# Genetic Analysis of *Striga* Resistance and Yield-influencing Traits in Tropical and Sub-tropical Maize

**By**

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**Thesis summary**

Maize (*Zea mays* L., 2n = 2x = 20) is a vital food security and economic crop in sub-Saharan Africa (SSA) and globally. In SSA maize production is challenged by an array of biotic and abiotic stresses. Two parasitic weeds belonging to the genus *Striga*, *S. hermonthica* (Del.) Benth (*Sh*) and *S. asiatica* (L.) Kuntze (*Sa*) causes marked yield losses varying from 10% to 100% in susceptible maize cultivars. *Striga*-resistant maize varieties released so far had partial or moderate resistance and were bred for *Sh* resistance only. There are therefore no commercially grown maize varieties with *Sa* resistance requiring to develop new-generation maize varieties with durable *Sa* and *Sh* resistance and wide adaptability using genetically diverse tropical and subtropical genetic resources and genomic resources. The overall objective of this study was therefore, to improve maize resistance to *Sa* and *Sh* by harnessing genetic diversity and identifying markers and genes for resistance breeding. The overall hypothesis of the study was that novel genetic resources, genetic markers and genes associated with *Sa* and *Sh* resistance could be identified for dual *Striga* resistance for maize breeding programs.

The study had further five specific objectives:

1) To undertake a meta-analysis and provide a detailed comparison of the *Striga* control methods in the production of maize, sorghum, and the major millets as a guide to effective *Striga* management.
2) To assess the response of 130 tropical and sub-tropical African maize germplasm to *Sh* and *Sa* resistance and desirable agronomic traits and select promising genotypes.
3) To determine the genetic diversity of 130 tropical and sub-tropical maize inbred lines, hybrids, and open-pollinated varieties using phenotypic traits and single nucleotide polymorphism (SNP) markers to select *Striga*-resistant and complementary genotypes for breeding.
4) To determine the combining ability and gene action controlling grain yield and *Striga* resistance among single crosses of maize to select desirable hybrids with *Sh* and *Sa* resistance and promising agronomic traits.
5) To undertake a genome-wide association analysis of grain yield and *Sh* and *Sa* resistance among tropical and sub-tropical maize populations to identify putative genetic markers and genes for marker-assisted resistance breeding and gene pyramiding.

In the first part of the study, a meta-analysis was conducted on already reported *Striga* control methods on the major cereal crops (i.e., maize, sorghum, and millets) using 66 research articles. The data collected included grain yield (GY), *Striga* emergence count (SEC), and *Striga* damage rating (SDR). The search showed mean yield for maize varieties with *Striga*-resistant genes at 2053.00 kg $ha^{-1}$, ranging from 281.00 to 6260.00 kg $ha^{-1}$, and a mean SDR of 4.70, varying from 2.00 to 7.00. Likewise, sorghum varieties with *Striga* resistance genes achieved greater GY with a mean yield response of 1738.00 kg $ha^{-1}$, ranging from 850.00 to 2162.00 kg $ha^{-1}$. A relatively low GY was achieved in maize and sorghum production when deploying integrated *Striga* management (ISM) (e.g., cultural control + host resistance, and host resistance + chemical herbicides) and chemical *Striga* control. The outcome of this part of the study was that SDR is the best selection criterion for improving GY performance in maize, while SEC and SDR were the parameters of choice in sorghum selection programs for better GY under *Striga* infestation. The meta-analysis revealed that host resistance is the most effective method for controlling *Striga* infestation and boosting GY in maize and sorghum.

The second part of the study focused on screening 130 tropical and sub-tropical maize germplasms, including checks, in a controlled environment for their reaction to *Sh* and *Sa* infestations using a 13×10 alpha lattice design with two replications over two seasons. The following data were collected on maize: days to 50% silking (DS), days to anthesis (DA), anthesis-silking interval (ASI), plant height (PLHT), ear height (EHT), Root lodging (RL), the number of ears per plant (EPP), husk cover (HUSK), ear aspect (EASP), and grain yield per plant (GY/plant). *Striga* parameters included the number of emerged *Sa* and *Sh* plants 8 and 10 weeks after planting, denoted as SEC8 and SEC10, and host plant damage by *Striga* 8 and 10 weeks after planting, designated as SDR8 and SDR10. The mean yield of maize and *Striga* parameters differed from one *Striga* species to the other. Under *Sa*-infested conditions, the mean SEC8 and SEC10 were 5.00 and 45.50, respectively, while the mean SDR8 and SDR10 were 3.35 and 3.07, respectively. Under *Sh*-infested conditions, SEC8 and SEC10 mean values were 3.66 and 3.77, respectively, while the SDR8 and SDR10 values were 5.25 and 2.75 respectively. The results suggested that dual resistance to the two *Striga* species exists in some tropical and sub-tropical maize lines. The study selected genotypes CML440, CML566, CML540, CML539, CLHP0343, CLHP0326, TZISTR1248, TZSTRI115, TZISTR25, TZISTR1205, TZSTRI113, TZISTR1119, TZISTR1174 and the OPVs B.King/1421, Shesha/1421, ZM1421, DTSTR-WSYN13, DTSTR-YSYN14, and 2*TZECOMP3DT/WhiteDTSTRSYN) C2 with dual resistance to *Sa* and *Sh*. These genotypes

are suitable for use as parents in developing high-performing maize varieties with *Striga* resistance and improved grain yield.

The third part of the study assessed the genetic diversity of 130 tropical and sub-tropical maize inbred lines, hybrids, and open-pollinated varieties using *Striga* resistance and agronomic traits, and SNP markers. The SNP markers demonstrated that the test genotypes had an average gene diversity of 0.34 and a polymorphic information content of 0.44, indicating significant phenotypic variation. Significant variation was recorded within populations (85%) compared to between populations using the analysis of molecular variance. The structure analysis allocated the test genotypes into eight major clusters (K = 8) in concordance with the principal coordinate analysis (PCoA). The following genetically distant inbred lines were selected, displaying good agronomic performance and *Sa* and *Sh* resistance: CML540, TZISTR25, TZISTR1248, CLHP0303, TZISTR1174, TZSTRI113, TZDEEI50, TZSTRI115, CML539, TZISTR1015, CZL99017, CML451, CML566, CLHP0343 and CML440. The new selections will now facilitate the breeding of maize varieties with *Striga* resistance and market-preferred traits.

In the fourth part of the study, a combining ability analysis was undertaken to determine the mode of gene action regulating *Sa* and *Sh* resistance and to select good combiner parental maize lines for hybrid breeding. Four preliminarily selected tropical high-yielding and *Sh*-resistant testers and eight sub-tropical lines with *Sa* resistance were crossed using a line-by-tester mating design, and 32 single cross hybrids were generated. The crosses and their parents were evaluated under field and controlled environments during the 2023/2024 growing season using a 7 x 6 alpha lattice design with two replications. Combined analysis of variance revealed a significant ($p \leq 0.05$) effect of the crosses on grain yield (GY), related agronomic traits, *Striga* emergence counts, and *Striga* damage rating 8 and 10 weeks after sowing. The ratio of the general combining ability effect (SCA) and the specific combining ability effect (SCA) was less than one for all the traits, indicating the predominance of non-additive genetic effects in trait inheritance and signifying the value of hybrid breeding. The best general combiner tester was TZISTR1248 in the *Sa*-infested environment, while tester TZISTR1174 was noteworthy under *Sh* environment. Lines CML540 and CLHP0343 were the best combiners in *Sa* environment, while CZL99017, CML566, CML540, and CLHP0343 were promising in *Sh* environment and CML540 was the best general combiner in all test environments. The crosses CML540 x TZISTR1174, CML540 x TZDEEI50, and CML539 x TZISTR1174 exhibited high

yields, significant SCA effects, and high heterosis for GY in *Sa* environment. Whereas, in *Sh* environment, cross CML440 x TZDEEI50 had the best GCA effect and heterosis for GY. Crosses CML451 x TZISTR1174, CML539 x TZISTR1174, CML440 x TZDEEI50, CML566 x TZDEEI50, CZL99017 x TZISTR1248, and CML539 x TZISTR1248 were relatively the best specific combiners for GY in both *Sa* and *Sh* environments. The selected lines and testers and the new experimental hybrids are recommended for multi-environment evaluation in *Sa* and *Sh*-prone agroecologies to enhance grain yield and *Striga* resistance.

In the fifth final part of the study, a genome-wide association analysis of grain yield and *Sh* and *Sa* resistance among tropical and sub-tropical maize populations was undertaken to identify putative genetic markers and genes for resistance breeding. The test genotypes were profiled for GY, SEC8, SEC10, SDR8, and SDR10. Population structure analysis and genome-wide association mapping were undertaken based on 16,000 single nucleotide polymorphism (SNP) markers using the Diversity Array Technology Sequencing platform. The genome-wide association study identified 50 significant loci associated with *Sh* resistance and 22 significant loci linked to *Sa* resistance, corresponding to 39 and 19 candidate genes, respectively. No significant loci were found associated with dual resistance, suggesting that breeding maize must be specific for resistance to each *Striga* species using germplasm adapted to the endemic region of each parasite.

Overall, the study finally revealed a novel result that host resistance is the most effective method for controlling *Striga* infestation and boosting GY despite that research institutions advocate integrated *Striga* management. Promising genotypes with *Sa* and *Sh* resistance were selected, and some tropical and sub-tropical genotypes showed dual resistance. Suitable parental lines and testers and new experimental hybrids were selected for *Sa* and *Sh* resistance breeding in SSA. The new selections could be explored for future *Striga* resistance breeding and the development of new varieties. Significant loci associated with *Sh* and *Sa* resistance with their corresponding genes were detected and could be used to facilitate selection for *Sh* and *Sa* resistance and GY in tropical and sub-tropical maize genetic resources.

## Declaration

I, Nanou Emeline Dossa, declare the following.

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.

4. This thesis does not contain other persons' writing, unless specifically acknowledged as being sourced from other researchers. Where other written sources have been quoted, then:

a. Their words have been re-written but the general information attributed to them has been referenced.

b. Where their exact words have been used, then their writing has been placed in italics and inside quotation marks, and referenced.

5. This thesis does not contain text, graphics or tables copied and pasted from the Internet, unless specifically acknowledged, and the source being detailed in the thesis and in the references sections.

Signed

**Nanou Emeline Dossa**

As the candidate's supervisor, I agree to the submission of this thesis:

**Prof. Hussein Shimelis** (Supervisor)

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- Most importantly, I am grateful and give glory to God for granting me the opportunity to pursue my studies and reach this stage in my life. I recognize that this achievement would not have been possible without his favour and intervention.

## Dedication

To

My mother, **Julienne Towadè,** and in memory of my late father, **Paul Dossa**

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## Publications emanating from the thesis

**Chapter 1:**

Dossa, E. N., Shimelis, H., Shayanowako, A. I. T., and Laing, M. D. (2023). A meta-analysis of the effects of *Striga* control methods on maize, sorghum, and major millets production in sub-Saharan Africa. Crop Science, 1-20. Doi: https://doi.org/10.1002/csc2.20889

**Chapter 2:**

Dossa, E. N., Shimelis, H., Shayanowako, A. I. T., and Laing, M. D. (2024). Screening tropical and sub-tropical maize germplasm for resistance to *Striga hermonthica* and *S. asiatica* and yield-related traits. Euphytica **220**: 1-23. Doi: https://doi.org/10.1007/s10681-024-03309-2

**Chapter 3:**

Dossa, E. N., Shimelis, H., and Shayanowako, A. I. T. (2024). Genetic diversity analysis of tropical and sub-tropical maize germplasm for *Striga* resistance and agronomic traits with SNP markers. PLoS One **19**, 1-21. Doi: https://doi.org/10.1371/journal. pone.0306263

**Chapter 5:**

Dossa, E. N., Shimelis, H., and Shayanowako, A. I. T. (2024). Genome-wide association analysis of grain yield and *Striga hermonthica* and *S. asiatica* resistance in tropical and sub-tropical maize populations. BMC Plant Biology **24**, 1-16. Doi: https://doi.org/10.1186/s12870-024-05590-8

## Background of study

Maize (*Zea mays* L., 2n = 2x = 20) is the major cereal crop worldwide, contributing to 30–70% of daily human calorie requirements (Kamara et al., 2005; Yacoubou et al., 2021). The annual global production of maize was estimated at 1,163,497,383.13 tons in 2022 (FAOSTAT, 2024). The main maize producers are the United States of America (348,750,930 tons), China (277,415,553.14 tons), Brazil (109,420,717 tons), Argentina (59,037,179 tons), India (33,729,540 tons), Mexico (26,625,693.83 tons), Ukraine (26,186,930 tons) accounting for 66% of the global production per annum (FAOSTAT, 2024). In Africa, annual maize production was estimated at 92,800,971.58 tons in 2022, representing 7.98% of the world's production (FAOSTAT, 2024). South Africa is the largest maize producer in Africa, with an estimated annual output of 16,137,000 tons, followed by Nigeria (12,948,920 tons), Ethiopia (10,200,000 tons), Egypt (7,500,000 tons), and Kenya (3,087,000 tons) (FAO, 2024).

In sub-Saharan Africa (SSA), 14 countries have the highest per capita consumption of maize (Ranum et al., 2014). For instance, in Benin, the mean per capita consumption of maize per annum is 85 kg. Maize is cultivated in all agroecological zones in Africa on small landholdings varying between 0.5 and 2 hectares (ha) (Achigan-Dako et al., 2014). Sub-Saharan Africa has the lowest maize yields globally, estimated at 3 tons/hectare (FAO 2022), compared to global mean yields of 5 to 10 tons $ha^{-1}$ (FAO 2022). The low productivity of maize and major crops in SSA is attributable to an array of production constraints, including biotic factors (e.g. parasitic and competitive weeds, field and storage insect pests, and pre-and post-harvest diseases) (Cairns et al., 2013; Rachidatou et al., 2018; Yacoubou et al., 2021), and abiotic factors including heat and drought stresses and poor soil fertility (Ali et al., 2015; Cairns et al., 2013). Heat and drought stress and low soil fertility are the common abiotic challenges affecting maize productivity throughout the region (Badu-Apraku and Fakorede, 2017; Lobulu et al., 2019), predisposing major cereal and legume crops to parasitic weeds of the genus *Striga*.

Forty *Striga* species have been reported worldwide (Gethi and Smith, 2004; Reda and Verkleij, 2004). Among these, 33 species have been reported in Africa, and 11 affect major grain crops (Ejeta et al., 2007; Gethi and Smith, 2004). *Striga hermonthica* (Del.) Benth and *S. asiatica* (L.) Kuntze are the most economically important in cereal production systems. *Striga hermonthica* is present in most sub-Saharan African regions, affecting cereal production in

Western, Central, and Eastern African countries, while *S. asiatica* is predominant in Southern Africa (Figure 0.1) (Ejeta and Gressel, 2007; Parker, 2012; Shayanowako et al., 2018a).

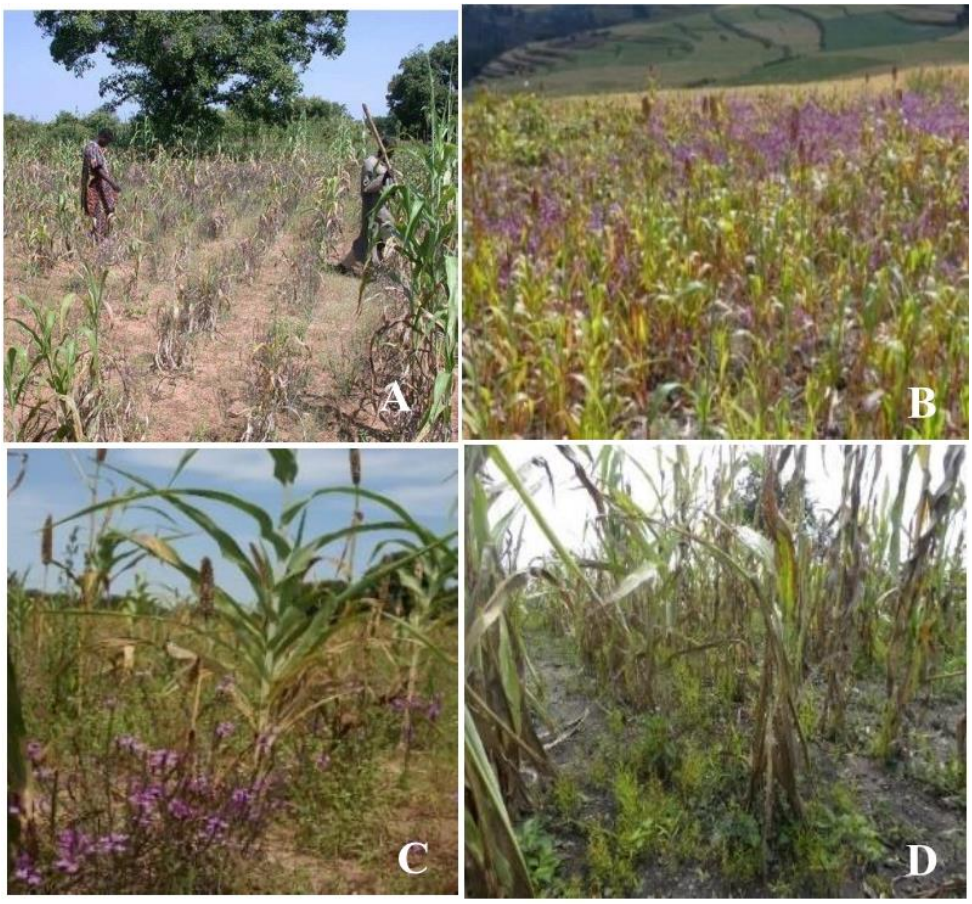


**Figure 0.1** *Striga hermonthica* infested-maize in Benin (A), sorghum in Ethiopia (B), pearl millet in Burkina-Faso (C), and *S. asiatica* infested maize in Tanzania (D). (Photo A supplied by EN Dossa, B by H Shimelis, C by S Al-Babili, and D by E Mrema).

Unlike sorghum, which has co-evolved with *Striga* in Africa, maize is exceptionally susceptible to the parasite, particularly in marginal and low input production environments (Adewale et al. 2020; Badu-Apraku et al. 2020a; Shayanowako et al. 2020). Maize yield losses exceeding 60% are common under *Striga* infestation (Jamil et al., 2012; Lobulu et al., 2019). The *Striga*-infested area in SSA is estimated to be 2.4 million hectares, leading to a yield loss of 1.6 tons per year with a monetary value US$ 383 million (Woomer et al., 2008).

Methods to control *Striga* include cultural practices, chemical herbicides, and biological agents. However, these are often inaccessible, unavailable or inadequate (Shayanowako et al., 2018b). Smallholder farmers often resort to manual weeding, which is ineffective because most of the damage to the maize plant occurs before the parasitic plants emerge (Ejeta, 2007; Stanley

et al., 2021). There is little use of selective herbicides in the region because of the high cost and the complex cropping systems (e.g., intercropping cereals and legumes) (Hearne, 2009). The use of host resistance against *Striga* parasitism is widely favoured because of its cost-effectiveness, safety, and practicality, making it readily deployable in low-input maize production environments (Adu et al., 2019; Badu-Apraku et al., 2016). There is a need to identify new sources of *Striga* resistance and quantitative trait loci (QTL) associated with *Striga* resistance and economic traits to guide the pace and precision of resistance breeding in maize. Breeding maize varieties resistant to *Striga* will significantly improve maize productivity in SSA.

Breeders in SSA strive to develop maize genotypes that are either (i) resistant, inhibiting or allowing few *Striga* seeds to germinate and attach onto the host roots through low production of strigolactones, root barriers for incompatibility, and hypersensitive and antibiosis reactions toxic to the parasite, or (ii) tolerant by being insensitive to high levels of parasitic attachments with minimum yield loss. However, only partial resistance has been reported so far (Shayanowako et al., 2018a). Also, most available resistant varieties have been bred for *Sh* resistance, while both *Sh* and *Sa* are challenging for maize production in the region. Moreover, the two *Striga* species occur in tandem, mainly in East Africa (Lobulu et al., 2021).

Tropical and sub-tropical germplasm with dual resistance will be valuable for controlling *Striga* in the continent. Hybrid breeding effectively combines genes from *Striga*-resistant inbred lines to exploit heterosis. *Striga asiatica* and *Sh*-resistant genes could be accumulated in hybrids or recurrent populations using hybridization. Therefore, genetic profiling and diversity analyses among the tropical and sub-tropical gene pool lines are the overriding considerations for breeding (Reif et al., 2005). Information on the genetic effects and mode of inheritance for yield and yield-influencing traits, and *Striga* resistance traits, are crucial to designing and deploying high-performing hybrids and open-pollinated varieties. This is achieved through effective genetic evaluation and general combining ability (GCA) and the specific combining ability (SCA) analyses of the available inbred lines in hybrid combinations.

Developing new maize hybrid varieties through conventional breeding can take more than 10 years. Integrating complementary modern plant breeding methods (e.g. marker-assisted selection, quantitative trait loci (QTL) analysis, next-generation sequencing, and genome editing) can enhance variety development through the demand-led breeding approach (Matova et al., 2022). Genomic tools such as molecular markers help identify, locate, and map genes

responsible for economic traits such as *Striga* resistance and agronomic traits in maize. With rapid genome-wide, high-density marker data using high-throughput and next-generation sequencing technologies, genome-wide association studies (GWAS) have become a standard tool for identifying resistance genes and loci (Adewale et al., 2020). GWAS, also known as whole-genome association study (WGAS), identifies genomic regions controlling quantitative economic traits (Adewale et al., 2020). It involves collecting a genetically diverse sample population, phenotyping, genotyping, and testing the association between phenotypes and genotypes using statistical approaches. GWAS is used to evaluate the association between each genotyped marker and a phenotype of interest that has been scored across many individuals to guide marker-assisted selection (MAS) (Korte and Farlow, 2013).

Few studies have reported on QTL and genes linked to *Sh* resistance in maize using GWAS. It is worth noting that none of the QTL and genes available today are related to *Sa* resistance except the single nucleotide polymorphism (SNPs) reported by (Pfunye et al., 2021) based on total emerged *Striga* plants. The availability of genes linked to the resistance of both *Sa* and *Sh* will facilitate the use of genetic engineering and gene editing for *Striga* resistance maize development as novel strategies to control the parasitic weeds in the continent. Therefore, there is a need to identify unique *Sa* and *Sh* resistance genes or QTL that confer durable resistance to maize using GWAS. With the ongoing advancements in high-throughput DNA sequencing technology and the continuous expansion of "omics" databases, identifying valuable *Striga* resistance traits for genome editing in maize is becoming increasingly important.

**Rational of the study**

The two *Striga* species, *Sh* and *Sa* are often referred to as witchweeds due to their heavy crop damage. Both species are the leading impediments to maize yield losses in SSA. Several control measures were reported to control the weeds in the field, but most of them are beyond the means of many smallholder farmers. Breeding maize for *Sa* and *Sh* is the most economical and environmentally friendly approach that smallholder maize producers can adopt for sustainable use. *Striga* resistance varieties were reported, but most were partial or moderately resistant and bred for *Sh* resistance, while no commercially grown varieties are resistant to *Sa*. Hence, there is a need for new sources to breed *Striga*-resistant maize with desirable product profiles. Understanding the genetic composition and profile of *Striga* resistance and yield-related traits in a tropical and sub-tropical maize gene pool and derived hybrids is a prerequisite

for *Striga* resistance breeding programs. Also, hybrid vigour is achieved by crossing inbred lines from complementary heterotic groups. Therefore, detailed information on genetic diversity, genetic interrelationship, and heterotic groups is needed for parental choice for effective *Striga* resistance breeding. To exploit heterosis in hybrid breeding, knowledge of combining ability and gene action of contrasting parents through progeny testing is crucial. This will allow maize breeders to discern best inbred lines that contribute unique and contrasting multiple alleles towards the desirable performance of a progeny or hybrid. Identifying QTL linked to *Sa* and *Sh* resistance is a precondition for marker-assisted and precision selection and accelerates cultivar development with desirable market profiles. The available QTL for *Striga* resistance in maize are associated to *Sh* resistance only. Also, most *Striga*-resistance QTL were detected from a biparental population with low mapping resolution, which needed further fine mapping to achieve higher resolution and accuracy. There is a need to identify genetic markers associated with both *Sa* and *Sh* using GWAS for MAS and deploy *Striga*-resistant maize with wide adaptability in the region.

**Overall research goal**

The overall goal of the study was to identify novel genetic resources, genetic markers, and genes associated with *Sa* and *Sh* resistance in tropical and sub-tropical maize for dual *Striga* resistance in maize hybrids.

**Specific objectives**

1) To undertake a meta-analysis and provide a detailed comparison of the *Striga* control methods in the production of maize, sorghum, and the major millets as a guide to effective *Striga* management spearheaded by resistance breeding.

2) To assess the response of 130 tropical and sub-tropical African maize germplasm to *Sh* and *Sa* resistance and desirable agronomic traits and select promising genotypes to develop experimental hybrids.

3) To determine the genetic diversity of 130 tropical and sub-tropical maize inbred lines, hybrids, and open-pollinated varieties using phenotypic traits and single nucleotide polymorphism (SNP) markers to select *Striga*-resistant and complementary genotypes for single-cross hybrid breeding.

4) To determine the combining ability and gene action controlling grain yield and *Striga* resistance among selected parents and single crosses of maize to select desirable parents and new hybrids with *Sh* and *Sa* resistance and promising agronomic traits to recommend breeding parents and new single crosses.

5) To undertake a genome-wide association analysis of grain yield and *Sh* and *Sa* resistance among tropical and sub-tropical maize populations to identify putative genetic markers and genes for marker-assisted resistance breeding and gene pyramiding for durable resistance and gene deployment.

**Hypotheses**

The overall hypothesis of the study was that novel genetic resources, genetic markers and genes associated with *Sa* and *Sh* resistance could be identified for dual *Striga* resistance maize breeding programs. The specific hypotheses were:

1) Effective *Striga* management options will be discerned to improve crop yield under *Striga* infestation.

2) There are promising tropical and sub-tropical African maize genotypes that exhibit better agronomic performance and resistance to *Sa* and *Sh* to select dual sources of resistance.

3) When assessed using phenotypic traits and single nucleotide polymorphism markers, there is sufficient genetic variation among the tropical and sub-tropical maize inbred lines, hybrids, and open-pollinated varieties germplasm for breeding.

4) When evaluated under *Sa* and *Sh* infestation, there are parental lines and single crosses with high combining ability for *Striga* parameters, yield, and yield-related traits.

5) Markers and genes controlling *Sa* and *Sh* in maize are detected using GWAS in genetically diverse tropical and sub-tropical maize populations.

**Outline of thesis**

This thesis consists of five different chapters in accordance with the number of objectives (Table 0.1). Chapter 1 is written as a separate review paper, while Chapters 2 to 5 are written as discrete research chapters, which follow the format of a stand-alone research paper. This is the dominant thesis format adopted by the University of KwaZulu-Natal. Consequently, there is some unavoidable repetition of references and introductory information between chapters. The referencing system used in this thesis chapter is adopted by the journal that published the papers. Chapter 1 was published in Crop Science doi: https://doi.org/10.1002/csc2.20889; Chapter 2 in Euphytica https://doi.org/10.1007/s10681-024-03309-2; Chapter 3 in PLOS One https://doi.org/10.1371/journal. pone.0306263, and Chapter 5 in BMC Plant Biology https://doi.org/10.1186/s12870-024-05590-8. Chapter 4 is under review in Plant Breeding.

For each chapter, as the PhD candidate, I contributed to conceptualising the study ideas, served as principal investigator, conducted the field and glasshouse experiments and collected the data independently. I performed the data analysis, wrote the original drafts, and handled the reviewing and editing process. Additionally, I was the corresponding author for each published paper resulting from this thesis.

**Table 0.1** Thesis structure

| Chapter | Title |
|---|---|
| - | Introduction To Thesis |
| **1** | Literature Review: A Meta-analysis of the Effects of *Striga* Control Methods on Maize, Sorghum, and Major Millets Production in Sub-Saharan Africa. |
| **2** | Screening Tropical and Sub-tropical Maize Germplasm for Resistance to *Striga hermonthica* and *S. asiatica* and Yield-related Traits. |
| **3** | Genetic Diversity Analysis of Tropical and Sub-tropical Maize Germplasm for *Striga* Resistance and Agronomic Traits with SNP Markers. |
| **4** | Genome-wide Association Analysis of Grain Yield and *Striga hermonthica* and *S. asiatica* Resistance in Tropical and Sub-tropical Maize Populations. |
| **5** | Progeny Testing of Tropical and Sub-tropical Maize Lines for Grain Yield and *Striga* Resistance. |
| - | General Overview |

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# A meta-analysis of the effects of *Striga* control methods on maize, sorghum, and major millets production in sub-Saharan Africa


## Abstract

Parasitic *Striga* weeds severely damage cereal crops in sub-Saharan Africa (SSA), leading to yield losses in susceptible varieties. A range of *Striga* control methods are commonly recommended, including cultural practices, chemical herbicides, biological control agents, and host resistance, either solo treatments or in combinations of these approaches (i.e., integrated *Striga* management [ISM]). A limited number of studies compared the relative efficacy of the recommended *Striga* control methods, or their combinations for ISM, in cereal crop production in SSA. The objective of this part of the study was to undertake a meta-analysis to provide a detailed comparison of the *Striga* control methods in the production of maize, sorghum, and the major millets, as a guide to effective *Striga* management. The study was conducted as a meta-analysis of 66 research articles that have been so far reported on various control measures. The following agronomic data were collected: grain yield (GY) response of the assessed crops and *Striga* parameters such as damage rating score (SDR) and emergence count (SEC). Maize varieties possessing *Striga*-resistant genes displayed high mean yield values at 2053.00 kg $ha^{-1}$, varying from 281.00 kg $ha^{-1}$ to 6260.00 kg $ha^{-1}$, and a mean SDR of 4.70, ranging from 2.00 to 7.00. Likewise, sorghum varieties with *Striga* resistance genes achieved greater GY with a mean yield response of 1738.00 kg $ha^{-1}$, ranging from 850.00 kg $ha^{-1}$ to 2162.00 kg $ha^{-1}$. A relatively low GY was achieved in maize and sorghum production when deploying ISM (e.g., cultural control + host resistance and host resistance + chemical herbicides), and chemical *Striga* control. Effective ISM and pre-and post-emergent herbicides have not yet been identified for *Striga* control and yield gains. *Striga* damage negatively affected GY in maize, as revealed by a significant correlation ($r=-0.36$, $P<0.001$) between GY and SDR. A relatively weak correlation was also found in maize between GY and SEC ($r=0.003$, $P=0.96$). Sorghum GY further negatively correlated with SEC, although non-significantly ($r=-0.30$, $P=0.36$). Few studies have evaluated *Striga* control methods in pearl millet and finger millet, limiting the opportunity for an effective comparison. The study recommends SDR as the best selection criterion for improving GY performance in maize, while SEC and SDR are the parameters of choice in sorghum selection programs for better GY under *Striga* infestation. The meta-analysis indicates that host resistance is the most effective method for controlling *Striga* infestation and boosting GY in maize and sorghum. There is an ongoing need for research into the best combinations of the reported control methods as a sound basis for the recommendation of an ISM package across target production environments of common cereals in Africa.



**Keywords:** cereal crops, meta-analysis, Integrated *Striga* Management, ISM, *Striga* control methods, *Striga* parameters

## 1.1 **Introduction**

Maize (*Zea mays* L.), rice (*Oryza sp.*), sorghum (*Sorghum bicolor* [L.] Moench), pearl millet (*Pennisetum glaucum* L.), and finger millet (*Eleusine coracana* L.) are key cereal crops globally (Sarwar 2013; Macauley 2015). In sub-Saharan Africa (SSA), the socio-economic role of maize is comparable to that of rice or wheat in Asia (Macauley 2015). Maize, sorghum, pearl millet, and finger millet are major food security crops in Africa, feeding more than 500 million people (Taylor 2003; Sarwar 2013; Macauley 2015). Despite the economic importance of the common cereals, their productivity in SSA is low due to various production constraints. Parasitic *Striga* weed species cause severe yield losses ranging from 10% to 100% (Sibhatu 2016). Reportedly, more than 35 species of parasitic weeds in SSA affect cereal crops. Nevertheless, *Striga hermonthica* (Del.) Benth. and *S. asiatica Striga asiatica* (L.) Kuntze are the most widespread and economically significant species causing yield losses varying from 10 to 100% in SSA (Badu-Apraku et al. 2020a). *Striga hermonthica* is widely found in most SSA regions and is reported in Western, Central, and Eastern Africa. *Striga asiatica* is predominantly found in the Southern Africa sub-region (Ejeta and Gressel 2007; Parker 2012; Shayanowako et al. 2018).

Various *Striga* control options have been reported, including cultural practices, chemical herbicides, host resistance, biological agents (bioherbicides), and a combination of two or more methods in an integrated *Striga* management (ISM) package (Rich and Ejeta 2008; Jamil et al. 2021; Yacoubou et al. 2021). Most cultural control practices aim to enhance soil fertility. *Striga* parasites thrive in low-fertility soils with a low cation exchange capacity (Adewale et al. 2020). Crop rotation, intercropping, catch-cropping, trap-cropping, and the application of organic and inorganic fertilizers are some of the recommended cultural practices for *Striga* management. Most cultural practices are fairly effective and are used in smallholder farming systems. However, they are tedious and require labor and resources. For example, 5 to 7 tonnes per hectare of livestock manure is required every two years to raise the soil's fertility and pH, and to suppress *Striga* (Weill and Duval 2009). Also, monoculture systems affect the implementation of cultural practices such as crop rotations and relay croppings (Kureh et al. 2006; Manyong et al. 2008). Biological control, such as the use of fungal pathogens, has been highly effective in hindering *Striga*'s germination, growth, and development. Selected strains of *Fusarium oxysporum f.sp. strigae* (FOS) are an important biological control agents. The efficacy of *FOS* in suppressing *Striga* infestation in sorghum and maize has been reported in

Ethiopia (Rebeka et al. 2013), Tanzania (Mrema et al. 2017), and South Africa (Shayanowako et al. 2020). However, not all strains of *FOS* are effective in controlling *Striga* infestations. In western Kenya, Avedi et al. (2014) reported that the *FOS* strain Foxy 2 did not suppress *S. hermonthica*. In contrast, Nzioki et al. (2016) in Kenya deployed an effective *FOS* strain, Foxy T14, a readily available and inexpensive control method for smallholder farmers.

Chemicals such as ethylene, and ethephon, when applied on cultivated lands before the sowing of the major crop, can trigger suicidal seed germination of *Striga*, resulting in a reduced soil seed bank of *Striga* seeds (Esilaba et al. 2000). Pre-emergent herbicides, including imidazolinones and sulfonylureas, are effective in *Striga* control. For example, seed treatment with imazapyr at a low dose suppresses *Striga* in maize and sorghum production for impazapyr-resistant cultivars (Kabambe et al. 2008; Tesso and Ejeta 2011). Herbicides such as 2,4-D can effectively control the parasite post-emergence (Eplee and Norris 1987; Kanampiu et al. 2002). However, environmental, and human safety concerns limit the use of herbicides. In addition, smallholder farmers often intercrop legumes and cereals, forestalling the uptake of selective herbicides.

Host resistance is one of the sustainable *Striga* control strategies available for low-input farming systems. *Striga*-resistant and tolerant crop cultivars are increasingly bred in Africa and Asia. The Consultative Group of International Agriculture Research (CGIAR) has championed *Striga* resistance breeding in SSA since the mid-1980s (Manyong 2000). For instance, the International Institute of Tropical Agriculture (IITA)/Nigeria has bred maize hybrids and open-pollinated cultivars with durable resistance to *S. hermonthica* for the west and central Africa region. Likewise, the International Crop Research Institute for the Semi-Arid Tropic (ICRISAT)/India has reported genetic gains for *Striga* resistance in sorghum. However, limited research and development efforts have been made in improving *Striga* resistance in pearl millet and finger millet. *Pennisetum glaucum* subsp. *monodii,* a wild progenitor of pearl millet, reportedly possesses *Striga* resistance genes, making it a candidate donor parent in resistance breeding programs (Wilson et al. 2000). Pearl millet landraces such as M141, M239, M029, M197, M017, and KBH have been reported to possess *Striga* resistance genes (Kountche et al. 2013). No studies were conducted on *Striga* resistance in other millets, including finger millet (Kountche et al. 2016).

*Striga* resistance is polygenic, and breeding gains are confounded by several constraints, including the variable *Striga*/host interaction and response, the influence of

genotype by environment interactions, and the involvement of additive and non-additive genes (Rich et al. 2004; Wilson et al. 2004; Menkir and Kling 2007). The *Striga* genome project (http://ppgp.huck.psu.edu/) could provide current and future opportunities for genetic resistance breeding programs (Westwood et al. 2017). The RNA interference (RNAi) technology has been explored as a genetic tool for engineering host resistance against parasitic weeds. The approach has been to transform host plants with a plasmid encoding a double-stranded hairpin RNA (hpRNA) targeted against one or more genes of *Striga* (Yoder et al. 2009; Runo et al. 2011).

The efficacy of a *Striga* control method is determined by its effect on three primary indices: host grain yield (GY), *Striga* damage rating (SDR), and *Striga* emergence count (SEC) (Olivier et al. 1991; Badu-Apraku et al. 2020c). These indices have been used extensively in studies involving *Striga* and host interactions. The *Striga* control methods described above have achieved varying levels of efficacy against the parasites in cereals. The control methods' interplay and efficacy have not been well documented and compared. Also, there is a lack of consensus regarding the most effective and reliable control method because no single control method has been developed that can effectively manage the parasites (Kountche et al. 2016; Sibhatu 2016). Additionally, the most effective and optimized ISM combinations remain unknown. In light of the above background, the objective of this part of the study was to undertake a meta-analysis of prior field studies, to generate a detailed comparison of the *Striga* control methods in the production of maize, sorghum, and major millets, as a guide for effective *Striga* management and sustainable cereal production.

## 1.2 **Materials and Methods**

### **1.2.1 Literature search**

A literature search was first conducted on Google Scholar to identify the major studies available on the topic, and to formulate the keywords related to the topic. These keywords were then combined using Boolean operators to search for studies to be included in this meta-analysis, using two different datasets, Web of Science (https://www.webofknowledge.com), and Scopus (https://www.scopus.com/). The keywords used were: [(*Striga* or "parasitic weeds") and (maize or corn or "*Zea mays*" or sorghum or millet)]. The quotation marks indicate that the term was used as a whole, and not each word alone. The search was limited to maize,

sorghum, and millet, while no limitation was given on the period of the studies. The search was completed in August 2021, and the studies were imported into the reference manager Endnote (EndNote version 20.3) for further screening.

### 1.2.2 Screening and selection of the reported studies

The screening process followed the critical steps in screening and selection, which are: (1) removing duplicates, (2) screening for relevant studies by title and abstract, and (3) inspecting full texts to ensure that they fulfilled the eligibility criteria following Mikolajewicz and Komarova (2019). The duplicates were removed using Endnote (https://endnote.com/downloads), and the remaining studies were imported into DistillerSR Evidence Partners (DistillerSR. Version 2.35. Evidence Partners; 2021). The following were the inclusion criteria of the reported studies: The study was not a review.

- The study was published in English or French.
- The study contained original results.
- The study reported the grain yield as well as the *Striga* parameters.
- The study used a control check for the treatments.
- The study did not deal with modeling, political discussions, or laboratory studies.
- The full text of the study is available.

### 1.2.3 Data extraction

Data extraction was done on DistillerSr using the variables presented in Table 1.1. The main variables for this study were grain yield (GY), *Striga* emergence count (SEC), and *Striga* damage rating (SDR). The reported grain yield of all the studies was standardized into kg/ha. *Striga* emergence count was recorded based on the number of *Striga* plants at 10 weeks after planting per 3.75$m^2$ for all the studies. *Striga* damage rating was recorded uniformly in all the studies, on a scale of 1 to 9 where 1= normal plant growth, no visible symptom, and 9= complete scorching of leaves, causing premature death and collapse of host plant and failure of ear formation (Kim 1991).

**Table 1.1** Variables definitions and units or descriptions extracted from searched publications.

| Variables | Definition | Unit or description |
|---|---|---|
| **Title** | Title of the publications | Text |
| **Country** | Countries where the experiments were conducted | Text |
| **Authors** | Authors of the publications | Text |
| **Journal** | Name of the journal where the study has been published | Text |
| ***Striga* species** | The *Striga* species examined during the experiments | Text |
| **Control method** | The control method used in the experiment | Text |
| ***Striga* damage rating** | *Striga* damage rating under each control method | Score |
| ***Striga* emergence count** | The number of *Striga* plants emerged | Count |
| **Grain yield** | Grain yield of each crop using each *Striga* control method | kg/ha |
| **Genetic control** | Studies including the use of improved varieties with *Striga*-resistant candidate genes | Text |
| **Cultural control** | Studies including the use of any cultural practice | Text |
| **Biological control** | Studies including the use of biological agents | Text |
| **Chemical control** | The use of any chemical to control the parasite | Text |
| **Integrated control** | The combination of any individual control methods | Text |
| **Experimental design** | The experimental design used in the study | Text |

### 1.2.4 Data analysis

The data collected were tested for normality, outliers, and variability using the following statistics: number of samples (N), minimum, maximum, median, mean, range, standard deviation, standard error mean, coefficient of variation (in percentage), skewness, and kurtosis. The statistics were computed using Genstat 20th Edition (Lane et al. 1987), based on individual data collected from the studies. The mean difference for GY, SEC, and SDR was calculated in Excel using the formula:

mean difference =Vf-Vi

where Vf =mean values of the treatments and Vi = mean values of the control, based on the individual data to determine the absolute difference between the control and the treatment involved in each study. Pearson correlation coefficients were calculated using the SPSS 27$^{th}$ (IBM SPSS Statistics for Windows, Version 27) (De Sá 2007) to determine the degree of associations among variables.

The Cohen's d parameter was used to compare the effect size of each control method (Kotrlik et al. 2011), where yield, SEC, and SDR from treatment and control were compared (Oda 2018; Behdad et al. 2022). The following formula was used to calculate Cohen's d effect on each control method: Cohen's d= (mean of experimental group)- (mean of the control group)/average standard deviation. The individual effect sizes were weighted using the following effect size ratio: individual mean difference/average standard deviation. The average standard deviation was calculated in Excel using the individual data of the control and experimental groups.

The meta-analysis was conducted using Jeffreys's Amazing Statistics Program (JASP) meta-analysis software version 016.10 (JASPTeam 2020), which provided results with 95% confidence interval (CI). Jeffreys's Amazing Statistics Program is user-friendly and freely available software. The statistical model used to estimate the mean effect size was based on the test of residual heterogeneity. When the residual heterogeneity test is significant, all effect sizes are equal, and a random model is applied. If this is not significant, a fixed effect model is used (Goss-Sampson 2020). The publication bias analysis was based on the normality test and funnel plots asymmetry (Richard et al. 2009). In addition to Cohen's d effect size, the percentage differences between the control and the treatment were calculated to support the meta-analysis using the formula:

percentage difference = (Vf-Vi)/Vi) x 100, where Vf =mean of values of the treatments and Vi = mean of the values of the controls. Bar graphs showing the comparison of the percentage differences were computed using the SPSS version 27$^{th}$ (De Sá 2007). Forest plots showing the comparison of the effect sizes of the *Striga* control methods on GY, SEC, and SDR were computed, based on the effect size and the standard error of the effect size values, using JASP. Forest plots provide graphical information about estimates of comparisons or associations, corresponding precision, and statistical significance. This visual representation also makes it easier to see variations between study results (Thapa et al. 2016).

## 1.3 **Results**

### **1.3.1 Search results, article screening, and inclusion**

The first step of the literature selection yielded 1751 publications on the Web of Science and Scopus. Duplicates were removed in the Distiller SR web-based (DistillerSR 2020), resulting

in 1021 unique articles. After title, abstract, and full-text screening, 66 publications met the inclusion criteria and were included in the study (Figure 1.1). From the 66 publications, 408 observations were extracted. The main reasons for the exclusion of a paper were that some trials were not performed under field conditions, the grain yields and *Striga* parameters were not reported, the studies were performed without a control treatment, and some were literature reviews. The list of the 66 studies used and the data extracted are presented in Table 1.2.

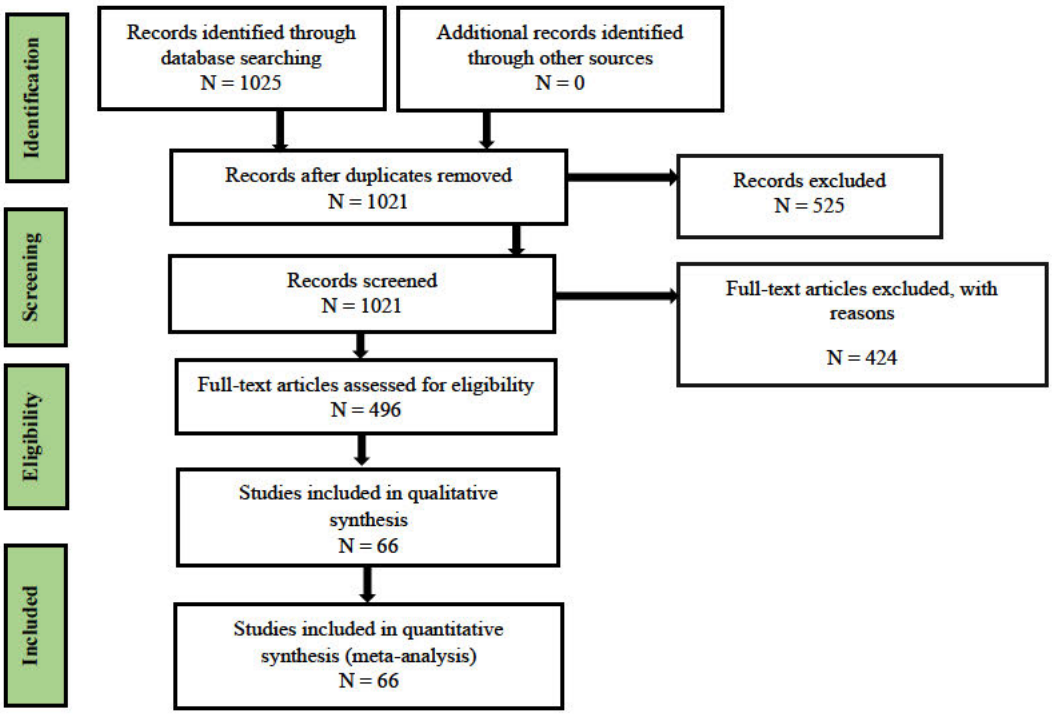



**Figure 1.1** Flow chart of the selection of studies included in the meta-analysis on Striga control methods on major cereal crops.

### 1.3.2 Characteristics of the articles included in the study

Most of the studies were conducted in Nigeria (57.57%), followed by Kenya (18.00%), and Ethiopia (7.50%). About 96.96% of the studies were on *S. hermonthica,* while the remaining were on *S. asiatica* (Table 1.2, Figure 1.2). The results indicated that *S. hermonthica* is widely distributed in Eastern and Western African countries, while *S. asiatica* is found in Southern Africa (Figure 1.2). Of the 66 papers evaluated, 31 reported genetic management of *Striga*, while 24 were cultural, 4 chemical, 1 biological control, and 6 integrated control methods. Most of the studies were conducted on maize (46), followed by sorghum (18), pearl millet (1), and finger millet (1) (Table 1.2).

**Table 1.2** List of references, and trial details, including the number of replications, *Striga* control methods, experimental designs, traits assessed, and countries of studies.

| No. | Reference | Number of replications | Crop | *Striga* species | *Striga* control method | Assessed traits | Experimental design | Countries |
|---|---|---|---|---|---|---|---|---|
| 1 | Efron (1993) | 2 | Maize | *S. hermonthica* | Genetic | SEC, GY | RCBD | Nigeria |
| 2 | Mumera and Below (1993) | 4 | Maize | *S. hermonthica* | Cultural | SEC, GY | LD | Nigeria |
| 3 | Soon-Kwon and Adetimirin (1997) | 4 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | SSP | Nigeria |
| 4 | Kim et al. (1998) | 2 | Maize | *S. hermonthica* | Genetic | SDR, GY | RCBD | West Africa |
| 5 | Carsky et al. (2000) | 3 | Maize | *S. hermonthica* | Cultural | SEC, GY | RCBD | Nigeria |
| 6 | Fred et al. (2001) | 3 | Maize | *S. hermonthica* | Chemical | SEC, GY | RCBD | Kenya |
| 7 | Oswald et al. (2002) | 4 | Maize | *S. hermonthica* | Cultural | SEC, GY | RCBD | Kenya |
| 8 | Oswald and Ransom (2002) | 4 | Maize | *S. hermonthica* | Cultural | SEC, GY | RCBD | Kenya |
| 9 | Khan et al. (2002) | 6 | Maize | *S. hermonthica* | Cultural | SEC, GY | LS | Kenya |
| 10 | Gworgwor et al. (2002) | 2 | Sorghum | *S. hermonthica* | Cultural | SEC, GY | SP | Nigeria |
| 11 | Kanampiu et al. (2003) | 3 | Maize | *S. hermonthica* | Integrated | SEC, GY | RCBD | Zimbabwe, Malawi |
| 12 | Kuchinda et al. (2003) | 12 | Maize | *S. hermonthica* | Integrated | SEC, SDR GY | RCBD | Nigeria |
| 13 | Olupot et al. (2003) | 5 | Sorghum | *S. hermonthica* | Cultural | SEC, GY | RCBD | Uganda |
| 14 | Ezeaku and Gupta (2004) | 3 | Sorghum | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |
| 15 | Hess and Dodo (2004) | 7 | Pearl Millet | *S. hermonthica* | Cultural | GY | RCBD | Niger |
| 16 | Marley et al. (2004a) | 3 | Sorghum | *S. hermonthica* | Cultural | SEC, SDR GY | RCBD | Nigeria |
| 17 | Marley et al. (2004b) | 10 | Sorghum | *S. hermonthica* | Integrated | SEC, SDR GY | RCBD | Nigeria |
| 18 | Dembélé and Westwood (2005) | 4 | Sorghum | *S. hermonthica* | Chemical | SEC, GY | RCBD | Mali |
| 19 | van Ast et al. (2005) | 2 | Sorghum | *S. hermonthica* | Cultural | SEC, GY | SSP | Mali |
| 20 | Reda et al. (2005) | 3 | Sorghum | *S. hermonthica* | Cultural | SEC, GY | RCBD | Ethiopia |
| 21 | Aliyu and Emechebe (2006) | 3 | Sorghum | *S. hermonthica* | Cultural | SEC, GY | RCBD | Nigeria |
| 22 | Kureh et al. (2006) | 3 | Maize | *S. hermonthica* | Cultural | SDR, GY | RCBD | Nigeria |
| 23 | Khan et al. (2006a) | 4 | Sorghum | *S. hermonthica* | Cultural | GY | RCBD | Kenya |
| 24 | Khan et al. (2006b) | 6 | Maize | *S. hermonthica* | Cultural | SEC, GY | LS | Kenya |
| 25 | Badu-Apraku (2006) | 2 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | LD | Nigeria |
| 26 | Menkir (2006) | 6 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |
| 27 | Menkir and Kling (2007) | 2 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | LD | Nigeria |
| 28 | Kamara et al. (2007) | 2 | Maize | *S. hermonthica* | Cultural | SEC, SDR, GY | SPD | Nigeria |
| 29 | Khan et al. (2007) | 4 | Sorghum | *S. hermonthica* | Cultural | SEC, GY | RCBD | Kenya |
| 30 | Badu-Apraku and Lum (2007) | 2 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |
| 31 | De Groote et al. (2007) | 3 | Maize | *S. hermonthica* | Chemical | SEC, GY | PWC | Kenya |
| 32 | Badu-Apraku et al. (2008a) | 4 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |
| 33 | Badu-Apraku et al. (2008b) | 2 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | IBD | Nigeria |
| 34 | Khan et al. (2008) | 3 | Maize | *S. hermonthica* | Cultural | GY | RCBD | Kenya |
| 35 | Kabambe et al. (2008) | 3 | Maize | *S.asiatica* | Chemical | SEC, GY | RCBD | Malawi |
| 36 | Badu-Apraku and Yallou (2009) | 4 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Ouest Africa |
| 37 | Khan et al. (2009) | 4 | Maize | *S. hermonthica* | Cultural | SEC, GY | RCBD | Kenya |
| 38 | Badu-Apraku et al. (2009) | 4 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |
| 39 | Menkir et al. (2010a) | 3 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | ALD | Nigeria |
| 40 | Menkir et al. (2010b) | 3 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |
| 41 | Midega et al. (2010) | 4 | Finger millet | *S. hermonthica* | Cultural | GY | RPS | Benin |
| 42 | Ibrahim et al. (2010) | 2 | Maize | *S. hermonthica* | Integrated | SEC, SDR GY | RCBD | Nigeria |
| 43 | Badu-Apraku et al. (2010a) | 4 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |
| 44 | Badu-Apraku et al. (2010b) | 4 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |

## Table 1.2 (continued)

| No. | Reference | Number of replications | Crop | *Striga* species | *Striga* control method | Assessed traits | Experimental design | Countries |
|---|---|---|---|---|---|---|---|---|
| 45 | Badu-Apraku and Lum (2010) | 4 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RIB | Nigeria |
| 46 | Odhiambo et al. (2011) | 4 | Maize | *S. hermonthica* | Cultural | SEC, GY | RCBD | Kenya |
| 47 | Tesso and Ejeta (2011) | 4 | Sorghum | *S. hermonthica* | Integrated | SEC, GY | RCBD | Ethiopia |
| 48 | Badu-Apraku and Akinwale (2011) | 4 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |
| 49 | Menkir et al. (2012) | 4 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | Crisscross | Nigeria |
| 50 | Badu-Apraku and Oyekunle (2012) | 3 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | LD | Nigeria |
| 51 | Menkir et al. (2012) | 4 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | LD | Kenya |
| 52 | Akaogu et al. (2013) | 2 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | IBD | Nigeria |
| 53 | Abate et al. (2017) | 3 | Sorghum | *S. hermonthica* | Genetic | SEC, GY | LD | Ethiopia |
| 54 | Konate et al. (2017) | 2 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |
| 55 | Midega et al. (2017) | 4 | Sorghum | *S. hermonthica* | Cultural | SEC, GY | RCBD | Kenya |
| 56 | Menkir and Meseka (2019) | 3 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | ALD | Nigeria |
| 57 | Badu-Apraku et al. (2020a) | 2 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | LD | Nigeria |
| 58 | Badu-Apraku et al. (2020b) | 3 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Ouest Africa |
| 59 | Zebire et al. (2020) | 2 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | AL | Nigeria |
| 60 | Shayanowako et al. (2020) | 2 | Maize | *S. asiatica* | Biological | SEC, SDR GY | ALD | South Africa |
| 61 | Kamara et al. (2020) | 3 | Sorghum | *S. hermonthica* | Integrated | SEC, SDR GY | RCBD | Nigeria |
| 62 | Afolabi et al. (2021) | 3 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | AL | Nigeria |
| 63 | Gebremedhin et al. (2021) | 3 | Sorghum | *S. hermonthica* | Cultural | SEC, GY | RCBD | Ethiopia |
| 64 | Woldemariam et al. (2021) | 3 | Sorghum | *S. hermonthica* | Cultural | SEC, GY | RCBD | Ethiopia |
| 65 | Shaibu et al. (2021) | 2 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | RCBD | Nigeria |
| 66 | Oyekale et al. (2021) | 2 | Maize | *S. hermonthica* | Genetic | SEC, SDR, GY | ALD | Nigeria |

No., serial number; RCBD, Randomized Complete Block Design; RIB, Randomized Incomplete Block; SSPD, Split-Split Plot Design; ALD, Alpha Lattice Design; LD, Lattice Design; IBD, Incomplete Block Design; RPS, Random-Paired Subplots; SPD, Split Plot Design; LS, Latin Square; SP, Strip-Plot, PWC, Pair-wise Comparison; GY, Grain yield; SEC, *Striga* emergence count; SDR, *Striga* damage rating.


**Figure 1.2** Distribution of the *Striga* species in sub-Saharan Africa, based on the present meta-analysis.

### 1.3.3 Crop performance for grain yield and *Striga* parameters under *Striga* infestation

#### 1.3.3.1 ***Maize***

The coefficient of variation (CV% in percent) for maize GY under *Striga* infestation ranged from 17.40% to 70.58% (Table 1.3). This suggests that GY performance varied considerably among studies under the different control methods. Less variation resulted from the biological and chemical control methods, with CV% values of 17.40% and 29.52%, respectively. ISM studies exhibited the highest variation, followed by genetic and cultural control methods, with CV% values of 78.52%, 55.50%, and 49.25%, respectively. The maximum attainable GY was 9900.00 kg/ha, and the minimum was 4.10 kg/ha. The SEC for maize varied from 18.39% to 95.67% across the control methods (Appendix 1.1). ISM trials exhibited the greatest variation for GY, with a value of 348.80% due to the wide variability of the assessed traits across the various combinations of individual *Striga* control methods. In contrast, biological control resulted in the lowest variation at 18.39% for GY. The minimum value for SEC was 0.00, while the maximum was 270.00. SDR varied between 3.02% and 19.26%. Cultural control resulted in the highest CV%, followed by genetic control with values of 19.26% and 16.76%, respectively, for SDR (Appendix 1.2). The lowest CV% was observed for ISM trials, followed

by biological control, with values of 3.02% and 5.46%, respectively, for SDR. The SDR minimum value was 2.00, while the maximum was 8.00.

**Table 1.3** Summary statistics for grain yield of maize under *Striga* infestation without *Striga* control (-) and with control (+) with five methods.

| | Control methods | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Statistics | Genetic | | Cultural | | Chemical | | Bioagent | | Integrated | |
| | - | + | – | + | – | + | – | + | – | + |
| Samples (N) | 274 | 274 | 53 | 53 | 6 | 6 | 9 | 9 | 14 | 14 |
| Mean (kg/ha) | 970.80 | 2060.00 | 1984.00 | 3118.00 | 2635.00 | 2859.00 | 2240.00 | 2558.00 | 2504.00 | 2450.00 |
| Mean difference (kg/ha) | 1089.20 | | 1134.00 | | 224.00 | | 318.00 | | 54.00 | |
| Mean difference (%) | 112.19 | | 57.15 | | 8.50 | | 14.19 | | 2.15 | |
| Median | 910.00 | 1779.00 | 2500.00 | 2800.00 | 2990.00 | 3010.00 | 2210.00 | 2800.00 | 3857.00 | 1962.00 |
| Minimum | 135.00 | 281.00 | 337.00 | 4.10 | 599.10 | 1291.00 | 1840.00 | 1900.00 | 139.60 | 227.60 |
| Maximum | 2931.00 | 6260.00 | 3620.00 | 9900.00 | 3250.00 | 3630.00 | 2620.00 | 3140.00 | 3857.00 | 5220.00 |
| Range | 2796.00 | 5979.00 | 3283.00 | 9896.00 | 2651.00 | 2339.00 | 780.00 | 1240.00 | 3717.00 | 4992.00 |
| Standard deviation | 535.70 | 1132.00 | 821.30 | 1535.00 | 1003.00 | 843.90 | 299.90 | 445.10 | 1644.00 | 1730.00 |
| Standard error the mean difference | 32.36 | 68.41 | 112.80 | 210.90 | 409.40 | 344.50 | 99.96 | 148.40 | 439.30 | 462.20 |
| Coefficient of variation (%) | 55.04 | 54.97 | 41.40 | 49.25 | 38.06 | 29.52 | 13.39 | 17.40 | 65.66 | 70.58 |
| Skewness | 0.61 | 1.21 | -0.23 | 1.77 | -1.74 | -1.13 | 0.23 | -0.20 | -0.37 | 0.39 |
| Kurtosis | 0.28 | 1.48 | -0.96 | 5.55 | 1.12 | 0.10 | -1.44 | -1.52 | -1.74 | -1.24 |

1.3.3.2 ***Sorghum***

The coefficient of variation for mean sorghum grain yield varied from 25.52% to 67.57% (Appendix 1.3) under *Striga* infestation. This suggests that grain yield performance varied considerably among studies under the different control methods. Genetic control resulted in the lowest variation, with a CV% of 25.52%. Cultural control resulted the highest variation, followed by ISM with CV% values of 64.93% and 67.57%, respectively, under *Striga* infestation. The maximum GY was 4640.00 kg/ha and the minimum was 1.60 kg/ha. The SEC on sorghum varied from 125.20 % to 186.70%. Cultural control resulted in the highest variation, followed by genetic control with CV% values of 186.70% and 133.90%, respectively (Appendix 1.4). The SEC had a minimum value of 3.69 and a maximum of 895.00. ISM resulted the lowest CV% of 125.20%, while the CV% of SDR ranged from 30.82% to 43.42%. The lowest variation for SDR was recorded for genetic control with a CV% value of 30.82%. The highest CV% for SDR was for ISM at 43.42%, followed by cultural control at 32.75%

(Appendix 1.5). SDR's minimum and maximum values were 1.00 and 5.50, respectively. No studies were found that reported on the genetic, biological, chemical, or ISM methods of *Striga* control for pearl millet and finger millet. In these two crops, the only studies involved cultural control methods. The CV% for the grain yield for pearl millet and finger millet was 35.63 %, showing marked variation between the studies (Appendix 1.4).

