1	0.78**	0.07	-0.23**	0.31**	0.38**	0.18*	0.17*	0.18*	0.13
EH	0.51**	0.55**	0.32**	0.78**	1	0.25**	-0.20**	0.44**	0.30**	0.35**	0.34**	0.36**	0.27**
DM	0.47**	0.44**	0.15	0.18*	0.34**	1	0.23**	0.74**	0.20*	0.21**	0.22**	0.18*	0.17*
GYD	-0.13	-0.23**	-0.26**	-0.31**	-0.29**	0.05	1	0.05	-0.22**	-0.02	0.00	-0.12	-0.12
AGB	0.54**	0.51**	0.18*	0.26**	0.52**	0.73**	0.03	1	0.23**	0.25**	0.25**	0.23**	0.18*
HKWT	0.11	0.14	0.13	0.38**	0.23**	0.32**	-0.11	0.23**	1	0.19*	0.21**	0.18*	0.17*
SaEC8	0.18*	0.23**	0.19*	0.06	0.21**	0.13	-0.05	0.16*	0.12	1	0.99**	0.78**	0.75**
SaEC10	0.18*	0.23**	0.19*	0.06	.21**	0.12	-0.04	0.16*	0.13	0.99**	1	0.75**	0.74**
SaDR8	0.16*	0.21**	0.16*	0.10	0.19*	0.09	-0.07	0.10	0.10	0.87**	0.85**	1	0.78**
SaDR10	0.26**	0.31**	0.22**	0.16*	0.26**	0.10	-0.04	0.18*	0.10	0.80**	0.81**	0.77**	1

*, **, *** Significant at $P < 0.05$, $P < 0.01$ and $P < 0.001$ probability level, respectively; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD – Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; PH – Plant height (cm); EH – Ear height (cm); DM – Days to maturity; FOS- *Fusarium oxysporium* f.sp. *strigae*; GYD – Grain yield/plant (g), AGB – Above ground biomass recorded as the weight (g) of all plants parts above the ground; HKWT – Weight of 100 kernel (g); SaEC8 – Number of emerged *S. asiatica* plants (count) recorded eight weeks after sowing; SaEC10 – Number of emerged *S. asiatica* plants (count) recorded ten weeks after sowing; SaDR8 – *S. asiatica* damage rating recorded eight weeks after sowing; SaDR10– *S. asiatica* damage rating recorded ten weeks after sowing.

3.3.7 Principal components analysis of the maize agronomic traits and *S. hermonthica* parameters under *Sh* infestation, with and without *FOS* treatment

A summary for the rotated component matrix of the PCA, following Varimax rotation with Kaiser Normalization is presented in Table 3.9 for maize agronomic traits under *Sh* infestation, with and without *FOS* treatment. Three principal components were important in allocating traits for both *FOS*-treated and untreated maize genotypes. From the untreated maize genotypes evaluated under *Sh* infestation, the first three principal components (PCs) with eigen values greater than 1 accounted for 75.47% of the total variation (Table 3.9). The first principal component (PC1) was dominated by four *Sh* resistance parameters (ShEC8, ShEC10, ShDR8, ShDR10) and explained 28.06% of the total variance relating to *Striga* infestation. The second principal component (PC2) was highly influenced by four maize agronomic traits (AGB, DM, AD and SD) with high positive loadings explaining 23.77% of the total variation. The third principal component (PC3) was mainly associated with three maize traits (PH, EH and ASI) with high positive loadings, and GYD with a high negative loading, contributing 23.64% of the total variation (Table 3.10). Likewise, in the *FOS*-treated genotypes under *Sh* infestation, three principal components were significant, and explained 74.19% of the total variance in the original data set (Table 3.9). *Sh* parameters (ShEC8, ShEC10, ShDR8, ShDR10) were the main contributors of PC1, accounting for 28.9% of the total variation. PC2 was governed by traits like AGB, AD, DM, explaining 23.85% of the total variance, whereas maize traits like PH, EH and ASI had high positive loadings into PC3, describing 21.43% of the total variance (Table 3.9).

3.3.8 Principal components analysis based on maize traits and *S. asiatica* resistance traits under *Sa* infestation with and without *FOS* treatment

Table 3.10 summarizes the rotated component matrix of the PCA, following Varimax rotation with Kaiser Normalization, for maize agronomic traits under *Sh* infestation, with and without *FOS* treatment. From the untreated genotypes, under *Sa* infestation, three principal components were important, explaining 77.47% of the total variance in the original data set. Traits contributing strongly to PC1 were SaEC8 (0.97), SaEC10 (0.97), SaDR8 (0.95), and SaDR10 (0.91), respectively, accounting for 29.61% of the total variance. PC2 was mainly influenced by AGB (0.92), DM (0.89), AD (0.80) and SD (0.79), respectively, explaining 26.44% of the total variance. Likewise, PC3 was dominated by three maize traits PH (0.88), GYD (-0.79) and EH (0.76), accounting for 21.42% of the total variance. Furthermore, in *FOS*-treated maize genotypes under *Sa* infestation, four principal components were important, explaining 82.08% of the total variation. Four *Sa* resistance traits, SaEC8, SaEC10, SaDR8, and SaDR10, had high positive loadings into PC1, contributing 28.91% to the total variance. PC2 in *FOS*-treated genotypes under *Sa* infestation was mainly contributed to by maize traits such as AD, SD, DM and AGB, which accounted for 25.72% of the total variance. Likewise, PC3 comprised of PH and EH, which

had high positive loadings and GYD with a negative loading, accounting for 16.29% of the total variance. PC4 was influenced by ASI, explaining 11.16% of the total variation in the original data set.

Table 3.10. Eigen-values, explained variance and rotated component matrix of nine agronomic traits and four *Striga hermonthica* (*Sh*) parameters among 56 maize genotypes evaluated under *Sh* infestation with and without *FOS* treatments in Tanzania

Traits – assessed under <i>Sh</i> infestation without <i>FOS</i> treatment	Rotated component matrix			Traits – assessed under <i>Sh</i> infestation with <i>FOS</i> treatment	Rotated component matrix		
	PC1	PC2	PC3		PC1	PC2	PC3
AD	0.30	0.81	0.29	AD	0.21	0.84	0.22
SD	0.27	0.76	0.49	SD	0.26	0.74	0.48
ASI	0.05	0.22	0.75	ASI	0.21	0.06	0.73
PH	0.07	0.23	0.84	PH	-0.01	0.30	0.82
EH	0.18	0.40	0.81	EH	0.17	0.39	0.80
DM	0.00	0.85	0.03	DM	0.10	0.82	0.00
GYD	0.07	0.18	-0.70	GYD	0.05	0.18	-0.59
HKWT	-0.17	0.12	0.57	HKWT	-0.07	0.13	0.55
AGB	-0.09	0.91	0.10	AGB	-0.06	0.92	0.07
ShEC8	0.96	0.03	-0.05	ShEC8	0.95	0.10	0.03
ShEC10	0.93	0.11	-0.02	ShEC10	0.95	0.14	0.05
ShDR8	0.89	0.05	0.09	ShDR8	0.93	0.06	0.03
ShDR10	0.91	0.08	-0.04	ShDR10	0.94	0.10	0.05
Eigen-value	3.65	3.09	3.07	Eigen-value	3.76	3.10	2.79
Proportion variance (%)	28.06	23.77	23.64	Proportion of Variance (%)	28.90	23.85	21.43
Cumulative variance (%)	28.06	51.83	75.47	Cumulative Variance (%)	28.90	52.76	74.19

AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD – Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; PH – Plant height (cm); EH – Ear height (cm); DM – Days to maturity; *FOS*- *Fusarium oxysporium* f.sp. *strigae*; GYD – Grain yield/plant (g); HKWT – Weight of 100 kernels (g); AGB – Above ground biomass recorded as the weight (g) of above ground plant parts; ShEC8 - Number of emerged *S. hermonthica* plants (count) recorded eight weeks after sowing; ShEC10 - Number of emerged *S. hermonthica* plants (count) recorded ten weeks after sowing; ShDR8 – *Striga hermonthica* damage rating recorded eight weeks after sowing; ShDR10 – *Striga hermonthica* damage rating recorded ten weeks after sowing; PC1; PC2; and PC3 – denote Principal components 1, 2 and 3, respectively.

Table 3.11. Eigen-values, explained variance and rotated component matrix of nine agronomic traits and four *Striga asiatica* (Sa) parameters among 56 maize genotypes assessed under Sa infestation with and without *FOS* treatments in Tanzania

Traits – assessed under Sa infestation without <i>FOS</i> treatment	Rotated component matrix			Traits – assessed under Sa infestation with <i>FOS</i> treatment	Rotated component matrix			
	PC1	PC2	PC3		PC1	PC2	PC3	PC4
AD	0.14	0.80	0.31	AD	0.24	0.89	0.15	-0.18
SD	0.24	0.79	0.43	SD	0.24	0.88	0.16	0.15
ASI	0.35	0.36	0.52	ASI	0.06	0.26	0.07	0.76
PH	0.04	0.24	0.88	PH	0.09	0.33	0.86	0.07
EH	0.15	0.46	0.76	EH	0.25	0.51	0.71	0.13
DM	0.08	0.89	-0.01	DM	0.15	0.75	-0.23	0.49
GYD	0.01	0.19	-0.79	GYD	-0.07	0.29	-0.73	-0.10
HKWT	0.05	0.19	0.43	HKWT	0.18	-0.03	0.44	0.61
AGB	0.05	0.92	0.14	AGB	0.15	0.75	0.04	0.39
SaEC8	0.97	0.12	0.05	SaEC8	0.94	0.23	0.10	0.06
SaEC10	0.97	0.12	0.05	SaEC10	0.94	0.23	0.10	0.06
SaDR8	0.95	0.04	0.06	SaDR8	0.92	0.12	0.14	0.12
SaDR10	0.91	0.15	0.16	SaDR10	0.93	0.12	0.08	0.10
Eigen-value	3.85	3.44	2.78	Eigen-value	3.76	3.34	2.12	1.45
Proportion of Variance (%)	29.61	26.44	21.42	Proportion of Variance (%)	28.91	25.72	16.29	11.16
Cumulative Variance (%)	29.61	56.05	77.47	Cumulative Variance (%)	28.91	54.63	70.92	82.08

AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD – Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; PH – Plant height (cm); EH – Ear height (cm); DM – Days to maturity; *FOS*- *Fusarium oxysporium* f.sp. *strigae*; GYD – Grain yield/plant (g); HKWT – Weight of 100 kernels (g); AGB – Above ground biomass recorded as the weight (g) of above ground plant parts; SaEC8 - Number of emerged *Striga asiatica* plants (count) recorded eight weeks after sowing; SaEC10 – Number of emerged *Striga asiatica* plants (count) recorded ten weeks after sowing; SaDR8 – *Striga asiatica* damage rating recorded eight weeks after sowing; SaDR10 – *Striga asiatica* damage rating recorded ten weeks after sowing. PC1; PC2; and PC3 – denote Principal components 1, 2 and 3, respectively.

3.4 Discussion

The present study identified highly significant differences for all maize agronomic traits and *Striga* parameters studied under both *Sh* and *Sa* infestation, with and without *FOS* treatments (Tables 3.2 and 3.5). This suggests that the test genotypes possess adequate genetic variability from which selection for *Sh* and *Sa* resistance breeding could be done. The higher the genetic variation present among the test genotypes, the greater the probability of success for developing new superior *Striga* resistant varieties. An effective maize breeding program depends primarily on the available genetic variation within and between the genetic resources [62,63]

The application of the *FOS* treatment to the maize genotypes significantly ($P < 0.001$) affected the test genotypes and *Striga* parameters. The high variability behaviour of the test genotypes for all the *Striga* parameters studied, with and without *FOS* treatment, could be ascribed to the genetic constitutions and *FOS* compatibility. *Striga* emergence count, *Striga* damage rating, and grain yield under *Striga* infestation are significant traits for describing the level of resistance of genotypes to *Striga* infestation [67,68]. The interaction between maize genotypes and *FOS* was significant ($P < 0.05$) for all the maize traits studied except for hundred kernel weight. Likewise, the interaction mean squares between maize genotypes and *FOS* exhibited significant ($P < 0.001$) difference for *Sh* and *Sa* emergence counts at eight and 10 weeks after sowing (Tables 3.2 and 3.5). This measures the compatibility of the test genotypes with the biocontrol agent, *FOS*, and thus selections could be made, based on the genotypes individual *Striga* resistance and their *FOS* compatibility, under *Sh* and *Sa* infestation. Significant interactions between *FOS* and genotypes suggests the presence of synergistic effects between them for the management of *Striga* spp. Compatibility between test genotypes and *FOS* allows the biocontrol agent to colonize the root rhizospheres of the host genotypes, and subsequently to suppress *Striga* growth and establishment [10,56,57], reducing *Striga* parasitism to the host plant roots and improving grain yield [7,10,56]. In the present study, *FOS*-treated genotypes recorded higher grain yields than the untreated genotypes under both *Sh* and *Sa* infestation (Tables 3.3 and 3.6). The mean grain yield for *FOS*-treated genotypes under *Sh* infestation increased by 5.12 g/plant yield relative to the untreated treatment, amounting to 6.80% (Table 3.3). Likewise, under *Sa* infestation, *FOS*-treated genotypes had a mean yield increase of 4.5% (Table 3.6). These findings agree with those reported by [56] and [57], when studying the effect of *FOS* on maize genotypes under *Sh* and *Sa* infestation, respectively.

Grain yield performance of some *FOS*-treated genotypes under both *Sh* and *Sa* infestation surpassed that of the control treatment. These included TZA3181 (28.47%), TZA1782 (19.07%), JL21 (14.73%), TZA3964 (12.2%), TZA604 (9.11%) and JL25 (10.40%) (Tables 3.3 and 3.6). Similar findings have been reported by [10] when screening sorghum genotypes for *FOS*

compatibility under *Sh* and *Sa* infestation. This confirms the effectiveness of *FOS* in enhancing the performance of the test genotypes assessed under *Sh* and *Sa* infestation. Furthermore, the present study recorded higher fresh biomass for *FOS*-treated genotypes compared to untreated genotypes under both *Sh* and *Sa* infestation (Tables 3.3 and 3.6). Under *Sh* infestation the following *FOS*-treated genotypes recorded higher fresh biomass than the un-infested and untreated control treatment: TZA3827 (33.3 g/plant), JL08 (28.3 g/plant), JL05 (31 g/plant) and TZA4203 (26 g/plant) (Tables 3.3 and 3.4). Likewise, under *Sa* infestation, the following *FOS*-treated genotypes had fresh biomass that surpassed that of the control (uninfested and untreated): TZA3827 (32.5g/plant), TZA599 (30 g/plant) and JL24 (21 g/plant) (Tables 3.4 and 3.6). This confirms the effectiveness of *FOS* in suppressing the *Striga* spp. and its ability to stimulate plant growth in compatible genotypes. Thus, water, nutrients and inorganic solutes from the host xylem could be translocated towards the upper plant parts, improving plant vigour, biomass and consequently grain yield. Studies done earlier on the efficacy of *FOS* on sorghum genotypes recorded higher fresh biomass on *FOS*-treated genotypes than untreated control under *Striga* spp. infestation [7,10]. Furthermore, *FOS*-treated genotypes recorded significantly lower numbers of emerged *Striga* plants at both eight and 10 weeks after sowing. Under *Sh* infestation, *FOS*-treated genotypes supported reduced *Striga* numbers by up to 90.72% (TZA4165) at 10 weeks after sowing (Table 3.3). Likewise, under *Sa* infestation, *FOS*- was able to reduce the number of emerged *Sa* plants up to 90.7% (TZA3417) 10 weeks after sowing (Table 3.6). This confirmed the ability of the mycoherbicide to attack *Striga* spp. at different growth stages before emergence and flowering. The reduction of *Striga* number in *FOS*-treated maize genotypes was reported earlier in field and pot experiments [56,57]. *FOS*- reduces *Striga* spp. through complete digestion of *Sh* and *Sa* seedlings inside the host and clogging of vessels of emerged *Striga* plants by hyphae, causing wilting and subsequent death of *Striga* plants [69]. The present study noted some cases where there were few or zero emerged *Striga* plants, as well as wilting of emerged *Striga* plants in some of *FOS*-treated pots, suggesting the efficacy of *FOS* in infecting *Striga* seeds, seedlings, and shoots. Comparable observations have been reported before in field and pot experiments involving maize and sorghum treated with *FOS* [10,70]. Some *FOS*-treated genotypes (TZA604, TZA3952, TZA4064 and JL01) under both *Sh* and *Sa* infestation supported an increased number of emerged *Striga* plants at eight and 10 weeks after planting, suggesting *FOS* incompatibility. Some *Striga* resistant genotypes excrete exudates that are inhibitory to fungal growth, rendering them *FOS* incompatible [57]. Conversely, *FOS* compatible maize genotypes release exudates that activate virulence genes of the *Striga* mycoherbicide to efficiently suppress the parasite [56]. *FOS* is highly host specific, and it may be more compatible with some maize genotypes than others [60,71,72]

In the present study, secondary traits such days to 50% anthesis, days to 50% silking, anthesis-silking-interval, plant height and ear height under *Sh* and *Sa* infestation, revealed significant and positive correlations with *Striga* parameters after *FOS* treatment (Tables 3.7 and 3.8). This suggested that selection of one trait may simultaneously improve the other under *FOS* treatment. It has been reported that secondary traits play a significant role in the selection for improved grain yield under *Striga* infestation [73]. The studied *Striga* parameters of *Striga* emergence counts at eight and 10 weeks after planting, and *Striga* damage rating at eight and ten weeks after planting were highly significant and positively correlated among each other. This suggests that selection for one trait may improve the performance of another simultaneously. Therefore, either of these parameters could serve as a selection criterion for the evaluation of genotypes for *Striga* resistance [41].

Principal component analysis performed on the mean values of each trait, identified the most important traits that accounted for most of the variance in the data set (Tables 3.9 and 3.10). *Striga* emergence count and *Striga* host damage rating at eight and 10 weeks after sowing were the most significant traits, which accounted for the highest proportion of the variance in the data set. These traits were loaded in the first principal component (PC1) under both *Sh* and *Sa* infestation, with and without *FOS* treatment. Comparable results have been reported earlier in sorghum study involving *FOS* treatment [7]. Maize traits like above ground biomass, days to 50% anthesis and days to maturity formed the second-best linear combinations of traits and were loaded in PC2 under both *Sh* and *Sa* infestation with and *FOS* application. The traits grouped by the principal components, reflected significant relationships with *Striga* parameters under the Pearson correlation matrix, while *Striga* traits had strong positive correlations with each other. This suggests their usefulness in discriminating between the genotypes and should be considered during evaluation for *Striga* resistance [56]. The strong negative loading found on grain yield per plant was expected because as *Striga* thrives, it causes damage to the host, thereby reducing grain yield.

3.5 Conclusions

The application of *FOS* to maize genotypes under both *S. hermonthica* and *S. asiatica* infestation enhanced the resistance of the test genotypes to *Striga* and significantly reduced the number of emerged *Striga* plants and the levels of *Striga*-induced host damage, and subsequently improved grain yield of many test genotypes, compared to the untreated ones. The study demonstrated the value of combining host plant resistance, farmers compatible cultural practices and *FOS* for integrated *Striga* control in maize in Tanzania. Additionally, the study identified 23 genotypes with variable resistance, high grain yield, farmers preferred traits and *FOS* compatible for a *Striga* resistance breeding program in Tanzania. Development and

deployment of *Striga*-resistant and *FOS* compatible crop genotypes is a fundamental component of an integrated *Striga* management strategy in *Striga* infested agricultural lands. However, the identified maize genotypes need to be evaluated in multiple field conditions after *FOS* treatment to substantiate the findings recorded in the screen house.

3.6 References

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CHAPTER FOUR: Genetic diversity of maize genotypes with differential resistance to *Striga asiatica* and *S. hermonthica* based on phenotypic and simple sequence repeats markers

Abstract

Parasitic weeds of *Striga* spp. are a serious problem affecting maize production in much of sub-Saharan Africa, including Tanzania. The aim of this study was to determine the genetic diversity present among maize germplasm of diverse geographic origins, to select for new sources of *Striga* resistance and to develop farmer-preferred, locally adapted and high yielding maize varieties in Tanzania. Fifty-one maize genotypes collected from different sources were evaluated for resistance to *Striga asiatica* (*Sa*) and *S. hermonthica* (*Sh*) under controlled conditions. The test genotypes were assessed using 10 diagnostic simple sequence repeat (SSR) markers to complement the phenotypic data. Data were recorded for agronomic performance, *Striga* resistance and genetic diversity parameters. Significant ($P < 0.05$) genotypic variation was recorded among the test genotypes for key agronomic traits and resistance to *Striga* spp. The genotypes TZA4320, JL18, TZA4205, JL12, TZA3952, TZA3964, TZA3942, and JL01 showed resistance reactions for *Sa* and *Sh* based on low *Striga* counts. The analysis of molecular variance (AMOVA) revealed that within genotypes variance, among genotypes variance, and population differences accounted for 66.8%, 32.6%, and 0.6% of the total genotypic variation. Cluster analysis based on morphological and molecular markers classified the genotypes into three main groups. The clusters were independent of the geographic origin of the germplasm. TZA2263 and JL08, TZA4320 and JL12, TZA4205 and JL20, TZA1780 and JL05, TZA2761 and JL01, TZA604 and JL18, TZA4010 and JL12 were the most genetically divergent pairs of genotypes, based on SSR markers. The selected complementary lines are new and useful sources of genetic variation for *Striga* resistance breeding in maize in Tanzania.

Keywords: Genetic diversity, maize, *Striga*, SSR marker, Tanzania

4.1 Introduction

In Tanzania maize is predominantly cultivated by resource-poor small-scale farmers, with mean grain yields ranging from 1 to 1.5 t/ha compared to the potential yields of 4 to 5 t/ha reported elsewhere (Bisanda *et al.*, 1998; Mbwaga and Massawe, 2002; Barreiro-Hurle, 2012; Lobulu *et al.*, 2019). The low maize productivity has been attributed to diverse production constraints including biotic, abiotic, and socio-economic constraints. The key biotic factors limiting maize production and productivity include parasitic weeds (e.g., *Striga* spp.), the use of low yielding varieties, and diseases and insect pests (Mbwaga and Massawe, 2002; Lobulu *et al.*, 2019). Abiotic factors include poor soil fertility, drought, and heat stress (Shiferaw *et al.*, 2011; Cairns *et al.*, 2013).

Striga spp. are parasitic weeds, some of which that have an impact on cereal production systems in SSA. The genus *Striga* comprises 43 spp. worldwide, of which 11 spp. are considered noxious weeds in agriculture (Ejeta, 2007b; Lobulu *et al.*, 2019). Among the spp., *Striga hermonthica* (Del.) Benth, *S. asiatica* (L.) Kuntze, *S. forbesii* (Benth.), *S. aspera* (Willd.) Benth. and *S. densiflora* (Benth.) cause substantial yield loss and crop failure in cereal crop production (Ejeta, 2007a; Parker, 2009; Timko *et al.*, 2012). Of all the cultivated cereals, maize is exceptionally susceptible to *Striga* infestations, especially under drought and suboptimal soil nitrogen conditions, which are common in marginal maize production areas of SSA (Ejeta, 2007a; Badu-Apraku and Akinwale, 2011; Menkir *et al.*, 2012b).

Cereal yield losses due to *Striga* in SSA range from 20 to 100%, depending on *Striga* seed density, cultivar susceptibility, soil fertility status, and climatic conditions (Massawe *et al.*, 2002; Teka, 2014; Lobulu *et al.*, 2019). More than 10 million tons of cereal grains are lost annually due to *Striga* damage in the SSA region (Watson *et al.*, 2007), worth an estimated 7 USD billion, and affecting the welfare and livelihoods of over 100 million people (Badu-Apraku and Akinwale, 2011). In East Africa, monetary losses due to *Striga* damage is about 335 USD million per year (Khan, 2011). In Tanzania, MacOpiyo *et al.* (2009) estimated annual grain yield loss due to *Striga* infestation in maize at 464,599 tons, followed by rice (232,913 tons) and sorghum (192,975 tons), causing economic losses valued at 173 million USD (Khan, 2011).

Striga control is more difficult than other weeds due to its biology and crop production systems. The weed produces large quantities of minute seeds that can remain viable in the soil for over 20 years (Gurney *et al.*, 2003; Gurney *et al.*, 2006). A single plant can produce up to 500,000 tiny dust-like seeds, which mature at different times (Berner *et al.*, 1994; Yoneyama *et al.*, 2010). Many of the seeds are held in the soil seed-bank, which increases the chance that some *Striga* seeds will find a suitable host (Ejeta, 2007b). Under smallholder farming systems, the available

cultural control practices such as manual weeding, are laborious and time-consuming, expensive and are seldom effective. Severe crop damage can occur even before *Striga* emerges above the ground (Massawe *et al.*, 2002; Sibhatu, 2016). Use of herbicides, organic and inorganic soil amendments such as fertilizer or manure are expensive and not widely used by smallholder farmers in low-input agricultural production systems in SSA. Hence, the use of host plant resistance combined with other control practices is essential for enhancing crop yields in the region.

The development of host plant resistance through breeding is a fundamental component of a sustainable integrated *Striga* management strategy to minimize yield losses in farmers' fields. A successful maize breeding program depends mainly on the available genetic variation within and between the germplasm resources (Yan *et al.*, 2016; Al-Naggar *et al.*, 2020). Maize landraces harbour useful and novel genes for multiple stress tolerance and for resistance to pests and diseases (Warburton *et al.*, 2008; Shimelis and Laing, 2012). Hence, it is imperative to exploit the genetic variability present among landraces and other locally adapted improved maize populations for breeding (Cholastova *et al.*, 2011). Landraces are genetically diverse and co-evolved with the diverse parasitic weeds, insect pests and diseases of their original agroecology, making them a good source of genetic variation with desirable traits.

Genetic diversity studies can be carried out using phenotypic or molecular markers. Phenotyping is the foremost step in identifying and categorizing germplasm for breeding purposes (Govindaraj *et al.*, 2015). Although phenotypic evaluations are limited by the effect of environment on traits' expression, it offers an unparalleled means of identifying phenotypic variation (Twumasi *et al.*, 2017; Al-Naggar *et al.*, 2020). Accurate phenotyping provides crucial information to describe genetic resources for ideotype breeding (Ignjatovic-Micic *et al.*, 2015). Maize genotypes are usually assessed using phenotypic traits based on standard descriptors such as those developed by the International Maize and Wheat Improvement Center/ International Board for Plant Genetic Resources (CIMMYT and IBPGR, 1991). The key phenotypic traits include days to flowering, days to maturity, anthesis-silking interval, plant height, ear height, 100 weight, grain yield and *Striga* parameters such as the number of *Striga* plants emerged, and *Striga* plant height and vigour. For efficient germplasm characterization, phenotyping is often complimented by DNA-based molecular markers because the latter is not affected by environmental influences.

Molecular markers are effective in elucidating the genetic variability among genotypes (Smith and Smith, 1992; Maniruzzaman *et al.*, 2018). The commonly used molecular markers in genetic diversity analyses include restriction fragment length polymorphisms (RFLP), random amplified

polymorphisms (RAPD), amplified fragment length polymorphisms (AFLP), microsatellite or simple sequence repeats (SSRs), and single nucleotide polymorphisms (SNP) (Smith *et al.*, 1997; Molin *et al.*, 2013; Nyaligwa *et al.*, 2016). SSR markers are frequently used because of their high polymorphism, detection of multi-allelic variation, co-dominance, reproducibility, ease of detection by polymerase chain reaction (PCR), relative abundance with a uniform coverage within the maize genome, and their requirement of a small amount of DNA (Powell *et al.*, 1996; Saxena *et al.*, 2010; Xu *et al.*, 2013; Maniruzzaman *et al.*, 2018). SSR markers have been widely used in maize genetic diversity studies to define potential heterotic groups for parental selection (Surender *et al.*, 2014; Vega-Alvarez *et al.*, 2017; Shayanowako *et al.*, 2018). In light of the above background, the objective of this study was to determine the genetic diversity among maize germplasm of diverse geographic origins to select new sources of *Striga* resistance that can be used to develop farmer-preferred, locally adapted and promising maize varieties in Tanzania.

4.2 Materials and methods

4.2.1 Plant material

The study used 51 maize genotypes consisting of 34 landraces acquired from the National Plant Genetic Resources Centre (NPGRC) – Tanzania, 12 improved open-pollinated varieties (OPVs) from the International Institute of Tropical Agriculture (IITA) – Nigeria, and five OPVs from the Tanzanian Agricultural Research Institute (TARI) – Tanzania. The IITA germplasm included 11 *Striga* resistant genotypes and one *Striga* susceptible genotype, which were used as checks. The details of the studied genotypes are presented in Table 4.1.

4.2.2 *Striga* inoculum

The *Striga* seeds were collected from maize and sorghum fields infested with either of the two *Striga* spp. or both in the 2016/2017 growing season. The seed of *S. asiatica* was collected at the TARI – Hombolo Research Centre, Dodoma region and the TARI - Tumbi Research Centre, Tabora region, while the seed of *S. hermonthica* was collected in the Mbutu and Igogo wards, Igunga district, Tabora region. *Striga* seeds from both spp. were separately processed, packed, labelled, and stored for further use.