For GY of maize, sorghum, and millet, the skewness and kurtosis values under all the control methods fall within the ranges of -1.00 to 1.00, except for cultural control in maize. Maize GY had kurtosis and skewness at 5.50 and 1. 77, respectively. For the SEC on maize, the skewness and the kurtosis were greater than 1.00 for genetic, cultural, and ISM control methods. The SEC values for maize were between -1.00 and 1.00 for the chemical and biological control methods. The skewness and the kurtosis values for SEC on sorghum were greater than 1.00. For the *Striga* damage rating, skewness and kurtosis were between -1.00 and 1.00.

### 1.3.4 Effect of *Striga* control methods on crop grain yield and *Striga* parameters

#### 1.3.4.1 *Comparative analysis based on percentage differences*

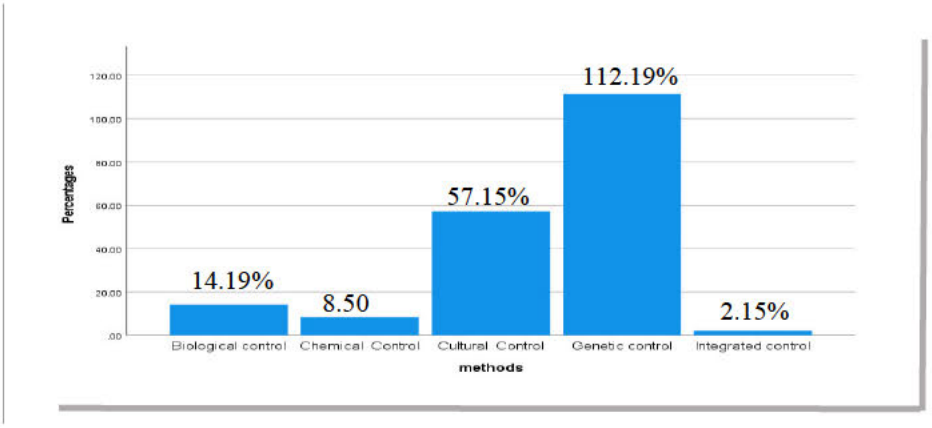



**Figure 1.3** Bar graph showing the effect of five *Striga* control methods on maize grain yield increase (%) under *Striga* infestation.

Genetic control increased maize yields by 112.19% followed by cultural control (57.15%), whereas ISM caused the lowest yield gain (2.15%) (Figure 1.3). Similarly, genetic control reduced SEC by 31.07%, which was lower than the chemical, cultural, and ISM methods, with reductions of 48.65%, 44.91%, and 42.24%, respectively (Appendix 1.1). However, the highest reduction in SDR was recorded with genetic control (27.14%), compared to ISM (22.85%) and cultural control (15.12%) (Appendix 1.2).

Genetic control on sorghum had the largest percentage increase of GY of 179.60%, which was twofold higher than that from cultural control (77.50%) (Figure 1.4). The overall impact of chemical control on sorghum was negative (-26.33%). Similarly, genetic control reduced SEC by 88.87%, followed by ISM, which caused a reduction of 58.87%. Cultural control caused a moderate reduction of SEC (33.21%). No study reported on SDR levels for chemical and biological control in sorghum. The SDR was much lower under cultural control than genetic and ISM control, which exhibited almost the same levels of 23.50% and 23.45%, respectively (Appendix 1.4). Millet grain yields increased to 158.24 % under cultural control.

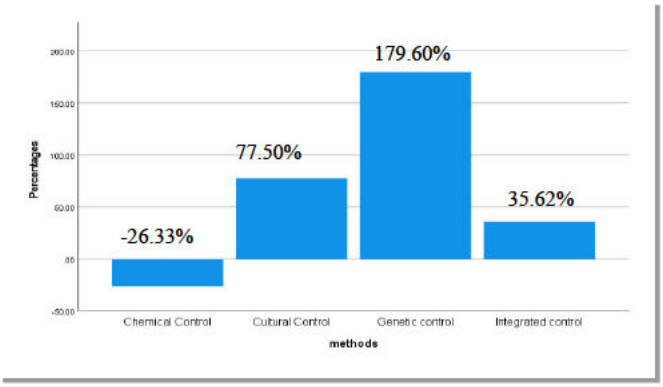



**Figure 1.4** Bar graph showing the effect of four *Striga* control methods on sorghum grain yield increase (%) under *Striga* infestation

### 1.3.4.2 *Comparative analysis based on Cohen'd parameter*

#### 1.3.4.2.1 **Effect of *Striga* control methods on grain yield**

The random effects model was used to compare the grain yield of sorghum and maize under *Striga* infestation. The summary statistics (Table 1.4) showed that the Omnibus test of model coefficients was significant (P=0.01). The residual heterogeneity of the test was highly significant (P<0.001). In addition, the Wald statistics of the overall effect size of the combined study was highly significant (Z= 2.48, P=0.01). Both heterogeneity variance ($\tau^2$) and test of heterogeneity ($I^2$) showed excess variance between the control methods with values of 1.40 and 97.85%, respectively.

**Table 1.4** Summary statistics calculated on Jeffreys's Amazing Statistics Program using effect sizes and standard error of effect sizes of five *Striga* control methods on maize and sorghum grain yields.

| Random-effects model (REM) | | | | | | Estimate standard error | | Residual heterogeneity estimates | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Omnibus test | | | Test of residual heterogeneity | | | Wald test | | Parameters | | | |
| Q | df | P | Q | df | P | Z | P | $\tau^2$ | $\tau$ | $I^2$ (%) | $H^2$ |
| 6.16 | 1.00 | 0.01 | 143.90 | 7.00 | <0.001 | 2.48 | 0.01 | 1.40 | 1.18 | 97.85 | 46.65 |

Q, probability of failure; df, degree of freedom; P, probability; Z, wald test, $\tau^2$, heterogeneity variance; $\tau$, ratio of the departure; $I^2$, test of heterogeneity, $H^2$, residual heterogeneity

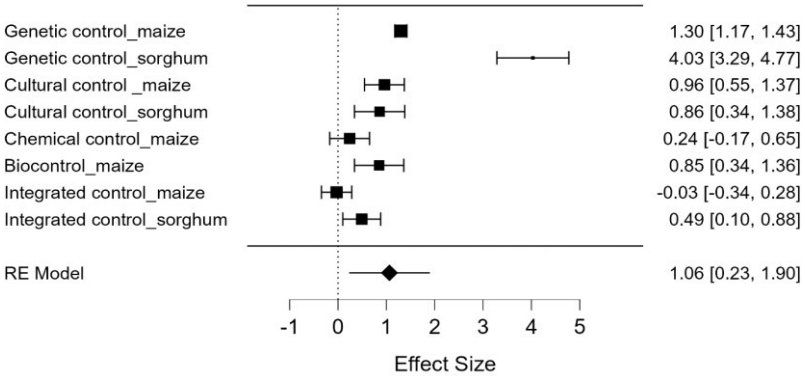
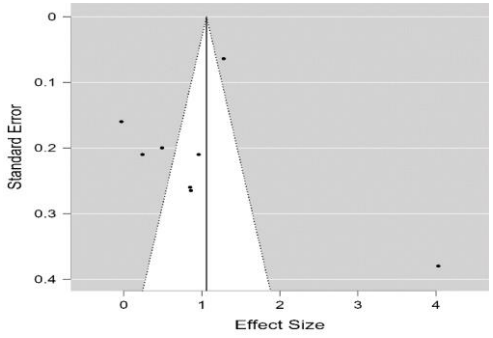



**Figure1.5** Forest plots showing the effect of the five *Striga* control methods on maize and sorghum grain yield based on random-effects model (REM). Right-hand values for each control method and plot denote the effect size and a 95% confidence interval for the effect size. The diamond shape denotes the effect size and confidence interval for the combined effect.

Figure 1.5 summarises the effect of the five control methods on maize and sorghum grain yields. The forest plots showed the mean weighted effect sizes and the 95% confidence intervals for each control method. The sizes of the squares reflect the weight of each control method. The confidence intervals (CIs) were used to determine the combined effect size (ES) (see the diamond shape in Figure 1.5). It was noted that the overall effect of *Striga* control had a significant positive effect on the maize and sorghum GY (ES=1.06) with a 95% CIs between 0.23 and 1.90. Genetic control generated the highest effect size for maize (ES=1.30), with a 95% CIs between 1.17 and 1.43, and sorghum (ES=4.03) with 95% CIs between 3.29 and 4.77. The effect sizes of ISM and chemical control methods on maize GY were overlapping, and the plots crossed the non-effect line (ES=-0.03). Cultural control exhibited almost the same ES on maize and sorghum with (ES=0.96), CIs [0.55, 1.37], and (ES=0.86), CIs [0.34, 1.38], respectively.




| Rank correlation test for Funnel plot asymmetry | | |
|---|---|---|
| **Variable** | **Kendall's τ** | **P-value** |
| Rank test | 0.32 | 0.26 |

**Figure 1.6** Funnel plot and rank correlation test showing the distribution of the effect sizes of the five control methods (left) and rank test (right) on maize and sorghum grain yield.

The funnel plot (Figure 1.6) showed that the observed effect sizes appear to be symmetrically distributed around the vertical axis. The Kendall's test showed a non-significant (P= 0.26) difference among the GY achieved across the studies suggesting that the trait had symmetrical distribution.

1.3.4.2.2 **Effect of *Striga* control methods on *Striga* emergence count**

The test of residual heterogeneity was not significant with the random effect model, suggesting that the comparison of the effect of the five control methods on *Striga* reduction is not under the random effect model. However, the fixed-effect model, the omnibus test, the test of residual heterogeneity, and the Wald test of the overall effect size of the combined study, were highly significant (P<0.001) (Table 1.5).

**Table 1.5** Statistical summaries computed based on Jeffreys's Amazing Statistics Program using effect sizes and standard error of effect sizes of five *Striga* control methods on *Striga* emergence count in maize and sorghum production.

| **Fixed-effect model** | | | | | | **Estimate standard error** | |
|---|---|---|---|---|---|---|---|
| **Omnibus test** | | | **Test of residual heterogeneity** | | | **Wald test** | |
| Q | df | P | Q | df | P | Z | P |
| 130.66 | 1.00 | <0.001 | 216.00 | 7.00 | <0.001 | -11.40 | 0.01 |

Q, probability of failure; df, degree of freedom; P, probability; Z, wald test statistic

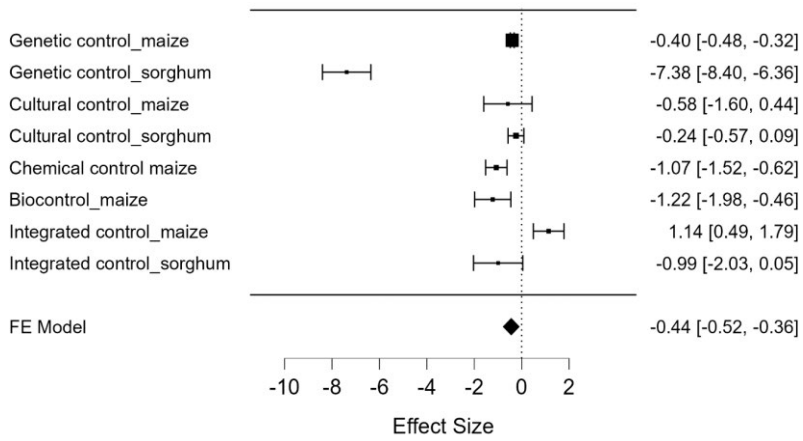
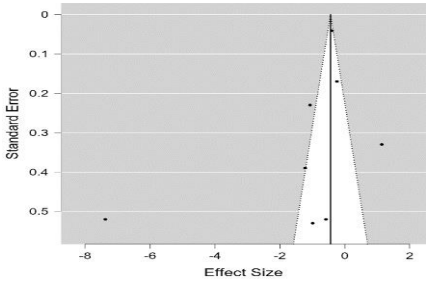



**Figure 1.7** Forest plots showing the effect of the five *Striga* control methods on *Striga* emergence count in maize and sorghum production. Right-hand values for each plot/control method denote the effect size and a 95% confidence interval for the effect size. The diamond shape denotes the effect size and confidence interval for the combined effect.

The forest plots showed that the overall effect of the control methods had a significant negative effect on *Striga* count based on SEC (ES=-0.44), with 95% CIs between -0.52 and -0.36 (Figure 1.7). Biological control caused the highest reduction in SEC for maize (ES=-1.22), CIs [-1.98, -0.46], followed by chemical control (ES=-1.07), CIs [-1.52, -0.62], but their forest plots were overlapping. This suggests that the biological and chemical control effects were not statistically significantly different on SEC reduction. Genetic control caused a high but non-significant effect on SEC reduction for sorghum (ES=-7.38), with wider 95% CIs between -8.40 and -6.36. ISM caused the least reduction in SEC for both maize and sorghum, and the plots crossed the non-effect line.




**Rank correlation test for Funnel plot asymmetry**

| Variables | Kendall's τ | P-value |
|---|---|---|
| Rank test | -0.32 | 0.26 |

**Figure 1.8** Funnel plot and rank correlation test showing the distribution of the effect sizes of the five control methods (left) and rank test (right) on SEC reduction for maize and sorghum.

The funnel plot (Figure 1.8) showed that the observed effect sizes are symmetrically distributed around the vertical axis. The Kendall's test showed a non-significant (P= 0.54) difference among SEC values. This suggests a symmetric distribution of SEC across the studies included in the current meta-analysis.

1.3.4.2.3 **Effect of *Striga* control methods on *Striga* damage rating**

The model used to compare the effect of *Striga* control methods on SDR reduction is the fixed effect model similar to the SEC. Table 1.6 showed that the omnibus test, the test of residual heterogeneity, and the estimate of the overall effect (Wald test) were highly significant with P<0.001.

**Table 1.6** Summary statistics computed based on Jeffreys's Amazing Statistics Program using effect sizes and standard error of effect sizes of five *Striga* control methods on *Striga* damage rating in maize and sorghum production.

| **Fixed-effects model** | | | | | | **Estimate standard error** | |
|---|---|---|---|---|---|---|---|
| Omnibus test | | | Test of residual heterogeneity | | | Wald test | |
| Q | df | P | Q | df | P | Z | P |
| 1054.84 | 1.00 | <0.001 | 432.97 | 4.00 | <0.001 | 32.47 | <0.001 |

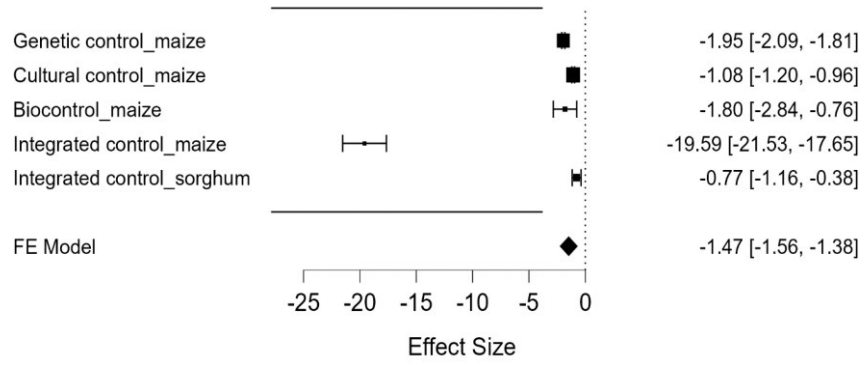
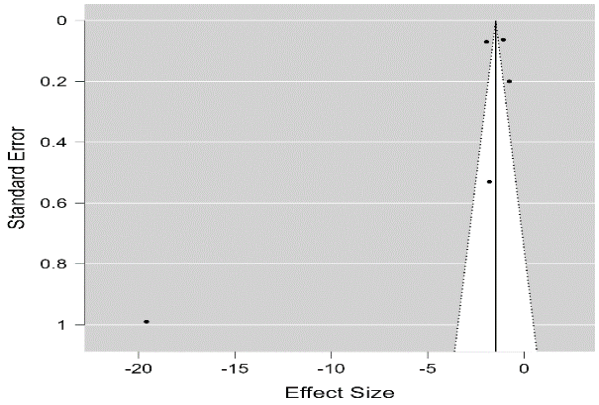



**Figure 1.9** Forest plots showing the effect of the five *Striga* control methods on *Striga* damage rating in maize and sorghum production. Values in the right side for each control plot/method denote the effect size and a 95% confidence interval for the effect size. The diamond shape denotes the effect size and confidence interval for the combined effect.

The forest plots (Figure 1.9) showed that the overall effect of the control methods on SDR was positively significant, ES=-1.47 and CIs between -1.56 and -1.38. Genetic control caused a high and significant effect on SDR reduction on maize GY (ES=-1.95) with CIs of between -2.09 and -1.81. ISM caused a greater effect on SDR (ES=-19.59) but with wider CIs [21.53, -17.65], indicating that the effect of ISM on SDR reduction was not significant.




| Rank correlation test for Funnel plot asymmetry | | |
|---|---|---|
| Variable | Kendall's τ | P-value |
| Rank test | -0.60 | 0.23 |

**Figure 1.10** Funnel plot and rank correlation test showing the distribution of the effect sizes of the five control methods (left) and rank test (right) on SDR reduction for maize and sorghum.

Figure 1.10 showed that the observed effect sizes were symmetrically distributed around the vertical axis. Also, the Kendall's test showed a non-significant (P= 0.23) difference among SDR values across the studies, indicating a symmetric distribution.

### 1.3.5 Association among *Striga* parameters and grain yield under *Striga* infestation and when using five control methods.

*Striga* emergence counts and *Striga* damage rating are used as complementary sets of traits that impact on the grain yield under *Striga* infestation. It is relevant to determine how well these traits correlate to the grain yield under *Striga* infestation as an indication of their significance and to guide control evaluations. The Pearson's correlation coefficients involving maize (Table 1.7) showed that with genetic control under *Striga* infestation, GY exhibited a significant (P<0.001) and highly negative correlation (r=-0.36) with the SDR, but a relatively weak correlation (r=0.003) with the SEC. The SDR and the SEC exhibited a significant (P=0.00) and positive correlation (r=0.18). Under cultural control, GY exhibited a significant (P=0.003) and highly negative correlation (r=-0.46) with SEC, and a positive (r=0.41) but non-significant

(P=0.36) correlation with SDR. The correlation between SDR and SEC was non-significant (P=0.62) but positive (r=0.56). Only GY and SEC were recorded for chemical control, exhibiting a significant (P=0.04) and highly positive correlation (0.81). GY exhibited a negative (P=-0.18) but non-significant correlation (P=0.64) with SDR, and a positive (r=0.04) but non-significant (P=0.91) correlation with SEC under biological control. The correlation between SEC and SDR was positive (0.47) but non-significant (r=0.19). With ISM, none of the traits was significantly correlated with GY. The correlation between SDR and GY was negative (r=-0.40), but positive between SEC and GY (r=0.42). The correlation between SDR and SEC was non-significant but highly positive (r=0.66).

The Pearson's correlation coefficients between *Striga* parameters and grain yield under the different control methods on sorghum are presented in Table 1.8. *Striga* damage ratings were not recorded for genetic and cultural control methods studies. None of the biological control studies on sorghum met our inclusion criteria. With genetic control the SEC and GY exhibited negative (r=-0.30) but non-significant (P=0.36) correlations. Conversely, with cultural control, the GY exhibited a highly negative (r=-0.48) and significant (P=0.03) correlation with SEC. For ISM none of the correlations between GY, SEC, and SDR were significant. Grain yield exhibited a positive correlation with SDR and SEC, with r=0.53 and r=0.87, respectively. The correlation between SDR and SEC was positive (r=0.45) but non-significant (P=0.14) under ISM.

**Table 1.7** Pearson's correlation coefficients and significant tests of *Striga* parameters and maize grain yield involving 53 and 274 samples, respectively for cultural (above diagonal) and genetic (below diagonal) control methods.

| Variables | SEC (+) | SEC (-) | SDR (-) | SDR (+) | GY (+) | GY (-) |
|---|---|---|---|---|---|---|
| SEC (+) | — | 0.923*** | na | 0.562 | 0.469** | -0.283 |
| | — | < 0.001 | na | 0.620 | 0.003 | 0.081 |
| SEC (-) | 0.799*** | — | na | na | -0.267 | -0.213 |
| | < .001 | — | | | 0.100 | 0.194 |
| SDR (-) | -0.490*** | -0.419*** | — | 0.750 | 0.737* | 1.000*** |
| | <0 .001 | < .001 | — | 0.052 | 0.059 | < .001 |
| SDR (+) | 0.186** | 0.048 | 0.211*** | — | 0.410 | 0.750* |
| | 0.003 | 0.443 | < .001 | — | 0.361 | 0.052 |
| GY (+) | 0.003 | 0.044 | -0.240*** | -0.365*** | — | -0.024 |
| | 0.966 | 0.474 | < .001 | < .001 | — | 0.864 |
| GY (-) | 0.354*** | 0.323*** | -0.561*** | -0.104 | 0.649*** | — |
| | < 0.001 | < .001 | < .001 | 0.093 | < .001 | — |

* p < 0.05, ** p < 0.01, *** p < 0.001; GY, grain yield; SEC, *Striga* emergence count; SDR, *Striga* damage rating; parameters followed by - denote without a control method and + with a control method; na, data not available.

**Table 1.8** Pearson's correlation coefficients of *Striga* parameters and sorghum grain yield involving 28 and 11 studies, respectively, for cultural (above diagonal) and genetic (below diagonal) control methods.

| Variables | SEC (-) | SEC (+) | GY (-) | GY (+) |
|---|---|---|---|---|
| SEC (-) | — | 0.212 | -0.388 | -0.365 |
| | — | 0.384 | 0.091 | 0.114 |
| SEC (+) | -0.721* | — | -0.460* | -0.481* |
| | 0.012 | — | 0.041 | 0.032 |
| GY (+) | 1.000*** | -0.721* | — | 0.943*** |
| | < .001 | 0.012 | — | < .001 |
| GY (+) | 0.856*** | -0.304 | 0.856*** | — |
| | < .001 | 0.363 | < .001 | — |

* $p < 0.05$, *** $p < 0.001$; GY, grain yield; SEC, *Striga* emergence count; parameters followed by - denote without a control method and + with a control method; na, data not available;

## 1.4 **Discussion**

### 1.4.1 Variation among studies for grain yield, *Striga* emergence, and damage rating

The kurtosis and skewness of most of the data included in this meta-analysis are between -1.00 and 1.00. This suggests that the data can be described as normally distributed. However, publication bias cannot be ruled out. The kurtosis and the skewness of some parameters suggested that the data distribution was not normal and was too peaked, e.g., GY for cultural control on maize, and SEC for both maize and sorghum. Publication bias may result from the use of the same control check for many treatments in several studies, making some data homogeneous. Fortunately the publication bias is expected to have a minor effect (Sileshi et al. 2008). In the current study, most of the publications excluded from the analysis did not record GY data. Some studies recorded the GY per plant with no possibility of standardizing the GY into kg/ha. Hence, the analysis focused on the studies that satisfied the minimum requirement, which is the record of at least one *Striga* parameter and GY.

The CV% for maize yield varied from 17.40% to 70.58% and sorghum yield from 25.52% to 67.57% across the control methods. SEC varied from 18.39% to 95.67% on maize and from 125.20% to 186.70% on sorghum under different control methods. The SDR varied between 3.02% and 19.26% on maize and from 30.82% to 43.42% on sorghum across the control methods. SDR is less variable than SEC since it was measured on a small scale. The wide variability for GY, SEC, and SDR under the different *Striga* control methods on maize and sorghum suggest that these parameters are directly affected by control method used and the crop type. This could also show the level of resilience of these two crops to different agro ecologies. The biological and chemical control methods resulted in the lowest variation for

maize GY, indicating that this trait did not vary widely under these control methods across the different observations.

The highest CV% was exhibited by ISM (78.52%), followed by genetic control (55.50%), and cultural control (49.25%), indicating that maize GY varied widely under these control methods across the studies. The ISM studies included in the meta-analysis were either a combination of cultural practices with resistant varieties, or the use of host plant resistance combined with chemical control. The high variation across the studies for GY showed that the trait varied widely across the different combinations of the individual *Striga* control methods. The same magnitude of variability was recorded for GY under genetic and cultural control methods. Genetic control included the use of improved varieties such as improved inbred lines, open-pollinated varieties, hybrids, and landraces/local varieties. Over the last decade, there have been considerable effort to breed maize varieties for enhanced *Striga* resistance/tolerance (Badu-Apraku and Oyekunle 2012; Akaogu et al. 2013; Akaogu et al. 2020). Wide variation in the cultural practices was also expected, which would result in variable effects. The cultural practices studied included intercropping, crop rotation, hand-weeding, fertilization, trap and catch cropping, transplanting, and mulching (Khan et al. 2006a; Khan et al. 2006b; Ronald et al. 2019). The coefficient of variations for SEC and SDR on maize showed almost the same extent of variation for GY for all the control methods. This indicates a probable association between GY, SDR, and SEC (Kim et al. 1997; Kim et al. 2002; Badu-Apraku and Akinwale 2011).

In contrast to its performance on maize, genetic control resulted in the lowest CV% for sorghum GY. The high CV% values for sorghum GY under cultural control and ISM (64.93% and 67.57%, respectively) indicated the wide variability of sorghum GY across the studies under these control methods. This is probably because most of the evaluations of *Striga* control methods in sorghum were focused on cultural management practices. There is inadequate information on the genetics of *Striga* resistance in sorghum (Haussmann et al. 2000), and on SDR in sorghum. The lack of studies on *Striga* control methods in pearl millet and finger millet indicates the lower value of these crops, and hence a lack of R&D funding for studies on *Striga* control, or that they are less susceptible to *Striga* spp. than maize and sorghum. For instance, millets are considerably more resistant to drought, insects pests, and diseases than other major food grains (Pray and Latha 2009).

### 1.4.2 Association among grain yield and *Striga* parameters

The correlation between maize GY and SEC was r=0.003. This weak correlation between maize GY and SEC indicates that maize resistance to *Striga* infection is partial but exhibits tolerance. For example,

Badu-Apraku et al. (2010a) reported weak phenotypic and genotypic correlations between GY and SEC in early maize germplasm and suggested its exclusion as a base index for selection for improved grain yield. The association between sorghum GY and SEC was also not significant under genetic control (r=-0.30), although the percentage increase of GY was high. This further indicates that SEC is not a reliable index for selecting for high GY in maize and sorghum. The correlation between GY and SEC on maize under chemical control was positive (r=0.81), which was not expected, but significant. This suggests that this control method was relatively ineffective. With ISM the correlation was negative (r=-0.40) between GY and SDR and was not significant.

### 1.4.3 Impact of *Striga* control methods on grain yield and *Striga* parameters

#### 1.4.3.1 Effect of *Striga* control methods on grain yield

The percentage increase of maize grain yield under genetic control was 112.19% compared to cultural control (57.15%), biological control (14.19%), chemical control (8.50%), and ISM (2.15%). The higher percentage increase of maize GY under genetic control agrees with evaluations by Badu-Apraku et al. (2007), Badu-Apraku et al. (2016), Menkir and Meseka (2019), and Zebire et al. (2021). A Cohen's d value of 1.06 was computed for maize and sorghum GY under all the control methods. Genetic control outperformed the other control methods for both maize (ES=1.30) and sorghum (ES=4.03). The non-overlapping 95% CIs of genetic control with the other control methods for both maize and sorghum indicates that genetic control was significantly different from all the other control methods. The 95% CIs for chemical, cultural, biological, and ISM methods overlap between 0 and 1, indicating that these control methods are not significantly different from each other. Under *Striga* infestation, the resistant/tolerant genotypes produced a greater yield than the susceptible or non-improved genotypes (Ejeta and Gressel 2007; Yacoubou et al. 2021).

The lowest percentage increase of GY as result of ISM could be attributed to a lack of optimized and effective combinations of *Striga* control methods. *Striga*-resistant varieties of maize were intercropped or planted in rotation with legumes such as groundnut (*Arachis hypogaea* L.), and soybean [*Glycine max* (L.) Merr.], or silverleaf desmodium [*Desmodium*

*uncinatum* (Jacq.) DC], or other cereal crops in SSA (Kanampiu et al. 2018; Kamara et al. 2020), leading to an overall effect size of -0.30 for maize and 0.49 for sorghum. Therefore, there is a need for more extensive studies to identify the best ISM strategy to achieve optimum control of the parasite. Based on the above results, it is not possible to recommend ISM as a viable strategy for farmers, especially since this strategy is costly and time-consuming. There is a need to conduct more research to identify better combinations of treatments to include in an ISM strategy.

#### 1.4.3.2 Effect of *Striga* control methods on *Striga* parameters

The percentage decrease of SEC on maize was 31.07% when using genetic control. With cultural control, chemical control and ISM, the percentage decrease in SEC was 48.65%, 44.91%, and 42.24%, respectively. This lower reduction of SEC on maize under genetic control could be explained by *Striga*-tolerant genotypes that support as many *Striga* plants as the susceptible genotypes under *Striga* infestation (Menkir et al. 2006), but which suffer less damage and less yield loss (Kim et al. 1994). Resistant genotypes support considerably fewer *Striga* plants and produce a greater yield than susceptible genotypes (Badu-Apraku et al. 2020c). As in this study, tolerant and resistant varieties were included. the limited effect of SEC (-0.40) was expected, as well as a high SDR effect (-1.95). ISM had a strong impact on SDR but wide 95% CIs, making it non-significant. For sorghum, the effect of genetic control on suppressing SEC appears to be pronounced, with a reduction percentage of 88. 87% and a high negative effect (ES=-7.38). However, the wide CIs [-8.40, -6.46] indicated that the effect is not statistically significant, which was confirmed by a weak correlation (r=-0.30, P=0.36). The 95% CIs of the effect for all the other control methods were overlapping, indicating that they were not significantly different. Overall, the SEC index did not significantly affect selecting high GY in maize and sorghum, especially for maize. Under *Striga* infestation, SDR is the more reliable selection criterion to improve maize GY, while both SEC and SDR are essential traits for selecting high GY in sorghum (Rodenburg et al. 2005).

## 1.5 **Conclusion and recommendations**

The high variability of GY under the different control methods, notably genetic control, reflects the positive contribution of breeding for high-yielding cereal grains under *Striga* infestation. This meta-analysis showed that maize and sorghum varieties possessing *Striga*-resistant genes

displayed high mean yields, and low SEC and SDR values. Similarly, maize GY increases were significantly associated with a reduction in SDR. Sorghum GY increase was also associated with SEC reductions, although the link was non-significant. This suggests that the best control method to manage *Striga* parasites in maize and sorghum is to use genetically improved varieties with *Striga* resistance genes. Given the above reasons, we recommend the use of SDR as the best selection criterion for high GY genotypes under *Striga* infestation for maize, while SEC and SDR should be used as selection traits for improving sorghum GY under *Striga* infestation. The analysis also showed that combining host-resistance with the other control methods in an ISM package does not improve the crops' grain yield. For instance, in this analysis, host resistance combined with herbicide or intercropped with legumes did not significantly increase maize and sorghum GY. The question of the best ISM combination of control treatments therefore remains unanswered. A detailed evaluation and analysis of a combination of diverse control methods is required to find the best ISM for effective control of the parasite. In addition to increasing the GY, ISM is need if the *Striga* seed bank in the soil is to be reduced, which is the reason for not relying only on the use of resistant varieties. The fact that ISM is not yet well studied and documented does not exclude its future implementation for controlling *Striga* in cereal crop production. Few studies have evaluated *Striga* control methods in pearl millet and finger millet, limiting the opportunity for an effective comparison. Therefore, we suggest more investigations on *Striga* control in the major millets. The results confirmed that effective *Striga* management options were discerned to improve crop yield under *Striga* infestation.

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**Appendix 1.1.** Summary statistics for *Striga* emergence counts of maize under *Striga* infestation without control (-) and with control (+) method using five methods.

| | **Control methods** | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Genetic | | Cultural | | Chemical | | Biocontrol | | Integrated | |
| Statistics | - | + | - | + | - | + | - | + | - | + |
| Samples (N) | 267 | 267 | 39 | 39 | 6 | 6 | 9 | 9 | 14 | 14 |
| Mean | 55.32 | 38.13 | 34.64 | 19.08 | 122.80 | 63.05 | 6.10 | 4.90 | 29.35 | 16.95 |
| Mean difference (%) | 31.07 | | 44.91 | | 48.65 | | 19.67 | | 42.24 | |
| Median | 43.00 | 32.00 | 23.04 | 11.00 | 145.90 | 64.69 | 5.70 | 4.38 | 18.00 | 0.43 |
| Minimum | 2.90 | 0.40 | 4.00 | 0.00 | 25.98 | 16.01 | 5.09 | 4.07 | 0.46 | 0.00 |
| Maximum | 244.00 | 227.00 | 102.00 | 92.00 | 145.90 | 108.00 | 8.01 | 6.64 | 270.40 | 222.40 |
| Range | 241.10 | 226.60 | 98.00 | 92.00 | 119.90 | 91.90 | 2.90 | 2.50 | 269.90 | 222.40 |
| Standard Deviation | 48.90 | 36.48 | 28.34 | 25.26 | 48.00 | 32.91 | 1.04 | 0.90 | 69.98 | 59.14 |
| Standard Error Mean | 2.93 | 2.23 | 4.53 | 4.04 | 19.60 | 13.44 | 0.34 | 0.30 | 18.70 | 15.81 |
| Coefficient of Variation (%) | 88.40 | 95.60 | 81.80 | 132.40 | 39.10 | 52.10 | 17.00 | 18.30 | 238.50 | 348.80 |
| Skewness | 2.08 | 2.09 | 1.41 | 1.65 | -1.69 | -0.07 | 0.87 | 0.76 | 3.22 | 3.32 |
| Kurtosis | 5.13 | 6.24 | 0.57 | 1.33 | 1.01 | -1.08 | -0.76 | -0.69 | 8.67 | 9.06 |

**Appendix 1.2.** Summary statistics for *Striga* damage rating of maize under *Striga* infestation without control (-) and with control (+) method using four methods.

| Statistics | Control methods | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Genetic | | Cultural | | Biological | | Integrated | |
| | - | + | - | + | - | + | - | + |
| Samples (N) | 262 | 262 | 7 | 7 | 9 | 9 | 4 | 4 |
| Mean | 6.41 | 4.67 | 4.96 | 4.21 | 4.67 | 3.96 | 3.50 | 2.70 |
| Mean difference (%) | 28.12 | | 15.12 | | 13.91 | | 22.85 | |
| Median | 6.20 | 4.60 | 4.50 | 4.00 | 4.59 | 3.89 | 3.50 | 2.70 |
| Minimum | 4.00 | 2.00 | 4.50 | 3.30 | 3.88 | 3.75 | 3.50 | 2.60 |
| Maximum | 8.00 | 7.00 | 5.58 | 5.67 | 5.42 | 4.33 | 3.50 | 2.80 |
| Range | 4.00 | 5.00 | 1.08 | 2.37 | 1.54 | 0.58 | 0.00 | 0.20 |
| Standard Deviation | 0.97 | 0.78 | 0.57 | 0.81 | 0.57 | 0.21 | 0.00 | 0.08 |
| Standard Error Mean | 0.06 | 0.04 | 0.21 | 0.30 | 0.19 | 0.07 | 0.00 | 0.04 |
| Coefficient of Variation (%) | 15.27 | 16.76 | 11.63 | 19.26 | 12.22 | 5.46 | 0.00 | 3.02 |
| Skewness | 2.08 | 0.38 | 0.28 | 0.83 | -0.02 | 0.86 | * | 0.00 |
| Kurtosis | 5.13 | -0.85 | -1.91 | -0.50 | -1.33 | -0.80 | * | -1.00 |

**Appendix 1.3.** Summary statistics for *Striga* emergence counts of sorghum under *Striga* infestation without control (-) and with control (+) method using three methods.

| | **Control methods** | | | | | |
|---|---|---|---|---|---|---|
| Statistics | Genetic | | Cultural | | Integrated | |
| | - | + | - | + | - | + |
| Samples (N) | 11 | 11 | 20 | 20 | 8 | 8 |
| Mean | 119.70 | 13.32 | 204.40 | 136.50 | 52.64 | 21.65 |
| Mean difference (%) | 88.87 | | 33.21 | | 58.87 | |
| Median | 126.20 | 6.69 | 52.67 | 25.16 | 48.05 | 13.59 |
| Minimum | 102.60 | 3.69 | 9.21 | 1.49 | 14.62 | 1.83 |
| Maximum | 126.20 | 64.85 | 895.00 | 822.00 | 113.50 | 81.37 |
| Range | 23.52 | 61.16 | 885.80 | 820.50 | 98.88 | 79.54 |
| Standard Deviation | 10.99 | 17.84 | 293.50 | 254.80 | 35.31 | 27.11 |
| Standard Error Mean | 3.31 | 5.37 | 65.64 | 56.98 | 12.48 | 9.58 |
| Coefficient of Variation (%) | 9.17 | 133.90 | 143.60 | 186.70 | 67.07 | 125.20 |
| Skewness | -1.02 | 2.45 | 1.47 | 2.02 | 0.47 | 1.44 |
| Kurtosis | -0.95 | 4.70 | 0.52 | 2.47 | -1.02 | 1.00 |

**Appendix 1.4.** Summary statistics for *Striga* damage rating of sorghum under *Striga* infestation without control (-) and with control (+) method using three methods.

| Statistics | Control methods | | | | | |
|---|---|---|---|---|---|---|
| | Genetic | | Cultural | | Integrated | |
| | - | + | - | + | - | + |
| Samples (N) | 3 | 3 | 3 | 3 | 6 | 6 |
| Mean | 2.00 | 1.53 | 4.70 | 1.50 | 4.05 | 3.10 |
| Mean difference (%) | 23.50 | | 68.00 | | 23.45 | |
| Median | 2.00 | 1.70 | 4.70 | 1.10 | 4.00 | 3.70 |
| Minimum | 2.00 | 1.00 | 4.70 | 1.00 | 2.70 | 1.30 |
| Maximum | 2.00 | 1.90 | 4.70 | 2.00 | 5.50 | 4.40 |
| Range | 0.00 | 0.90 | 0.00 | 1.00 | 2.70 | 3.00 |
| Standard Deviation | 0.00 | 0.40 | 0.00 | 0.50 | 1.00 | 1.30 |
| Standard Error Mean | 0.00 | 0.20 | 0.00 | 0.20 | 0.40 | 0.50 |
| Coefficient of Variation (%) | 0.00 | 30.80 | 0.00 | 32.70 | 26.30 | 43.40 |
| Skewness | * | -0.50 | * | -0.40 | 0.10 | -0.50 |
| Kurtosis | * | -1.50 | * | -1.50 | -1.30 | -1.40 |

## Chapter 2: Screening tropical and sub-tropical maize germplasm for resistance to *Striga hermonthica* and *S. asiatica* and yield-related traits


### Abstract

Identification of maize germplasm with dual resistance to *Striga hermonthica (Sh)* and *S. asiatica (Sa),* could lead to the development of cultivars with stable resistance. 130 tropical and sub-tropical maize germplasms, including checks, were evaluated in a controlled environment for their reaction to *Sh* and *Sa* infestations using a 13x10 alpha lattice design with two replications over two seasons. Significant differences ($P<0.05$) were detected among the assessed genotypes for all the recorded traits in *Sh* and *Sa*-infested treatments. Under *Sa*-infested conditions, mean *Striga* emergence counts 8 weeks after planting (SEC8) and 10 weeks after planting (SEC10) were 5.00 and 45.50, respectively, while the mean *Striga* damage rate 8 weeks after planting (SDR8) and 10 weeks after planting (SDR10) were 3.35 and 3.07, respectively. Under *Sh*-infested conditions, SEC8 and SEC10 mean values were 3.66 and 3.77, respectively, while the SDR8 and SDR10 values were 5.25 and 2.75 respectively. Positive and significant ($P<0.05$) correlations were found between anthesis-silking interval (ASI) and SDR8 (r=0.18) and SDR10 (0.32) under *Sa*-infested conditions. Negative and significant correlations were recorded between ear per plant (EPP) and SEC8, SDR8, and SDR10, with r=-0.18, r=-0.27, and r=-0.24, respectively. Under *Sh*-infested conditions, significant and negative correlations were recorded between SDR8 and EPP (r=-0. 20), EHT and SEC8 (r=-0.22), EHT and SDR8 (r=-0.36), PLHT and SDR8 (-0.48), and PLHT and SDR10 (-0.22). The results suggest that dual resistance to the two *Striga* species exists in some tropical and sub-tropical maize lines. The following genotypes have dual resistance to *Sa* and *Sh*: CML440, CML566, CML540, CML539, CLHP0343, CLHP0326, TZISTR1248, TZSTRI115, TZISTR25, TZISTR1205, TZSTRI113, TZISTR1119, TZISTR1174 and the OPVs B.King/1421, Shesha/1421, ZM1421, DTSTR-W SYN13, DTSTR-Y SYN14, and 2*TZECOMP3DT/WhiteDTSTRSYN) C2. The identified genotypes are suitable for use as parents in developing high-performing maize varieties with *Striga* resistance and improved grain yield.



**Keywords:** Dual resistance, *Striga asiatica*, *Striga hermonthica*, maize breeding

## 2.1 **Introduction**

Maize (*Zea mays* L., 2n=2x=20) is the world's third most widely cultivated cereal crop, after wheat and rice. It is a vital food security crop in sub-Saharan Africa (SSA), constituting 85-95% of the region's carbohydrate intake (Johnmark et al., 2022). In SSA, maize is a source of livelihood for more than 300 million Africans (Regassa et al., 2021; Kansiime et al., 2023). It is a raw material for manufacturing industrial products, including livestock feed (Dabija et al., 2021). Despite the importance of the cereal, one out of five people living in communal and small-scale maize farming systems are at risk of starvation (Arndt et al., 2023). This is because the crop is vulnerable to many stress factors, one major biotic stress being parasitic weeds of the genus *Striga*.

*Striga,* popularly known as witchweed, is endemic and widespread throughout SSA. The species *S. asiatica* (red flower type) is predominant in Southern Africa, and *S. hermonthica* (purple flower) is widely distributed in Western, Central, and Eastern Africa (Dossa et al., 2023b). *Striga hermonthica* has the largest geographical distribution in Africa, spreading from latitudes of 5° N and 20° S. The two holoparasites cause severe crop damage through stunting and leaf chlorosis, leading to yield losses ranging from 30% to 100% under severe infestation (Mutsvanga et al., 2022). Maize suffers yield losses caused by these parasites due to the paucity of *Striga* resistance sources in the maize gene pool, and only partial resistance has been reported. Over 50 million hectares of agricultural land under cereal cultivations, including maize, have been infested by *Striga* spp (Dafaallah, 2019; David et al., 2022). The annual losses caused by *Striga* have been estimated to USD 10 billion across SSA (Dafaallah, 2019; Samejima and Sugimoto, 2022). Under heavy, *Striga* infestations farmers are often forced to abandon their farms.

Cultural practices, crop protection chemicals, biological control, host plant resistance, and integrated *Striga* management approach are the main control strategies recommended for *Striga* management. Germination stimulants such as ethylene and ethephon, when applied on infested croplands before sowing, can deplete *Striga* seed banks by inducing suicidal germination without a host (Samejima et al., 2016). Imidazolinone herbicides are also effective against *Striga* (Kanampiu et al., 2003). Maize seeds with imazapyr resistance can be coated with small doses of the herbicide, significantly reducing *Striga* emergence (David et al., 2011; Kamara et al., 2020). However, using imazapyr-coated maize in a smallholder maize production system is difficult since the chemical is toxic to other crops (Souto et al., 2020). Most of the proposed

control methods are impractical to implement under communal and small-scale farming systems. Most farmers do not have enough land to crop rotate, nor do they have access to large quantities of organic matter for effective cultural control practices (Shayanowako et al., 2020). Furthermore, they cannot afford to buy agrochemicals and sprayers. Hence, the development and use of *Striga*-resistant cultivars is the most feasible management option (Gasura et al., 2021; Dossa et al., 2023a).

*Striga*-resistant cultivars can reduce *Striga* seed production and the *Striga* seed bank in infested soils (Badu-Apraku et al., 2020a). Resistant cultivars can induce the germination of *Striga* seeds but prevent the parasite from attaching to the maize plant. Concerted efforts have been made by the International Institute of Tropical Agriculture (IITA) in Nigeria and national maize research programs to develop tropical maize genotypes with resistance to *Sh* (Badu-Apraku et al., 2020b; Yacoubou et al., 2021a). However, the performance of their germplasm against *Sa* is unknown. High-yielding and *Striga*-resistant sub-tropical maize varieties are yet to be developed (Shayanowako et al., 2018a). Therefore, the IITA genetic resources can serve as breeding parents with resistance to *Sh* and need to be evaluated for their levels of resistance to *Sa*, and for yield improvements under *Sa*-infestation. Likewise, sub-tropical maize varieties should be screened for *Striga* resistance and yield performance under both *Sa* and *Sh* infestation. This can also benefit West and Central Africa with a diversity of resistance genes that could be useful for accumulating improved levels of partial resistance.

*Striga* emergence count, *Striga* damage rating, and grain yield under *Striga* infestation are the major selection indices used in resistance breeding (Menkir et al., 2007). The choice of the selection method to be used in the genetic improvement of maize depends on the type of gene action controlling *Striga* resistance in maize. *Striga* resistance in maize is quantitatively inherited with many minor genes with small additive effects and is significantly influenced by the environment (Lane et al., 1997; Badu-Apraku et al., 2020a), making breeding complex and challenging. Hybrid breeding, backcrossing, and recurrent selection are common methods widely used in incorporating *Striga* tolerance/resistance genes into well-adapted maize varieties. However, the initial steps of these methods include the collection and evaluation of maize germplasm with different genetic backgrounds to identify potential sources of resistance (Yacoubou et al., 2021b). Screening for *Striga* resistance in maize includes field, greenhouse, and laboratory conditions (Shayanowako et al., 2018b). However, the use of greenhouse conditions is the most efficient for managing the level of *Striga* infestation and environmental conditions (Kountche et al., 2019; Yacoubou et al., 2021b).

The existing *Striga*-resistant cultivars of maize in SSA are bred for *Sh* resistance, while no commercially grown maize varieties are resistant to *Sa*. In most of the East African countries, the two species occur in tandem (Gethi and Smith, 2004). Germplasm with dual resistance to both parasites would be extremely valuable across the continent. This part of the study aimed to evaluate 130 tropical and sub-tropical maize germplasms in a controlled environment for their reaction to *Sh* and *Sa* infestations and resistance breeding. This study is, therefore, one of the few attempts to report on the performance of tropical and sub-tropical maize germplasm under both *Sa* and *Sh* infestation to select inbred lines with dual resistance to the two dominant *Striga* species. The study focused on identifying tropical and sub-tropical maize germplasm resistant to both *Striga* species.

## 2.2 **Materials and Methods**

### **2.2.1 Plant material and study sites**

The study screened maize genotypes for *Striga* resistance at the University of Kwazulu-Natal Controlled Environment Facilities (UKZN-CEF) in two cropping seasons (December 2021 to April 2022, and August 2022 to December 2022). During the two summer seasons, average maximum temperatures are between 26 and 28°C, while minimum temperature is 10°C. The UKZN CEF is situated at the UKZN College of Agriculture, Engineering, and Science (29.62° S, 30.40° E). The study used 130 maize genotypes, comprising 74 acquired from the International Institute of Tropical Agriculture (IITA)/Nigeria, 45 from the International Maize and Wheat Improvement Centre, Zimbabwe (CIMMYT)/Zimbabwe, and 10 from the National Plant Genetic Resources Centre, South Africa (NPGRC)/South Africa (Table 2.1). The germplasm from IITA/Nigeria comprised 55 inbred lines (genotypes number 1 to 55 in Table 2.1), 4 single cross hybrids (genotypes number 127 to 130 in Table 2.1), and 15 open-pollinated varieties (OPV) (genotypes number 112 to 126 in Table 2.1). Out of the 55 inbred lines, 21 were generated from multi-parent crosses of elite *Striga*-resistant lines, while the remaining were derived from synthetics IWD-SYN, Syn-Y-STR, and ACR97SYN, composites TZL CompI and TZE Comp5. The CIMMYT/Zimbabwe germplasm included 43 inbred lines (genotype number 56 to 98 in Table 2.1), and 1 OPV (genotype number 110 in Table 2.1). The NPGRC/South Africa germplasm included 5 OPVs (genotype 99 to 103 Table 2.1) and 6 hybrids (genotype 104 to 109 Table 2.1). The Nigerian accessions were tropical varieties developed for *Sh* resistance, generated from multi-parent populations (Menkir, 2006; Simon et al., 2018; Gasura et al., 2019). CIMMYT provided sub-tropical maize germplasm. Their

material was developed for drought tolerance. The OPVs and hybrids germplasms from NPGRC/South Africa and CIMMYT/Zimbabwe were used as local checks, while the OPVs and hybrids from IITA were *Sh*-resistant checks. The *Sa* and *Sh* seeds were collected from sorghum and maize-infested fields in Tanzania and Kenya, respectively.

**Table 2.1** List and source of maize genotypes evaluated in the present study

| No° | Germplasm name/designation | Source/Origin | *Striga* resistance /genotype description | Pedigree |
|---|---|---|---|---|
| 1 | TZISTR1154 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-1-B*4)-4-B*4 |
| 2 | TZISTR1261 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-5-BBB)-3-B*4 |
| 3 | TZISTR1248 | IITA/Nigeria | Resistant/inbred line | (ACR97TZLComp1-YS155-4-1-3-B*4/ACR97SYN-Y-S1-76-B*4)-32-1-BB-B |
| 4 | TZISTR1263 | IITA/Nigeria | Resistant/inbred line | (TZECOMP5-Y-C7-S3-56-B*4/TZECOMP5-25-1-1-3-#-2-B*4)-38-1-BB-B |
| 5 | TZISTR1275 | IITA/Nigeria | Resistant/inbred line | (TZECOMP5-Y-C7-S3-150-B*4/TZECOMP5-Y-C7-S3-56-B*4)-24-1-BB-B |
| 6 | TZISTR1157 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-1-B*4)-28-B*4 |
| 7 | TZISTR1160 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-1-B*4)-50-B*4 |
| 8 | TZISTR1162 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-5-BBB)-17-B*4 |
| 9 | TZISTR1165 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-1-B*4)-21-B*4 |
| 10 | TZISTR1175 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-5-BBB)-3-1-1-BB |
| 11 | TZISTR1178 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-5-BBB)-56-1-1-BB |
| 12 | TZISTR1163 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-5-BBB)-25-B*4 |
| 13 | TZISTR1166 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-1-B*4)-54-B*4 |
| 14 | TZISTR1190 | IITA/Nigeria | Resistant/inbred line | (ZDiploBC4-472-2-2-1-2-3-B-1-B*5/ZDiploBC4-19-4-1-#-3-1-B-1-B*4)-2-1-BB-B |
| 15 | TZISTR1199 | IITA/Nigeria | Resistant/inbred line | (ZDiploBC4-472-2-2-1-2-3-B-1-B*5/ZDiploBC4-19-4-1-#-3-1-B-1-B*4)-44-1-BB-B |
| 16 | TZISTR1231 | IITA/Nigeria | Resistant/inbred line | (ACR97SYN-Y-S1-79-B*4/ACR97TZLComp1-YS155-4-1-3-B*4)-46-1-BB-B |
| 17 | TZISTR1232 | IITA/Nigeria | Resistant/inbred line | (ACR97SYN-Y-S1-79-B*4/ACR97TZLComp1-YS155-4-1-3-B*4)-50-1-BB-B |
| 18 | TZISTR1259 | IITA/Nigeria | Resistant/inbred line | (TZECOMP5-Y-C7-S3-56-B*4/TZECOMP5-25-1-1-3-#-2-B*4)-28-1-BB-B |
| 19 | TZISTR1262 | IITA/Nigeria | Resistant/inbred line | |
| 20 | TZISTR1159 | IITA/Nigeria | Resistant/inbred line | (ACRSYN-W-S2-173-B*4/TZLCompIC4S1-37-1-B*4)-36-B*4 |
| 21 | TZISTR1223 | IITA/Nigeria | Resistant/inbred line | IWD-SYN-STR-C3-11-1-B*5 |
| 22 | TZISTR1225 | IITA/Nigeria | Resistant/inbred line | (ACR97SYN-Y-S1-79-B*4/ACR97TZLComp1-YS155-4-1-3-B*4)-14-1-BB-B |
| 23 | TZISTR1244 | IITA/Nigeria | Resistant/inbred line | (ACR97TZLComp1-YS155-4-1-3-B*4/ACR97SYN-Y-S1-76-B*4)-21-1-BB-B |
| 23 | TZISTR1244 | IITA/Nigeria | Resistant/inbred line | (ACR97TZLComp1-YS155-4-1-3-B*4/ACR97SYN-Y-S1-76-B*4)-21-1-BB-B |
| 24 | TZSTRI101 | IITA/Nigeria | Resistant/inbred line | TZL Comp. IC4 S1-37-1-B-B-B |
| 25 | TZSTRI102 | IITA/Nigeria | Resistant/inbred line | TZL Comp. IC4 S1-37-5-B-B-B |
| 26 | TZSTRI104 | IITA/Nigeria | Resistant/inbred line | Z.diplo.BC4-472-2-2-1-2-3-B-B-B-B-B |
| 27 | TZSTRI107 | IITA/Nigeria | Resistant/inbred line | Z.Diplo.BC4-472-2-3-1-1-B-1-B*5 |

CIMMYT, International Maize and Wheat Improvement Centre; IITA, International Institute of Tropical Agriculture; NPGRC/SA, National Plant Genetic Resources Centre/South Africa, OPV, open-pollinated variety.

**Table 2.1** (continued)

| No° | Germplasm name/designation | Source/Origin | *Striga* resistance /genotype description | Pedigree |
|---|---|---|---|---|
| 28 | TZSTRI108 | IITA/Nigeria | Resistant/inbred line | Z. Diplo.BC4-472-2-1-1-2-1-B-1-B-B-B-B |
| 29 | TZSTRI109 | IITA/Nigeria | Resistant/inbred line | ACR97SYN-Y-S1-79-B-B-B |
| 30 | TZSTRI110 | IITA/Nigeria | Resistant/inbred line | ACR97SYN-Y-S1-24-B-B-B |
| 31 | TZSTRI112 | IITA/Nigeria | Resistant/inbred line | TZE COMP5-25-1-1-3-#-2-B-B-B |
| 32 | TZSTRI114 | IITA/Nigeria | Resistant/inbred line | TZECOMP5-Y-C7-S3-55-B-B-B |
| 33 | TZSTRI115 | IITA/Nigeria | Resistant/inbred line | TZECOMP5-Y-C7-S3-56-B-B-B |
| 34 | TZISTR25 | IITA/Nigeria | Resistant/inbred line | 9450-B-B |
| 35 | TZISTR1001 | IITA/Nigeria | Resistant/inbred line | ZDiploBC4-467-4-1-2-1-1-B-1-B*6 |
| 36 | TZISTR1003 | IITA/Nigeria | Resistant/inbred line | TZLCompIC4S1-37-1-B*7 |
| 37 | TZISTR1004 | IITA/Nigeria | Resistant/inbred line | ZdiploBC4-472-2-3-4-3-B-2-B*8 |
| 38 | TZISTR1008 | IITA/Nigeria | Resistant/inbred line | TZLCompIC4S1-38-5-B*6 |
| 39 | TZISTR1011 | IITA/Nigeria | Resistant/inbred line | Syn-Y-STR-(43-2)-1-1-5-1-B*6 |
| 40 | TZISTR1018 | IITA/Nigeria | Resistant/inbred line | ACR97TZL-CCOMP1-Y-S3-34-2-B*9 |
| 41 | TZEEI21 | IITA/Nigeria | Resistant/inbred line | |
| 42 | TZEEI13 | IITA/Nigeria | Resistant/inbred line | |
| 43 | TZEEI14 | IITA/Nigeria | Resistant/inbred line | |
| 44 | TZEEI49 | IITA/Nigeria | Resistant/inbred line | |
| 45 | TZDEEI55 | IITA/Nigeria | Resistant/inbred line | |
| 46 | TZDEEI50 | IITA/Nigeria | Resistant/inbred line | |
| 47 | TZEEI34 | IITA/Nigeria | Resistant/inbred line | |
| 48 | TZISTR1174 | IITA/Nigeria | Resistant/inbred line | |
| 49 | TZISTR1205 | IITA/Nigeria | Resistant/inbred line | |
| 50 | TZSTRI113 | IITA/Nigeria | Resistant/inbred line | |
| 51 | TZISTR1119 | IITA/Nigeria | Resistant/inbred line | |
| 52 | TZISTR1015 | IITA/Nigeria | Resistant/inbred line | |
| 53 | TZDEEI64 | IITA/Nigeria | Resistant/inbred line | |
| 54 | TZDEEI54 | IITA/Nigeria | Resistant/inbred line | |

CIMMYT, International Maize and Wheat Improvement Centre; IITA, International Institute of Tropical Agriculture; NPGRC/SA, National Plant Genetic Resources Centre/South Africa, OPV, open-pollinated variety.

**Table 2.1** (continued)

| No° | Germplasm name/designation | Source/Origin | *Striga* resistance /genotype description | Pedigree |
|---|---|---|---|---|
| 55 | TZEEI10 | IITA/Nigeria | Resistant/inbred line | |
| 56 | CML312 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 57 | CML444 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 58 | CML442 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 59 | CML550 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 60 | CML547 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 61 | CML539 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 62 | CML440 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 63 | CML566 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 64 | CML540 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 65 | CML545 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 66 | CML571 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 67 | CML390 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 68 | CLHP0352 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 69 | HA04A-2107-36 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 70 | CLHP0303 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 71 | CLHP0221 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 72 | CLHP0020 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 73 | CLHP0058 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 74 | CKDHL0378 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 75 | CLHP0312 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 76 | CLHP0310 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 77 | CLHP0003 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 78 | CKDHL0467 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 79 | CLHP00378 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 80 | CLHP0156 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 81 | CLHP0113 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 82 | CLHP03302 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 83 | CLHP0404 | CIMMYT/Zimbabwe | Unknown/Inbred line | |

CIMMYT, International Maize and Wheat Improvement Centre; IITA, International Institute of Tropical Agriculture; NPGRC/SA, National Plant Genetic Resources Centre/South Africa, OPV, open-pollinated variety.

**Table 2.1** (continued)

| No° | Germplasm name/designation | Source/Origin | *Striga* resistance /genotype description | Pedigree |
|---|---|---|---|---|
| 84 | CLHP0343 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 85 | CZL1380 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 86 | CLHP0326 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 87 | CZL99017 | CIMMYT/Zimbabe | Unknown/Inbred line | |
| 88 | CLHP0049 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 89 | CLHP00478 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 90 | CLHP00286 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 91 | CML451 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 92 | CLHP0302 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 93 | CLHP0364 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 94 | CLHP0350 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 95 | CLHP00294 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 96 | CLHP0005 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 97 | CLHP0022 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 98 | CML304 | CIMMYT/Zimbabwe | Unknown/Inbred line | |
| 99 | ZM1423/Z.DLO | NPGRC/South Africa | Unknown/local OPV | |
| 100 | NC.QPM/Z.DPLO | NPGRC/South Africa | Unknown/local OPV | |
| 101 | M.Pearl/DT-STR | NPGRC/South Africa | Unknown/local OPV | |
| 102 | NC.QPM/DT-STR | NPGRC/South Africa | Unknown/local OPV | |
| 103 | ZM1421/DT-STR | NPGRC/South Africa | Unknown/local OPV | |
| 104 | N.Choice/1421 | NPGRC/South Africa | Unknown/local hybrid | |
| 105 | B.King/1421 | NPGRC/South Africa | Unknown/local hybrid | |
| 106 | Colorado/1421 | NPGRC/South Africa | Unknown/local hybrid | |
| 107 | Hickory/1421 | NPGRC/South Africa | Unknown/local hybrid | |
| 108 | Kep/1421 | NPGRC/South Africa | Unknown/local hybrid | |
| 109 | Shesha/1421 | NPGRC/South Africa | Unknown/local hybrid | |
| 110 | ZM1423 | CIMMYT/Zimbabwe | Unknown/local OPV | |
| 111 | ZM1421 | CIMMYT/Zimbabwe | Unknown/local hybrid | |

CIMMYT, International Maize and Wheat Improvement Centre; IITA, International Institute of Tropical Agriculture; NPGRC/SA, National Plant Genetic Resources Centre/South Africa, OPV, open-pollinated variety.

**Table 2.1** (continued)

| No° | Germplasm name/designation | Source/Origin | *Striga* resistance /genotype description | Pedigree |
|---|---|---|---|---|
| 112 | STR-SYN-Y2 | IITA/Nigeria | Resistant/OPV | |
| 113 | Z.diplo-BC4-C3-W/DOGONA-1/Z.diplo-BC4-C3-W | IITA/Nigeria | Resistant/OPV | |
| 114 | STR-SYN-Y2 | IITA/Nigeria | Resistant/OPV | |
| 115 | TZBSTR (Susceptible)(RE) | IITA/Nigeria | Resistant/OPV | |
| 116 | STR-SYN-W1 | IITA/Nigeria | Resistant/OPV | |
| 117 | DTSTR-W SYN13 | IITA/Nigeria | Resistant/OPV | |
| 118 | DTSTR-Y SYN15 | IITA/Nigeria | Resistant/OPV | |
| 119 | ((IWD C3 SYN*2/(White DT STR Syn))-DT C1 | IITA/Nigeria | Resistant/OPV | |
| 120 | DTSTR-W SYN11 | IITA/Nigeria | Resistant/OPV | |
| 121 | SAMMMZ16 | IITA/Nigeria | Resistant/OPV | |
| 122 | (TZEOMP5C7/TZECOMP3DTC2) C2 | IITA/Nigeria | Resistant/OPV | |
| 123 | ((TZL COMP1-W C6*2/(White DT STR Syn))-DT C1 | IITA/Nigeria | Resistant/OPV | |
| 124 | TZCOM1/ZDPSYN | IITA/Nigeria | Resistant/OPV | |
| 125 | DTSTR-Y SYN14 | IITA/Nigeria | Resistant/OPV | |
| 126 | (2*TZECOMP3DT/WhiteDTSTRSYN) C2 | IITA/Nigeria | Resistant/OPV | |
| 127 | TZSTR1137/TZSTR1132 | IITA/Nigeria | Resistant/hybrid | |
| 128 | TZSTR1159/TZSTR1132 | IITA/Nigeria | Resistant/hybrid | |
| 129 | TZSTR1160/TZSTR1132 | IITA/Nigeria | Resistant/hybrid | |
| 130 | TZSTR1166/TZSTR1132 | IITA/Nigeria | Resistant/hybrid | |

CIMMYT, International Maize and Wheat Improvement Centre; IITA, International Institute of Tropical Agriculture; NPGRC/SA, National Plant Genetic Resources Centre/South Africa, OPV, open-pollinated variety.

### 2.2.2 Experimental design and trial management

The 130 genotypes were evaluated under two *Striga* treatments using a 13 x 10 alpha lattice design with two replications in each *Striga*-infested environment. The maize genotypes were evaluated under *Sa* and *Sh* infestations. The experimental unit consisted of 4 plastic pots of 15-L capacity, filled with a composted pine bark potting mix for each *Striga*-infested environment. Two weeks before planting, each pot was infested with a scoop of sand mixed with 0.03 g of two years old *Sa* or *Sh* seed containing approximately 3000 *Striga* seeds. Standard agronomic practices recommended for maize production were followed. Hand weeding was routinely done to remove all weeds except *Striga*. Figure 2.1 shows the experimental setup with artificial infestations of maize with *Sa* (A, B, and C), and *Sh* (D and E) in the greenhouse condition at the University of KwaZulu-Natal, South Africa.

### 2.2.3 Data collection

Data were collected on maize phenotypic traits and *Striga* parameters in the *Sa* and *Sh*-infested environments. The following phenotypic traits were evaluated on maize: Days to 50% silking (DS), recorded as the number of days taken by 50% of the plants to silk in each plot; Days to anthesis (DA), recorded as the number of days from planting until 50% of the plants have emerged silks and shed pollen, respectively; Anthesis-silking interval (ASI), measured as the difference between days to 50% silking and 50% anthesis; Plant height (PLHT) and ear height (EHT), measured as the distance from the base of the plant to the height of the first tassel branch and the node bearing the upper ear, respectively; Root lodging (RL) was recorded as a percentage of plants leaning more than 30° from the vertical; Stalk lodging (SLG) (percentage broken at or below the highest ear node); and Number of rotten ears (EROT). The number of ears per plant (EPP) was obtained by dividing the total number of ears per plot by the number of plants harvested. Husk cover (HUSK) was rated on a scale of 1 to 5, where 1 = husks tightly arranged and extended beyond the ear tip and 5 = ear tips exposed. Ear aspect (EASP) was recorded based on a scale of 1 to 9, where 1 = clean, uniform, large, and well-filled ears and 9 = ears with undesirable features. Grain yield per plant (GY/plant) was determined as the weight (g) of the grain from the ears of individual plants after shelling, adjusted to a constant moisture of 12.5%.

The *Striga* parameters were recorded, including the number of emerged *Sa* and *Sh* plants 8 and 10 weeks after planting, denoted as SEC8 and SEC10. A rating of host plant damage 8 and 10 weeks after planting, designated as SDR8 and SDR10, was done using a visual rating score of 1 to 9 where 1 = no damage, indicating normal plant growth and a high level of tolerance, and 9 = complete collapse or death of the maize plant, i.e., highly susceptible (Kim, 1994).

### 2.2.4 Data-analysis

The collected data from *Sa* and *Sh*-infested environments were subjected to analysis of variance using a lattice procedure, using the package *agricolae* in RStudio version 2023. 06.1 (R Core Team, 2023). The normality of the data was tested using kurtosis and skewness values, which were coumputed using Genstat version 23.1.0.651. The mean values of the test genotypes for the assessed traits were compared at the 5% significance level using Fisher's least significance difference (LSD). Broad sense heritability ($H^2$) (hereafter referred to as heritability) was computed using DeltaGen (Jahufer and Luo, 2018) with the following formula:

$$(H^2)= \frac{\sigma^2 g}{\sigma^2 g+\frac{\sigma^2 s}{ns}+\frac{\sigma^2 r}{nr}+\frac{\sigma^2 b}{nb}+\frac{\sigma_\varepsilon^2}{ns+nr+nb}}$$

where $\sigma^2 g, \sigma^2 s, \sigma^2 r, \sigma^2 b,$ and $\sigma_\varepsilon^2$ are the variance components for genotypes, season, replication, block, and the pooled error, respectively, and ns, nr, and nb are the number of seasons, replications, and blocks, respectively.

Pearson's correlation coefficients (r) were calculated separately for *Sa* and *Sh*-infested conditions using RStudio version 4.3.1 (Team, 2010). The rotated component matrix and principal component analysis biplots (PCA) were generated separately for the assessed traits under *Sa*, and *Sh*-infested conditions using the packages *ggplot2*, *factoextra*, and *FactoMiner* (Alboukadel, 2017) in RStudio version 4.3.1. Cluster heatmap plots were generated based on the mean values of the traits recorded in both *Sa* and *Sh* environments to establish the Clustering of the genotypes using Deltagen (Jahufer and Luo, 2018).

## 2.3 **Results**

### 2.3.1 Analysis of variance (ANOVA)

The analysis of variance revealed significant differences among the evaluated genotypes for all the recorded traits (P<0.001) (Table 2.2) under both *Sa* and *Sh*-infested environments. Testing seasons exerted significant effects (P<0.001) on all the traits under *Sa*-infested conditions

except for EPP, PLHT, HUSK, and SEC10, and under *Sh*-conditions except for EPP, PLHT, EHT, and HUSK. Significant differences were recorded for all the assessed traits except for EPP due to the block nested to replication-by-season interaction effect under both *Sa* and *Sh*-infested environments.

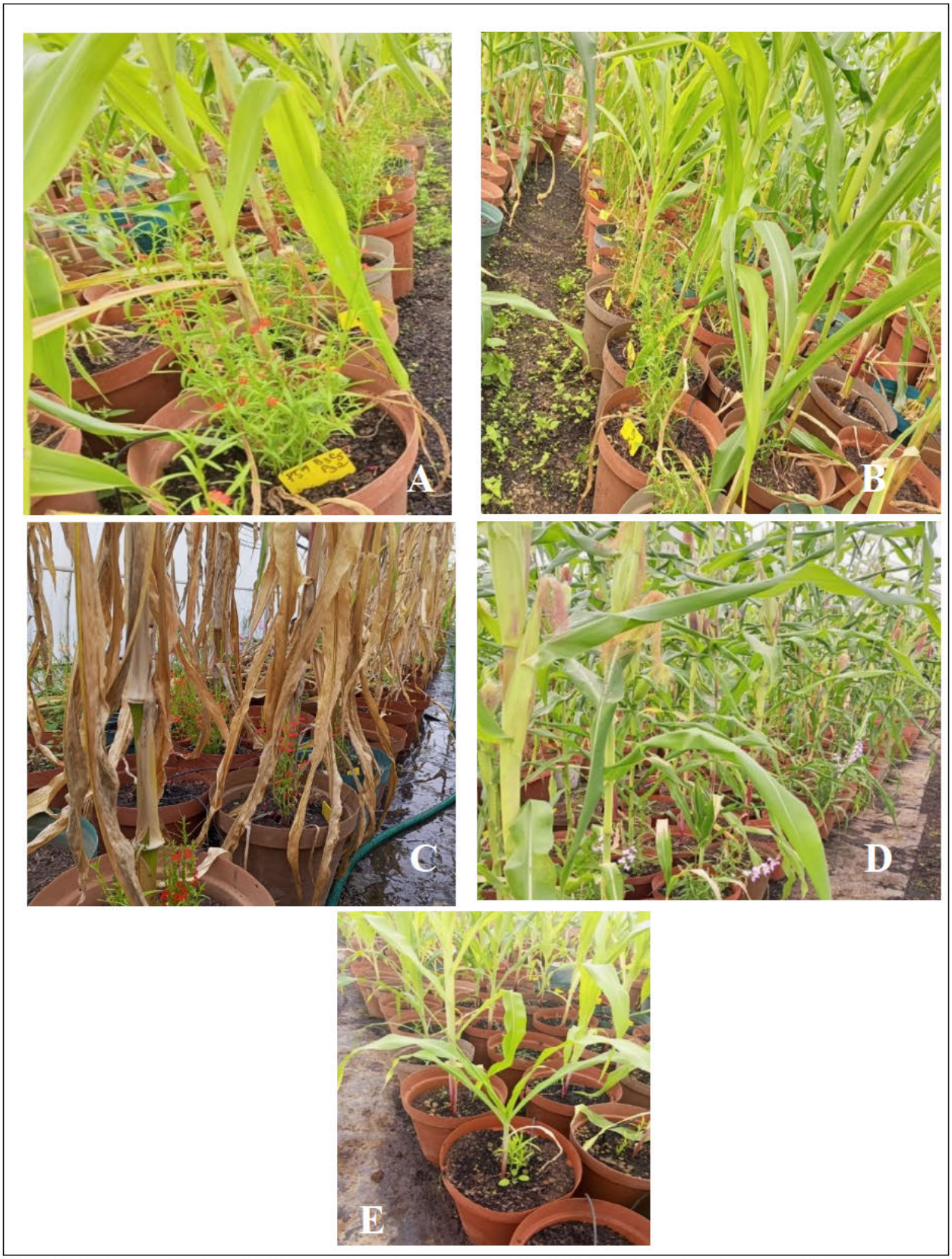


**Figure 2.1** Photographs showing the experimental setup with artificial infestations of maize with *Striga asiatica* (A, B, and C), and *S. hermonthica* (D and E) in the African Center for Crop Improvement greenhouse at the University of KwaZulu-Natal, South Africa.

**Table 2.2** Analysis of variance for yield components and *Striga* parameters of 126 maize genotypes evaluated under *Sa* and *Sh* infestation conditions.

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | ***S. asiatica*** | | | | | | | |
| **Source of variation** | Df | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
| **Genotype (G)** | 125 | 9.34*** | 7.27*** | 4.06*** | 6.49*** | 2.10*** | 5.82*** | 3.65*** | 9.95*** | 2.47*** | 4.05*** | 2.79*** | 2.19*** | 2.41*** | 2.91*** |
| **Season (S)** | 1 | 273.78*** | 100.64*** | 33.01*** | 0.00 | 0.27 | 20.82*** | 0.00 | 29.74*** | 43.79*** | 54.71*** | 1518.79*** | 3.48 | 56.80*** | 37.88*** |
| **G x S** | 125 | 0.0666 | 0.00 | 0.084 | 0.00 | 0.00 | 0.00 | 0.06 | 0.00 | 0.036 | 0.00 | 0.54 | 0.00 | 0.00 | 0.00 |
| **Replication in season** | 1 | 0.35 | 0.00 | 0.44 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.39 | 0.00 | 51.62*** | 0.00 | 0.00 | 0.00 |
| **Block/(replication x season)** | 13 | 0.46** | 9.29** | 4.36** | 0.00 | 0.59** | 5.73** | 0.07** | 1.51** | 0.08** | 0.06** | 2.06** | 2.69** | 2.00** | 0.90** |
| **Error** | 238 | 15.40 | 20.03 | 12.28 | 0.03 | 106.99 | 0.05 | 0.28 | 2.08 | 3.47 | 1439.00 | 1.51 | 144.80 | 2.22 | 2.13 |
| | | | | | | | ***S. hermonthica*** | | | | | | | |
| **Source of variation** | df | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
| **Genotype (G)** | 125 | 2.43*** | 2.29*** | 1.76*** | 3.01*** | 2.17*** | 1.84*** | 1.48** | 1.47** | 2.76*** | 2.45*** | 4.97*** | 2.13*** | 2.08*** | 2.24*** |
| **Season (S)** | 1. | 125.84*** | 158.08*** | 32.01*** | 0.00 | 3.14 | 23.37 | 1.03 | 17.77*** | 18.89*** | 72.91*** | 3255.33*** | 78.31*** | 222.49*** | 71.81*** |
| **G x S** | 125 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.25 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| **Replication in season** | 1 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.26 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| **Block/(replication x season)** | 13 | 10.73** | 7.20** | 0.58** | 0.00 | 0.52** | 4.70* | 3.83** | 10.61** | 2.82* | 5.07** | 4.05** | 2.00** | 2.54** | 1.98** |
| **Error** | 233 | 36.00 | 51.00 | 15.75 | 0.03 | 3.61 | 0.08 | 0.49 | 7.09 | 5.40 | 1473.00 | 1.20 | 6.44 | 2.27 | 1.76 |

*, **, and *** denote significant difference at P < 0.05, P < 0.01 and P < 0.001, respectively, Df = degrees of freedom, DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

### 2.3.2 Mean performance and statistical summary

#### 2.3.2.1 *Under Sa-infested conditions*

Appendix 2.1 summarizes the mean performance and the statistics of the 126 genotypes evaluated under *Sa* infestation. The kurtosis values ranged from -7 to 7, except for EPP, HUSK, GY, and SEC10, while the skewness varied from -2 to 2. The coefficient of variation (CV%) of all the traits under *Sa* infestation ranged from 4.89% to 426.82% (Table 2.3). Smaller variations were obtained for DA followed by DS, with CV values of 4.89% and 5.60%, respectively. The highest variation was exhibited by PLHT followed by ASI, with CV values of 426.82% and 268.88%, respectively. Inbred lines had a mean ASI of 2.77, while the OPV and hybrid checks had mean ASI values of 1.86 and 1.77, respectively. The EPP ranged from 1.00 to 2.00. The mean yield ranged from 0.00 g/plant to 277.50 g/plant for TZISTR1262 and CML540, respectively, with a mean of 62.77 g/plant for the inbred lines, while ranging from 00.00 g/plant to 214.00 g/plant for Hickory/1421 and N.Choice/1421, respectively for the hybrid checks, and from 35.00 g/plant to 169.50 g/plant (((IWD C3 SYN*2/(White DT STR Syn)) -DT C1 and NC.QPM/Z.DPLO respectively) for the OPVs checks. The top inbred lines and checks are shown in Table 2.3. The best-yielding genotypes were generally taller than the poorer-performing genotypes, with the longest cobs and moderate or high EASP. The greatest reduction in *Striga* emergence in SEC8 occurred with relatively high-yielding genotypes, e.g., TZISTR1154 (2.00), TZISTR1263 (2.00), TZISTR1261 (2.50), TZISTR1015 (2.50), TZISTR1174 (3.00), TZSTRI113 (3.00), TZISTR1119 (3.00), TZISTR1205 (3.50), TZISTR1248 (3.50), the local OPVs M.Pearl/DT-STR (2.00), ZM1421/DT-STR (2.50), and the *Striga*-resistant checks DTSTR-Y SYN14 (2.50), and NC.QPM/DT-STR (3.00). The SEC10 mean was 45.50, 10.32, and 9.07 for the inbred lines, the OPVs, and the hybrids, respectively. Genotypes such as inbred line TZISTR1174 and *Striga*-resistant check OPV DTSTR-W SYN11 exhibited high numbers for SEC10 and are still relatively high yielding. The inbred lines exhibited an SDR8 mean value of 3.35, while the OPVs and hybrids showed an SDR8 of 3.14 and 2.36, respectively. SDR10 mean scores were 3.07, 4.30, and 2.71 for the inbred lines, the OPVs, and the hybrid checks, respectively. Genotypes with high yields generally showed moderate or large reductions in SDR8 and SDR10 values. The following high-yielding genotypes displayed relatively high and moderate reductions in scores for SDR8 and SDR10: CML566, CML440, TZISTR1248, ZM1421, and local check (B.King/1421). None of the genotypes exhibited SLG, RL, and EROT under *Sa* infestation. High broad-sense

heritability was recorded for CL (0.97), EHT (0.96), EASP (0.96), DS (0.94), ASI (0.94), DA (0.90), and GY (0.88) under *Sa*-infested conditions. However, the low heritability of *Sa* resistance is worth noting, reflected in the *Striga* parameters SEC10, SDR8, and SDR10 under *Sa*-infested conditions. In contrast, under *Sh*-infested conditions, high heritability values were estimated for all the traits except for GY (0.02).

**Table 2.3** Mean responses for 14 traits of 126 maize genotypes evaluated under *Sa* infestation, showing the top 10 inbred lines, the top 4 hybrids, and 6 OPVs.

| Genotype | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP (1 to 9) | GY (g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Top 10 inbred lines** | | | | | | | | | | | | | | |
| **CML540** | 77.00 | 81.50 | 4.50 | 1.00 | 2.03 | 0.77 | 1.00 | 11.00 | 3.50 | 277.50 | 4.00 | 1.50 | 3.50 | 3.00 |
| **CML566** | 82.50 | 79.00 | 3.50 | 1.00 | 2.22 | 1.15 | 1.00 | 12.00 | 1.50 | 155.50 | 4.00 | 5.50 | 1.50 | 1.50 |
| **TZISTR1001** | 82.00 | 82.00 | 0.00 | 1.00 | 2.10 | 1.28 | 1.00 | 11.00 | 1.50 | 140.00 | 4.50 | 4.50 | 3.00 | 2.50 |
| **TZISTR1205** | 81.50 | 75.50 | 6.00 | 1.00 | 1.85 | 0.91 | 1.00 | 11.00 | 1.00 | 114.25 | 3.50 | 13.00 | 3.00 | 2.50 |
| **TZSTRI115** | 77.50 | 77.00 | 0.50 | 1.00 | 2.10 | 1.20 | 1.00 | 11.50 | 1.50 | 112.50 | 5.00 | 2.00 | 3.50 | 2.50 |
| **CLHP0350** | 75.00 | 76.00 | 1.00 | 1.00 | 2.35 | 0.81 | 3.00 | 14.00 | 3.50 | 102.75 | 5.00 | 3.50 | 2.00 | 3.50 |
| **CLHP0049** | 80.50 | 78.00 | 2.50 | 1.00 | 1.25 | 0.70 | 1.00 | 10.00 | 3.00 | 101.25 | 7.00 | 4.00 | 1.00 | 2.50 |
| **CLHP0302** | 81.00 | 80.50 | 0.50 | 1.00 | 1.76 | 1.00 | 3.00 | 13.25 | 3.00 | 98.00 | 4.50 | 7.00 | 2.00 | 3.50 |
| **CML440** | 82.50 | 76.00 | 6.50 | 1.00 | 2.36 | 1.08 | 1.00 | 11.00 | 1.50 | 96.25 | 4.50 | 13.50 | 3.00 | 1.50 |
| **CLHP0303** | 84.50 | 83.50 | 1.00 | 1.50 | 1.87 | 1.15 | 1.00 | 7.25 | 3.00 | 92.50 | 4.50 | 8.50 | 3.00 | 3.00 |
| **Top 4 hybrids and 6 OPVs** | | | | | | | | | | | | | | |
| **N.Choice/1421** | 82.00 | 76.50 | 5.50 | 1.00 | 1.90 | 1.03 | 1.00 | 13.25 | 1.50 | 214.00 | 5.00 | 4.00 | 3.50 | 3.50 |
| **Shesha/1421** | 75.50 | 72.50 | 3.00 | 1.00 | 2.03 | 1.75 | 1.00 | 18.75 | 1.50 | 165.75 | 7.50 | 18.50 | 2.00 | 2.00 |
| **B.King/1421** | 80.50 | 78.50 | 2.00 | 1.00 | 2.05 | 1.15 | 2.00 | 23.50 | 1.50 | 157.25 | 5.00 | 4.50 | 1.00 | 2.00 |
| **ZM1421/DT-STR** | 77.00 | 76.50 | 0.50 | 1.00 | 2.38 | 1.10 | 1.50 | 10.75 | 3.00 | 93.50 | 2.50 | 19.00 | 2.50 | 2.00 |
| **NC.QPM/Z.DPLO** | 71.50 | 71.50 | 0.00 | 1.00 | 2.25 | 1.03 | 0.00 | 12.50 | 4.50 | 154.25 | 3.00 | 5.00 | 3.50 | 2.00 |
| **Z.diplo-BC4-C3-W/DOGONA-1/Z.diplo-BC4-C3-W** | 81.00 | 83.00 | 2.00 | 1.00 | 2.36 | 1.05 | 1.00 | 11.50 | 1.50 | 112.00 | 6.00 | 8.50 | 3.00 | 3.50 |
| **DTSTR-W SYN13** | 85.50 | 85.50 | 0.00 | 1.00 | 1.25 | 0.85 | 1.50 | 13.00 | 3.50 | 107.50 | 4.50 | 3.50 | 1.50 | 1.00 |
| **TZBSTR** | 83.00 | 83.50 | 0.50 | 1.00 | 2.65 | 1.30 | 1.50 | 14.50 | 1.00 | 103.00 | 6.50 | 3.00 | 3.00 | 2.50 |
| **ZM1423** | 69.00 | 69.50 | 0.50 | 1.00 | 0.85 | 1.39 | 1.00 | 10.50 | 1.50 | 99.25 | 4.50 | 16.50 | 5.00 | 3.00 |
| **(2*TZECOMP3DT/WhiteDTSTRSYN) C2** | 69.00 | 78.00 | 9.00 | 1.00 | 1.75 | 0.85 | 1.50 | 12.25 | 2.50 | 89.00 | 6.00 | 0.50 | 2.00 | 1.50 |
| **Trial statistics** | | | | | | | | | | | | | | |
| **LSD (5%)** | 3.94 | 4.44 | 3.69 | 0.15 | 10.57 | 0.23 | 0.52 | 1.55 | 1.93 | 37.73 | 1.87 | 12.44 | 1.64 | 1.61 |
| **Skewness** | 0.33 | 0.74 | -0.81 | 3.88 | -0.15 | 0.59 | 2.79 | 1.20 | 0.70 | 3.49 | 0.61 | 3.31 | 0.27 | 0.34 |
| **Kurtosis** | 0.33 | 0.53 | 4.25 | 13.06 | -0.53 | 0.82 | 11.77 | 3.53 | -0.36 | 25.56 | -0.83 | 13.64 | -0.89 | -0.61 |
| **SEM** | 7.64 | 8.75 | 7.27 | 0.21 | 20.82 | 0.46 | 1.02 | 3.05 | 3.80 | 74.31 | 3.69 | 24.51 | 3.23 | 3.17 |
| **%CV** | 4.89 | 5.60 | 268.88 | 14.65 | 426.82 | 25.36 | 41.21 | 13.63 | 58.57 | 56.12 | 40.91 | 129.74 | 50.29 | 49.50 |
| **Heritability** | 0.90 | 0.94 | 0.94 | 0.11 | 0.11 | 0.96 | 0.96 | 0.97 | 0.96 | 0.88 | 0.34 | 0.01 | 0.11 | 0.16 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing. LSD= least significant difference, SEM= standard error of mean, %CV= coefficient of variation, m= meter, cm= centimeter, g= gramme.

2.3.2.2 ***Under Sh-infested conditions***

Appendix 2.2 shows the mean performances and the summary statistics of the evaluated genotypes for all traits under *Sh*-infested conditions. The kurtosis values varied from -7 to 7, except for ASI, EPP, PLHT, and HUSK, while the skewness ranged from -2 to 2 except for EPP, PLHT, and HUSK. The CV% of the traits ranged from 7.15% to 597.49% (Table 2.4). The DA exhibited the lowest variation of 7.15%, while PLHT exhibited the highest variation of 597.49%, as was the case under *Sa* infested environment. The mean ASI was 1.52 for the inbred lines, 1.26, and 2.03 for the OPVs and the hybrids, respectively. The mean yield ranged from 10.05 g/plant to 151 g/plant, with a mean of 63.83 g/plant for the inbred lines, from 34.75 g/plant to 133.25 g/plant with a mean of 79.79 g/plant for the hybrids, and 33.60 g/plant to 144.25 g/plant with a mean of 70.81 g/plant for the OPVs. The sub-tropical inbred line CML304, which exhibited the lowest SDR10 under *Sa*, showed the highest GY under *Sh*. The lowest GY among the inbred lines was exhibited by the sub-tropical line HA04A-2107-36. The local check OPV ZM1423 exhibited the highest GY, whereas the *Striga* susceptible check TZBSTR showed the lowest GY. The top 10 inbred lines, as well as the top 10 check genotypes showing high GY under *Sh,* are presented in Table 2.4. The SEC8 mean was 63.89, 70.81, and 79.79, whereas the SEC10 mean was 3.25, 4.43, and 3.28 for the inbred lines, the OPVs, and the hybrids, respectively. The following high-yielding genotypes displayed the greatest reduction in SEC10 scores: TZDEEI50 (1.70) CML550 (2.63), TZISTR1001 (2.70), and B.King/1421 (2.63). The mean SDR8 was 5.25, 3.86, and 3.11 for the inbred lines, the OPVs, and the hybrids checks, respectively while the SDR10 means were 2.75, 3.05, and 3.11 in the same order. The high-yielding genotypes CML539 and ZM1421 resulted in the greatest reduction in SDR8. The genotype TZDEEI54 resulted in the greatest reduction of 0.75 in SDR10, while the least reductions were displayed by the low-yielding genotypes CKDHL0378 (5.75) and CZL1380 (5.50).

**Table 2.4** Mean responses for 14 traits of 126 maize genotypes evaluated under *Sh* infestation, showing the top 10 inbred lines, the top 4 hybrids, and 6 OPVs

| Genotypes | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP (1 to 9) | GY (g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Top 10 lines** | | | | | | | | | | | | | | |
| **CML304** | 79.25 | 79.63 | 0.38 | 1.00 | 1.44 | 0.75 | 1.00 | 12.00 | 4.75 | 151.00 | 3.18 | 2.00 | 4.75 | 2.75 |
| **TZSTRI101** | 90.00 | 87.50 | 2.50 | 1.00 | 1.45 | 0.75 | 1.00 | 12.46 | 3.25 | 144.00 | 3.63 | 6.50 | 3.75 | 3.00 |
| **CLHP0404** | 74.75 | 74.25 | 0.50 | 1.00 | 2.07 | 0.75 | 1.00 | 10.00 | 6.25 | 137.35 | 3.18 | 5.00 | 6.00 | 2.00 |
| **TZISTR1119** | 78.75 | 77.00 | 1.75 | 1.00 | 1.81 | 0.95 | 1.00 | 10.50 | 3.75 | 135.75 | 3.68 | 4.50 | 5.50 | 3.50 |
| **TZISTR25** | 75.75 | 75.50 | 0.25 | 1.00 | 2.25 | 1.05 | 1.00 | 12.00 | 1.25 | 131.00 | 3.20 | 2.00 | 3.75 | 2.00 |
| **TZISTR1205** | 81.00 | 83.00 | 2.00 | 1.00 | 2.21 | 1.00 | 1.00 | 9.50 | 1.75 | 129.00 | 4.18 | 1.00 | 3.75 | 2.50 |
| **CML566** | 78.00 | 76.00 | 2.00 | 1.00 | 2.07 | 1.20 | 1.00 | 12.00 | 1.25 | 127.00 | 2.25 | 4.50 | 1.75 | 2.75 |
| **TZISTR1001** | 79.63 | 78.25 | 1.38 | 1.00 | 2.10 | 1.03 | 1.00 | 11.50 | 1.75 | 120.00 | 2.70 | 1.50 | 3.50 | 2.50 |
| **TZISTR1174** | 79.25 | 79.63 | 0.38 | 1.00 | 1.44 | 0.75 | 1.00 | 12.00 | 4.75 | 151.00 | 3.18 | 2.00 | 4.75 | 2.75 |
| **TZSTRI113** | 74.50 | 73.00 | 1.50 | 1.00 | 1.41 | 0.90 | 1.00 | 9.00 | 1.75 | 111.75 | 2.68 | 3.50 | 3.75 | 2.75 |
| **Top 4 hybrids and 6 OPVs** | | | | | | | | | | | | | | |
| **N.Choice/1421** | 81.25 | 75.25 | 6.00 | 1.00 | 1.62 | 0.85 | 1.50 | 10.96 | 1.75 | 133.25 | 3.13 | 3.50 | 4.00 | 3.00 |
| **Shesha/1421** | 71.50 | 70.75 | 0.75 | 1.00 | 1.82 | 0.88 | 1.50 | 10.71 | 1.75 | 112.25 | 4.63 | 2.50 | 4.00 | 2.75 |
| **B.King/1421** | 81.00 | 77.75 | 3.25 | 1.00 | 2.35 | 1.05 | 1.50 | 11.71 | 3.25 | 91.75 | 2.63 | 4.50 | 2.25 | 2.25 |
| **ZM1421** | 82.38 | 80.75 | 1.63 | 1.00 | 2.10 | 0.95 | 1.50 | 10.71 | 2.25 | 88.00 | 2.63 | 2.00 | 1.75 | 3.25 |
| **ZM1423** | 70.25 | 71.88 | 1.63 | 1.00 | 2.17 | 0.94 | 1.00 | 13.71 | 1.25 | 144.25 | 4.63 | 2.50 | 1.75 | 2.50 |
| **STR-SYN-Y2** | 85.25 | 85.25 | 0.00 | 1.00 | 1.60 | 0.80 | 1.00 | 11.25 | 3.25 | 126.85 | 8.18 | 3.50 | 3.25 | 2.50 |
| **DTSTR-W SYN13** | 89.25 | 88.50 | 0.75 | 1.00 | 0.98 | 0.75 | 1.50 | 10.00 | 3.75 | 115.35 | 4.68 | 5.50 | 3.50 | 2.50 |
| **ZM1423/Z.DLO** | 81.25 | 83.25 | 2.00 | 1.00 | 12.41 | 1.03 | 1.00 | 10.75 | 4.75 | 96.75 | 2.68 | 5.00 | 3.75 | 2.75 |
| **DTSTR-Y SYN14** | 80.13 | 79.75 | 0.38 | 1.00 | 1.36 | 0.75 | 1.50 | 11.50 | 1.75 | 93.25 | 3.68 | 1.00 | 3.75 | 3.75 |
| **DTSTR-Y SYN15** | 83.75 | 84.25 | 0.50 | 1.00 | 1.78 | 0.65 | 1.00 | 9.00 | 6.25 | 87.35 | 3.18 | 4.50 | 4.00 | 2.75 |
| **Trial statistics** | | | | | | | | | | | | | | |
| **LSD (5%)** | 5.71 | 7.10 | 2.58 | 0.09 | 1.58 | 1.15 | 0.62 | 2.18 | 1.39 | 34.87 | 34.87 | 2.37 | 1.62 | 1.17 |
| **Skewness** | 0.40 | -0.32 | -6.16 | 5.34 | 10.00 | -0.35 | 3.02 | 0.20 | 0.23 | 1.44 | 0.21 | 0.63 | 0.25 | 0.62 |
| **Kurtosis** | 0.26 | 4.13 | 69.13 | 26.53 | 105.80 | -0.20 | 12.58 | 1.54 | -0.97 | 2.72 | -0.93 | 0.49 | -0.23 | 0.68 |
| **SEM** | 8.19 | 15.88 | 5.08 | 0.18 | 2.58 | 2.26 | 1.39 | 4.87 | 4.20 | 77.95 | 77.95 | 5.31 | 3.62 | 2.61 |
| **%CV** | 7.15 | 8.95 | 597.49 | 12.24 | 87.15 | 28.59 | 49.30 | 21.39 | 43.80 | 52.81 | 52.81 | 64.59 | 47.58 | 41.79 |
| **Heritability** | 0.42 | 0.89 | 0.89 | 0.88 | 0.92 | 0.92 | 0.88 | 0.92 | 0.88 | 0.002 | 0.87 | 0.92 | 0.82 | 0.91 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing. LSD= least significant difference, SEM= standard error of mean, %CV= coefficient of variation, m= meter, cm= centimeter, g= gramme.

### 2.3.3 Principal component and biplot analyses

The rotated components matrix showing the percentages of variances of different principal components (PC) and the respective loadings of recorded traits are shown in Table 2.5. The first four PCs under *Sa*-infested conditions had a cumulative variance of 50.80%. The first PC had the highest variation of 17.38% followed by PC2 with 13.32%. DS, DA, EHT, CL, GY, and SDR8 contributed the most to PC1, while EPP, EASP, SDR8, and SDR10 contributed strongly to PC2. The highest loadings for PC3 were DS, GY, and DA, followed by SEC10, while the highest loadings for PC4 were SEC8, and CL, followed by HUSK, EPP, and SEC10. Under *Sh*-infested conditions, DS, DA, EHT, SDR8, and SEC8 had high positive loadings into the first PC, explaining 17.06% of the total variance. PC2 was highly influenced by GY, SEC8, CL, and EHT, which had a high loading, explaining 31.82% of the total variance. SDR8, SDR10, DA, and DS had the highest loadings into PC3, while PC4 was most influenced by HUSK, PLHT, and ASI.

**Table 2.5** Rotated component matrix for 10 yield components and 4 *Striga* parameters in 126 maize genotypes under *Sa* and *Sh*-infested conditions.

| | ***Sa*** | | | | ***Sh*** | | | |
|---|---|---|---|---|---|---|---|---|
| **Traits** | **PC1** | **PC2** | **PC3** | **PC4** | **PC1** | **PC2** | **PC3** | **PC4** |
| DA | 17.17 | 9.90 | 16.59 | 0.90 | 18.58 | 2.32 | 18.85 | 0.93 |
| DS | 22.02 | 1.17 | 21.56 | 0.80 | 26.88 | 3.70 | 14.19 | 1.26 |
| ASI | 1.44 | 8.42 | 1.31 | 0.44 | 8.96 | 1.55 | 0.00 | 16.19 |
| EPP | 1.77 | 18.61 | 0.42 | 10.40 | 3.65 | 0.08 | 3.75 | 14.48 |
| PLHT | 2.44 | 4.09 | 0.11 | 15.37 | 2.42 | 3.41 | 0.48 | 21.22 |
| EHT | 12.49 | 2.32 | 2.57 | 0.05 | 11.45 | 12.91 | 0.22 | 0.00 |
| HUSK | 3.26 | 3.76 | 4.41 | 13.84 | 0.39 | 1.21 | 0.37 | 34.65 |
| CL | 11.47 | 0.00 | 0.91 | 17.26 | 0.00 | 12.91 | 1.83 | 3.15 |
| EASP | 5.33 | 15.95 | 12.88 | 0.05 | 0.35 | 25.29 | 4.19 | 0.65 |
| GY | 9.46 | 4.52 | 20.73 | 5.10 | 0.03 | 25.52 | 7.97 | 1.43 |
| SEC8 | 1.10 | 0.54 | 1.10 | 21.64 | 10.09 | 0.02 | 2.58 | 0.12 |
| SEC10 | 0.05 | 2.77 | 14.31 | 9.02 | 0.10 | 5.48 | 0.06 | 0.94 |
| SDR8 | 8.64 | 12.92 | 2.99 | 3.64 | 11.85 | 3.51 | 18.57 | 0.09 |
| SDR10 | 3.35 | 15.03 | 0.10 | 1.50 | 5.25 | 2.09 | 26.94 | 4.89 |
| Eigenvalue | 2.43 | 1.91 | 1.53 | 1.24 | 2.39 | 2.07 | 1.66 | 1.29 |
| Variance percentage (%) | 17.38 | 13.63 | 10.96 | 8.82 | 17.06 | 14.77 | 11.85 | 9.24 |
| Cumulative variance percentage (%) | 17.38 | 31.01 | 41.97 | 50.80 | 17.06 | 31.82 | 43.67 | 52.91 |

PC: principal component, DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP= ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

Biplots based on principal components are presented to decipher the performance of the maize germplasm with *Sa* and *Sh* infestations using Figure 2.2 and Figure 2.3, respectively. Smaller angles between vectors of recorded traits indicate a high correlation between the traits in discriminating genotypes. Genotypes plotted closer to and further along a vector line scored highly in that trait. Under *Sa*-infested conditions, the genotypes were evenly scattered across both PC1 and PC2 (Figure 2.2). The angles between vectors of GY and those of PLHT and HUSK, were acute, indicating a strong positive correlation between the traits and with high-yielding genotypes TZSTRI115 (34), TZISTR1001 (36), CML451 (86), TZISTR1015 (98), TZBSTR (110), ZM1423 (104), TZISTR1205 (95), and NC.QPM/Z.DPLO (106). The same analysis can be made with all the *Striga* parameters SEC8, SEC10, SDR8, and SDR10, which showed small angles with each other and with ASI, pointing to a high positive correlation between the traits. Genotypes CML312 (49), CML571 (60), CML539 (55), CLHP0049 (83), CLHP00286 (85), CML304 (93), STR -SYN -Y2 (107), and SAMMMZ16 (115) showed more susceptibility to *Sa* because they were closely associated with vectors of SEC8, SEC10, SDR8, and SDR10. However, the angles formed between the vectors of GY, SEC8, SEC10, SDR8, and SDR10 were close to 90°, which means that the association between the traits is weak. EASP, DA, DS, and EPP showed a negative correlation with poor yielding genotypes including TZISTR1154 (1), TZISTR1275 (5), TZISTR1165 (9), TZISTR1159 (20), and TZSTRI109 (30).

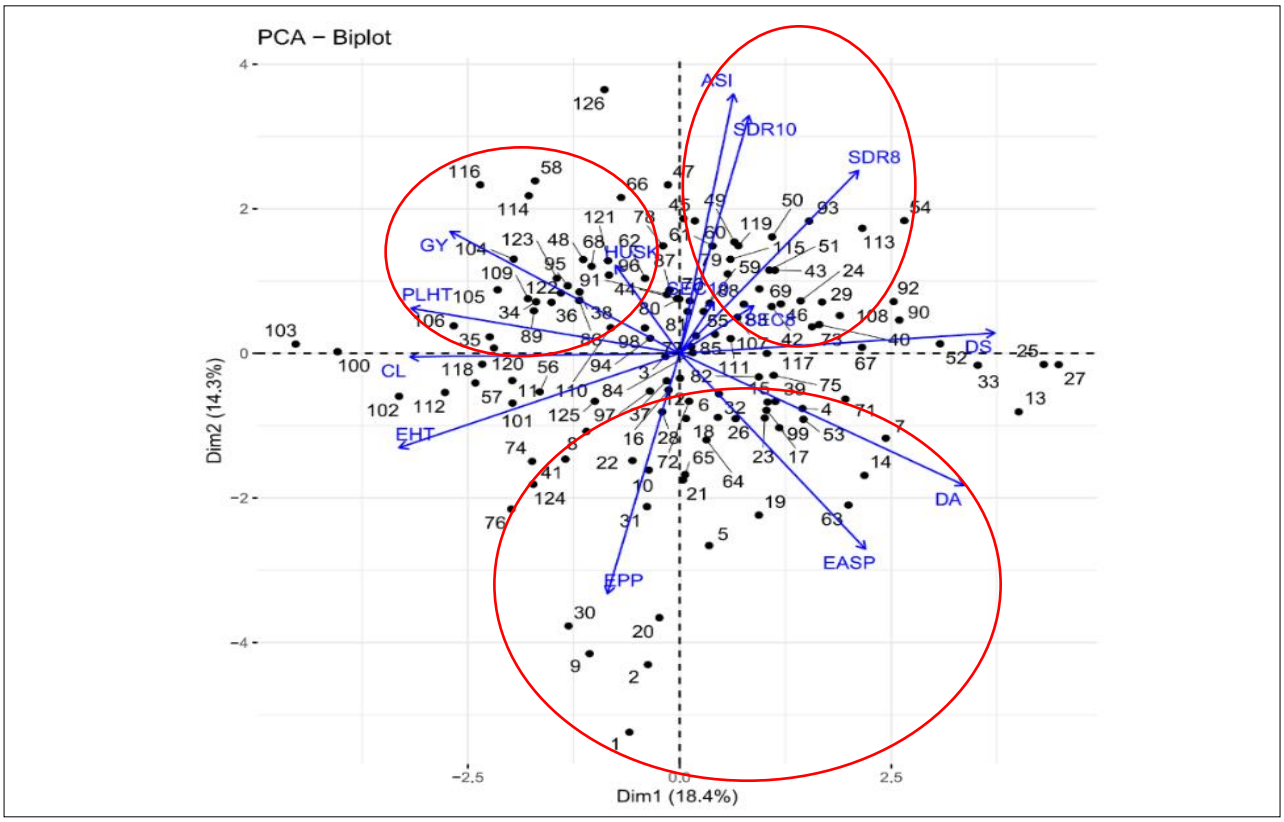


**Figure 2.2** Principal component of 126 maize population under *Sa*-infested condition. Genotypes are coded with numbers as recorded in Appendix 2.1. Dim= dimension, DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

Under *Sh*-infested conditions (Figure 2.3), GY had a strong correlation with EHT, PLHT, and EPP and with the high-yielding genotypes, including CML304 (93) and ZM1423 (104), which showed a high score in these traits. The *Striga* parameters SEC8, SEC10, SDR8, and SDR10 positively correlated with EASP, and all plotted far from the vector of GY, indicating a negative correlation between the traits and low *Striga* emergence counts genotypes, including TZISTR1263 and Colorado/1421. The same summary is made with low SDR8 and SDR10 reduction genotypes CLHP0404, CKDHL0378, CZL1380, M.Pearl/DT-STR, and Colorado/1421, which were negatively correlated with GY.

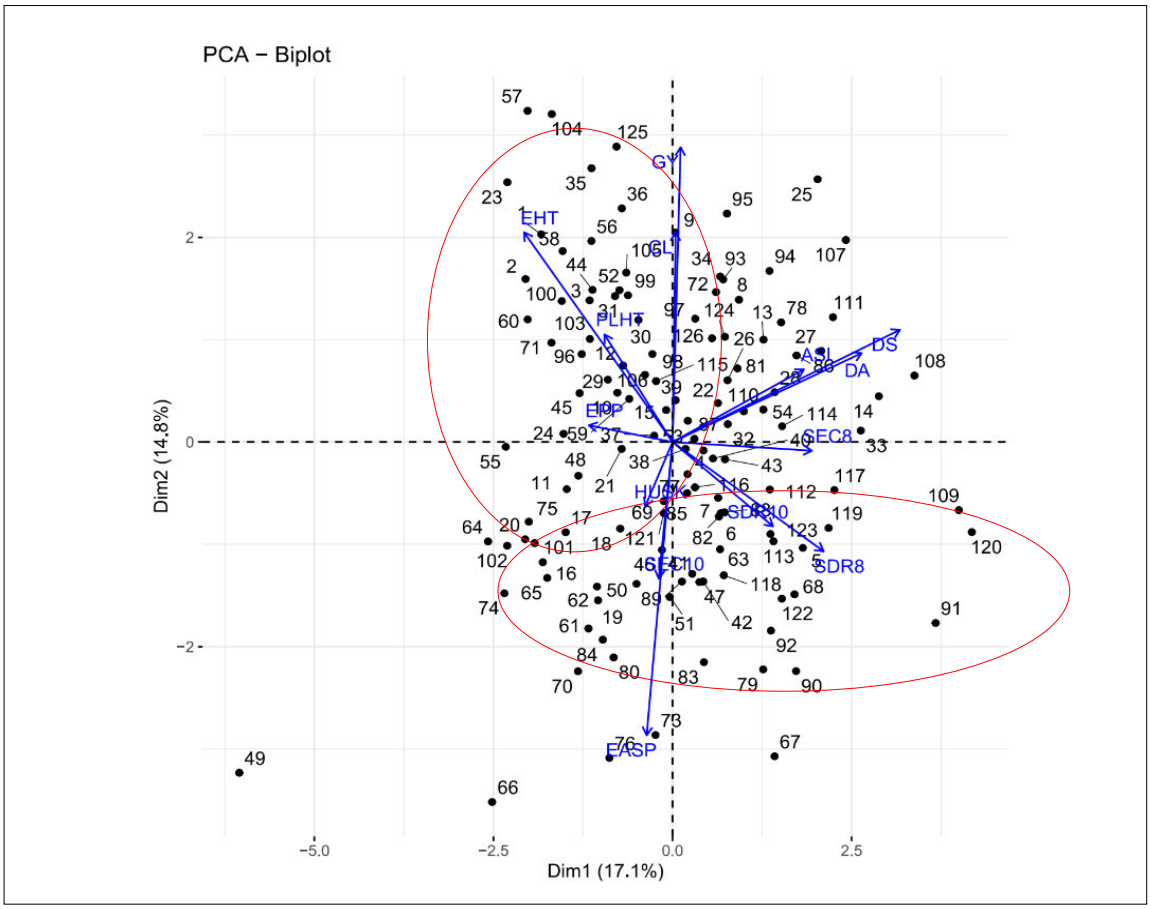


**Figure 2.3** Principal component of 126 maize population under *Sh*-infested condition. Genotypes are coded with numbers as recorded in Appendix 2.2. Dim= dimension, DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

### 2.3.4 Correlation of maize yield components and *Striga* parameters

Phenotypic correlation coefficients showing the relationship between GY and agronomic traits, within agronomic traits, within *Striga* parameters, and between GY and *Striga* parameters under both *Sa* and *Sh* infested conditions are shown in Figure 2.4A and Figure 2.4B, respectively**.** Under *Sa* conditions (Figure 2.4A), GY had a positive and significant correlation with CL and PLHT, with correlation coefficients of r=0.33 and r=0.18, respectively. Negative and significant correlations were found between GY and EASP (r=-0.50). The agronomic traits PLHT and EHT showed positive and significant correlations of r=0.28 and r=0.29 with CL, respectively. A positive and significant correlation was also recorded between DA and DS (r=0.83). The correlation between EPP and EASP, DS and ASI, and PLHT and EHT were also positive and significant (r=0.18, r=0.30, and r=0.54, respectively). However, negative and significant correlations were recorded between the following agronomic traits: DA and ASI

(r=-0.29), EPP and ASI (r=-0.22), EHT and DS (r=-0.18), CL and DA (r=-0.20), CL and DS (r=-0.21), PLHT and DA (-0.18), PLHT and DS (r=-0.20). ASI showed a positive and significant correlation between SDR8 (r=0.18) and SDR10 (0.32). PLHT and SDR10 had a positive and significant correlation of r=0.18. EPP exhibited a negative and significant correlation with SEC8, SDR8, and SDR10 (r=-0.18, r=-0.27, and r=-0.24, respectively). SDR8 exhibited negative and significant correlations with EHT (r=-0.32) and CL (r=-0.22). The correlation between SDR8 and SDR10 was positive and significant (r=0.54).

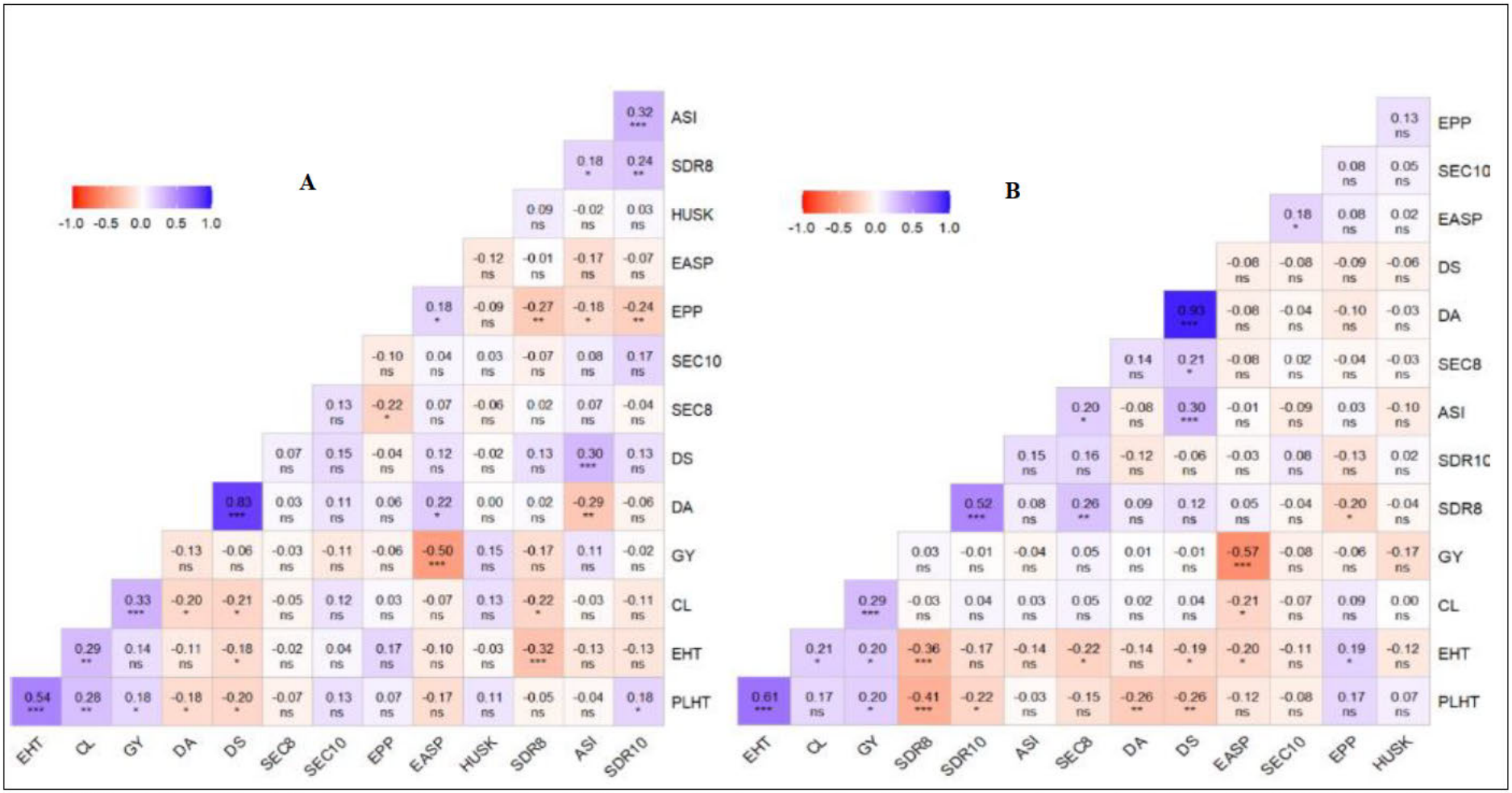


**Figure 2.4** Correlation matrix plot between yield components and *Striga* parameters in a population of 126 maize genotypes under *Sa* (A) and *Sh* (B) infestation. The colour variation indicates the magnitude of correlations; traits with deep blue are strongly and positively correlated, while deep red are strongly negatively correlated. Note *, ** and *** denote the level of significance associations of traits at 0.05, 0.01, and <0.001 probability values, respectively, and ns=non-significant. EHT= ear height, CL= cob length, GY= grain yield, DA= days to 50% anthesis, DS= days to 50% silking, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, EPP = ear per plant, EASP= ear aspect, HUSK= husk cover, SDR8= *Striga* damage rating eight days after sowing, ASI= anthesis-silking interval, SDR10= *Striga* damage rating 10 days after sowing, PLHT= plant height.

Under *Sh* conditions (Figure 2.4B), GY was positively correlated with EHT (r=0.20), CL (r=0.29), and PLHT (0.20), whereas with EASP, GY and CL exhibited a negative correlation of r=-0.57 and r=-0.21, respectively. Positive and significant correlations were revealed between the agronomic parameters DS and DA (r=0.93), ASI and DS (r=0.30), and PLHT and EHT (r=0.61). However, negative and significant correlations were found between EHT and DS (r=-0.19), PLHT and DA (r=-0.26), and PLHT and DS (r=-0.26). Positive and significant correlations were observed between maize agronomic traits and *Striga* parameters. These include the positive correlation recorded between DS and SEC8 (r=0.21), EASP and SEC10 (r=0.18), and ASI and SEC8 (r=0.20). However, negative, and significant correlations were recorded for SDR8 with EPP (r=-0.20) and EHT (r-0.20). A negative correlation was recorded for EHT with SEC8 (r=-0.22) and SDR8 (r=-0.36), and PLHT with SDR10 (r=-0.22), and SDR8 (r=-0.48). The *Striga* parameter SDR8 was positively correlated with SEC8 (r=0.26) and SDR10 (r=0.52).

### 2.3.5 Cluster analysis based on yield components and *Striga* parameters

Cluster heatmap analysis based on eight maize and *Striga* phenotypic traits is presented for both *Sa* (Figure 2.5 and Appendix 2.3) and *Sh*-infested environments (Figure 2.6 and Appendix 2.4). The heatmap shows clusters based on the mean performances of each trait from the lowest performance (blue colour) to the highest performance (red colour). In a *Sa*-infested environment, the heatmap revealed six clusters (Figure 2.5) where genotypes in the first cluster (I) had the highest scores in EASP, ASI, and SDR8 reduction. For instance, the IITA lines TZISTR1154, TZISTR1225, TZISTR1018, TZISTR1178, TZISTR1163, and hybrid ZM1421, which exhibited high SDR8 reductions and high scores in EASP, are classified in that cluster. Genotypes in the second cluster (II) had low ASI and high SEC10 values, including some IITA lines TZISTR1166, TZISTR1244, TZSTRI101, TZSTRI104, some CMMYT lines CLHP0326, CLHP00378, CLHP0049, CLHP0022, and IITA OPVs DTSTR-W SYN13, and TZL COMP1-W C6*2/(White DT STR Syn-DT C1, which all exhibited low SEC10 reductions. Genotypes from the third cluster (III) had moderate EASP and moderate SEC8 values and included some CIMMYT lines CML312, CML444, CML442, CML571, CML390, IITA lines TZSTRI108, TZEEI14, TZEEI49, TZISTR1011, and TZDEEI50 and OPVs STR-SYN-Y2, and Z. Diplo.BC4C3-W-DT C1. Cluster IV comprised genotypes exhibiting the lowest SEC10 reduction, moderate ASI, moderate PLHT, and moderate SDR10 reduction. The genotype CML304, which showed a high SEC10 number, was clustered together with the IITA OPVs

(2*TZECOMP3DT/WhiteDTSTRSYN) C2, NC.QPM/DT-STR, ZM1421/DT-STR, and DTSTR-Y SYN14. Cluster V consisted of genotypes with high SDR10 reduction, moderate PLHT, and moderate SDR10, and comprised some good-yielding genotypes, including CKDHL0378, CML451, CLHP0350, CLHP0005, ZM1423/Z.DLO, TZISTR1174, (TZEOMP5C7/TZECOMP3DTC2) C2, and Colorado/1421. Cluster VI comprised genotypes that exhibited high GY, moderate PLHT, and high SDR10 reduction. The cluster had the high-yielding CIMMYT lines CML440, CML566, CML540, CML545, CLHP0156, and the IITA OPVs TZBSTR, Z.diplo-BC4-C3-W/DOGONA-1/Z.diplo-BC4-C3-W, and showed high GY under *Sa* infestation.

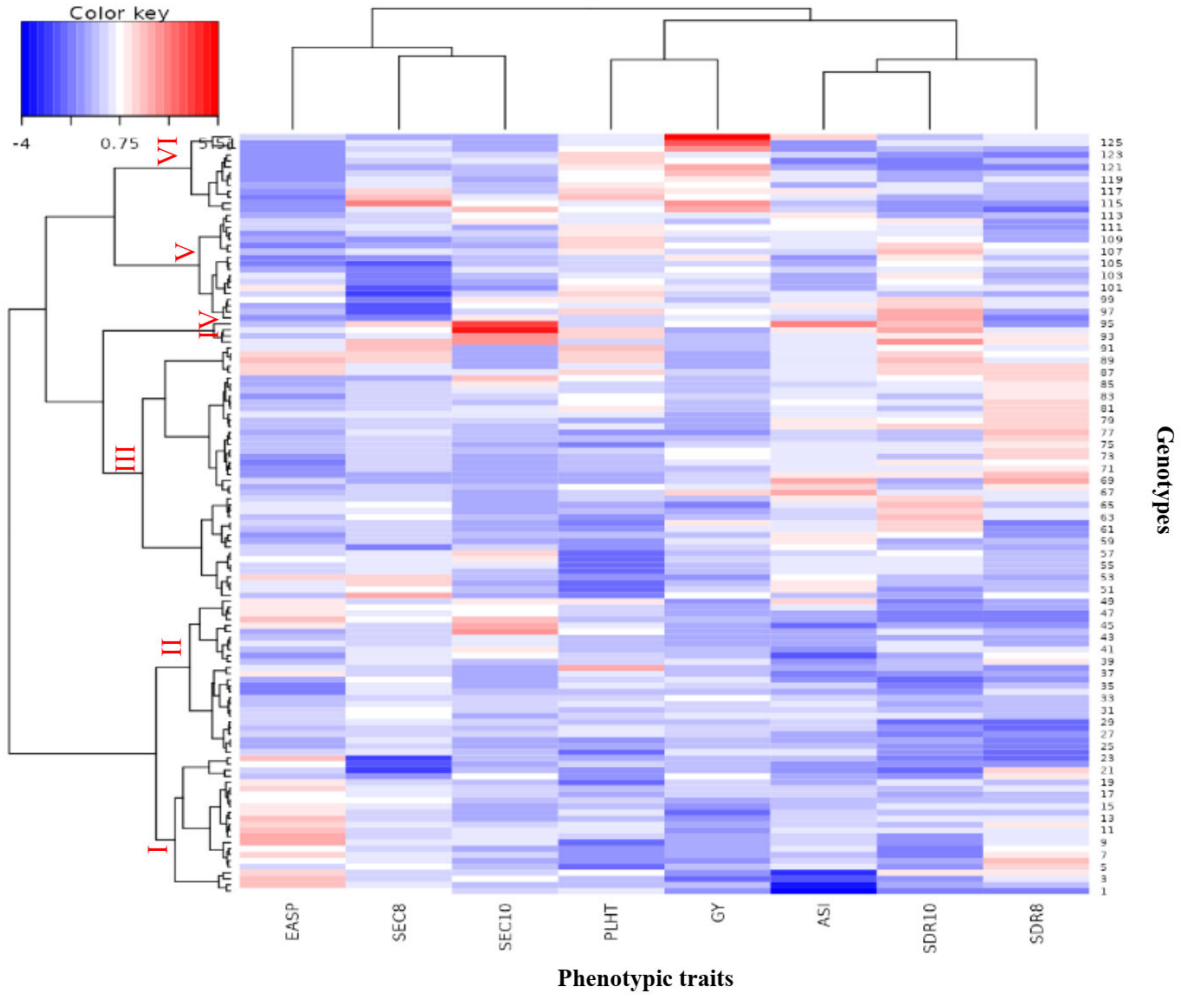


**Figure 2.5** Six clusters (I to VI) heatmap plot showing a colour pattern of 126 maize genotypes based on 4 maize yield components and 4 *Striga* parameters recorded in *Sa*-infested environment. Blue: lowest performance; red: highest performance. The numbers at the right represent the genotype numbers as coded in Appendix 2.1. EASP= ear aspect, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, PLHT= Plant height, GY= grain yield, ASI= anthesis-silking interval, SDR10= *Striga* damage rating 10 days after sowing, SDR8= *Striga* damage rating eight days after sowing.