4.2.3 Experimental procedure

The experiment was established following completely randomised design during the 2017/2018 growing season in a screen house facility at TARI - Tumbi Research Centre situated in Tabora Municipal, western Tanzania. The centre is located at 5°03'S latitude and 32°41'E longitude with an altitude of 1190 metre above sea level (masl). The test genotypes were sown in a screen house using 20 litre-capacity polyethylene plastic pots were initially filled with a growing medium

consisting of topsoil and sandy soil mixed at a ratio of 6:3. A total of 816 pots were filled with the growing medium and divided into two equal sets of 408. The first set of 408 pots was infested with one-year old *S. asiatica* (*Sa*) seeds uniformly distributed at a depth of 2 cm in the growing medium. The second set of 408 pots was infested with one year old *S. hermonthica* (*Sh*) seeds. Each infested pot received 0.03 g of viable *Striga* seeds. After 12 days of *Striga* seed preconditioning, maize seeds were planted in all the pots, with two seeds of each genotype were planted in each pot. After emergence, maize plants were thinned to one seedling per pot. An experimental plot consisted of four pots, and these were replicated twice for each treatment. The trial was maintained following standard maize agronomic practices. Weeds other than the two *Striga* spp. were uprooted manually.

4.2.4 Phenotypic data collection

Phenotypic data were collected, based on maize agronomic traits and *Striga* resistance traits. Maize genotypes were assessed for the following traits: anthesis date (AD) was recorded as the number of days from sowing to when 50% of the plants in a plot shed pollen. The days to silking (SD) was recorded as the number of days from sowing to when 50% of the plants in a plot produced silks. Anthesis-silking interval (ASI) was determined as the difference between days to 50% silking and 50% anthesis. The days to maturity (DM) were recorded as the number of days from planting to when 75% of the plants reached physiological maturity (Verheye, 2010). Plant height (PH) was measured from the base of the plant (cm) to the top of the first tassel branch. Ear height (EH) was measured (cm) from the ground level to the node bearing the uppermost ear. Grain yield/plant (GYD) was determined as the average weight (g), of the grain from the ears of individual plants after shelling, converted to a constant moisture of 12.5%. Hundred kernel weight was recorded based on a weight of hundred kernels at field moisture content and converted to a constant moisture of 12.5%.

The following *Striga* parameters were recorded: days to *Striga* emergence (DES) were recorded as the number of days taken for the first *Striga* plant to emerge above the ground. The *Striga* emergence (Sn) counts were recorded as the number of emerged *Striga* plants per genotype. *Striga* plant height (cm) was measured from the base of the plant to the tip of the plant and *Striga* plant vigour (SV) was recorded following a rating scale of 0 – 9 (Hausmann *et al.*, 2000), where 0 = not emerged, 1 < 5 cm, 2 = 6 – 20 cm, 3 = 6 – 20 cm with ≥ 1 branch, 4 = 21 – 30 cm and ≤ 5 branches, 5 = 21 – 30 cm with ≥ 5 branches, 6 = 31 – 40 cm with ≤ 10 branches, 7 = 31 – 40 cm with ≥ 10 branches, 8 = >40 cm with ≤ 10 branches and 9 = > 40 cm with >10 branches.

Table 4.1. List and source of maize genotypes used for the study.

S/No	Genotype code	Name/designation/pedigree	Source/origin	Description
1	JL23	Staha	TARI/Tanzania	OPV
2	TZA 3951	Mwarabu	NPGRC/Tanzania	Landrace
3	TZA 3942	Mwarabu	NPGRC/Tanzania	Landrace
4	TZA 4092	Mahindi ya Kisukuma	NPGRC/Tanzania	Landrace
5	TZA 4205	Katumbili	NPGRC/Tanzania	Landrace
6	TZA 4000	Nchanana	NPGRC/Tanzania	Landrace
7	TZA 3964	Amakuria	NPGRC/Tanzania	Landrace
8	TZA 4010	Kagire	NPGRC/Tanzania	Landrace
9	TZA 3827	Mahindi	NPGRC/Tanzania	Landrace
10	TZA 4016	Mahindi	NPGRC/Tanzania	Landrace
11	TZA 1782	Mahindi	NPGRC/Tanzania	Landrace
12	TZA 4165	Ibahakazi	NPGRC/Tanzania	Landrace
13	TZA 4203	Gembe	NPGRC/Tanzania	Landrace
14	TZA 3417	Mahindi	NPGRC/Tanzania	Landrace
15	TZA 2881	Mahindi	NPGRC/Tanzania	Landrace
16	TZA 3095	Fumandoli	NPGRC/Tanzania	Landrace
17	TZA 3181	Uruwanga	NPGRC/Tanzania	Landrace
18	TZA 1784	Mahindi	NPGRC/Tanzania	Landrace
19	TZA 2263	Mahindi	NPGRC/Tanzania	Landrace
20	TZA 599	Ipukile	NPGRC/Tanzania	Landrace
21	TZA 3502	Katumbili	NPGRC/Tanzania	Landrace
22	TZA 615	Mahindi	NPGRC/Tanzania	Landrace
23	TZA 4062	Chalana	NPGRC/Tanzania	Landrace
24	TZA 3561	Oloman	NPGRC/Tanzania	Landrace
25	TZA 3614	Magereza	NPGRC/Tanzania	Landrace
26	TZA 4078	Mnana	NPGRC/Tanzania	Landrace
27	TZA 4064	Ya kienyeji	NPGRC/Tanzania	Landrace
28	TZA 1775	Mahindi	NPGRC/Tanzania	Landrace
29	TZA 604	Ipukele	NPGRC/Tanzania	Landrace
30	TZA 4320	Mahindi	NPGRC/Tanzania	Landrace
31	TZA 1780	Mahindi	NPGRC/Tanzania	Landrace
32	TZA 1771	Katumani	NPGRC/Tanzania	Landrace
33	TZA 687	Nyamula	NPGRC/Tanzania	Landrace
34	JL25	T105	TARI/Tanzania	OPV
35	JL24	T104	TARI/Tanzania	OPV
36	TZA 2761	Mahindi	NPGRC/Tanzania	Landrace
37	TZA 3570	Oloman	NPGRC/Tanzania	Landrace
38	JL22	Situka M1	TARI/Tanzania	OPV
39	JL26	Kilima	TARI/Tanzania	OPV
40	JL13	TZECOMP5C7/TZECOM3DT.C2	IITA/Nigeria	OPV
41	JL12	SAMMAZ – 16	IITA/Nigeria	OPV
42	JL15	1 WDC3SYN *2 white DSTR-SYN-DTC1	IITA/Nigeria	OPV
43	JL08	Z. DIPLO.BC4C3-W-DTC1	IITA/Nigeria	OPV
44	JL19	DT-STR-W-SYN12	IITA/Nigeria	OPV
45	JL01	DT-STR-Y-SYN14	IITA/Nigeria	OPV
46	JL09	TZECOMP3DT/white DT-STRR-SYNDC2	IITA/Nigeria	OPV
47	JL05	STR-SYN-Y2	IITA/Nigeria	OPV
48	JL20	Z. DIPLO-BC4C3-W/ DOGONA-1/Z.DIPLO-BC4-C3-W	IITA/Nigeria	OPV
49	JL17	TZLCOMP1-WCB*2C White DT-STR-SYNJ-DTC1	IITA/Nigeria	OPV
50	JL18	STR-SYN-W1	IITA/Nigeria	OPV
51	JL16	2*TZECOMP3DT/White DSTR/SYN DC2	IITA/Nigeria	OPV

OPV – Open Pollinated Variety; NPGRC – National Plant Genetic Resources Centre for Tanzania; S/No – Serial number; TARI - Tanzania Agricultural Research Institute; IITA – International Institute of Tropical Agriculture.

4.2.5 Phenotypic data analysis

Phenotypic data were subjected to analysis of variance (ANOVA) using Genstat 18.2th Edition and significant tests were carried out at 5% probability level. Mean separation was performed using the least significant difference (LSD) at 5%. Hierarchical cluster analysis based on phenotypic traits was performed using the Euclidean distance based on the unweighted pair group method with arithmetic averages (UPGMA) algorithm using R software (Grum and Atieno, 2007). The correlation analysis was computed to test the relationship between agronomic and *Striga* parameters. A principal component analysis (PCA) was performed using the mean values of the 51 maize genotypes using the Statistical Package for the Social Sciences (SPSS) version 24.0 (SPSS, 2017), to elucidate the genetic relationships among the test genotypes.

4.2.6 Genotyping

4.2.6.1 DNA extraction and polymerase chain reaction

Maize genotypes were raised in artificial media in 400 mm diameter pots at the University of KwaZulu-Natal – Controlled Environment Facility, South Africa. Fresh young leaf samples from three randomly selected four weeks old maize plants were collected for DNA extraction. The DNA was extracted following the Cetyl-tetramethyl ammonium bromide (CTAB) method. Approximately 200 mg of ground plant tissue combined with 500 µL of CTAB buffer, was incubated for one hour at 65°C, and subjected to centrifugation at 3500 rpm for 10 min. The supernatant was then transferred into new micro-tubes, and 400 µL chloroform: iso-amyl alcohol (24:1) was added into the tubes and mixed gently. After the second centrifugation (centrifuged at 3500 rpm for 30 min), the DNA was precipitated from the aqueous layer by adding salt and ethanol. The upper aqueous phase containing DNA was transferred to a clean microfuge tube. The resulting pellet was dried and re-suspended in TE buffer. The PCR amplification reaction contained a total volume of 12 µL of PCR mix. The PCR mix contained 1.2 µL dNTPs (25 µM), 0.12 µL Taq (5U/ µL), 0.72 µL Magnesium chloride (50 mM MgCl₂), 0.06 µL forward primer (10 µM), 0.3 µL reverse primer (10 µM), 1.2 µL reaction buffer (10x), 6.16 µL PCR grade water, 0.24 µL dye and 2µL of genomic DNA. The touchdown PCR amplification cycle consisted of an initial denaturation step of 2 min at 94°C, 9 cycles of denaturation for 30 sec at 94°C, an annealing temperature of 60°C for 30 sec, and an extension of 72°C for 45 sec, followed by 26 cycles of denaturation at 94°C for 30 sec, annealing temperature of 52°C for 30 sec, an extension temperature of 72°C for 45 sec and final extension at 72°C for 5 min. The PCR products were fluorescently analysed using a Genetic Analyzer 3130xl (Applied Biosystems, Pietermaritzburg, South Africa) and separated by capillary electrophoresis on an ABI 3013 automatic sequencer. Analysis of the electropherograms was done using Gene Mapper 4.0, and the marker data was presented as fragment sizes in an Excel spreadsheet.

4.2.6.2 Simple sequence repeats markers analysis

Ten diagnostic simple sequence repeats (SSRs) molecular markers distributed across the 10 maize chromosomes were used in this study. The markers were chosen based on their high polymorphic information content (PIC) value, and their frequent use in maize diversity analysis (Senior *et al.*, 1998; Legesse *et al.*, 2007; André *et al.*, 2015; Kumari *et al.*, 2018). One primer (Phi046) out of 10 showed a monomorphic pattern and thus was dropped in further analysis. Forward and reverse primers of the SSR markers used in this study are presented in Table 4.2.

4.2.6.3 Genetic parameters analysis

Genetic diversity analyses were performed using GenAlex version 6.5 (Peakall and Smouse, 2012). The following parameters were computed: total number of alleles per locus (N_a), number of effective alleles per locus (N_e), Shannon's information index (I), observed heterozygosity (H_o), gene diversity (H_e), and fixation index (F) (Nei, 1978). The PIC values were calculated for each SSR locus, according to Smith *et al.* (1997) as:

$PIC = 1 - \sum (p_i^2)$, where p_i is the frequency of i^{th} allele.

Cluster analysis was conducted among the 51 maize genotypes using the genetic distance matrix, and the dendrogram was drawn using the unweighted pair group method (UPGMA) using Darwin 6.0.5 software (Perrier and Jacquemoud-Collet, 2006). Furthermore, an analysis of molecular variance (AMOVA) was performed to analyse genetic variation among the 51 genotypes.

Table 4.2. List and sequence of SSRs markers used for genotyping 51 maize genotypes

S/No	Primer Code	Primer sequence	Reference(s)
1	Phi064	F: CCGAATTGAAATAGCTGCGAGAACCT R: ACAATGAACGGTGGTTATCAACACGC	Kumari <i>et al.</i> (2018)
2	Nc130	F: GCACATGAAGATCCTGCTGA R: TGTGGATGACGGTGATGC	Senior <i>et al.</i> (1998) and Kumari <i>et al.</i> (2018)
3	Nc133	F: AATCAAACACACACCTTGCG R: GCAAGGGAATAAGGTGACGA	Senior <i>et al.</i> (1998) and Kumari <i>et al.</i> (2018)
4	Bnlg391	F: CAGATATCACAGCATCAGAAGATCA R: CAGATATCACAGCATCAGAAGATCA	Kumari <i>et al.</i> (2018)
5	Phi014	F: AGATGACCAGGGCCGTC AACGAC R: CCAGCTTCACCAGCTTGCTCTTCGTG	Kumari <i>et al.</i> (2018)
6	Phi046	F: ATCTCGCGAACGTGTGTGCAGATTCT R: TCGATCTTTCCCGGAACTCTGAC	Kumari <i>et al.</i> (2018)
7	Phi037	F: CCCAGCTCCTGTTGTGGCTCAGAC R: TCCAGATCCGCCGCACCTCAGTCA	André <i>et al.</i> (2015)
8	Bnlg619	F: ACCCATCCCCTTTCCACCTCCTCCT R: GCTTTCAGCGAATACTGAATAACGCGGA	Legesse <i>et al.</i> (2007) and André <i>et al.</i> (2015)
9	Nc003	F: ACCCTTGCCCTTTACTGAAACACAACAGG R: GCACACCGTGTGGCTGGTTC	Legesse <i>et al.</i> (2007) and André <i>et al.</i> (2015)
10	Bnlg2190	F: TCCTCCTTCATCCCCTTCTT R: CCCAGTATCATTGCCCAATC	Legesse <i>et al.</i> (2007)

Notes: F - Forward primers; R - Reverse primers; S/No – Serial number

4.3 Results

4.3.1 Phenotyping maize populations

Analysis of variance (ANOVA) based on phenotypic traits revealed significant ($P < 0.05$) variation for yield and yield components among maize genotypes studied when infested with both *Sa* and *Sh* (Table 4.3). Under *Sa* infestation, the mean squares for the genotypes were significantly different ($P < 0.01$) for most studied traits except grain yield and anthesis-silking interval. Furthermore, test genotypes showed significant variation for *Sa* parameters except for the number of days to *Sa* emergence. The mean squares for the test genotypes exhibited significant variation ($P < 0.05$) for all the traits under *Sh* conditions (Table 4.3). Likewise, test genotypes exhibited significant variation ($P < 0.05$) for all the *Sh* parameters studied under *Sh* infestation.

4.3.2 Performance of maize genotypes under *Striga asiatica* infestation

The mean number of days to anthesis was 63.86 under *Sa* infestation. Anthesis days varied from 52.00 days (genotype JL 22) to 77.00 days (TZA1782) (Table 4.4). The days to silking varied from 55.00 days (JL22) to 82.00 days (TZA1782). Furthermore, the days to maturity ranged from 107.00 (TZA4000 and TZA3502) to 138.00 days (TZA1780). The mean grain yield per plant was 74.84 g. Grain yield varied from 36.03 g/plant for the genotype TZA4000 to 107.21 g/plant for the genotype TZA2263. The mean plant height was 275.50 cm. The minimum plant

height (209.30cm) was observed from the genotype JL19, while the maximum (351.50cm) was recorded from TZA4064. The mean hundred kernel weight was 24.92g, and the genotype TZA4064 recorded the highest hundred kernel weight of 35.47g, whilst JL06 had the lowest hundred kernel weight at 19.80 g.

The mean number of days for *S. asiatica* emergence across the test genotypes was 47.30 days. *Sa* emerged relatively early (18.00 days) for genotypes TZA3570 and TZA3942, and late (70.50 days) for TZA4205 (Table 4.4). The mean number of emerged *Sa* was 19.00. The lowest mean number (1.50) of emerged *Sa* plants was recorded for the genotype TZA4320 and the highest *Sa* count (59.50) was observed for TZA599. The mean *Sa* vigour was 3.38 with a minimum of 1.50 observed for TZA4320 and a maximum of seven was scored for ZA2881.

4.3.3 Performance of maize genotypes under *Striga hermonthica* infestation

Day to anthesis varied from 53.00 days (JL 22) to 76.50 days (TZA1782) with a mean of 64.29 under *Sh* infestation (Table 4.5). The days to silking ranged from 55.50 (JL22) to 81.00 (TZA1782). The anthesis-silking interval varied from -1.00 day (TZA4165) to 6.00 days (TZA4165) with a mean of 2.00 days. The mean number of days to physiological maturity was 117.63. A relatively early maturing genotype was TZA3417 with a mean of 105.5 days, while the latest maturing (135.50 days) genotype was TZA1780. Grain yield varied from 34.22 g/plant for the genotype TZA3561 to 130.44 g/plant for the genotype TZA2263, with a mean of 75.20 g/plant. Heavier grain weight was recorded for TZA4064 (35.17 g/100 kernels). The lowest value was 19.08 g/100 kernels for genotype JL06.

The number of emerged *Sh* plants ranged from 0.00 (TZA4320) to 22.50 for the susceptible check (JL06). Days to *Sh* emergence varied from 0.00 (TZA4320) to 81.00 days (TZA4203), with a mean of 52.80 days (Table 4.5). The mean vigour of *Sh* plants was 4.03 with a minimum of 1.00 observed for TZA4000 and a maximum of 9.00 for JL25.

Table 4.3. Mean squares for eight phenotypic traits of 51 maize genotypes under *Striga* infestation evaluated in western Tanzania in 2017/18

Source of variation	Maize traits									<i>Striga asiatica</i> parameters			
	DF	AD	SD	ASI	DM	PH	EH	GYD	HKWT	DESa	SNSa	HTSa	SVSa
Replication	1	43.75	128.57	22.32	18.08	3917.60	358.90	2077.10	0.40	367.90	1255.60	98.25	1.29
Genotype	50	32.94**	49.65**	6.53ns	84.08***	2492.60***	2499.60***	651.70ns	30.37***	205.70ns	330.50*	166.04***	3.88**
Residual	50	5.31	7.46	4.36	29.66	841.80	513.20	487.90	2.60	242.30	201.90	72.53	1.74
Total	101												

Source of variation	Maize traits									<i>Striga hermonthica</i>			
	DF	AD	SD	ASI	DM	PH	EH	GYD	HKWT	DESh	SNSh	HTSh	SVSh
Replication	1	40.08	98.44	12.89	2.58	70.10	1815.30	459.80	11.28	908.60	170.04	400.5	0.72
Genotype	50	31.83***	46.81***	5.24*	89.65***	2165.50***	2459.80***	878.90***	30.65***	326.70*	38.61**	832.4**	8.66*
Residual	50	3.86	8.77	3.15	32.53	636.90	619.90	312.30	2.57	187.60	16.69	363.3	4.65
Total	101												

*, **, *** Significant at $P < 0.05$; $P < 0.01$ and $P < 0.001$ probability level respectively; ns – Not significant at $P < 0.05$ probability level; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; ASI – Anthesis-silking interval; DESa - Number of days taken for the first *S. asiatica* plant to emerge above the ground; DESh - Number of days taken for the first *S. hermonthica* plant to emerge above the ground; DF – Degree of freedom; DM – Days to maturity; EH - Ear height (cm); GYD – Grain yield/plant (g); HKWT - Weight of 100 kernel/plant (g); HTSa – *S. asiatica* plant height; HTSh – *S. hermonthica* plant height; PH - Plant height (cm); SD - Number of days from sowing to when 50% of the plants in a plot produce silk; SNSa - Number of emerged *S. asiatica* plants; SNSh - Number of emerged *S. hermonthica* plants; SVSa – *S. asiatica* plant vigour; and SVSh - *S. hermonthica* plant vigour.

Table 4.4. Mean performance of the top 15 and bottom five genotypes amongst 51 maize genotypes evaluated based on phenotypic traits under *Striga asiatica* infestation in western Tanzania during 2017/18. Genotypes were ranked based on number of emerged *Striga* plants.

Accession	Maize traits									<i>Striga asiatica</i> parameters			
	AD	SD	ASI	DM	PH	EH	EP	GYD	HKWT	DESa	SNSa	HTSa	SVSa
Top 15 genotypes													
TZA4320	70.50	76.50	6.00	132.00	307.00	210.50	0.69	63.80	23.93	38.50	1.50	3.00	1.00
JL12	64.50	65.50	1.00	117.00	300.00	168.20	0.56	85.03	23.27	34.00	2.50	7.00	1.00
TZA3952	65.50	68.50	3.00	124.50	328.00	158.00	0.48	63.33	30.52	64.50	2.50	9.50	3.00
TZA3942	61.50	62.00	0.50	120.00	225.50	145.80	0.65	61.64	27.58	18.00	4.00	11.00	1.50
TZA4205	60.50	62.50	2.00	111.50	255.00	132.50	0.52	93.67	24.54	70.50	4.50	21.00	4.00
JL18	63.50	64.00	0.50	123.50	242.20	122.50	0.50	86.83	24.48	53.50	5.50	13.00	2.50
TZA3964	62.00	64.50	2.50	125.00	307.50	169.50	0.56	39.27	33.07	28.00	5.50	8.00	3.00
JL01	62.00	64.00	2.00	112.50	256.20	134.50	0.52	82.43	23.53	53.00	6.00	8.50	2.00
TZA3502	54.50	57.50	3.00	107.00	248.70	101.50	0.41	48.13	19.47	44.00	7.00	12.00	2.50
JL03	63.00	66.00	3.00	112.50	286.20	180.20	0.63	73.81	24.11	44.00	7.50	9.50	2.00
TZA3570	65.50	66.50	1.00	114.50	332.50	213.80	0.64	63.22	23.08	18.00	7.50	10.00	1.50
TZA4165	63.00	63.50	0.50	118.00	248.70	132.50	0.53	86.01	23.86	63.00	8.00	17.00	3.00
JL04	63.00	65.50	2.50	118.50	251.00	126.00	0.50	66.87	25.45	45.50	8.50	11.00	2.00
JL21	62.00	64.00	2.00	117.50	308.80	171.20	0.55	71.69	23.24	45.50	9.00	11.00	2.50
TZA1775	64.00	65.50	1.50	122.50	270.20	161.50	0.59	88.45	25.26	56.50	10.50	36.50	6.00
Bottom five genotypes													
TZA3561	69.00	71.50	2.50	115.50	345.20	216.20	0.63	53.70	22.64	41.00	38.00	26.50	4.50
JL13	57.00	61.00	4.00	117.00	213.50	118.00	0.55	84.57	19.72	51.50	42.00	21.00	3.00
JL06	64.50	67.50	3.00	116.00	251.50	155.80	0.62	74.38	19.08	37.00	43.50	31.50	5.50
TZA2881	69.00	75.00	6.00	118.00	293.00	208.80	0.73	47.26	23.01	38.50	53.50	41.00	7.00
TZA599	71.50	74.00	2.50	129.50	262.70	191.80	0.73	81.93	32.39	44.50	59.50	33.50	6.00
Mean	63.86	66.52	2.66	117.9	275.5	157.8	0.57	74.84	24.92	47.3	19.3	18.88	3.38
CV%	3.60	4.10	78.50	4.60	10.50	14.40	11.50	29.50	6.50	32.90	73.60	45.10	39.10
<i>P</i> < 5%	**	**	ns	***	***	***	***	ns	***	ns	*	**	**
Sed	2.305	2.732	2.088	5.446	29.01	22.65	0.066	22.089	1.612	15.57	14.21	8.516	1.319
LSD	4.62	5.475	4.184	10.915	58.15	45.4	0.132	44.267	3.231	31.2	28.47	17.067	2.644

*, **, *** Significant at $P < 0.05$; $P < 0.01$ and $P < 0.001$ probability level, respectively; ns – Not significant at $P < 0.05$ probability level; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; ASI – Anthesis-silking interval; CV% - Coefficient of variation; DESa - Number of days taken for the first *S. asiatica* plant to emerge above the ground; DM – Days to maturity; EH - Ear height (cm); GYD – Grain yield/plant (g); HKWT - Weight of 100 kernel/plant (g); HTSa – *S. asiatica* plant height; LSD – Least significant difference; PH - Plant height (cm); Sed – Standard error of difference; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; SNSa - Number of emerged *S. asiatica* plants; and SVSa – *S. asiatica* plant vigour.

Table 4.5. Mean performance of the top 15 and bottom five genotypes amongst 51 maize genotypes evaluated based on phenotypic traits under *Striga hermonthica* infestation in western Tanzania during 2017/18. Genotypes were ranked based on number of emerged *Striga*

Accession	Maize traits									<i>Striga hermonthica</i> parameters			
	AD	SD	ASI	DM	PH	EH	EP	GYD	HKWT	DESh	SNSh	HTSh	SVSh
Top 15 genotypes													
TZA4320	68.50	73.50	5.00	128.00	275.00	168.80	0.61	94.76	23.19	0.00	0.00	0.00	0.00
JL09	63.00	62.00	1.00	111.50	218.80	112.80	0.51	85.91	22.02	51.50	1.00	23.50	4.00
TZA4010	59.00	62.00	3.00	117.00	303.50	164.50	0.55	83.21	30.75	27.00	1.00	3.00	1.00
JL04	60.50	62.00	0.50	122.50	256.80	146.20	0.57	42.82	25.30	24.50	1.00	5.50	1.00
JL05	62.00	62.00	0.50	119.00	240.00	136.80	0.57	90.29	21.25	62.00	1.50	7.50	2.00
JL20	63.50	64.00	0.50	121.00	257.20	142.00	0.55	74.85	23.20	72.50	1.50	15.00	2.50
TZA3502	56.50	61.00	4.50	107.00	252.50	136.50	0.54	55.77	19.10	49.00	1.50	13.50	3.00
TZA4203	71.00	73.50	2.50	125.00	271.00	157.50	0.57	82.49	24.65	81.00	2.00	8.00	2.50
JL18	63.00	64.00	1.00	123.50	239.50	112.80	0.47	93.86	24.90	55.50	3.00	64.00	5.50
TZA4064	65.50	67.00	1.50	118.00	339.50	217.50	0.64	83.84	35.17	67.00	3.00	13.00	2.50
JL17	64.50	66.50	2.00	113.00	283.80	141.00	0.50	76.17	22.70	72.00	3.00	14.50	2.50
TZA3952	65.50	71.50	6.00	126.00	297.00	176.00	0.59	38.00	30.00	50.50	3.00	18.00	3.00
JL12	64.50	64.50	0.00	114.50	281.50	150.50	0.53	48.56	22.95	49.50	3.50	11.00	2.50
TZA2749	61.50	63.50	2.00	116.00	253.20	146.50	0.58	86.66	25.21	63.00	4.00	13.50	3.00
JL22	53.00	55.50	2.50	107.00	235.50	114.80	0.49	66.29	24.25	53.00	4.00	14.50	2.50
Bottom five genotypes													
TZA3570	66.50	68.50	2.00	110.00	299.50	182.70	0.61	65.92	22.45	53.50	12.00	36.50	5.50
JL13	60.50	62.00	1.50	118.50	238.20	102.00	0.44	66.80	19.34	52.50	14.00	46.00	8.00
TZA1782	76.50	81.00	4.50	128.50	331.80	227.20	0.68	55.55	25.30	61.50	15.00	54.00	5.50
TZA1771	63.50	64.00	0.50	114.00	273.00	143.80	0.52	86.78	23.45	38.00	17.50	53.20	7.50
JL06	61.00	63.00	0.00	118.50	210.80	108.00	0.51	91.44	19.08	51.00	22.50	38.20	6.00
Mean	64.29	66.29	2.00	117.63	275.30	157.80	0.57	75.20	24.54	52.80	6.55	26.70	4.03
CV%	3.10	4.50	88.70	4.80	9.20	15.80	13.00	23.50	6.50	26.00	62.30	71.30	53.60
<i>P</i> < 5%	***	***	*	***	***	***	**	***	***	*	**	**	*
Sed	1.965	2.961	1.774	5.703	25.24	24.90	0.074	17.673	1.603	13.70	4.085	19.06	2.156
LSD	3.938	5.933	3.555	11.429	50.57	49.90	0.149	35.417	3.212	27.45	8.187	38.20	4.322

*, **, *** Significant at $P < 0.05$; $P < 0.01$ and $P < 0.001$ probability level, respectively; ns – Not significant at $P < 0.05$ probability level; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; ASI – Anthesis-silking interval; CV% - Coefficient of variation; DESh - Number of days taken for the first *S. hermonthica* plant to emerge above the ground; DM – Days to maturity; EH - Ear height (cm); GYD – Grain yield/plant (g); HKWT - Weight of 100 kernel/plant (g); HTSh – *S. hermonthica* plant height; LSD – Least significant difference; PH - Plant height (cm); Sed – Standard error of difference; SD - Number of days from sowing to when 50% of the plants in a plot produce silks; SNSh - Number of emerged *S. hermonthica* plants; and SVSh – *S. hermonthica* plant vigour.