Under *Sh*-infested conditions (Figure 2.6 and Appendix 2.4), the genotypes clustered into four, with Cluster I consisting of genotypes exhibiting low reductions in SDR8, SDR10, SEC8, and SEC10. This cluster included TZBSTR, CZL1380, and Colorado/1421, characterized by low GY, SDR10, and lowest SEC10 reduction under *Sh*. Cluster II was composed of two types of genotypes. The first group comprised genotypes that showed low GY, low SEC8, and SEC10 reduction, and included the genotype HA04A-2107-36, which showed the lowest GY in a *Sh*-infested environment. The second group comprised genotypes that showed average GY and moderate resistance to *Sh*. Cluster III genotypes had high values in GY, and EASP, and had moderate reduction in all *Sh* parameters. These included the CIMMYT lines CML540, CML566, CML304, CML550, CML539, CML440, CML545, and the IITA genotypes TZISTR25, TZISTR1174, TZISTR1119, TZISTR1166, TZSTRI113, B.King/1421, Shesha/1421, ZM1423, N.Choice/1421, DTSTR-W SYN13 all exhibited high mean yields under *Sh* infestation. Cluster IV comprised the NPGRC/SA OPV ZM1423/Z.DLO and the CIMMYT line CML571 showed exceptional scores in PLHT and GY.

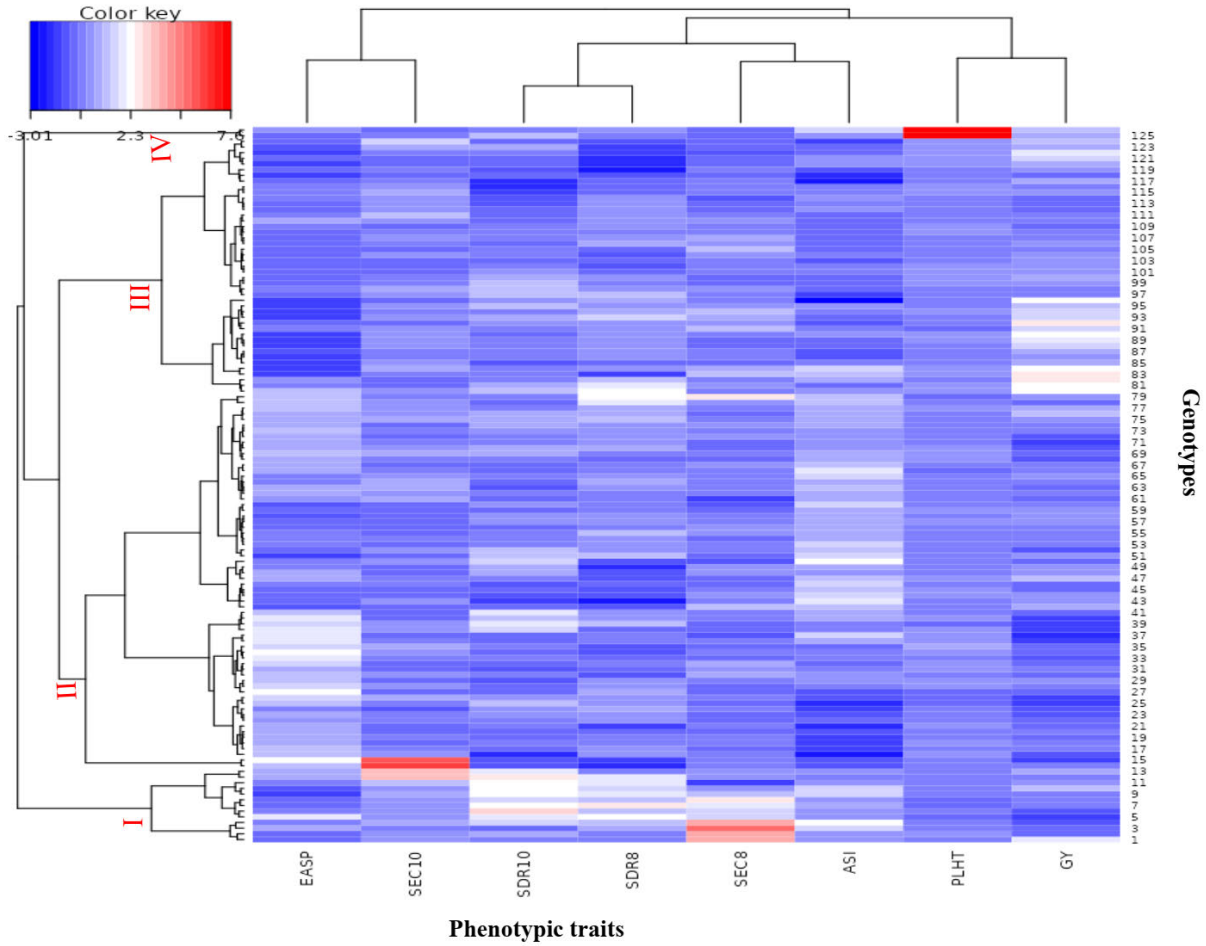


**Figure 2.6** Four clusters (I to IV) heatmap plot showing a colour pattern of 126 maize genotypes based on 4 maize yield components and 4 *Striga* parameters recorded in *Sh*-infested environment. Blue: lowest performance; red: highest performance. The numbers at the right represent the genotype numbers as coded in Appendix 2.2. EASP= ear aspect, SEC10= *Striga* emergence counts ten days after sowing, SDR10= *Striga* damage rating 10 days after sowing, SDR8= *Striga* damage rating eight days after sowing, SEC8= *Striga* emergence counts eight days after sowing, ASI= anthesis-silking interval, PLHT= plant height, GY= grain yield.

## 2.4 **Discussion**

Breeding *Striga*-resistant maize genotypes adaptable to wide agro-ecological areas in SSA would be a sustainable solution to manage *Striga* infestations in maize. The mean values, genotypic and phenotypic variances, heritability, and the correlation coefficients of agronomic traits are key parameters used in breeding programs to select superior genotypes (Nzuve et al., 2014). The present study discerned genotypic differences for agronomic and *Striga* resistance traits, indicating that the target traits are amenable to selection. The skewness and kurtosis values for most of the evaluated traits ranged from -2 to 2, and -7 to 7, respectively, suggesting a normal distribution of the data. The high variation of some parameters, such as PLHT, EPP,

and EHT was expected due to the variability of the test populations, including inbred lines, OPVs, and hybrids. The genotype-by-season interaction effect was significant for any of the evaluated traits in both *Striga* species environments, suggesting the strong influence of environment on *Striga* traits. The significant effect of cropping season on some agronomic and *Striga* resistance traits suggested that the two seasons and associated growing conditions influenced trait responses. It shows that using two or more testing seasons supports the repeatability of the study for genotype comparison and selection. Nonetheless, in the current study, there were statistically non-significant effects of the G x S interaction, suggesting that the test season/environment did not influence the ranking of genotypes for the studied traits.

The rotated component matrix showed that DA, DS, EHT, CL, GY, and SDR8 were the most discriminating traits under both *Sa* and *Sh* environments. This indicates that these traits are important selection indices. In addition to these traits, EPP, EASP, SDR8, and SDR10, which were loaded in the second PC in a *Sa*-infested environment, can also be considered during selection. Badu-Apraku et al. (2010) reported that SDR8, SDR10, EASP, and EPP were the best traits for selection under *Striga*-infested conditions. SDR was also reported to be the best selection criterion for improving GY performance in maize under *Striga* infestation by Dossa et al. (2023a). All the traits exhibited high heritability values in both the *Sa* and *Sh* environments, except for GY under *Sh*-infested conditions. This indicates a large contribution of the genotypes to the phenotypic variance (Ngugi, 2013). Traits having high heritability are improved by selection based on phenotypic traits (Shekhawat and Singhania, 2005; Boghara et al., 2016). However, it is important to note the low heritability of the *Striga* parameters SEC10, SDR8, and SDR10, with values of only 0.008, 0.11, and 0.16, respectively, under *Sa* infested conditions, and of GY, with a value of 0.02 under *Sh* infested conditions. Notably, maize selection parameters recorded high heritabilities compared to the heritability of *Sa* parameters. This suggests that the genotypic variance of the *Striga* resistance traits was low compared to the phenotypic variance, making direct selection difficult for these traits. This is also indicative of the complex nature of the *Striga* resistance traits. Badu-Apraku et al. (2007) reported low heritability values in a previous study for SDR and SEC.

The PC biplots confirmed the positive and significant correlation between GY and secondary traits, including PLHT, EHT, and CL, under both *Sa* and *Sh*-infested conditions, indicating the importance of these traits in improving maize GY under *Striga* infestation. Previous studies reported similar findings (Golam et al., 2011; Nzuve et al., 2014; Yahaya et al., 2021).

The ASI showed a positive correlation between SDR8 (r=0.18) and SDR10 (0.32) under *Sa*-infested conditions, indicating that severe *Striga* damage prolongs the ASI. This confirms the stunted growth symptom of *Striga*-infested plants (Waweru et al., 2019). This is also supported by the positive correlation between EASP and SEC10, indicating that higher numbers of *Striga* plants increased the EASP score. The negative and significant associations between yield components, including EPP, CL, PLHT, and EHT, and *Striga* parameters, including SEC8, SEC10, SDR8, and SDR10, under both *Sa* and *Sh* infestation, were expected because when the parasitic weeds proliferate, damage to maize yield components increase (Shayanowako et al., 2020). Therefore, reducing *Striga* damage scores and the parasitic plant counts at 8 and 10 days after planting will have a positive impact on yield component and enhance GY under *Striga* infestation (Menkir and Meseka, 2019; Badu-Apraku et al., 2021).

With *Sa* infestation, the yield of the evaluated inbred lines was higher than the yield of the OPVs checks. This was not expected, but it can be explained by the fact that most of these OPVs were bred for resistance or tolerance to *Sh*, with no screening activities done under *Sa*. These results indicate that these OPVs that have been bred for *Sh* resistance are not resistant to *Sa*. However, some OPVs and hybrids showed lower grain yield than inbred lines under *Sh* environment, likely because they were not bred for *Sh* resistance or, if tropical, did not perform well in sub-tropical environments.

In the present study, some genotypes, e.g. TZISTR1174, showed excellent GY performance and relatively high SEC under *Sa*-infested conditions compared to others and could be used as a source of resistance. Resistant genotypes support fewer *Striga* plants and produce a higher grain yield than susceptible ones. Conversely, in the case of tolerance, the host supports an equally severe level of the parasitic weed without losses in GY (Rodenburg et al., 2005). The following lines showed resistance to both *Sa* and *Sh*: sub-tropical lines CML440, CML566, CML540, CML539, CML451, CLHP0343, CLHP0326, and the tropical lines TZISTR1248, TZSTRI115, TZISTR25, TZISTR1205, TZSTRI113, TZISTR1119. The local hybrids B.King/1421, Shesha/1421, ZM1421, and the *Striga*-resistant check OPV DTSTR-W SYN13.

The phenotypic clustering analysis based on eight morphological traits clustered 126 maize genotypes into six clusters under *Sa* infestation and four clusters under *Sh* infestation. This indicates that the studied genotypes exhibited genetic divergence regarding morphological traits. The formation of different clusters using phenotypic traits in maize genotypes agreed with other reports (Saiyad and Kumar, 2017; Han et al., 2018; Kasoma et al., 2020;

Shayanowako et al., 2020). All clusters consisted of a mixture of genotypes from different sources (IITA, CIMMYT, and NPGRC). Cluster mean values of evaluated genotypes in the *Sa* environment suggested that Cluster VI was the best with outstanding trait values, especially for GY and SDR. In a *Sh*-infested environment, cluster mean values showed that Cluster IV was best, with outstanding values for all the evaluated traits. Therefore, these clusters containing tropical and sub-tropical maize genotypes should be good sources for hybrid breeding through the exploitation of their heterotic affinities in *Striga* resistance breeding programs.

## 2.5 **Conclusions**

This study identified IITA, CIMMYT, and NPGRC/SA conserved maize genetic resources that could be used as breeding parents to improve for both *Sa*, *Sh*, and dual resistance. The top five most resistant to *Sa* included tropical and sub-tropical maize inbred lines: CML540 (277.50 g/plant), CML566 (155.50 g/plant), TZISTR1001 (140.00 g/plant), TZISTR1205 (114.25 g/plant) and TZSTRI115 (112.50 g/plant). On the other hand, the top five yielding inbred lines under *Sh* were CML304 (151.00 g/plant), TZSTRI101 (144.00 g/plant), CLHP0404 (137.35 g/plant), TZISTR1119 (135.75 g/plant), and TZISTR25 (131.00 g/plant). The genotypes CML440, CML566, CML540, CML539, CLHP0343, CLHP0326, TZISTR1248, TZSTRI115, TZISTR25, TZISTR1205, TZSTRI113, and TZISTR1119, showed resistance to both *Striga* species, whereas TZISTR1174 showed tolerance to *Sa*. The identified tolerant and resistant inbred lines could be used to produce new hybrids combining tolerance and resistance to both *Sa* and *Sh* and market-preferred agronomic traits. The results of this study confirmed that promising tropical and sub-tropical African maize genotypes are present as sources of dual *Striga* resistance and with better agronomic performance.

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**Appendix 2.1.** Mean values for 10 yield components and 4 *Striga* parameters measured for 126 maize genotypes evaluated under *Sa* infestation.

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | TZISTR1154 | 85.50 | 83.00 | 2.50 | 2.00 | 1.52 | 1.53 | 1.00 | 10.75 | 6.50 | 47.50 | 2.00 | 5.00 | 1.00 | 1.50 |
| 2 | TZISTR1261 | 87.50 | 82.00 | 5.50 | 2.00 | 1.73 | 0.85 | 1.00 | 13.75 | 4.50 | 51.25 | 2.50 | 2.00 | 2.00 | 2.00 |
| **3** | **TZISTR1248** | **78.00** | **73.50** | 4.50 | **1.00** | **1.30** | **0.59** | **1.00** | **13.25** | **3.00** | **98.25** | **3.50** | 17.50 | **4.50** | **2.00** |
| 4 | TZISTR1263 | 87.50 | 82.00 | 5.50 | 1.00 | 1.40 | 0.53 | 3.00 | 10.50 | 3.50 | 52.50 | 2.00 | 5.50 | 5.00 | 1.00 |
| 5 | TZISTR1275 | 89.50 | 76.00 | 13.50 | 1.00 | 1.60 | 0.75 | 2.00 | 14.75 | 6.00 | 54.50 | 5.00 | 5.00 | 3.00 | 2.50 |
| 6 | TZISTR1157 | 82.00 | 77.50 | 4.50 | 1.00 | 1.59 | 0.62 | 2.00 | 10.75 | 3.00 | 44.50 | 4.50 | 11.50 | 2.50 | 2.50 |
| 7 | TZISTR1160 | 84.50 | 83.50 | 1.00 | 1.00 | 1.00 | 0.60 | 1.50 | 12.50 | 7.00 | 35.00 | 5.00 | 14.50 | 3.50 | 2.00 |
| 8 | TZISTR1162 | 80.50 | 78.00 | 2.50 | 1.00 | 1.54 | 1.13 | 1.00 | 13.50 | 2.00 | 57.50 | 4.50 | 2.50 | 1.50 | 2.00 |
| 9 | TZISTR1165 | 79.50 | 75.50 | 4.00 | 2.00 | 1.85 | 1.15 | 1.00 | 11.50 | 5.00 | 32.50 | 5.00 | 16.50 | 1.50 | 1.50 |
| 10 | TZISTR1175 | 76.00 | 72.50 | 3.50 | 1.00 | 1.58 | 0.65 | 1.00 | 14.50 | 6.50 | 55.00 | 5.50 | 28.00 | 1.50 | 1.50 |
| 11 | TZISTR1178 | 76.00 | 74.50 | 1.50 | 1.00 | 2.00 | 1.55 | 1.00 | 10.15 | 1.00 | 64.55 | 5.00 | 3.50 | 3.00 | 1.50 |
| 12 | TZISTR1163 | 82.00 | 78.00 | 4.00 | 1.00 | 1.70 | 1.01 | 1.00 | 9.25 | 1.00 | 57.25 | 5.00 | 5.00 | 3.50 | 2.00 |
| 13 | TZISTR1166 | 99.00 | 101.00 | 2.00 | 1.00 | 1.00 | 0.78 | 1.00 | 10.50 | 4.00 | 62.50 | 5.50 | 7.50 | 3.00 | 2.00 |
| 14 | TZISTR1190 | 86.00 | 84.00 | 2.00 | 1.00 | 1.75 | 0.88 | 1.00 | 8.25 | 7.00 | 31.00 | 4.50 | 12.00 | 3.50 | 1.75 |
| 15 | TZISTR1199 | 81.00 | 78.50 | 2.50 | 1.00 | 1.85 | 0.90 | 1.00 | 7.75 | 4.50 | 36.00 | 5.50 | 5.00 | 3.00 | 3.00 |
| 16 | TZISTR1231 | 75.00 | 73.00 | 2.00 | 1.00 | 1.55 | 0.90 | 1.00 | 10.05 | 4.50 | 62.50 | 5.00 | 8.00 | 3.00 | 2.50 |
| 17 | TZISTR1232 | 85.50 | 86.00 | 0.50 | 1.00 | 1.75 | 1.04 | 1.00 | 11.50 | 5.00 | 35.00 | 5.50 | 15.50 | 2.50 | 2.00 |
| 18 | TZISTR1259 | 77.00 | 74.00 | 3.00 | 1.00 | 1.40 | 0.76 | 1.00 | 15.50 | 5.50 | 43.25 | 5.00 | 10.00 | 4.50 | 1.50 |
| 19 | TZISTR1262 | 83.50 | 74.50 | 9.00 | 1.00 | 1.65 | 0.82 | 2.00 | 11.50 | 6.50 | 0.00 | 4.50 | 16.50 | 3.50 | 2.00 |
| 20 | TZISTR1159 | 86.50 | 71.00 | 15.50 | 1.00 | 1.90 | 0.97 | 1.00 | 9.75 | 4.50 | 29.25 | 5.50 | 8.00 | 1.50 | 1.50 |
| 21 | TZISTR1223 | 87.00 | 83.50 | 3.50 | 1.00 | 1.95 | 1.30 | 1.00 | 9.50 | 3.50 | 60.00 | 4.50 | 8.00 | 2.00 | 1.50 |
| 22 | TZISTR1225 | 85.50 | 84.50 | 1.00 | 1.00 | 1.90 | 1.45 | 1.00 | 10.50 | 3.00 | 62.50 | 4.50 | 4.50 | 1.00 | 2.00 |
| 23 | CML550 | 85.50 | 85.00 | 0.50 | 1.00 | 2.03 | 1.15 | 1.00 | 12.50 | 6.50 | 28.75 | 4.50 | 11.50 | 3.50 | 3.50 |
| 24 | TZISTR1244 | 76.00 | 76.50 | 0.50 | 1.00 | 1.00 | 0.45 | 2.00 | 9.00 | 3.50 | 47.50 | 5.00 | 7.50 | 3.00 | 3.50 |
| 25 | TZSTRI101 | 99.00 | 98.50 | 0.50 | 1.00 | 1.00 | 0.55 | 1.00 | 9.00 | 3.50 | 52.50 | 5.00 | 14.00 | 3.00 | 3.50 |
| 26 | TZSTRI102 | 87.50 | 78.00 | 9.50 | 1.00 | 1.85 | 0.85 | 1.00 | 10.50 | 1.50 | 52.25 | 5.00 | 15.50 | 4.00 | 2.50 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.1 (continued)**

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 27 | TZSTRI104 | 100.00 | 99.00 | 1.00 | 1.00 | 1.00 | 0.45 | 1.50 | 10.50 | 3.50 | 57.50 | 5.00 | 23.00 | 3.00 | 4.00 |
| 28 | TZSTRI107 | 77.50 | 73.50 | 4.00 | 1.00 | 1.40 | 0.84 | 1.00 | 8.50 | 2.00 | 57.00 | 5.00 | 1.50 | 1.50 | 2.50 |
| 29 | TZSTRI108 | 81.00 | 80.00 | 1.00 | 1.00 | 1.40 | 0.77 | 2.00 | 9.00 | 2.00 | 28.00 | 5.00 | 4.50 | 5.50 | 3.00 |
| 30 | TZSTRI109 | 80.00 | 73.00 | 7.00 | 2.00 | 2.03 | 0.97 | 1.00 | 11.00 | 5.00 | 57.25 | 4.50 | 2.50 | 2.50 | 2.00 |
| 31 | TZSTRI110 | 82.00 | 74.50 | 7.50 | 1.00 | 2.03 | 1.45 | 1.00 | 7.75 | 5.00 | 37.00 | 4.50 | 29.50 | 2.00 | 2.50 |
| 32 | TZSTRI112 | 81.00 | 76.50 | 4.50 | 1.00 | 1.08 | 0.80 | 1.00 | 12.50 | 5.00 | 68.75 | 4.50 | 4.50 | 3.00 | 3.50 |
| 33 | TZSTRI114 | 93.00 | 93.50 | 0.50 | 1.00 | 1.05 | 0.55 | 1.00 | 10.50 | 4.50 | 65.00 | 5.00 | 19.00 | 3.00 | 3.50 |
| 34 | **TZSTRI115** | **77.50** | **77.00** | 0.50 | **1.00** | **2.10** | **1.20** | **1.00** | **11.50** | **1.50** | **112.50** | **5.00** | 2.00 | **3.50** | **2.50** |
| 35 | **TZISTR25** | **76.50** | **72.50** | 4.00 | **1.00** | **2.25** | **1.13** | **1.00** | **13.50** | **2.00** | **97.25** | **5.00** | 4.50 | **3.00** | **3.50** |
| 36 | **TZISTR1001** | **82.00** | **82.00** | 0.00 | **1.00** | **2.10** | **1.28** | **1.00** | **11.00** | **1.50** | **140.00** | **4.50** | 4.50 | **3.00** | **2.50** |
| 37 | TZISTR1003 | 84.50 | 80.00 | 4.50 | 1.00 | 2.05 | 1.42 | 1.00 | 8.75 | 2.00 | 44.50 | 4.50 | 32.00 | 3.00 | 3.50 |
| 38 | TZISTR1004 | 70.50 | 72.50 | 2.00 | 1.00 | 1.58 | 1.13 | 1.00 | 9.25 | 1.50 | 54.50 | 4.50 | 4.50 | 2.00 | 4.00 |
| 39 | TZISTR1008 | 85.50 | 83.50 | 2.00 | 1.00 | 2.00 | 1.13 | 1.00 | 11.00 | 5.50 | 38.75 | 5.00 | 9.50 | 4.50 | 3.00 |
| 40 | TZISTR1011 | 91.00 | 91.50 | 0.50 | 1.00 | 1.80 | 1.15 | 1.00 | 10.75 | 2.50 | 58.00 | 4.50 | 12.50 | 4.50 | 3.50 |
| 41 | TZISTR1018 | 75.50 | 74.50 | 1.00 | 1.00 | 1.70 | 1.15 | 1.00 | 12.00 | 3.50 | 47.75 | 5.00 | 8.00 | 1.00 | 1.00 |
| 42 | TZEEI21 | 81.50 | 82.00 | 0.50 | 1.00 | 1.18 | 0.80 | 1.00 | 12.50 | 3.00 | 67.50 | 4.50 | 2.50 | 4.50 | 3.50 |
| 43 | TZEEI13 | 77.00 | 76.00 | 1.00 | 1.00 | 1.30 | 0.72 | 2.00 | 8.50 | 3.00 | 58.25 | 5.50 | 5.50 | 3.50 | 5.50 |
| 44 | TZEEI14 | 82.00 | 82.00 | 0.00 | 1.00 | 2.10 | 1.13 | 2.00 | 10.25 | 1.50 | 63.00 | 4.50 | 9.50 | 4.50 | 3.00 |
| 45 | TZEEI49 | 72.50 | 74.50 | 2.00 | 1.00 | 1.97 | 0.77 | 2.00 | 11.25 | 3.00 | 36.00 | 4.50 | 7.00 | 5.00 | 5.00 |
| 46 | TZDEEI55 | 76.50 | 75.50 | 1.00 | 1.00 | 1.59 | 0.61 | 2.00 | 8.50 | 4.00 | 36.25 | 5.00 | 2.00 | 3.50 | 5.00 |
| 47 | TZDEEI50 | 70.00 | 72.50 | 2.50 | 1.00 | 1.42 | 0.75 | 2.00 | 10.50 | 1.50 | 69.25 | 4.00 | 2.00 | 5.50 | 4.50 |
| 48 | TZDEEI64 | 69.50 | 72.50 | 3.00 | 1.00 | 1.74 | 1.25 | 2.00 | 11.00 | 3.50 | 57.50 | 4.50 | 3.50 | 3.50 | 5.00 |
| 49 | **CML312** | **80.50** | **85.00** | 4.50 | **1.00** | **2.05** | **0.91** | **2.00** | **8.75** | **2.00** | **86.25** | **4.50** | 5.00 | **4.50** | **3.00** |
| 50 | CML444 | 78.50 | 81.00 | 2.50 | 1.00 | 1.50 | 0.67 | 2.00 | 12.50 | 3.00 | 31.75 | 4.50 | 9.50 | 5.00 | 4.00 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.1 (continued)**

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 51 | CML442 | 85.50 | 86.00 | 0.50 | 1.00 | 1.69 | 0.80 | 2.00 | 11.50 | 1.50 | 55.00 | 4.50 | 3.00 | 4.50 | 3.50 |
| 52 | TZDEEI54 | 90.50 | 91.00 | 0.50 | 1.00 | 1.00 | 0.75 | 2.00 | 10.50 | 3.50 | 47.50 | 5.50 | 6.50 | 5.00 | 2.00 |
| 53 | TZEEI10 | 86.50 | 84.50 | 2.00 | 1.00 | 1.65 | 0.92 | 2.00 | 12.75 | 6.50 | 26.00 | 4.50 | 3.00 | 3.50 | 3.50 |
| 54 | CML547 | 83.50 | 90.50 | 7.00 | 1.00 | 1.45 | 0.60 | 1.50 | 9.50 | 3.50 | 62.50 | 4.00 | 3.50 | 6.00 | 2.50 |
| 55 | **CML539** | **80.50** | **74.50** | 6.00 | **1.00** | **1.85** | **0.60** | **1.00** | **10.50** | **3.00** | **74.75** | **5.00** | 5.00 | **4.50** | **3.00** |
| 56 | **CML440** | **82.50** | **76.00** | 6.50 | **1.00** | **2.36** | **1.08** | **1.00** | **11.00** | **1.50** | **96.25** | **4.50** | 13.50 | **3.00** | **1.50** |
| 57 | **CML566** | **82.50** | **79.00** | 3.50 | **1.00** | **2.22** | **1.15** | **1.00** | **12.00** | **1.50** | **155.50** | **4.00** | 5.50 | **1.50** | **1.50** |
| 58 | **CML540** | **77.00** | **81.50** | 4.50 | **1.00** | **2.03** | **0.77** | **1.00** | **11.00** | **3.50** | **277.50** | **4.00** | 1.50 | **3.50** | **3.00** |
| 59 | CML545 | 75.50 | 74.00 | 1.50 | 1.00 | 1.73 | 0.67 | 1.00 | 10.25 | 3.00 | 53.00 | 4.50 | 6.00 | 5.00 | 3.00 |
| 60 | CML571 | 76.00 | 75.50 | 0.50 | 1.00 | 2.05 | 0.68 | 1.00 | 9.80 | 2.00 | 45.50 | 4.00 | 26.50 | 5.00 | 4.00 |
| 61 | CML390 | 80.00 | 81.00 | 1.00 | 1.00 | 2.10 | 0.74 | 1.00 | 11.30 | 2.50 | 56.00 | 4.50 | 7.00 | 5.00 | 3.50 |
| 62 | CLHP0352 | 76.50 | 76.50 | 0.00 | 1.00 | 2.30 | 0.85 | 1.00 | 11.75 | 3.00 | 51.25 | 4.50 | 11.50 | 5.00 | 3.00 |
| 63 | HA04A-2107-36 | 97.50 | 86.00 | 11.50 | 1.00 | 2.14 | 1.35 | 1.00 | 8.50 | 5.50 | 27.50 | 4.50 | 8.00 | 4.50 | 4.50 |
| 64 | **CLHP0303** | **84.50** | **83.50** | 1.00 | **1.50** | **1.87** | **1.15** | **1.00** | **7.25** | **3.00** | **92.50** | **4.50** | 8.50 | **3.00** | **3.00** |
| 65 | **CLHP0221** | **79.50** | **77.50** | 2.00 | **1.50** | **1.65** | **1.10** | **1.00** | **10.25** | **5.50** | **72.50** | **5.00** | 9.50 | **3.50** | **3.00** |
| 66 | **CLHP0020** | **71.00** | **77.00** | 6.00 | **1.00** | **1.80** | **0.57** | **1.00** | **12.00** | **2.50** | **119.00** | **4.50** | 2.00 | **3.50** | **3.50** |
| 67 | CLHP0058 | 78.50 | 76.50 | 2.00 | 1.00 | 1.40 | 0.46 | 1.00 | 8.50 | 4.50 | 26.00 | 5.00 | 3.00 | 5.50 | 2.50 |
| **68** | **CKDHL0378** | **72.00** | **75.00** | 3.00 | **1.00** | **1.90** | **0.75** | **1.00** | **11.75** | **2.00** | **85.00** | **4.50** | 17.50 | **3.00** | **2.50** |
| 69 | CLHP0312 | 80.50 | 79.50 | 1.00 | 1.00 | 1.75 | 0.76 | 1.00 | 9.50 | 2.00 | 45.75 | 4.50 | 18.50 | 4.50 | 3.50 |
| 70 | CLHP0310 | 76.00 | 76.50 | 0.50 | 1.00 | 1.91 | 1.03 | 1.00 | 11.75 | 4.00 | 35.75 | 5.00 | 13.50 | 5.00 | 3.50 |
| 71 | CLHP0003 | 82.00 | 83.00 | 1.00 | 1.00 | 1.40 | 0.82 | 1.00 | 9.00 | 5.50 | 30.00 | 6.00 | 4.50 | 2.50 | 3.00 |
| 72 | CKDHL0467 | 79.50 | 75.50 | 4.00 | 1.00 | 1.65 | 0.86 | 1.00 | 11.25 | 4.00 | 42.75 | 4.50 | 14.50 | 2.50 | 3.50 |
| 73 | CLHP00378 | 77.00 | 79.00 | 2.00 | 1.00 | 1.03 | 0.60 | 2.50 | 9.50 | 4.00 | 57.50 | 6.00 | 3.00 | 3.00 | 3.00 |
| 74 | **CLHP0156** | **80.50** | **78.50** | 2.00 | **1.50** | **2.40** | **0.98** | **1.00** | **12.00** | **1.50** | **74.50** | **5.00** | 8.00 | **1.50** | **2.00** |
| 75 | CLHP0113 | 77.50 | 74.50 | 3.00 | 1.00 | 1.65 | 0.50 | 2.50 | 10.00 | 5.00 | 30.50 | 5.00 | 4.00 | 3.50 | 3.50 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.1 (continued)**

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 76 | **CLHP03302** | **75.50** | **70.50** | 5.00 | **1.50** | **1.80** | **0.95** | **1.00** | **12.00** | **2.00** | **75.25** | **5.50** | 4.00 | **2.00** | **1.00** |
| 77 | CLHP0404 | 77.00 | 75.50 | 1.50 | 1.00 | 1.68 | 0.70 | 1.00 | 11.00 | 3.50 | 62.50 | 5.50 | 8.00 | 3.00 | 3.00 |
| 78 | **CLHP0343** | **77.50** | **77.00** | 0.50 | **1.00** | **1.60** | **0.77** | **1.00** | **11.50** | **1.00** | **82.00** | **4.50** | 2.00 | **4.00** | **4.50** |
| 79 | CZL1380 | 78.50 | 78.50 | 0.00 | 1.00 | 2.38 | 0.87 | 1.00 | 10.50 | 5.50 | 62.50 | 5.00 | 13.50 | 5.00 | 5.00 |
| 80 | **CLHP0326** | **75.00** | **77.00** | 2.00 | **1.00** | **1.40** | **0.66** | **1.00** | **10.50** | **2.00** | **82.25** | **4.50** | 2.00 | **3.00** | **2.50** |
| 81 | CZL99017 | 79.50 | 79.00 | 0.50 | 1.00 | 2.03 | 0.77 | 1.00 | 8.50 | 2.50 | 62.50 | 5.00 | 8.50 | 3.00 | 2.50 |
| 82 | TZEEI34 | 74.50 | 74.50 | 0.00 | 1.00 | 1.30 | 0.53 | 1.00 | 10.50 | 4.50 | 36.50 | 4.50 | 3.50 | 4.00 | 1.50 |
| 83 | **CLHP0049** | **80.50** | **78.00** | 2.50 | **1.00** | **1.25** | **0.70** | **1.00** | **10.00** | **3.00** | **101.25** | **7.00** | 4.00 | **1.00** | **2.50** |
| 84 | CLHP00478 | 79.50 | 74.50 | 5.00 | 1.00 | 1.73 | 0.70 | 1.00 | 11.50 | 3.00 | 56.00 | 5.00 | 20.50 | 3.50 | 3.50 |
| **85** | **CLHP00286** | **83.00** | **83.00** | 0.00 | **1.00** | **1.88** | **0.88** | **1.00** | **11.50** | **3.50** | **82.50** | **5.50** | 3.50 | **3.00** | **3.50** |
| 86 | **CML451** | **79.00** | **79.00** | 0.00 | **1.00** | **2.30** | **0.96** | **1.00** | **12.00** | **1.50** | **83.00** | **4.50** | 10.50 | **2.50** | **3.50** |
| 87 | **CLHP0302** | **81.00** | **80.50** | 0.50 | **1.00** | **1.76** | **1.00** | **3.00** | **13.25** | **3.00** | **98.00** | **4.50** | 7.00 | **2.00** | **3.50** |
| 88 | **CLHP0364** | **80.00** | **80.50** | 0.50 | **1.00** | **1.30** | **0.85** | **1.00** | **12.00** | **3.00** | **79.00** | **4.50** | 4.00 | **2.00** | **5.00** |
| 89 | **CLHP0350** | **75.00** | **76.00** | 1.00 | **1.00** | **2.35** | **0.81** | **3.00** | **14.00** | **3.50** | **102.75** | **5.00** | 3.50 | **2.00** | **3.50** |
| 90 | CLHP00294 | 88.00 | 87.50 | 0.50 | 1.00 | 2.00 | 0.75 | 1.00 | 9.50 | 5.50 | 40.00 | 5.00 | 1.50 | 5.00 | 5.00 |
| 91 | CLHP0005 | 76.00 | 77.50 | 1.50 | 1.00 | 2.03 | 0.76 | 1.00 | 10.50 | 3.50 | 58.75 | 4.50 | 19.00 | 2.00 | 4.50 |
| 92 | CLHP0022 | 81.00 | 81.50 | 0.50 | 1.00 | 1.50 | 0.55 | 1.00 | 7.00 | 4.00 | 12.50 | 5.50 | 3.00 | 3.00 | 5.50 |
| 93 | **CML304** | 82.50 | 82.50 | 0.00 | 1.00 | 1.75 | 0.95 | 2.00 | 11.00 | 4.00 | 59.25 | 6.50 | 33.50 | 4.50 | 6.50 |
| 94 | **TZISTR1174** | **84.00** | **82.50** | 1.50 | **1.00** | **1.80** | **1.00** | **1.50** | **12.25** | **2.00** | **93.25** | **3.00** | 47.00 | **3.00** | **3.50** |
| 95 | **TZISTR1205** | **81.50** | **75.50** | 6.00 | **1.00** | **1.85** | **0.91** | **1.00** | **11.00** | **1.00** | **114.25** | **3.50** | 13.00 | **3.00** | **2.50** |
| 96 | **TZSTRI113** | **78.00** | **77.00** | 1.00 | **1.00** | **1.75** | **0.95** | **1.00** | **10.50** | **1.50** | **87.00** | **3.00** | 7.50 | **1.50** | **6.00** |
| 97 | **TZISTR1119** | **84.00** | **80.50** | 3.50 | **1.00** | **1.91** | **1.15** | **1.00** | **11.25** | **4.00** | **84.75** | **3.00** | 19.00 | **2.50** | **4.50** |
| 98 | **TZISTR1015** | **81.00** | **77.00** | 4.00 | **1.00** | **1.77** | **0.85** | **1.00** | **10.50** | **1.00** | **73.25** | **2.50** | 5.50 | **3.50** | **4.00** |
| 99 | **ZM1421** | **80.50** | **81.00** | **0.50** | **1.00** | **1.00** | **0.70** | **1.00** | **9.00** | **3.50** | **77.50** | **5.00** | 4.50 | **1.00** | **2.00** |
| 100 | **B.King/1421** | **80.50** | **78.50** | **2.00** | **1.00** | **2.05** | **1.15** | **2.00** | **23.50** | **1.50** | **157.25** | **5.00** | 4.50 | **1.00** | **2.00** |
| 101 | Hickory/1421 | 70.50 | 69.50 | 1.00 | 1.00 | 1.95 | 1.30 | 2.00 | 15.50 | 5.00 | 0.00 | 4.50 | 27.00 | 3.00 | 3.00 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.1 (continued)**

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 102 | Kep/1421 | 69.50 | 73.00 | 3.50 | 1.00 | 2.30 | 1.75 | 1.00 | 17.50 | 5.00 | 25.75 | 4.50 | 2.00 | 2.50 | 1.50 |
| 103 | **Shesha/1421** | **75.50** | **72.50** | **3.00** | **1.00** | **2.03** | **1.75** | **1.00** | **18.75** | **1.50** | **165.75** | **7.50** | 18.50 | **2.00** | **2.00** |
| 104 | **ZM1423** | **69.00** | **69.50** | **0.50** | **1.00** | **0.85** | **1.39** | **1.00** | **10.50** | **1.50** | **99.25** | **4.50** | 16.50 | **5.00** | **3.00** |
| 105 | **N.Choice/1421** | **82.00** | **76.50** | **-5.50** | **1.00** | **1.90** | **1.03** | **1.00** | **13.25** | **1.50** | **214.00** | **5.00** | 4.00 | **3.50** | **3.50** |
| 106 | NC.QPM/Z.DPLO | **79.50** | **74.50** | **-5.00** | **1.00** | **2.05** | **0.88** | **1.00** | **15.50** | **1.50** | **169.50** | **4.50** | 3.50 | **2.50** | **3.00** |
| 107 | STR-SYN-Y2 | 81.50 | 82.00 | 0.50 | 1.00 | 2.40 | 0.98 | 1.00 | 11.50 | 6.00 | 44.50 | 6.00 | 2.50 | 3.50 | 5.50 |
| 108 | Z. Diplo.BC4C3-W-DT C1 | 88.00 | 88.50 | 0.50 | 1.00 | 2.45 | 0.95 | 1.50 | 9.00 | 5.50 | 42.50 | 6.00 | 2.00 | 4.00 | 5.00 |
| 109 | **TZBSTR (Susceptible)** | **83.00** | **83.50** | **0.50** | **1.00** | **2.65** | **1.30** | **1.50** | **14.50** | **1.00** | **103.00** | **6.50** | 3.00 | **3.00** | **2.50** |
| 110 | STR-SYN-W1 | 80.00 | 79.50 | -0.50 | 1.00 | 2.55 | 1.18 | 1.50 | 13.50 | 4.00 | 53.50 | 6.50 | 14.50 | 3.50 | 4.00 |
| 111 | **DTSTR-W SYN13** | **85.50** | **85.50** | **0.00** | **1.00** | **1.25** | **0.85** | **1.50** | **13.00** | **3.50** | **107.50** | **4.50** | 3.50 | **1.50** | **5.00** |
| 112 | DTSTR-Y SYN15 | 77.00 | 72.50 | -4.50 | 1.00 | 2.80 | 1.30 | 1.00 | 12.75 | 4.00 | 57.50 | 4.50 | 2.50 | 2.00 | 3.00 |
| 113 | ((IWD C3 SYN*2/(White DT STR Syn))-DT C1 | 89.00 | 91.50 | 2.50 | 1.00 | 2.45 | 0.75 | 1.50 | 11.50 | 4.00 | 35.00 | 5.50 | 3.50 | 3.50 | 6.00 |
| 114 | **DTSTR-W SYN11** | **78.50** | **77.50** | **-1.00** | **1.00** | **2.30** | **1.23** | **1.50** | **13.00** | **2.50** | **71.25** | **5.00** | 52.50 | **3.50** | **5.50** |
| 115 | SAMMMZ16 | 86.50 | 87.00 | 0.50 | 1.00 | 2.50 | 1.10 | 1.00 | 11.75 | 3.00 | 54.25 | 5.00 | 11.00 | 4.50 | 4.50 |
| 116 | **(TZEOMP5C7/TZEOMP3DTC2) C2** | **75.00** | **75.50** | **0.50** | **1.00** | **2.38** | **1.10** | **1.50** | **14.00** | **1.00** | **89.50** | **4.00** | 32.00 | **4.00** | **5.00** |
| 117 | ((TZL COMP1-W C6*2/(White DT STR Syn))-DT C1 | 85.00 | 86.50 | 1.50 | 1.00 | 1.40 | 0.85 | 1.00 | 11.00 | 3.50 | 62.50 | 3.00 | 2.50 | 2.50 | 3.00 |
| 118 | TZCOM1/ZDPSYN | 74.00 | 69.50 | -4.50 | 1.00 | 2.15 | 1.02 | 1.00 | 15.00 | 3.50 | 61.25 | 3.00 | 10.00 | 3.00 | 4.00 |
| 119 | **Colorado/1421** | **87.50** | **89.50** | **2.00** | **1.00** | **2.03** | **0.70** | **1.00** | **13.75** | **2.00** | **75.25** | **2.50** | 3.00 | **3.50** | **5.00** |
| 120 | M.Pearl/DT-STR | 73.50 | 74.00 | 0.50 | 1.00 | 2.38 | 1.04 | 0.50 | 13.50 | 3.50 | 61.50 | 2.00 | 17.00 | 2.50 | 3.00 |
| 121 | **Z.diplo-BC4-C3-W/DOGONA-1/Z.diplo-BC4-C3-W** | **81.00** | **83.00** | **2.00** | **1.00** | **2.36** | **1.05** | **1.00** | **11.50** | **1.50** | **112.00** | **6.00** | 8.50 | **3.00** | **3.50** |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.1 (continued)**

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 122 | NC.QPM/DT-STR | 71.50 | 71.50 | 0.00 | 1.00 | 2.25 | 1.03 | 0.00 | 12.50 | 4.50 | 54.25 | 3.00 | 5.00 | 3.50 | 5.00 |
| 123 | **ZM1421/DT-STR** | **77.00** | **76.50** | **-0.50** | **1.00** | **2.38** | **1.10** | **1.50** | **10.75** | **3.00** | **93.50** | **2.50** | 19.00 | **2.50** | **2.00** |
| 124 | **DTSTR-Y SYN14** | **78.50** | **74.50** | **4.00** | **1.00** | **2.23** | **1.10** | **0.50** | **13.75** | **5.00** | **78.50** | **2.50** | 8.50 | **3.50** | **3.50** |
| 125 | **(2*TZECOMP3DT/WhiteDTSTRSYN) C2** | **69.00** | **78.00** | **9.00** | **1.00** | **1.75** | **0.85** | **1.50** | **12.25** | **2.50** | **89.00** | **6.00** | 0.50 | **2.00** | **1.50** |
| 126 | ZM1423/Z.DLO | 84.50 | 85.00 | 0.50 | 1.00 | 2.50 | 1.05 | 1.50 | 13.25 | 2.00 | 64.25 | 3.50 | 6.00 | 2.50 | 4.00 |
| | | **DA** | **DS** | **ASI** | **EPP** | **PLHT** | **EHT** | **HUSK** | **CL** | **EASP** | **GY** | **SEC8** | **SEC10** | **SDR8** | **SDR10** |
| | **Trial statistics** | | | | | **Inbred lines** | | | | | | | | | |
| | Minimum | 69.5 | 70.5 | 0.00 | 1 | 1.00 | 0.45 | 1.00 | 7.00 | 1.00 | 0.00 | 2.00 | 1.50 | 1.00 | 1.00 |
| | Maximum | 100 | 101 | 15.50 | 2 | 2.4 | 1.55 | 3 | 15.5 | 7 | 277.50 | 7 | 47 | 6 | 6.5 |
| | Mean | 81.14 | 79.44 | 2.77 | 1.06 | 1.71 | 0.88 | 1.28 | 10.79 | 3.42 | 62.77 | 5 | 45.5 | 3.35 | 3.07 |
| | | | | | | **Open-pollinated varieties checks** | | | | | | | | | |
| | Minimum | 69.00 | 69.50 | 0.00 | 1.00 | 0.85 | 0.70 | 0.50 | 9.00 | 1.00 | 35.00 | 2.00 | 0.50 | 1.50 | 2.50 |
| | Maximum | 89.00 | 91.50 | 9.00 | **1.00** | 2.80 | 1.39 | 1.50 | 15.50 | 6.00 | 169.50 | 6.50 | 52.50 | 5.00 | 6.00 |
| | Mean | 79.73 | 79.77 | 1.86 | **1.00** | 2.18 | 1.04 | 1.18 | 12.63 | 3.11 | 76.33 | 4.39 | 10.32 | 3.14 | 4.30 |
| | | | | | | **Hybrids checks** | | | | | | | | | |
| | Minimum | 69.00 | 69.50 | 0.5 | 1.00 | 0.85 | 0.70 | 0.50 | 9.00 | 1.00 | 00.00 | 2.00 | 0.50 | 1.50 | 2.50 |
| | Maximum | 87.50 | 89.50 | 5.50 | 1.00 | 2.30 | 0.70 | 2.00 | 23.50 | 5.00 | 214.00 | 7.50 | 27.00 | 3.50 | 5.00 |
| | Mean | 78.00 | 77.21 | 1.77 | 1.00 | 1.89 | 1.20 | 1.29 | 15.89 | 2.86 | 102.21 | 4.86 | 9.07 | 2.36 | 2.71 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.2.** Mean values for 10 yield components and 4 *Striga* parameters measured for 126 maize genotypes evaluated under *Sh* infestation.

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | TZISTR1154 | 78.50 | 79.50 | 1.00 | 1.50 | 2.25 | 1.25 | 1.00 | 11.00 | 3.00 | 67.25 | 2.50 | 1.50 | 3.00 | 2.25 |
| 2 | **TZISTR1261** | **78.63** | **80.63** | 2.00 | **2.00** | **2.20** | **0.97** | **2.00** | **10.96** | **3.25** | **70.25** | **3.75** | 4.50 | **2.00** | **1.75** |
| 3 | **TZISTR1248** | **75.88** | **77.25** | 1.38 | **1.50** | **1.75** | **0.77** | **2.00** | **11.96** | **2.25** | **81.25** | **4.75** | 1.50 | **2.25** | **2.00** |
| 4 | **TZISTR1263** | **76.25** | **78.25** | 2.00 | **1.00** | **1.35** | **0.59** | **1.00** | **10.96** | **3.75** | **76.00** | **3.25** | 9.00 | **3.75** | **2.75** |
| 5 | TZISTR1275 | 82.00 | 83.00 | 1.00 | 1.00 | 1.50 | 0.49 | 1.00 | 9.96 | 5.25 | 65.25 | 3.25 | 6.00 | 4.50 | 3.50 |
| 6 | TZISTR1157 | 81.13 | 81.25 | 0.13 | 1.00 | 1.55 | 0.54 | 2.00 | 9.96 | 5.25 | 65.25 | 3.75 | 3.50 | 2.25 | 3.50 |
| 7 | TZISTR1160 | 79.88 | 80.50 | 0.63 | 1.00 | 1.47 | 0.54 | 2.00 | 10.46 | 3.75 | 57.25 | 2.75 | 6.50 | 3.75 | 2.75 |
| 8 | TZISTR1162 | 81.70 | 84.13 | 2.43 | 1.00 | 1.70 | 0.71 | 1.00 | 12.21 | 2.25 | 63.75 | 2.25 | 3.00 | 3.00 | 3.00 |
| 9 | TZISTR1165 | 82.38 | 81.75 | 0.63 | 1.00 | 2.10 | 0.99 | 1.00 | 13.46 | 2.75 | 66.25 | 3.25 | 3.50 | 2.75 | 3.00 |
| 10 | TZISTR1175 | 79.00 | 78.25 | 0.75 | 1.00 | 2.10 | 0.92 | 1.00 | 11.71 | 5.75 | 59.75 | 3.75 | 5.50 | 2.75 | 1.75 |
| 11 | TZISTR1178 | 74.50 | 74.00 | 0.50 | 1.00 | 2.35 | 0.94 | 1.00 | 9.96 | 6.75 | 65.25 | 3.25 | 3.50 | 3.75 | 1.75 |
| 12 | TZISTR1163 | 76.75 | 77.50 | 0.75 | 1.00 | 2.25 | 1.07 | 1.00 | 9.46 | 3.25 | 65.00 | 3.25 | 1.00 | 3.50 | 3.00 |
| 13 | TZISTR1166 | 90.00 | 87.50 | 2.50 | 1.00 | 1.60 | 0.77 | 1.00 | 9.46 | 3.25 | 65.00 | 3.25 | 6.50 | 2.75 | 2.00 |
| 14 | TZISTR1190 | 93.50 | 92.00 | 1.50 | 1.00 | 1.45 | 0.69 | 1.50 | 8.46 | 3.25 | 67.00 | 3.75 | 5.00 | 4.25 | 2.25 |
| 15 | TZISTR1199 | 82.75 | 81.00 | 1.75 | 1.00 | 1.85 | 0.97 | 1.50 | 8.46 | 3.25 | 64.25 | 3.25 | 2.00 | 3.25 | 2.75 |
| 16 | TZISTR1231 | 73.25 | 72.25 | 1.00 | 1.00 | 1.85 | 0.94 | 1.00 | 9.21 | 7.25 | 62.50 | 2.75 | 6.50 | 3.75 | 2.25 |
| 17 | TZISTR1232 | 77.50 | 76.75 | 0.75 | 1.00 | 1.83 | 0.94 | 1.00 | 10.71 | 8.75 | 46.75 | 3.25 | 2.00 | 2.00 | 2.00 |
| 18 | TZISTR1259 | 77.75 | 78.75 | 1.00 | 1.00 | 1.78 | 0.89 | 2.00 | 13.46 | 8.25 | 25.75 | 3.25 | 3.50 | 3.00 | 2.25 |
| 19 | TZISTR1262 | 76.75 | 74.50 | 2.25 | 1.00 | 1.65 | 0.73 | 2.50 | 10.71 | 5.75 | 39.25 | 2.63 | 5.00 | 3.75 | 3.00 |
| 20 | TZISTR1159 | 76.50 | 72.75 | 3.75 | 1.00 | 1.85 | 0.86 | 1.50 | 8.46 | 5.25 | 46.25 | 3.13 | 2.00 | 1.75 | 2.75 |
| 21 | TZISTR1223 | 80.88 | 78.00 | 2.88 | 1.00 | 2.10 | 0.97 | 1.00 | 9.46 | 5.25 | 55.00 | 3.13 | 2.50 | 3.25 | 2.75 |
| 22 | TZISTR1225 | 84.75 | 83.25 | 1.50 | 1.00 | 2.00 | 0.88 | 1.00 | 8.71 | 3.25 | 65.25 | 2.63 | 4.50 | 3.25 | 3.75 |
| 23 | CML550 | **73.25** | **73.25** | 0.00 | **1.00** | **2.13** | **1.00** | **1.00** | **13.21** | **1.25** | **86.00** | **2.63** | 5.00 | **1.50** | **2.00** |
| 24 | TZISTR1244 | 79.25 | 75.25 | 4.00 | 1.00 | 1.55 | 0.82 | 1.50 | 8.46 | 1.75 | 48.25 | 2.63 | 7.00 | 2.25 | 2.00 |
| 25 | TZSTRI101 | **90.00** | **87.50** | 2.50 | **1.00** | **1.45** | **0.75** | **1.00** | **12.46** | **3.25** | **144.00** | **3.63** | 6.50 | **3.75** | **3.00** |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.2** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 25 | TZSTRI101 | **90.00** | **87.50** | 2.50 | **1.00** | **1.45** | **0.75** | **1.00** | **12.46** | **3.25** | **144.00** | **3.63** | 6.50 | **3.75** | **3.00** |
| 26 | TZSTRI102 | 87.75 | 84.75 | 3.00 | 1.00 | 1.45 | 0.75 | 1.00 | 12.96 | 5.25 | 51.75 | 3.13 | 4.50 | 3.00 | 2.00 |
| 27 | TZSTRI104 | 89.50 | 90.75 | 1.25 | 1.00 | 1.45 | 0.75 | 1.00 | 12.96 | 5.25 | 51.75 | 3.13 | 7.50 | 3.50 | 1.75 |
| **28** | **TZSTRI107** | **88.00** | **86.75** | 1.25 | **1.00** | **1.25** | **0.66** | **1.00** | **8.75** | **3.25** | **70.25** | **3.63** | 8.00 | **2.25** | **2.50** |
| 29 | TZSTRI108 | **77.25** | **75.00** | 2.25 | **1.00** | **1.55** | **0.88** | **1.00** | **8.75** | **1.25** | **77.00** | **3.13** | 1.50 | **3.50** | **2.50** |
| 30 | TZSTRI109 | **80.75** | **78.00** | 2.75 | **1.00** | **1.75** | **0.97** | **1.00** | **11.00** | **2.25** | **78.00** | **3.13** | 4.50 | **3.75** | **2.50** |
| 31 | TZSTRI110 | **80.75** | **79.75** | 1.00 | **1.00** | **1.95** | **1.10** | **1.00** | **10.25** | **3.25** | **71.00** | **3.13** | 4.00 | **2.25** | **2.75** |
| 32 | TZSTRI112 | 80.38 | 82.50 | 2.13 | 1.00 | 1.55 | 0.82 | 1.00 | 9.25 | 4.25 | 62.00 | 3.13 | 5.50 | 3.75 | 2.75 |
| 33 | TZSTRI114 | 87.75 | 91.00 | 3.25 | 1.00 | 1.10 | 0.47 | 1.00 | 10.00 | 5.25 | 62.25 | 3.13 | 2.50 | 3.00 | 2.00 |
| 34 | **TZSTRI115** | **84.75** | **87.75** | 3.00 | **1.00** | **1.65** | **0.77** | **1.00** | **10.50** | **3.25** | **70.00** | **3.20** | 1.50 | **1.00** | **1.25** |
| 35 | **TZISTR25** | **75.75** | **75.50** | 0.25 | **1.00** | **2.25** | **1.05** | **1.00** | **12.00** | **1.25** | **131.00** | **3.20** | 2.00 | **3.75** | **2.00** |
| 36 | **TZISTR1001** | **79.63** | **78.25** | 1.38 | **1.00** | **2.10** | **1.03** | **1.00** | **11.50** | **1.75** | **120.00** | **2.70** | 1.50 | **3.50** | **2.50** |
| 37 | TZISTR1003 | 81.38 | 79.50 | 1.88 | 1.00 | 1.53 | 0.91 | 1.00 | 10.00 | 3.75 | 59.00 | 3.20 | 1.50 | 3.50 | 2.25 |
| 38 | TZISTR1004 | 80.25 | 78.75 | 1.50 | 1.00 | 1.45 | 0.84 | 1.00 | 9.00 | 3.25 | 62.25 | 4.20 | 3.50 | 3.75 | 2.50 |
| 39 | TZISTR1008 | 81.25 | 79.25 | 2.00 | 1.00 | 1.70 | 0.89 | 1.00 | 9.00 | 3.25 | 62.25 | 4.70 | 1.50 | 2.75 | 2.75 |
| 40 | TZISTR1011 | 86.50 | 84.75 | 1.75 | 1.00 | 2.05 | 0.96 | 1.00 | 10.00 | 7.25 | 39.75 | 4.20 | 1.50 | 3.00 | 2.00 |
| 41 | TZISTR1018 | 81.00 | 81.50 | 0.50 | 1.00 | 2.05 | 1.03 | 1.00 | 9.50 | 8.25 | 22.75 | 3.20 | 6.00 | 3.75 | 4.00 |
| 42 | TZEEI21 | 77.00 | 77.88 | 0.88 | 1.00 | 1.37 | 0.75 | 1.00 | 9.50 | 6.25 | 45.25 | 3.20 | 5.00 | 3.75 | 4.75 |
| 43 | TZEEI13 | 80.75 | 81.25 | 0.50 | 1.00 | 1.27 | 0.65 | 1.00 | 8.50 | 3.25 | 55.00 | 3.70 | 2.00 | 3.25 | 2.25 |
| 44 | TZEEI14 | 77.25 | 79.00 | 1.75 | 1.00 | 1.97 | 1.10 | 1.00 | 10.75 | 2.75 | 51.75 | 3.20 | 3.50 | 2.00 | 2.00 |
| 45 | TZEEI49 | 76.25 | 74.75 | 1.50 | 1.00 | 2.05 | 1.06 | 1.00 | 11.75 | 4.25 | 48.25 | 3.20 | 2.00 | 3.75 | 2.50 |
| 46 | TZDEEI55 | 78.38 | 76.75 | 1.63 | 1.00 | 1.38 | 0.61 | 1.00 | 9.50 | 4.75 | 51.50 | 2.70 | 2.00 | 3.75 | 2.75 |
| **47** | **TZDEEI50** | **74.50** | **74.50** | 0.00 | **1.00** | **1.29** | **0.57** | **1.00** | **10.50** | **3.75** | **70.00** | **1.70** | 5.50 | **5.50** | **5.00** |
| 48 | TZDEEI64 | 70.75 | 74.25 | 3.50 | 1.00 | 1.72 | 0.85 | 1.00 | 10.50 | 4.25 | 52.00 | 2.20 | 2.00 | 2.00 | 4.25 |
| 49 | CML312 | 74.50 | 72.63 | 1.87 | 1.00 | 2.02 | 0.88 | 1.00 | 8.50 | 6.25 | 27.25 | 3.20 | 2.00 | 3.75 | 1.00 |
| 50 | CML444 | 77.75 | 77.50 | 0.25 | 1.00 | 1.57 | 0.68 | 1.00 | 7.00 | 4.25 | 42.50 | 2.20 | 1.50 | 3.75 | 1.75 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.2** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 51 | CML442 | 79.25 | 80.25 | 1.00 | 1.00 | 1.32 | 0.63 | 1.00 | 6.75 | 4.75 | 45.00 | 1.70 | 2.00 | 3.25 | 2.25 |
| **52** | **TZDEEI54** | **83.75** | **79.25** | 4.50 | **1.00** | **1.52** | **0.80** | **1.50** | **13.00** | **3.25** | **82.50** | **3.20** | 1.50 | **2.75** | **0.75** |
| 53 | TZEEI10 | 82.25 | 81.25 | 1.00 | 1.00 | 1.32 | 0.71 | 1.00 | 11.25 | 3.25 | 40.00 | 2.70 | 2.00 | 3.50 | 1.50 |
| 54 | CML547 | 86.75 | 86.25 | 0.50 | 1.00 | 1.32 | 0.71 | 1.50 | 11.25 | 3.25 | 40.00 | 2.70 | 2.00 | 3.50 | 2.25 |
| **55** | **CML539** | **75.50** | **73.00** | 2.50 | **1.00** | **1.59** | **0.77** | **1.50** | **8.00** | **3.25** | **70.25** | **3.18** | 5.50 | **0.75** | **1.50** |
| **56** | **CML440** | **80.50** | **79.25** | 1.25 | **1.00** | **1.62** | **1.17** | **1.00** | **9.50** | **1.25** | **84.50** | **2.70** | 6.50 | **2.75** | **1.75** |
| **57** | **CML566** | **78.00** | **76.00** | 2.00 | **1.00** | **2.07** | **1.20** | **1.00** | **12.00** | **1.25** | **127.00** | **2.25** | 4.50 | **1.75** | **2.75** |
| **58** | **CML540** | **77.25** | **76.75** | 0.50 | **1.00** | **2.17** | **0.89** | **1.00** | **11.00** | **3.25** | **108.00** | **2.60** | 4.00 | **1.50** | **2.00** |
| **59** | **CML545** | **77.50** | **76.00** | 1.50 | **1.00** | **2.15** | **0.87** | **1.00** | **10.00** | **3.25** | **83.00** | **2.68** | 5.00 | **3.75** | **3.50** |
| **60** | **CML571** | **76.25** | **75.75** | 0.50 | **1.00** | **12.45** | **0.78** | **3.00** | **10.00** | **3.25** | **87.75** | **2.63** | 2.00 | **3.25** | **3.75** |
| 61 | CML390 | 74.00 | 73.75 | 0.25 | 1.00 | 2.05 | 0.80 | 3.00 | 10.75 | 5.75 | 37.30 | 2.68 | 7.50 | 4.25 | 3.25 |
| 62 | CLHP0352 | 78.50 | 74.75 | 3.75 | 1.00 | 1.10 | 0.98 | 1.00 | 11.25 | 6.75 | 17.05 | 2.68 | 8.00 | 3.75 | 3.75 |
| 63 | HA04A-2107-36 | 86.25 | 88.25 | 2.00 | 1.00 | 2.00 | 0.96 | 1.50 | 8.50 | 8.25 | 10.05 | 2.18 | 0.00 | 3.00 | 2.00 |
| 64 | CLHP0303 | 77.25 | 73.75 | 3.50 | 1.50 | 1.52 | 1.06 | 1.50 | 8.00 | 6.25 | 54.55 | 2.68 | 4.00 | 3.75 | 2.00 |
| 65 | CLHP0221 | 83.75 | 81.25 | 2.50 | 1.50 | 1.75 | 0.89 | 1.50 | 10.00 | 6.25 | 54.55 | 3.18 | 5.00 | 1.50 | 1.50 |
| 66 | CLHP0020 | 74.25 | 71.75 | 2.50 | 1.00 | 1.64 | 0.71 | 1.50 | 10.50 | 8.75 | 22.30 | 3.18 | 2.50 | 1.75 | 1.50 |
| 67 | CLHP0058 | 76.75 | 76.25 | 0.50 | 1.00 | 1.13 | 0.58 | 1.50 | 10.50 | 7.75 | 22.30 | 5.18 | 2.00 | 5.75 | 4.75 |
| 68 | CKDHL0378 | 80.00 | 79.75 | 0.25 | 1.00 | 1.55 | 0.78 | 1.50 | 10.00 | 4.25 | 28.05 | 5.18 | 2.00 | 4.75 | 5.75 |
| 69 | CLHP0312 | 76.25 | 78.00 | 1.75 | 1.00 | 1.35 | 0.95 | 1.50 | 8.50 | 2.75 | 35.55 | 3.18 | 1.50 | 3.75 | 3.75 |
| 70 | CLHP0310 | 72.75 | 72.50 | 0.25 | 1.00 | 1.20 | 0.77 | 1.50 | 8.00 | 5.75 | 23.55 | 2.68 | 2.50 | 3.75 | 2.75 |
| **71** | **CLHP0003** | **72.75** | **74.25** | 1.50 | **1.00** | **1.85** | **0.88** | **1.00** | **12.75** | **5.25** | **90.80** | **2.68** | 7.00 | **2.00** | **2.50** |
| **72** | **CKDHL0467** | **82.00** | **82.75** | 0.75 | **1.00** | **1.40** | **1.04** | **1.00** | **13.50** | **5.25** | **96.80** | **2.68** | 3.00 | **4.25** | **3.50** |
| 73 | CLHP00378 | 75.25 | 74.25 | 1.00 | 1.00 | 1.10 | 0.72 | 1.00 | 8.25 | 7.25 | 25.05 | 2.68 | 4.00 | 4.50 | 4.50 |
| 74 | CLHP0156 | 73.25 | 72.50 | 0.75 | 1.50 | 2.28 | 0.86 | 1.00 | 11.75 | 7.75 | 26.30 | 2.68 | 3.00 | 2.50 | 4.25 |
| 75 | CLHP0113 | 77.25 | 76.00 | 1.25 | 1.50 | 1.25 | 0.92 | 1.00 | 12.00 | 8.25 | 39.05 | 2.68 | 2.00 | 2.75 | 2.50 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.2** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 76 | CLHP03302 | 74.00 | 71.75 | 2.25 | 1.00 | 0.90 | 0.47 | 1.00 | 8.25 | 8.75 | 46.05 | 2.68 | 2.50 | 4.25 | 2.25 |
| **77** | **CLHP0404** | **74.75** | **74.25** | 0.50 | **1.00** | **2.07** | **0.75** | **1.00** | **10.00** | **6.25** | **137.35** | **3.18** | 5.00 | **6.00** | **2.00** |
| **78** | **CLHP0343** | **79.13** | **81.00** | 1.88 | **1.00** | **1.37** | **0.92** | **1.00** | **11.50** | **2.25** | **101.10** | **3.68** | 2.50 | **5.00** | **5.25** |
| 79 | CZL1380 | 80.25 | 79.25 | 1.00 | 1.00 | 1.23 | 0.79 | 1.00 | 9.50 | 5.25 | 54.85 | 3.68 | 5.00 | 5.25 | 5.50 |
| 80 | CLHP0326 | **72.75** | **72.25** | 0.50 | **1.00** | **1.60** | **0.72** | **1.50** | **8.50** | **5.25** | **85.35** | **3.68** | 2.00 | **3.25** | **4.75** |
| **81** | **CZL99017** | **81.75** | **82.25** | 0.50 | **1.00** | **1.70** | **0.68** | **1.50** | **10.75** | **2.25** | **71.10** | **3.18** | 5.50 | **3.50** | **3.00** |
| 82 | TZEEI34 | 79.25 | 80.25 | 1.00 | 1.00 | 1.26 | 0.58 | 1.50 | 10.25 | 4.25 | 60.10 | 3.18 | 6.50 | 4.00 | 2.25 |
| 83 | CLHP0049 | 78.25 | 79.25 | 1.00 | 1.00 | 1.25 | 0.47 | 1.50 | 5.50 | 5.25 | 60.35 | 3.18 | 2.50 | 3.25 | 2.50 |
| 84 | CLHP00478 | 77.75 | 75.25 | 2.50 | 1.00 | 1.60 | 0.55 | 1.00 | 5.25 | 5.75 | 57.35 | 2.68 | 2.00 | 2.50 | 2.00 |
| 85 | CLHP00286 | 77.88 | 79.50 | 1.63 | 1.00 | 1.25 | 0.70 | 1.00 | 9.75 | 5.75 | 57.60 | 3.68 | 3.00 | 3.25 | 2.00 |
| 86 | CML451 | 85.75 | 86.25 | 0.50 | 1.00 | 1.65 | 0.84 | 1.00 | 11.25 | 4.25 | 62.85 | 3.68 | 4.50 | 4.50 | 2.50 |
| 87 | CLHP0302 | 82.75 | 79.75 | 3.00 | 1.00 | 1.40 | 0.79 | 2.00 | 13.75 | 4.25 | 32.10 | 3.18 | 3.50 | 4.25 | 3.00 |
| 88 | CLHP0364 | 80.25 | 80.25 | 0.00 | 1.00 | 1.45 | 0.57 | 2.00 | 12.50 | 5.25 | 39.35 | 3.68 | 4.50 | 3.75 | 2.75 |
| 89 | CLHP0350 | 77.25 | 78.25 | 1.00 | 1.00 | 1.85 | 0.62 | 1.00 | 10.50 | 6.25 | 40.85 | 3.18 | 2.00 | 3.25 | 3.25 |
| 90 | CLHP00294 | 88.50 | 85.75 | 2.75 | 1.00 | 1.07 | 0.47 | 1.50 | 9.25 | 7.25 | 25.10 | 3.18 | 2.50 | 3.50 | 3.00 |
| 91 | CLHP0005 | 84.25 | 85.75 | 1.50 | 1.00 | 1.10 | 0.32 | 1.50 | 8.75 | 6.25 | 67.10 | 6.68 | 5.50 | 5.75 | 2.50 |
| 92 | CLHP0022 | 71.75 | 73.88 | 2.13 | 1.00 | 1.45 | 0.45 | 1.00 | 9.00 | 5.25 | 44.60 | 9.68 | 2.00 | 4.00 | 2.00 |
| **93** | **CML304** | **79.25** | **79.63** | 0.38 | **1.00** | **1.44** | **0.75** | **1.00** | **12.00** | **4.75** | **151.00** | **3.18** | 2.00 | **4.75** | **2.75** |
| **94** | **TZISTR1174** | **83.75** | **82.00** | 1.75 | **1.00** | **1.68** | **0.91** | **1.00** | **11.00** | **1.75** | **112.75** | **4.18** | 4.50 | **5.00** | **3.50** |
| **95** | **TZISTR1205** | **81.00** | **83.00** | 2.00 | **1.00** | **2.21** | **1.00** | **1.00** | **9.50** | **1.75** | **129.00** | **4.18** | 1.00 | **3.75** | **2.50** |
| **96** | **TZSTRI113** | **74.50** | **73.00** | 1.50 | **1.00** | **1.41** | **0.90** | **1.00** | **9.00** | **1.75** | **111.75** | **2.68** | 3.50 | **3.75** | **2.75** |
| **97** | **TZISTR1119** | **78.75** | **77.00** | 1.75 | **1.00** | **1.81** | **0.95** | **1.00** | **10.50** | **3.75** | **135.75** | **3.68** | 4.50 | **5.50** | **3.50** |
| **98** | **TZISTR1015** | **80.00** | **80.50** | 0.50 | **1.00** | **1.51** | **0.92** | **1.00** | **9.50** | **3.75** | **74.50** | **3.68** | 4.00 | **1.25** | **3.50** |
| **99** | **ZM1421** | **82.38** | **80.75** | 1.63 | **1.00** | **2.10** | **0.95** | **1.50** | **10.71** | **2.25** | **88.00** | **2.63** | 2.00 | **1.75** | **3.25** |
| **100** | **B.King/1421** | **81.00** | **77.75** | 3.25 | **1.00** | **2.35** | **1.05** | **1.50** | **11.71** | **3.25** | **91.75** | **2.63** | 4.50 | **2.25** | **2.25** |
| 101 | Hickory/1421 | 79.25 | 77.75 | 1.50 | 1.00 | 2.40 | 1.18 | 1.50 | 7.96 | 7.25 | 39.75 | 2.63 | 5.00 | 2.00 | 2.50 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.2** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 102 | Kep/1421 | 72.50 | 73.50 | 1.00 | 1.00 | 2.10 | 1.12 | 2.00 | 8.21 | 5.75 | 34.75 | 2.63 | 4.00 | 2.50 | 2.75 |
| **103** | **Shesha/1421** | **71.50** | **70.75** | 0.75 | **1.00** | **1.82** | **0.88** | **1.50** | **10.71** | **1.75** | **112.25** | **4.63** | 2.50 | **4.00** | **2.75** |
| **104** | **ZM1423** | **70.25** | **71.88** | 1.63 | **1.00** | **2.17** | **0.94** | **1.00** | **13.71** | **1.25** | **144.25** | **4.63** | 2.50 | **1.75** | **2.50** |
| **105** | **N.Choice/1421** | **81.25** | **75.25** | 6.00 | **1.00** | **1.62** | **0.85** | **1.50** | **10.96** | **1.75** | **133.25** | **3.13** | 3.50 | **4.00** | **3.00** |
| 106 | NC.QPM/Z.DPLO | 82.50 | 81.25 | 1.25 | 1.00 | 1.77 | 0.86 | 1.50 | 11.25 | 4.25 | 68.00 | 3.20 | 5.00 | 2.75 | 1.25 |
| **107** | **STR-SYN-Y2** | **85.25** | **85.25** | 0.00 | **1.00** | **1.60** | **0.80** | **1.00** | **11.25** | **3.25** | **126.85** | **8.18** | 3.50 | **3.25** | **2.50** |
| 108 | Z. Diplo.BC4C3-W-DT C1 | 87.75 | 87.75 | 0.00 | 1.00 | 0.98 | 0.82 | 1.00 | 12.25 | 3.25 | 60.35 | 6.68 | 2.50 | 4.75 | 4.25 |
| 109 | TZBSTR (Susceptible)(RE) | 84.25 | 87.75 | 3.50 | 1.00 | 1.65 | 0.66 | 1.00 | 10.50 | 4.25 | 33.60 | 8.18 | 1.50 | 4.75 | 4.25 |
| 110 | STR-SYN-W1 | 79.00 | 79.00 | 0.00 | 1.00 | 2.12 | 0.94 | 1.50 | 10.50 | 2.75 | 51.10 | 8.18 | 5.00 | 3.25 | 3.25 |
| **111** | **DTSTR-W SYN13** | **89.25** | **88.50** | 0.75 | **1.00** | **0.98** | **0.75** | **1.50** | **10.00** | **3.75** | **115.35** | **4.68** | 5.50 | **3.50** | **2.50** |
| **112** | **DTSTR-Y SYN15** | **83.75** | **84.25** | 0.50 | **1.00** | **1.78** | **0.65** | **1.00** | **9.00** | **6.25** | **87.35** | **3.18** | 4.50 | **4.00** | **2.75** |
| 113 | ((IWD C3 SYN*2/(White DT STR Syn))-DT C1 | 84.25 | 84.50 | 0.25 | 1.00 | 1.48 | 0.65 | 1.00 | 8.50 | 6.25 | 57.10 | 3.18 | 3.50 | 3.75 | 3.00 |
| 114 | DTSTR-W SYN11 | 87.25 | 89.75 | 2.50 | 1.00 | 1.73 | 0.73 | 1.50 | 8.00 | 3.75 | 45.10 | 2.68 | 3.00 | 2.75 | 1.75 |
| 115 | SAMMMZ16 | 85.75 | 84.75 | 1.00 | 1.00 | 1.93 | 1.03 | 2.00 | 8.50 | 3.75 | 56.50 | 3.18 | 4.50 | 2.75 | 0.75 |
| 116 | (TZEOMP5C7/TZECOMP3DTC2) C2 | 84.50 | 82.75 | 1.75 | 1.00 | 1.33 | 0.96 | 2.00 | 9.25 | 5.75 | 59.50 | 3.68 | 3.00 | 3.75 | 2.25 |
| 117 | ((TZL COMP1-W C6*2/(White DT STR Syn))-DT C1 | 87.75 | 88.75 | 1.00 | 1.00 | 1.73 | 0.66 | 2.00 | 9.25 | 5.75 | 59.50 | 3.68 | 4.50 | 3.75 | 3.25 |
| 118 | TZCOM1/ZDPSYN | 79.25 | 75.75 | 3.50 | 1.00 | 1.66 | 0.31 | 2.00 | 11.50 | 3.25 | 62.50 | 3.18 | 5.50 | 4.75 | 3.75 |
| 119 | Colorado/1421 | 77.75 | 79.63 | 1.88 | 1.00 | 1.63 | 0.49 | 2.00 | 10.50 | 1.25 | 58.75 | 4.68 | 7.50 | 5.25 | 5.25 |
| 120 | M.Pearl/DT-STR | 87.25 | 87.75 | 0.50 | 1.00 | 0.73 | 0.65 | 1.00 | 9.00 | 3.25 | 57.25 | 5.68 | 2.00 | 6.50 | 5.00 |
| 121 | Z.diplo-BC4-C3-W/DOGONA-1/Z.diplo-BC4-C3-W | 79.13 | 78.75 | 0.38 | 1.00 | 1.34 | 0.75 | 0.50 | 9.75 | 6.25 | 47.00 | 4.18 | 2.00 | 2.25 | 2.50 |
| 122 | NC.QPM/DT-STR | 79.65 | 80.75 | 1.10 | 1.00 | 1.31 | 0.50 | 0.50 | 9.75 | 6.25 | 47.00 | 3.68 | 5.00 | 5.50 | 2.00 |
| 123 | ZM1421/DT-STR | 82.50 | 80.75 | 1.75 | 1.00 | 1.32 | 0.50 | 1.00 | 10.00 | 3.75 | 58.25 | 3.68 | 4.00 | 3.75 | 4.00 |
| **124** | **DTSTR-Y SYN14** | **80.13** | **79.75** | 0.38 | **1.00** | **1.36** | **0.75** | **1.50** | **11.50** | **1.75** | **93.25** | **3.68** | 1.00 | **3.75** | **3.75** |
| **125** | **ZM1423/Z.DLO** | **81.25** | **83.25** | 2.00 | **1.00** | **12.41** | **1.03** | **1.00** | **10.75** | **4.75** | **96.75** | **2.68** | 5.00 | **3.75** | **2.75** |
| **126** | **(2*TZECOMP3DT/WhiteDTSTRSYN) C2** | **77.25** | **79.25** | 2.00 | **1.00** | **1.21** | **0.91** | **1.00** | **11.25** | **1.75** | **72.50** | **2.68** | 2.50 | **4.75** | **3.75** |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing.

**Appendix 2.2** (continued)

| Trial statistics | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Inbred lines** | | | | | | | | | | | | | | |
| Minimum | 70.75 | 71.75 | 0.00 | 1.00 | 0.9 | 0.32 | 1.00 | 5.25 | 1.25 | 10.05 | 1.70 | 0.00 | 0.75 | 0.75 |
| Maximum | 93.5 | 92.00 | 4.50 | 2.00 | 12.45 | 1.25 | 3.00 | 13.75 | 8.75 | 151 | 9.68 | 9.00 | 6.00 | 5.75 |
| Mean | 79.52 | 79.03 | 1.52 | 1.04 | 1.75 | 0.81 | 1.23 | 10.18 | 4.51 | 63.89 | 3.25 | 3.66 | 5.25 | 2.75 |
| **OPVs** | | | | | | | | | | | | | | |
| Minimum | 70.25 | 71.88 | 0.00 | 1.00 | 0.73 | 0.31 | 0.50 | 8.00 | 1.25 | 33.60 | 2.68 | 1.00 | 1.75 | 0.75 |
| Maximum | 89.25 | 71.88 | 3.50 | 1.00 | 12.41 | 1.03 | 2.00 | 13.71 | 6.25 | 144.25 | 8.18 | 7.50 | 6.50 | 5.25 |
| Mean | 82.53 | 82.81 | 1.26 | 1.00 | 2.01 | 0.74 | 1.30 | 13.71 | 3.93 | 70.81 | 4.43 | 3.77 | 3.86 | 3.05 |
| **Hybrids** | | | | | | | | | | | | | | |
| Minimum | 71.50 | 70.75 | 0.50 | 1.00 | 1.62 | 0.49 | 1.50 | 7.96 | 1.25 | 34.75 | 2.63 | 2.00 | 1.75 | 2.25 |
| Maximum | 82.38 | 80.75 | 6.00 | 1.00 | 2.40 | 1.18 | 2.00 | 11.71 | 7.25 | 133.25 | 4.68 | 7.50 | 5.25 | 5.25 |
| Mean | 77.95 | 76.48 | 2.03 | 1.00 | 2.00 | 0.93 | 1.64 | 10.11 | 3.32 | 79.79 | 3.28 | 4.14 | 3.11 | 3.11 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight days after sowing, SEC10= *Striga* emergence counts ten days after sowing, SDR8= *Striga* damage rating eight days after sowing, and SDR10= *Striga* damage rating 10 days after sowing

**Appendix 2.3.** Clusters and their member genotypes of 126 maize genotypes evaluated under *Sa* infestation.

| Cluster | Genotypes[a] | Total |
|---|---|---|
| I | 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20, 25, 27, 29, 30, 31, 38, 40, 36, 54, 61, 21, 22, 59, 55, 69, 70, 71, 73, 78, 89, 90, 47, 81, 82, 83, 87, 111, 107, 108, 118 | 49 |
| II | 13, 23, 24, 26, 32, 37, 42, 93, 45, 53, 77, 86, 79, 88, 97, 117, 123, 110, 60 | 19 |
| III | 56, 57, 58, 28, 43, 44, 39, 41, 46, 66, 67, 68, 72, 75, 76, 84, 85, 92, 95, 112, 114, 116 | 22 |
| IV | 98, 126, 102, 103, 125, 119, 121 | 7 |
| V | 74, 91, 94, 96, 99, 48, 49, 50, 51, 52, 120, 122, 124, 106, 101 | 15 |
| VI | 33, 34, 35, 62, 63, 64, 65, 80, 105, 109, 104, 100, 115, 113 | 14 |
| | Grand total | 126 |

[a]genotypes entry codes as listed in Table 2.1

**Appendix 2.4.** Clusters and their member genotypes of 126 maize genotypes evaluated under *Sh* infestation.

| Cluster | Genotypes[a] | Total |
|---|---|---|
| I | 46, 85, 86, 73, 74, 97, 106, 101, 84, 112, 114, 115, 116 | 13 |
| II | 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18, 19, 20, 21, 25, 26, 31, 32, 33, 39, 40, 41, 42, 43, 45, 53, 56, 58, 67, 68, 69, 70, 71, 72, 75, 76, 77, 78, 79, 80, 81, 82, 87, 47, 88, 89, 90, 91, 92, 93, 94, 95, 96, 52, 107, 108, 118, 119, 120, 123, 113, 102, 126 | 67 |
| III | 13, 14, 15, 22, 23, 24, 27, 28, 29, 30, 34, 35, 36, 37, 38, 44, 57, 54, 55, 59, 60, 61, 62, 63, 64, 65, 83, 98, 48, 49, 50, 51, 111, 105, 109, 110, 104, 100, 117, 121, 122, 124, 103, 125 | 44 |
| IV | 66, 99 | 2 |
| | Grand total | 126 |

[a]genotypes entry codes as listed in Table 2.1

## Chapter 3: Genetic diversity analysis of tropical and sub-tropical maize germplasm for *Striga* resistance and agronomic traits with SNP markers


### Abstract

*Striga hermonthica (Sh)* and *S. asiatica (Sa)* are major parasitic weeds limiting cereal crop production and productivity in sub-Saharan Africa (SSA). Under severe infestation, *Striga* causes yield losses of up to 100%. The deployment of *Striga*-resistant maize varieties is the most effective and economical approach to control the parasite. Well-characterized and genetically differentiated maize germplasm is vital in developing inbred lines, hybrids, and synthetic varieties with *Striga* resistance and desirable product profiles. The objective of this study was to determine the genetic diversity of 130 tropical and sub-tropical maize inbred lines, hybrids, and open-pollinated varieties germplasm using phenotypic traits and single nucleotide polymorphism (SNP) markers to select *Striga*-resistant and complementary genotypes for breeding. The test genotypes were phenotyped with *Sh* and *Sa* infestations using a 13x10 alpha lattice design with two replications. Agro-morphological traits and *Striga*-resistance damage parameters were recorded under a controlled environment. Further, high-density Diversity Array Technology Sequencing-derived SNP markers were used to profile the test genotypes. Significant phenotypic differences ($P<0.001$) were detected among the assessed genotypes for the assessed traits. The SNP markers revealed mean gene diversity and polymorphic information content of 0.34 and 0.44, respectively, supporting the phenotypic variation of the test genotypes. Significant variation was recorded within populations (85%) than between populations using the analysis of molecular variance. The Structure analysis allocated the test genotypes into eight major clusters ($K = 8$) in concordance with the principal coordinate analysis (PCoA). The following genetically distant inbred lines were selected, displaying good agronomic performance and *Sa* and *Sh* resistance: CML540, TZISTR25, TZISTR1248, CLHP0303, TZISTR1174, TZSTRI113, TZDEEI50, TZSTRI115, CML539, TZISTR1015, CZL99017, CML451, CML566, CLHP0343 and CML440. Genetically diverse and complementary lines were selected among the tropical and sub-tropical maize populations that will facilitate the breeding of maize varieties with *Striga* resistance and market-preferred traits.



**Keywords:** genetic diversity analysis, population structure, single nucleotide polymorphism, *Striga* resistance breeding, tropical and sub-tropical maize

## 3.1 **Introduction**

Maize (*Zea maize* L., 2n=2x=20) is the key food security crop in sub-Saharan Africa (SSA). However, the mean maize yield in the region is low (<3 t/ha) compared with the global average of 5 to 10 t/ha (FAO, 2022). Low yields are attributable to a plethora of challenges, including biotic (e.g. field and storage pests, plant diseases, and *Striga* infestation) and abiotic (e.g. poor soil health, drought, and heat). *Striga hermonthica (Sh)* and *S. asiatica (Sa)* are parasitic weeds that significantly impede cereal crop production in SSA, with yield losses of up to 100% under severe infestation [1].

*Striga hermonthica* is prevalent in most SSA regions, notably in Western, Central, and Eastern Africa, while *Sa* is predominant in Southern Africa [2-4]. Maize is relatively more susceptible to both species than sorghum and pearl millet due to the co-evolution of the latter with *Striga* [5]. *Striga* extracts the host's metabolites in exchange for phytotoxic compounds, reducing photosynthesis that causes yield loss varying from 10% to 100% [6,7]. More than 40 million households are affected by the scourge of *Striga* every year across Africa [7,8]. Several *Striga* control methods have been reported globally. However, the use of *Striga*-resistant cultivars is the most economical, sustainable, and environmentally friendly approach that can be deployed and adopted by small-holder maize producers [9]. The major components of *Striga* resistance/tolerance in maize are high grain yield, reduced *Striga* emergence, and low *Striga* damage symptoms [10].

The genetic base of maize has been enhanced by breeders at the Institute of Tropical Agriculture (IITA), the International Maize and Wheat Improvement (CIMMYT), and national breeding programs for *Striga* resistance and major economic traits [10]. Genetically diverse maize germplasm has been developed and dispatched by IITA and CIMMYT globally for more than three decades [11-13]. The germplasms can be phenotyped in the target production environments for selection and as parents in *Striga* resistance breeding programs by the public and private sectors. Genetic resources of maize selected by the breeders at IITA possess mainly *S. hermonthica* resistance. Conversely, CIMMYT-bred lines in East and Southern Africa display drought and heat stress tolerance. *Striga asiatica* is increasingly a major parasitic weed in South and East Africa due to poor soil fertility and drought stress conditions, which are conducive to the proliferation of the parasite and host susceptibility. Reportedly, both species occur in tandem in the major cereal crops [14,15]. Breeding for *Striga*-resistant maize cultivars is vital for sustainable *Striga* management [3].

*Striga*-resistant maize varieties are bred with major genes conditioning *Sh* resistance. Gene introgression using the tropical genetic resources into locally adapted sub-tropical varieties will enable the suppression of both *Sh* and *Sa* in SSA. Well-characterized and genetically differentiated maize germplasm is vital to developing inbred lines, hybrids, and synthetic varieties with durable *Striga* resistance. Enhanced hybrid vigour is achieved from crosses of inbred lines from complementary heterotic groups [16,17]. Hence, detailed information on genetic diversity, genetic interrelationships, and heterotic groups is crucial for developing maize cultivars with desirable product profiles.

Various molecular markers have been developed and applied to determine genetic diversity, population structure, quantitative trait loci (QTL), and linkage maps in maize. These include Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPDs), Amplified Fragment Length polymorphic (AFLPs), Single Sequence Repeats (SSR), and Single Nucleotide Polymorphisms (SNPs). SNPs have emerged as the markers of choice for genetic diversity analysis and marker-assisted breeding. This is attributed to their low cost per data point, high genomic abundance, locus specificity, co-dominance, the potential for high throughput analysis, and lower genotyping error rates [18]. SNPs can be identified using various protocols, including Genotyping by sequencing (GBS), restriction-associated DNA (RAD), complexity reduction of polymorphic sequences (CRoPS), and diversity arrays technology (DArT). DArT is a sequence-independent, high throughput, reproducible, cost-effective, and whole genome genotyping technology. DArTseq SNP markers have been routinely used in genetic diversity analysis in maize and other crops.

Results using DArTseq SNP markers enabled the selection of parents for breeding [19]. Successful genetic diversity and grouping of pigeonpea [20], cowpea [21], sorghum [22,23] maize [24,25] have been reported using DArTseq SNPs. Genetic diversity analysis of *Striga*-resistant maize populations was reported using DArTseq SNP markers. For instance, Badu-Apraku, et al. [19], Yacoubou, *et al.* [26], and Gasura, et al. [6] discerned the genetic diversity and population structure of maize germplasm. Zebire, *et al.* [27] identified suitable testers for *Striga*-resistant lines using DArTseq SNP markers and agronomic traits. Quantitative trait loci conditioning resistance/tolerance to *S. hermonthica* have been identified using this marker system [9,28-31].

In an attempt to select novel inbred lines with *Striga* resistance and morpho-agronomic traits, genetically diverse tropical and sub-tropical maize genotypes were assembled by the University

of KwaZulu-Natal's African Center for Crop Improvement (ACCI) from IITA/Ibadan, CIMMYT/ Zimbabwe, and the National Plant Genetic Resources Centre (NGRC) in South Africa. The genetic diversity and the population structure of the accessions should be characterized to delineate heterotic groups for developing inbred lines, hybrids, and synthetic varieties with *Striga* resistance and desirable product profiles. Therefore, this part of the study aimed to determine the genetic diversity of 130 tropical and sub-tropical maize germplasm using phenotypic traits and single nucleotide polymorphism (SNP) markers to select *Striga*-resistant and complementary genotypes for breeding. The novelty of this study is that the selected inbred lines are tropical and sub-tropical genetic pools with dual resistance to the two *Striga* species. Both genetic resources can be used for *Striga* resistance breeding in *Striga*-prone environments in sub-Saharan Africa.

## 3.2 **Materials and methods:**

### 3.2.1 Plant material

A panel of 130 maize germplasm was used for this study. The test genotypes comprised 74 accessions acquired from IITA/Nigeria, 45 from CIMMYT/Zimbabwe, and 10 from the National Plant Genetic Resources Centre (NPGRC)/South Africa (Appendix 3.1). The population included released tropical inbred lines, hybrids, and open-pollinated varieties with *Striga* resistance and sub-tropical varieties bred for their agronomic performance and drought tolerance in South Africa and East Africa. Seeds of *Sa* were collected from Zimbabwe in 2016, while *Sh* seeds were collected from maize-infested fields in Kenya in 2021. The seeds were stored in airtight plastic jars at room temperature in dry conditions.

### 3.2.2 Phenotyping

The 130 accessions were phenotyped at the University of Kwazulu-Natal Controlled Environment Facilities (UKZN-CEF) in two seasons (December 2021–April 2022, and August 2022–December 2022). The UKZN CEF is situated at the UKZN College of Agriculture, Engineering, and Science (29.62° S, 30.40° E). Treatments were laid out using a 13 x 10 alpha lattice design with two replications in each *Striga*-infested environment. Two weeks before planting, each pot was infested with a scoop of sand mixed with 0.03 g of 2-year-old *Sa* or *Sh* seed containing approximately 3000 *Striga* seeds [32]. The experimental unit consisted of 4

plastic pots of 5-L capacity, filled with a composted pine bark potting mix for each *Striga*-infested environment. Maize and *Striga* parameters were used for phenotyping. Days to 50% silking (DS) was recorded as the number of days taken by 50% of the plants to silk in each plot; days to anthesis (DA), was recorded as the number of days from planting until 50% of the plants have shed pollen; anthesis-silking interval (ASI), was measured as the difference between days to 50% silking and 50% anthesis; plant height (PLHT) and ear height (EHT) were measured as the distance from the base of the plant to the height of the first tassel branch and the node bearing the upper ear, respectively; root lodging (RL) tolerance was recorded as a percentage of plants leaning more than 30° from the vertical; stalk lodging (SLG) tolerance (percentage broken at or below the highest ear node); and ear rot (EROT) was assessed as the number of rotten ears per plant. The number of ears per plant (EPP) was obtained by dividing the total number of ears per plot by the number of plants harvested. Husk cover (HUSK) was rated on a scale of 1 to 5, where 1 = husks tightly arranged and extended beyond the ear tip and 5 = ear tips exposed. Ear aspect (EASP) was recorded on a scale of 1 to 9, where 1 = clean, uniform, large, well-filled ears and 9 = ears with undesirable features. The grain yield per plant (GY/plant) adjusted to a constant moisture of 12.5% was determined as the grain weight (g) from the ears of an individual plant after shelling. This was determined by dividing the grain yield per plot by the number of plants harvested.

The *Striga* parameters were recorded, including the number of emerged *Sa* and *Sh* plants 8 and 10 weeks after planting, denoted as SEC8 and SEC10. Host plant damage was rated 8 and 10 weeks after planting, designated as SDR8 and SDR10 using a visual rating score of 1 to 9 where 1 = no damage, indicating normal plant growth and a high level of tolerance, and 9 = complete collapse or death of the maize plant, i.e., highly susceptible [33].

### 3.2.3 Phenotypic data analysis

Before data analysis, the ASI values were standardized and expressed in positive figures using the corrective value (cv) following [34], where cv =1 – the smallest ASI value. Phenotypic data collected in both *Sh* and *Sa*-infested environments were subjected to Bartlet's homogeneity of variance test prior to combined analysis of variance (ANOVA) using a lattice procedure in RStudio version 2023. 06.1 (R Core Team, 2023). Genotypes mean comparisons were made at the 5% significance level using Fisher's least significance difference (LSD). Phenotypic clusters based on the dissimilarity matrix were generated using the Gower method implemented in the "cluster" and "graphics" procedures in R statistical package version 4.2.1 (R Core Team,

2018). Broad sense heritability ($H^2$) was computed using DeltaGen [35] with the following formula:

$$(H^2)= \frac{\sigma^2 g}{\sigma^2 g+\frac{\sigma^2 s}{ns}+\frac{\sigma^2 r}{nr}+\frac{\sigma^2 b}{nb}+\frac{\sigma_\varepsilon^2}{ns+nr+nb}}$$

where $\sigma^2 g, \sigma^2 s, \sigma^2 r, \sigma^2 b,$ and $\sigma_\varepsilon^2$ are the variance components for genotypes, season, replication, block, and the pooled error, respectively, and ns, nr, and nb are the number of seasons, replications, and blocks, respectively. A hierarchical cluster was constructed using the ward D2 method in "cluster" in R package version 4.2.1 (R Core Team, 2018). Cluster analyses were conducted to classify the germplasm and study their genetic relationships.

### 3.2.4 DNA extraction and genotyping

The seeds of the 130 accessions were planted in plastic pots filled with a growing medium in a greenhouse at the University of Kwazulu-Natal. Two weeks after planting, the fresh leaves of the three leaves stage were harvested for genomic DNA extraction. Genomic DNA was extracted using the DArTseq protocol as described by Kilian, *et al.* [36]. DNA quality was checked for nucleic acid concentration and purity using a NanoDrop 2000 spectrophotometer (ND-2000 V3.5, NanoDrop Technologies Inc) as described by Desjardins and Conklin [37]. An estimated 20 µl of DNA sample of each genotype with concentrations between 50 and 100 ng ul-1, and absorbances ranging from 1.75 to 2.05 were submitted to *Sequential art (SEQAT) (https://www.seqart.net/)* in Kenya for high throughput genotyping. The Diversity Array Technology Sequencing (DArTseq) protocol was used for genotyping the samples as previously described by Elshire et al. (2011). SNPs obtained were used for data analysis in this study.

### 3.2.5 Genotypic Data Analysis

#### 3.2.5.1 *SNPs filtering*

The numerical genotyping output was used for genotypic data analysis. The initial 70197 SNPs were imputed by removing SNPs with >20% missing data and < 5% minor allele frequency (MAF) on the KDCompute server (https://kdcompute.igssafrica.org/kdcompute/). A total of 16000 informative SNP markers and 130 genotypes were used for further analysis after data imputation.

3.2.5.2 ***Analysis of genetic diversity parameters and genetic relationship among germplasms***

The polymorphic information content (PIC), minor allele frequency (MAF), heterozygosity (Ho), and gene diversity (GD) were calculated using RStudio version 4.3.0 (R Core Team, 2023). Analysis of molecular variance (AMOVA), inbreeding coefficient (Fis), and the genetic distance between the individuals were calculated using GenAlex version 6.5 [38].

3.2.5.3 ***Population Structure Analysis:***

The clustering of the 130 genotypes was assessed using the admixture model-based clustering method in Structure software version 2.3.4 [39]. The burn-in period length and the Markov Chain Monte Carlo (MCMC) replications were set at 10,000. The Structure analysis was done for K ranging from 1 to 10 with 5 iterations at each K to determine the optimum number of clusters. The best K value was predicted following the simulation method of Evanno, *et al.* [40] using Structure harvester version 0.6.94 [41], and the bar plot for the optimum K was confirmed through the clustering markov packager across k (CLUMPAK) beta version [42]. Maize genotypes with inferred ancestries ≥ 70% were assigned to a different population, and those ≤ 70% were treated as admixtures. The dendrograms were generated using the genetic dissimilarity matrix using the "phylogenetics" and "evolution" procedures in RStudio version 4.3.0 (R Core Team, 2023).

3.2.5.4 ***Joint analysis using phenotypic and SNP data***

Genetic groups were defined using a combination of the phenotypic and genotypic dissimilarity matrices. The joint matrix was generated by the summation of the genotypic and phenotypic dissimilarity matrices. The phenotypic dissimilarity matrix was generated using Gower's distance matrix, while the genotypic dissimilarity matrix was based on Jaccard's coefficients. The groups generated from the phenotypic and genotypic sets were compared using the "viridis" procedure in R version 4.3.0 (R Core Team, 2023), and the similarity of the two dendrograms was assessed using the tanglegram function developed by the "dendextend" R package (R Core Team, 2020).

## 3.3 **Results**

### 3.3.1 Phenotyping

Genotypic variation was significant for all the assessed traits in both *Sa* and *Sh* environments (Table 3.1). Under *Sa*-infested conditions, testing seasons had a significant effect ($P<0.001$) on all the traits except for EPP, PLHT, HUSK, and SEC10. Also, significant effects were noted for all traits except for EPP, PLHT, EHT, and HUSK under *Sh*-conditions. Block nested in replication-by-season interaction significantly affected all the assessed traits under both *Sa* and *Sh*-infested environments, except for EPP.

**Table 3.1** Analyse of variance and significant tests for yield components and *Striga* parameters of 126 maize genotypes evaluated under *Striga asiatica* and *S. hermonthica* infestations.

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | ***S. asiatica*** | | | | | | | | |
| **Source of variation** | Df | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
| **Genotypes (G)** | 125 | 9.34*** | 7.27*** | 4.06*** | 6.49*** | 2.10*** | 5.82*** | 3.65*** | 9.95*** | 2.47*** | 4.05*** | 2.79*** | 2.19*** | 2.41*** | 2.91*** |
| **Seasons (S)** | 1.00 | 273.78*** | 100.64*** | 33.01*** | 0.00 | 0.27 | 20.82*** | 0.00 | 29.74*** | 43.79*** | 54.71*** | 1518.79*** | 3.48 | 56.80*** | 37.88*** |
| **G x S** | 125 | 0.0666 | 0.00 | 0.084 | 0.00 | 0.00 | 0.00 | 0.06 | 0.00 | 0.036 | 0.00 | 0.54 | 0.00 | 0.00 | 0.00 |
| **Replications in seasons** | 1.00 | 0.35 | 0.00 | 0.44 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.39 | 0.00 | 51.62*** | 0.00 | 0.00 | 0.00 |
| **Block/(replication x season)** | 13 | 0.46** | 9.29** | 4.36** | 0.00 | 0.59** | 5.73** | 0.07** | 1.51** | 0.08** | 0.06** | 2.06** | 2.69** | 2.00** | 0.90** |
| **Error** | 238.00 | 15.40 | 20.03 | 12.28 | 0.03 | 106.99 | 0.05 | 0.28 | 2.08 | 3.47 | 1439.00 | 1.51 | 144.80 | 2.22 | 2.13 |
| | | | | | | ***S. hermonthica*** | | | | | | | | |
| **Source of variation** | df | DA | DS | ASI | EPP | PLHT | EHT | HUSK | CL | EASP | GY | SEC8 | SEC10 | SDR8 | SDR10 |
| **Genotypes (G)** | 125 | 2.43*** | 2.29*** | 1.76*** | 3.01*** | 2.17*** | 1.84*** | 1.48** | 1.47** | 2.76*** | 2.45*** | 4.97*** | 2.13*** | 2.08*** | 2.24*** |
| **Seasons (S)** | 1.00 | 125.84*** | 158.08*** | 32.01*** | 0.00 | 3.14 | 23.37 | 1.03 | 17.77*** | 18.89*** | 72.91*** | 3255.33*** | 78.31*** | 222.49*** | 71.81*** |
| **G x S** | 125 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.25 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| **Replications in seasons** | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.26 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| **Block/(replication x season)** | 13 | 10.73** | 7.20** | 0.58** | 0.00 | 0.52** | 4.70* | 3.83** | 10.61** | 2.82* | 5.07** | 4.05** | 2.00** | 2.54** | 1.98** |
| **Error** | 233.00 | 36.00 | 51.00 | 15.75 | 0.03 | 3.61 | 0.08 | 0.49 | 7.09 | 5.40 | 1473.00 | 1.20 | 6.44 | 2.27 | 1.76 |

*, **, and *** denote significance at P < 0.05, P < 0.01 and P < 0.001, respectively, Df = degrees of freedom, DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing.

Tables 3.2 and 3.3 summarize the mean performances of the top 10 inbred lines and check genotypes with high GY under *Sa* and *Sh*-infested conditions, respectively. In a *Sa*-infested environment, the highest variation was exhibited by PLHT, followed by ASI, with a coefficient of variation values of 426.82% and 268.88%, respectively (Table 3.2). Inbred lines had a mean ASI of 2.77, while the OPV and hybrid checks had mean ASI values of 1.86 and 1.77, respectively (Table 3.2). The mean yield of the inbred lines ranged from 0.00 g/plant (TZISTR1262) to 277.50 g/plant (CML540). Further, the mean grain yield of the hybrid checks ranged from 00.00 g/plant (Hickory/1421) to 214.00 g/plant (N.Choice/1421). Whereas the OPV checks had mean grain yields varying from 35.00 g/plant ((IWD C3 SYN*2/(White DT STR Syn)) -DT C1) to 169.50 g/plant (NC.QPM/Z.DPLO).

In a *Sh*-infested environment, PLHT exhibited the highest coefficient of variation of 597.49% (Table 3.3). The grain yield of the inbred lines varied from 0.05 g/plant (HA04A-2107-36) to 151 g/plant (CML304), with a mean of 63.89 g/plant. A mean grain yield of 79.79 g/plant was recorded for the hybrids varying from 34.75 g/plant (Kep/1421) to 133.25 g/plant (N.Choice/1421), while the OPVs recorded an overall mean yield of 70.81 g/plant varying from 33.60 g/plant (TZBSTR) to 144.25 g/plant (ZM1423) (Table 3.3). Low broad-sense heritability values were computed for SEC10, SDR8, and SDR10 in *Sa*-infested conditions. In contrast, high heritability values were recorded for all the traits except for GY ($H^2$=0.02) under *Sh*-infested conditions.

Dendrograms based on phenotypic traits resolved the test genotypes into three clusters under *Sa* (Figure 3.1) and *Sh* (Figure 3.2) conditions. In a *Sa*-infested environment, Cluster I recorded the highest number of genotypes (91), followed by Cluster II (18), and Cluster III (17). Cluster I comprised tropical and sub-tropical genotypes from all sources. This Cluster had two sub-groups. The first sub-group is characterized by genotypes with low yield and moderate *Striga* resistance, whereas the second consists of genotypes with high yield and relatively high *Striga* resistance. Cluster II comprised 18 inbred lines mainly from IITA, while the genotypes in Cluster III were a mixture of *Striga*-resistant lines, drought-tolerant lines, and synthetic hybrids from IITA/Nigeria and CIMMYT/Zimbabwe. Under *Sh*-infested conditions, Cluster I was the largest (with 90 genotypes), followed by Cluster II (19) and Cluster III (17). Clusters I and II were composed of inbred lines from IITA and CIMMYT. Genotypes from Cluster III were from all sources; however, most were OPVs and hybrids sourced from IITA and NPGRC.

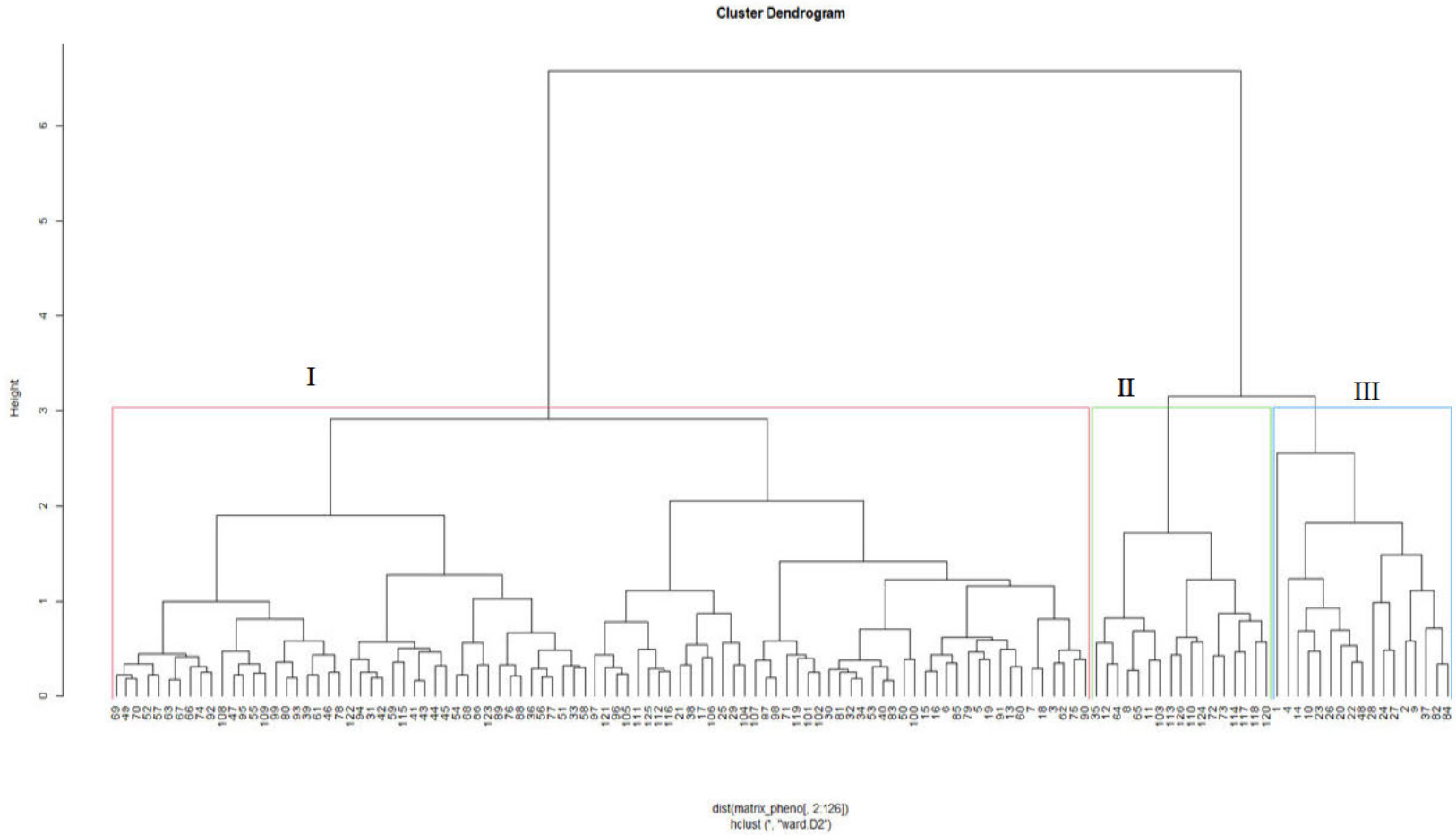


**Figure 3.1** Dendrogram showing genetic relatedness among the 126 maize genotypes (G1 to G126) based on phenotypic traits under *Striga asiatica*-infested conditions. See Appendix 3.2 for the code of genotypes.

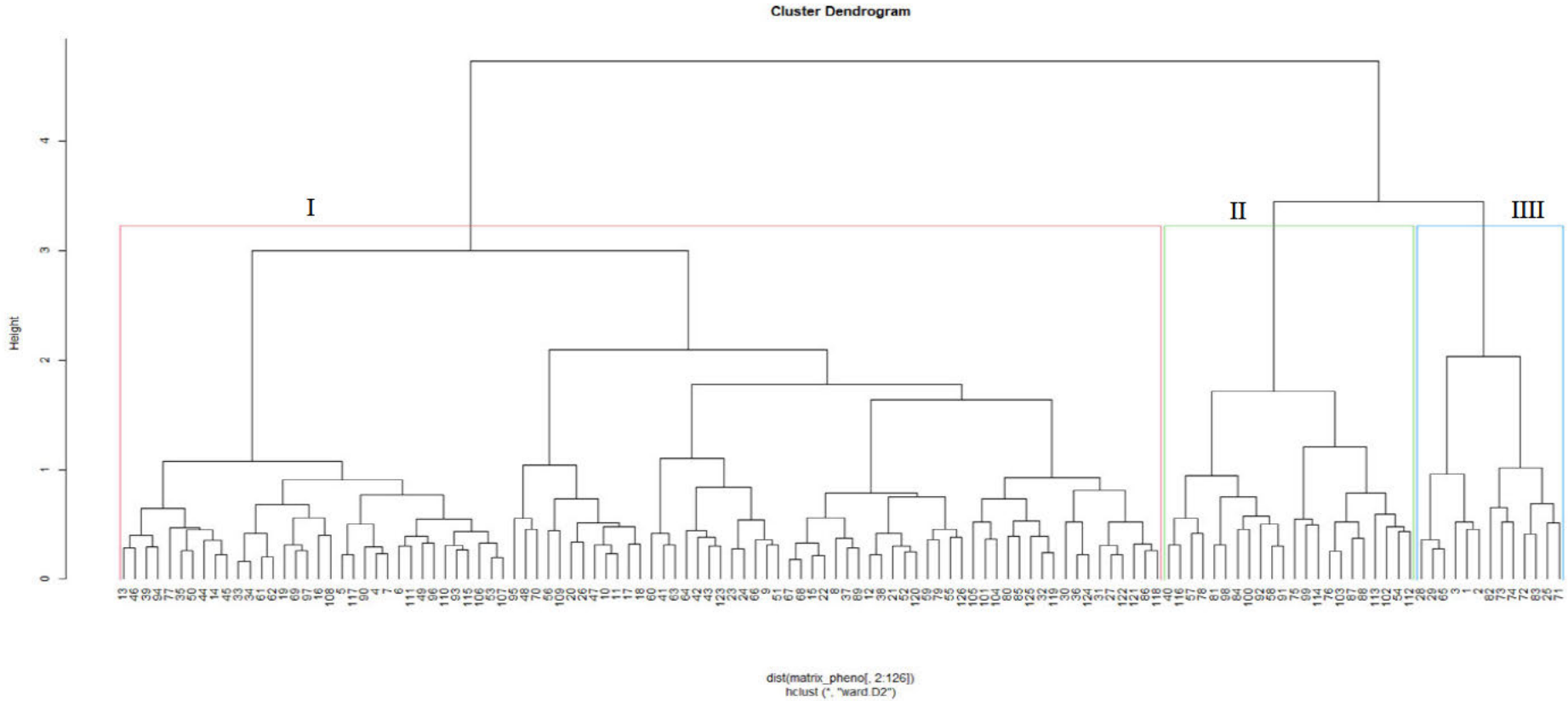


**Figure 3.2** Dendrogram showing genetic relatedness among the 126 maize genotypes (G1 to G126) based on phenotypic traits under *Striga hermonthica*-infested conditions. See Appendix 3.3 for the code of genotypes.

**Table 3.2** Mean values for 14 traits of 126 maize genotypes evaluated under *Striga asiatica* infestation, showing the top 10 inbred lines, the top 4 hybrids, and 6 OPVs based on grain yield.

| Genotype | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP (1 to 9) | GY (g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Top 10 inbred lines** | | | | | | | | | | | | | | |
| **CML540** | 77.00 | 81.50 | 4.50 | 1.00 | 2.03 | 0.77 | 1.00 | 11.00 | 3.50 | 277.50 | 4.00 | 1.50 | 3.50 | 3.00 |
| **CML566** | 82.50 | 79.00 | -3.50 | 1.00 | 2.22 | 1.15 | 1.00 | 12.00 | 1.50 | 155.50 | 4.00 | 5.50 | 1.50 | 1.50 |
| **TZISTR1001** | 82.00 | 82.00 | 0.00 | 1.00 | 2.10 | 1.28 | 1.00 | 11.00 | 1.50 | 140.00 | 4.50 | 4.50 | 3.00 | 2.50 |
| **TZISTR1205** | 81.50 | 75.50 | -6.00 | 1.00 | 1.85 | 0.91 | 1.00 | 11.00 | 1.00 | 114.25 | 3.50 | 13.00 | 3.00 | 2.50 |
| **TZSTRI115** | 77.50 | 77.00 | -0.50 | 1.00 | 2.10 | 1.20 | 1.00 | 11.50 | 1.50 | 112.50 | 5.00 | 2.00 | 3.50 | 2.50 |
| **CLHP0350** | 75.00 | 76.00 | 1.00 | 1.00 | 2.35 | 0.81 | 3.00 | 14.00 | 3.50 | 102.75 | 5.00 | 3.50 | 2.00 | 3.50 |
| **CLHP0049** | 80.50 | 78.00 | -2.50 | 1.00 | 1.25 | 0.70 | 1.00 | 10.00 | 3.00 | 101.25 | 7.00 | 4.00 | 1.00 | 2.50 |
| **CLHP0302** | 81.00 | 80.50 | -0.50 | 1.00 | 1.76 | 1.00 | 3.00 | 13.25 | 3.00 | 98.00 | 4.50 | 7.00 | 2.00 | 3.50 |
| **CML440** | 82.50 | 76.00 | -6.50 | 1.00 | 2.36 | 1.08 | 1.00 | 11.00 | 1.50 | 96.25 | 4.50 | 13.50 | 3.00 | 1.50 |
| **CLHP0303** | 84.50 | 83.50 | -1.00 | 1.50 | 1.87 | 1.15 | 1.00 | 7.25 | 3.00 | 92.50 | 4.50 | 8.50 | 3.00 | 3.00 |
| **Top 4 hybrids and 6 OPVs** | | | | | | | | | | | | | | |
| **N.Choice/1421** | 82.00 | 76.50 | -5.50 | 1.00 | 1.90 | 1.03 | 1.00 | 13.25 | 1.50 | 214.00 | 5.00 | 4.00 | 3.50 | 3.50 |
| **Shesha/1421** | 75.50 | 72.50 | -3.00 | 1.00 | 2.03 | 1.75 | 1.00 | 18.75 | 1.50 | 165.75 | 7.50 | 18.50 | 2.00 | 2.00 |
| **B.King/1421** | 80.50 | 78.50 | -2.00 | 1.00 | 2.05 | 1.15 | 2.00 | 23.50 | 1.50 | 157.25 | 5.00 | 4.50 | 1.00 | 2.00 |
| **ZM1421/DT-STR** | 77.00 | 76.50 | -0.50 | 1.00 | 2.38 | 1.10 | 1.50 | 10.75 | 3.00 | 93.50 | 2.50 | 19.00 | 2.50 | 2.00 |
| **NC.QPM/Z.DPLO** | 71.50 | 71.50 | 0.00 | 1.00 | 2.25 | 1.03 | 0.00 | 12.50 | 4.50 | 154.25 | 3.00 | 5.00 | 3.50 | 2.00 |
| **Z.diplo-BC4-C3-W/DOGONA-1/Z.diplo-BC4-C3-W** | 81.00 | 83.00 | 2.00 | 1.00 | 2.36 | 1.05 | 1.00 | 11.50 | 1.50 | 112.00 | 6.00 | 8.50 | 3.00 | 3.50 |
| **DTSTR-W SYN13** | 85.50 | 85.50 | 0.00 | 1.00 | 1.25 | 0.85 | 1.50 | 13.00 | 3.50 | 107.50 | 4.50 | 3.50 | 1.50 | 1.00 |
| **TZBSTR** | 83.00 | 83.50 | 0.50 | 1.00 | 2.65 | 1.30 | 1.50 | 14.50 | 1.00 | 103.00 | 6.50 | 3.00 | 3.00 | 2.50 |
| **ZM1423** | 69.00 | 69.50 | 0.50 | 1.00 | 0.85 | 1.39 | 1.00 | 10.50 | 1.50 | 99.25 | 4.50 | 16.50 | 5.00 | 3.00 |
| **(2*TZECOMP3DT/WhiteDTSTRSYN) C2** | 69.00 | 78.00 | 9.00 | 1.00 | 1.75 | 0.85 | 1.50 | 12.25 | 2.50 | 89.00 | 6.00 | 0.50 | 2.00 | 1.50 |
| **Trial statistics** | | | | | | | | | | | | | | |
| **LSD (5%)** | 3.94 | 4.44 | 3.69 | 0.15 | 10.57 | 0.23 | 0.52 | 1.55 | 1.93 | 37.73 | 1.87 | 12.44 | 1.64 | 1.61 |
| **SEM** | 7.64 | 8.75 | 7.27 | 0.21 | 20.82 | 0.46 | 1.02 | 3.05 | 3.80 | 74.31 | 3.69 | 24.51 | 3.23 | 3.17 |
| **%CV** | 4.89 | 5.60 | 268.88 | 14.65 | 426.82 | 25.36 | 41.21 | 13.63 | 58.57 | 56.12 | 40.91 | 129.74 | 50.29 | 49.50 |
| **Heritability** | 0.90 | 0.94 | 0.94 | 0.11 | 0.11 | 0.96 | 0.96 | 0.97 | 0.96 | 0.88 | 0.34 | 0.01 | 0.11 | 0.16 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP= ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing. LSD= least significant difference, SEM= standard error of the mean, %CV= coefficient of variation, m= meter, cm= centimetre, g= gram.