4.3.4 Correlations between maize and *Striga* parameters under *S. asiatica* and *S. hermonthica* infestations

Coefficients of phenotypic correlations for the studied traits among 51 maize genotypes under *Sa* infestation are summarised in Table 4.6. Grain yield exhibited significant ($P<0.05$) and positive correlation with days to maturity ($r=0.19$). Grain yield showed significant ($P<0.01$) positive correlation with days to *Sa* emergence ($r=0.25$). Furthermore, grain yield had a significant ($P<0.05$) negative correlation with the anthesis-silking interval ($r=-0.27$) and plant height ($r=-0.21$). Days to *Sa* emergence exhibited a significant ($P<0.01$) negative correlation with plant height ($r=-0.24$). Days to 50% anthesis showed significant ($P<0.01$) positive correlations with days to 50% silking ($r=0.91$), plant height ($r=0.5$), ear height ($r=0.63$) and days to maturity ($r=0.49$) (Table 4.6). Plant height and ear height showed a strong significant ($P<0.01$) correlation ($r=0.78$). Likewise, *Sa* plant height showed a significant positive correlation ($P<0.01$) with *Sa* plant vigour ($r=0.92$).

Pearson correlation coefficients for key phenotypic traits among the 51 maize genotypes under *Sh* infestation are presented in Table 4.6. Days to 50% anthesis were strongly correlated ($P<0.01$) with days to 50% silking ($r=0.93$), the anthesis-silking interval ($r=0.35$), plant height ($r=0.32$), ear height ($r=0.46$) and days to maturity ($r=0.44$). In addition, grain yield showed a significant ($P<0.01$) negative correlation with the anthesis-silking interval ($r=-0.36$). Furthermore, grain yield exhibited a significant ($P<0.05$) negative correlation with hundred kernel weight ($r=-0.19$). Likewise, hundred kernel weight showed significant ($P<0.01$) positive correlations with the anthesis-silking interval ($r=0.23$), plant height ($r=0.43$) and ear height ($r=0.38$). Moreover, there were significant ($P<0.01$) positive correlations between days to 50% silking and the anthesis-silking interval ($r=0.67$), plant height ($r=0.35$), ear height ($r=0.5$) and days to maturity ($r=0.41$). Number of emerged *Sh* plants revealed significant ($P<0.01$) correlations with *Sh* height ($r=0.62$) and *Sh* vigour ($r=0.65$). Also, *Sh* height exhibited a significant ($P<0.01$) positive correlation with *Sh* vigour ($r=0.89$).

Table 4.6. Pearson correlation coefficients of phenotypic traits among 51 maize genotypes assessed under *Striga asiatica* (Sa) (upper diagonal), *S. hermonthica* (Sh) (lower diagonal) infestation in western Tanzania during 2017/2018

Traits	AD	SD	ASI	PH	EH	DM	GYD	HKWT	DESa	SNSa	HTSa	SVSa
AD		0.91**	0.22*	0.50**	0.63**	0.49**	-0.07	0.19*	-0.06	0.15	0.13	0.15
SD	0.93**		0.61**	0.49**	0.66**	0.47**	-0.17	0.21*	-0.08	0.20*	0.16	0.19*
ASI	0.35**	0.67**		0.23*	0.33**	0.17	-0.27*	0.13	-0.08	0.17	0.13	0.15
PH	0.32**	0.35**	0.21*		0.78**	0.16	-0.21*	0.33**	-0.12	-0.02	-0.15	-0.11
EH	0.46**	0.50**	0.33**	0.77**		0.36**	-0.13	0.27**	-0.24**	0.20*	0.04	0.07
DM	0.44**	0.41**	0.16	0.10	0.20*		0.19*	0.30**	0.07	0.11	0.15	0.16
GYD	-0.04	-0.17	-0.36**	-0.17	-0.15	0.04		-0.13	0.25**	-0.09	0.06	0.03
HKWT	0.09	0.16	0.23*	0.43**	0.38**	0.16	-0.19*		-0.03	0.10	-0.04	-0.03
DESh	0.19*	0.12	-0.07	0.20*	0.16	0.05	0.02	0.06		-0.07	0.15	0.18
SNSh	0.22*	0.15	-0.08	0.03	0.07	0.09	0.11	-0.10	0.01		0.59**	0.54**
HTSh	0.23*	0.18	-0.01	-0.12	-0.07	0.28**	0.09	-0.02	0.02	0.62**		0.92**
SVSh	0.19*	0.17	0.05	-0.05	-0.02	0.20*	-0.02	0.03	0.05	0.65**	0.89**	

*, **, Significant at $P < 0.05$ and $P < 0.01$ probability level respectively; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; DM – Days to maturity; PH - Plant height (cm); EH - Ear height (cm); GYD – Grain yield/plant (g); HKWT - Weight of 100 kernel/plant (g); DESa - Number of days taken for the first *S. asiatica* plant to emerge above the ground; SNSa - Number of emerged *S. asiatica* plants; HTSa – *S. asiatica* plant height and SVSa – *S. asiatica* plant vigour; DESh - Number of days taken for the first *S. hermonthica* plant to emerge above the ground; SNSh - Number of emerged *S. hermonthica* plants, HTSh – *S. hermonthica* plant height and SVSh - *S. hermonthica* plant vigour.

4.3.5 Clustering of maize genotypes under *Striga asiatica* and *S. hermonthica* infestations

Figures 4.1 and 4.2 show the phenotypic clustering patterns of 51 maize genotypes evaluated under *Sh* and *Sa* infestation. Under both *Sh* and *Sa* infestations, the genotypes were grouped into three major clusters that were independent of the geographic origin or source of the genotypes. Under *Sh*, Cluster I comprised of 19 genotypes (representing 37.3% of the test genotypes), while Clusters II and III had eight (15.7%), and 24 (47.06%) genotypes, respectively. Most of the genotypes sourced from IITA, which are resistant to *Sh*, fall under Cluster III (Figure 4.1). The genotype TZA4320, which supported no emerged *Sh* plants under *Sh* infestation was grouped in Sub-cluster II. TZA4010, TZA3502 and JL04 were allocated in Sub-cluster II, based on fewer number of emerged *Sh* plants (Figure 4.1).

There were three clusters representing the test genotypes during evaluation under *Sa* infestation. Only 13 genotypes (25.5%) were found in Cluster I, while Clusters II and III comprised 21 (41.2%), and 17 (33%) of the assessed maize genotypes, respectively (Figure 4.2). Many of the genotypes sourced from IITA were found in Cluster II. The genotype TZA4320, which had smallest *Sa* count (1.5) was allocated to Sub-cluster III. The accessions sourced from NPGRC (TZA4320, TZA3952 and TZA3964) with fewer number of emerged *Sa* plants were grouped in Cluster III, while most of the IITA collections were in Cluster II (Figure 4.2).

4.3.6 Principal components analysis on maize phenotypic traits under *Striga asiatica* and *S. hermonthica* infestation

Principal components analysis (PCA) was performed to elucidate the relationships between maize genotypes based on their phenotypic traits. The first three principal components (PCs) with Eigen-values greater than 1 accounted for 68.15% of the total variation under *Sa* infestation (Table 4.7). Principal component 1 (PC1) accounted for 35.39%, while PC2 and PC3 contributed to 21.89% and 10.87% of the total variation, respectively. Traits with the largest contribution to the total variation observed in PC1 included; silking days (20.26), anthesis days (16.41), ear height (16.92), anthesis-silking interval (10.98), plant height (9.68), and days to maturity (9.34). *Sa* plant height (30.59), *Sa* plant vigour (28.56), number of emerged *Sa* plants (15.87), and plant height (10.37) made the largest contribution to PC2. Traits accounting for the largest variation observed in PC3, included grain yield (40.38), days to *Sa* emergence (32.3), and the number of emerged *Sa* plants (7.93).

The relationships among the maize and *Sa* parameters and the test genotypes and their association with the respective principal components are further illustrated by the principal component biplot presented in Figure 4.3. The biplot dimension vectors showed a high positive

correlation among traits such as days to 50% anthesis, days to 50% silking, days to maturity, plant height, ear height, hundred kernel weight. The biplot revealed positive correlations among *Sa* parameters such as number of emerged *Sa* plants, *Sa* plant vigour and *Sa* plant height. The test genotypes were scattered throughout the biplot, with most of the *Sa* susceptible genotypes being on the right side (Quadrant I) of the biplot (PC1) (TZA599 and JL06, the *Striga* susceptible check). On the left side (Quadrant III) (PC2), *Sa* resistant genotypes were allocated, most of them being collections from the IITA and NPGRC (Figure 4.3). Genotypes TZA4320, TZA4064, TZA1782, TZA2881 and TZA599 contributed strongly to days to 50% anthesis, days 50% silking, plant height, ear height as well as days to maturity.

Under *Sh* infestation, the PCA showed that the first three PCs with Eigen-values larger than 1 explained more than 67% of the total variation exhibited by the assessed phenotypic traits (Table 4.8). PC1 accounted for 36%, while PC2 and PC3 explained 20.11% and 11.09% of the total variation, respectively. The highest contributing traits related to PC1 were days to 50% silking (17.33), days to 50% anthesis (14.49), ear height (14.65), anthesis-silking interval (8.7), plant height (8.45) and days to maturity (7.35). Traits contributing strongly PC2 included *Sh* plant height (26.93), *Sh* vigour (23.01), number of *Sh* plants emerged (17.04), maize plant height (10.37) and grain yield (6.15). The biplot further illustrates the relationships between maize and *Sh* parameters, and test genotypes, and their respective principal components (Figure 4.4). The dimension vectors on the biplot displayed positive associations among traits, namely plant height, ear height, hundred kernel weight, days to maturity, days to 50% anthesis, days to 50% silking and anthesis-silking interval and *Sh* characteristics such as *Sh* count, *Sh* plant vigour and *Sh* plant height. All the accessions sourced from IITA, which are resistant to *Sh*, are situated on PC2 while most of the genotypes from NPGRC and TARI Tanzania are found on PC1, including those with low *Sh* counts (TZA4320, TZA4010, TZA4203, TZA4064 and TZA 3952), relative to the resistant check (Figure 4.4 and Table 4.5).

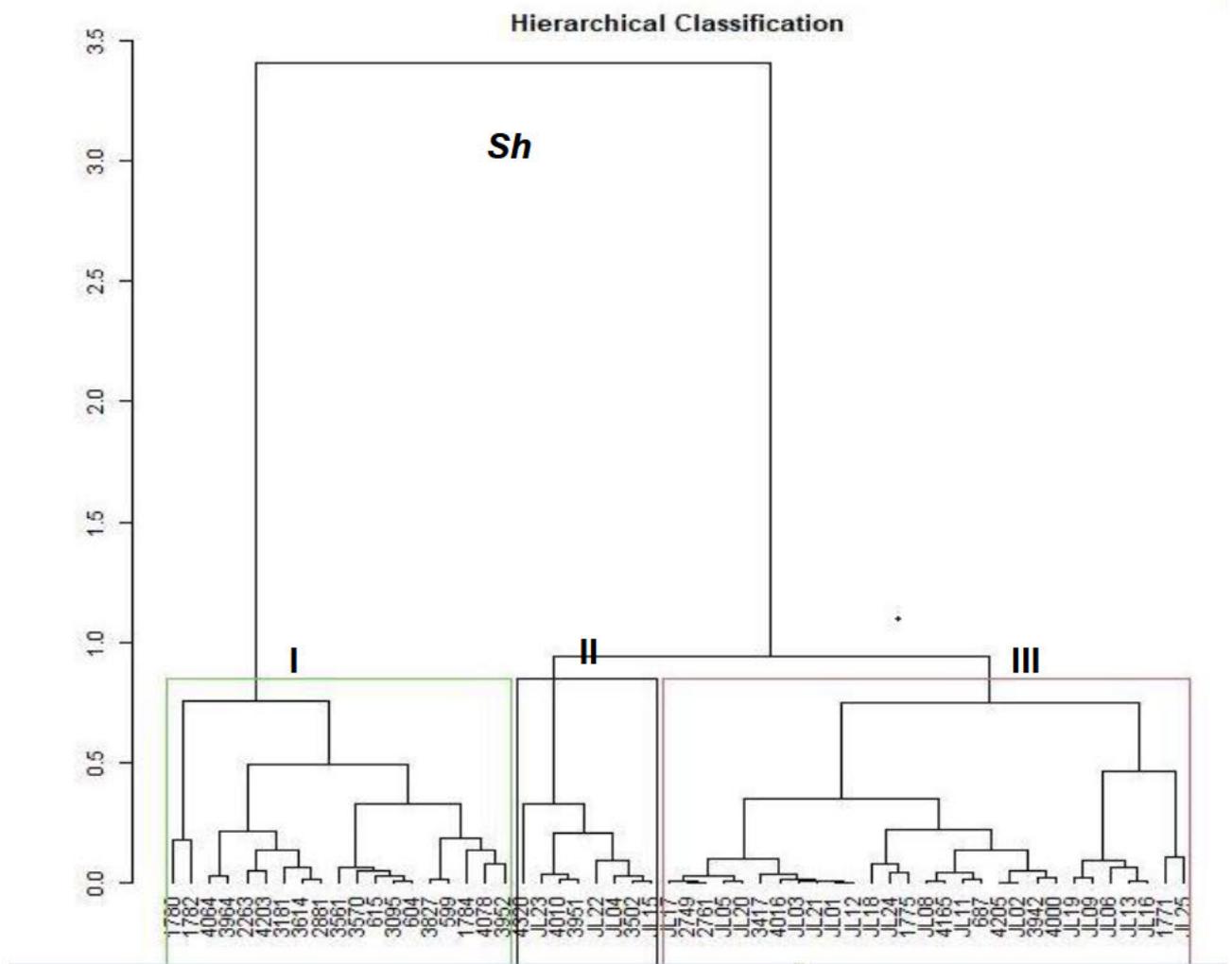


Figure 4.1. Genetic relationship among 51 maize genotypes using eight phenotypic traits and four *Striga* parameters under *S. hermonthica* infestation

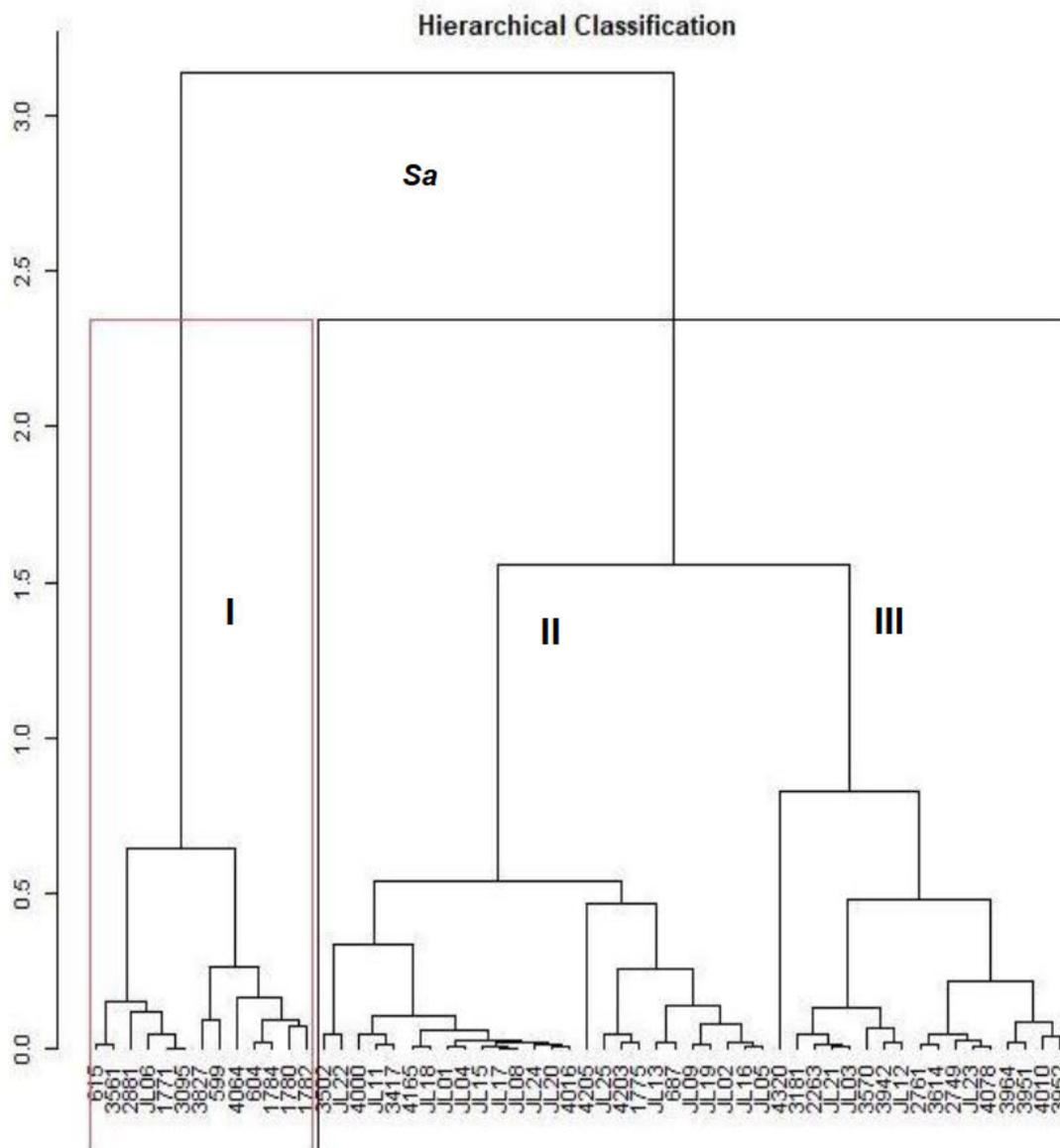


Figure 4.2. Genetic relationship among 51 maize genotypes using eight phenotypic traits and four *Striga* parameters under *S. asiatica* infestation

Table 4.7. Eigen-values, variances and loading scores of eight phenotypic traits and four *Sa* parameters among 51 maize genotypes evaluated under *Sa* infestation in western Tanzania in 2017/2018

Traits	PC1	PC2	PC3
AD	16.41	0.71	2.22
SD	20.26	0.31	1.27
ASI	10.98	0.13	0.06
DM	9.34	0.03	11.23
PH	9.68	10.37	2.27
EH	16.92	4.79	2.21
GYD	0.06	2.20	40.38
HKWT	3.88	1.41	0.04
DESA	1.00	5.02	32.30
SANO	5.34	15.87	7.93
SAHT	2.75	30.59	0.00
SVSA	3.38	28.56	0.09
Eigen-value	4.25	2.63	1.30
Proportion of variance (%)	35.39	21.89	10.87
Cumulative variance (%)	35.39	57.28	68.15

AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; DM – Days to maturity; PH - Plant height (cm); EH - Ear height (cm); GYD – Grain yield/plant (g); HKWT - Weight of 100 kernel (g); DESA - Number of days taken for the first *S.asiatica* plant to emerge above the ground; SANO - Number of emerged *S. asiatica* plants; SAHT – *S. asiatica* plant height and SVSA – *S.asiatica* plant vigour.

Table 4.8. Eigen-values, variances and loading scores of eight phenotypic traits and four *Sh* parameters among 51 maize genotypes evaluated under *Sh* infestation in western Tanzania during 2017/18

Traits	PC1	PC2	PC3
AD	14.49	1.10	0.23
SD	17.33	0.14	1.48
ASI	8.70	2.26	19.94
DM	7.35	1.78	8.52
PH	8.45	8.22	9.35
EH	14.65	5.75	5.44
EP	12.93	2.48	1.61
GYD	1.60	6.15	14.03
HKWT	3.66	5.10	0.00
DESh	0.86	0.04	33.14
ShNO	2.63	17.04	5.35
HTSh	3.08	26.93	0.71
SVSh	4.29	23.01	0.20
Eigen-values	4.68	2.61	1.44
Proportion of variance (%)	36.00	20.11	11.09
Cumulative variance (%)	36.00	56.10	67.20

AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; DM – Days to maturity; PH - Plant height (cm); EH - Ear height (cm); GYD – Grain yield/plant (g); HKWT - Weight of 100 kernel (g); DESh - Number of days taken for the first *S. hermonthica* plant to emerge above the ground; ShNO - Number of emerged *S. hermonthica* plants; HTSh – *S. hermonthica* plant height and SVSh - *S. hermonthica* plant vigour.

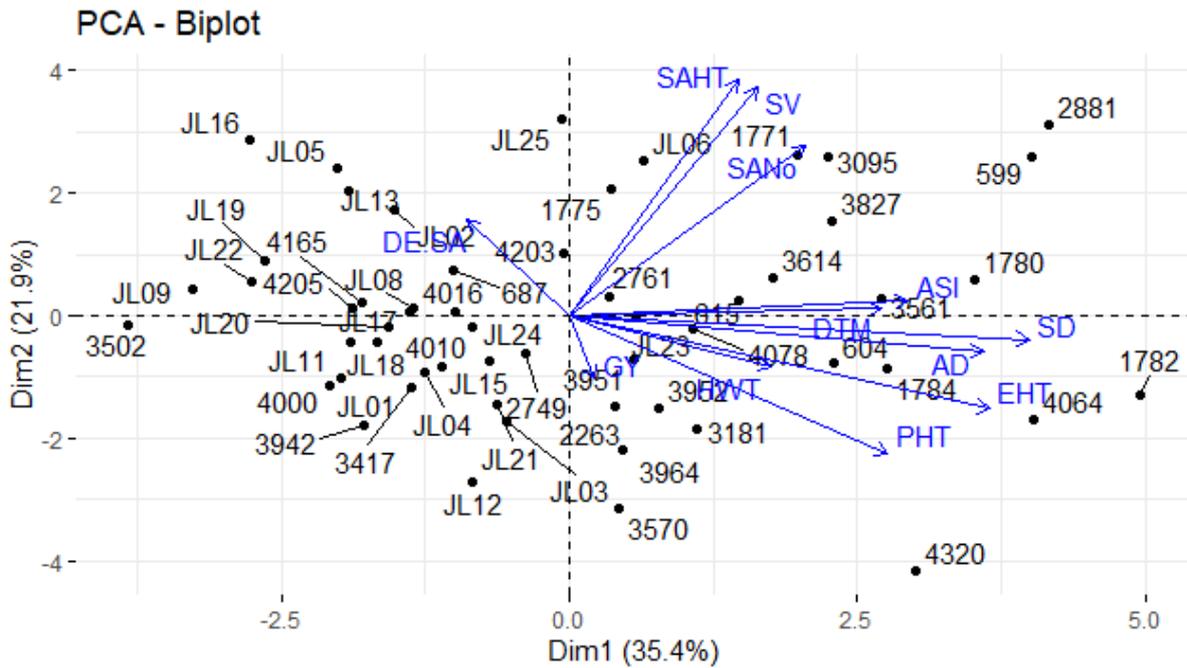


Figure 4.3. PCA-biplot showing the relationships of eight maize traits and four *Striga asiatica* (*Sa*) parameters in 51 maize genotypes evaluated under *Sa* infestation in western Tanzania, during 2017/18 cropping season.

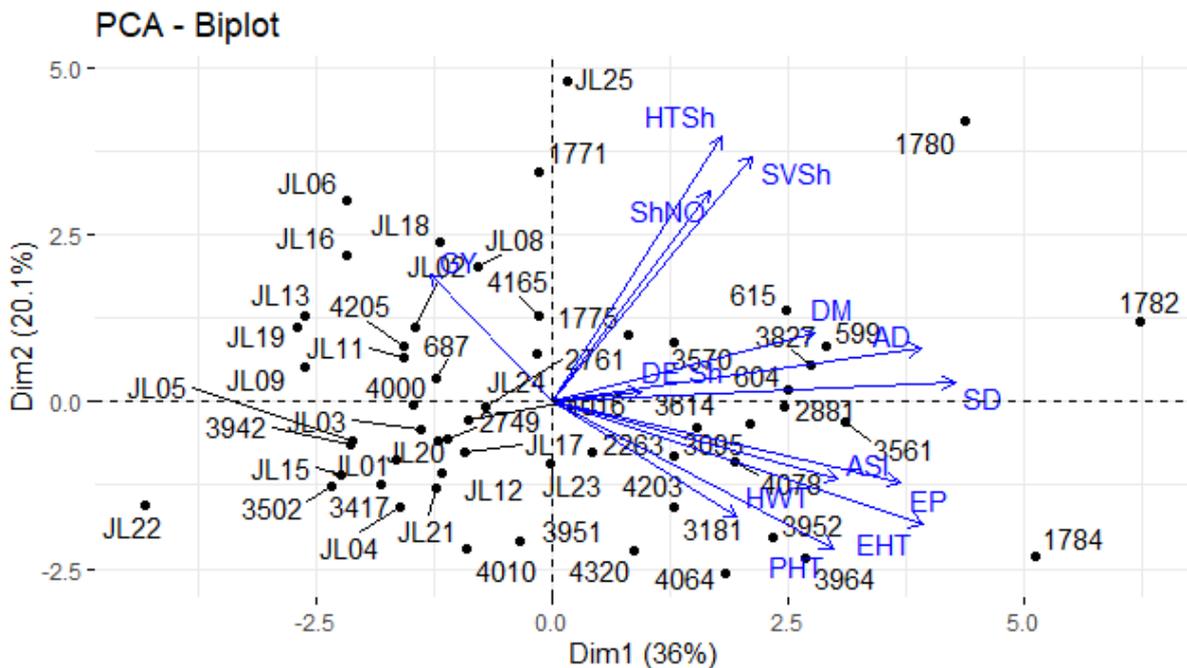


Figure 4.4. PCA-biplot showing the relationships of eight maize traits and four *Striga hermonthica* (*Sh*) parameters in 51 maize genotypes evaluated under *Sh* infestation in western Tanzania during 2017/18 cropping season.

4.3.7 Polymorphism and allelic diversity of SSR markers

The genetic diversity among the 51 maize genotypes was assessed using nine polymorphic SSR markers. The number of alleles (N_a) detected per locus ranged from three (Nc133) to 21 (Bnl619), with a mean of 10.22 allele per locus (Table 4.9). The number of effective alleles (N_e) per locus varied from 1.69 (Nc133) to 12.92 (Bnl619), with a mean of 5.82. The observed heterozygosity (H_o) ranged from 0.33 (Nc133) to 0.86 (Bnl391) with a mean of 0.53 (Table 4.9). The expected heterozygosity (H_e) ranged from 0.41 (Nc133) to 0.92 (Bnl619) with a mean of 0.73 (Table 4.9). Shannon's information index (I) values ranged from 0.68 (Nc133) to 2.76 (Bnl619), with a mean of 1.73. Furthermore, the inbreeding coefficient (F_{IS}) varied from -0.06 (Bnl391) to 0.53 (Nc003) with a mean of 0.25. The SSR markers used in this study were highly polymorphic, with PIC values varying from 0.41 (Nc133) to 0.92 (Bnl619) with a mean of 0.73.

Table 4.9. Genetic parameters generated by SSR markers when evaluating 51 maize genotypes

Locus	N	N_a	N_e	I	H_o	H_e	F_{IS}	PIC
Phi064	46	13	7.72	2.21	0.78	0.87	0.10	0.87
Nc130	49	5	2.14	1.01	0.53	0.53	0.01	0.53
NC133	48	3	1.69	0.68	0.33	0.41	0.19	0.41
Bnl391	49	9	5.32	1.85	0.86	0.81	-0.06	0.81
Phi014	49	4	2.30	0.96	0.43	0.56	0.24	0.56
Phi037	45	5	3.34	1.33	0.49	0.70	0.30	0.70
Bnl619	42	21	12.92	2.76	0.48	0.92	0.48	0.92
Nc003	44	15	7.32	2.33	0.41	0.86	0.53	0.86
Bnl2190	46	17	9.62	2.45	0.46	0.90	0.49	0.90
Mean	46.44	10.22	5.82	1.73	0.53	0.73	0.25	0.73
SE	0.79	2.15	1.25	0.28	0.07	0.09	0.07	0.06

N_a - Total number of alleles per locus; N_e = Number of effective alleles per locus; I - Shannon's information index; H_o = Observed heterozygosity; H_e - Expected heterozygosity; F_{IS} - Inbreeding coefficient; PIC - Polymorphic information content and SE - Standard error.

4.3.8 Genetic variability within and among 51 maize genotypes based on SSR markers

The genetic relationship and parameters among maize genotypes based on the source of the collection are presented in Table 4.10. The mean values for N_a ranged from 4.3 for genotypes acquired from TARI to 8.0 (from NPGRC) with a mean of 5.9. The N_e ranged from 3.83 (IITA genotypes) to 4.83 (NPGRC genotypes) with a mean of 4.04. Shannon's information index ranged from 1.19 for TARI genotypes to 1.48 for NPGRC genotypes, with a mean of 1.33. The highest values of H_o (0.54) and H_e (0.65) were observed for maize genotypes collected from TARI and NPGRC, respectively. Similarly, the lowest values of H_o (0.41) and H_e (0.60) were recorded for IITA and TARI genotypes, with a grand mean of 0.48 for H_o and 0.63 for H_e . Among the three maize populations, the F_{IS} varied from 0.17 (TARI genotypes) to 0.33 (IITA genotypes) with a mean of 0.23.