**Table 3.3** Mean responses for 14 traits of 126 maize genotypes evaluated under *Striga hermonthica* infestation, showing the top 10 inbred lines, the top 4 hybrids, and 6 OPVs.

| Genotypes | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP (1 to 9) | GY (g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Top 10 lines** | | | | | | | | | | | | | | |
| **CML304** | 79.25 | 79.63 | 0.38 | 1.00 | 1.44 | 0.75 | 1.00 | 12.00 | 4.75 | 151.00 | 3.18 | 2.00 | 4.75 | 2.75 |
| **TZSTRI101** | 90.00 | 87.50 | -2.50 | 1.00 | 1.45 | 0.75 | 1.00 | 12.46 | 3.25 | 144.00 | 3.63 | 6.50 | 3.75 | 3.00 |
| **CLHP0404** | 74.75 | 74.25 | -0.50 | 1.00 | 2.07 | 0.75 | 1.00 | 10.00 | 6.25 | 137.35 | 3.18 | 5.00 | 6.00 | 2.00 |
| **TZISTR1119** | 78.75 | 77.00 | -1.75 | 1.00 | 1.81 | 0.95 | 1.00 | 10.50 | 3.75 | 135.75 | 3.68 | 4.50 | 5.50 | 3.50 |
| **TZISTR25** | 75.75 | 75.50 | -0.25 | 1.00 | 2.25 | 1.05 | 1.00 | 12.00 | 1.25 | 131.00 | 3.20 | 2.00 | 3.75 | 2.00 |
| **TZISTR1205** | 81.00 | 83.00 | 2.00 | 1.00 | 2.21 | 1.00 | 1.00 | 9.50 | 1.75 | 129.00 | 4.18 | 1.00 | 3.75 | 2.50 |
| **CML566** | 78.00 | 76.00 | -2.00 | 1.00 | 2.07 | 1.20 | 1.00 | 12.00 | 1.25 | 127.00 | 2.25 | 4.50 | 1.75 | 2.75 |
| **TZISTR1001** | 79.63 | 78.25 | -1.38 | 1.00 | 2.10 | 1.03 | 1.00 | 11.50 | 1.75 | 120.00 | 2.70 | 1.50 | 3.50 | 2.50 |
| **TZISTR1174** | 79.25 | 79.63 | 0.38 | 1.00 | 1.44 | 0.75 | 1.00 | 12.00 | 4.75 | 151.00 | 3.18 | 2.00 | 4.75 | 2.75 |
| **TZSTRI113** | 74.50 | 73.00 | -1.50 | 1.00 | 1.41 | 0.90 | 1.00 | 9.00 | 1.75 | 111.75 | 2.68 | 3.50 | 3.75 | 2.75 |
| **Top 4 hybrids and 6 OPVs** | | | | | | | | | | | | | | |
| **N.Choice/1421** | 81.25 | 75.25 | -6.00 | 1.00 | 1.62 | 0.85 | 1.50 | 10.96 | 1.75 | 133.25 | 3.13 | 3.50 | 4.00 | 3.00 |
| **Shesha/1421** | 71.50 | 70.75 | -0.75 | 1.00 | 1.82 | 0.88 | 1.50 | 10.71 | 1.75 | 112.25 | 4.63 | 2.50 | 4.00 | 2.75 |
| **B.King/1421** | 81.00 | 77.75 | -3.25 | 1.00 | 2.35 | 1.05 | 1.50 | 11.71 | 3.25 | 91.75 | 2.63 | 4.50 | 2.25 | 2.25 |
| **ZM1421** | 82.38 | 80.75 | -1.63 | 1.00 | 2.10 | 0.95 | 1.50 | 10.71 | 2.25 | 88.00 | 2.63 | 2.00 | 1.75 | 3.25 |
| **ZM1423** | 70.25 | 71.88 | 1.63 | 1.00 | 2.17 | 0.94 | 1.00 | 13.71 | 1.25 | 144.25 | 4.63 | 2.50 | 1.75 | 2.50 |
| **STR-SYN-Y2** | 85.25 | 85.25 | 0.00 | 1.00 | 1.60 | 0.80 | 1.00 | 11.25 | 3.25 | 126.85 | 8.18 | 3.50 | 3.25 | 2.50 |
| **DTSTR-W SYN13** | 89.25 | 88.50 | -0.75 | 1.00 | 0.98 | 0.75 | 1.50 | 10.00 | 3.75 | 115.35 | 4.68 | 5.50 | 3.50 | 2.50 |
| **ZM1423/Z.DLO** | 81.25 | 83.25 | 2.00 | 1.00 | 12.41 | 1.03 | 1.00 | 10.75 | 4.75 | 96.75 | 2.68 | 5.00 | 3.75 | 2.75 |
| **DTSTR-Y SYN14** | 80.13 | 79.75 | -0.38 | 1.00 | 1.36 | 0.75 | 1.50 | 11.50 | 1.75 | 93.25 | 3.68 | 1.00 | 3.75 | 3.75 |
| **DTSTR-Y SYN15** | 83.75 | 84.25 | 0.50 | 1.00 | 1.78 | 0.65 | 1.00 | 9.00 | 6.25 | 87.35 | 3.18 | 4.50 | 4.00 | 2.75 |
| **Trial statistics** | | | | | | | | | | | | | | |
| **LSD (5%)** | 5.71 | 7.10 | 2.58 | 0.09 | 1.58 | 1.15 | 0.62 | 2.18 | 1.39 | 34.87 | 34.87 | 2.37 | 1.62 | 1.17 |
| **SEM** | 8.19 | 15.88 | 5.08 | 0.18 | 2.58 | 2.26 | 1.39 | 4.87 | 4.20 | 77.95 | 77.95 | 5.31 | 3.62 | 2.61 |
| **%CV** | 7.15 | 8.95 | 597.49 | 12.24 | 87.15 | 28.59 | 49.30 | 21.39 | 43.80 | 52.81 | 52.81 | 64.59 | 47.58 | 41.79 |
| **Heritability** | 0.42 | 0.89 | 0.89 | 0.88 | 0.92 | 0.92 | 0.88 | 0.92 | 0.88 | 0.002 | 0.87 | 0.92 | 0.82 | 0.91 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing. LSD= least significant difference, SEM= standard error of the mean, %CV= coefficient of variation, m= meter, cm= centimetre, g=gram.

### 3.3.2 Genetic analysis using SNP markers

#### 3.3.2.1 *Genetic diversity and Population structure*

Table 3.4 summarizes the genetic diversity parameters of the biological types. The tested SNP markers were moderately polymorphic with a mean PIC value of 0.34 for the whole population, 0.33 for the inbred lines, 0.34 for the hybrids, and 0.35 for the OPVs. The whole population had a mean GD of 0.44. The OPVs exhibited the highest mean GD of 0.45 followed by the hybrids (0.44), and the inbred lines (0.42). The highest MAF was 0.37 observed among OPVs while the whole population exhibited an MAF of 0.36. The mean values of heterozygosity ranged from 0.22 to 0.28 with the highest Ho of 0.28 exhibited by the inbred lines. Overall, the level of fixation index ranged from 0.33 to 0.52. The OPVs exhibited the highest F of 0.52 followed by the hybrids (0.50).

The structure analysis based on the Evanno method indicated that the highest value of ΔK was eight (Figure 3.3A), revealing eight main genetic clusters (Figure 3.3B). About 55.31% of the tested genotypes exhibited membership coefficient values ≥ 0.70. The rest, accounting for 44.69%, were considered admixtures. Sub-population II was the largest group, with 22 accessions (21.15%) representing OPVs and synthetic hybrids from IITA/Nigeria, CIMMYT/Zimbabwe, and NPGRC/South Africa. Sub-population III comprised 21 accessions (20.19%), comprising IITA/Nigeria inbred lines and hybrids. Sub-population IV composed of 19 accessions (18.26%) that were IITA hybrids and some IITA inbred lines. About 14 accessions (13.46%) were allocated to the sub-population I comprising CIMMYT/Zimbabwe inbred lines. Sub-population V constituted 10 accessions (9.61%) that were CIMMYT/Zimbabwe inbred lines. Sub-populationsVI, VII, and VIII comprised ten, five, and four accessions, respectively. Members of these populations were inbred lines from IITA/Nigeria. Principal coordinate analysis assigned the accessions to four admixture groups (Figure 3.4). In particular, sub-populations I and II were clustered in PC1, while sub-population V was dominant in PC2. Sub-populations VI, VII, and VIII were clustered in PC3, whereas sub-populations III and IV were dominants in PC4.

**Table 3.4** Genetic diversity parameters of 126 maize genotypes assessed based on 16000 SNP markers

| | Whole population | | | | | Inbred lines | | | | | Hybrids | | | | | OPVs | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Diversity** | GD | PIC | MAF | Ho | F | GD | PIC | MAF | Ho | F | GD | PIC | MAF | Ho | F | GD | PIC | MAF | Ho | F |
| Lower | 0.19 | 0.17 | 0.10 | 0.08 | 0.13 | 0.11 | 0.11 | 0.06 | 0.09 | 0.08 | 0.00 | 0.00 | 0.00 | 0.08 | 0.27 | 0.08 | 0.08 | 0.04 | 0.08 | 0.17 |
| Upper | 0.50 | 0.38 | 0.50 | 0.38 | 0.81 | 0.50 | 0.38 | 0.50 | 0.38 | 0.78 | 0.50 | 0.38 | 0.50 | 0.33 | 0.81 | 0.50 | 0.38 | 0.50 | 0.37 | 0.81 |
| Mean | 0.44 | 0.34 | 0.36 | 0.26 | 0.41 | 0.42 | 0.33 | 0.33 | 0.28 | 0.33 | 0.44 | 0.34 | 0.36 | 0.22 | 0.50 | 0.45 | 0.35 | 0.37 | 0.22 | 0.52 |

GD= gene diversity, PIC= polymorphism information content, MAF= minor allele frequency, Ho= observed heterozygosity, F= fixation index.

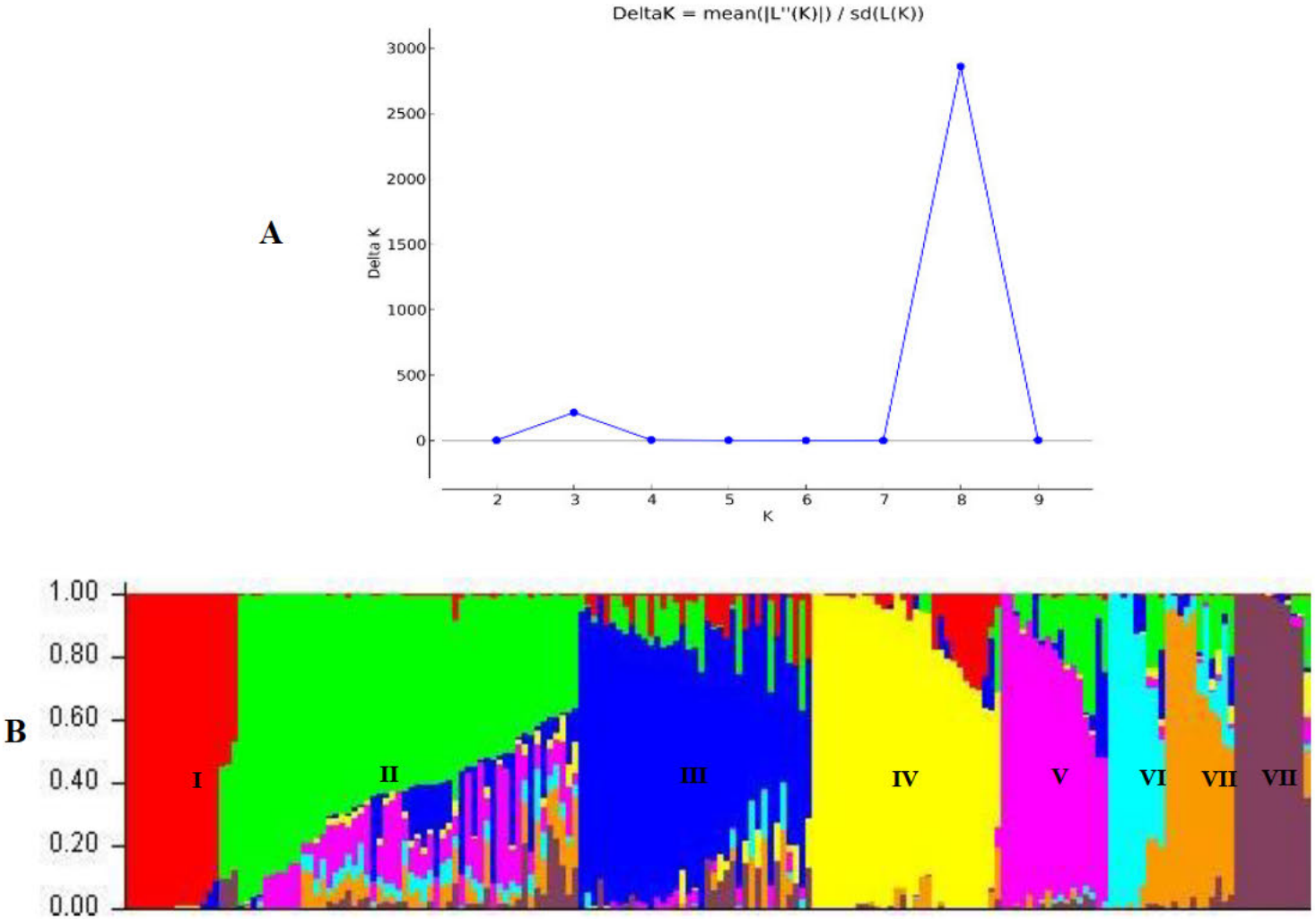


**Figure 3.3** Sub-population inference among the 126 maize genotypes based on 16000 SNPs: (A) likelihood and delta K values for different numbers of assumed clusters and (B) population structure among the 126 maize genotypes based on 16000 SNPs at K=8.

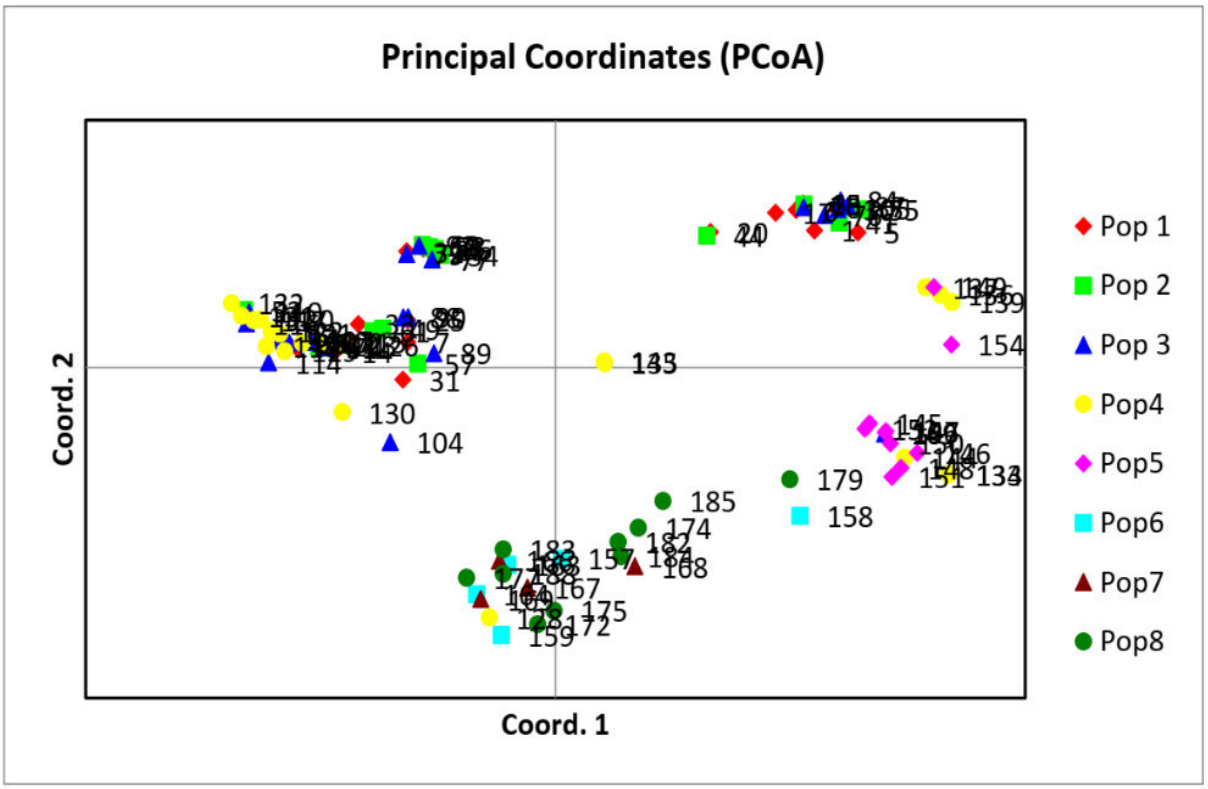


**Figure 3.4** Principal coordinate analysis clustering of the test genotypes. See Appendix 3.3 for the code of genotypes.

3.3.2.2 ***Genetic distance***

The inbreeding coefficient ranged from -0.06 to 0.59, with a mean of 0.34 representing the population pairs VI and VIII, and V and VII (Table 3.5, bottom diagonal). The pairwise genetic distance among the eight populations ranged from 0.16 to 0.48, with a mean of 0.32 (Table 3.5, upper diagonal). Sub-populations III and VIII, and IV and III were the most distantly related, while sub-population VII had relatively the shortest distances from sub-populations II and VI. It was noticed that the genetic distances between the sub-populations III, IV, V, VI, and VII are beyond the average. The same extent was noticed with sub-populations I, V, VI, VII, and VIII. The sub-population III consists of the genotype NC.QPM/Z.DPLO, Shesha/1421, and NC.QPM/Z.DPLO and was associated with high GY under *Sa*-infested conditions. Sub-population VIII and IV consisted of IITA inbred lines including TZISTR1175, TZISTR1225, TZISTR1190, TZISTR1174, and TZISTR1166 that were associated with high SDR8 and SDR10 reduction under *Sa* infested-conditions, and TZISTR1205 and TZSTRI108 associated with high GY under *Sh*-infested conditions. Nei's genetic distance between the individuals based on the 16000 SNP markers ranged from 0.01 to 0.34 within the inbred lines with a mean

of 0.18 (Appendices 3.4 and Table 3.5). TZISTR1008 and CLHP0221 had the lowest genetic distance of 0.01, while CLHP0343 and TZISTR1223 exhibited the highest genetic distance of 0.34. CLHP0343 was associated with good GY under *Sa* infestation and exhibited a relatively high genetic distance from all the other inbred lines. The accessions CML540, TZISTR25, TZISTR1248, CLHP0303, TZISTR1174, TZSTRI113, TZDEEI50, TZSTRI115, CML539, TZISTR1015, CZL99017, CML451, CML566, CLHP0343 and CML440 which showed high GY and reduce *Striga* damage under both *Sa* and *Sh* infested conditions, exhibited high and average genetic distances from each other.

**Table 3.5** Genetic distance (upper diagonal), and pairwise inbreeding coefficients (lower diagonal), among eight populations resulting from 130 maize genotypes based on 16000 SNP profiling.

| Populations | Fst (genetic distance) | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | **C1** | **C2** | **C3** | **C4** | **C5** | **C6** | **C7** | **C8** |
| **C1** | - | 0.30 | 0.29 | 0.25 | 0.42 | 0.39 | 0.34 | 0.42 |
| **C2** | -0.04 | - | 0.29 | 0.26 | 0.20 | 0.19 | 0.16 | 0.29 |
| **C3** | 0.00 | 0.00 | - | 0.44 | 0.42 | 0.38 | 0.34 | 0.48 |
| **C4** | 0.13 | 0.14 | 0.04 | - | 0.35 | 0.31 | 0.26 | 0.34 |
| **C5** | 0.46 | 0.50 | 0.45 | 0.33 | - | 0.31 | 0.28 | 0.36 |
| **C6** | 0.54 | 0.55 | 0.49 | 0.39 | 0.54 | - | 0.18 | 0.35 |
| **C7** | 0.57 | 0.58 | 0.51 | 0.39 | 0.59 | -0.02 | - | 0.30 |
| **C8** | 0.52 | 0.52 | 0.48 | 0.39 | 0.50 | -0.06 | 0.04 | - |
| | **Fis (inbreeding coefficient)** | | | | | | | |

C1 to C8 represent the clusters generated by the Structure analysis.

The analysis of molecular variance (AMOVA) showed a significant variation within populations (Table 3.6). The within-population variation accounted for 85% of the total variation. The variation detected among the population was low (15%).

**Table 3.6** Analysis of molecular variance involving 130 maize accessions based on 16000 SNP markers.

| Source | df | SS | MS | Estimated Variance | Proportion of variance |
|---|---|---|---|---|---|
| Among Populations | 7 | 88048.86 | 12578.41 | 696.07 | 0.15 |
| Within Populations | 96 | 369493.72 | 3848.89 | 3848.89 | 0.85 |
| Total | 103 | 457542.59 | | 4544.96 | 1.00 |

Df, degrees of freedom; SS, sum of squares; MS, mean squares.

The dendrogram based on the 16000 SNP markers clustered the accessions into three major clusters (Figure 3.5). The largest is Cluster III, containing mainly CIMMYT and IITA inbred lines, followed by Cluster II, consisting of admixtures of IITA and CIMMYT lines and synthetic hybrids. Cluster I form genotypes from all sources, mainly OPVs from IITA.

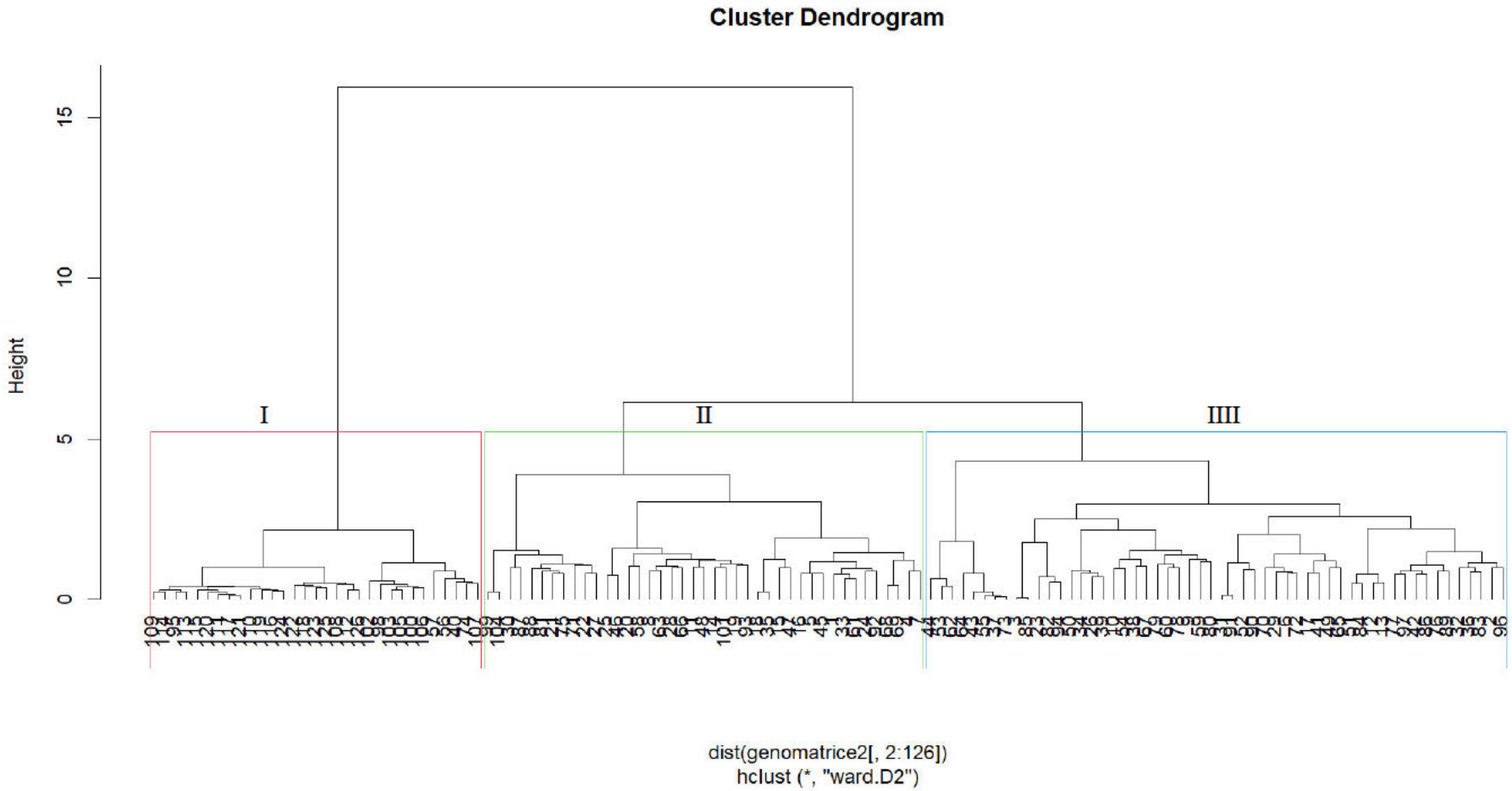


**Figure 3.5** Hierarchical cluster dendrogram showing the genetic relationships among 126 maize accessions using 16000 SNP markers. See Appendix 3.3 for the code of genotypes.

### 3.3.3 Comparison of test genotypes using phenotypic and genotypic analyses

Figures 3.6 and 3.7 present the joint analysis that revealed three clusters for both tested conditions using the phenotypic and molecular data. Under *Sa* conditions, Cluster III was the largest, with 68 genotypes, followed by Cluster I (35), and Cluster II (23). Under *Sh* conditions, Cluster I was the largest, followed by Clusters II and III with 84, 28, and 14 genotypes, respectively.

The phylogenetic tree generated from the phenotypic data was compared to the genotype grouping based on the SNPs data (Figures 3.8 and 3.9). Only a few genotypes (21.42%) maintained their positions across the hierarchical clusters. Furthermore, the correlation between the phenotypic and genotypic dissimilarity matrices was low according to the Mantel test in *Sh* ($r^2 = 0.0009$, P=0.01) and *Sa* ($r^2 = 0.0006$, P= 0.02) infested environments.

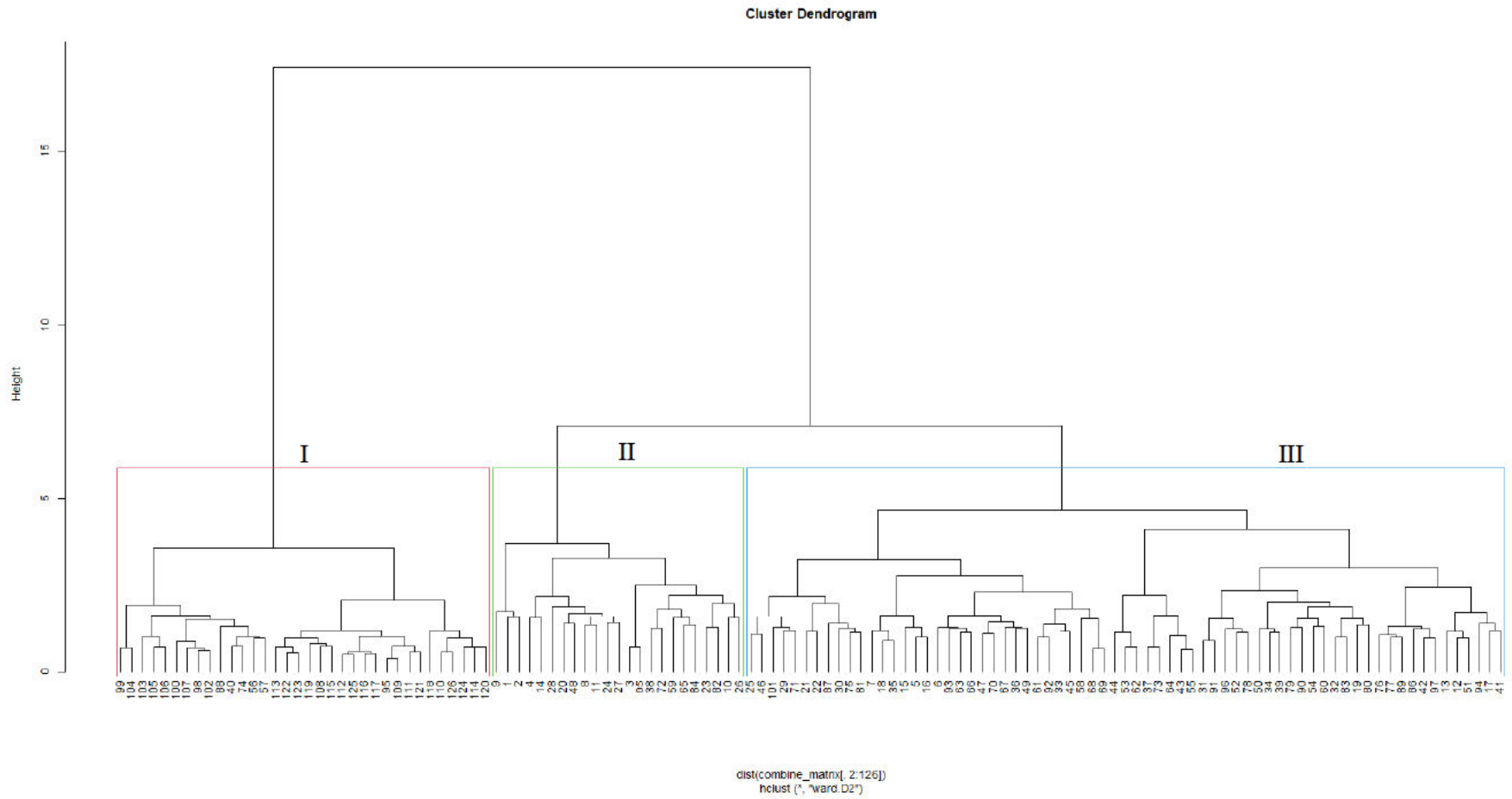


**Figure 3.6** Dendrogram showing relatedness among the 126 maize genotypes under *Striga asiatica*-infested conditions using genotypic and phenotypic data. See Appendix 3.4 for the code of genotypes.

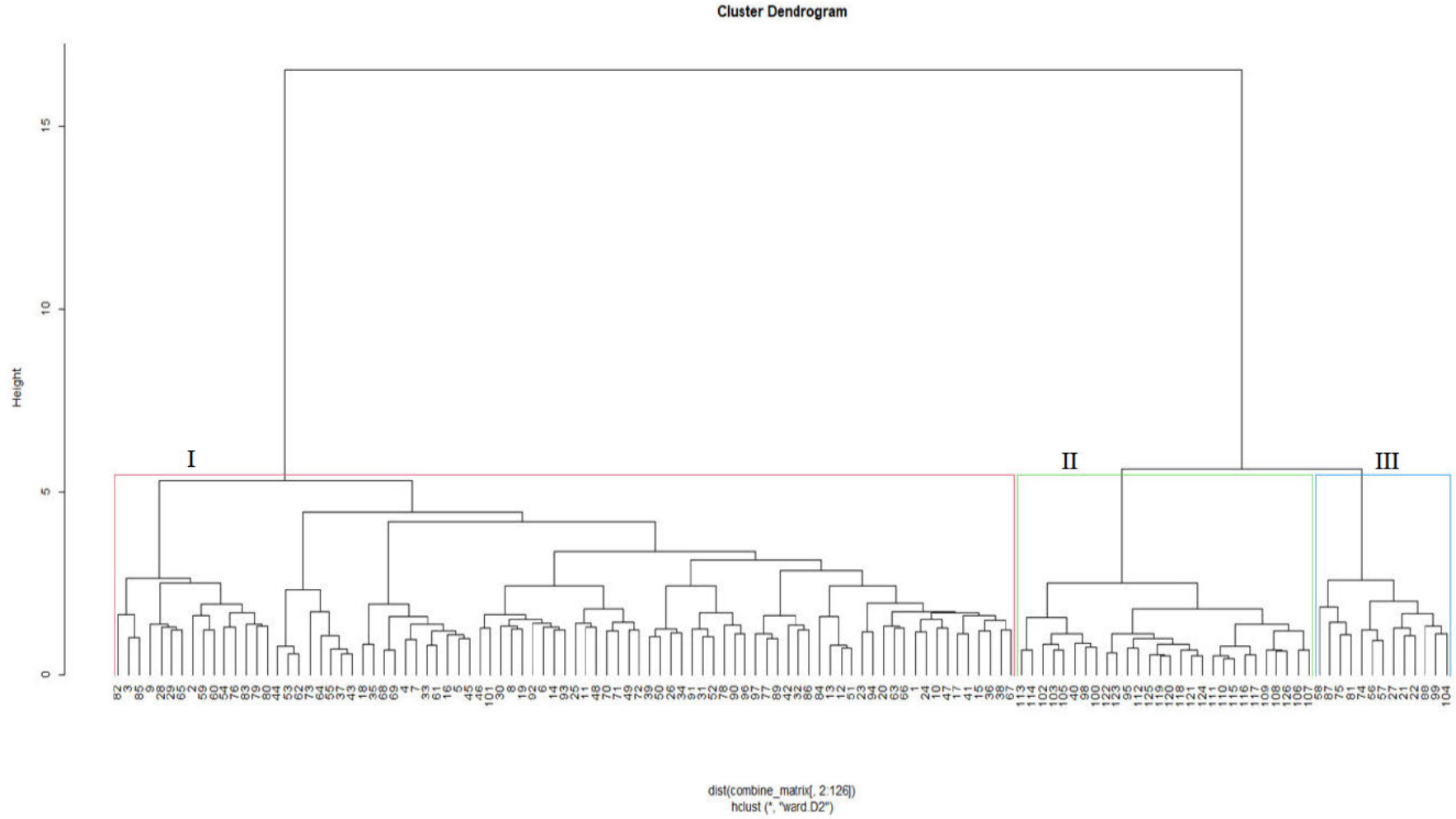


**Figure 3.7** Dendrogram showing relatedness among the 126 maize genotypes under *Striga hermonthica* conditions using genotypic and phenotypic data. Appendix 3.4 for the code of genotypes.

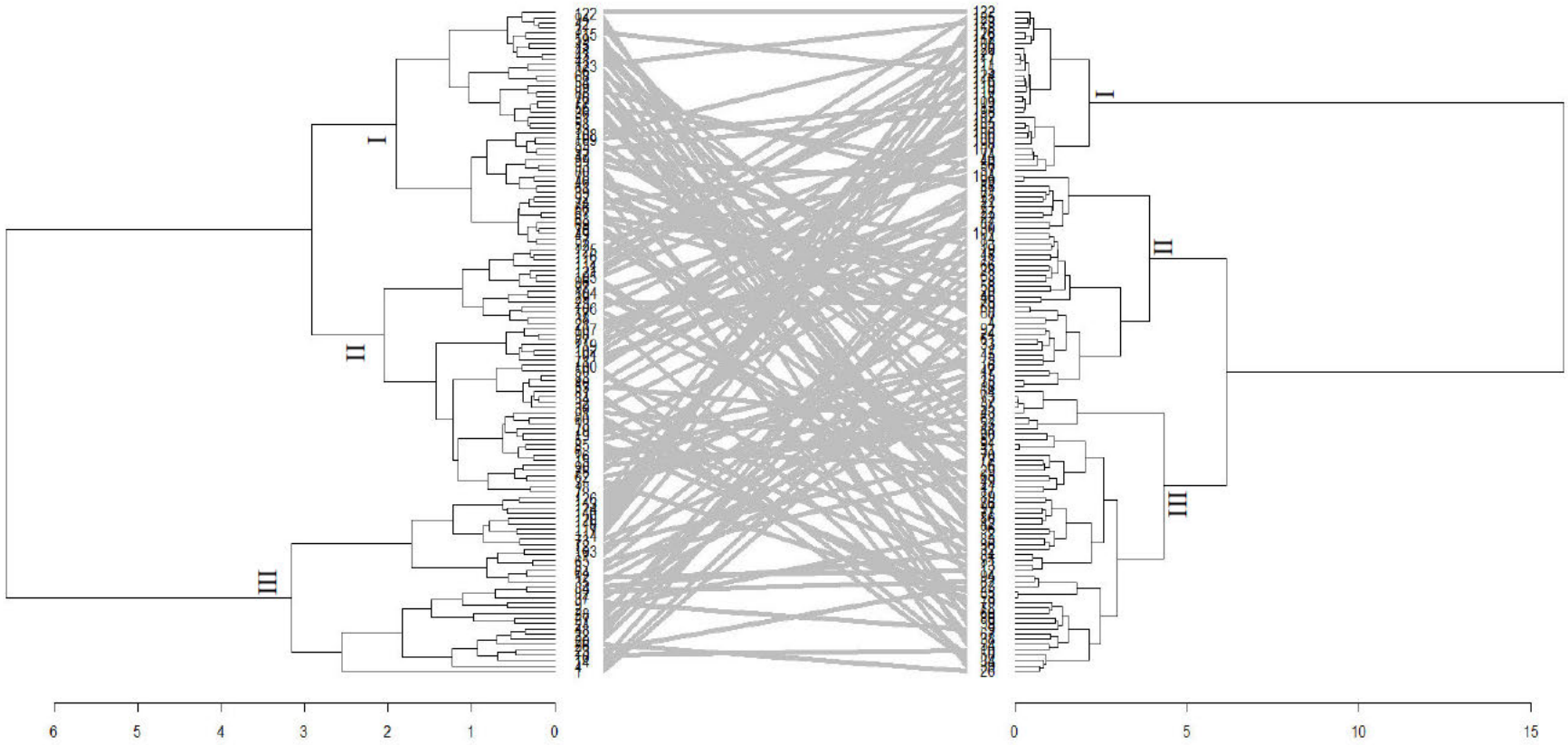


**Figure 3.8** Tanglegram comparing dendrograms based on evaluation of 126 maize genotypes evaluated using phenotypic (left) and genotypic data (right) under *Striga asiatica* conditions. See Appendix 3.4 for the code of genotypes.

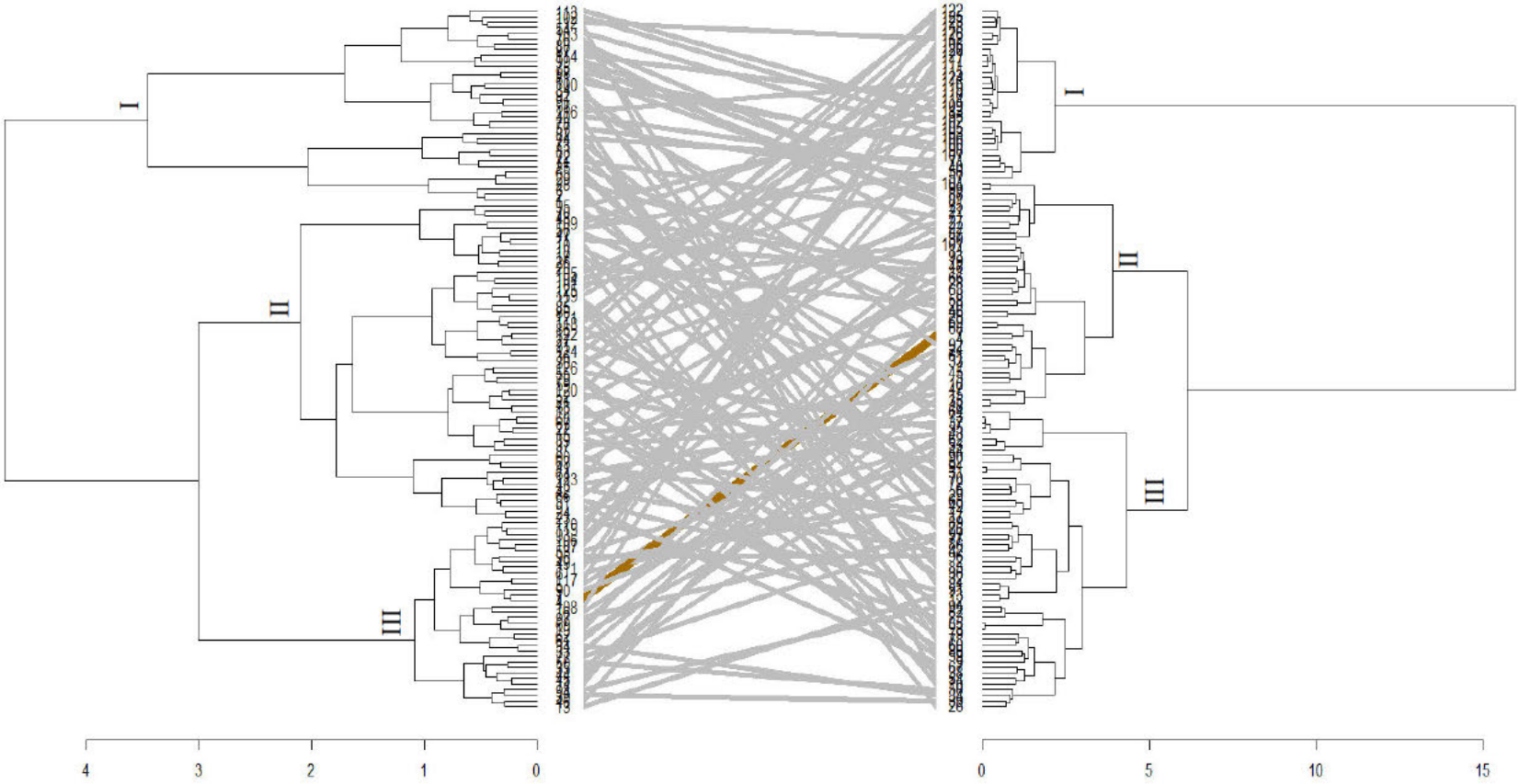


**Figure 3.9** Tanglegram comparing dendrograms based on evaluation of 126 maize genotypes evaluated using phenotypic (left) and genotypic data (right) under *Striga hermonthica* conditions. See Appendix 3.4 for the code of genotypes.

## 3.4 **Discussion**

Genetic variation is fundamental for any crop breeding programs. The development of open-pollinated, hybrid and synthetic maize varieties with high hybrid vigour relies on genetically contrasting parents and heterotic groups emanating from well-characterized genetic resources. The present study assessed the genetic diversity of 126 maize genotypes (Appendix 3.1) sourced from IITA/Nigeria, CIMMYT/Zimbabwe, and NPGRC/South Africa using agro-morphological traits and high-density SNP markers. Morphological traits are useful in preliminary genetic diversity assessments [43] and ideotype breeding [44,45].

In the current study, a wide variability was recorded among accessions of different sources using phenotypic traits (Table 3.1). Each source of genotype group presented a unique selection with specific and unique traits (Tables 3.2 and 3.3). For instance, genotypes CML540 and CML566 were higher yielders in a *Sa*-infested environment (Table 3.2), while genotypes CML304 and TZSTRI101 were higher yielders in a *Sh*-infested environment (Table 3.3). These genotypes are ideal candidates for *Striga* resistance breeding. Some of the tropical genotypes bred for *Sh* resistance were susceptible to *Sa*. This is consistent with the previous finding of Gasura, *et al.* [46], who reported the susceptibility to *Sa* of some tropical inbred lines bred for *Sh* resistance. Under *Sa* infestation, the yield of most of the evaluated inbred lines was higher than that of the OPV and hybrid checks. This result can be explained by the fact that most OPVs and hybrids were bred for resistance or tolerance to *Sh*, without screening for *Sa*. These findings indicate that genotypes bred for *Sh* resistance are not necessarily resistant to *Sa*.

Low broad sense heritability values were computed for SEC10, SDR8, and SDR10 in *Sa*-infested environment (Table 3.2), indicating that *Sa*-resistance has low heritability, and therefore, the phenotype was a poor measure of the genetic merit of the evaluated genotypes, which reduces the effectiveness of selection under *Sa* infestation. These findings differ from those of Olakojo and Olaoye [47], who reported a high heritability of *Striga* syndrome rating and *Striga* emergence count under *Sa*-infested conditions. Meanwhile, high heritability values were recorded for the same traits under *Sh*-infested conditions (Table 3.3). This suggests that, unlike *Sa* resistance, *Sh* resistance is highly heritable. This shows that the results would be repeatable, which is ideal for *Sh* resistance breeding. Kaewchumnong and Price [48] and Stanley, et al. [30] reported high heritability estimates for *Striga* resistance traits in a *Sh*-infested environment. This finding, however, differs from those of Badu-Apraku, *et al.* [49],

who recorded low heritability estimates for emerged *Striga* plants and damage ratings. All these results suggest that the gene actions controlling *Sa* and *Sh* are not the same.

Based on phenotypic traits, the dendrogram delineated the genotypes into three major clusters, subdivided into six sub-clusters under *Sa*-infested conditions (Figure 3.1) and four under *Sh*-conditions (Figure 3.2). The clusters were formed based on reaction to Sa and Sh infestations and yield component performances. This suggests the presence of considerable genetic variation among the assessed genotypes that could be used in developing *Striga*-resistance germplasm. Reports on the clustering of genotypes based on phenotypic traits are common in genetic studies in maize [50,51].

Compared with morphological traits, molecular markers are independent of environmental effects and can provide additional and accurate information for assessing genetic diversity [52,53]. This study used SNP markers to assess the genetic diversity of tropical and sub-tropical maize germplasm. The test germplasm exhibited a high heterozygosity of 0.26 (Table 3.4), suggesting that alternative alleles were represented in the population. The inbred lines exhibited the highest heterozygosity estimates. The observed heterozygosity in the inbred lines (28%) exceeded the expectations (6.25%) for inbred lines derived after four generations of selfing needing continuous selfing, given that the inbred lines are relatively in the early generation of inbreeding [54]. The PIC and GD values were useful for assessing the population's genetic diversity and identifying divergent parental lines for breeding programs. The mean PIC and GD values were 0.34 and 0.44, respectively, for the whole population, and the same trend was observed for the inbred lines, the hybrid checks, and the OPV checks (Table 3.4). This shows that the 16000 SNP markers in this study were polymorphic to distinguish the test population, inbred lines, and checks. The PIC value corresponds to the ability of the test markers to detect the polymorphism among individuals in the population [55]. The PIC values in this study are higher compared to PIC values reported in some of the past related studies. Adu, et al. [17] reported PIC values within the range of 0.01 to 0.38 using 15,047 SNP markers on 94 maize inbred lines. Badu-Apraku, et al. [19] reported PIC values ranging from 0.029 to 0.37 with a mean of 0.21 using 9642 SNP markers. The mean PIC values observed in this study are comparable to Yang, *et al.* [56]. The mean GD of the population in this study (0.44) was similar to the one reported by Eschholz, *et al.* [57] when using SSR markers. Yacoubou, et al. [26] reported a gene diversity value of 0.44 in early-generation maize lines. According to the formula of Anderson, *et al.* [58], the theoretical maximum gene diversity for bi-allelic markers is 0.50. This signifies that the gene diversity obtained in this study was high, suggesting a

significant genetic segregation in the test population in this study. Genetic diversity reflects the population's genetic constitution and its adaptability in various environments [59].

The genetic differentiation recorded in this study ranged from 0.16 to 0.48 (Table 3.5). According to Wright [60] an Fst of 0–0.005 indicates low, 0.05–0.15 moderate, 0.15–0.25 high, and above 0.25 very significant genetic differentiations. The Fst value in the present study is indicative of high genetic differentiation among the heterotic groups, which was expected. This result is confirmed by the high rate of inbreeding coefficient, reflecting a low level of genetic identity for the populations in this study. Genetic differentiation occurs when there is restricted gene flow between populations [61]. The high genetic differentiation observed in this study agrees with previous studies on maize [62,63].

The analysis of molecular variance is a suitable criterion for assessing the overall diversity distribution within and among populations. The AMOVA results in this study showed a higher level of genetic variation within populations than among populations of the test genotypes (Table 3.6), which supports the high genetic differentiation. Related findings were reported by Leng, *et al.* [64] and Mathiang, *et al.* [65]. Based on phenotyping, the test genotypes were resolved into six clusters under *Sa*-infested (Figure 1.1) conditions and four clusters under *Sh*-infested conditions (Figure 1.2). The model-based population structure analysis (Figure 1.3), principal coordinate analysis (Figure 1.4), and neighbor-joining cluster analysis (Figure 1.5) revealed the presence of eight groups, which is fairly consistent with pedigree information and with putative heterotic groups. This is supported by the very low and significant correlation exhibited by the phenotypic and genotypic distance matrices, revealing the discordance between the two matrices. The discordance between phenotypic and genotypic matrices is partially attributed to the environmental effect on the phenotypic trait's expression [21]. Other studies reported inconsistency between phenotypic and genotypic matrices [53,66].

## 3.5 **Conclusion**

The results of the present study revealed significant phenotypic and molecular diversity of the tropical and sub-tropical maize populations. Significant differences were recorded for all the assessed quantitative traits. The SNPs used in this study revealed the genetic variation among the test population. The mean gene diversity and polymorphic information content were 0.34 and 0.44, respectively, reflecting a moderate level of genetic variation among the test genotypes when assessed using SNP markers. The overall mean genetic distance among the inbred lines was 0.18, ranging from 0.01 to 0.34. Divergent parents were selected for hybridization and the

development of new *Striga*-resistant varieties in SSA. The following genetically distant genotypes were selected, displaying good agronomic performance and *Sa* and *Sh* resistance: CML540, TZISTR25, TZISTR1248, CLHP0303, TZISTR1174, TZSTRI113, TZDEEI50, TZSTRI115, CML539, TZISTR1015, CZL99017, CML451, CML566, CLHP0343 and CML440. Genetically diverse and complementary lines were selected among the tropical and sub-tropical maize populations that will facilitate the breeding of maize varieties with *Striga* resistance and market-preferred traits. Both molecular and morphological features are useful and will facilitate the selection and breeding process for *Striga* resistance in maize. The results suggested that there is sufficient genetic variation among the tropical and sub-tropical maize inbred lines, hybrids, and open-pollinated varieties for breeding when assessed using phenotypic traits and single nucleotide polymorphism markers.

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**Appendix 3.1**. List and source of maize genotypes evaluated in the present study.

| N° | Name /designation | Source/origin | *Striga* resistance /genotype description | N° | Name /designation | Source/origin | *Striga* resistance /genotype description |
|---|---|---|---|---|---|---|---|
| **1** | TZISTR1154 | IITA/Nigeria | Resistant/inbred line | 29 | TZSTRI109 | IITA/Nigeria | Resistant/inbred line |
| **2** | TZISTR1261 | IITA/Nigeria | Resistant/inbred line | 30 | TZSTRI110 | IITA/Nigeria | Resistant/inbred line |
| **3** | TZISTR1248 | IITA/Nigeria | Resistant/inbred line | 31 | TZSTRI112 | IITA/Nigeria | Resistant/inbred line |
| **4** | TZISTR1263 | IITA/Nigeria | Resistant/inbred line | 32 | TZSTRI114 | IITA/Nigeria | Resistant/inbred line |
| **5** | TZISTR1275 | IITA/Nigeria | Resistant/inbred line | 33 | TZSTRI115 | IITA/Nigeria | Resistant/inbred line |
| **6** | TZISTR1157 | IITA/Nigeria | Resistant/inbred line | 34 | TZISTR25 | IITA/Nigeria | Resistant/inbred line |
| **7** | TZISTR1160 | IITA/Nigeria | Resistant/inbred line | 35 | TZISTR1001 | IITA/Nigeria | Resistant/inbred line |
| **8** | TZISTR1162 | IITA/Nigeria | Resistant/inbred line | 36 | TZISTR1003 | IITA/Nigeria | Resistant/inbred line |
| **9** | TZISTR1165 | IITA/Nigeria | Resistant/inbred line | 37 | TZISTR1004 | IITA/Nigeria | Resistant/inbred line |
| **10** | TZISTR1175 | IITA/Nigeria | Resistant/inbred line | 38 | TZISTR1008 | IITA/Nigeria | Resistant/inbred line |
| **11** | TZISTR1178 | IITA/Nigeria | Resistant/inbred line | 39 | TZISTR1011 | IITA/Nigeria | Resistant/inbred line |
| **12** | TZISTR1163 | IITA/Nigeria | Resistant/inbred line | 40 | TZISTR1018 | IITA/Nigeria | Resistant/inbred line |
| **13** | TZISTR1166 | IITA/Nigeria | Resistant/inbred line | 41 | TZEEI21 | IITA/Nigeria | Resistant/inbred line |
| **14** | TZISTR1190 | IITA/Nigeria | Resistant/inbred line | 42 | TZEEI13 | IITA/Nigeria | Resistant/inbred line |
| **15** | TZISTR1199 | IITA/Nigeria | Resistant/inbred line | 43 | TZEEI14 | IITA/Nigeria | Resistant/inbred line |
| **16** | TZISTR1231 | IITA/Nigeria | Resistant/inbred line | 44 | TZEEI49 | IITA/Nigeria | Resistant/inbred line |
| **17** | TZISTR1232 | IITA/Nigeria | Resistant/inbred line | 45 | TZDEEI55 | IITA/Nigeria | Resistant/inbred line |
| **18** | TZISTR1259 | IITA/Nigeria | Resistant/inbred line | 46 | TZDEEI50 | IITA/Nigeria | Resistant/inbred line |
| **19** | TZISTR1262 | IITA/Nigeria | Resistant/inbred line | 47 | TZEEI34 | IITA/Nigeria | Resistant/inbred line |
| **20** | TZISTR1159 | IITA/Nigeria | Resistant/inbred line | 48 | TZISTR1174 | IITA/Nigeria | Resistant/inbred line |
| **21** | TZISTR1223 | IITA/Nigeria | Resistant/inbred line | 49 | TZISTR1205 | IITA/Nigeria | Resistant/inbred line |
| **22** | TZISTR1225 | IITA/Nigeria | Resistant/inbred line | 50 | TZSTRI113 | IITA/Nigeria | Resistant/inbred line |
| **23** | TZISTR1244 | IITA/Nigeria | Resistant/inbred line | 51 | TZISTR1119 | IITA/Nigeria | Resistant/inbred line |
| **24** | TZSTRI101 | IITA/Nigeria | Resistant/inbred line | 52 | TZISTR1015 | IITA/Nigeria | Resistant/inbred line |
| **25** | TZSTRI102 | IITA/Nigeria | Resistant/inbred line | 53 | TZDEEI64 | IITA/Nigeria | Resistant/inbred line |
| **26** | TZSTRI104 | IITA/Nigeria | Resistant/inbred line | 54 | TZDEEI54 | IITA/Nigeria | Resistant/inbred line |
| **27** | TZSTRI107 | IITA/Nigeria | Resistant/inbred line | 55 | TZEEI10 | IITA/Nigeria | Resistant/inbred line |
| **28** | TZSTRI108 | IITA/Nigeria | Resistant/inbred line | 56 | CML312 | CIMMYT/Zimbabwe | Unknown/Inbred line |

**Appendix 3.1**. **(**Continued)

| N° | Name /designation | Source/origin | *Striga* resistance /breed description | N° | Name /designation | Source/origin | *Striga* resistance /genotype description |
|---|---|---|---|---|---|---|---|
| **57** | CML444 | CIMMYT/Zimbabwe | Unknown/Inbred line | 85 | CZL1380 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **58** | CML442 | CIMMYT/Zimbabwe | Unknown/Inbred line | 86 | CLHP0326 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **59** | CML550 | CIMMYT/Zimbabwe | Unknown/Inbred line | 87 | CZL99017 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **60** | CML547 | CIMMYT/Zimbabwe | Unknown/Inbred line | 88 | CLHP0049 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **61** | CML539 | CIMMYT/Zimbabwe | Unknown/Inbred line | 89 | CLHP00478 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **62** | CML440 | CIMMYT/Zimbabwe | Unknown/Inbred line | 90 | CLHP00286 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **63** | CML566 | CIMMYT/Zimbabwe | Unknown/Inbred line | 91 | CML451 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **64** | CML540 | CIMMYT/Zimbabwe | Unknown/Inbred line | 92 | CLHP0302 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **65** | CML545 | CIMMYT/Zimbabwe | Unknown/Inbred line | 93 | CLHP0364 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **66** | CML571 | CIMMYT/Zimbabwe | Unknown/Inbred line | 94 | CLHP0350 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **67** | CML390 | CIMMYT/Zimbabwe | Unknown/Inbred line | 95 | CLHP00294 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **68** | CLHP0352 | CIMMYT/Zimbabwe | Unknown/Inbred line | 96 | CLHP0005 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **69** | HA04A-2107-36 | CIMMYT/Zimbabwe | Unknown/Inbred line | 97 | CLHP0022 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **70** | CLHP0303 | CIMMYT/Zimbabwe | Unknown/Inbred line | 98 | CML304 | CIMMYT/Zimbabwe | Unknown/Inbred line |
| **71** | CLHP0221 | CIMMYT/Zimbabwe | Unknown/Inbred line | 99 | ZM1423/Z.DLO | NPGRC/South Africa | Unknown/OPV check |
| **72** | CLHP0020 | CIMMYT/Zimbabwe | Unknown/Inbred line | 100 | NC.QPM/Z.DPLO | NPGRC/South Africa | Unknown/OPV check |
| **73** | CLHP0058 | CIMMYT/Zimbabwe | Unknown/Inbred line | 101 | M.Pearl/DT-STR | NPGRC/South Africa | Unknown/OPV check |
| **74** | CKDHL0378 | CIMMYT/Zimbabwe | Unknown/Inbred line | 102 | NC.QPM/DT-STR | NPGRC/South Africa | Unknown/OPV check |
| **75** | CLHP0312 | CIMMYT/Zimbabwe | Unknown/Inbred line | 103 | ZM1421/DT-STR | NPGRC/South Africa | Unknown/OPV check |
| **76** | CLHP0310 | CIMMYT/Zimbabwe | Unknown/Inbred line | 104 | N.Choice/1421 | NPGRC/South Africa | Unknown/hybrids check |
| **77** | CLHP0003 | CIMMYT/Zimbabwe | Unknown/Inbred line | 105 | B.King/1421 | NPGRC/South Africa | Unknown/hybrids check |
| **78** | CKDHL0467 | CIMMYT/Zimbabwe | Unknown/Inbred line | 106 | Colorado/1421 | NPGRC/South Africa | Unknown/hybrids check |
| **79** | CLHP00378 | CIMMYT/Zimbabwe | Unknown/Inbred line | 107 | Hickory/1421 | NPGRC/South Africa | Unknown/hybrids check |
| **80** | CLHP0156 | CIMMYT/Zimbabwe | Unknown/Inbred line | 108 | Kep/1421 | NPGRC/South Africa | Unknown/hybrids check |
| **81** | CLHP0113 | CIMMYT/Zimbabwe | Unknown/Inbred line | 109 | Shesha/1421 | NPGRC/South Africa | Unknown/hybrids check |
| **82** | CLHP03302 | CIMMYT/Zimbabwe | Unknown/Inbred line | 110 | ZM1423 | CIMMYT/Zimbabwe | Unknown/OPV check |
| **83** | CLHP0404 | CIMMYT/Zimbabwe | Unknown/Inbred line | 111 | ZM1421 | CIMMYT/Zimbabwe | Unknown/hybrids check |
| **84** | CLHP0343 | CIMMYT/Zimbabwe | Unknown/Inbred line | 112 | STR-SYN-Y2 | IITA/Nigeria | Resistant/OPV check |

**Appendix 3.1**. (Continued)

| N° | Name /designation | Source/origin | *Striga* resistance /genotype description |
|---|---|---|---|
| **113** | Z.diplo-BC4-C3-W/DOGONA-1/Z.diplo-BC4-C3-W | IITA/Nigeria | Resistant/OPV check |
| **114** | Z. Diplo.BC4C3-W-DT C1 | IITA/Nigeria | Resistant/OPV check |
| **115** | TZBSTR (Susceptible)(RE) | IITA/Nigeria | Resistant/OPV check |
| **116** | STR-SYN-W1 | IITA/Nigeria | Resistant/OPV check |
| **117** | DTSTR-W SYN13 | IITA/Nigeria | Resistant/OPV check |
| **118** | DTSTR-Y SYN15 | IITA/Nigeria | Resistant/OPV check |
| **119** | ((IWD C3 SYN*2/(White DT STR Syn))-DT C1 | IITA/Nigeria | Resistant/OPV check |
| **120** | DTSTR-W SYN11 | IITA/Nigeria | Resistant/OPV check |
| **121** | SAMMMZ16 | IITA/Nigeria | Resistant/OPV check |
| **122** | (TZEOMP5C7/TZECOMP3DTC2) C2 | IITA/Nigeria | Resistant/OPV check |
| **123** | ((TZL COMP1-W C6*2/(White DT STR Syn))-DT C1 | IITA/Nigeria | Resistant/OPV check |
| **124** | TZCOM1/ZDPSYN | IITA/Nigeria | Resistant/OPV check |
| **125** | DTSTR-Y SYN14 | IITA/Nigeria | Resistant/OPV check |
| **126** | (2*TZECOMP3DT/WhiteDTSTRSYN) C2 | IITA/Nigeria | Resistant/OPV check |
| **127** | TZSTR1137/TZSTR1132 | IITA/Nigeria | Resistant/hybrid check |
| **128** | TZSTR1159/TZSTR1132 | IITA/Nigeria | Resistant/hybrid check |
| **129** | TZSTR1160/TZSTR1132 | IITA/Nigeria | Resistant/hybrid check |
| **130** | TZSTR1166/TZSTR1132 | IITA/Nigeria | Resistant/hybrid check |

**Appendix 3.2**. Mean responses for 14 maize and *Striga* parameters assessed from 126 maize genotypes evaluated under *Striga asiatica* infestation.