Table 4.10. Genetic diversity among 51 maize genotypes based on the sources of collection

Source	Genetic Parameters					
	Na	Ne	I	Ho	He	F _{IS}
NPGRC/Tanzania	8.000	4.831	1.484	0.493	0.647	0.206
TARI/Tanzania	4.300	3.457	1.191	0.540	0.602	0.165
IITA/West Africa	5.500	3.834	1.313	0.408	0.624	0.333
Overall mean	5.933	4.041	1.329	0.480	0.625	0.234
SE	0.708	0.447	0.129	0.052	0.049	0.058

Na - total number of alleles per locus; Ne - Number of effective alleles per locus; I - Shannon's information index; Ho - Observed heterozygosity; He - Expected heterozygosity; F_{IS} - Inbreeding coefficient; and SE - Standard error of the mean; NPGRC – National Plant Genetic Resources Centre for Tanzania; TARI -Tanzania Agricultural Research Institute; IITA – International Institute of Tropical Agriculture.

The results from the analysis of molecular variances (AMOVA) exhibited significant differences ($P < 0.01$) among and within genotypes (Table 4.11). The variation within genotypes accounted for the largest proportion of genetic dissimilarity (66.8%), while 32.6% of the variation was explained by among genotypes. However, among populations differences were non-significant.

Table 4.11. Analysis of molecular variance among and within 49 maize genotypes

Source	DF	SS	MS	Estimated variance	Proportion of variance (%)	F-probability	F- statistics
Among populations	2	9.921	4.961ns	0.020	0.6	0.197	F _{ST} = 0.006
Among individuals	46	206.058	4.479**	1.107	32.6	0.001	F _{IS} = 0.328
Within individual	49	111.000	2.265***	2.265	66.8	0.001	F _{IT} = 0.332
Total	97	326.980		3.392	100.0		

, *, significant at ($P < 0.01$), ($P < 0.001$), respectively; ns – Not significant at ($P < 0.05$); DF – Degree of freedom; SS - Sum of squares; and MS – means square; F_{ST} - Genetic differentiation index; F_{IS} - Inbreeding coefficient; F_{IT} = Overall fixation

4.3.9 Population differentiation based on the sources of collection

The pairwise population matrix of Nei genetic distance (GD) between maize populations indicated that maximum genetic distance (0.19) was detected between genotypes collected from TARI and IITA, followed by NPGRC and TARI (0.18), and NPGRC and IITA (0.08) (Table 4.12). The maximum genetic identity (0.93) was recorded between NPGRC and TARI genotypes, followed by TARI and IITA (0.83), and NPGRC and TARI (0.83) genotypes. The genetic differentiation index (F_{st}) ranged from 0.02 between IITA and NPGRC genotypes to 0.05 between IITA and TARI collections, with a mean of 0.04. Gene flow (Nm) among sources varied from 0.47 for IITA and TARI genotypes to 1.70 for IITA and NPGRC genotypes.

Table 4.12. Pairwise population matrix of Nei genetic distance (above diagonal off brackets) and Nei genetic identity (above diagonal within brackets) and genetic differentiation index (lower diagonal off brackets) and gene flow index (lower diagonal within brackets) among 51 genotypes when assessed using 9 SSR marker.

Source	NPGRC	TARI	IITA
NPGRC		0.18 (0.83)	0.08 (0.93)
TARI	0.04 (0.98)		0.19 (0.83)
IITA	0.02 (1.70)	0.05 (0.47)	

NPGRC – National Plant Genetic Resources Centre for Tanzania; TARI - Tanzania Agricultural Research Institute; IITA – International Institute of Tropical Agriculture.

4.3.10 Cluster analysis of maize genotypes based on SSR markers

The 51 maize genotypes were classified into three major distinct clusters that were independent of the geographical sources of collection (Figure 4.5). Cluster B comprised of 32 maize genotypes, accounting for 65.32% of the total genotypes evaluated. Genotype allocation was independent of the sources of genotypes. For instance, 50% of the IITA accessions were allocated on Cluster C, while the rest of the genotypes were distributed in Clusters A and B. Cluster C comprised of 15 genotypes. Results show that the following pair of genotypes were highly dissimilar and can be used as suitable parents in future breeding programs (Figure 4.5): TZA4062 and JL24, TZA1780 and JL05, TZA4016 and JL20, TZA3942 and JL22, TZA2263 and JL17, TZA4320 and JL01.

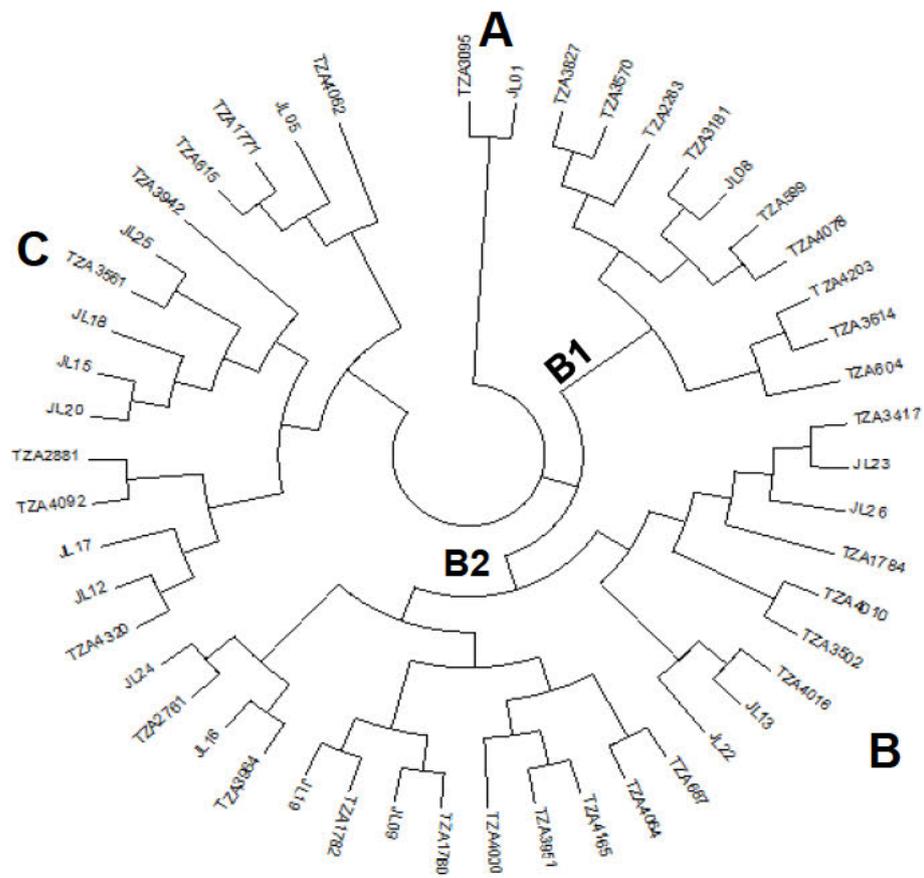


Figure 4.5. Genetic relationship among 51 maize genotypes sourced from Tanzania Agricultural Research Institute, National Plant Genetic Resources Centre for Tanzania and International Institute of Tropical Agriculture when assessed using nine SSR markers

4.4 Discussion

The 51 maize genotypes exhibited significant differences for key agronomic traits and *Striga* parameters when evaluated under *Striga asiatica* and *S. hermonthica* infestation (Table 4.3). The significant variations detected among the test genotypes for most of the measured traits showed that the germplasm evaluated in the current study were genetically diverse and thus, resistant parental lines could be used for *Striga* resistance breeding programs in Tanzania or in similar agro-ecologies.

A high level of genetic variability was detected, especially for the number of emerged *Striga* plants and grain yield performance under *Striga* infestation, which is essential for defining the level of resistance of the test genotypes to *Striga* (Menkir *et al.*, 2007). *Striga* resistance has been described as the capacity of a genotype to support significantly fewer emerged *Striga* plants and produce significantly more grain yield than a susceptible genotype when grown under *Striga* infestation (Ejeta *et al.*, 1991; Menkir *et al.*, 2012a). *Striga* resistance and tolerance are derived from gene combinations favouring low production of *Striga* seed germination stimulants, mechanical root barriers, strong post-attachment hypersensitive reactions, and insensitivity to *Striga* toxins, all of which rely on a large reservoir of genetic variation (Hausmann *et al.*, 2001; Shayanowako *et al.*, 2018).

Significant correlations among phenotypic traits, and *Striga* parameters, were identified, to guide selection (Table 4.6). The significant correlations measured between traits enables direct or indirect selection. For example, a positive correlation for *Striga* resistance traits under *Sa* and *Sh* infestation, suggests that selection of one trait will simultaneously improve the other. Grain yield was negatively correlated with the anthesis-silking interval ($r=-0.36^{**}$) and the hundred kernel weight ($r=-0.19^{*}$) under *Sh*, and with plant height ($r=-0.21^{*}$) under *Sa* infestation, respectively (Table 4.6), suggesting the potential for indirect selection for grain yield. These findings are in agreement with those reported by previous authors (Iqbal *et al.*, 2015; Aci *et al.*, 2018; Kasoma *et al.*, 2020), when working with genetically diverse maize germplasm, using phenotypic and molecular markers. Hence, the studied genotypes possess substantial variability which could be used for *Striga* resistance breeding and other traits of economic importance such as heat and drought stress tolerance.

The principal component analysis (Table 4.7) discriminated between the test genotypes based on key phenotypic traits. The first three PCs with eigen-values greater than 1 accounted for more than 68.15% of the total variation exhibited by the test genotypes when assessed under *Sa* infestation. The most discriminatory traits were hundred kernel weight, grain yield, days to

50% anthesis, days to 50% silking, ear height and plant height. These findings agree with Aci *et al.* (2018), who reported genetic variation among Algerian maize populations. In addition, cluster analysis based on phenotypic traits grouped the test genotypes into three distinct clusters, independent of the origin of the genotype under both *Sa* and *Sh* infestation (Figures 4.1 and 4.2, respectively). Using phenotypic cluster analysis, most of the *Striga* resistant genotypes were grouped under Clusters II (*Sa*) (Figure 4.1) and III (*Sh*) (Figure 4.2). Clustering based on molecular data grouped the test genotypes into three main clusters, with half of the accessions known to be resistant to *S. hermonthica* grouping in Cluster C (Figure 4.5). The pattern revealed by clustering suggests the presence of genetic variation for *Striga* resistance breeding in Tanzania.

The AMOVA exposed highly significant differences ($P < 0.01$) within and among genotypes (Table 4.11). Variation within genotypes accounted for the largest proportion of genetic dissimilarity (66.8%) detected, while 32.6% of the variation was explained by among genotypes' variability. These results agree with earlier findings that outcrossing spp., including maize, tend to keep a consistent level of genetic variation within populations due to reshuffling of genes (Da Silva *et al.*, 2015; Vega-Alvarez *et al.*, 2017; Belalia *et al.*, 2018). Warburton *et al.* (2008) reported the presence of high levels of genetic variability among landraces, broad-based open-pollinated, and synthetic varieties. The mean PIC from the present study was 0.73 (Table 4.9). This suggests that the SSR markers used had high discriminating ability, and therefore, they are suitable to be used in genetic diversity and relationship analyses. PIC values provide a measure of the genetic diversity and show the discriminatory power of a marker by considering the relative frequency of each alleles in the studied population (Senior *et al.*, 1998). PIC values have been classified into three groups: (i) if the PIC value of the marker is greater than 0.5 the marker is considered highly informative; (ii) if the PIC value is between 0.25 and 0.5 the marker is moderately informative; and (iii) if the PIC value is less than 0.25 then the marker is slightly informative (Botstein *et al.*, 1980; Adu *et al.*, 2019). More than 66% of the markers used in the present study showed PIC values greater than 0.70, signifying that they were highly informative and could detect differences among maize genotypes based on their genetic relationships. The PIC values reported in the present study are higher than the PIC values reported by Adu *et al.* (2018), who recorded a mean PIC value of 0.68 when studying 70 maize genotypes using 31 SSR markers. Patel *et al.* (2017) reported a mean PIC value of 0.68 using 17 SSR markers and eight inbred lines. In contrast, Maniruzzaman *et al.* (2018) reported a higher mean PIC of 0.77 using 10 SSR markers. The PIC value of a marker reflects the likelihood of the marker being

detected in the progeny and is a good measure of a marker's usefulness for genetic linkage and genetic diversity analysis, and QTL mapping (Adu *et al.*, 2019; Suvi *et al.*, 2019).

The mean observed heterozygosity and gene diversity within genotypes were 0.53 and 0.73, respectively (Table 4.9). The high level of gene diversity reported implies that the accessions studied possess high levels of genotypic variation, which is useful for maize breeding. Gene diversity refers to the probability that two randomly chosen alleles in a sample are different (André *et al.*, 2015; Adu *et al.*, 2019). The mean gene diversity value (0.73) detected in the present study is comparable to that reported by Enoki *et al.* (2002) (0.72), Shayanowako *et al.* (2018) (0.74), and Adu *et al.* (2019) (0.71) using 60, 18 and 31 SSR markers, respectively. In addition, the mean gene diversity reported in the present study was higher than that reported by Kumar *et al.* (2018) (0.37) and Vega-Alvarez *et al.* (2017) (0.49), using 22 and 31 SSR markers, respectively. The high level of gene diversity described in this study may have been related to the outcrossing nature of maize. Outcrossing spp., including maize are characterized by a wider genetic base and are quick to adapt to changes in the environment.

The genetic diversity indices recorded in this study suggests that useful levels of genetic variation exist among and within test genotypes. Among the calculated indices, the inbreeding coefficient ($F_{IS} = 0.33$), overall fixation index ($F_{IT} = 0.33$) (Table 4.11) and mean pairwise genetic differentiation index (F_{ST}) of 0.04 (Table 4.12), provided further understanding into the nature of the tested maize genotypes. The magnitude of the F_{ST} (0.04) showed a low level of genetic differentiation among the test populations (Wright, 1978; Balloux and Lugon-Moulin, 2002). The low level of genetic differentiation among populations was due to the high variability within the populations, which could be due to gene flow (Gepts and Papa, 2003; Qi-Lun *et al.*, 2008) as depicted by high mean pairwise gene flow (1.05) (Table 4.12). The use of landraces or open-pollinated varieties or synthetics in developing the assessed maize genotypes would be the main reason for the low level of genetic differentiation among the studied populations. In addition, low levels of genetic differentiation has been attributed to the exchange of genetic material among farmers from different locations (Loveless and Hamrick, 1984). Qi-Lun *et al.* (2008) reported an F_{ST} of 0.13 with 45 SSR among landraces from China. Aci *et al.* (2018) reported F_{ST} of = 0.33 with 18 SSR when studying the genetic diversity of 47 Algerian landraces.

4.5 Conclusions

The present study found considerable genetic variability among maize genotypes, which could be exploited for breeding, germplasm management and conservation. Both phenotypic traits and molecular markers were effective in evaluating the germplasm for *Striga* resistance

breeding. Based on *Striga* count, an index of *Striga* resistance, the following genotypes were resistant for both *Sa* and *Sh*: TZA4320, TZA3942, TZA4205, TZA3942, TZA3964, JL01, JL12 and JL18. These genotypes supported a maximum of six (6) *Striga* plants of the two *Striga* spp. which is below the maximum (seven) count of a resistant check genotype (JL11) under *Sh* infestation. The results from SSR markers, revealed that eight out of the nine selected markers were highly polymorphic and could distinguish the tested genotypes. The markers could be used in maize diversity studies. The dendrogram based on SSR markers grouped the genotypes into three clusters, regardless of their geographical origins. *Striga* resistant accessions such as JL01 (Cluster A), JL12, JL 18, TZA4320 and TZA3942 (Cluster C) could be used as a source of novel genes for *Striga* resistance breeding purposes.

4.6 References

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4.7. Appendices

Appendix 4.1. Mean performance of the 51 maize genotypes evaluated based on phenotypic traits under *Striga asiatica* infestation in western Tanzania during 2017/18. Genotypes were ranked based on the number of emerged *Striga* plants

Accession	Maize traits									<i>Striga asiatica</i> parameters			
	AD	SD	ASI	DM	PH	EH	EP	GYD	HKWT	DESa	SNSa	HTSa	SVSa
TZA4320	70.50	76.50	6.00	132.00	307.00	210.50	0.69	63.80	23.93	38.50	1.50	3.00	1.00
JL12	64.50	65.50	1.00	117.00	300.00	168.20	0.56	85.03	23.27	34.00	2.50	7.00	1.00
TZA3952	65.50	68.50	3.00	124.50	328.00	158.00	0.48	63.33	30.52	64.50	2.50	9.50	3.00
TZA3942	61.50	62.00	0.50	120.00	225.50	145.80	0.65	61.64	27.58	18.00	4.00	11.00	1.50
TZA4205	60.50	62.50	2.00	111.50	255.00	132.50	0.52	93.67	24.54	70.50	4.50	21.00	4.00
JL18	63.50	64.00	0.50	123.50	242.20	122.50	0.50	86.83	24.48	53.50	5.50	13.00	2.50
TZA3964	62.00	64.50	2.50	125.00	307.50	169.50	0.56	39.27	33.07	28.00	5.50	8.00	3.00
JL01	62.00	64.00	2.00	112.50	256.20	134.50	0.52	82.43	23.53	53.00	6.00	8.50	2.00
TZA3502	54.50	57.50	3.00	107.00	248.70	101.50	0.41	48.13	19.47	44.00	7.00	12.00	2.50
JL03	63.00	66.00	3.00	112.50	286.20	180.20	0.63	73.81	24.11	44.00	7.50	9.50	2.00
TZA3570	65.50	66.50	1.00	114.50	332.50	213.80	0.64	63.22	23.08	18.00	7.50	10.00	1.50
TZA4165	63.00	63.50	0.50	118.00	248.70	132.50	0.53	86.01	23.86	63.00	8.00	17.00	3.00
JL04	63.00	65.50	2.50	118.50	251.00	126.00	0.50	66.87	25.45	45.50	8.50	11.00	2.00
JL21	62.00	64.00	2.00	117.50	308.80	171.20	0.55	71.69	23.24	45.50	9.00	11.00	2.50
TZA1775	64.00	65.50	1.50	122.50	270.20	161.50	0.59	88.45	25.26	56.50	10.50	36.50	6.00
JL20	62.00	64.00	2.00	118.50	241.00	133.20	0.56	84.45	23.43	51.50	11.00	14.50	2.50
TZA4203	67.50	68.50	1.00	120.00	273.70	121.20	0.44	73.07	25.08	56.50	11.50	26.50	4.50
TZA3181	67.50	73.50	6.00	110.00	300.00	175.00	0.58	58.21	21.85	38.50	12.50	9.00	2.00
TZA2749	62.50	66.50	4.00	111.50	288.50	155.20	0.54	52.51	26.14	53.00	12.50	13.50	3.00
TZA4000	61.00	62.00	1.00	107.00	278.00	132.00	0.47	36.03	27.56	44.00	13.00	11.00	2.00
TZA4010	61.50	63.00	1.50	114.00	293.50	144.20	0.49	99.85	31.62	61.50	13.50	12.00	2.50
JL15	65.00	68.00	3.00	116.00	262.50	128.80	0.49	78.12	22.62	43.00	13.50	14.25	2.00
JL19	65.00	65.00	0.00	111.00	209.30	97.20	0.46	101.86	19.83	55.00	15.00	17.50	3.00
JL24	61.50	63.50	2.00	121.00	253.70	138.80	0.55	90.61	28.84	44.00	15.00	16.50	3.00
TZA2263	65.00	68.00	3.00	111.50	296.20	177.00	0.60	107.21	28.35	37.00	15.50	13.25	2.50
TZA3417	62.00	63.00	1.00	110.00	291.20	174.80	0.60	63.49	20.96	43.50	15.50	10.00	2.50
JL09	61.00	61.00	0.00	111.50	217.70	98.50	0.45	77.07	22.35	53.00	16.00	13.50	2.50
TZA604	68.00	71.00	3.00	128.50	299.20	215.80	0.72	103.07	25.63	45.50	16.50	18.50	3.50
TZA1780	71.50	76.00	4.50	138.00	296.80	196.20	0.66	96.99	20.84	56.50	16.50	27.00	4.50
TZA2761	62.00	66.00	4.00	120.50	258.80	174.00	0.69	106.50	26.40	45.00	17.00	20.50	4.00
JL05	61.50	62.00	0.50	117.00	219.70	109.70	0.50	94.95	21.84	55.50	17.50	29.50	5.00
TZA4016	64.00	65.50	1.50	115.50	281.70	144.00	0.52	78.12	21.75	63.00	17.50	18.50	2.50
JL11	62.00	63.00	1.00	111.50	264.20	137.00	0.52	76.11	20.51	42.00	17.50	13.00	2.50
JL16	59.50	59.50	0.00	115.50	214.20	104.70	0.48	82.21	20.12	59.50	18.00	29.30	5.50
TZA687	59.00	63.00	4.00	114.50	278.00	152.50	0.55	79.96	19.51	52.00	18.00	17.00	4.50
TZA4078	65.00	68.50	3.50	111.50	312.20	193.00	0.61	48.10	28.48	55.00	19.00	23.25	3.50
TZA1782	77.00	82.00	5.00	126.00	326.20	233.80	0.72	56.05	25.59	47.50	21.50	17.00	3.50
JL08	62.50	64.00	1.50	116.00	246.00	142.50	0.57	95.11	22.37	48.00	22.00	13.50	3.00
TZA615	66.50	70.50	4.00	114.00	289.00	206.00	0.71	62.26	21.00	42.50	23.00	24.50	4.00
JL02	61.50	62.00	0.50	117.50	244.20	123.20	0.50	80.96	23.07	50.00	24.50	29.00	4.00
JL22	52.00	55.00	3.00	108.50	282.00	135.80	0.48	86.11	24.33	45.50	27.00	19.00	3.00
JL23	63.50	66.50	3.00	117.50	303.70	164.80	0.54	93.10	27.28	50.00	27.50	17.75	3.50
JL17	63.00	63.50	0.50	117.50	258.70	130.20	0.51	88.48	22.49	44.50	27.50	15.00	2.50
TZA3614	66.50	70.50	4.00	113.00	319.20	178.80	0.56	46.82	25.59	47.50	28.50	27.00	4.50
TZA3951	62.50	64.00	1.50	121.50	308.20	181.80	0.59	73.51	32.00	48.00	30.50	16.75	2.50
TZA1771	63.00	69.50	6.50	122.50	268.00	158.00	0.59	81.30	23.87	41.00	31.50	38.00	6.00
TZA4064	68.00	74.00	6.00	123.50	351.50	223.50	0.64	76.63	35.47	45.50	31.50	15.50	2.50
JL25	61.50	66.00	4.50	124.50	211.20	104.20	0.49	88.46	27.94	59.50	32.50	34.00	5.00
TZA3095	64.50	71.50	7.00	119.00	245.70	157.50	0.65	53.36	26.68	35.50	33.50	37.00	6.00
TZA1784	66.50	70.50	4.00	131.00	311.80	207.00	0.66	42.44	29.59	45.50	33.50	13.50	3.00
TZA3827	67.50	70.00	2.50	123.50	300.20	165.50	0.55	61.71	32.46	56.50	37.50	30.50	5.00
TZA3561	69.00	71.50	2.50	115.50	345.20	216.20	0.63	53.70	22.64	41.00	38.00	26.50	4.50
JL13	57.00	61.00	4.00	117.00	213.50	118.00	0.55	84.57	19.72	51.50	42.00	21.00	3.00
JL06	64.50	67.50	3.00	116.00	251.50	155.80	0.62	74.38	19.08	37.00	43.50	31.50	5.50
TZA2881	69.00	75.00	6.00	118.00	293.00	208.80	0.73	47.26	23.01	38.50	53.50	41.00	7.00
TZA599	71.50	74.00	2.50	129.50	262.70	191.80	0.73	81.93	32.39	44.50	59.50	33.50	6.00
Mean	63.86	66.52	2.66	117.90	275.50	157.80	0.57	74.84	24.92	47.30	19.30	18.88	3.38
CV%	3.60	4.10	78.50	4.60	10.50	14.40	11.50	29.50	6.50	32.90	73.60	45.10	39.10
P< 5%	**	**	ns	***	***	***	***	ns	***	ns	*	**	**
Sed	2.31	2.73	2.09	5.45	29.01	22.65	0.07	22.09	1.61	15.57	14.21	8.52	1.32
LSD	4.62	5.48	4.18	10.92	58.15	45.40	0.13	44.27	3.23	31.20	28.47	17.07	2.64

*, **, *** Significant at P<0.05; P<0.01 and P<0.001 probability level, respectively; ns – Not significant at P< 0.05 probability level; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; CV% - Coefficient of variation; DM – Days to maturity; LSD – Least significant different; PH - Plant height (cm); EH - Ear height (cm); GYD – Grain yield/plant (g); HKWT - Weight of 100 kernel/plant (g); DESa - Number of days taken for the first *S.asiatica* plant to emerge above the ground; SED – Standard error of different; SNSa - Number of emerged *S. asiatica* plants; HTSa – *S.asiatica* plant height and SVSa – *S.asiatica* plant vigour

Appendix 4.2. Mean performance of 51 maize genotypes evaluated based on phenotypic traits under *Striga hermonthica* infestation in western Tanzania during 2017/18. Genotypes were ranked based on number of emerged *Striga* plants

Accession	Maize traits										<i>Striga hermonthica</i> parameters			
	AD	SD	ASI	DM	PH	EH	EP	GYP	HKWT	DESh	SNSh	HTSh	SVSh	
TZA4320	68.50	73.50	5.00	128.00	275.00	168.80	0.61	94.76	23.19	0.00	0.00	0.00	0.00	
JL09	63.00	62.00	1.00	111.50	218.80	112.80	0.51	85.91	22.02	51.50	1.00	23.50	4.00	
4010	59.00	62.00	3.00	117.00	303.50	164.50	0.55	83.21	30.75	27.00	1.00	3.00	1.00	
JL04	60.50	62.00	0.50	122.50	256.80	146.20	0.57	42.82	25.30	24.50	1.00	5.50	1.00	
JL05	62.00	62.00	0.50	119.00	240.00	136.80	0.57	90.29	21.25	62.00	1.50	7.50	2.00	
JL20	63.50	64.00	0.50	121.00	257.20	142.00	0.55	74.85	23.20	72.50	1.50	15.00	2.50	
TZA3502	56.50	61.00	4.50	107.00	252.50	136.50	0.54	55.77	19.10	49.00	1.50	13.50	3.00	
TZA4203	71.00	73.50	2.50	125.00	271.00	157.50	0.57	82.49	24.65	81.00	2.00	8.00	2.50	
JL18	63.00	64.00	1.00	123.50	239.50	112.80	0.47	93.86	24.90	55.50	3.00	64.00	5.50	
TZA4064	65.50	67.00	1.50	118.00	339.50	217.50	0.64	83.84	35.17	67.00	3.00	13.00	2.50	
JL17	64.50	66.50	2.00	113.00	283.80	141.00	0.50	76.17	22.70	72.00	3.00	14.50	2.50	
TZA3952	65.50	71.50	6.00	126.00	297.00	176.00	0.59	38.00	30.00	50.50	3.00	18.00	3.00	
JL12	64.50	64.50	0.00	114.50	281.50	150.50	0.53	48.56	22.95	49.50	3.50	11.00	2.50	
TZA2749	61.50	63.50	2.00	116.00	253.20	146.50	0.58	86.66	25.21	63.00	4.00	13.50	3.00	
JL22	53.00	55.50	2.50	107.00	235.50	114.80	0.49	66.29	24.25	53.00	4.00	14.50	2.50	
TZA3417	61.00	62.00	1.00	105.50	270.00	155.50	0.58	58.45	20.25	66.00	4.00	7.80	2.50	
JL21	62.00	64.00	2.00	116.00	262.60	145.20	0.56	57.45	23.11	51.50	4.00	5.70	2.00	
TZA3827	69.50	74.00	4.50	120.50	294.50	151.50	0.52	47.46	32.10	61.00	4.00	45.50	7.50	
TZA3942	58.00	59.00	1.00	108.50	258.00	150.00	0.57	92.88	27.45	65.50	4.50	18.00	3.00	
JL19	65.50	66.50	1.00	119.50	199.50	83.80	0.42	72.68	19.42	54.00	4.50	15.00	2.50	
JL15	62.00	63.50	1.50	113.00	250.80	133.00	0.53	69.01	22.05	52.50	4.50	20.00	3.00	
3181	69.00	72.50	3.50	110.00	330.80	183.80	0.56	67.40	21.75	56.00	4.50	12.50	2.50	
JL01	63.00	64.00	1.00	113.00	280.00	143.80	0.51	77.84	23.05	43.00	5.00	7.50	2.00	
TZA3951	63.50	65.50	2.00	111.50	295.80	160.00	0.54	50.16	31.30	36.50	5.00	8.50	2.00	
TZA1784	67.00	72.50	5.50	132.00	311.00	260.20	0.84	44.84	29.40	51.00	5.00	21.70	4.00	
TZA3964	67.50	69.00	1.50	126.00	346.00	215.00	0.62	36.99	32.00	59.50	5.00	18.50	2.50	
TZA687	63.00	63.00	0.00	114.50	281.20	162.80	0.58	105.12	19.15	64.50	5.50	20.50	3.50	
TZA2761	64.50	65.50	1.00	115.50	249.20	147.00	0.60	94.81	26.95	51.50	5.50	18.80	3.00	
TZA4205	61.50	62.50	1.00	114.50	292.50	131.00	0.45	91.48	23.75	55.50	5.50	30.50	5.00	
TZA4016	65.50	67.00	1.50	113.00	270.00	142.50	0.53	70.77	21.20	52.00	5.50	17.00	2.50	
JL03	64.50	62.50	1.00	115.50	278.80	134.20	0.48	59.35	23.40	56.00	5.50	13.20	3.00	
TZA4078	62.50	67.50	5.00	111.50	310.00	197.50	0.64	53.14	28.35	50.00	5.50	35.00	6.00	
JL23	63.50	66.50	3.00	118.50	266.00	144.20	0.54	36.33	27.15	50.00	6.00	17.20	3.00	
JL24	62.00	63.00	1.00	123.50	317.50	153.80	0.48	92.75	29.00	42.50	6.50	37.00	5.50	
TZA2263	65.00	66.50	1.50	118.50	293.80	188.80	0.64	130.44	28.56	48.00	7.00	12.20	2.00	
TZA1775	65.50	67.50	2.00	122.50	278.80	163.20	0.58	90.86	24.46	56.50	7.00	33.00	5.50	
JL11	62.50	63.00	0.50	115.50	268.20	141.80	0.53	90.26	19.72	55.50	7.00	21.50	3.50	
TZA3614	67.00	69.50	2.50	114.50	312.50	195.00	0.62	97.47	25.20	67.50	7.50	21.00	4.00	
TZA599	67.00	70.00	3.00	132.00	282.50	178.20	0.63	69.97	31.75	61.50	7.50	41.80	6.50	
TZA2881	68.00	69.50	1.50	114.00	336.00	224.50	0.67	79.62	22.85	70.50	8.00	46.20	4.00	
JL02	62.50	62.00	1.00	114.50	276.20	134.20	0.49	92.55	22.90	52.50	8.50	28.50	4.50	
TZA3095	66.50	71.50	5.00	114.00	268.20	183.50	0.68	70.21	26.40	50.00	8.50	25.00	4.50	
TZA3561	70.50	74.00	3.50	113.00	304.50	207.50	0.68	34.22	22.05	40.00	9.50	28.50	5.50	
TZA1780	74.50	79.00	4.50	135.50	242.50	166.00	0.67	93.97	20.10	42.00	10.00	79.50	8.50	
TZA4165	67.50	66.50	-1.00	114.50	263.00	158.80	0.60	93.16	23.40	61.50	10.00	27.00	4.50	
TZA4000	62.00	62.00	0.00	107.00	291.50	156.00	0.54	96.12	26.65	44.00	11.00	19.00	2.50	
JL16	61.00	62.00	1.00	119.50	233.50	115.00	0.49	86.50	19.50	43.00	11.00	96.00	8.50	
TZA604	66.00	69.00	3.00	125.00	291.20	202.50	0.70	75.86	25.60	51.50	11.00	29.00	4.50	
TZA615	66.50	69.00	2.50	126.00	288.20	197.20	0.68	62.35	20.20	48.00	11.00	36.50	7.00	
JL08	64.50	63.50	0.00	120.00	255.50	146.00	0.57	117.60	21.75	63.00	11.50	43.10	6.00	
JL25	64.50	67.00	2.50	121.00	211.00	98.80	0.47	81.39	28.11	47.50	11.50	87.50	9.00	
TZA3570	66.50	68.50	2.00	110.00	299.50	182.70	0.61	65.92	22.45	53.50	12.00	36.50	5.50	
JL13	60.50	62.00	1.50	118.50	238.20	102.00	0.44	66.80	19.34	52.50	14.00	46.00	8.00	
TZA1782	76.50	81.00	4.50	128.50	331.80	227.20	0.68	55.55	25.30	61.50	15.00	54.00	5.50	
TZA1771	63.50	64.00	0.50	114.00	273.00	143.80	0.52	86.78	23.45	38.00	17.50	53.20	7.50	
JL06	61.00	63.00	0.00	118.50	210.80	108.00	0.51	91.44	19.08	51.00	22.50	38.20	6.00	
Mean	64.29	66.29	2.00	117.63	275.30	157.80	0.57	75.20	24.54	52.80	6.55	26.70	4.03	
CV%	3.10	4.50	88.70	4.80	9.20	15.80	13.00	23.50	6.50	26.00	62.30	71.30	53.60	
P< 5%	***	***	*	***	***	***	**	***	***	*	**	**	*	
Sed	1.97	2.96	1.77	5.70	25.24	24.90	0.07	17.67	1.60	13.70	4.09	19.06	2.16	
LSD	3.94	5.93	3.56	11.43	50.57	49.90	0.15	35.42	3.21	27.45	8.19	38.20	4.32	

*, **, *** Significant at P< 0.05; P< 0.01 and P< 0.001 probability level, respectively; ns – not significant at P< 0.05 probability level; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; CV% - Coefficient of variation; DM – Days to maturity; PH - Plant height (cm); EH - Ear height (cm); GYP – Grain yield/plant (g); HKWT - Weight of 100 kernel/plant (g); DESh - Number of days taken for the first *S. hermonthica* plant to emerge above the ground; SNSh - Number of emerged *S. hermonthica* plants; HTSh – *S. hermonthica* plant height and SVSh - *S. hermonthica* plant vigour

CHAPTER FIVE: Progeny testing of maize genotypes for grain yield and yield components, *Striga* resistance and *Fusarium oxysporum* f.sp. *strigae* compatibility

Abstract

Developing and deploying maize genotypes with resistance to *Striga* spp. and compatibility to *Fusarium oxysporum* f.sp. *strigae* (FOS) to control *Striga* is an economical, sustainable, and environmentally friendly option. The objective of this study was to assess the performance of F1 progenies of maize genotypes, and to determine the type and magnitude of gene action controlling grain yield and yield-related components, *Striga* resistance, FOS compatibility, and to select promising maize genotypes for an integrated *Striga* management approach. Ninety-nine experimental hybrids, generated by a North Carolina Design II, were evaluated with and without FOS treatment at three *Striga*-infested sites in western Tanzania using a 9 x 12 alpha lattice design with two replications. The F1 progenies were developed from a set of nine Tanzania adapted and FOS-compatible, relatively high-yielding landraces serving as female parents, and 11 *Striga*-resistant, open-pollinated varieties that were used as the male parents. The general combining ability (GCA) and specific combining ability (SCA) effects were significant for days to 50% anthesis, days to 50% silking, anthesis-silking interval, grain yield, hundred kernel weight, *Striga* emergence count at eight (SEC8), and 10 (SEC10) weeks after planting, *Striga* damage ratings at eight (SDR8) and 10 (SDR10) weeks after planting, with and without FOS treatment. FOS-treated progenies had fewer emerged *Striga* plants infecting their roots than untreated controls. Parental genotypes such as SITUKA M1, TZA4010, TZA4016, TZA4203, JL01, JL05, JL13, JL16, and JL17 showed negative GCA effects for all *Striga* parameters and relatively positive GCA effects for grain yield in a desirable direction. Experimental hybrids such as TZA4010xJL13, TZA4010xJL05, TZA2263xJL13, and TZA4203xJL18 were selected with desirable grain yield and *Striga* resistance. The new progenies are recommended for *Striga* resistance breeding in Tanzania or similar agro-ecologies.

Keywords: *Fusarium oxysporium* f. sp. *strigae*, gene action, maize, resistance breeding, *Striga* resistance, *Striga hermonthica*, *Striga asiatica*

5.1 Introduction

Striga spp. are popularly known as witchweed due to the enormity of crop damage. *Striga* spp. infestation is one of the major constraints to cereal and legume crop production in sub-Saharan Africa (SSA) and Asia (Satish *et al.*, 2011; Lobulu *et al.*, 2021). Due to *Striga* infestation, maize grain losses range from 20% to 100% in SSA, depending on the extent of the infestation, susceptibility of the variety, soil fertility level, and prevailing climatic conditions (Watson *et al.*, 2007; Teka, 2014; Lobulu *et al.*, 2019). Millions of hectares of crop fields in Africa are infested by *Striga* spp. affecting over 300 million resource-poor farmers engaged in cereal and legume crop production (Ejeta, 2007; Nzioki *et al.*, 2016; Yacoubou *et al.*, 2021). The predominant *Striga* spp. devastating cereal crop yield in SSA, including Tanzania, are *Striga hermonthica* (Del.) Benth, *S. asiatica* (L.) Kuntze, *S. forbesii* (Benth.), and *S. aspera* (Willd.) Benth. (Timko *et al.*, 2012; Gebretsadik *et al.*, 2013; Lobulu *et al.*, 2019). Thus far, there is no single effective method to control *Striga* due to its reproductive biology, habitat colonisation, and interaction with other biophysical factors.

The use of host plant resistance, combined with other management practices, is considered to be the most sustainable, reliable, and economically viable option accessible to resource-poor farmers (Badu-Apraku *et al.*, 2004; Teka, 2014; Akaogu *et al.*, 2019). Host-plant resistance against *Striga* spp. involves two complementary mechanisms: resistance and tolerance (Rodenburg and Bastiaans, 2011). Resistant genotypes support significantly fewer *Striga* plants and produce a higher grain yield than susceptible genotypes (Gebisa *et al.*, 1992; Haussmann *et al.*, 2001; Badu-Apraku *et al.*, 2020). Tolerance is associated with the ability of a host plant to endure the effects of parasitic plants that are already attached, irrespective of their quantity, with minimum yield loss (Kim, 1994; Badu-Apraku *et al.*, 2020; Lobulu *et al.*, 2021). Maize genotypes that combine resistance and tolerance to *S. hermonthica* have been developed by the International Institute of Tropical Agriculture (Akaogu *et al.*, 2019; Badu-Apraku *et al.*, 2020). These genotypes are useful genetic resources for *Striga* resistance breeding programs in SSA, including Tanzania. However, only partial *Striga* resistance has been reported in maize. Thus, it is essential to supplement the existing host plant resistance with cultural practices and a biocontrol agent for effective *Striga* control.

The use of *Striga*-resistant genotypes, combined with a biological control agent against *Striga* spp. may create an effective *Striga* control strategy. Pathogenic isolates of *Fusarium oxysporum* f. sp. *strigae* (FOS) reportedly control both *S. asiatica* and *S. hermonthica* infestations, and boost productivity in compatible maize and sorghum genotypes (Venne *et al.*, 2009; Gebretsadik *et al.*, 2013; Shayanowako *et al.*, 2020). FOS can symbiotically colonize the root system of the

host plant, subsequently causing infection to *Striga* plants at different growth phases, including the seedlings (Elzein *et al.*, 2006; Beed *et al.*, 2007). *FOS* is highly aggressive and rapidly establishes itself in the rhizosphere of compatible host genotypes (Gebretsadik *et al.*, 2013; Shayanowako *et al.*, 2018). *FOS*-compatible maize genotypes release root exudates that activate virulence genes in *FOS*, stimulating it to suppress *Striga* (Handelsman and Stabb, 1996; Shayanowako *et al.*, 2020; Lobulu *et al.*, 2021). The biocontrol agent affects *Striga* parasites by blocking the xylem and phloem vessels, which causes wilting symptoms (Elzein *et al.*, 2010; Ndambi *et al.*, 2011). The synergistic effects of *Striga*-resistant maize genotypes and *FOS* can reduce *Striga* emergence by over 90% (Venne *et al.*, 2009). Gebretsadik *et al.* (2013) reported a 92% reduction in *Striga* emergence counts on *Striga* resistant sorghum when the seed was coated with *FOS*. *FOS* is most effective when combined with *Striga*-resistant genotypes and other control measures (Gebretsadik *et al.*, 2013; Mrema *et al.*, 2017b). However, *Striga*-resistant maize genotypes are not available in Tanzania at this time. Preliminary studies in the country identified maize populations with differential resistance to *S. asiatica* and *S. hermonthica*, and *FOS* compatibility (Lobulu *et al.*, 2021). The selected parental genotypes are excellent candidates for *Striga*-resistance breeding. Knowledge of the combining ability effects of the selected parents through progeny testing is vital to discern the gene action controlling yield and yield-limiting factors, including *Striga* resistance and *FOS* compatibility, as a basis for the choice of mating designs in subsequent breeding programs.

Combining ability effects are categorized into general and specific combining ability. The general combining ability (GCA) refers to the average performance of a progeny in all its crosses, expressed as a deviation from the overall mean of all the crosses. The specific combining ability (SCA) denotes the deviation of the F1 progeny performance from the expected value (Sprague and Tatum, 1942; Christie and Shattuck, 1992). GCA measures additive and additive x additive gene effects, whereas SCA measures non-additive gene effects, including dominance and epistasis (Sprague and Tatum, 1942; Fasahat *et al.*, 2016). Various studies have reported the presence of both GCA and SCA effects for *Striga* resistance in maize. Kim (1994) and Badu-Apraku (2007) reported that additive gene action was more important in normal-endosperm maize inbreds for *Striga* damage, while non-additive gene action was more important for *Striga* emergence. Other studies reported a larger proportion of the GCA sum of squares over the SCA for *Striga* damage and the number of emerged *Striga* plants at eight and 10 weeks after planting (WAP) for early-maturing and normal-endosperm maize inbred lines (Gethi and Smith, 2004; Ifie *et al.*, 2015).

Conversely, some studies reported a larger proportion of the SCA sum of squares over the GCA for *Striga* damage and the number of emerged *Striga* plants at eight and 10 WAP, indicating the importance of non-additive gene action conditioning the inheritance of *Striga* resistance (Badu-Apraku *et al.*, 2016). Combining ability effects of parental genotypes are deduced through a suitable mating design. The commonly used mating designs in maize breeding programs are the diallels (Hallauer *et al.*, 2010), North Carolina Design II (NCD II) (Hallauer *et al.*, 2010; Fasahat *et al.*, 2016; Amegbor *et al.*, 2020), and line by tester (Davis, 1927; Hallauer *et al.*, 2010).

The NCD II mating scheme is a cross-classification design whereby different parents are used as males and females (Hallauer *et al.*, 2010; Acquah, 2012; Fasahat *et al.*, 2016; Ngaboyisonga *et al.*, 2019). In NCD II, each member of a group of males is mated to each member of a group of females. The design is better for handling a large number of parents than the diallel, yet it provides the same type of genetic information following proper data computation (Hallauer *et al.*, 2010). The main effects of males and females correspond to the GCA effect, and the female x male interaction corresponds to the SCA effect (Cach *et al.*, 2006; Hallauer *et al.*, 2010; Fasahat *et al.*, 2016). The NCD II has been used widely to study combining ability effects and to estimate genetic variance components for yield and agronomic traits in maize (Derera *et al.*, 2008; Wegary *et al.*, 2011; Salami and Agbowuro, 2016; Ngaboyisonga *et al.*, 2019).

Striga spp. are widely distributed in Tanzania, with variable levels of infestation across different agro-ecologies. The major cereal crop production regions with high *Striga* densities in the country include Mwanza, Mara, and Shinyanga (Lake zone) (Khan, 2011); Tabora and parts of Kigoma (Western zone); Dodoma and Singida (Central zone); and Morogoro in the Eastern zone (Mbwaga and Obilana, 1993; Mbwaga, 1996; MacOpiyo *et al.*, 2009; Mrema *et al.*, 2017a). Infestations extend to the Ruvuma region in the south, the Iringa and Mbeya regions in the Southern Highlands, and Tanga, Pwani, Lindi, and Mtwara (Coastal regions) (MacOpiyo *et al.*, 2009; Khan, 2011). Grain yield losses of 18 to 90% have been reported in Tanzania due to *Striga* infestation (Mbwaga, 1996; Massawe *et al.*, 2002). The objective of this study was to assesses the performance of F1 progenies of maize genotypes and determine the type and magnitude of gene action controlling grain yield and yield-related components, *Striga* resistance, FOS compatibility, and to select promising maize genotypes for an integrated *Striga* management program.

5.2 Materials and methods

5.2.1 Germplasm and crosses

Twenty parents were used to develop 99 experimental hybrids using NCD II during the 2018 off-season. The description of the 20 parental genotypes is presented in Table 5.1. The parents consisted of 11 open-pollinated varieties (OPVs) used as males and nine landraces designated as female genotypes. The parental genotypes were selected from a previous study (Lobulu *et al.*, 2021). The parents were mainly selected for their desirable agronomic attributes, resistance to both *S. asiatica* and *S. hermonthica* and for *FOS* compatibility.

5.2.2 *Fusarium oxysporium f. sp. strigae (FOS) inoculum*

A virulent strain of *FOS* was used as the biocontrol agent. The *FOS* was initially isolated from severely diseased *Striga* plants in sorghum fields in north-eastern Ethiopia (Gebretsadik *et al.*, 2013). The host specificity and pathogenicity of the *FOS* isolate on *Striga* spp. have been previously described by Gebretsadik *et al.* (2013). The Phytomedicine Department of Humboldt University in Berlin, Germany, confirmed the taxonomic identification of *FOS* (Gebretsadik *et al.*, 2013). Pure *FOS* spores were produced and preserved by Plant Health Products (Pty) Ltd., KwaZulu-Natal, South Africa. *FOS* in a dry powder formulation was used to coat the maize seeds before sowing. Approximately 19.3 mg of *FOS* inoculum was applied to the whole surface of the seed.

Table 5.1. Description of maize parents used in the crosses

S/N	Female	Description	Source	Attributes	S/N	Male	Description	Source	Attributes
1	SITUKA M1	OPV	TARI	Early maturing, <i>FOS</i> compatible, <i>Striga</i> tolerant	10	JL01	OPV	IITA	Early maturing, <i>Striga</i> resistant
2	T104	OPV	TARI	Medium maturing, drought tolerant	11	JL05	OPV	IITA	<i>FOS</i> compatible, <i>Striga</i> resistant
3	TZA1780	Landrace	NPGRC	<i>Striga</i> tolerance, late maturing	12	JL08	OPV	IITA	Medium maturing, <i>Striga</i> resistant
4	TZA2263	Landrace	NPGRC	<i>Striga</i> tolerant, <i>FOS</i> compatible	13	JL09	OPV	IITA	Medium maturing, <i>Striga</i> resistant
5	TZA4010	Landrace	NPGRC	<i>FOS</i> compatible, <i>Striga</i> tolerant	14	JL13	OPV	IITA	<i>FOS</i> compatible, <i>Striga</i> resistant
6	TZA4016	Landrace	NPGRC	<i>FOS</i> compat ble	15	JL15	OPV	IITA	<i>FOS</i> compatible, <i>Striga</i> resistant
7	TZA4165	Landrace	NPGRC	<i>FOS</i> compat ble, <i>Striga</i> tolerant	16	JL16	OPV	IITA	Early maturing, <i>Striga</i> resistant
8	TZA4203	Landrace	NPGRC	<i>FOS</i> compat ble, <i>Striga</i> tolerant	17	JL17	OPV	IITA	<i>FOS</i> compatible, <i>Striga</i> resistant
9	TZA4205	Landrace	NPGRC	<i>FOS</i> compatible, <i>Striga</i> tolerant, late maturing	18	JL18	OPV	IITA	Medium maturing, <i>Striga</i> resistant
					19	JL19	OPV	IITA	<i>FOS</i> , compatible, <i>Striga</i> resistant

IITA - International Institute of Tropical Agriculture - Nigeria; NPGRC – Tanzania’s National Plant Genetic Resources Centre; OPV – Open pollinated variety; TARI – Tanzania Agricultural Research Institute; *FOS* – *Fusarium oxysporum* f. sp. strigae; S/N – Serial number.

5.2.3 Experimental sites

The 99 hybrids and three three-way hybrid checks, designated as HB 9022-13, HB 8338-1 and DKC8053, were evaluated for *Striga* resistance and FOS compatibility at three sites with high levels of *S. asiatica* and *S. hermonthica* inoculum in the soil during the 2018/19 cropping season. The sites were TARI - Tumbi Research Farm (5.05°S; 32.683°E) situated in Tabora district, Nzenda (5.081°S; 32.081°E) – Urambo district, and Igogo (4.293°S; 33.769°E) - Igunga district. The Urambo and Tumbi sites are characterized by sandy soils, while the Igunga site is characterized by sandy-loam soil. Tabora and Urambo districts receive unimodal rainfall, with a mean total annual rainfall of 880 mm. The districts are also characterized by long dry seasons of about five to six months, with temperatures ranging from 14.6°C in June to 32.5°C in October and a mean daily temperature of 23°C. Igunga district is located in the eastern part of the Tabora region and receives unimodal rainfall with a mean of 700 mm and temperatures ranging from 17.50°C to 32.5°C (URT, 1998; URT, 2020). All three sites are hotspots for *S. hermonthica* or *S. asiatica* species

5.2.4 Trial establishment and management

The experiment at each site was laid out in a 9 x 12 alpha lattice design with two replications. Two sets of treatments were compared in this study: (1) maize genotypes treated with FOS with *Striga* infestation, and (2) maize genotypes with *Striga* infestation without FOS treatment (untreated control). Before planting, artificial *Striga* infestation was created as described by Berner *et al.* (1997) depending on the prominent *Striga* spp. in a particular site. *Striga* seeds were mixed with fine sand at a ratio of 1:99 (*Striga* seed: sand) so that each scoop would deliver more than 3000 viable *Striga* seeds. The *Striga* seed in the sand was preconditioned by drenching in water and incubating for a week at room temperature. The experimental units were single-row plots of 4 m length, each with inter-row and intra-row spacing of 0.75 and 0.25 m, respectively. Two maize seeds per hill were sown and thinned to one seedling per hill 14 days after planting to achieve a maize plant density of 53,333/ha. To ensure good germination of the *Striga* seeds and to enhance the attachment of *Striga* plants to the roots of the maize plants, fertilizer application was delayed until 21 days after planting. This was followed by an application of 60 kg/ha of NPK 20-10-5 fertilizer when maize plants reach a height of 60 cm. Weeds other than *Striga* were removed manually immediately upon emergence. To control fall armyworm, stem borer and termites, chlorpyrifos (DKFOS480EC™) (C₉H₁₁Cl₃NO₃PS), a non-systemic organophosphate insecticide, was used by mixing it with water at a ratio of 30 ml to 16 litres (insecticide: water) and foliar-sprayed.

5.2.5 Data collection

Data were collected based on maize agronomic traits and *Striga* resistance parameters. Days to 50% anthesis (AD) were recorded as the number of days from sowing to when 50% of the plants in a plot shed pollen. The days to 50% silking (SD) were recorded as the number of days from planting to when 50% of the plants produced silks in a plot. Anthesis-silking interval (ASI) was determined as the difference between days to 50% silking and 50% anthesis. The days to 75% maturity (DM) were recorded as the number of days from planting to when 75% of the plants reached physiological maturity (Verheye, 2010). Plant height (PH) was measured from the base of the plant (expressed in cm) to the top of the first tassel branch. Ear height (EH) was measured (cm) from the ground level to the node bearing the uppermost ear. Grain yield/plot (GYD) was determined as the weight (kg) of the grain from all the ears harvested from individual plants in a plot after dehusking, shelling. The plot yield was converted to tons/ha at a constant kernel moisture content of 12.5%. Before weighing, the moisture content of the grains was obtained. Hundred kernel weight (HKWT) was recorded as a weight (g) of 100 kernels at field moisture content and converted to constant moisture of 12.5%. *Striga* emergence counts were recorded at eight weeks after planting (SEC8) and 10 weeks after planting (SEC10) as the number of emerged *Striga* plants per plot. The host plant damage syndrome rating was recorded at 8 and 10 weeks after planting, denoted as SDR8 and SDR10, using a scale of 1 to 9 as described by Kim (1994).

5.2.6 Data analysis

Maize agronomic traits and *Striga* parameters were subjected to a combined analysis of variance (ANOVA) after the homogeneity of variance test following an unbalanced design procedure in Genstat 21st Edition (Payne, 2020). Mean separation was performed using Fisher's unprotected least significant difference (LSD) test at the 5% probability level. Data on the *Striga* emergence counts were square-root transformed ($y = \sqrt{x + 0.5}$) prior to analysis to meet normalization assumptions. Correlation analysis was conducted separately between FOS-treated and untreated maize genotypes under *Striga* infestation to determine the relationship among maize agronomic traits and *Striga* parameters using the Statistical Package for Social Science Studies (SPSS) Version 24.0.

The genetic variance components for yield and yield-related traits were estimated following the Henderson method (Rodriguez *et al.*, 2018), using the Analysis of Genetic Designs with R (AGD-R) for Windows software version 5 (AGD-R v5.0) (Rodriguez *et al.*, 2018). The main effects due to female and male are independent estimates of the GCA effect, while female x male interaction effects represent estimates of the SCA effect (Hallauer *et al.*, 2010). The general combining

ability effects of females and males (GCA females and males), the interaction effects of crosses (SCA crosses), and their interactions with the locations were computed according to Rodriguez *et al.* (2018), following the linear model for the NCD II as follows:

$$Y_{ijk} = \mu + Ed + Rk(Ed) + mi + fj + mi*fj + Ed*mi + Ed*fj + Ed*mi*fj + B(Rk) + e_{ijk},$$

where, Y_{ijk} is the performance of the cross between the i th male and j th female, in the k th location;

μ is the grand mean;

Ed is the location effects ($d = 1, 2, 3, \dots, s$);

$Rk(Ed)$ is the effect of the replicate k nested in location d ($k = 1, 2, 3, \dots, r$);

mi is the male effect ($i = 1, 2, 3, \dots, m$);

fj is the female effects ($j = 1, 2, 3, \dots, f$);

$B(Rk)$ is the random effect of block nested in replicate k ; and

e_{ijk} is the residual.

The relative importance of the GCA and SCA effects for each trait was determined following the general predictability ratio: $GCA/SCA = 2 MSGCA/(2MSGCA + MSSCA)$ (Baker, 1978). The closer the ratio is to unity, the greater the predictability based on the additive gene effects (GCA). If the ratio is less than unity, then the performance of the progeny could be predicted based on the non-additive gene effects (SCA). The broad-sense heritability (H^2) and the narrow-sense heritability (h^2) estimates for the assessed traits were computed according to Rodriguez *et al.* (2018) as follows:

$$H^2 = (\sigma^2_A + \sigma^2_D) / \sigma^2_P$$

$$h^2 = \sigma^2_A / \sigma^2_P$$

where;

σ^2_A represents the additive genetic variance; σ^2_D represents the dominance genetic variance; σ^2_P is the total phenotypic variance given by $\sigma^2_A + \sigma^2_D + \sigma^2_E$; and σ^2_E is the location variance.

5.3 Results

5.3.1 Analysis of variance

The combined analysis of variance across locations revealed highly significant ($P < 0.01$) differences among the maize hybrids for all the traits studied and *Striga* parameters except the *Striga* damage ratings at eight weeks after planting with FOS treatment (Table 5.2). The mean squares were partitioned into female parent effects (GCA_F) and male parent effects (GCA_M),

attributed to GCA. Likewise, the variations due to male x female interaction were attributed to SCA. The mean squares were highly significant ($P<0.05$) for GCA for all the characters studied for both maize traits and *Striga* parameters with and without *FOS* inoculation (Table 5.2). Further, SCA effects exhibited significant ($P<0.05$) difference for all the assessed traits except *Striga* damage rating at eight and ten weeks after planting with *FOS* application. In addition, the experimental hybrids showed significant ($P<0.01$) interactions with locations for grain yield, days to 50% anthesis, days to 50% silking, and *Striga* emergence count at eight and 10 WAP with and without *FOS* application and *Striga* damage ratings at eight and 10 WAP without *FOS* treatment.

Furthermore, the interaction of GCA with locations was significant ($P<0.05$) for grain yield, days to 50% anthesis, days to 50% silking, and *Striga* emergence count at eight weeks after planting with and without *FOS* inoculation, and *Striga* emergence count at ten weeks after planting without *FOS* treatment. Likewise, the SCA and locations interaction effect was significant ($P<0.01$) for days to 50% anthesis, days to 50% silking, *Striga* emergence count at both eight and 10 WAP with and without *FOS* inoculation, and *Striga* damage rating at eight and 10 WAP without *FOS* application.

5.3.2 Effects of *FOS* on maize hybrids evaluated under *Striga* infestation

The mean performances of the top 15 and bottom five maize hybrids, plus the three checks for the measured traits, are presented in Table 5.3. Maize genotypes treated with *FOS* produced a higher grain yield than untreated genotypes. For *FOS*-treated genotypes, a high grain yield was recorded from the cross T104/JL18 (3.18 t/ha), while a low grain yield (1.21 t/ha) was noted from HB8338 -1 (*Striga* susceptible). For untreated genotypes, a high grain yield (2.98 t/ha) was recorded from the varietal cross T104/JL18, and a low yield (0.97 t/ha) was recorded from a *Striga* susceptible genotype, HB8331. A *Striga* resistant check (HB9022-13) recorded a grain yield of 1.86 t/ha with *FOS* and 1.64 t/ha without *FOS* (Appendix 5.3). Overall, there was an increase of 6.7 to 25% in grain yields for genotypes treated with *FOS* relative to the untreated genotypes. Further, grain yield performance for some crosses surpassed the checks both with and without *FOS* treatment. The respective yield performance of hybrids with and without *FOS* was T104/JL18 (3.18, 2.98 t/ha), TZA4205/JL01 (2.99, 2.76 t/ha), T104/JL17 (2.65, 2.44 t/ha), and TZA4010/JL08 (2.65, 2.42 t/ha) (Table 5.3).