| N° | Accessions | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP 1 to 9) | GY g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | TZISTR1154 | 85.50 | 83.00 | -2.50 | 2.00 | 1.52 | 1.53 | 1.00 | 10.75 | 6.50 | 47.50 | 2.00 | 5.00 | 1.00 | 1.50 |
| 2 | TZISTR1261 | 87.50 | 82.00 | -5.50 | 2.00 | 1.73 | 0.85 | 1.00 | 13.75 | 4.50 | 51.25 | 2.50 | 2.00 | 2.00 | 2.00 |
| **3** | **TZISTR1248** | **78.00** | **73.50** | -4.50 | **1.00** | **1.30** | **0.59** | **1.00** | **13.25** | **3.00** | **98.25** | **3.50** | 17.50 | **4.50** | **2.00** |
| 4 | TZISTR1263 | 87.50 | 82.00 | -5.50 | 1.00 | 1.40 | 0.53 | 3.00 | 10.50 | 3.50 | 52.50 | 2.00 | 5.50 | 5.00 | 1.00 |
| 5 | TZISTR1275 | 89.50 | 76.00 | -13.50 | 1.00 | 1.60 | 0.75 | 2.00 | 14.75 | 6.00 | 54.50 | 5.00 | 5.00 | 3.00 | 2.50 |
| 6 | TZISTR1157 | 82.00 | 77.50 | -4.50 | 1.00 | 1.59 | 0.62 | 2.00 | 10.75 | 3.00 | 44.50 | 4.50 | 11.50 | 2.50 | 2.50 |
| 7 | TZISTR1160 | 84.50 | 83.50 | -1.00 | 1.00 | 1.00 | 0.60 | 1.50 | 12.50 | 7.00 | 35.00 | 5.00 | 14.50 | 3.50 | 2.00 |
| 8 | TZISTR1162 | 80.50 | 78.00 | -2.50 | 1.00 | 1.54 | 1.13 | 1.00 | 13.50 | 2.00 | 57.50 | 4.50 | 2.50 | 1.50 | 2.00 |
| 9 | TZISTR1165 | 79.50 | 75.50 | -4.00 | 2.00 | 1.85 | 1.15 | 1.00 | 11.50 | 5.00 | 32.50 | 5.00 | 16.50 | 1.50 | 1.50 |
| 10 | TZISTR1175 | 76.00 | 72.50 | -3.50 | 1.00 | 1.58 | 0.65 | 1.00 | 14.50 | 6.50 | 55.00 | 5.50 | 28.00 | 1.50 | 1.50 |
| 11 | TZISTR1178 | 76.00 | 74.50 | -1.50 | 1.00 | 2.00 | 1.55 | 1.00 | 10.15 | 1.00 | 64.55 | 5.00 | 3.50 | 3.00 | 1.50 |
| 12 | TZISTR1163 | 82.00 | 78.00 | -4.00 | 1.00 | 1.70 | 1.01 | 1.00 | 9.25 | 1.00 | 57.25 | 5.00 | 5.00 | 3.50 | 2.00 |
| 13 | TZISTR1166 | 99.00 | 101.00 | 2.00 | 1.00 | 1.00 | 0.78 | 1.00 | 10.50 | 4.00 | 62.50 | 5.50 | 7.50 | 3.00 | 2.00 |
| 14 | TZISTR1190 | 86.00 | 84.00 | -2.00 | 1.00 | 1.75 | 0.88 | 1.00 | 8.25 | 7.00 | 31.00 | 4.50 | 12.00 | 3.50 | 1.75 |
| 15 | TZISTR1199 | 81.00 | 78.50 | -2.50 | 1.00 | 1.85 | 0.90 | 1.00 | 7.75 | 4.50 | 36.00 | 5.50 | 5.00 | 3.00 | 3.00 |
| 16 | TZISTR1231 | 75.00 | 73.00 | -2.00 | 1.00 | 1.55 | 0.90 | 1.00 | 10.05 | 4.50 | 62.50 | 5.00 | 8.00 | 3.00 | 2.50 |
| 17 | TZISTR1232 | 85.50 | 86.00 | 0.50 | 1.00 | 1.75 | 1.04 | 1.00 | 11.50 | 5.00 | 35.00 | 5.50 | 15.50 | 2.50 | 2.00 |
| 18 | TZISTR1259 | 77.00 | 74.00 | -3.00 | 1.00 | 1.40 | 0.76 | 1.00 | 15.50 | 5.50 | 43.25 | 5.00 | 10.00 | 4.50 | 1.50 |
| 19 | TZISTR1262 | 83.50 | 74.50 | -9.00 | 1.00 | 1.65 | 0.82 | 2.00 | 11.50 | 6.50 | 0.00 | 4.50 | 16.50 | 3.50 | 2.00 |
| 20 | TZISTR1159 | 86.50 | 71.00 | -15.50 | 1.00 | 1.90 | 0.97 | 1.00 | 9.75 | 4.50 | 29.25 | 5.50 | 8.00 | 1.50 | 1.50 |
| 21 | TZISTR1223 | 87.00 | 83.50 | -3.50 | 1.00 | 1.95 | 1.30 | 1.00 | 9.50 | 3.50 | 60.00 | 4.50 | 8.00 | 2.00 | 1.50 |
| 22 | TZISTR1225 | 85.50 | 84.50 | -1.00 | 1.00 | 1.90 | 1.45 | 1.00 | 10.50 | 3.00 | 62.50 | 4.50 | 4.50 | 1.00 | 2.00 |
| 23 | CML550 | 85.50 | 85.00 | -0.50 | 1.00 | 2.03 | 1.15 | 1.00 | 12.50 | 6.50 | 28.75 | 4.50 | 11.50 | 3.50 | 3.50 |
| 24 | TZISTR1244 | 76.00 | 76.50 | 0.50 | 1.00 | 1.00 | 0.45 | 2.00 | 9.00 | 3.50 | 47.50 | 5.00 | 7.50 | 3.00 | 3.50 |
| 25 | TZSTRI101 | 99.00 | 98.50 | -0.50 | 1.00 | 1.00 | 0.55 | 1.00 | 9.00 | 3.50 | 52.50 | 5.00 | 14.00 | 3.00 | 3.50 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

**Appendix 3.2** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP 1 to 9) | GY g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 26 | TZSTRI102 | 87.50 | 78.00 | -9.50 | 1.00 | 1.85 | 0.85 | 1.00 | 10.50 | 1.50 | 52.25 | 5.00 | 15.50 | 4.00 | 2.50 |
| 27 | TZSTRI104 | 100.00 | 99.00 | -1.00 | 1.00 | 1.00 | 0.45 | 1.50 | 10.50 | 3.50 | 57.50 | 5.00 | 23.00 | 3.00 | 4.00 |
| 28 | TZSTRI107 | 77.50 | 73.50 | -4.00 | 1.00 | 1.40 | 0.84 | 1.00 | 8.50 | 2.00 | 57.00 | 5.00 | 1.50 | 1.50 | 2.50 |
| 29 | TZSTRI108 | 81.00 | 80.00 | -1.00 | 1.00 | 1.40 | 0.77 | 2.00 | 9.00 | 2.00 | 28.00 | 5.00 | 4.50 | 5.50 | 3.00 |
| 30 | TZSTRI109 | 80.00 | 73.00 | -7.00 | 2.00 | 2.03 | 0.97 | 1.00 | 11.00 | 5.00 | 57.25 | 4.50 | 2.50 | 2.50 | 2.00 |
| 31 | TZSTRI110 | 82.00 | 74.50 | -7.50 | 1.00 | 2.03 | 1.45 | 1.00 | 7.75 | 5.00 | 37.00 | 4.50 | 29.50 | 2.00 | 2.50 |
| 32 | TZSTRI112 | 81.00 | 76.50 | -4.50 | 1.00 | 1.08 | 0.80 | 1.00 | 12.50 | 5.00 | 68.75 | 4.50 | 4.50 | 3.00 | 3.50 |
| 33 | TZSTRI114 | 93.00 | 93.50 | 0.50 | 1.00 | 1.05 | 0.55 | 1.00 | 10.50 | 4.50 | 65.00 | 5.00 | 19.00 | 3.00 | 3.50 |
| 34 | **TZSTRI115** | **77.50** | **77.00** | -0.50 | **1.00** | **2.10** | **1.20** | **1.00** | **11.50** | **1.50** | **112.50** | **5.00** | 2.00 | **3.50** | **2.50** |
| 35 | **TZISTR25** | **76.50** | **72.50** | -4.00 | **1.00** | **2.25** | **1.13** | **1.00** | **13.50** | **2.00** | **97.25** | **5.00** | 4.50 | **3.00** | **3.50** |
| 36 | **TZISTR1001** | **82.00** | **82.00** | 0.00 | **1.00** | **2.10** | **1.28** | **1.00** | **11.00** | **1.50** | **140.00** | **4.50** | 4.50 | **3.00** | **2.50** |
| 37 | TZISTR1003 | 84.50 | 80.00 | -4.50 | 1.00 | 2.05 | 1.42 | 1.00 | 8.75 | 2.00 | 44.50 | 4.50 | 32.00 | 3.00 | 3.50 |
| 38 | TZISTR1004 | 70.50 | 72.50 | 2.00 | 1.00 | 1.58 | 1.13 | 1.00 | 9.25 | 1.50 | 54.50 | 4.50 | 4.50 | 2.00 | 4.00 |
| 39 | TZISTR1008 | 85.50 | 83.50 | -2.00 | 1.00 | 2.00 | 1.13 | 1.00 | 11.00 | 5.50 | 38.75 | 5.00 | 9.50 | 4.50 | 3.00 |
| 40 | TZISTR1011 | 91.00 | 91.50 | 0.50 | 1.00 | 1.80 | 1.15 | 1.00 | 10.75 | 2.50 | 58.00 | 4.50 | 12.50 | 4.50 | 3.50 |
| 41 | TZISTR1018 | 75.50 | 74.50 | -1.00 | 1.00 | 1.70 | 1.15 | 1.00 | 12.00 | 3.50 | 47.75 | 5.00 | 8.00 | 1.00 | 1.00 |
| 42 | TZEEI21 | 81.50 | 82.00 | 0.50 | 1.00 | 1.18 | 0.80 | 1.00 | 12.50 | 3.00 | 67.50 | 4.50 | 2.50 | 4.50 | 3.50 |
| 43 | TZEEI13 | 77.00 | 76.00 | -1.00 | 1.00 | 1.30 | 0.72 | 2.00 | 8.50 | 3.00 | 58.25 | 5.50 | 5.50 | 3.50 | 5.50 |
| 44 | TZEEI14 | 82.00 | 82.00 | 0.00 | 1.00 | 2.10 | 1.13 | 2.00 | 10.25 | 1.50 | 63.00 | 4.50 | 9.50 | 4.50 | 3.00 |
| 45 | TZEEI49 | 72.50 | 74.50 | 2.00 | 1.00 | 1.97 | 0.77 | 2.00 | 11.25 | 3.00 | 36.00 | 4.50 | 7.00 | 5.00 | 5.00 |
| 46 | TZDEEI55 | 76.50 | 75.50 | -1.00 | 1.00 | 1.59 | 0.61 | 2.00 | 8.50 | 4.00 | 36.25 | 5.00 | 2.00 | 3.50 | 5.00 |
| 47 | TZDEEI50 | 70.00 | 72.50 | 2.50 | 1.00 | 1.42 | 0.75 | 2.00 | 10.50 | 1.50 | 69.25 | 4.00 | 2.00 | 5.50 | 4.50 |
| 48 | TZDEEI64 | 69.50 | 72.50 | 3.00 | 1.00 | 1.74 | 1.25 | 2.00 | 11.00 | 3.50 | 57.50 | 4.50 | 3.50 | 3.50 | 5.00 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

**Appendix 3.2** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP 1 to 9) | GY g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 49 | **CML312** | **80.50** | **85.00** | 4.50 | **1.00** | **2.05** | **0.91** | **2.00** | **8.75** | **2.00** | **86.25** | **4.50** | 5.00 | **4.50** | **3.00** |
| 50 | CML444 | 78.50 | 81.00 | 2.50 | 1.00 | 1.50 | 0.67 | 2.00 | 12.50 | 3.00 | 31.75 | 4.50 | 9.50 | 5.00 | 4.00 |
| 51 | CML442 | 85.50 | 86.00 | 0.50 | 1.00 | 1.69 | 0.80 | 2.00 | 11.50 | 1.50 | 55.00 | 4.50 | 3.00 | 4.50 | 3.50 |
| 52 | TZDEEI54 | 90.50 | 91.00 | 0.50 | 1.00 | 1.00 | 0.75 | 2.00 | 10.50 | 3.50 | 47.50 | 5.50 | 6.50 | 5.00 | 2.00 |
| 53 | TZEEI10 | 86.50 | 84.50 | -2.00 | 1.00 | 1.65 | 0.92 | 2.00 | 12.75 | 6.50 | 26.00 | 4.50 | 3.00 | 3.50 | 3.50 |
| 54 | CML547 | 83.50 | 90.50 | 7.00 | 1.00 | 1.45 | 0.60 | 1.50 | 9.50 | 3.50 | 62.50 | 4.00 | 3.50 | 6.00 | 2.50 |
| 55 | **CML539** | **80.50** | **74.50** | -6.00 | **1.00** | **1.85** | **0.60** | **1.00** | **10.50** | **3.00** | **74.75** | **5.00** | 5.00 | **4.50** | **3.00** |
| 56 | **CML440** | **82.50** | **76.00** | -6.50 | **1.00** | **2.36** | **1.08** | **1.00** | **11.00** | **1.50** | **96.25** | **4.50** | 13.50 | **3.00** | **1.50** |
| 57 | **CML566** | **82.50** | **79.00** | -3.50 | **1.00** | **2.22** | **1.15** | **1.00** | **12.00** | **1.50** | **155.50** | **4.00** | 5.50 | **1.50** | **1.50** |
| 58 | **CML540** | **77.00** | **81.50** | 4.50 | **1.00** | **2.03** | **0.77** | **1.00** | **11.00** | **3.50** | **277.50** | **4.00** | 1.50 | **3.50** | **3.00** |
| 59 | CML545 | 75.50 | 74.00 | -1.50 | 1.00 | 1.73 | 0.67 | 1.00 | 10.25 | 3.00 | 53.00 | 4.50 | 6.00 | 5.00 | 3.00 |
| 60 | CML571 | 76.00 | 75.50 | -0.50 | 1.00 | 2.05 | 0.68 | 1.00 | 9.80 | 2.00 | 45.50 | 4.00 | 26.50 | 5.00 | 4.00 |
| 61 | CML390 | 80.00 | 81.00 | 1.00 | 1.00 | 2.10 | 0.74 | 1.00 | 11.30 | 2.50 | 56.00 | 4.50 | 7.00 | 5.00 | 3.50 |
| 62 | CLHP0352 | 76.50 | 76.50 | 0.00 | 1.00 | 2.30 | 0.85 | 1.00 | 11.75 | 3.00 | 51.25 | 4.50 | 11.50 | 5.00 | 3.00 |
| 63 | HA04A-2107-36 | 97.50 | 86.00 | -11.50 | 1.00 | 2.14 | 1.35 | 1.00 | 8.50 | 5.50 | 27.50 | 4.50 | 8.00 | 4.50 | 4.50 |
| 64 | **CLHP0303** | **84.50** | **83.50** | -1.00 | **1.50** | **1.87** | **1.15** | **1.00** | **7.25** | **3.00** | **92.50** | **4.50** | 8.50 | **3.00** | **3.00** |
| 65 | **CLHP0221** | **79.50** | **77.50** | -2.00 | **1.50** | **1.65** | **1.10** | **1.00** | **10.25** | **5.50** | **72.50** | **5.00** | 9.50 | **3.50** | **3.00** |
| 66 | **CLHP0020** | **71.00** | **77.00** | 6.00 | **1.00** | **1.80** | **0.57** | **1.00** | **12.00** | **2.50** | **119.00** | **4.50** | 2.00 | **3.50** | **3.50** |
| 67 | CLHP0058 | 78.50 | 76.50 | -2.00 | 1.00 | 1.40 | 0.46 | 1.00 | 8.50 | 4.50 | 26.00 | 5.00 | 3.00 | 5.50 | 2.50 |
| **68** | **CKDHL0378** | **72.00** | **75.00** | 3.00 | **1.00** | **1.90** | **0.75** | **1.00** | **11.75** | **2.00** | **85.00** | **4.50** | 17.50 | **3.00** | **2.50** |
| 69 | CLHP0312 | 80.50 | 79.50 | -1.00 | 1.00 | 1.75 | 0.76 | 1.00 | 9.50 | 2.00 | 45.75 | 4.50 | 18.50 | 4.50 | 3.50 |
| 70 | CLHP0310 | 76.00 | 76.50 | 0.50 | 1.00 | 1.91 | 1.03 | 1.00 | 11.75 | 4.00 | 35.75 | 5.00 | 13.50 | 5.00 | 3.50 |
| 71 | CLHP0003 | 82.00 | 83.00 | 1.00 | 1.00 | 1.40 | 0.82 | 1.00 | 9.00 | 5.50 | 30.00 | 6.00 | 4.50 | 2.50 | 3.00 |
| 72 | CKDHL0467 | 79.50 | 75.50 | -4.00 | 1.00 | 1.65 | 0.86 | 1.00 | 11.25 | 4.00 | 42.75 | 4.50 | 14.50 | 2.50 | 3.50 |
| 73 | CLHP00378 | 77.00 | 79.00 | 2.00 | 1.00 | 1.03 | 0.60 | 2.50 | 9.50 | 4.00 | 57.50 | 6.00 | 3.00 | 3.00 | 3.00 |
| 74 | **CLHP0156** | **80.50** | **78.50** | -2.00 | **1.50** | **2.40** | **0.98** | **1.00** | **12.00** | **1.50** | **74.50** | **5.00** | 8.00 | **1.50** | **2.00** |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

**Appendix 3.2** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP 1 to 9) | GY g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 75 | CLHP0113 | 77.50 | 74.50 | -3.00 | 1.00 | 1.65 | 0.50 | 2.50 | 10.00 | 5.00 | 30.50 | 5.00 | 4.00 | 3.50 | 3.50 |
| 76 | **CLHP03302** | **75.50** | **70.50** | -5.00 | **1.50** | **1.80** | **0.95** | **1.00** | **12.00** | **2.00** | **75.25** | **5.50** | 4.00 | **2.00** | **1.00** |
| 77 | CLHP0404 | 77.00 | 75.50 | -1.50 | 1.00 | 1.68 | 0.70 | 1.00 | 11.00 | 3.50 | 62.50 | 5.50 | 8.00 | 3.00 | 3.00 |
| 78 | **CLHP0343** | **77.50** | **77.00** | -0.50 | **1.00** | **1.60** | **0.77** | **1.00** | **11.50** | **1.00** | **82.00** | **4.50** | 2.00 | **4.00** | **4.50** |
| 79 | CZL1380 | 78.50 | 78.50 | 0.00 | 1.00 | 2.38 | 0.87 | 1.00 | 10.50 | 5.50 | 62.50 | 5.00 | 13.50 | 5.00 | 5.00 |
| 80 | **CLHP0326** | **75.00** | **77.00** | 2.00 | **1.00** | **1.40** | **0.66** | **1.00** | **10.50** | **2.00** | **82.25** | **4.50** | 2.00 | **3.00** | **2.50** |
| 81 | CZL99017 | 79.50 | 79.00 | -0.50 | 1.00 | 2.03 | 0.77 | 1.00 | 8.50 | 2.50 | 62.50 | 5.00 | 8.50 | 3.00 | 2.50 |
| 82 | TZEEI34 | 74.50 | 74.50 | 0.00 | 1.00 | 1.30 | 0.53 | 1.00 | 10.50 | 4.50 | 36.50 | 4.50 | 3.50 | 4.00 | 1.50 |
| 83 | **CLHP0049** | **80.50** | **78.00** | -2.50 | **1.00** | **1.25** | **0.70** | **1.00** | **10.00** | **3.00** | **101.25** | **7.00** | 4.00 | **4.00** | **2.50** |
| 84 | CLHP00478 | 79.50 | 74.50 | -5.00 | 1.00 | 1.73 | 0.70 | 1.00 | 11.50 | 3.00 | 56.00 | 5.00 | 20.50 | 3.50 | 3.50 |
| **85** | **CLHP00286** | **83.00** | **83.00** | 0.00 | **1.00** | **1.88** | **0.88** | **1.00** | **11.50** | **3.50** | **82.50** | **5.50** | 3.50 | **3.00** | **3.50** |
| 86 | **CML451** | **79.00** | **79.00** | 0.00 | **1.00** | **2.30** | **0.96** | **1.00** | **12.00** | **1.50** | **83.00** | **4.50** | 10.50 | **2.50** | **3.50** |
| 87 | **CLHP0302** | **81.00** | **80.50** | -0.50 | **1.00** | **1.76** | **1.00** | **3.00** | **13.25** | **3.00** | **98.00** | **4.50** | 7.00 | **5.00** | **3.50** |
| 88 | **CLHP0364** | **80.00** | **80.50** | 0.50 | **1.00** | **1.30** | **0.85** | **1.00** | **12.00** | **3.00** | **79.00** | **4.50** | 4.00 | **2.00** | **5.00** |
| 89 | **CLHP0350** | **75.00** | **76.00** | 1.00 | **1.00** | **2.35** | **0.81** | **3.00** | **14.00** | **3.50** | **102.75** | **5.00** | 3.50 | **2.00** | **3.50** |
| 90 | CLHP00294 | 88.00 | 87.50 | -0.50 | 1.00 | 2.00 | 0.75 | 1.00 | 9.50 | 5.50 | 40.00 | 5.00 | 1.50 | 5.00 | 5.00 |
| 91 | CLHP0005 | 76.00 | 77.50 | 1.50 | 1.00 | 2.03 | 0.76 | 1.00 | 10.50 | 3.50 | 58.75 | 4.50 | 19.00 | 2.00 | 4.50 |
| 92 | CLHP0022 | 81.00 | 81.50 | 0.50 | 1.00 | 1.50 | 0.55 | 1.00 | 7.00 | 4.00 | 12.50 | 5.50 | 3.00 | 3.00 | 5.50 |
| 93 | **CML304** | 82.50 | 82.50 | 0.00 | 1.00 | 1.75 | 0.95 | 2.00 | 11.00 | 4.00 | 59.25 | 6.50 | 33.50 | 4.50 | 6.50 |
| 94 | **TZISTR1174** | **84.00** | **82.50** | -1.50 | **1.00** | **1.80** | **1.00** | **1.50** | **12.25** | **2.00** | **93.25** | **3.00** | 47.00 | **3.00** | **3.50** |
| 95 | **TZISTR1205** | **81.50** | **75.50** | -6.00 | **1.00** | **1.85** | **0.91** | **1.00** | **11.00** | **1.00** | **114.25** | **3.50** | 13.00 | **3.00** | **4.50** |
| 96 | **TZSTRI113** | **78.00** | **77.00** | -1.00 | **1.00** | **1.75** | **0.95** | **1.00** | **10.50** | **1.50** | **87.00** | **3.00** | 7.50 | **1.50** | **6.00** |
| 97 | **TZISTR1119** | **84.00** | **80.50** | -3.50 | **1.00** | **1.91** | **1.15** | **1.00** | **11.25** | **4.00** | **84.75** | **3.00** | 19.00 | **2.50** | **4.50** |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

**Appendix 3.2** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP 1 to 9) | GY g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 98 | **TZISTR1015** | **81.00** | **77.00** | -4.00 | **1.00** | **1.77** | **0.85** | **1.00** | **10.50** | **1.00** | **73.25** | **2.50** | 5.50 | **3.50** | **4.00** |
| 99 | **ZM1421** | **80.50** | **81.00** | 0.50 | **1.00** | **1.00** | **0.70** | **1.00** | **9.00** | **3.50** | **77.50** | **5.00** | 4.50 | **1.00** | **2.00** |
| 100 | **B.King/1421** | **80.50** | **78.50** | -2.00 | **1.00** | **2.05** | **1.15** | **2.00** | **23.50** | **1.50** | **157.25** | **5.00** | 4.50 | **1.00** | **2.00** |
| 101 | Hickory/1421 | 70.50 | 69.50 | -1.00 | 1.00 | 1.95 | 1.30 | 2.00 | 15.50 | 5.00 | 0.00 | 4.50 | 27.00 | 3.00 | 3.00 |
| 102 | Kep/1421 | 69.50 | 73.00 | 3.50 | 1.00 | 2.30 | 1.75 | 1.00 | 17.50 | 5.00 | 25.75 | 4.50 | 2.00 | 2.50 | 1.50 |
| 103 | **Shesha/1421** | **75.50** | **72.50** | -3.00 | **1.00** | **2.03** | **1.75** | **1.00** | **18.75** | **1.50** | **165.75** | **7.50** | 18.50 | **2.00** | **2.00** |
| 104 | **ZM1423** | **69.00** | **69.50** | 0.50 | **1.00** | **0.85** | **1.39** | **1.00** | **10.50** | **1.50** | **99.25** | **4.50** | 16.50 | **5.00** | **3.00** |
| 105 | **N.Choice/1421** | **82.00** | **76.50** | -5.50 | **1.00** | **1.90** | **1.03** | **1.00** | **13.25** | **1.50** | **214.00** | **5.00** | 4.00 | **3.50** | **3.50** |
| 106 | NC.QPM/Z.DPLO | **79.50** | **74.50** | -5.00 | **1.00** | **2.05** | **0.88** | **1.00** | **15.50** | **1.50** | **169.50** | **4.50** | 3.50 | **2.50** | **3.00** |
| 107 | STR-SYN-Y2 | 81.50 | 82.00 | 0.50 | 1.00 | 2.40 | 0.98 | 1.00 | 11.50 | 6.00 | 44.50 | 6.00 | 2.50 | 3.50 | 5.50 |
| 108 | Z. Diplo.BC4C3-W-DT C1 | 88.00 | 88.50 | 0.50 | 1.00 | 2.45 | 0.95 | 1.50 | 9.00 | 5.50 | 42.50 | 6.00 | 2.00 | 4.00 | 5.00 |
| 109 | **TZBSTR (Susceptible)** | **83.00** | **83.50** | 0.50 | **1.00** | **2.65** | **1.30** | **1.50** | **14.50** | **1.00** | **103.00** | **6.50** | 3.00 | **3.00** | **2.50** |
| 110 | STR-SYN-W1 | 80.00 | 79.50 | -0.50 | 1.00 | 2.55 | 1.18 | 1.50 | 13.50 | 4.00 | 53.50 | 6.50 | 14.50 | 3.50 | 4.00 |
| 111 | **DTSTR-W SYN13** | **85.50** | **85.50** | 0.00 | **1.00** | **1.25** | **0.85** | **1.50** | **13.00** | **3.50** | **107.50** | **4.50** | 3.50 | **1.50** | **5.00** |
| 112 | DTSTR-Y SYN15 | 77.00 | 72.50 | -4.50 | 1.00 | 2.80 | 1.30 | 1.00 | 12.75 | 4.00 | 57.50 | 4.50 | 2.50 | 2.00 | 3.00 |
| 113 | ((IWD C3 SYN*2/(White DT STR Syn))-DT C1 | 89.00 | 91.50 | 2.50 | 1.00 | 2.45 | 0.75 | 1.50 | 11.50 | 4.00 | 35.00 | 5.50 | 3.50 | 3.50 | 6.00 |
| 114 | **DTSTR-W SYN11** | **78.50** | **77.50** | -1.00 | **1.00** | **2.30** | **1.23** | **1.50** | **13.00** | **2.50** | **71.25** | **5.00** | 52.50 | **3.50** | **5.50** |
| 115 | SAMMMZ16 | 86.50 | 87.00 | 0.50 | 1.00 | 2.50 | 1.10 | 1.00 | 11.75 | 3.00 | 54.25 | 5.00 | 11.00 | 4.50 | 4.50 |
| 116 | **(TZEOMP5C7/TZE COMP3DTC2) C2** | **75.00** | **75.50** | 0.50 | **1.00** | **2.38** | **1.10** | **1.50** | **14.00** | **1.00** | **89.50** | **4.00** | 32.00 | **4.00** | **5.00** |
| 117 | ((TZL COMP1-W C6*2/(White DT STR Syn))-DT C1 | 85.00 | 86.50 | 1.50 | 1.00 | 1.40 | 0.85 | 1.00 | 11.00 | 3.50 | 62.50 | 3.00 | 2.50 | 2.50 | 3.00 |
| 118 | TZCOM1/ZDPSYN | 74.00 | 69.50 | -4.50 | 1.00 | 2.15 | 1.02 | 1.00 | 15.00 | 3.50 | 61.25 | 3.00 | 10.00 | 3.00 | 4.00 |
| 119 | **Colorado/1421** | **87.50** | **89.50** | 2.00 | **1.00** | **2.03** | **0.70** | **1.00** | **13.75** | **2.00** | **75.25** | **2.50** | 3.00 | **3.50** | **5.00** |
| 120 | M.Pearl/DT-STR | 73.50 | 74.00 | 0.50 | 1.00 | 2.38 | 1.04 | 0.50 | 13.50 | 3.50 | 61.50 | 2.00 | 17.00 | 2.50 | 3.00 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

**Appendix 3.2** (continued)

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 121 | **Z.diplo-BC4-C3-W/DOGONA-1/Z.diplo-BC4-C3-W** | **81.00** | **83.00** | **2.00** | **1.00** | **2.36** | **1.05** | **1.00** | **11.50** | **1.50** | **112.00** | **6.00** | **8.50** | **3.00** | **3.50** |
| 122 | NC.QPM/DT-STR | 71.50 | 71.50 | 0.00 | 1.00 | 2.25 | 1.03 | 0.00 | 12.50 | 4.50 | 54.25 | 3.00 | 5.00 | 3.50 | 5.00 |
| 123 | **ZM1421/DT-STR** | **77.00** | **76.50** | -0.50 | **1.00** | **2.38** | **1.10** | **1.50** | **10.75** | **3.00** | **93.50** | **2.50** | 19.00 | **2.50** | **6.00** |
| 124 | **DTSTR-Y SYN14** | **78.50** | **74.50** | -4.00 | **1.00** | **2.23** | **1.10** | **0.50** | **13.75** | **5.00** | **78.50** | **2.50** | 8.50 | **3.50** | **3.50** |
| 125 | **(2*TZECOMP3DT/WhiteDTSTRSYN) C2** | **69.00** | **78.00** | 9.00 | **1.00** | **1.75** | **0.85** | **1.50** | **12.25** | **2.50** | **89.00** | **6.00** | 0.50 | **2.00** | **5.50** |
| 126 | ZM1423/Z.DLO | 84.50 | 85.00 | 0.50 | 1.00 | 2.50 | 1.05 | 1.50 | 13.25 | 2.00 | 64.25 | 3.50 | 6.00 | 2.50 | 4.00 |
| | | **DA** | **DS** | **ASI** | **EPP** | **PLHT** | **EHT** | **HUSK** | **CL** | **EASP** | **GY** | **SEC8** | **SEC10** | **SDR8** | **SDR10** |
| | **Trial Statistic** | **Inbred lines** | | | | | | | | | | | | | |
| | Minimum | 69.50 | 70.50 | 0.00 | 1.00 | 1.00 | 0.45 | 1.00 | 7.00 | 1.00 | 0.00 | 2.00 | 1.50 | 1.00 | 1.00 |
| | Maximum | 100.00 | 101.00 | 15.50 | 2.00 | 2.40 | 1.55 | 3.00 | 15.50 | 7.00 | 277.50 | 7.00 | 47.00 | 6.00 | 6.50 |
| | Mean | 81.14 | 79.44 | 2.77 | 1.06 | 1.71 | 0.88 | 1.28 | 10.79 | 3.42 | 62.77 | 5.00 | 45.50 | 3.35 | 3.07 |
| | | **Open-pollinated varieties checks** | | | | | | | | | | | | | |
| | Minimum | 69.00 | 69.50 | 0.00 | 1.00 | 0.85 | 0.70 | 0.50 | 9.00 | 1.00 | 35.00 | 2.00 | 0.50 | 1.50 | 2.50 |
| | Maximum | 89.00 | 91.50 | 9.00 | **1.00** | 2.80 | 1.39 | 1.50 | 15.50 | 6.00 | 169.50 | 6.50 | 52.50 | 5.00 | 6.00 |
| | Mean | 79.73 | 79.77 | 1.86 | **1.00** | 2.18 | 1.04 | 1.18 | 12.63 | 3.11 | 76.33 | 4.39 | 10.32 | 3.14 | 4.30 |
| | | **Hybrids checks** | | | | | | | | | | | | | |
| | Minimum | 69.00 | 69.50 | 0.5 | 1.00 | 0.85 | 0.70 | 0.50 | 9.00 | 1.00 | 00.00 | 2.00 | 0.50 | 1.50 | 2.50 |
| | Maximum | 87.50 | 89.50 | 5.50 | 1.00 | 2.30 | 0.70 | 2.00 | 23.50 | 5.00 | 214.00 | 7.50 | 27.00 | 3.50 | 5.00 |
| | Mean | 78.00 | 77.21 | 1.77 | 1.00 | 1.89 | 1.20 | 1.29 | 15.89 | 2.86 | 102.21 | 4.86 | 9.07 | 2.36 | 2.71 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

**Appendix 3.3**. Mean responses for 14 maize and *Striga* parameters assessed from 126 maize genotypes evaluated under *Striga hermonthica* infestation

| N° | Accessions | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP (1 to 9) | GY (g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | TZISTR1154 | 78.50 | 79.50 | 1.00 | 1.50 | 2.25 | 1.25 | 1.00 | 11.00 | 3.00 | 67.25 | 2.50 | 1.50 | 3.00 | 2.25 |
| 2 | **TZISTR1261** | **78.63** | **80.63** | 2.00 | **2.00** | **2.20** | **0.97** | **2.00** | **10.96** | **3.25** | **70.25** | **3.75** | 4.50 | **2.00** | **1.75** |
| 3 | **TZISTR1248** | **75.88** | **77.25** | 1.37 | **1.50** | **1.75** | **0.77** | **2.00** | **11.96** | **2.25** | **81.25** | **4.75** | 1.50 | **2.25** | **2.00** |
| 4 | **TZISTR1263** | **76.25** | **78.25** | 2.00 | **1.00** | **1.35** | **0.59** | **1.00** | **10.96** | **3.75** | **76.00** | **3.25** | 9.00 | **3.75** | **2.75** |
| 5 | TZISTR1275 | 82.00 | 83.00 | 1.00 | 1.00 | 1.50 | 0.49 | 1.00 | 9.96 | 5.25 | 65.25 | 3.25 | 6.00 | 4.50 | 3.50 |
| 6 | TZISTR1157 | 81.13 | 81.25 | 0.12 | 1.00 | 1.55 | 0.54 | 2.00 | 9.96 | 5.25 | 65.25 | 3.75 | 3.50 | 2.25 | 3.50 |
| 7 | TZISTR1160 | 79.88 | 80.50 | 0.62 | 1.00 | 1.47 | 0.54 | 2.00 | 10.46 | 3.75 | 57.25 | 2.75 | 6.50 | 3.75 | 2.75 |
| 8 | TZISTR1162 | 81.70 | 84.13 | 2.43 | 1.00 | 1.70 | 0.71 | 1.00 | 12.21 | 2.25 | 63.75 | 2.25 | 3.00 | 3.00 | 3.00 |
| 9 | TZISTR1165 | 82.38 | 81.75 | -0.63 | 1.00 | 2.10 | 0.99 | 1.00 | 13.46 | 2.75 | 66.25 | 3.25 | 3.50 | 2.75 | 3.00 |
| 10 | TZISTR1175 | 79.00 | 78.25 | -0.75 | 1.00 | 2.10 | 0.92 | 1.00 | 11.71 | 5.75 | 59.75 | 3.75 | 5.50 | 2.75 | 1.75 |
| 11 | TZISTR1178 | 74.50 | 74.00 | -0.50 | 1.00 | 2.35 | 0.94 | 1.00 | 9.96 | 6.75 | 65.25 | 3.25 | 3.50 | 3.75 | 1.75 |
| 12 | TZISTR1163 | 76.75 | 77.50 | 0.75 | 1.00 | 2.25 | 1.07 | 1.00 | 9.46 | 3.25 | 65.00 | 3.25 | 1.00 | 3.50 | 3.00 |
| 13 | TZISTR1166 | 90.00 | 87.50 | -2.50 | 1.00 | 1.60 | 0.77 | 1.00 | 9.46 | 3.25 | 65.00 | 3.25 | 6.50 | 2.75 | 2.00 |
| 14 | TZISTR1190 | 93.50 | 92.00 | -1.50 | 1.00 | 1.45 | 0.69 | 1.50 | 8.46 | 3.25 | 67.00 | 3.75 | 5.00 | 4.25 | 2.25 |
| 15 | TZISTR1199 | 82.75 | 81.00 | -1.75 | 1.00 | 1.85 | 0.97 | 1.50 | 8.46 | 3.25 | 64.25 | 3.25 | 2.00 | 3.25 | 2.75 |
| 16 | TZISTR1231 | 73.25 | 72.25 | -1.00 | 1.00 | 1.85 | 0.94 | 1.00 | 9.21 | 7.25 | 62.50 | 2.75 | 6.50 | 3.75 | 2.25 |
| 17 | TZISTR1232 | 77.50 | 76.75 | -0.75 | 1.00 | 1.83 | 0.94 | 1.00 | 10.71 | 8.75 | 46.75 | 3.25 | 2.00 | 2.00 | 2.00 |
| 18 | TZISTR1259 | 77.75 | 78.75 | 1.00 | 1.00 | 1.78 | 0.89 | 2.00 | 13.46 | 8.25 | 25.75 | 3.25 | 3.50 | 3.00 | 2.25 |
| 19 | TZISTR1262 | 76.75 | 74.50 | -2.25 | 1.00 | 1.65 | 0.73 | 2.50 | 10.71 | 5.75 | 39.25 | 2.63 | 5.00 | 3.75 | 3.00 |
| 20 | TZISTR1159 | 76.50 | 72.75 | -3.75 | 1.00 | 1.85 | 0.86 | 1.50 | 8.46 | 5.25 | 46.25 | 3.13 | 2.00 | 1.75 | 2.75 |
| 21 | TZISTR1223 | 80.88 | 78.00 | -2.88 | 1.00 | 2.10 | 0.97 | 1.00 | 9.46 | 5.25 | 55.00 | 3.13 | 2.50 | 3.25 | 2.75 |
| 22 | TZISTR1225 | 84.75 | 83.25 | -1.50 | 1.00 | 2.00 | 0.88 | 1.00 | 8.71 | 3.25 | 65.25 | 2.63 | 4.50 | 3.25 | 3.75 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

**Appendix 3.3** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP (1 to 9) | GY (g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 23 | CML550 | **73.25** | **73.25** | 0.00 | **1.00** | **2.13** | **1.00** | **1.00** | **13.21** | **1.25** | **86.00** | **2.63** | 5.00 | **1.50** | **2.00** |
| 24 | TZISTR1244 | 79.25 | 75.25 | -4.00 | 1.00 | 1.55 | 0.82 | 1.50 | 8.46 | 1.75 | 48.25 | 2.63 | 7.00 | 2.25 | 2.00 |
| 25 | TZSTRI101 | **90.00** | **87.50** | -2.50 | **1.00** | **1.45** | **0.75** | **1.00** | **12.46** | **3.25** | **144.00** | **3.63** | 6.50 | **3.75** | **3.00** |
| 26 | TZSTRI102 | 87.75 | 84.75 | -3.00 | 1.00 | 1.45 | 0.75 | 1.00 | 12.96 | 5.25 | 51.75 | 3.13 | 4.50 | 3.00 | 2.00 |
| 27 | TZSTRI104 | 89.50 | 90.75 | 1.25 | 1.00 | 1.45 | 0.75 | 1.00 | 12.96 | 5.25 | 51.75 | 3.13 | 7.50 | 3.50 | 1.75 |
| **28** | **TZSTRI107** | **88.00** | **86.75** | -1.25 | **1.00** | **1.25** | **0.66** | **1.00** | **8.75** | **3.25** | **70.25** | **3.63** | 8.00 | **2.25** | **2.50** |
| 29 | TZSTRI108 | **77.25** | **75.00** | -2.25 | **1.00** | **1.55** | **0.88** | **1.00** | **8.75** | **1.25** | **77.00** | **3.13** | 1.50 | **3.50** | **2.50** |
| 30 | TZSTRI109 | **80.75** | **78.00** | -2.75 | **1.00** | **1.75** | **0.97** | **1.00** | **11.00** | **2.25** | **78.00** | **3.13** | 4.50 | **3.75** | **2.50** |
| 31 | TZSTRI110 | **80.75** | **79.75** | -1.00 | **1.00** | **1.95** | **1.10** | **1.00** | **10.25** | **3.25** | **71.00** | **3.13** | 4.00 | **2.25** | **2.75** |
| 32 | TZSTRI112 | 80.38 | 82.50 | 2.12 | 1.00 | 1.55 | 0.82 | 1.00 | 9.25 | 4.25 | 62.00 | 3.13 | 5.50 | 3.75 | 2.75 |
| 33 | TZSTRI114 | 87.75 | 91.00 | 3.25 | 1.00 | 1.10 | 0.47 | 1.00 | 10.00 | 5.25 | 62.25 | 3.13 | 2.50 | 3.00 | 2.00 |
| 34 | **TZSTRI115** | **84.75** | **87.75** | 3.00 | **1.00** | **1.65** | **0.77** | **1.00** | **10.50** | **3.25** | **70.00** | **3.20** | 1.50 | **1.00** | **1.25** |
| 35 | **TZISTR25** | **75.75** | **75.50** | -0.25 | **1.00** | **2.25** | **1.05** | **1.00** | **12.00** | **1.25** | **131.00** | **3.20** | 2.00 | **3.75** | **2.00** |
| 36 | **TZISTR1001** | **79.63** | **78.25** | -1.38 | **1.00** | **2.10** | **1.03** | **1.00** | **11.50** | **1.75** | **120.00** | **2.70** | 1.50 | **3.50** | **2.50** |
| 37 | TZISTR1003 | 81.38 | 79.50 | -1.88 | 1.00 | 1.53 | 0.91 | 1.00 | 10.00 | 3.75 | 59.00 | 3.20 | 1.50 | 3.50 | 2.25 |
| 38 | TZISTR1004 | 80.25 | 78.75 | -1.50 | 1.00 | 1.45 | 0.84 | 1.00 | 9.00 | 3.25 | 62.25 | 4.20 | 3.50 | 3.75 | 2.50 |
| 39 | TZISTR1008 | 81.25 | 79.25 | -2.00 | 1.00 | 1.70 | 0.89 | 1.00 | 9.00 | 3.25 | 62.25 | 4.70 | 1.50 | 2.75 | 2.75 |
| 40 | TZISTR1011 | 86.50 | 84.75 | -1.75 | 1.00 | 2.05 | 0.96 | 1.00 | 10.00 | 7.25 | 39.75 | 4.20 | 1.50 | 3.00 | 2.00 |
| 41 | TZISTR1018 | 81.00 | 81.50 | 0.50 | 1.00 | 2.05 | 1.03 | 1.00 | 9.50 | 8.25 | 22.75 | 3.20 | 6.00 | 3.75 | 4.00 |
| 42 | TZEEI21 | 77.00 | 77.88 | 0.88 | 1.00 | 1.37 | 0.75 | 1.00 | 9.50 | 6.25 | 45.25 | 3.20 | 5.00 | 3.75 | 4.75 |
| 43 | TZEEI13 | 80.75 | 81.25 | 0.50 | 1.00 | 1.27 | 0.65 | 1.00 | 8.50 | 3.25 | 55.00 | 3.70 | 2.00 | 3.25 | 2.25 |
| 44 | TZEEI14 | 77.25 | 79.00 | 1.75 | 1.00 | 1.97 | 1.10 | 1.00 | 10.75 | 2.75 | 51.75 | 3.20 | 3.50 | 2.00 | 2.00 |
| 45 | TZEEI49 | 76.25 | 74.75 | -1.50 | 1.00 | 2.05 | 1.06 | 1.00 | 11.75 | 4.25 | 48.25 | 3.20 | 2.00 | 3.75 | 2.50 |
| 46 | TZDEEI55 | 78.38 | 76.75 | -1.63 | 1.00 | 1.38 | 0.61 | 1.00 | 9.50 | 4.75 | 51.50 | 2.70 | 2.00 | 3.75 | 2.75 |
| **47** | **TZDEEI50** | **74.50** | **74.50** | 0.00 | **1.00** | **1.29** | **0.57** | **1.00** | **10.50** | **3.75** | **70.00** | **1.70** | 5.50 | **5.50** | **5.00** |
| 48 | TZDEEI64 | 70.75 | 74.25 | 3.50 | 1.00 | 1.72 | 0.85 | 1.00 | 10.50 | 4.25 | 52.00 | 2.20 | 2.00 | 2.00 | 4.25 |
| 49 | CML312 | 74.50 | 72.63 | -1.87 | 1.00 | 2.02 | 0.88 | 1.00 | 8.50 | 6.25 | 27.25 | 3.20 | 2.00 | 3.75 | 1.00 |
| 50 | CML444 | 77.75 | 77.50 | -0.25 | 1.00 | 1.57 | 0.68 | 1.00 | 7.00 | 4.25 | 42.50 | 2.20 | 1.50 | 3.75 | 1.75 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

**Appendix 3.3** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP (1 to 9) | GY (g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 51 | CML442 | 79.25 | 80.25 | 1.00 | 1.00 | 1.32 | 0.63 | 1.00 | 6.75 | 4.75 | 45.00 | 1.70 | 2.00 | 3.25 | 2.25 |
| **52** | **TZDEEI54** | **83.75** | **79.25** | -4.50 | **1.00** | **1.52** | **0.80** | **1.50** | **13.00** | **3.25** | **82.50** | **3.20** | 1.50 | **2.75** | **0.75** |
| 53 | TZEEI10 | 82.25 | 81.25 | -1.00 | 1.00 | 1.32 | 0.71 | 1.00 | 11.25 | 3.25 | 40.00 | 2.70 | 2.00 | 3.50 | 1.50 |
| 54 | CML547 | 86.75 | 86.25 | -0.50 | 1.00 | 1.32 | 0.71 | 1.50 | 11.25 | 3.25 | 40.00 | 2.70 | 2.00 | 3.50 | 2.25 |
| **55** | **CML539** | **75.50** | **73.00** | -2.50 | **1.00** | **1.59** | **0.77** | **1.50** | **8.00** | **3.25** | **70.25** | **3.18** | 5.50 | **0.75** | **1.50** |
| **56** | **CML440** | **80.50** | **79.25** | -1.25 | **1.00** | **1.62** | **1.17** | **1.00** | **9.50** | **1.25** | **84.50** | **2.70** | 6.50 | **2.75** | **1.75** |
| **57** | **CML566** | **78.00** | **76.00** | -2.00 | **1.00** | **2.07** | **1.20** | **1.00** | **12.00** | **1.25** | **127.00** | **2.25** | 4.50 | **1.75** | **2.75** |
| **58** | **CML540** | **77.25** | **76.75** | -0.50 | **1.00** | **2.17** | **0.89** | **1.00** | **11.00** | **3.25** | **108.00** | **2.60** | 4.00 | **1.50** | **2.00** |
| **59** | **CML545** | **77.50** | **76.00** | -1.50 | **1.00** | **2.15** | **0.87** | **1.00** | **10.00** | **3.25** | **83.00** | **2.68** | 5.00 | **3.75** | **3.50** |
| **60** | **CML571** | **76.25** | **75.75** | -0.50 | **1.00** | **12.45** | **0.78** | **3.00** | **10.00** | **3.25** | **87.75** | **2.63** | 2.00 | **3.25** | **3.75** |
| 61 | CML390 | 74.00 | 73.75 | -0.25 | 1.00 | 2.05 | 0.80 | 3.00 | 10.75 | 5.75 | 37.30 | 2.68 | 7.50 | 4.25 | 3.25 |
| 62 | CLHP0352 | 78.50 | 74.75 | -3.75 | 1.00 | 1.10 | 0.98 | 1.00 | 11.25 | 6.75 | 17.05 | 2.68 | 8.00 | 3.75 | 3.75 |
| 63 | HA04A-2107-36 | 86.25 | 88.25 | 2.00 | 1.00 | 2.00 | 0.96 | 1.50 | 8.50 | 8.25 | 10.05 | 2.18 | 0.00 | 3.00 | 2.00 |
| 64 | CLHP0303 | 77.25 | 73.75 | -3.50 | 1.50 | 1.52 | 1.06 | 1.50 | 8.00 | 6.25 | 54.55 | 2.68 | 4.00 | 3.75 | 2.00 |
| 65 | CLHP0221 | 83.75 | 81.25 | -2.50 | 1.50 | 1.75 | 0.89 | 1.50 | 10.00 | 6.25 | 54.55 | 3.18 | 5.00 | 1.50 | 1.50 |
| 66 | CLHP0020 | 74.25 | 71.75 | -2.50 | 1.00 | 1.64 | 0.71 | 1.50 | 10.50 | 8.75 | 22.30 | 3.18 | 2.50 | 1.75 | 1.50 |
| 67 | CLHP0058 | 76.75 | 76.25 | -0.50 | 1.00 | 1.13 | 0.58 | 1.50 | 10.50 | 7.75 | 22.30 | 5.18 | 2.00 | 5.75 | 4.75 |
| 68 | CKDHL0378 | 80.00 | 79.75 | -0.25 | 1.00 | 1.55 | 0.78 | 1.50 | 10.00 | 4.25 | 28.05 | 5.18 | 2.00 | 4.75 | 5.75 |
| 69 | CLHP0312 | 76.25 | 78.00 | 1.75 | 1.00 | 1.35 | 0.95 | 1.50 | 8.50 | 2.75 | 35.55 | 3.18 | 1.50 | 3.75 | 3.75 |
| 70 | CLHP0310 | 72.75 | 72.50 | -0.25 | 1.00 | 1.20 | 0.77 | 1.50 | 8.00 | 5.75 | 23.55 | 2.68 | 2.50 | 3.75 | 2.75 |
| **71** | **CLHP0003** | **72.75** | **74.25** | 1.50 | **1.00** | **1.85** | **0.88** | **1.00** | **12.75** | **5.25** | **90.80** | **2.68** | 7.00 | **2.00** | **2.50** |
| **72** | **CKDHL0467** | **82.00** | **82.75** | 0.75 | **1.00** | **1.40** | **1.04** | **1.00** | **13.50** | **5.25** | **96.80** | **2.68** | 3.00 | **4.25** | **3.50** |
| 73 | CLHP00378 | 75.25 | 74.25 | -1.00 | 1.00 | 1.10 | 0.72 | 1.00 | 8.25 | 7.25 | 25.05 | 2.68 | 4.00 | 4.50 | 4.50 |
| 74 | CLHP0156 | 73.25 | 72.50 | -0.75 | 1.50 | 2.28 | 0.86 | 1.00 | 11.75 | 7.75 | 26.30 | 2.68 | 3.00 | 2.50 | 4.25 |
| 75 | CLHP0113 | 77.25 | 76.00 | -1.25 | 1.50 | 1.25 | 0.92 | 1.00 | 12.00 | 8.25 | 39.05 | 2.68 | 2.00 | 2.75 | 2.50 |
| 76 | CLHP03302 | 74.00 | 71.75 | -2.25 | 1.00 | 0.90 | 0.47 | 1.00 | 8.25 | 8.75 | 46.05 | 2.68 | 2.50 | 4.25 | 2.25 |
| **77** | **CLHP0404** | **74.75** | **74.25** | -0.50 | **1.00** | **2.07** | **0.75** | **1.00** | **10.00** | **6.25** | **137.35** | **3.18** | 5.00 | **6.00** | **4.00** |
| **78** | **CLHP0343** | **79.13** | **81.00** | 1.87 | **1.00** | **1.37** | **0.92** | **1.00** | **11.50** | **2.25** | **101.10** | **3.68** | 2.50 | **5.00** | **5.25** |
| 79 | CZL1380 | 80.25 | 79.25 | -1.00 | 1.00 | 1.23 | 0.79 | 1.00 | 9.50 | 5.25 | 54.85 | 3.68 | 5.00 | 5.25 | 5.50 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

**Appendix 3.3** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP (1 to 9) | GY (g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 80 | CLHP0326 | **72.75** | **72.25** | -0.50 | **1.00** | **1.60** | **0.72** | **1.50** | **8.50** | **5.25** | **85.35** | **3.68** | 2.00 | **3.25** | **4.75** |
| **81** | **CZL99017** | **81.75** | **82.25** | 0.50 | **1.00** | **1.70** | **0.68** | **1.50** | **10.75** | **2.25** | **71.10** | **3.18** | 5.50 | **3.50** | **3.00** |
| 82 | TZEEI34 | 79.25 | 80.25 | 1.00 | 1.00 | 1.26 | 0.58 | 1.50 | 10.25 | 4.25 | 60.10 | 3.18 | 6.50 | 4.00 | 2.25 |
| 83 | CLHP0049 | 78.25 | 79.25 | 1.00 | 1.00 | 1.25 | 0.47 | 1.50 | 5.50 | 5.25 | 60.35 | 3.18 | 2.50 | 3.25 | 2.50 |
| 84 | CLHP00478 | 77.75 | 75.25 | -2.50 | 1.00 | 1.60 | 0.55 | 1.00 | 5.25 | 5.75 | 57.35 | 2.68 | 2.00 | 2.50 | 2.00 |
| 85 | CLHP00286 | 77.88 | 79.50 | 1.62 | 1.00 | 1.25 | 0.70 | 1.00 | 9.75 | 5.75 | 57.60 | 3.68 | 3.00 | 3.25 | 2.00 |
| 86 | CML451 | 85.75 | 86.25 | 0.50 | 1.00 | 1.65 | 0.84 | 1.00 | 11.25 | 4.25 | 62.85 | 3.68 | 4.50 | 4.50 | 2.50 |
| 87 | CLHP0302 | 82.75 | 79.75 | -3.00 | 1.00 | 1.40 | 0.79 | 2.00 | 13.75 | 4.25 | 32.10 | 3.18 | 3.50 | 4.25 | 3.00 |
| 88 | CLHP0364 | 80.25 | 80.25 | 0.00 | 1.00 | 1.45 | 0.57 | 2.00 | 12.50 | 5.25 | 39.35 | 3.68 | 4.50 | 3.75 | 2.75 |
| 89 | CLHP0350 | 77.25 | 78.25 | 1.00 | 1.00 | 1.85 | 0.62 | 1.00 | 10.50 | 6.25 | 40.85 | 3.18 | 2.00 | 3.25 | 3.25 |
| 90 | CLHP00294 | 88.50 | 85.75 | -2.75 | 1.00 | 1.07 | 0.47 | 1.50 | 9.25 | 7.25 | 25.10 | 3.18 | 2.50 | 3.50 | 3.00 |
| 91 | CLHP0005 | 84.25 | 85.75 | 1.50 | 1.00 | 1.10 | 0.32 | 1.50 | 8.75 | 6.25 | 67.10 | 6.68 | 5.50 | 5.75 | 2.50 |
| 92 | CLHP0022 | 71.75 | 73.88 | 2.13 | 1.00 | 1.45 | 0.45 | 1.00 | 9.00 | 5.25 | 44.60 | 9.68 | 2.00 | 4.00 | 2.00 |
| **93** | **CML304** | **79.25** | **79.63** | 0.38 | **1.00** | **1.44** | **0.75** | **1.00** | **12.00** | **4.75** | **151.00** | **3.18** | 2.00 | **4.75** | **2.75** |
| **94** | **TZISTR1174** | **83.75** | **82.00** | -1.75 | **1.00** | **1.68** | **0.91** | **1.00** | **11.00** | **1.75** | **112.75** | **4.18** | 4.50 | **5.00** | **3.50** |
| **95** | **TZISTR1205** | **81.00** | **83.00** | 2.00 | **1.00** | **2.21** | **1.00** | **1.00** | **9.50** | **1.75** | **129.00** | **4.18** | 1.00 | **3.75** | **2.50** |
| **96** | **TZSTRI113** | **74.50** | **73.00** | -1.50 | **1.00** | **1.41** | **0.90** | **1.00** | **9.00** | **1.75** | **111.75** | **2.68** | 3.50 | **3.75** | **2.75** |
| **97** | **TZISTR1119** | **78.75** | **77.00** | -1.75 | **1.00** | **1.81** | **0.95** | **1.00** | **10.50** | **3.75** | **135.75** | **3.68** | 4.50 | **5.50** | **3.50** |
| **98** | **TZISTR1015** | **80.00** | **80.50** | 0.50 | **1.00** | **1.51** | **0.92** | **1.00** | **9.50** | **3.75** | **74.50** | **3.68** | 4.00 | **1.25** | **3.50** |
| **99** | **ZM1421** | **82.38** | **80.75** | -1.63 | **1.00** | **2.10** | **0.95** | **1.50** | **10.71** | **2.25** | **88.00** | **2.63** | 2.00 | **1.75** | **3.25** |
| **100** | **B.King/1421** | **81.00** | **77.75** | -3.25 | **1.00** | **2.35** | **1.05** | **1.50** | **11.71** | **3.25** | **91.75** | **2.63** | 4.50 | **2.25** | **2.25** |
| 101 | Hickory/1421 | 79.25 | 77.75 | -1.50 | 1.00 | 2.40 | 1.18 | 1.50 | 7.96 | 7.25 | 39.75 | 2.63 | 5.00 | 2.00 | 2.50 |
| 102 | Kep/1421 | 72.50 | 73.50 | 1.00 | 1.00 | 2.10 | 1.12 | 2.00 | 8.21 | 5.75 | 34.75 | 2.63 | 4.00 | 2.50 | 2.75 |
| **103** | **Shesha/1421** | **71.50** | **70.75** | -0.75 | **1.00** | **1.82** | **0.88** | **1.50** | **10.71** | **1.75** | **112.25** | **4.63** | 2.50 | **4.00** | **2.75** |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

**Appendix 3.3** (continued)

| N° | Accessions | DA | DS | ASI | EPP | PLHT (m) | EHT (m) | HUSK (1 to 5) | CL (cm) | EASP (1 to9) | GY (g/plant) | SEC8 | SEC10 | SDR8 (1 to 9) | SDR10 (1 to 9) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **104** | **ZM1423** | **70.25** | **71.88** | 1.63 | **1.00** | **2.17** | **0.94** | **1.00** | **13.71** | **1.25** | **144.25** | **4.63** | 2.50 | **1.75** | **2.50** |
| **105** | **N.Choice/1421** | **81.25** | **75.25** | -6.00 | **1.00** | **1.62** | **0.85** | **1.50** | **10.96** | **1.75** | **133.25** | **3.13** | 3.50 | **4.00** | **3.00** |
| 106 | NC.QPM/Z.DPLO | 82.50 | 81.25 | -1.25 | 1.00 | 1.77 | 0.86 | 1.50 | 11.25 | 4.25 | 68.00 | 3.20 | 5.00 | 2.75 | 1.25 |
| **107** | **STR-SYN-Y2** | **85.25** | **85.25** | 0.00 | **1.00** | **1.60** | **0.80** | **1.00** | **11.25** | **3.25** | **126.85** | **8.18** | 3.50 | **3.25** | **2.50** |
| 108 | Z. Diplo.BC4C3-W-DT C1 | 87.75 | 87.75 | 0.00 | 1.00 | 0.98 | 0.82 | 1.00 | 12.25 | 3.25 | 60.35 | 6.68 | 2.50 | 4.75 | 4.25 |
| 109 | TZBSTR (Susceptible)(RE) | 84.25 | 87.75 | 3.50 | 1.00 | 1.65 | 0.66 | 1.00 | 10.50 | 4.25 | 33.60 | 8.18 | 1.50 | 4.75 | 4.25 |
| 110 | STR-SYN-W1 | 79.00 | 79.00 | 0.00 | 1.00 | 2.12 | 0.94 | 1.50 | 10.50 | 2.75 | 51.10 | 8.18 | 5.00 | 3.25 | 3.25 |
| **111** | **DTSTR-W SYN13** | **89.25** | **88.50** | -0.75 | **1.00** | **0.98** | **0.75** | **1.50** | **10.00** | **3.75** | **115.35** | **4.68** | 5.50 | **3.50** | **2.50** |
| **112** | **DTSTR-Y SYN15** | **83.75** | **84.25** | 0.50 | **1.00** | **1.78** | **0.65** | **1.00** | **9.00** | **6.25** | **87.35** | **3.18** | 4.50 | **4.00** | **2.75** |
| 113 | ((IWD C3 SYN*2/(White DT STR Syn))-DT C1 | 84.25 | 84.50 | 0.25 | 1.00 | 1.48 | 0.65 | 1.00 | 8.50 | 6.25 | 57.10 | 3.18 | 3.50 | 3.75 | 3.00 |
| 114 | DTSTR-W SYN11 | 87.25 | 89.75 | 2.50 | 1.00 | 1.73 | 0.73 | 1.50 | 8.00 | 3.75 | 45.10 | 2.68 | 3.00 | 2.75 | 1.75 |
| 115 | SAMMMZ16 | 85.75 | 84.75 | -1.00 | 1.00 | 1.93 | 1.03 | 2.00 | 8.50 | 3.75 | 56.50 | 3.18 | 4.50 | 2.75 | 0.75 |
| 116 | (TZEOMP5C7/TZECOMP3DTC2) C2 | 84.50 | 82.75 | -1.75 | 1.00 | 1.33 | 0.96 | 2.00 | 9.25 | 5.75 | 59.50 | 3.68 | 3.00 | 3.75 | 2.25 |
| 117 | ((TZL COMP1-W C6*2/(White DT STR Syn))-DT C1 | 87.75 | 88.75 | 1.00 | 1.00 | 1.73 | 0.66 | 2.00 | 9.25 | 5.75 | 59.50 | 3.68 | 4.50 | 3.75 | 3.25 |
| 118 | TZCOM1/ZDPSYN | 79.25 | 75.75 | -3.50 | 1.00 | 1.66 | 0.31 | 2.00 | 11.50 | 3.25 | 62.50 | 3.18 | 5.50 | 4.75 | 3.75 |
| 119 | Colorado/1421 | 77.75 | 79.63 | 1.88 | 1.00 | 1.63 | 0.49 | 2.00 | 10.50 | 1.25 | 58.75 | 4.68 | 7.50 | 5.25 | 5.25 |
| 120 | M.Pearl/DT-STR | 87.25 | 87.75 | 0.50 | 1.00 | 0.73 | 0.65 | 1.00 | 9.00 | 3.25 | 57.25 | 5.68 | 2.00 | 6.50 | 5.00 |
| 121 | Z.diplo-BC4-C3-W/DOGONA-1/Z.diplo-BC4-C3-W | 79.13 | 78.75 | -0.38 | 1.00 | 1.34 | 0.75 | 0.50 | 9.75 | 6.25 | 47.00 | 4.18 | 2.00 | 2.25 | 2.50 |
| 122 | NC.QPM/DT-STR | 79.65 | 80.75 | 1.10 | 1.00 | 1.31 | 0.50 | 0.50 | 9.75 | 6.25 | 47.00 | 3.68 | 5.00 | 5.50 | 2.00 |
| 123 | ZM1421/DT-STR | 82.50 | 80.75 | -1.75 | 1.00 | 1.32 | 0.50 | 1.00 | 10.00 | 3.75 | 58.25 | 3.68 | 4.00 | 3.75 | 4.00 |
| **124** | **DTSTR-Y SYN14** | **80.13** | **79.75** | -0.38 | **1.00** | **1.36** | **0.75** | **1.50** | **11.50** | **1.75** | **93.25** | **3.68** | 1.00 | **3.75** | **3.75** |
| **125** | **ZM1423/Z.DLO** | **81.25** | **83.25** | 2.00 | **1.00** | **12.41** | **1.03** | **1.00** | **10.75** | **4.75** | **96.75** | **2.68** | 5.00 | **3.75** | **2.75** |
| **126** | **(2*TZECOMP3DT/WhiteDTSTRSYN) C2** | **77.25** | **79.25** | 2.00 | **1.00** | **1.21** | **0.91** | **1.00** | **11.25** | **1.75** | **72.50** | **2.68** | 2.50 | **4.75** | **3.75** |
| | **Trial statistics** | **DA** | **DS** | **ASI** | **EPP** | **PLHT** | **EHT** | **HUSK** | **CL** | **EASP** | **GY** | **SEC8** | **SEC10** | **SDR8** | **SDR10** |
| | **Inbred lines** | | | | | | | | | | | | | | |
| | Minimum | 70.75 | 71.75 | 0.00 | 1.00 | 0.9 | 0.32 | 1.00 | 5.25 | 1.25 | 10.05 | 1.70 | 0.00 | 0.75 | 0.75 |
| | Maximum | 82.38 | 80.75 | 6.00 | 1.00 | 2.40 | 1.18 | 2.00 | 11.71 | 7.25 | 133.25 | 4.68 | 7.50 | 5.25 | 5.25 |
| | Mean | 77.95 | 76.48 | 2.03 | 1.00 | 2.00 | 0.93 | 1.64 | 10.11 | 3.32 | 79.79 | 3.28 | 4.14 | 3.11 | 3.11 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= Plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, m= meter, cm= centimetre, g= gramme. Boldface entries denote best-performing genotypes.