Striga emergence count and *Striga* damage rating at eight and 10 weeks after planting were reduced significantly ($P<0.05$) for *FOS*-treated genotypes compared to the untreated set. For example, the minimum number of emerged *Striga* plants for untreated genotypes was 21.20

(HB9022-13) and the maximum number was 141.01 (TZA4165/JL15), recorded 10 weeks after planting (Table 5.3). In contrast, the lowest number of *Striga* emergence count for *FOS-treated* genotypes 10 weeks after planting was 8.63 (1780/JL01), and the highest number was 68.82 recorded from the hybrid 4165/JL15 (Appendix 5.3). This accounted for an over 50% reduction in the number of emerged *Striga* plants. For the untreated genotypes, the maximum damage rating recorded ten weeks after planting (SDR10) was 4.33 (HB8338-1), while under *FOS* treatment, the highest damage rating observed ten weeks after planting was 2.67 (HB8338-1) (Table 5.3), with a damage reduction of over 38%.

Furthermore, the average number of emerged *Striga* plants eight and 10 WAP for the untreated genotypes was 42.79 and 61.10, respectively. For *FOS-treated* genotypes, the average *Striga* emergence count at eight and 10 WAP was 21.93 and 31.21, respectively (Table 5.3). This shows a reduction of *Striga* emergence count of 20.8 and 29.89 at eight and 10 WAP, accounting for about 49% reduction of *Striga* emergence count.

Table 5.2. Mean squares of general combining ability and specific combining ability effects for grain yield, and other agronomic traits and *Striga* parameters of 99 maize hybrids evaluated in three locations during 2018/2019 cropping season with (+) and without (-) *FOS* treatment, in western Tanzania.

Source variation	of DF	AD		SD		ASI		GYD		HKWT		SEC8		SEC10		SDR8		SDR10	
		-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
Loc	2	277.88***	312.78***	184.14***	153.08***	6.26**	23.95***	15.89***	21.05***	363.66***	378.79***	596.09***	343.41**	765.62***	568.23***	40.69***	43.06***	43.67***	17.75***
Rep (Loc)	3	15.09***	13.40***	17.31***	13.96***	2.52***	4.07***	0.61***	0.62***	179.60***	179.89***	17.25***	6.45***	19.88***	10.32***	1.93***	2.387***	3.06***	1.08***
Hybrids	98	24.39***	24.17***	28.10***	27.32***	3.51***	2.37***	0.44***	0.44***	36.23***	36.23***	7.49***	5.02***	9.15***	6.01***	0.43***	0.553ns	0.55***	0.43**
GCA _M	10	89.52***	84.89***	96.94***	89.76***	8.30***	3.74***	1.26***	1.24***	72.34***	72.36***	8.94**	5.26**	11.86**	6.09*	0.53*	0.382ns	0.74*	0.43ns
GCA _F	8	106.99***	111.22***	130.18***	130.85***	6.73***	5.82***	1.13***	1.13***	101.40***	101.37***	20.60***	13.75***	26.48***	15.23***	1.00***	1.713***	0.99**	1.22***
SCA	80	8.02***	7.91***	9.29***	9.17***	2.59***	1.85***	0.27**	0.27**	25.29***	25.28***	6.06***	4.24***	7.16***	5.27***	0.36*	0.459ns	0.49**	0.36ns
Hybrids X Loc	196	3.15***	3.19***	3.66***	3.59***	0.87ns	0.86ns	0.24**	0.24**	13.17ns	13.19ns	5.90***	3.83***	7.32***	4.73***	0.39***	0.558ns	0.49**	0.35ns
GCA _M x Loc	20	3.72**	3.94***	4.56***	4.23**	0.89ns	0.97ns	0.34**	0.33*	13.04ns	13.01ns	5.93*	3.48*	6.61*	3.74ns	0.42*	0.620ns	0.55*	0.34ns
GCA _F x Loc	16	6.37***	5.77***	5.37***	4.87***	1.27ns	1.30ns	0.52***	0.53***	13.51ns	13.57ns	5.95*	3.52*	7.94*	4.95*	0.24ns	0.492ns	0.41ns	0.39ns
SCA X Loc	160	2.73***	2.81***	3.37***	3.36***	0.83ns	0.80ns	0.20ns	0.20ns	13.09ns	13.12ns	5.86***	3.85***	7.30***	4.73***	0.40***	0.557ns	0.49**	0.34ns
Error	240	1.57	1.64	1.72	1.85	0.89	1.05	0.17	0.17	12.91	12.93	3.04	2.01	3.96	2.58	0.26	0.45	0.32	0.28

*, **, *** Significant at $P < 0.05$; $P < 0.01$ and $P < 0.001$ probability level respectively; ns – Not significant at $P < 0.05$ probability level; DF - Degrees of freedom; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; GCA_F – General combining ability of female genotype; GCA_M – General combining ability of male genotype; GYD – Grain yield (t/ha); HKWT - Weight of 100 kernels (g); Loc - Location; Rep – Replication; Rep (Loc); Replication within location; SCA – Specific combining ability effect; SDR8 – *Striga* damage rating recorded eight weeks after sowing; SDR10 – *Striga* damage rating recorded 10 WAP; SEC8 - Number of emerged *Striga* plants (count) recorded eight WAP; SEC10 - Number of emerged *Striga* plants (count) recorded 10 WAP; *FOS* = *Fusarium oxysporium* f. sp. *strigae*.

Table 5.3. Mean performance of the top 15 and bottom five maize hybrids ranked based on reduced *Striga* emergence count eight weeks after planting and desirable agronomic traits and *Striga* parameters when evaluated in three locations during 2018/2019 cropping season with (+) and without(-) FOS in western Tanzania

Genotypes	AD		SD		ASI		HKWT		GYD		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
Top 15 hybrids																		
T104/JL18	60.00	62.50	61.67	63.83	1.67	1.33	44.33	44.88	2.98	3.18	12.02	6.92	22.16	9.05	1.33	1.33	1.50	1.33
HB9022-13	64.17	66.67	65.33	67.67	1.17	1.00	28.49	29.05	1.64	1.86	12.92	8.88	21.20	14.78	1.67	1.33	1.83	1.17
TZA1780/JL16	57.12	59.13	59.12	61.25	2.00	2.13	29.89	30.33	1.45	1.63	14.97	5.67	23.90	13.74	1.63	1.25	1.63	1.50
TZA4010/JL20	59.33	61.50	59.83	61.83	0.50	0.33	28.77	29.33	1.90	2.11	16.24	7.69	25.00	12.57	1.83	1.33	1.83	1.50
T104/JL17	62.17	64.00	62.33	64.67	0.17	0.67	40.37	40.93	2.44	2.65	18.58	19.44	27.34	19.70	2.17	1.50	2.17	2.00
TZA4205/JL01	57.67	60.00	61.67	62.50	4.00	2.50	38.09	38.65	2.76	2.99	18.60	6.33	29.01	13.99	1.83	1.33	2.00	1.50
TZA4205/JL20	59.67	61.83	59.67	62.00	0.00	0.17	29.39	29.94	1.86	2.06	19.78	9.54	26.40	15.07	1.83	1.33	1.83	1.33
TZA1780/JL01	58.00	60.00	58.83	61.17	0.83	1.17	38.08	38.64	2.01	2.22	20.28	8.43	26.89	8.63	1.83	1.33	2.00	1.50
TZA4010/JL08	57.00	59.17	58.00	60.00	1.00	0.83	33.65	34.21	2.42	2.65	21.00	12.30	30.48	20.60	2.00	1.50	2.00	1.84
TZA2263/JL20	61.67	63.83	62.00	64.33	0.33	0.50	27.91	28.46	1.61	1.82	21.57	4.98	35.45	11.33	1.83	1.50	2.00	1.50
TZA2263/JL16	54.33	56.67	55.33	57.33	1.00	0.67	32.56	33.12	1.91	2.12	22.88	14.38	32.91	20.28	1.83	1.33	2.17	1.50
TZA1780/JL18	59.67	61.83	61.50	63.50	1.83	1.67	34.12	34.67	1.76	1.90	23.91	12.97	39.42	15.29	1.67	1.33	1.67	1.50
TZA4165/JL16	58.33	59.83	59.17	61.33	0.83	1.50	33.89	34.45	2.10	2.29	24.81	13.91	40.32	19.67	1.67	1.50	1.83	1.50
TZA4203/JL09	58.67	60.83	61.17	62.67	2.50	1.83	36.72	37.27	1.82	1.99	25.26	13.68	31.37	20.76	1.83	1.50	2.17	1.50
TZA4165/JL13	58.67	61.17	61.00	62.83	2.33	1.67	32.44	33.00	1.87	2.08	25.39	9.18	41.22	15.48	1.83	1.33	1.83	1.67
Bottom 5 hybrids																		
TZA4016/JL17	61.17	63.50	62.00	64.00	0.83	0.50	32.86	33.41	2.28	2.48	81.46	41.82	109.58	52.37	2.33	2.00	2.50	2.00
HB8338-1	60.67	62.83	63.50	65.67	2.83	2.83	25.48	26.05	0.97	1.21	82.67	50.49	114.85	63.69	3.50	2.67	4.33	2.67
DKC8053	61.50	64.00	63.83	65.67	2.33	1.67	39.19	39.74	1.95	2.17	83.46	43.14	104.26	53.30	2.50	2.17	2.83	2.33
TZA1780/JL19	57.33	59.67	59.00	60.67	1.67	1.00	33.78	34.34	2.21	2.43	88.69	43.34	113.95	60.89	2.83	2.17	2.83	2.33
TZA4165/JL15	61.33	63.67	63.50	65.50	2.17	1.83	33.41	33.97	1.80	2.02	98.72	50.42	141.01	68.82	2.50	2.33	2.83	2.50
Trial statistics																		
Overall mean	59.82	62.08	61.45	63.43	1.64	1.36	33.51	34.06	1.87	2.09	42.79	21.93	61.10	31.21	2.15	1.72	2.35	1.79
CV%	2.30	2.20	2.40	2.40	59.10	77.80	12.00	11.80	25.40	22.67	30.70	34.30	29.70	31.80	24.70	38.80	25.60	31.70
LSD (0.05)	2.48	2.50	2.61	2.76	1.65	1.81	10.80	10.81	0.87	0.86	11.31	7.27	15.52	8.89	0.94	1.19	1.09	1.05
F- test	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	*	***	***
Maximum	64.33	66.67	66.50	68.33	4.00	2.83	44.33	44.88	2.98	3.18	98.72	50.49	141.01	68.82	3.50	3.17	4.33	2.67
Minimum	53.67	56.17	54.33	56.17	-0.50	0.00	25.48	26.05	0.97	1.21	12.02	4.98	21.20	8.63	1.33	1.17	1.50	1.17

*, *** Significant at $P < 0.05$ and $P < 0.001$ probability level, respectively; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; CV% - Coefficient of variation; HKWT - Weight of 100 kernel (g); GYD – Grain yield (t/ha); LSD- Least significant difference; SDR8 – *Striga* damage rating recorded eight weeks after sowing; SDR10 – *Striga* damage rating recorded 10 WAP; SEC8 - Number of emerged *Striga* plants (count) recorded eight weeks after sowing; SEC10 - Number of emerged *Striga* plants (count) recorded 10 WAP.

5.3.3 Estimates of variance components, broad-sense, and narrow-sense heritability

Estimates of genetic variance components, heritabilities, prediction ratio for the maize traits and the *Striga* parameters with and without *FOS* treatment are presented in Table 5.4. The variance due to the general combining ability (δ^2_{GCA}) was greater than the variance due to specific combining ability (δ^2_{SCA}) for days to 50% anthesis, days to 50% silking and grain yield with and without inoculation and *Striga* damage ratings at eight weeks after planting for *FOS*-treated genotypes. Conversely, the δ^2_{SCA} was relatively larger than δ^2_{GCA} for the anthesis-silking interval, hundred kernel weight, *Striga* emergence count at eight and ten weeks after planting for both *FOS*-treated and untreated genotypes and *Striga* damage rating eight and 10 WAP for untreated genotypes (Table 5.4).

Days to 50% anthesis, days to 50% silking, anthesis-silking interval, grain yield, hundred kernel weight, *Striga* emergence count at eight (SEC8) and 10 (SEC10) weeks after planting recorded high (>60%) broad sense heritability with and without *FOS* application. *Striga* damage rating at eight and SDR10 recorded moderate (30 to 60%) broad-sense heritability under the same conditions, except for SDR8 under *FOS* treatment, which recorded low broad sense heritability (27%). In addition, moderate narrow-sense heritability estimates were noted for days to 50% anthesis (0.54), days to 50% silking (0.54), and grain yield (0.36) under *Striga* infestation with and without *FOS* treatment. The rest of the studied traits recorded low narrow-sense heritability values (10 to 28%).

The relative importance of GCA and SCA was determined as the proportion of the genotypic variance attributable to the GCA due to female and male contributions, and the SCA due the interaction of female and male populations. A high predictability ratio close to unity ($\geq 70\%$) was recorded for days to 50% anthesis, days to 50% silking, grain yield with and without *FOS* application, and *Striga* damage rating at eight WAP under *FOS* treatment (Table 5.4).

5.3.4 General combining ability effects of female and male parents

A summary of the GCA effects of nine female and 11 male parents for the studied maize traits and *Striga* parameters is presented in Table 5.5. The genotype SITUKA M1 displayed significant ($P < 0.05$) negative GCA values for days to 50% anthesis and days to 50% silking under *Striga* infestation, with and without *FOS* treatment. This genotype also revealed non-significant negative GCA values for all *Striga* parameters studied, with and without *FOS* application. The genotype TZA4016 exhibited significant ($P < 0.05$) negative GCA values for hundred kernel weight and non-significant negative GCA values for both *Striga* emergence count and *Striga* damage ratings at both eight and 10 weeks after planting, with and without *FOS*.

In addition, the male genotype JL16 exhibited significant ($P<0.05$) positive GCA values for days to 50% anthesis and 50% silking, with and without *FOS* inoculation. Likewise, the genotype JL17 displayed significant ($P<0.05$) positive GCA values for hundred kernel weight and significant ($P<0.05$) negative GCA values for the anthesis-silking interval under *Striga* infestation, with and without *FOS* treatment. Further, the genotype JL17 exhibited low non-significant GCA values for *Striga* traits, with and without *FOS* treatment. Additionally, the genotype JL13 recorded significant ($P<0.05$) negative GCA values for *Striga* damage rating at eight weeks after planting, without *FOS* application, and *Striga* damage ratings at 10 WAP, with and without *FOS* inoculation. The genotype displayed further negative non-significant GCA values for *Striga* emergence count at eight and 10 WAP, with and without *FOS* treatment.

Table 5.4. Estimates of variance components, heritabilities and prediction ratio for yield and yield components, and *Striga* traits among 99 maize hybrids evaluated under *Striga* infestation at three locations in the 2018/19 cropping season with (+) and without (-) FOS treatment in western Tanzania

Variance component	AD		SD		ASI		GYD		HKWT		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
δ^2_g	3.81	3.76	4.40	4.25	0.44	0.22	0.04	0.04	3.90	3.89	0.75	0.52	0.88	0.60	0.03	0.02	0.04	0.03
δ^2_{GCAM}	1.51	1.43	1.62	1.49	0.11	0.03	0.02	0.02	0.87	0.87	0.05	0.02	0.09	0.02	0.00	0.00	0.01	0.00
δ^2_{GCAF}	1.50	1.57	1.83	1.84	0.06	0.06	0.01	0.01	1.15	1.15	0.22	0.14	0.29	0.15	0.01	0.02	0.01	0.01
δ^2_{SCA}	1.07	1.05	1.26	1.22	0.28	0.13	0.02	0.02	2.06	2.06	0.50	0.37	0.53	0.45	0.02	0.00	0.03	0.01
$\delta^2_{GCA (GCAM + GCAF)}$	3.01	2.99	3.45	3.34	0.17	0.10	0.03	0.03	2.02	2.02	0.27	0.16	0.38	0.17	0.01	0.02	0.01	0.01
Predictability ratio	0.85	0.85	0.85	0.85	0.54	0.59	0.80	0.78	0.66	0.66	0.52	0.47	0.59	0.43	0.58	0.95	0.47	0.68
δ^2_A	6.02	5.98	6.90	6.66	0.34	0.19	0.06	0.06	4.04	4.04	0.54	0.32	0.76	0.33	0.03	0.03	0.02	0.03
δ^2_D	4.30	4.18	5.05	4.89	1.13	0.54	0.06	0.06	8.25	8.23	2.01	1.49	2.13	1.79	0.07	0.01	0.11	0.05
δ^2_{EW}	0.79	0.79	0.93	0.89	0.15	0.17	0.05	0.05	2.24	2.24	1.46	0.94	1.78	1.15	0.09	0.11	0.11	0.07
H^2	0.93	0.93	0.93	0.93	0.91	0.81	0.71	0.71	0.85	0.85	0.64	0.66	0.62	0.65	0.53	0.27	0.55	0.54
h^2	0.54	0.55	0.54	0.54	0.21	0.21	0.36	0.35	0.28	0.28	0.14	0.12	0.16	0.10	0.14	0.23	0.10	0.19

δ^2_A – Additive variance in the population; δ^2_D – Dominance variance; δ^2_g – Genotypic variance; δ^2_{EW} – Environmental variance; δ^2_{GCAF} – Variance due to general combining ability of female or additive variance of female; δ^2_{GCAM} – Variance due to general combining ability of male or additive variance of male; δ^2_{GCA} – Variance due general combining ability of female and male or additive variance of female and male, δ^2_{SCA} – additive variance for female and male interaction; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-si king interval; GYD – Grain yield (t/ha); HKWT – Hundred kernels weight (g); H^2 – Broad-sense heritability; h^2 - Narrow-sense heritability.

Table 5.5. Estimates of the general combining ability effects of nine female (GCA_F) and 11 male (GCA_M) maize parents used in the crosses when evaluated under *Striga* infestation at three locations in the 2018/19 cropping season with (+) and without (-) FOS, in western Tanzania

Parents	AD		SD		ASI		GYD		HKWT		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
Female																		
SITUKA M1	-3.05*	-3.07*	-3.38*	-3.40*	-0.34	-0.32	0.02	0.01	-0.51	-0.50	-0.63	-0.40	-0.71	-0.35	-0.20	-0.21	-0.16	-0.16
T104	1.13	1.17	1.04	1.00	-0.11	-0.18	0.26	0.26	0.91	0.90	0.36	0.26	0.41	0.19	0.03	-0.03	0.01	0.04
TZA1780	-0.47	-0.48	-0.14	-0.09	0.32	0.39	-0.05	-0.06	1.21	1.21	0.05	0.32	-0.02	0.34	0.02	0.03	0.12	-0.04
TZA2263	1.43	1.50	1.85	1.89	0.42	0.36	-0.07	-0.07	-0.49	-0.50	0.90	0.77	1.08	0.81	0.21	0.23	0.22	0.28*
TZA4010	-0.50	-0.52	-0.17	-0.27	0.32	0.27	0.08	0.08	1.27	1.28	-0.53	-0.60	-0.62	-0.55	-0.05	-0.15	-0.06	-0.13
TZA4016	0.28	0.19	-0.24	-0.22	-0.55	-0.41	-0.18	-0.18	-2.93*	-2.93*	-0.76	-0.60	-0.87	-0.58	-0.09	-0.03	-0.09	-0.08
TZA4165	0.47	0.41	0.52	0.43	0.04	0.00	-0.02	-0.02	0.60	0.60	-0.07	-0.08	0.07	-0.12	-0.03	0.01	-0.06	0.05
TZA4203	0.38	0.45	0.25	0.25	-0.11	-0.20	0.14	0.14	0.56	0.55	-0.06	-0.23	-0.11	-0.34	-0.04	-0.11	-0.10	-0.10
TZA4205	0.32	0.37	0.28	0.44	0.00	0.08	-0.16	-0.15	-0.62	-0.62	0.65	0.41	0.66	0.53	0.16	0.27	0.13	0.12
Male																		
JL01	-0.84	-0.86	-1.17	-1.10	-0.33	-0.24	0.17	0.17	-1.70	-1.70	-0.57	-0.35	-0.68	-0.31	-0.06	-0.09	-0.08	0.00
JL05	-0.58	-0.52	-0.46	-0.57	0.15	0.00	0.09	0.11	-0.87	-0.86	-0.55	-0.49	-0.74	-0.50	-0.09	0.14	-0.10	-0.09
JL08	-0.39	-0.39	-0.28	-0.21	0.10	0.19	-0.02	-0.02	-0.83	-0.83	0.36	0.26	0.42	0.39	-0.04	-0.14	0.05	0.00
JL09	-0.54	-0.65	-0.78	-0.71	-0.29	-0.11	0.09	0.09	0.07	0.07	0.49	0.25	0.57	0.25	0.02	-0.03	0.13	0.07
JL13	-2.11	-1.96	-1.97	-1.95	0.14	-0.02	0.03	0.02	-0.24	-0.24	-0.70	-0.50	-0.60	-0.61	-0.22*	0.08	-0.27*	-0.19*
JL15	0.19	0.23	0.37	0.41	0.19	0.17	0.00	0.00	-0.03	-0.03	0.47	-0.02	0.49	0.25	0.10	-0.08	0.04	0.04
JL16	2.82*	2.77*	3.29*	3.09*	0.43	0.26	-0.41*	-0.40*	0.91	0.91	0.16	0.38	0.31	0.17	0.16	-0.01	0.19	0.07
JL17	0.76	0.66	-0.13	0.11	-0.90*	-0.57*	0.14	0.14	2.96*	2.96*	0.00	-0.10	-0.20	-0.25	-0.03	0.08	0.04	-0.04
JL18	-1.01	-0.99	-0.53	-0.65	0.51	0.41	-0.08	-0.09	-0.08	-0.08	-0.19	0.05	-0.10	-0.01	0.03	0.05	0.00	-0.08
JL19	0.66	0.61	0.65	0.51	0.03	-0.07	0.10	0.09	0.36	0.36	0.30	0.14	0.30	0.31	0.10	-0.03	0.05	0.09
JL20	1.05	1.12	1.02	1.12	-0.03	0.00	-0.09	-0.08	-0.56	-0.56	0.13	0.18	0.10	0.23	0.03	0.03	-0.01	0.10

*, Significant at $P < 0.05$ probability level; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI – Anthesis-silking interval; GYD – Grain yield (t/ha); HKWT – Hundred kernels weight (g); SDR8 – *Striga* damage rating recorded eight weeks after sowing, SDR10 – *Striga* damage rating recorded ten weeks after sowing; SEC8 - Number of emerged *Striga* plants (count) recorded eight weeks after sowing; SEC10 - Number of emerged *Striga* plants (count) recorded 10 weeks after sowing.

5.3.5 Specific combining ability effects of crosses

The new hybrids exhibited significant negative and positive SCA effects for different traits measured under this study (Table 5.6). The hybrid TZA4010xJL13 recorded highly significant ($P<0.01$) and positive SCA effects for grain yield (0.85) and hundred kernel weight (8.89) under *Striga* infestation, with and without FOS treatment. Likewise, the progeny TZA4010xJL05 displayed highly significant ($P<0.01$) and positive SCA values for grain yield under *Striga* infestation under the same conditions. Furthermore, the genotype TZA4205/JL20 showed significant ($P<0.05$) positive SCA effects for grain yield, with and without FOS inoculation. The cross TZA1780/JL18 exhibited a highly significant ($P<0.01$) and negative SCA effects for days to 50% silking, anthesis-silking interval under *Striga* infestation, with and without FOS treatment, and significant ($P<0.05$) negative SCA effects for days to 50% anthesis under FOS inoculation. In addition, the experimental hybrids TZA4165/JL01 and TZA4203/JL09 showed significant negative ($P<0.05$) SCA effects for days to 50% anthesis and 50% silking, with and without FOS application. The cross TZA4010xJL13 showed significant ($P<0.05$) negative SCA effects for *Striga* damage rating at eight weeks after planting, without FOS. Additionally, the experimental hybrid TZA2263xJL13 revealed significant ($P<0.05$) negative SCA effects for *Striga* emergence count at eight and 10 WAP when treated with FOS. Likewise, the genotype TZA4203xJL18 exhibited significant ($P<0.05$) negative SCA effects for *Striga* emergence count and *Striga* damage rating at eight and 10 WAP without FOS treatment. In addition, the cross TZA1780/JL19 revealed significant ($P<0.05$) desirable SCA effects for *Striga* emergence count at ten and *Striga* damage rating at eight weeks after planting without FOS treatment.

Table 5.6. Estimates of the specific combining ability (SCA) effects of 99 maize hybrids evaluated under *Striga* infestation at three locations in 2018/19 cropping season with (+) and without (-) FOS, in western Tanzania

Hybrid	AD		SD		ASI		GYD		HKWT		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
TZA4010*JL13	2.94**	3.05**	2.59*	2.88*	-0.41	-0.25	0.86***	0.85***	8.90***	8.89***	-1.53	-0.95	-1.57	-1.47	-0.55*	-0.09	-0.50	-0.16
TZA4010*JL05	-0.95	-0.96	0.99	0.03	1.91**	0.90	0.60**	0.59**	3.09	3.08	-1.03	-1.42	-0.92	-0.95	-0.19	-0.15	-0.19	-0.15
TZA4205*JL20	-1.06	-0.93	-1.25	-1.34	-0.09	-0.25	0.47*	0.49*	2.38	2.38	-0.88	-0.93	-1.37	-1.08	-0.11	-0.40	-0.22	-0.13
TZA1780*JL09	2.36*	1.93	2.24*	2.29*	0.02	0.55	-0.46*	-0.44*	-3.98*	-3.97*	-0.40	-0.41	-0.17	-0.38	-0.24	-0.15	-0.11	-0.19
TZA2263*JL17	0.56	0.63	1.09	0.82	0.52	0.21	-0.46*	-0.47*	-2.66	-2.66	1.27	0.83	1.50	0.95	0.35	0.09	0.09	0.08
TZA4010*JL16	0.27	0.42	0.73	0.63	0.46	0.30	-0.43*	-0.43*	-5.45**	-5.45**	2.51**	1.71*	2.49*	1.76*	0.34	0.42	0.42	0.30
TZA2263*JL15	0.94	0.92	0.90	0.71	-0.07	-0.20	0.29	0.33	0.65	0.66	-1.05	-0.97	-1.03	-1.24	-0.44*	0.02	-0.42	-0.11
TZA1780*JL17	1.12	1.33	1.66	1.32	0.63	0.17	0.28	0.30	-0.86	-0.85	-0.92	-0.67	-1.29	-0.96	-0.29	-0.05	-0.52	-0.05
TZA4165*JL01	-2.22*	-2.27*	-2.46*	-2.42*	-0.34	-0.26	0.27	0.28	1.05	1.04	-0.97	-0.51	-1.41	-0.41	0.01	-0.14	-0.14	0.02
TZA1780*JL15	-0.82	-0.76	-1.21	-1.27	-0.46	-0.56	0.26	0.21	1.59	1.58	1.25	1.42	1.30	1.42	0.52*	0.37	0.28	0.33
TZA4203*JL16	-0.33	-0.27	-1.94	-1.39	-1.61**	-1.23*	0.25	0.27	-0.17	-0.17	-0.51	-0.99	-0.94	-0.92	-0.12	-0.13	-0.05	-0.03
TZA1780*JL01	1.75	1.73	1.77	1.65	0.05	0.01	0.23	0.21	0.85	0.84	1.33	0.99	1.07	0.81	0.04	0.34	-0.08	0.26
TZA1780*JL18	-1.99	-2.12*	-3.65**	-3.26**	-1.78**	-1.29**	0.22	0.24	0.32	0.31	0.08	0.08	0.10	-0.05	0.14	-0.38	0.21	-0.26
SITUKA M1*JL18	1.46	1.68	1.75	1.93	0.37	0.25	0.22	0.23	0.06	0.06	0.39	-0.39	0.99	-0.18	0.05	-0.30	0.02	-0.16
TZA4016*JL09	-1.43	-1.09	-1.03	-0.92	0.38	0.18	0.20	0.19	0.81	0.80	0.33	0.82	0.05	0.62	-0.22	0.24	-0.03	0.20
TZA4203*JL19	1.28	1.18	0.51	0.41	-0.87	-0.89	0.20	0.22	3.09	3.10	0.39	0.28	0.43	-0.14	-0.31	0.09	-0.42	0.05
TZA4205*JL16	0.48	0.50	-0.05	-0.02	-0.55	-0.66	0.20	0.19	1.54	1.54	0.87	0.91	1.21	1.07	0.04	-0.01	0.02	0.19
SITUKA M1*JL19	0.08	0.23	-0.19	-0.20	-0.31	-0.44	0.20	0.20	-1.61	-1.61	-0.02	-0.18	-0.03	-0.31	-0.05	0.03	-0.24	0.00
TZA2263*JL01	-0.94	-0.94	-1.00	-1.04	-0.05	-0.12	0.19	0.20	-0.17	-0.17	0.33	0.31	0.32	0.60	-0.03	-0.19	-0.18	-0.14
TZA4165*JL19	0.94	1.10	0.39	0.39	-0.53	-0.59	0.19	0.17	-0.65	-0.67	0.22	-0.23	0.52	0.28	-0.03	-0.02	0.05	-0.20
T104*JL09	0.30	0.44	0.21	0.04	-0.06	-0.37	0.15	0.14	-1.57	-1.57	-1.28	-1.20	-1.23	-1.09	-0.34	-0.26	-0.29	-0.38
TZA4203*JL17	-0.69	-0.59	0.29	0.38	0.89	0.78	0.15	0.14	0.76	0.75	-0.57	-1.34	-0.51	-1.17	-0.39	-0.08	0.07	-0.28
TZA4165*JL16	-0.58	-0.56	-0.32	-0.12	0.23	0.41	0.15	0.14	-1.71	-1.71	-0.95	0.36	-0.48	-0.14	-0.06	0.08	-0.08	0.01
SITUKA M1*JL09	2.175*	1.60	2.03	2.15	-0.16	0.59	0.15	0.14	0.42	0.42	-0.76	-0.11	-0.59	-0.54	-0.24	-0.08	-0.39	-0.16
T104*JL17	0.56	0.17	0.18	0.34	-0.45	0.09	0.14	0.13	3.06	3.06	2.70**	-0.71	-2.86**	-1.19	-0.05	-0.15	-0.31	0.15
T104*JL18	0.09	0.05	0.63	0.66	0.48	0.45	0.12	0.12	0.24	0.24	1.31	0.99	1.15	1.48	0.10	0.34	0.08	0.70**
T104*JL20	-0.74	-0.79	-1.43	-1.50	-0.65	-0.65	0.12	0.11	-2.31	-2.31	2.12*	1.33	2.26*	1.34	0.15	0.23	0.18	0.03

Table 5.6. Continued.

Hybrid	AD		SD		ASI		GYD		HKWT		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
TZA4016*JL16	-1.85	-1.84	-0.64	-1.14	1.158*	0.65	0.12	0.12	0.14	0.15	-0.58	-0.51	-0.50	-0.49	-0.02	-0.05	-0.09	-0.10
TZA4205*JL15	-0.74	-0.79	-0.11	-0.14	0.69	0.75	0.10	0.09	0.76	0.76	0.79	0.94	1.05	1.26	0.04	0.30	0.10	0.43
TZA2263*JL09	-0.47	-0.39	-0.75	-0.72	-0.26	-0.42	0.09	0.10	0.13	0.13	0.81	1.03	1.08	1.17	0.12	0.31	0.28	0.32
TZA4205*JL09	-0.62	-0.47	-0.39	-0.56	0.17	-0.13	0.09	0.09	0.50	0.50	-0.43	-0.70	-0.22	-0.60	-0.17	-0.23	-0.32	-0.11
TZA2263*JL05	1.05	1.16	-0.11	0.47	-1.20*	-0.69	0.08	0.08	0.76	0.77	1.01	0.92	0.93	0.99	0.23	0.31	0.53*	0.36
TZA2263*JL08	0.43	0.50	0.42	0.32	0.02	-0.05	0.08	0.08	1.82	1.82	1.73	1.14	1.99*	1.07	0.17	0.40	0.25	0.29
TZA4016*JL18	0.54	0.53	0.28	0.16	-0.25	-0.33	0.08	0.08	-0.44	-0.44	0.41	0.47	0.22	0.22	0.03	0.01	0.04	-0.01
TZA1780*JL08	-1.44	-1.53	-1.42	-1.36	-0.04	0.09	0.07	0.09	1.04	1.05	0.99	-0.02	1.32	0.48	0.17	0.10	0.23	0.05
TZA1780*JL20	1.28	1.35	1.63	1.46	0.42	0.27	0.07	0.08	-0.15	-0.15	-0.72	-0.86	-0.56	-0.91	-0.14	0.18	-0.05	-0.01
TZA2263*JL20	-1.36	-1.26	-1.14	-0.92	0.15	0.14	0.06	0.04	-0.35	-0.36	-0.97	-0.60	-0.90	-0.73	-0.22	-0.02	-0.02	-0.15
TZA4010*JL19	-0.65	-0.69	-0.78	-0.98	0.04	-0.04	0.06	0.07	-0.01	-0.01	0.80	1.31	0.74	1.50	0.20	0.46	0.07	0.35
TZA4203*JL09	-2.24*	-2.06*	-1.79	-2.19*	0.44	-0.03	0.06	0.06	-0.80	-0.80	2.31*	1.86*	2.21*	2.18**	0.73**	0.47	0.49	0.45*
TZA4016*JL17	-1.21	-1.59	-1.92	-2.07	-0.68	-0.36	0.06	0.06	1.49	1.49	1.36	0.66	1.26	0.74	0.13	0.18	-0.01	0.10
SITUKA M1*JL08	-1.98	-1.92	-2.45*	-2.51*	-0.39	-0.54	0.05	0.05	0.23	0.23	-1.39	-0.81	-1.73	-1.09	-0.08	-0.16	-0.07	-0.12
SITUKA M1*JL17	-1.05	-1.00	-1.07	-1.25	-0.05	-0.27	0.04	0.06	0.24	0.24	1.21	0.86	0.87	1.16	0.24	0.36	0.49	0.34
TZA4165*JL08	0.45	0.61	0.69	0.72	0.23	0.15	0.04	0.03	0.20	0.18	-0.37	-0.56	-0.62	-1.21	-0.26	-0.05	-0.33	0.00
TZA4205*JL17	0.66	0.71	0.48	0.75	-0.22	-0.16	0.04	0.04	-0.25	-0.24	1.54	1.88*	1.69	1.65	0.39	0.05	0.71**	0.22
TZA2263*JL18	0.28	0.08	0.09	-0.02	-0.22	-0.11	0.03	0.04	3.05	3.06	-0.12	0.04	-0.32	0.14	0.06	-0.24	0.05	-0.13
TZA4016*JL01	0.14	0.18	-0.08	-0.16	-0.25	-0.35	0.03	0.03	0.21	0.21	-1.54	-1.24	-1.63	-1.35	-0.12	-0.26	-0.29	-0.22
SITUKA M1*JL16	-0.61	-0.60	-0.13	-0.31	0.45	0.23	0.02	0.02	1.25	1.25	-0.58	-0.53	-0.73	-0.48	-0.28	-0.02	-0.18	-0.05
TZA4165*JL17	-0.86	-0.84	-1.35	-1.12	-0.43	-0.26	0.02	0.02	1.67	1.68	-0.01	0.00	0.25	0.36	-0.29	-0.03	-0.19	-0.08
T104*JL05	0.86	0.81	0.73	0.69	-0.17	-0.15	0.02	0.09	1.50	1.49	0.48	0.25	0.29	0.10	-0.17	-0.10	-0.18	-0.25
TZA4203*JL05	0.43	0.21	0.04	-0.05	-0.34	-0.14	0.01	0.00	0.32	0.31	0.06	0.20	0.21	0.31	0.36	0.15	0.23	0.16
TZA4203*JL15	-0.65	-0.55	-0.23	-0.18	0.46	0.36	0.01	0.02	1.52	1.53	-0.07	0.22	-0.14	-0.17	-0.20	-0.15	-0.08	-0.21
T104*JL16	0.37	0.43	0.28	0.45	0.05	0.25	0.01	0.01	0.95	0.96	-0.23	-0.52	-0.29	-0.47	-0.11	0.12	-0.14	0.11
TZA4016*JL08	1.45	1.40	2.17	2.42*	0.66	0.90	0.01	0.01	0.50	0.50	0.90	0.31	0.97	0.84	0.11	0.00	0.34	0.20
TZA4016*JL05	0.14	0.08	-1.09	-0.63	-1.23*	-0.75	0.00	-0.02	-0.24	-0.25	-0.73	-0.44	-1.05	-0.62	-0.10	-0.26	-0.30	-0.23

Table 5.6. Continued.

Hybrid	AD		SD		ASI		GYD		HKWT		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
TZA4010*JL08	-1.44	-1.85	-1.85	-1.95	-0.37	-0.13	0.00	-0.01	-0.19	-0.18	-0.88	-0.46	-0.54	0.11	-0.21	-0.05	0.06	-0.18
TZA4205*JL08	0.93	1.15	1.03	0.80	0.11	-0.26	-0.02	-0.03	-1.71	-1.72	-0.16	0.27	-0.37	-0.06	0.05	-0.14	-0.06	-0.08
TZA1780*JL13	-1.62	-1.51	-1.80	-1.55	-0.24	-0.21	-0.04	-0.05	-0.43	-0.43	-0.84	-0.58	-0.92	-0.77	-0.12	-0.10	-0.03	-0.02
SITUKA M1*JL20	0.67	0.76	1.13	1.26	0.41	0.49	-0.05	-0.05	1.98	1.97	-0.05	-0.09	-0.36	0.20	0.24	-0.08	0.04	0.12
TZA4205*JL13	0.09	-0.06	0.33	0.34	0.24	0.44	-0.05	-0.05	-2.30	-2.31	-1.13	-0.89	-1.08	-0.38	-0.13	-0.18	-0.25	0.11
TZA2263*JL13	-0.23	-0.22	-0.08	-0.18	0.15	-0.01	-0.05	-0.05	-0.59	-0.60	-1.32	-1.78*	-1.37	-1.66*	-0.34	-0.47	-0.46	-0.22
TZA4165*JL05	-0.43	-0.05	-0.67	-0.62	-0.32	-0.67	-0.06	-0.07	1.84	1.84	0.54	0.65	0.44	0.38	0.05	0.35	0.06	0.26
T104*JL01	0.35	0.39	0.50	0.30	0.14	-0.08	-0.07	-0.06	0.17	0.17	-0.54	-0.82	-0.17	-1.08	-0.28	-0.26	-0.08	-0.30
TZA4203*JL13	-1.26	-1.36	-1.49	-1.73	-0.15	-0.12	-0.07	-0.06	-1.44	-1.44	0.34	0.42	0.24	0.60	0.37	0.20	0.30	0.11
TZA4010*JL15	0.28	0.29	0.26	0.46	-0.13	0.06	-0.08	-0.06	-1.56	-1.56	0.56	-0.02	0.59	0.35	0.34	-0.44	0.38	-0.50*
TZA4165*JL20	1.36	0.89	0.31	0.18	-0.97	-0.67	-0.08	-0.08	-2.79	-2.78	-0.28	-0.54	-0.15	-0.19	-0.01	0.02	-0.16	0.07
TZA4016*JL19	0.20	0.23	0.43	0.21	0.40	0.14	-0.09	-0.08	-0.38	-0.37	0.51	0.26	1.05	0.86	0.06	0.18	0.09	0.28
TZA4165*JL15	0.94	0.82	1.57	1.41	0.64	0.50	-0.09	-0.11	0.36	0.36	0.26	0.45	-0.20	-0.12	0.08	0.06	0.14	0.21
T104*JL19	0.21	0.09	0.63	1.04	0.29	0.76	-0.10	-0.12	0.37	0.36	0.14	0.16	0.01	-0.26	0.26	-0.32	0.45	-0.28
SITUKA M1*JL05	-0.18	-0.34	0.65	0.40	0.89	0.82	-0.10	-0.12	-3.82*	-3.82*	0.24	0.24	0.44	0.34	-0.04	-0.08	-0.01	0.17
T104*JL08	-0.05	0.13	-0.44	-0.28	-0.45	-0.50	-0.11	-0.10	-1.91	-1.91	-1.19	-0.77	-1.50	-0.96	-0.01	-0.17	-0.29	-0.31
TZA4165*JL09	0.53	0.78	0.83	0.80	0.29	-0.05	-0.11	-0.11	1.58	1.57	0.84	0.00	0.77	0.60	0.55*	0.02	0.63*	0.01
TZA4203*JL01	0.27	0.44	1.15	1.30	0.98	0.94	-0.11	-0.12	-3.45	-3.46	0.22	0.18	0.44	0.47	0.17	-0.02	0.41	-0.01
TZA4205*JL19	-0.37	-0.60	-1.11	-0.85	-0.81	-0.33	-0.12	-0.10	2.18	2.19	-0.25	-0.69	-0.39	-0.70	0.11	-0.12	0.18	-0.12
TZA4016*JL13	1.31	1.33	1.38	1.38	0.12	0.09	-0.13	-0.10	-2.81	-2.80	1.16	1.01	1.18	0.89	0.29	0.29	0.20	0.15
TZA2263*JL16	0.31	-0.15	-0.06	-0.26	-0.31	0.04	-0.14	-0.16	1.82	1.81	-1.42	-1.02	-2.02*	-1.51	-0.12	-0.13	-0.30	-0.45*
TZA4203*JL18	0.59	0.40	0.43	0.57	-0.19	0.12	-0.14	-0.18	0.80	0.80	-2.13*	-1.36	-2.21*	-1.62	-0.50*	-0.41	-0.59*	-0.16
TZA4016*JL15	1.56	1.50	0.71	1.08	-0.93	-0.59	-0.14	-0.14	-1.87	-1.87	-1.58	-1.76	-1.46	-1.96*	-0.30	-0.23	-0.26	-0.24
TZA4165*JL18	0.56	0.53	0.98	0.57	0.49	0.25	-0.14	-0.12	-0.17	-0.16	0.80	0.40	1.24	0.32	0.06	-0.03	0.06	0.08
TZA4203*JL08	1.66	1.50	1.84	1.81	0.22	0.34	-0.14	-0.14	0.02	0.03	0.45	1.04	0.58	0.90	0.06	0.08	-0.13	0.16
T104*JL13	0.20	0.44	0.56	0.29	0.35	-0.13	-0.15	-0.17	-0.08	-0.08	1.43	1.64*	1.75	1.30	0.49*	0.46	0.69**	0.29
TZA1780*JL19	-1.12	-1.18	-0.51	-0.83	0.54	0.18	-0.15	-0.18	1.46	1.46	-1.54	-1.03	-2.16*	-1.49	-0.44*	-0.21	-0.37	-0.22

Table 5.6. Continued.

Hybrid	AD		SD		ASI		GYD		HKWT		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
T104*JL15	-2.15*	-2.16*	-1.87	-2.06	0.46	0.34	-0.16	-0.16	-0.42	-0.43	0.56	-0.15	0.72	0.91	-0.03	0.10	-0.15	0.25
TZA4016*JL20	-0.84	-0.76	-0.24	-0.37	0.62	0.41	-0.16	-0.18	2.59	2.59	-0.15	0.60	0.02	0.34	0.12	-0.10	0.29	-0.12
TZA4010*JL18	-0.49	-0.25	-0.31	-0.52	0.22	-0.19	-0.17	-0.16	-3.57	-3.57	0.24	0.35	-0.15	0.62	0.21	-0.03	0.19	0.29
SITUKA M1*JL01	-0.46	-0.49	-0.19	0.15	0.21	0.56	-0.17	-0.16	2.15	2.16	-0.26	0.06	-0.11	0.03	0.10	0.25	0.21	-0.07
SITUKA M1*JL13	-0.75	-0.66	-1.51	-1.62	-0.76	-0.99*	-0.17	-0.20	0.12	0.11	1.96*	1.12	2.11*	1.35	0.09	0.14	0.11	0.10
TZA4010*JL09	-0.60	-0.76	-1.37	-0.93	-0.82	-0.32	-0.18	-0.18	2.92	2.92	-1.35	-1.13	-1.80	-1.89*	-0.19	-0.31	-0.27	-0.16
TZA4010*JL01	-0.02	-0.05	-0.66	-0.62	-0.61	-0.53	-0.19	-0.18	0.03	0.04	0.48	0.58	0.76	0.07	0.00	0.19	0.02	0.25
TZA4205*JL01	1.14	1.00	0.95	0.81	-0.13	-0.17	-0.20	-0.21	-0.83	-0.84	1.03	0.60	0.82	0.93	0.10	0.10	0.10	0.23
TZA1780*JL16	1.93	2.06*	2.11	2.13	0.13	0.02	-0.20	-0.18	1.63	1.62	0.97	0.76	1.36	1.25	0.33	-0.27	0.39	0.04
TZA4010*JL20	-0.26	-0.36	-0.20	0.17	-0.08	0.40	-0.20	-0.21	-0.71	-0.71	1.40	1.57*	1.35	1.47	0.14	0.35	0.15	0.46*
TZA2263*JL19	-0.57	-0.36	0.63	0.79	1.263*	1.21*	-0.20	-0.20	-4.45*	-4.45*	-0.17	0.29	-0.07	0.32	0.21	-0.08	0.16	0.16
TZA4165*JL13	-0.68	-1.03	0.01	0.17	0.70	1.19*	-0.21	-0.19	-1.35	-1.34	0.02	0.17	-0.25	0.23	-0.10	-0.26	-0.07	-0.35
SITUKA M1*JL15	0.65	0.72	-0.03	-0.04	-0.65	-0.68	-0.21	-0.19	-1.02	-1.02	-0.63	0.02	-0.74	-0.39	-0.02	-0.04	0.00	-0.15
TZA4203*JL20	0.95	1.09	1.16	1.04	0.18	-0.13	-0.24	-0.23	-0.64	-0.64	-0.39	-0.32	-0.18	-0.36	-0.16	-0.19	-0.24	-0.25
TZA4205*JL18	-1.04	-0.91	-0.20	-0.12	0.87	0.85	-0.25	-0.26	-0.28	-0.29	-0.89	-0.43	-0.91	-0.83	-0.15	1.04***	-0.09	-0.33
TZA4205*JL05	0.54	0.38	0.29	0.28	-0.28	-0.08	-0.27	-0.26	-1.99	-1.97	-0.39	-0.77	-0.31	-1.18	-0.17	-0.40	-0.19	-0.39
TZA4010*JL17	0.92	1.15	0.61	0.79	-0.21	-0.20	-0.29	-0.32	-3.45	-3.46	-1.08	-1.36	-0.81	-1.46	-0.09	-0.36	-0.35	-0.49*
TZA1780*JL05	-1.46	-1.31	-0.84	-0.61	0.74	0.77	-0.30	-0.31	-1.46	-1.45	-0.09	0.53	0.06	0.70	0.03	0.17	0.03	0.08

*, **, *** Significant at $P < 0.05$; $P < 0.01$ and $P < 0.001$ probability level; respectively; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI - Anthesis-silking interval; HKWT - Hundred kernels weight (g); GYD – Grain yield (t/ha); SDR8 – *Striga* damage rating recorded eight WAP; SDR10 – *Striga* damage rating recorded 10 WAP; SEC8 - Number of emerged *Striga* plants (count) recorded eight WAP; SEC10 - Number of emerged *Striga* plants (count) 10 weeks after planting.

5.4 Discussion

The combined analysis of variance across sites revealed highly significant differences among maize hybrids for all the traits assessed and *Striga* parameters except *Striga* damage rating at eight weeks after planting with *FOS* treatment (Table 5.2). The significant variation suggests the presence of considerable genetic variability among the studied genotypes, and thus selection and genetic improvement could be achieved. There were significant mean squares for the GCA and the SCA effects for all the assessed characters except for SDR8 and SDR10 with *FOS* application. This suggests the importance of both additive and non-additive gene effects, respectively. However, the combined mean square values for GCA were higher than the SCA mean squares for all the traits studied, indicating the preponderance of additive gene action in controlling these traits. These findings agree with those reported by earlier researchers (Gethi and Smith, 2004; Badu-Apraku, 2007; Abimiku *et al.*, 2020), for resistance to *S. hermonthica*. Recurrent selection methods, including S1 family selection and half-sib family selection with test crosses, could be adopted to improve this maize population for *Striga* resistance and grain yield (Badu-Apraku, 2007; Badu-Apraku *et al.*, 2007). This will provide superior OPVs for maize production in *Striga* affected areas of western Tanzania. The present results suggest that the creation of a generation of inbred lines resistant to *Striga* and compatible with *FOS* is possible because additive x additive interactions can be fixed in inbred lines (Gethi and Smith, 2004).

Significant genotypes x site interactions were recorded for grain yield, days to 50% anthesis, days to 50% silking, *Striga* emergence count at eight and 10 WAP with and without *FOS* treatment, and *Striga* damage rating at eight and 10 WAP without *FOS* application (Table 5.2). This suggested the need for evaluating maize genotypes across multiple environments to identify stable and location-specific genotypes (Machado *et al.*, 2009; Gurmu *et al.*, 2018; Abimiku *et al.*, 2020). Significant GCA_F and GCA_M and their interaction with location ($GCA \times Location$) effects suggest the need for selecting diverse parental genotypes for hybrids development in a specific location. These findings align with those reported by Machado *et al.* (2009) and Abimiku *et al.* (2020), who found that both the GCA and SCA effects can interact with the environment in response to maize grain yield productivity.

The application of *FOS* to maize genotypes significantly ($P < 0.001$) improved agronomic performance. Also, it significantly ($P < 0.05$) reduced *Striga* parameters and, thus, increased grain yield (Table 5.3). The present study observed an average grain yield increase from 6.7 to 24.7% for *FOS*-treated genotypes relative to untreated controls. Further, the study recorded minimum and maximum reduction of *Striga* emergence count 10 WAP at 51.2 and 59.3%, respectively (Table 5.3). This result suggests the efficacy of *FOS* in reducing the effects of *Striga* damage in

the FOS-treated genotypes. This is also relevant in terms of reducing the seedbank of *Striga* seeds in the long term. The findings corroborate with those reported by (Venne *et al.*, 2009; Shayanowako *et al.*, 2020; Lobulu *et al.*, 2021), when evaluating FOS effects on maize genotypes under both *S. asiatica* and *S. hermonthica* infestations. In addition, Gebretsadik *et al.* (2013) and Mrema *et al.* (2017b) reported improved sorghum agronomic traits and reduced numbers of *S. asiatica* and *S. hermonthica* plants due to FOS.

The prediction ratios of GCA to SCA variances were close to unity (≥ 0.70) for grain yield, days to 50% anthesis, days to 50% silking with and without FOS treatment, and *Striga* damage rating at eight and 10 weeks after planting for FOS-treated genotypes (Table 5.4). The findings signify the predominance of additive gene action in controlling these traits. Therefore, progeny performance can be predicted based on GCA alone for these characters (Baker, 1978; Fasahat *et al.*, 2016). In addition, high broad-sense heritability was recorded for all the characters measured, except for *Striga* damage ratings at eight and 10 weeks after planting. The result suggests that the traits have a highly heritable portion of variation due to additive and non-additive gene actions with little environmental influence (Fasahat *et al.*, 2016; Oponng-Sekyere *et al.*, 2019). Hence, these traits are amenable to genetic improvement. Heritability in the narrow-sense is important, in that the effectiveness of selection depends on the additive portion of genetic variance to the total variance (Oponng-Sekyere *et al.*, 2019). The present study recorded moderate (35 to 55%) narrow-sense heritability estimates for days to 50% anthesis (54%), days to 50% silking (54%), and grain yield (35%), with and without FOS treatment (Table 5.4). The rest of the characters under study recorded low (10 to 28%) narrow-sense heritability estimates. This suggests an adequate genetic variation to allow further improvement of these traits (Badu-Apraku, 2007).

The GCA effects for *Striga* emergence count (SEC) and *Striga* damage rating (SDR) were generally low, with some parents recording significant negative values (Tables 5.5). Low GCA levels for *Striga* traits are desirable and suggest that the genotypes are resistant or tolerant. For example, the male genotype JL13 showed significant ($P < 0.05$) negative *Striga* damage rating at eight weeks after planting without FOS inoculation and significant ($P < 0.05$) negative *Striga* damage ratings 10 weeks after planting with and without FOS application. The female genotypes SITUKA M1, TZA4010, TZA4016, TZA4203, and the male parents JL01, JL05, JL16, and JL17 exhibited non-significant negative low GCA values for SEC and SDR at eight and 10 weeks after planting, with and without FOS treatment. These genotypes are valuable genetic resources for *Striga* resistance breeding. The genotype SITUKA M1 exhibited significant ($P < 0.05$) negative GCA for days to 50% anthesis and silking. Early flowering and maturity are escape mechanisms

against heavy *Striga* infestation and terminal drought, which usually occur during the late stages of crop development (Oswald and Ransom, 2004; Badu-Apraku *et al.*, 2014; Mrema *et al.*, 2019). Generally, the male genotypes were good general combiners and would be valuable for *Striga* resistance breeding. For example, the experimental hybrid TZA4010xJL13 recorded significant ($P<0.05$) and positive SCA effects for grain yield, hundred kernel weight, days to 50% anthesis, and days to 50% silking, with and without *FOS* treatment (Table 5.6). In addition, this genotype showed significant negative SCA effects for *Striga* damage rating at eight weeks after planting, without *FOS* inoculation. Likewise, the hybrid TZA4010 x JL05 displayed significant positive ($P<0.05$) SCA effects for grain, with and without *FOS* application. This suggests that grain yield could be improved significantly through cross-breeding and continuous selection.

Furthermore, the experimental hybrid TZA4203 x JL18 recorded significant ($P<0.05$) negative SCA effects for *Striga* emergence count eight and ten weeks after planting without *FOS* inoculation. Likewise, the genotype 2263 x JL13, exhibited significant ($P<0.05$) negative SCA effects for *Striga* emergence count at eight and ten weeks after planting with *FOS* treatment. This indicates that these genotypes contain genes for the reduction of *Striga* emergence count and *Striga* damage rating. Thus, if deployed widely, they could contribute to the reduction of *Striga* seed multiplication and deposition in the soil.

5.5 Conclusions

The present study found that both with and without *FOS* treatments and locations influenced the genetic expression of traits in the assessed maize progenies. A combination of additive and non-additive gene action invariably controlled the genetic variation of the studied traits. Parents such as SITUKA M1, TZA4010, TZA4016, TZA4203, and JL01, JL05, JL13, JL17, and JL18 showed low GCA values for all *Striga* parameters, but relatively high positive GCA effects for grain yield, in a desirable direction for selection. Crosses such as TZA4010xJL13, TZA4010xJL05 displayed significantly higher SCA effects for grain yield and low SCA effects for the *Striga* parameters SEC8 and SEC10 WAP, and SDR8 and SDR10 WAP, respectively. The hybrid TZA1780xJL18 exhibited high negative SCA values for early flowering and maturity. The above parents and hybrids are recommended for further hybrid breeding or production in the *Striga*-infested locations, using *FOS* as a biological control agent to enhance their performance.

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5.7 Appendix

Appendix 5.1. Mean performance of 102 maize hybrids ranked based on reduced *Striga* emergence count eight weeks after planting and desirable agronomic traits and *Striga* parameters when evaluated in three locations during the 2018/2019 cropping season with (+) and without (-) FOS in western Tanzania

Hybrids	AD		SD		ASI		HKWT		GYD		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
T104/JL18	60.00	62.50	61.67	63.83	1.67	1.33	44.33	44.88	2.98	3.18	12.02	6.92	22.16	9.05	1.33	1.33	1.50	1.33
HB9022-13	64.17	66.67	65.33	67.67	1.17	1.00	28.49	29.05	1.64	1.86	12.92	8.88	21.20	14.78	1.67	1.33	1.83	1.17
TZA1780/JL16	57.12	59.13	59.12	61.25	2.00	2.13	29.89	30.33	1.45	1.63	14.97	5.67	23.90	13.74	1.63	1.25	1.63	1.50
TZA4010/JL20	59.33	61.50	59.83	61.83	0.50	0.33	28.77	29.33	1.90	2.11	16.24	7.69	25.00	12.57	1.83	1.33	1.83	1.50
T104/JL17	62.17	64.00	62.33	64.67	0.17	0.67	40.37	40.93	2.44	2.65	18.58	19.44	27.34	19.70	2.17	1.50	2.17	2.00
TZA4205/JL01	57.67	60.00	61.67	62.50	4.00	2.50	38.09	38.65	2.76	2.99	18.60	6.33	29.01	13.99	1.83	1.33	2.00	1.50
TZA4205/JL20	59.67	61.83	59.67	62.00	0.00	0.17	29.39	29.94	1.86	2.06	19.78	9.54	26.40	15.07	1.83	1.33	1.83	1.33
TZA1780/JL01	58.00	60.00	58.83	61.17	0.83	1.17	38.08	38.64	2.01	2.22	20.28	8.43	26.89	8.63	1.83	1.33	2.00	1.50
TZA4010/JL08	57.00	59.17	58.00	60.00	1.00	0.83	33.65	34.21	2.42	2.65	21.00	12.30	30.48	20.60	2.00	1.50	2.00	1.84
TZA2263/JL20	61.67	63.83	62.00	64.33	0.33	0.50	27.91	28.46	1.61	1.82	21.57	4.98	35.45	11.33	1.83	1.50	2.00	1.50
TZA2263/JL16	54.33	56.67	55.33	57.33	1.00	0.67	32.56	33.12	1.91	2.12	22.88	14.38	32.91	20.28	1.83	1.33	2.17	1.50
TZA1780/JL18	59.67	61.83	61.50	63.50	1.83	1.67	34.12	34.67	1.76	1.90	23.91	12.97	39.42	15.29	1.67	1.33	1.67	1.50
TZA4165/JL16	58.33	59.83	59.17	61.33	0.83	1.50	33.89	34.45	2.10	2.29	24.81	13.91	40.32	19.67	1.67	1.50	1.83	1.50
TZA4203/JL09	58.67	60.83	61.17	62.67	2.50	1.83	36.72	37.27	1.82	1.99	25.26	13.68	31.37	20.76	1.83	1.50	2.17	1.50
TZA4165/JL13	58.67	61.17	61.00	62.83	2.33	1.67	32.44	33.00	1.87	2.08	25.39	9.18	41.22	15.48	1.83	1.33	1.83	1.67
TZA4016/JL16	55.33	57.50	56.50	58.83	1.17	1.33	33.07	33.64	1.82	2.05	25.75	14.94	41.06	24.88	2.00	1.67	2.33	1.67
TZA4203/JL18	58.83	61.00	61.00	62.50	2.17	1.50	33.96	34.52	1.48	1.69	27.35	15.25	41.80	22.65	1.83	1.50	2.17	1.67
TZA4016/JL18	55.33	57.83	57.17	59.33	1.83	1.50	33.59	34.14	1.87	2.04	27.90	14.73	42.57	20.28	1.83	1.50	2.17	1.50
T104/JL01	61.00	63.33	61.83	64.17	0.83	0.83	33.96	34.50	1.76	1.96	27.94	8.39	42.80	13.26	2.00	1.17	2.00	1.17
SITUKA M1/JL20	61.00	63.17	63.67	65.00	2.67	1.83	31.87	32.43	1.43	1.64	28.26	16.14	44.64	21.55	2.17	1.67	2.33	1.67
SITUKA M1/JL08	62.33	64.50	64.67	66.50	2.33	2.00	33.81	34.36	1.68	1.89	30.42	25.61	56.23	27.07	2.17	1.83	2.33	1.83
TZA4010/JL19	59.67	62.17	61.83	64.00	2.17	1.83	29.80	30.35	2.15	2.37	30.82	14.72	43.38	23.90	2.17	1.50	2.50	1.67
T104/JL13	57.33	59.83	59.50	61.50	2.17	1.67	33.31	33.86	1.99	2.19	31.64	12.99	55.17	22.05	2.00	1.33	2.17	1.33
TZA4010/JL17	60.33	62.67	61.67	63.50	1.33	0.83	33.58	34.13	2.42	2.63	32.28	13.03	52.22	19.11	1.83	1.33	2.17	1.50
TZA4010/JL01	58.33	60.50	59.33	61.33	1.00	0.83	32.64	33.21	1.95	2.18	33.11	16.61	50.28	21.29	2.00	1.67	2.17	1.84
T104/JL16	58.50	60.83	60.17	62.33	1.67	1.50	34.68	35.24	1.80	2.01	33.33	18.76	45.18	32.90	2.17	1.50	2.17	1.83
TZA4016/JL20	60.17	62.50	61.83	63.83	1.67	1.33	32.23	32.78	1.51	1.72	33.91	23.73	51.38	30.74	2.17	1.67	2.50	1.67

Appendix 5.1. Continued.

Hybrids	AD		SD		ASI		HKWT		GYD		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
T104/JL19	60.00	62.33	61.50	63.67	1.50	1.33	37.66	38.20	2.31	2.51	33.98	8.83	47.03	13.85	1.67	1.50	2.33	1.33
TZA4165/JL01	57.33	59.17	59.00	60.83	1.67	1.67	34.00	34.56	1.93	2.15	34.14	17.33	55.35	31.24	1.83	1.50	2.33	1.50
T104/JL09	61.33	63.67	63.00	65.00	1.67	1.33	36.32	36.88	2.13	2.36	34.45	21.23	44.23	24.20	1.83	1.67	2.00	1.67
TZA1780/JL17	60.67	63.00	61.83	63.67	1.17	0.67	32.89	33.44	2.35	2.55	34.59	15.50	54.05	24.44	1.83	1.50	2.17	1.50
SITUKA M1/JL16	57.67	60.00	58.50	60.50	0.83	0.50	32.11	32.67	1.69	1.91	35.31	20.16	48.30	26.89	2.00	1.50	2.17	1.50
TZA4165/JL18	56.33	58.50	57.00	59.33	0.67	0.83	35.01	35.54	1.99	2.19	35.33	22.40	50.89	29.92	2.33	1.50	2.67	1.33
T104/JL08	60.17	62.33	60.50	62.83	0.33	0.50	39.38	39.94	2.11	2.32	35.90	16.55	52.88	26.23	1.83	1.67	2.17	1.67
TZA2263/JL18	57.67	60.17	60.33	62.00	2.67	1.83	31.59	32.14	1.74	1.95	36.10	18.15	47.18	29.78	2.33	1.67	2.50	1.84
TZA4205/JL13	57.33	59.33	59.83	61.83	2.50	2.50	31.90	32.46	1.60	1.82	37.03	20.60	52.97	29.25	1.83	1.33	2.00	1.33
SITUKA M1/JL19	62.33	64.67	62.67	64.83	0.33	0.17	35.95	36.50	2.01	2.25	37.04	14.37	50.99	19.90	2.17	1.50	2.33	1.67
TZA4010/JL16	57.33	59.67	58.33	60.17	1.00	0.50	32.45	33.00	2.22	2.41	37.35	17.86	51.20	27.36	2.00	1.50	2.00	1.67
TZA4205/JL16	58.00	60.50	61.00	63.17	3.00	2.67	33.03	33.57	1.48	1.68	37.45	21.06	55.84	26.59	2.17	3.17	2.33	1.50
TZA4203/JL13	59.67	61.83	61.00	62.83	1.33	1.00	29.38	29.92	1.59	1.80	38.15	23.72	51.44	28.96	2.17	1.83	2.33	1.67
TZA4016/JL09	61.67	64.00	64.00	66.00	2.33	2.00	33.68	34.24	1.75	1.97	38.34	19.47	56.26	29.63	2.00	2.00	2.33	1.84
TZA4016/JL05	60.17	62.67	61.67	63.83	1.50	1.17	34.18	34.74	2.07	2.32	38.48	16.64	47.59	24.89	2.17	1.67	2.17	1.84
TZA1780/JL09	61.33	63.00	63.00	65.17	1.67	2.17	31.33	31.90	1.47	1.69	39.05	19.09	56.93	28.14	1.83	1.67	2.33	1.50
TZA4205/JL19	60.00	62.17	61.33	63.17	1.33	1.00	33.39	33.94	2.07	2.27	39.39	16.23	56.40	24.00	2.33	1.67	2.33	1.67
TZA4205/JL08	59.00	61.67	60.50	62.33	1.50	0.67	36.82	37.38	2.07	2.29	39.53	20.82	54.99	24.56	2.00	2.00	2.17	2.00
TZA4205/JL09	57.17	59.67	60.00	62.17	2.83	2.50	32.33	32.90	1.69	1.90	39.90	26.83	58.88	40.17	2.17	1.83	2.50	1.83
TZA4016/JL08	62.50	64.33	63.17	65.00	0.67	0.67	31.35	31.92	1.73	1.96	40.45	19.05	63.04	30.88	2.17	1.83	2.17	2.00
SITUKA M1/JL17	64.00	66.33	66.00	68.00	2.00	1.67	37.08	37.64	1.79	2.01	40.47	21.49	63.29	27.54	2.17	1.83	2.33	2.00
TZA4016/JL15	60.67	63.17	62.83	65.00	2.17	1.83	31.56	32.11	1.82	2.02	41.12	24.44	60.29	32.24	2.17	2.00	2.50	2.00
TZA1780/JL13	59.33	61.67	60.67	62.67	1.33	1.00	27.11	27.67	1.48	1.70	41.39	23.38	58.85	29.86	2.17	1.83	2.17	1.67
TZA4205/JL05	60.00	62.17	61.50	63.50	1.50	1.33	30.11	30.69	1.55	1.80	41.59	13.96	59.53	18.66	2.00	1.50	2.17	1.33
TZA4205/JL17	61.00	63.33	62.50	64.33	1.50	1.00	35.89	36.44	2.35	2.64	41.98	20.27	56.01	26.82	1.83	1.50	2.00	1.50
TZA2263/JL19	59.50	62.00	61.67	63.67	2.17	1.67	35.95	36.50	2.09	2.31	42.21	20.18	60.87	27.89	2.00	1.50	2.17	1.50
SITUKA M1/JL13	53.67	56.17	54.33	56.17	0.67	0.00	33.65	34.21	1.89	2.06	42.65	20.22	61.72	30.51	1.83	1.50	2.00	1.50
TZA4165/JL17	60.33	62.83	61.50	63.67	1.17	0.83	31.14	31.69	2.05	2.26	42.68	21.67	59.41	30.71	2.17	1.50	2.17	1.50
TZA4016/JL19	62.00	64.50	63.67	65.50	1.67	1.00	32.56	33.11	1.69	1.91	43.21	18.22	63.85	26.10	2.00	1.50	2.00	1.50
TZA4010/JL18	57.00	59.33	58.50	60.33	1.50	1.00	31.94	32.49	1.84	2.06	43.38	22.78	59.55	32.61	2.33	1.67	2.33	1.67

Appendix 5.1. Continued.

Hybrids	AD		SD		ASI		HKWT		GYD		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
TZA4010/JL15	59.33	61.67	61.00	63.00	1.67	1.33	32.15	32.71	2.26	2.49	43.42	25.66	60.53	39.81	2.17	1.67	2.17	1.83
TZA4203/JL17	61.67	63.83	63.50	65.67	1.83	1.83	35.77	36.31	2.20	2.39	44.14	20.88	57.41	26.43	2.50	1.33	2.83	1.50
SITUKA M1/JL15	64.33	66.17	66.50	68.17	2.17	2.00	36.34	36.88	1.25	1.45	44.32	25.23	59.59	28.72	2.50	1.83	2.50	1.67
TZA4203/JL08	62.00	64.33	63.17	65.00	1.17	0.67	33.95	34.48	2.14	2.33	44.71	18.32	66.69	32.75	2.17	1.67	2.33	1.67
TZA4165/JL08	60.33	62.67	62.33	64.33	2.00	1.67	33.47	34.01	1.83	2.02	44.77	19.26	61.26	22.70	1.83	1.67	2.00	1.83
TZA4165/JL20	61.00	63.17	62.83	65.17	1.83	2.00	30.19	30.74	1.68	1.89	45.36	19.03	63.55	36.18	2.17	1.67	2.67	2.00
TZA2263/JL01	59.67	62.00	61.67	63.83	2.00	1.83	33.44	33.99	1.94	2.16	46.79	16.05	65.42	31.97	2.50	1.17	2.67	1.17
TZA4203/JL01	59.33	61.50	61.33	63.00	2.00	1.50	35.95	36.51	2.14	2.36	47.32	30.86	64.87	46.41	2.33	2.00	2.33	2.17
TZA1780/JL20	58.00	60.33	59.17	61.33	1.17	1.00	31.60	32.14	1.92	2.12	47.54	26.19	64.69	36.26	1.83	2.00	2.33	2.00
TZA4203/JL19	62.00	64.17	62.67	64.33	0.67	0.17	37.91	38.46	2.36	2.58	48.68	21.06	70.63	28.06	1.83	1.67	1.83	1.84
TZA4203/JL20	61.00	63.17	62.50	64.17	1.50	1.00	30.60	31.15	1.65	1.86	48.74	25.57	77.50	42.88	2.17	1.83	2.33	2.17
TZA2263/JL15	62.33	64.67	64.50	66.33	2.17	1.67	32.64	33.20	2.01	2.26	48.91	21.90	73.13	32.83	2.00	2.00	2.17	2.00
TZA4203/JL16	59.62	61.88	62.12	63.63	2.50	1.75	27.28	27.92	1.97	2.22	49.22	27.60	73.93	41.19	2.13	1.63	2.25	1.88
SITUKA M1/JL18	59.83	62.00	62.50	64.00	2.67	2.00	34.15	34.70	1.59	1.81	50.17	26.51	83.72	32.95	2.17	1.83	2.33	1.83
TZA4205/JL18	56.50	58.67	56.83	58.83	0.33	0.17	36.15	36.72	2.02	2.25	50.94	27.24	61.85	39.47	2.17	1.83	2.67	2.00
TZA4016/JL01	60.00	62.17	61.83	64.17	1.83	2.00	33.99	34.54	1.77	1.99	51.53	29.30	68.86	41.80	2.17	2.00	2.33	2.17
T104/JL20	59.67	61.33	59.17	61.33	-0.50	0.00	34.68	35.24	1.75	1.97	52.97	24.02	67.94	31.34	2.17	1.83	2.33	1.83
TZA1780/JL05	58.67	61.00	60.17	62.17	1.50	1.17	33.47	34.04	1.91	2.14	54.38	21.85	79.85	33.13	2.17	1.83	2.33	1.83
TZA1780/JL08	60.17	62.50	61.83	63.67	1.67	1.17	35.30	35.85	1.85	2.07	55.03	21.88	75.29	36.34	2.67	1.83	3.00	1.83
TZA4010/JL13	60.33	62.50	62.67	64.50	2.33	2.00	35.61	36.17	1.82	2.03	55.44	30.31	78.14	42.94	2.50	1.83	2.67	1.83
TZA2263/JL08	61.33	63.50	63.83	65.50	2.50	2.00	33.61	34.15	1.68	1.87	55.86	29.61	73.32	35.37	2.33	1.83	2.50	2.17
SITUKA M1/JL09	64.00	66.33	66.50	68.33	2.50	2.00	37.44	37.99	1.25	1.47	56.14	38.14	86.01	54.81	2.67	1.50	3.00	1.83
TZA4165/JL05	60.67	63.17	62.50	64.50	1.83	1.33	29.94	30.49	1.57	1.79	58.84	33.84	76.55	43.51	2.33	1.83	2.50	1.83
TZA4203/JL05	60.33	62.33	61.17	63.33	0.83	1.00	35.83	36.40	1.73	1.96	58.85	22.14	80.39	35.37	2.50	1.83	2.67	1.83
TZA4010/JL09	60.17	62.33	61.83	63.83	1.67	1.50	33.09	33.64	2.15	2.34	59.52	35.79	75.71	46.68	2.17	2.00	2.33	2.00
TZA4016/JL13	59.83	62.17	62.33	64.17	2.50	2.00	34.89	35.44	2.18	2.37	61.09	36.34	81.00	51.56	2.33	2.17	2.50	2.50
TZA4010/JL05	60.17	62.33	61.33	63.33	1.17	1.00	29.90	30.45	1.75	1.96	61.78	28.77	79.85	46.34	2.33	2.00	2.50	2.17
TZA4165/JL19	61.33	63.50	63.17	65.17	1.83	1.67	33.78	34.33	1.82	2.03	62.56	38.30	90.55	47.72	2.17	1.67	2.17	1.83
TZA2263/JL13	59.00	61.67	61.00	62.67	2.00	1.00	34.28	34.85	1.94	2.13	63.32	38.20	94.29	42.72	2.50	2.00	2.83	1.83
TZA4203/JL15	61.33	63.83	64.67	66.67	3.33	2.83	28.90	29.45	1.60	1.81	64.00	36.47	94.76	51.02	2.67	1.83	2.83	2.33

Appendix 5.1. Continued.

Hybrids	AD		SD		ASI		HKWT		GYD		SEC8		SEC10		SDR8		SDR10	
	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+
TZA2263/JL17	59.00	61.33	61.17	63.00	2.17	1.67	34.33	34.87	2.00	2.20	66.05	24.93	94.29	49.44	2.17	1.83	2.17	2.17
TZA4165/JL09	57.33	59.50	59.33	61.50	2.00	2.00	35.03	35.59	1.85	2.07	66.94	28.13	96.27	45.56	2.33	1.83	2.83	1.83
TZA4205/JL15	61.67	64.17	62.67	65.17	1.00	1.00	33.32	33.88	1.88	2.10	67.13	36.54	87.67	48.43	2.50	2.17	3.00	2.33
SITUKA M1/JL05	63.33	65.67	64.83	66.67	1.50	1.00	35.16	35.71	1.49	1.71	67.65	39.78	99.52	52.61	2.50	2.00	2.67	2.17
TZA2263/JL09	58.67	61.00	60.33	62.33	1.67	1.33	35.64	36.18	2.07	2.22	70.11	42.52	94.99	60.45	2.83	2.17	2.83	2.17
T104/JL05	61.33	63.67	61.83	64.33	0.50	0.67	35.66	36.22	1.90	2.11	70.41	43.96	93.14	54.33	2.67	2.00	3.17	2.00
TZA2263/JL05	59.50	61.83	62.00	64.17	2.50	2.33	33.74	34.30	1.84	2.06	70.60	36.80	99.04	59.56	2.50	2.33	2.67	2.50
TZA1780/JL15	60.00	62.33	61.50	63.50	1.50	1.17	33.45	34.01	2.05	2.28	76.10	46.42	110.91	60.31	2.50	2.33	3.00	2.50
SITUKA M1/JL01	62.33	64.67	65.17	66.83	2.83	2.17	29.53	30.09	1.16	1.39	77.75	39.43	102.14	50.79	2.67	2.00	3.00	2.00
T104/JL15	62.33	64.67	64.00	66.00	1.67	1.33	34.04	34.59	1.56	1.77	78.92	41.32	107.72	51.38	2.67	2.00	2.67	2.17
TZA4016/JL17	61.17	63.50	62.00	64.00	0.83	0.50	32.86	33.41	2.28	2.48	81.46	41.82	109.58	52.37	2.33	2.00	2.50	2.00
HB8338-1	60.67	62.83	63.50	65.67	2.83	2.83	25.48	26.05	0.97	1.21	82.67	50.49	114.85	63.69	3.50	2.67	4.33	2.67
DKC8053	61.50	64.00	63.83	65.67	2.33	1.67	39.19	39.74	1.95	2.17	83.46	43.14	104.26	53.30	2.50	2.17	2.83	2.33
TZA1780/JL19	57.33	59.67	59.00	60.67	1.67	1.00	33.78	34.34	2.21	2.43	88.69	43.34	113.95	60.89	2.83	2.17	2.83	2.33
TZA4165/JL15	61.33	63.67	63.50	65.50	2.17	1.83	33.41	33.97	1.80	2.02	98.72	50.42	141.01	68.82	2.50	2.33	2.83	2.50
Overall mean	59.82	62.08	61.45	63.43	1.64	1.36	33.51	34.06	1.87	2.09	42.79	21.93	61.10	31.21	2.15	1.72	2.35	1.79
CV%	2.30	2.20	2.40	2.40	59.10	77.80	12.00	11.80	25.40	22.67	30.70	34.30	29.70	31.80	24.70	38.80	25.60	31.70
LSD (0.05)	2.48	2.50	2.61	2.76	1.65	1.81	10.80	10.81	0.87	0.86	11.31	7.27	15.52	8.89	0.94	1.19	1.09	1.05
F- test	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	*	***	***
Maximum	64.33	66.67	66.50	68.33	4.00	2.83	44.33	44.88	2.98	3.18	98.72	50.49	141.01	68.82	3.50	3.17	4.33	2.67
Minimum	53.67	56.17	54.33	56.17	-0.50	0.00	25.48	26.05	0.97	1.21	12.02	4.98	21.20	8.63	1.33	1.17	1.50	1.17

*, *** Significant at $P < 0.05$ and $P < 0.001$ probability level respectively; AD – Number of days from sowing to when 50% of the plants in a plot shed pollen; SD - Number of days from sowing to when 50% of the plants in a plot produce silk; ASI - Anthesis-silking interval; CV% - Coefficient of variation; LSD – Least significant difference; HKWT - Hundred kernels weight (g); GYD – Grain yield (t /ha); SDR8 – *Striga* damage rating recorded eight weeks after sowing; SDR10 – *Striga* damage rating recorded 10 weeks after sowing; SEC8 - Number of emerged *Striga* plants (count) recorded eight weeks after sowing; SEC10 - Number of emerged *Striga* plants (count) recorded 10 weeks after sowing.

CHAPTER SIX: General overview of the research findings

6.1 Introduction and objectives of the study

Maize is a major staple food crop after wheat and rice worldwide. In Tanzania maize is grown in nearly all agro-ecological zones, accounting for 31% of the total food crops production and constituting more than 75% of the cereal consumption. Despite its role, maize production and productivity are affected by various biotic and abiotic stresses and socio-economic constraints. *Striga* is one of the main biotic constraints, causing yield losses of 18 to 100% in Tanzania. The weed is persistent and well distributed across the country. Several *Striga* control options have been suggested and deployed, including cultural, chemical, biological, and host resistance. However, none of these works effectively when deployed in isolation. An integrated *Striga* management approach is proposed that combines the use of host resistance at the centre, together with a biocontrol agent of *Striga* (*Fusarium oxysporum* f. sp. *strigae* [FOS]), and farmer-compatible agronomic practices that would be effective, economical, and environmentally friendly. *Striga* resistance breeding requires the integration of novel genes into locally adapted FOS compatible and productive maize genotypes with farmer preferred traits. Therefore, the overall aim of this study was to develop maize genotypes resistant to *Striga asiatica* and *S. hermonthica* and compatible with FOS in Tanzania, in varieties acceptable to farmers. This chapter highlights the objectives of the study, the major findings of the research and their implication in the development of an integrated *Striga* control option to enhance maize production in western Tanzania.

6.1.1 The specific objectives of the study were:

- i. To assess maize production constraints, traits preference and current *Striga* control options in western Tanzania for farmers consultation and to guide breeding.
- ii. To characterize maize genotypes for resistance to *S. asiatica* and *S. hermonthica* and compatibility with FOS in Tanzania.
- iii. To determine the genetic diversity of maize genotypes with differential resistance to *S. asiatica* and *S. hermonthica* based on phenotypic and simple sequence repeats markers.
- iv. To assess diverse progenies of maize genotypes for yield and yield components, *Striga* resistance and FOS compatibility to select experimental hybrids.

6.2 Summary of the major findings

6.2.1 Maize production constraints, traits preference and current *Striga* control options in western Tanzania: farmers consultation and implications for breeding

A participatory rural appraisal (PRA) study was conducted across four districts, eight wards and 16 villages of western Tanzania, involving 324 farmers. Data were collected using a semi-structured questionnaire with 166 farmers, focus group discussions with 158 farmers and field observations following transect walks.

The core findings of the study were:

- ❖ The major constraints affecting maize production in the study areas included drought (reported by 97.2% of the respondents), *Striga* infestation (93.1%), field insect pests (90.1%), storage insects (72.7%) and lack of capital (55.6%).
- ❖ Hand-hoe weeding (>59%), uprooting/hand-picking (53%), manure application (42%) and crop rotation (30%) were the most common practices of farmers for reducing *Striga* infestations.
- ❖ Uprooted *Striga* residues placed at the farm borders contributed to the spread of *Striga* in farmers' fields.
- ❖ About 59% and 45% of the interviewed farmers used *Striga* susceptible introduced varieties and farmer-saved maize seed, respectively.
- ❖ About half (49%) of the interviewed farmers used inorganic fertilizers.
- ❖ More than 10% of the respondents grow both improved and local maize varieties concurrently.
- ❖ Drought and *Striga* resistance, high grain yield, and field insect pest resistance were the most important farmers preferred traits. These traits should be incorporated into *FOS* compatible maize genotypes for sustainable maize production.

6.2.2 Characterization of maize genotypes for resistance to *Striga asiatica* and *S. hermonthica* and compatibility with *Fusarium oxysporum* f.sp. *strigae* (*FOS*) in Tanzania

Fifty-six genetically diverse maize genotypes were screened for resistance to *S. hermonthica* (*Sh*) and *S. asiatica* (*Sa*), and *FOS* compatibility. The experiment was laid out using a split-plot design; *FOS* as the main plot and maize genotypes are the sub-plot treatments, with three replications. Data on crop growth and grain yield parameters, and *Striga* incidence were collected. The major findings of the study were:

- ❖ Inoculation of maize seeds with *FOS* significantly ($P < 0.001$) enhanced both *Sh* and *Sa* management. This suggests that the test genotypes possess sufficient genetic variability from which selection of maize genotypes for resistance to *Sh* and *Sa* could be made.

- ❖ Compared to untreated controls, maize genotypes inoculated with *FOS* and evaluated in *Sh* infested soil had increased seed yield gains of 5.2%; and treated genotypes screened under *Sa* infestation had increased seed yields of 3.4%.
- ❖ Three principal components were important for both *FOS*-treated and untreated maize genotypes under *Sh* infestation, accounting cumulatively for 74.19% and 75.47% of the total variation, respectively.
- ❖ Likewise, under *S. asiatica* infestation, three principal components were important for untreated genotypes, accounting cumulatively for 77.47% of the total variance. In contrast, four principal components were important for *FOS*-treated genotypes accounting cumulatively for 82.08% of the total variance under the same condition.
- ❖ Twenty-three maize genotypes were identified with variable resistance to *Striga*, high grain yield, farmers preferred traits and *FOS* compatibility. These genotypes are useful genetic materials for developing *Striga* resistant cultivars in Tanzania.

6.2.3 Genetic diversity of maize genotypes with differential resistance to *Striga asiatica* and *S. hermonthica* based on phenotypic and simple sequence repeats markers

A set of 51 maize genotypes were assessed using phenotypic traits for resistance to *Striga asiatica* (*Sa*) and *S. hermonthica* (*Sh*) under controlled conditions. The test genotypes were further profiled using 10 diagnostic simple sequence repeat (SSR) markers to complement the phenotypic data.

The main findings of the study were:

- ❖ Significant ($P < 0.05$) genotypic variation was recorded among the test genotypes for key agronomic traits and resistance to *Striga* spp. The genetic variation indicates that test genotypes are diverse, and resistant genotypes could be selected for *Striga* resistance breeding in Tanzania.
- ❖ Significant ($P < 0.05$) correlations among phenotypic traits and *Striga* parameters were identified to guide direct or indirect selection.
- ❖ The mean PIC value was 0.73 with a range of 0.41 to 0.92, suggesting high allelic diversity among assessed maize genotypes.
- ❖ Analysis of molecular variance revealed that within genotypes variance, among genotypes variance, and population differences accounted for 66.8%, 32.6%, and 0.6% of the total genotypic variation, respectively.
- ❖ Cluster analysis based on morphological and molecular markers grouped the genotypes into three main groups, independent of their geographic origin.

- ❖ SSR markers showed that maize genotypes TZA2263 and JL08, TZA4320 and JL12, TZA4205 and JL20, TZA1780 and JL05, TZA2761 and JL01, TZA604 and JL18, TZA4010 and JL12 were the most genetically divergent pairs. These are valuable sources of genetic variation for *Striga* resistance breeding in Tanzania.

6.2.4 Progeny testing of maize (*Zea mays* L.) genotypes for yield and yield components, *Striga* resistance and *Fusarium oxysporum* f.sp. *strigae* compatibility

Twenty parental genotypes involving nine female parents selected for their *FOS* compatibility, adaptability, and farmer preferred traits, and 11 male parents possessing *Striga* resistance were crossed using a North Carolina Design II. The 99 experimental hybrids and three checks were field evaluated, with and without *FOS* treatment, at three *Striga*-infested sites in western Tanzania, using a 9 x 12 α -lattice design with two replications. Data on maize agro-morphological traits and *Striga* parameters were collected and processed.

Key findings were:

- ❖ There were significant ($P < 0.05$) effects for both the general and specific combining ability for the assessed maize agronomic traits and *Striga* parameters, with and without *FOS* treatment except for *Striga* damage ratings at eight and ten weeks after planting under *FOS* treatment. This finding suggests the importance of both additive and non-additive gene action.
- ❖ Additive gene action was more important than non-additive gene action. Recurrent selection methods, including S1 family and half-sib family selection with test crosses, could be adopted to improve the population for *Striga* resistance and grain yield.
- ❖ Hybrid x location interaction effect were significant ($P < 0.01$) for days to 50% anthesis, days to 50% silking, grain yield, *Striga* emergence count eight, and 10 WAP with and without *FOS* treatment, and *Striga* damage rating eight and 10 WAP without *FOS* inoculation.
- ❖ *FOS*-treated progenies had fewer emerged *Striga* plants than untreated controls, suggesting the efficacy of *FOS* in controlling *Striga*.
- ❖ Parental genotypes SITUKA M1, TZA4010, TZA4016, TZA4203, JL01, JL05, JL13, and JL17 showed negative GCA effects for all *Striga* parameters and relatively positive GCA effects for grain yield in a desirable direction.
- ❖ Maize hybrids TZA4010xJL13, TZA4010xJL05, TZA1780xJL18 were selected for their desirable grain yield and *Striga* resistance.
- ❖ The progenies TZA2263xJL13 and TZA4203xJL18 were selected for *Striga* resistance.

- ❖ The new progenies are recommended for *Striga* resistance breeding in Tanzania or similar agro-ecologies.

6.3 Implications of the research findings for breeding and *Striga* management

- ❖ Farmers use hand-hoe weeding and uprooting/hand-picking *Striga* plants like other weed spp. and place their residues at the farm border. This shows a lack of education on appropriate technologies for *Striga* control. Farmers` awareness creation on the biology of *Striga*, improvement of the linkage between farmers and agricultural extension officer/agent is essential.
- ❖ Given the lack of an efficient seed delivery system in the study area, community seed production should be initiated to provide farmers with affordable seed of improved maize varieties with *Striga* resistance and FOS compatibility.
- ❖ Breeding of new maize varieties to meet farmers` preferences would target *Striga* and drought resistance, FOS compatibility, and farmer preferred traits like earliness and good milling qualities.
- ❖ FOS applications to maize seed is effective in controlling *Striga* infestation, reducing the number of emerged *Striga* plants and reducing the levels of *Striga* damage, thus improving maize yields. Therefore, the integrated use of FOS with *Striga* resistant maize genotypes and farmer-compatible agronomic practices could form an effective suite of *Striga* control options for farmers in Tanzania.
- ❖ Maize genotypes with partial resistance to *S. asiatica* and *S. hermonthica* and FOS compatibility were identified among Tanzanian landraces. The identified maize genotypes are useful genetic resources for *Striga* resistance breeding and integrated *Striga* management in Tanzania.
- ❖ Phenotypic profiling of maize genotypes, complemented with SSR markers, revealed adequate levels of genetic variability among the studied genotypes for breeding purposes. Diverse genotypes, identified by genetic and phenotypic clustering, could be used for *Striga* resistance breeding in Tanzania and elsewhere.
- ❖ Both additive and non-additive gene effects were detected as influencing maize agronomic traits and *Striga* resistance-related parameters, which is relevant to the breeding strategies adopted for genetic improvements, ideally through hybrid breeding and recurrent selection