## Chapter 4: Progeny testing of tropical and sub-tropical maize lines for grain yield and *Striga* resistance


### Abstract

Maize (*Zea mays* L., 2n=2x=20) and the major cereal crop production are challenged by *Striga hermonthica (Sh)* and *S. asiatica (Sa)* infestation, leading to significant yield and monetary losses. High-yielding and *Striga*-resistant hybrids are yet to be deployed to enhance maize productivity in *Striga*-infested areas. Choice of genetically complementary inbred lines and derived hybrids with good combining ability for yield and *Striga* resistance traits are preconditions to exploit hybrid vigor. The objective of the present study was to undertake progeny testing and determine the genetic components of grain yield and *Sa* and *Sh* resistance in tropical and sub-tropical maize inbred lines to guide breeding. Four preliminarily selected tropical high-yielding and *Sh*-resistant testers and eight sub-tropical lines with resistance to *Sa* were crossed in a line-by-tester mating design, and 32 single cross hybrids were generated. The crosses and their parents were evaluated under field and controlled environments during the 2023/2024 growing season using a 7 x 6 alpha lattice design with two replications. Combined analysis of variance revealed a significant ($p \leq 0.05$) effect of the crosses on grain yield (GY), related agronomic traits, *Striga* emergence counts, and *Striga* damage rating 8 and 10 weeks after sowing. The ratio of the general combining ability and the specific combining ability effects was less than one for all the traits, indicating the predominance of non-additive genetic effects in trait inheritance and signifying the value of hybrid breeding. The best general combiner tester was TZISTR1248 in the *Sa*-infested environment, while tester TZISTR1174 was noteworthy under *Sh* environment. Lines CML540 and CLHP0343 were the best combiners in *Sa* environment, while CZL99017, CML566, CML540, and CLHP0343 were promising in *Sh* environment and CML540 was the best general combiner in all test environments. The crosses CML540 x TZISTR1174, CML540 x TZDEEI50, and CML539 x TZISTR1174 exhibited high yields at 7.16 t/ha, 7.00 t/ha, and 6.33 t/ha and significant specific combining ability effects of 13.55, 31.52, and 17.69, and heterosis at 32.08%, 37.28%, and 39.02%, respectively for GY in *Sa* environment. Whereas, in *Sh* environment, cross CML440 x TZDEEI50 had the best specific combining ability effect (54.13) and heterosis (73.66%) for GY. Crosses CML451 x TZISTR1174, CML539 x TZISTR1174, CML440 x TZDEEI50, CML566 x TZDEEI50, CZL99017 x TZISTR1248, and CML539 x TZISTR1248 were relatively the best specific combiners for GY in both *Sa* and *Sh* environments. The selected lines and testers and the new experimental hybrids are recommended for multi-environment evaluation in *Sa* and *Sh*-prone agro-ecologies to enhance grain yield and *Striga* resistance.



**Keywords**: Combining ability, heterosis, maize hybrids, *S. asiatica, S. hermonthica*

## 4.1 **Introduction**

Maize (*Zea mays*. L, 2n = 2x = 20) is the principal food staple in sub-Saharan Africa (SSA) and a commercial crop globally. It provides more than 30% of daily caloric needs across Africa (Adu et al., 2022). Nonetheless, maize yield in SSA is the lowest (about 3 tons $ha^{-1}$) compared to a global average of 5 to 10 tons $ha^{-1}$ (Aramburu-Merlos et al., 2024). Infestations by the parasitic weed *Striga spp* are among the leading causes of the region's low maize productivity and yield gap. The major factors for low maize productivity in Africa are biotic stresses (e.g. foliar diseases, field and storage insect pests, and parasitic weeds), abiotic stresses (heat, drought, and low soil fertility), and limited access to improved and quality seeds (Badu-Apraku et al., 2017; Chimonyo et al., 2020; Mncube et al., 2023).

The parasitic weed *Striga hermonthica* (*Sh*) (relatively tall and purple flour plants) and *S. asiatica* (*Sa*) (short and red flour types) are the most destructive, inflicting yield losses varying from 10 to 100% in susceptible maize cultivars (Belay, 2022a; Benjamin et al., 2024; David et al., 2022). *Striga hermonthica* is fertile and prolific owing to its highly allogamous mating system (Olivier et al., 1998). This species has the most extensive geographical distribution in SSA, particularly in Western, Central, and Eastern Africa (Belay, 2022a). In contrast, *Sa* is an autogamous species that occurs predominantly in Southern and East Africa. It is noteworthy that the two species occur in the same fields in tandem in some regions, mainly in East Africa (Lobulu et al., 2019; Lobulu et al., 2021; Lobulu et al., 2023), although there is limited information about their co-infestation in the literature. *Striga* is a prolific seed producer, capable of releasing up to 200,000 seeds per plan. *Striga* seeds are tiny, light and dust-like dispersed by wind and remaining viable in soil seed-bank for more than 20 years (Belay, 2022a; Ejeta, 2007; Parker and Riches, 1993). The parasite depends solely on its host crop for nourishment, which it “rewards” with devastating phytotoxins, causing rapid leaf chlorosis, thin stalk, stunted plant height, wilted silk, and total crop loss under heavy infestations (David et al., 2022).

Several management practices have been recommended for *Striga* control, including cultural practices (e.g. crop rotation, intercropping, catch and trap cropping, push-pull technology), crop protection chemicals (e.g. ethylene and ethephon) (David et al., 2022; Sibhatu, 2016), biological agents (e.g. *Fusarium oxysporum* f.sp. *strigae*) and host resistance (Mrema et al., 2019; Shayanowako et al., 2020). However, most of these methods have been unable to effectively control the weeds because of inaccessibility in communal maize production systems

and impracticality in specific cropping systems (e.g., maize-legume intercrops). Farmers often resort to hand weeding, which is ineffective as most damage occurs before the parasitic plant emerges (Dossa et al., 2023a). The use of resistant or tolerant cultivars is the most cost-effective, practical, environmentally friendly, and sustainable method for controlling *Striga* (Belay, 2022a).

Reportedly, maize yield losses due to *Striga* infestations are cultivar-dependent (Akinwale et al., 2013; Badu-Apraku et al., 2007; Dossa et al., 2024). Hence, *Striga* resistance breeding programs are crucial to developing and deploying maize varieties with durable resistance. *Striga* resistance is difficult to achieve because it involves many minor genes (Stanley et al., 2021). In some instances, major gene resistance are reported (Gowda et al., 2021; Okunlola et al., 2023a). Major gene resistance is ephemeral and failed, suggesting the need for screening and selecting new sources of resistance followed by combining ability tests. There is a need to select the best parental lines for gene introgression, pyramiding, and development of *Striga*-resistant hybrids. Continuous and concerted efforts in maize improvement for *Striga* resistance are necessary for integrated control of the witchweed.

Hybrid breeding is crucial for attaining maximum genetic gains and buffering climate change effects (Rehman et al., 2021; Tchounke et al., 2023). Knowledge of combining ability and gene action of contrasting parents through progeny testing is crucial to exploiting heterosis in hybrid breeding. Combining ability is the ability of inbred lines to contribute unique and contrasting multiple alleles towards the desirable performance of a progeny or hybrid. Combining ability is distinguished into two: general combining ability (GCA) and specific combining ability (SCA) (Rukundo et al., 2016; Shamuyarira et al., 2023; Yadav et al., 2021). The GCA refers to the average performance of a genotype in a series of hybrid combinations, and its significance indicates a greater role of additive gene action (Abady et al., 2021; Baker, 1978). In contrast, specific combining ability refers to the performance of parents in specific crosses and is a measure of non-additive gene effects (Baker, 1978; Sun et al., 2018). The magnitude of the mode of gene action (additive or non-additive) is important to guide breeding strategies such as hybrid breeding or recurrent selection in maize. Additive gene action involves the cumulative effect of individual genes, where each gene contributes a small, additive effect to the overall phenotype. Additive gene action is vital in recurrent selection programs, where the goal is to accumulate favorable alleles over successive generations (Yu et al., 2020). By selecting and interbreeding individuals with desirable traits, breeders can gradually enhance the genetic composition of populations such as *Striga* resistance. Non-additive gene action

includes interactions between genes, such as dominance and epistasis, where the combined effect of genes is not simply the sum of their individual minor effects. Non-additive gene action is required in hybrid breeding, which aims to produce hybrids with superior performance through heterosis (WU et al., 2019). Breeders exploit non-additive effects by crossing genetically diverse inbred lines to achieve higher yields, improved stress resistance, and other beneficial traits in hybrid maize varieties (Zhang et al., 2023). Also, estimating the additive and non-additive gene action is important in determining the possibility of commercial exploitation of heterosis and isolation of inbred lines among the progenies of good hybrids (Belay, 2022b).

The combining ability effects of inbred lines can be determined using various mating designs, including diallel, factorial designs, and the line-by-tester. The line-by-tester mating design is useful when a set of selected inbred lines is to be evaluated with a few testers harboring some economic traits such as disease and pest resistance, and quality traits (Amegbor et al., 2020). For instance, the combining ability of yellow maize testers with various reactions to *S. hermonthica* was evaluated by Zebire et al. (2020), using a line-by-tester mating design. The authors reported promising tolerance and resistance testers to identify superior *Striga*-resistant yellow endosperm inbred lines for hybridizing and developing resistant hybrids. Further, Oluwaseun et al. (2022) identified the combining ability of extra early maturing provitamin A maize inbred lines using a line-by-tester mating design. The authors found that additive and non-additive gene effects were important in the inheritance of grain yield and *Striga*-resistant traits in *Striga*-infested environments. Previous research has indicated inconsistencies in the gene action of *Striga* resistance traits. Some studies (Gethi and Smith, 2004; Konaté et al., 2017) reported the predominance of additive gene action, while others (Adu et al., 2022; Badu-Apraku et al., 2016) reported the predominance of nonadditive gene action of *Striga* resistance traits. Hence, there is a need to discern the specific genetic mechanisms underlying *Striga* resistance for the given test populations and conditions.

The existing *Striga*-resistant cultivars of maize in SSA are bred with major gene resistance for *Sh* resistance, while no commercially grown maize varieties are resistant to *Sa.* The two species occur in tandem, and no genetic resources were reported with dual resistance in the region. In an attempt to broaden *Striga* resistance genetic resources, sub-tropical and tropical maize genotypes were acquired from the International Institute of Tropical Agriculture (IITA) and the International Maize and Wheat Improvement Centre (CIMMYT). The genetic materials were screened at the University of KwaZulu-Natal's African Centre for Crop Improvement

(ACCI) (Dossa et al., 2024). Unique *S. asiatica* resistance lines and *S. hermonthica* resistance testers were selected for hybrid breeding. The selected genetically complementary inbred lines and derived hybrids need to be evaluated for their combining ability effects for grain yield and *Striga* resistance to exploit heterosis and design new hybrids. Therefore, the objective of the present study was to undertake progeny testing and determine the genetic components of grain yield and *Sa* and *Sh* resistance in tropical and sub-tropical maize inbred lines to guide breeding.

## 4.2 **Materials and Methods**

### 4.2.1 Study sites

Experiments were conducted at two sites, namely the University of KwaZulu-Natal's Controlled Environment Facilities (UKZN-CEF) and Ukulinga Research Farm during the 2023/2024 growing season. The UKZN CEF (29.6213° S, 30.3966° E) was used to conduct the glasshouse evaluations under controlled conditions. The field test was conducted at Ukulinga Research Farm (29.6627° S, 30.4050° E), which receives a mean annual rainfall of 750mm, with a yearly mean temperature of 18.4°C. The field at this site had undergone at least 20 years of maize monocropping.

### 4.2.2 Plant materials

The study used eight female lines initially acquired from CIMMYT/Zimbabwe and four tester inbred lines from the IITA/Nigeria. The details of the inbred lines used in this study are presented in Table 4.1. The inbred lines from CIMMYT are drought tolerant and were selected for their *Sa* resistance after screening 126 tropical and sub-tropical maize populations (Dossa et al., 2024). Inbred lines from IITA were tropically adapted genotypes developed for *Sh* resistance, generated from multi-parent populations, and were selected for their agronomic performance under *Sa* and *Sh* infestation (Dossa et al., 2024).

**Table 4.1** Description of the lines and testers used in the study

| Entry number | Name/designation | Role in a cross | Resistance reaction to *Striga* sp. | Source/origin |
|---|---|---|---|---|
| 1 | CLHP0303 | Line | *S. asiatica* | CIMMYT/Zimbabwe |
| 2 | CZL99017 | Line | *S. asiatica* | CIMMYT/Zimbabwe |
| 3 | CML440 | Line | *S. asiatica* | CIMMYT/Zimbabwe |
| 4 | CML451 | Line | *S. asiatica* | CIMMYT/Zimbabwe |
| 5 | CML566 | Line | *S. asiatica* | CIMMYT/Zimbabwe |
| 6 | CML540 (check) | Line | *S. asiatica* | CIMMYT/Zimbabwe |
| 7 | CLHP0343 | Line | *S. asiatica* | CIMMYT/Zimbabwe |
| 8 | CML539 | Line | *S. asiatica* | CIMMYT/Zimbabwe |
| 9 | TZISTR1174 | Tester | *S. hermonthica* | IITA/Nigeria |
| 10 | TZDEEI50 | Tester | *S. hermonthica* | IITA/Nigeria |
| 11 | TZISTR1248 | Tester | *S. hermonthica* | IITA/Nigeria |
| 12 | TZISTR1015 | Tester | *S. hermonthica* | IITA/Nigeria |

CIMMYT/Zimbabwe, International Maize and Wheat Improvement Centre/Zimbabwe; IITA/Nigeria, International Institute of Tropical Agriculture/Nigeria.

### Cross formation

The eight lines and four testers were crossed using a line-by-tester mating design from July 2023 to December 2023 at the controlled environment facilities of the University of KwaZulu-Natal, South Africa. A total of 32 crosses were made using the line-by-tester genetic design. The testers and lines were planted in three sequences staggered at an interval of seven days for flower synchronization. Four blocks were established, and each block was assigned to a tester. In each block, each tester was planted in 8 rows of 4 x 5 litre (L) plastic pots, while each line was planted in a single row of 4 x 5L pots so that each row of the line would be manually crossed to each row of the tester. The glasshouse conditions were maintained at temperature and humidity ranges of 30° C/20° C, and 50% to 55%, respectively. Plant nutrients were supplied through fertigation. Thirty successful F1 crosses were harvested in December 2023 for genetic analysis.

### 4.2.3 Evaluation of crosses

The 42 genotypes, including 30 $F_1$ single crosses hybrids and 12 parental lines, were evaluated using a 7 x 6 alpha lattice design with two replications. The genotypes were evaluated under three *Striga* treatment conditions. The first treatment comprised *Sa*-infested, the second *Sh*-infested conditions, and the third was a *Striga*-free or control. Studies were conducted during the 2023/2024 growing season. Genotype evaluations were conducted under plastic pot conditions and *Striga* infestation conditions to limit escapes and ensure better genotype

comparison. Each trial consisted of experimental units consisting of 5 pots of 5L capacity with 30 cm and 28 cm height and diameter, respectively, filled with composted pine bark medium for each of the three test conditions. Briefly, *Striga* infestation was achieved as follows: each pot received 0.10g of 2-year-old *Sa* and *Sh* seeds, which had been conditioned for two weeks in each pot before planting. Standard maize agronomic practices were applied for both testing environments (CIMMYT, 1985). Figures 4.1, 4.2, and 4.3 show the experimental setup with artificial infestations of maize with *Sa* and *Sh*, and control assays in the greenhouse and in the field conditions at the University of KwaZulu-Natal, South Africa.

### 4.2.4 Data collection

Data were collected on maize phenotypic traits and *Striga* parameters in the *Sa* and *Sh*-infested environments. The following phenotypic traits were evaluated and collected on maize: Days to 50% silking (DS), recorded as the number of days taken by 50% of the plants to silk in each plot; days to 50% anthesis (DA), recorded as the number of days from planting until 50% of the plants have emerged silks and shed pollen; anthesis-silking interval (ASI), measured as the difference between days to 50% silking and 50% anthesis; plant height (PLHT) and ear height (EHT), measured as the distance from the base of the plant to the height of the first tassel branch and the node bearing the upper ear, respectively; the number of ears per plant (EPP) was obtained by dividing the total number of ears per plot by the number of plants harvested. Husk cover (HUSK) was rated on a scale of 1–5, where 1=husks tightly arranged and extended beyond the ear tip and 5=ear tips exposed. Ear aspect (EASP) was recorded on a scale of 1–9, where 1=clean, uniform, large, well-filled ears and 9=ears with undesirable features. Grain yield per plant was determined as the weight (g) of the grain from the ears of individual plants after shelling adjusted to a constant moisture of 12.5% and converted in tons/ha using plant populations of 53,333 plants per ha. The *Striga* parameters included the number of emerged *Sa* and *Sh* plants 8 and 10 weeks after planting, denoted as SEC8 and SEC10, and *Striga* damage rating 8 and 10 weeks after planting, denoted as SDR8 and SDR10, respectively.

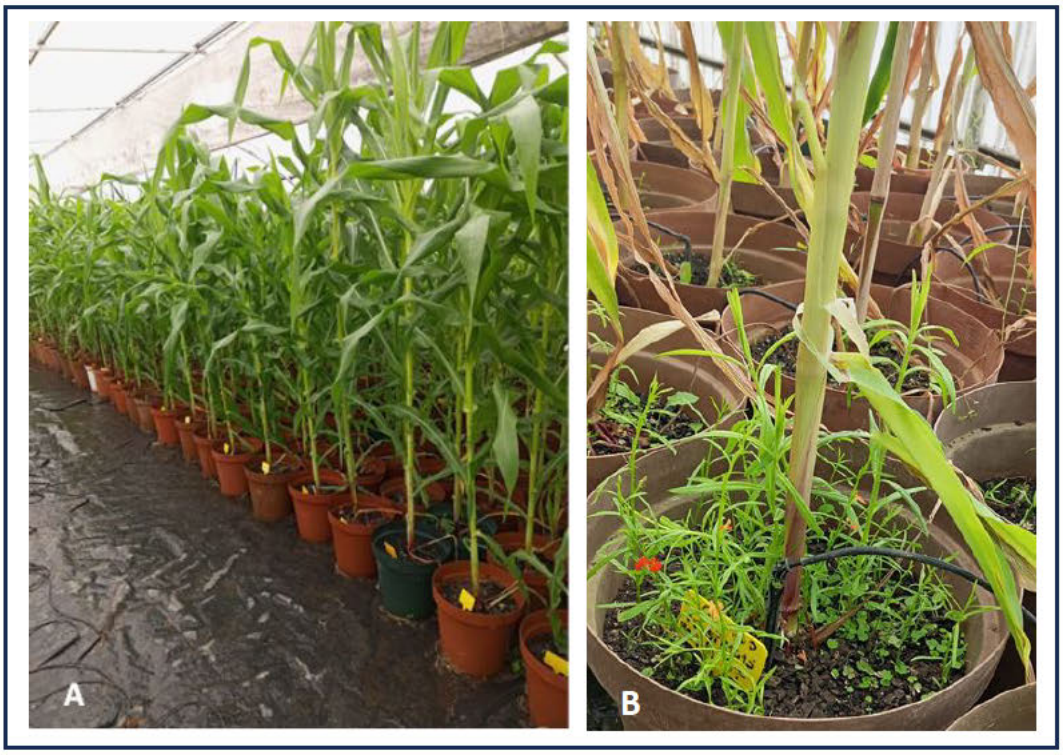


**Figure 4.1** Photographs showing the experimental setup in *Striga*-free environment (A) and with an artificial infestation of maize with *Striga asiatica* (B) in the greenhouse conditions at the University of KwaZulu-Natal, South Africa. Note: red flower plants are *Striga asiatica* (photo B) infesting maize.

**Figure 4.2:** Photographs showing the experimental setup with artificial infestation of maize with *Striga hermonthica* (purple flowers) in the greenhouse condition at the University of KwaZulu-Natal, South Africa. Note: purple flower plants are *Striga hermonthica* infesting maize.


**Figure 4.3** Photographs showing the experimental setup at the Ukulinga research farm of the University of KwaZulu-Natal, South Africa, in *Striga*-infested (A and B) and *Striga*-free conditions (C).

### 4.2.5 Data analysis

#### 4.2.5.1 *Analysis of variance (ANOVA), genotype performances and heritability estimates*

A separate analysis of variance was performed per test conditions using the R software version 4.4.1 (R Core Team, 2024) using the lattice procedure. This was followed by a combined analysis of variance across the two study sites for the 12 parents and 30 $F_1$ crosses after testing for homogeneity of variance with Bartlet's test. The test genotypes were compared based on mean values of the assessed traits using Fisher`s Protected Least Significant Difference at a 5% probability level.

Broad-sense heritability ($H^2$) and narrow-sense heritability ($h^2$) for the assessed traits were computed using the Analysis of Genetic Designs with R (AGD-R) version 5.0 (Rodríguez et al., 2015) using the following formula: $H^2$ (bs) = VG⁄VP and $h^2$ (ns) = VA⁄VP, where VG is the genetic variance, VA is the additive genetic variance, and VP is the total phenotypic variance.

4.2.5.2 ***Estimation of general and specific combining ability effects and heterosis***

Genetic analysis for a line-by-tester mating design was computed separately for each test condition using R software version 4.4.1 (R Core Team, 2024). The GCA and SCA were estimated using the general linear modal Yijk = μ + rk + gi + gj + sij + Ɛijk, where Yijk is the observed performance of the cross between the ith line and jth tester; μ is the overall trial mean; rk is the effect of replicate k; gi general combining ability of the $i^{th}$ line; gj is the general combining ability of the $j^{th}$ tester; sij is the specific combining ability of the cross between line i and tester j, and εijk is the residual.

The ratio of the GCA and the SCA effects was determined using the general prediction ratio (GPR) according to Baker (1978) using the following formula:

GCA⁄SCA = 2MSGCA⁄(2MSGCA + MSSCA), where MSGCA and MSSCA are the mean squares of GCA and SCA effects, respectively.

A Bakers' ratio close to 1.00 indicates that the GCA effects were more important in conditioning the heritability of that trait, whereas a ratio close to zero would indicate that SCA effects would be more important in controlling trait heritability.

Standard heterosis was calculated according to (Falconer, 1981), using the following formula:

Standard heterosis (%) = $[(F_1 – CV) / CV] \times 100$

Where $F_1$ and CV represented the mean performance of hybrid and commercial check variety (CV).

## 4.3 **Results**

### 4.3.1 Analysis of variance

The combined ANOVA and significant tests for grain yield and *Striga*-resistant traits for parental lines and $F_1$ hybrids in *Sa*, *Sh* and *Striga*-free environments across the two locations are presented in Table 4.2. Highly significant differences ($P<0.01$) were observed in all the evaluated traits among the test genotypes and across locations in *Sa*-infested environments. The mean squares due to genotype by location were significant only for DA, DS, SDR8, and GY in *Sa* infested environment. In *Sh* infested environment, significant differences ($P<0.05$) were recorded for all traits except for SEC8 and SEC10, while the location effect was significant for all the evaluated traits. The mean square due to genotype by location interaction effect was significant for DA, DS, ASI, SDR8, PLHT, and CL.

In *Striga*-free environment, the mean squares due to genotype, location, and genotype by location interaction effect were significant for all the studied traits except genotype by location interaction effects for CL.

**Table 4.2** Mean squares and significant tests from a combined analysis of variance of 12 maize parental lines and 30 F1 hybrids evaluated in *S. asiatica*, *S. hermonthica*, and *Striga* free environments for yield components and *Striga*-resistant traits.

| ***S. asiatica*** | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Source of variation** | **Df** | **DA** | **DS** | **ASI** | **SEC8** | **SEC10** | **SDR8** | **SDR10** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** |
| Genotype (G) | 41 | 79.70*** | 66.90*** | 26.21* | 8.92** | 45.03* | 5.12** | 9.64** | 0.19* | 0.07*** | 7.25* | 23.31*** | 3665.4*** |
| Location (L) | 1 | 15486.70*** | 10880.40*** | 405.48*** | 509.26*** | 1105.72*** | 4.34 | 330.12*** | 9.85*** | 2.47*** | 408.60*** | 429.12*** | 11128** |
| G x L | 41 | 27.00** | 34.50* | 21.20 | 12.64 | 49.22 | 4.53* | 6.45 | 0.09 | 0.03 | 5.21 | 5.48 | 2076.7** |
| Block/(Replication x L) | 6 | 26.40 | 32.40 | 9.40 | 30.11* | 97.25 | 5.69* | 13.22* | 0.39* | 0.09** | 9.06* | 3.05 | 995.80 |
| Residual | 70 | 14.30 | 24.00 | 15.85 | 14.85 | 56.58 | 2.64 | 4.68 | 0.12 | 0.03 | 4.45 | 4.42 | 1182.40 |
| ***S. hermonthica*** | | | | | | | | | | | | | |
| **Source of variation** | **Df** | **DA** | **DS** | **ASI** | **SEC8** | **SEC10** | **SDR8** | **SDR10** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** |
| Genotype (G) | 41 | 80.60*** | 73.40*** | 24.29* | 51.03 | 91.04 | 5.07** | 8.00** | 0.33*** | 0.12*** | 8.63** | 19.27*** | 4337.10*** |
| Location (L) | 1 | 16740.10*** | 11188.30*** | 557.36*** | 896.10*** | 1162.88*** | 35.29*** | 490.29*** | 10.9*** | 2.69*** | 271.32*** | 174.67*** | 80.50 |
| G x L | 41 | 32.20*** | 38.20* | 43.13*** | 39.81 | 90.62 | 4.65* | 5.82 | 0.14* | 0.04 | 5.02 | 12.17* | 2364.10 |
| Block/(Replication x L) | 6 | 26.20* | 52.10* | 17.34 | 175.42** | 223.01* | 2.48 | 7.80 | 0.15 | 0.05 | 14.84** | 11.31 | 5182.50** |
| Residual | 70 | 10.30 | 21.30 | 15.62 | 43.26 | 90.91 | 2.51 | 4.20 | 0.10 | 0.04 | 3.99 | 7.76 | 1659.30 |
| ***Striga* free environment** | | | | | | | | | | | | | |
| **Source of variation** | **Df** | **DA** | **DS** | **ASI** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** | | | | |
| Genotype (G) | 41 | 63.30*** | 64.20*** | 15.21*** | 0.30*** | 0.07*** | 12.38*** | 18.59*** | 8473.00*** | | | | |
| Location (L) | 1 | 14025.10*** | 13038.10*** | 18.01* | 29.67*** | 5.57*** | 2.26 | 23.48 | 146645.00*** | | | | |
| G x L | 41 | 28.30*** | 29.90*** | 20.31*** | 0.16*** | 0.03** | 4.68** | 6.66 | 4755.00*** | | | | |
| Block/(Replication x L) | 6 | 17.10* | 6.80 | 33.55*** | 0.05 | 0.01 | 0.45 | 1.66 | 2877 | | | | |
| Residual | 70 | 7.90 | 7.30 | 5.96 | 0.05 | 0.02 | 2.26 | 5.14 | 1415 | | | | |

*, **, and *** denote significance at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively, Df = degrees of freedom, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

### 4.3.2 Mean performances of parental lines and F1 hybrids

The performances of the lines and testers and F1 hybrids evaluated in *Striga*-free, *Sa* and *Sh*-infested environments are presented in Appendices 4.1, 4.2, and 4.3, respectively. Table 4.3 presents the top parental lines, testers, and crosses in *Sa*, *Sh,* and *Striga*-free environments. There was marked genetic variation in agronomic performance and *Striga* resistance traits among the lines and testers. For instance, the lines CZL99017 (4.79 t/ha) and CML540 (4.61 t/ha) exhibited the highest performances in GY in *Sa* infested environment. The CML540 had notable GY in *Striga*-infested and *Striga*-free environments (Table 4.3). The same line showed the lowest mean SDR8, SDR10, and EASP in all environments compared to other lines. Tester TZISTR1015 showed the highest performance in GY (6.39 t/ha) in *Sa* infested environment (Table 4.3), which was considerably reduced by *Sh* infestation (3.23 t/ha) (Table 4.3). The same tester showed the lowest ASI under *Sh* conditions. Under the three treatments, almost all lines and testers had 1 EPP with HUSK scores equal to 1. The tallest parental line in the *Striga*-free environment was CML540, whose height was slightly influenced by *Sa* and *Sh* infestation (Table 4.3).

The mean yield of the $F_1$ hybrids ranged from 3.16 t/ha (CLHP0303 x TZDEEI50) to 11.09 t/ha (CML540 x TZISTR1248) with a mean of 7.60 t/ha under *Striga*-free conditions (Appendix 4.1). The following F1 hybrids exhibited high GY under *Striga* free conditions: CZL99017 x TZISTR1174, CML440 x TZISTR1174, CML451 x TZISTR1174, CML540 x TZISTR1174, CLHP0343 x TZISTR1174, CML539 x TZISTR1174, CZL99017 x TZDEEI50, CML440 x TZDEEI50, CML566 x TZDEEI50, CML540 x TZDEEI50, CZL99017 x TZISTR1248, CML540 x TZISTR1248, and CML539 x TZISTR1015. Most of the above genotypes exhibited relatively high PLHT and CL, with the lowest EASP.

Most of the $F_1$ hybrids outperformed their parental lines in agronomic performance and *Striga* resistance. Under *Sa* conditions, the mean yield of the parental lines was 3.54 t/ha, whereas the mean yield of the hybrids was 4.59 t/ha (Appendix 4.2). Under *Sh* conditions, the parental lines had a mean yield of 3.08 t/ha, while the hybrids had a mean yield of 4.97 t/ha (Appendix 4.3).

*Sa* infestation had impacted the performance of some hybrids, while some were affected by *Sh* infestation. The following crosses were the best yield performing under *Sa* infestation: CML451 x TZISTR1174, CML540 x TZISTR1174, CLHP0343 x TZISTR1174, CML539 x TZISTR1174, CML540 x TZDEEI50, CML440 x TZDEEI50, CZL99017 x TZISTR1248, CLHP0343 x TZISTR1248, and CML539 x TZISTR1248 (Appendix 4.2). Among these,

CML451 x TZISTR1174, CML540 x TZISTR1174, CLHP0343 x TZISTR1174, CML539 x TZISTR1174, CML540 x TZDEEI50 were consistent from *Striga* free to *Sa* environment (Appendix 4.1 and 4.2, and Table 4.3). On the other hand, CZL99017 x TZISTR1174, CML440 x TZISTR1174, CZL99017 x TZDEEI50, CML440 x TZDEEI50, CML566 x TZDEEI50, CZL99017 x TZISTR1248, CML540 x TZISTR1248, CML440 x TZISTR1248, CZL99017 x TZISTR1015, CML540 x TZISTR1015, and CLHP0343 x TZISTR1015 were higher performing in *Sh* environment (Appendix 4.3). Among them, CZL99017 x TZISTR1174, CML440 x TZISTR1174, CZL99017 x TZDEEI50, CML440 x TZDEEI50, CML566 x TZDEEI50, CZL99017 x TZISTR1248, CML540 x TZISTR1248 showed consistent performance across *Striga* free and *Sh* infested environments. None of the F1 hybrids showed high yield performance in both *Striga*-infested environments.

**Table 4.3** Mean response for 10 traits of the top two lines, a tester, and five F1 hybrids of maize evaluated in *Striga asiatica*, *S. hermonthica*, and *Striga* free-infested environments.

| Genotypes | DA | DS | ASI (days) | SEC8 | SEC10 | SDR8 | SDR10 | PLHT (cm) | EHT (cm) | EASP | CL (cm) | GY (tons/ha) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Striga asiatica*** | | | | | | | | | | | | |
| **Top lines** | | | | | | | | | | | | |
| **CZL99017** | 79.00 | 77.50 | 10.50 | 3.25 | 4.25 | 4.00 | 5.50 | 130.00 | 46.00 | 2.50 | 12.87 | 4.79 |
| **CML540** | 70.25 | 72.75 | 14.50 | 3.00 | 6.50 | 1.25 | 3.00 | 172.00 | 75.00 | 1.50 | 11.75 | 4.61 |
| **Top tester** | | | | | | | | | | | | |
| **TZISTR1015** | 82.75 | 84.00 | 13.25 | 2.00 | 2.50 | 3.75 | 7.00 | 124.00 | 70.00 | 5.50 | 6.00 | 6.39 |
| **Top $F_1$ hybrids** | | | | | | | | | | | | |
| **CML540 xTZISTR1174** | 73.00 | 72.00 | 11.00 | 1.00 | 1.50 | 1.75 | 1.75 | 191.00 | 95.00 | 1.75 | 12.25 | 7.16 |
| **CML540 x TZDEEI50** | 70.25 | 72.75 | 14.50 | 4.00 | 5.25 | 1.50 | 3.00 | 171.00 | 85.00 | 3.00 | 14.00 | 7.00 |
| **CML539 x TZISTR1174** | 76.75 | 78.00 | 13.25 | 1.75 | 3.00 | 1.25 | 2.75 | 198.00 | 122.00 | 2.75 | 16.00 | 6.33 |
| **CML539 x TZISTR1248** | 75.25 | 76.75 | 13.50 | 7.00 | 8.75 | 1.25 | 3.00 | 146.00 | 79.00 | 2.75 | 12.37 | 6.33 |
| **CLHP0343 x TZDEEI50** | 76.75 | 81.25 | 16.50 | 1.25 | 2.75 | 1.25 | 3.75 | 176.00 | 88.00 | 2.75 | 14.12 | 6.99 |
| ***Striga hermonthica*** | | | | | | | | | | | | |
| **Genotypes** | **DA** | **DS** | **ASI (days)** | **SEC8** | **SEC10** | **SDR8** | **SDR10** | **PLHT (cm)** | **EHT (cm)** | **EASP** | **CL (cm)** | **GY (tons/ha)** |
| **Top lines** | | | | | | | | | | | | |
| **CML540** | 70.00 | 70.75 | 14.75 | 7.50 | 4.75 | 1.25 | 2.25 | 156.00 | 72.00 | 2.50 | 13.25 | 5.11 |
| **CML539** | 76.00 | 75.00 | 13.00 | 1.50 | 1.75 | 3.25 | 5.25 | 138.00 | 82.00 | 3.50 | 11.00 | 4.35 |
| **Top tester** | | | | | | | | | | | | |
| **TZISTR1015** | 82.25 | 76.50 | 8.25 | 0.75 | 0.75 | 4.75 | 7.25 | 128.00 | 62.00 | 3.25 | 5.75 | 3.23 |
| **Top $F_1$ hybrids** | | | | | | | | | | | | |
| **CML440 x TZDEEI50** | 70.50 | 70.00 | 13.50 | 1.50 | 4.00 | 1.25 | 1.75 | 152.00 | 88.00 | 1.75 | 13.62 | 9.30 |
| **CZL99017 x TZDEEI50** | 70.00 | 72.00 | 16.00 | 5.50 | 4.50 | 1.25 | 2.25 | 183.00 | 85.00 | 1.75 | 12.25 | 7.46 |
| **CML540 x TZISTR1015** | 76.50 | 76.50 | 14.00 | 0.75 | 2.00 | 1.75 | 3.25 | 164.00 | 86.00 | 2.75 | 11.12 | 7.25 |
| **CZL99017 x TZISTR1248** | 70.00 | 70.00 | 14.00 | 8.75 | 5.25 | 1.00 | 1.50 | 161.00 | 78.00 | 1.50 | 13.12 | 7.20 |
| **CML540 x TZISTR1248** | 72.00 | 70.50 | 12.50 | 1.00 | 2.25 | 1.25 | 1.00 | 143.00 | 74.00 | 2.50 | 12.87 | 6.72 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, cm= centimetre, ha= hectare.

**Table 4.3** (continued)

| ***Striga*-free environment** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Genotypes** | **DA** | **DS** | **ASI (days)** | **PLHT (cm)** | **EHT (cm)** | **EASP** | **CL (cm)** | **GY (tons/ha)** |
| **Top lines** | | | | | | | | |
| **CML540** | 73.75 | 72.75 | 10.00 | 190.00 | 106.00 | 1.00 | 12.37 | 6.96 |
| **CML539** | 79.75 | 77.00 | 8.25 | 168.00 | 94.00 | 2.25 | 13.50 | 5.58 |
| **Top tester** | | | | | | | | |
| **TZISTR1174** | 80.25 | 80.00 | 10.75 | 135.00 | 80.00 | 1.50 | 10.12 | 5.21 |
| **Top F1 hybrids** | | | | | | | | |
| **CML540 x TZISTR1248** | 77.00 | 73.75 | 7.75 | 177.00 | 89.00 | 1.00 | 14.87 | 11.09 |
| **CML539 x TZISTR1174** | 76.75 | 78.50 | 12.75 | 202.00 | 105.00 | 1.00 | 15.87 | 10.35 |
| **CML440 x TZISTR1174** | 72.50 | 76.25 | 14.75 | 208.00 | 95.00 | 1.50 | 15.12 | 10.11 |
| **CZL99017 x TZISTR1248** | 70.25 | 70.25 | 11.00 | 184.00 | 87.00 | 1.00 | 15.25 | 10.09 |
| **CML540 x TZDEEI50** | 72.00 | 73.75 | 12.75 | 193.00 | 97.00 | 1.00 | 16.25 | 9.85 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, cm= centimetre, ha= hectare.

### 4.3.3 Combining ability for agronomic and *Striga* resistance parameters

Combined analysis of variance revealed significant ($p<0.05$) differences among lines, testers, and crosses for most of the studied traits in both *Striga*-free and *Striga*-infested environments (Table 4.4). In both *Sa* and *Sh* environments, the effect of parents was significant for all the studied traits except for SEC10 in the *Sa* environment, and SEC8, PLHT, and EHT in *Sh* environment (Table 4.4). The mean squares due to crosses were significantly ($P<0.05$) different in the two *Striga*-infested environments for all the traits except for EHT. The mean squares due to parents vs crosses were highly significant for all the studied traits in the two *Striga*-infested environments except for ASI and SEC8 in *Sa* infested environment, and DS in *Sh* environment. The effects of lines were significant for all the traits in the two *Striga*-infested environments except for SDR8, PLHT, and EHT in *Sa*-infested environments. In contrast, significant effects due to testers were recorded for all the traits except for SDR8 and EHT in *Sh* infested environment. Significant line-by-tester interaction effect was recorded for all the traits except for SDR8, PLHT, and EHT in *Sa* infested environment and DA in *Sh* infested environment.

In *Striga*-free environment, the effect due to parents was significant for all the studied traits except for PLHT, whereas the effect due to crosses was significant for DA, ASI, CL, and GY (Table 4.4). The mean squares due to parents vs crosses revealed significant differences for all the traits except for ASI. Line effects were significant for DA, DS, ASI, CL, and GY, while tester effects were significant for ASI, CL, and GY. In both *Striga*-infested and *Striga*-free environments, the GCA/SCA ratio was less than 1.00, ranging from 0.39 to 0.92 (Table 4.4).

In *Sa* infested environment, all the traits showed broad-sense heritability higher than 0.50 except for SEC10 (0.39) and SDR8 (0.25) (Table 4.4). Highest $H^2$ values were recorded for DA (0.85), DS (0.76), CL (0.90), and GY (0.76). Moderate narrow sense heritability ($h^2$) (<0.5) values were recorded for all the traits except for DA (0.66) and DS (0.51), which showed relatively high $h^2$. In *Sh* infested environment, high $H^2$ (>0.5) values were recorded for all the assessed traits except for SEC8 and SEC10. The $h^2$ values were relatively moderate for all traits, ranging from 0.10 (SDR10) to 0.45 (SDR8 and EASP). In *Striga*-free environment, high $H^2$ values ranging from 0.55 to 0.75 were recorded for all the traits except for ASI with $H^2$= 0.31 (Table 4.4). The same trait exhibited the lowest narrow-sense heritability ($h^2$=0.13), while the rest of the traits showed moderate $h^2$ ranging from 0.41 to 0.69.

**Table 4.4** Mean squares and significant tests for lines, testers, and crosses of maize in *Striga asiatica*, *S. hermonthica* and *Striga*-free environments

| Source of variation | Df | DA | DS | ASI | SEC8 | SEC10 | SDR8 | SDR10 | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Striga asiatica*** | | | | | | | | | | | | | |
| **Replication** | 1 | 22.15 | 27.52 | 146.72*** | 136.62*** | 47.15** | 4.34* | 4.83 | 0.55** | 0.16 | 10.50** | 5.91 | 51.81 |
| **Treatments** | 41 | 79.73** | 66.92* | 94.9*** | 8.92* | 45.03* | 5.12* | 9.64** | 0.19** | 0.07 | 7.25* | 23.31** | 3665.41*** |
| **Parents (P)** | 11 | 85.93*** | 74.65** | 90.61*** | 5.54* | 25.02 | 7.96* | 6.75** | 0.18** | 0.06 | 9.61* | 17.89** | 3122.19** |
| **Crosses (Cr)** | 29 | 66.16** | 63.86* | 98.6*** | 10.43* | 53.96** | 2.55 | 6.59* | 0.15* | 0.07 | 6.34* | 23.19** | 3589.29*** |
| **P vs Cr** | 1 | 405.13*** | 70.44** | 34.57 | 2.63 | 6.31 | 48.35*** | 129.81*** | 1.36* | 0.42** | 7.80* | 86.41*** | 11848.20** |
| **Line (L)** | 7 | 171.05*** | 152.79*** | 197.82* | 10.83* | 43.45** | 2.50 | 6.48* | 0.23 | 0.06 | 7.66* | 25.19*** | 5431.33*** |
| **Tester (T)** | 3 | 126.48*** | 101.44*** | 153.64*** | 26.3** | 40.07* | 5.68* | 9.30*** | 0.51*** | 0.24** | 5.99*** | 76.12*** | 4238.74*** |
| **L x T** | 19 | 17.99** | 25.16** | 53.36** | 7.77* | 60.02*** | 2.08 | 6.21** | 0.06 | 0.04 | 5.92* | 14.10* | 2808.10** |
| **Error** | 125 | 85.93 | 118.63 | 149.37 | 20.42 | 65.95 | 3.34 | 9.04 | 0.21 | 0.05 | 8.13 | 8.42 | 1722.68 |
| **Trial statistics** | | | | | | | | | | | | | |
| **SE gca(L)** | | 0.39 | 0.39 | 0.14 | 0.16 | 0.29 | 0.64 | 0.16 | 0.16 | 0.08 | 0.10 | 1.00 | 1.67 |
| **SEgca(T)** | | 0.28 | 0.27 | 0.10 | 0.11 | 0.20 | 0.65 | 0.71 | 0.11 | 0.05 | 0.71 | 0.72 | 1.37 |
| **SEgca(LxT)** | | 0.11 | 0.11 | 0.38 | 0.45 | 0.81 | 0.18 | 0.30 | 0.46 | 0.23 | 2.85 | 0.29 | 4.15 |
| **SE(sca)** | | 0.80 | 0.78 | 0.27 | 0.32 | 0.57 | 0.12 | 0.21 | 0.03 | 0.16 | 2.00 | 0.25 | 29.34 |
| **$H^2$** | | 0.85 | 0.76 | 0.45 | 0.56 | 0.39 | 0.25 | 0.56 | 0.59 | 0.66 | 0.61 | 0.90 | 0.76 |
| **$h^2$** | | 0.66 | 0.51 | 0.18 | 0.28 | 0.20 | 0.25 | 0.24 | 0.31 | 0.33 | 0.02 | 0.25 | 0.15 |
| **GCA/SCA** | | 0.61 | 0.63 | 0.69 | 0.79 | 0.81 | 0.39 | 0.66 | 0.63 | 0.70 | 0.57 | 0.72 | 0.70 |
| ***Striga hermonthica*** | | | | | | | | | | | | | |
| **Source of variation** | **Df** | **DA** | **DS** | **ASI** | **SEC8** | **SEC10** | **SDR8** | **SDR10** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** |
| **Replication** | 1 | 30.01 | 0.48 | 22.88* | 126.88*** | 0.86 | 0.15 | 3.72 | 0.08 | 0.14** | 0.93 | 6.76 | 865.41 |
| **Treatments** | 41 | 80.58** | 73.4** | 24.29** | 51.03* | 91.04*** | 5.07* | 8.00*** | 0.33* | 0.12** | 8.63*** | 19.26* | 4337.08*** |
| **Parents (P)** | 11 | 85.79** | 70.14** | 19.29** | 19.19 | 31.66** | 5.49* | 6.07* | 0.10 | 0.05 | 9.52** | 19.46** | 1714.69* |
| **Crosses (Cr)** | 29 | 72.25* | 76.57*** | 21.95* | 62.14** | 116.19*** | 4.39* | 6.71* | 0.29* | 0.10 | 7.54** | 17.39* | 3999.46** |
| **P vs Cr** | 1 | 264.81*** | 17.20 | 147.03*** | 79.3*** | 14.67* | 20.15*** | 66.80*** | 4.16*** | 1.34*** | 30.54*** | 71.42*** | 42974.59*** |

*, **, and *** denote significance at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively, Df = degrees of freedom, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield. $H^2$ = broad sense heritability, $h^2$= narrow sense heritability, SE = standard error of the mean difference, GCA (gca)= general combining ability, SCA (sca)= specific combining ability.

**Table 4.4** (continued)

| Source of variation | Df | DA | DS | ASI | SEC8 | SEC10 | SDR8 | SDR10 | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Line (L)** | 7 | 83.95** | 145.10*** | 33.80** | 51.10*** | 72.94* | 4.05*** | 9.94** | 0.45 | 0.19* | 15.37* | 21.95** | 6876.18*** |
| **Tester (T)** | 3 | 126.34*** | 85.72** | 27.43*** | 63.10** | 70.35* | 1.06 | 4.11** | 0.78*** | 0.11 | 4.45* | 27.00** | 1751.93* |
| **L x T** | 19 | 59.40** | 49.88 | 16.72*** | 66.06** | 139.37*** | 5.03** | 5.93** | 0.15* | 0.06 | 5.14** | 14.20*** | 3294.49** |
| **Error** | 125 | 152.57 | 118.54 | 29.17 | 63.11 | 112.13 | 3.50 | 9.15 | 0.21 | 0.07 | 7.75 | 11.50 | 2141.41* |
| **Trial statistics** | | | | | | | | | | | | | |
| **SEgca(L)** | | 4.36 | 3.08 | 0.19 | 0.28 | 3.75 | 0.66 | 1.06 | 0.16 | 0.09 | 0.98 | 1.19 | 1.6 |
| **SEgca(T)** | | 3.08 | 0.27 | 1.35 | 1.98 | 0.26 | 0.46 | 0.75 | 0.11 | 0.06 | 0.69 | 0.84 | 1.1 |
| **SEgca(LxT)** | | 1.35 | 0.10 | 0.54 | 0.74 | 0.10 | 0.19 | 3.06 | 0.45 | 0.25 | 0.28 | 3.39 | 3.22 |
| **SE(sca)** | | 0.87 | 0.79 | 3.81 | 0.56 | 0.74 | 0.13 | 0.21 | 0.03 | 0.18 | 0.19 | 2.40 | 2.30 |
| **$H^2$** | | 0.93 | 0.69 | 0.8 | 0.28 | 0.40 | 0.75 | 0.60 | 0.72 | 0.63 | 0.47 | 0.66 | 0.68 |
| **$h^2$** | | 0.11 | 0.25 | 0.15 | 0.40 | 0.32 | 0.45 | 0.10 | 0.36 | 0.44 | 0.45 | 0.29 | 0.15 |
| **GCA/SCA** | | 0.70 | 0.65 | 0.64 | 0.38 | 0.35 | 0.71 | 0.64 | 0.41 | 0.50 | 0.72 | 0.69 | 0.46 |
| ***Striga* free environment** | | | | | | | | | | | | | |
| **Source of variation** | **Df** | **DA** | **DS** | **ASI** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** | | | | |
| **Replication** | 1 | 37.15 | 94.50*** | 3.72 | 0.01 | 0.00 | 0.01 | 14.18* | 15.79 | | | | |
| **Treatments** | 41 | 63.32** | 64.19* | 18.00 | 0.30 | 0.07 | 12.38*** | 18.59*** | 8473.22*** | | | | |
| **Parents (P)** | 11 | 51.93*** | 81.56*** | 21.16*** | 0.22 | 0.09** | 22.11*** | 13.92* | 3724.37* | | | | |
| **Crosses (Cr)** | 29 | 50.87*** | 47.20 | 17.12** | 0.09 | 0.04 | 3.90 | 13.00** | 5289.16** | | | | |
| **P vs Cr** | 1 | 549.71*** | 365.87*** | 9.01 | 7.24*** | 0.76*** | 151.20*** | 232.07*** | 153048.35*** | | | | |
| **Line (L)** | 7 | 169.17** | 139.04*** | 15.32* | 0.04 | 0.06 | 3.14 | 21.44** | 11368.08*** | | | | |
| **Tester (T)** | 3 | 7.04 | 21.10 | 79.99*** | 0.07 | 0.04 | 7.45 | 18.84** | 3214.99* | | | | |
| **L x T** | 19 | 14.21 | 17.48 | 7.85 | 0.11 | 0.03 | 3.62 | 8.97 | 3377.06* | | | | |
| **Error** | 125 | 127.63 | 120.20 | 14.75 | 0.33 | 0.07 | 2.89 | 5.88 | 3753.42 | | | | |
| **Trial statistics** | | | | | | | | | | | | | |
| **SEgca(L)** | | 3.99 | 3.87 | 1.35 | 0.20 | 0.09 | 0.60 | 0.85 | 21.66 | | | | |
| **SEgca(T)** | | 0.28 | 2.74 | 0.96 | 0.14 | 0.06 | 0.42 | 0.60 | 15.31 | | | | |
| **SEgca(LxT)** | | 1.19 | 1.96 | 0.34 | 0.57 | 0.25 | 1.70 | 2.42 | 61.26 | | | | |
| **SE(sca)** | | 0.79 | 0.77 | 0.271 | 0.04 | 0.02 | 1.20 | 0.27 | 0.43 | | | | |
| **$H^2$** | | 0.64 | 0.70 | 0.31 | 0.61 | 0.75 | 0.55 | 0.68 | 0.57 | | | | |
| **$h^2$** | | 0.53 | 0.45 | 0.13 | 0.53 | 0.69 | 0.45 | 0.50 | 0.41 | | | | |
| **GCA/SCA** | | 0.67 | 0.78 | 0.71 | 0.83 | 0.82 | 0.92 | 0.68 | 0.58 | | | | |

*, **, and *** denote significance at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively, Df = degrees of freedom, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield. $H^2$ = broad sense heritability, $h^2$= narrow sense heritability, SE = standard error of the mean difference, GCA (gca)= general combining ability, SCA (sca)= specific combining ability.

#### 4.3.3.1 **General combining ability effects**

Table 4.5 presents the general combining ability of the lines and testers evaluated in *Sa*, *Sh*, and *Striga*-free environments. Some lines and testers exhibited significant GCA effects in the desirable direction for studied traits. In *Sa* environment, lines CML540, CLHP0343, and tester TZISTR1248 exhibited a positive and significant GCA for GY. CML 540 recorded a negative and significant GCA for ASI and all the *Striga* parameters in the desirable direction, while CLHP0343 had good and significant scores for ASI, SEC8, and CL. The tester TZISTR1248 also showed a significant GCA effect for ASI, SDR8, and CL.

In *Sh* infested environment, lines CZL99017, CML566, CML540, CLHP0343, and tester TZISTR1174 showed highly positive and significant GCA for GY (Table 4.5). Negative and significant GCA effects for ASI, SDR8, SDR10, and EASP were recorded for CML540 in the desirable direction, whereas CZL99017 recorded negative and significant scores for SDR8, SDR10, and EASP in the desirable direction.

**Table 4.5** General combining ability effects of maize eight lines and four testers of maize evaluated in *Striga asiatica*, *S. hermonthica*, and *Striga*-free environments.

| **Genotypes** | **DA** | **DS** | **ASI** | **SEC8** | **SEC10** | **SDR8** | **SDR10** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Striga asiatica*** | | | | | | | | | | | | |
| CLHP0303 | 1.96*** | 4.89*** | 2.98**** | -0.39ns | -1.91* | 0.50*** | 0.32* | 0.29ns | 0.29ns | 1.15ns | -0.28ns | -30.56*** |
| CZL99017 | -3.04*** | -0.23*** | -1.83*** | 0.36ns | -1.60ns | 0.06*** | 0.32ns | 0.04ns | 0.04ns | 0.06ns | 0.51ns | -0.16ns |
| CML440 | -1.42*** | -2.80*** | -1.08* | -0.20ns | 1.72* | 0.56*** | 0.73** | -0.20ns | -0.20ns | -0.6ns | -0.09ns | 0.81ns |
| CML451 | -2.17*** | -0.92*** | -1.7*** | 1.23* | -0.78ns | -0.25*** | 0.01ns | -0.04ns | -0.04ns | -0.35ns | 0.23ns | 3.22ns |
| CML566 | 5.96*** | 3.64*** | 5.98*** | -0.14ns | 2.34** | 0.44*** | 0.57* | -0.01ns | -0.01ns | 1.28ns | -2.49*** | -30.13*** |
| CML540 | -3.67*** | -5.11*** | -5.83*** | -0.70ns | -0.72*** | -0.38*** | -1.30* | 0.08ns | 0.08ns | -0.22ns | 0.07ns | 13.22*** |
| CLHP0343 | 2.77*** | 2.58*** | 0.98* | -1.27*** | -1.60ns | -0.25*** | -0.18ns | 0.04ns | 0.04ns | -0.72ns | 2.10*** | 28.56*** |
| CML539 | 0.58*** | 0.39*** | 1.98*** | 0.92* | 1.59ns | -0.44*** | -0.30* | -0.06ns | -0.06ns | -0.03ns | -0.18ns | -0.25ns |
| TZISTR1174 | 0.86*** | 2.11*** | 0.92* | -0.30* | -1.19ns | 0.41*** | 0.56* | 0.18ns | 0.18ns | 0.14ns | 0.69* | 2.48ns |
| TZDEEI50 | -2.19*** | -1.30*** | -1.7*** | 0.55ns | -0.41ns | -0.5*** | -0.71** | 0.05ns | 0.05ns | 0.15ns | 0.35ns | 4.34ns |
| TZISTR1248 | -0.81*** | -1.91*** | -1.87*** | 0.93ns | 0.04ns | -0.18*** | -0.04ns | -0.14ns | -0.14ns | -0.72ns | 1.22*** | 8.43* |
| TZISTR1015 | 2.33*** | 0.98*** | 2.77*** | -1.21* | 1.79* | 0.29*** | 0.21ns | -0.11ns | -0.11ns | 0.39ns | -2.41*** | -16.23*** |
| ***Striga hermonthica*** | | | | | | | | | | | | |
| Genotypes | DA | DS | ASI | SEC8 | SEC10 | SDR8 | SDR10 | PLHT | EHT | EASP | CL | GY |
| CLHP0303 | 2.01ns | 4.96*** | 2.95*** | -3.08*** | -2.80** | 0.23ns | -0.38* | 0.47ns | 0.32ns | -1.28*** | 1.70ns | -16.06* |
| CZL99017 | -4.24*** | -4.54*** | -0.30ns | 1.60* | -0.05ns | -0.78*** | -1.13*** | 0.08ns | 0.03ns | -1.59*** | 1.33ns | 30.00** |
| CML440 | -0.12ns | -0.73*** | -0.61ns | -0.21ns | 3.89*** | 0.48** | 0.19ns | -0.24ns | -0.12ns | 0.10ns | -0.95ns | -44.00*** |
| CML451 | -1.30ns | 0.52ns | 1.83*** | 0.60ns | -2.80** | 0.73*** | 1.13*** | -0.12ns | -0.10ns | 1.35*** | -1.60ns | 18.00* |
| CML566 | 3.01* | 3.58*** | 0.58ns | -0.27ns | 0.39ns | -0.15ns | 0.44* | 0.09ns | 0.07ns | 0.79** | -1.24ns | 888.00*** |
| CML540 | -1.18ns | -3.67*** | -2.49*** | 2.92*** | 1.08ns | -0.59** | -1.13*** | 0.03ns | -0.04ns | -0.78** | 0.70ns | 26.00** |
| CLHP0343 | 0.88ns | 0.58ns | -0.3ns | -2.33*** | -1.80ns | 0.16ns | 0.25ns | -0.04ns | 0.03ns | 0.23ns | 0.95ns | 706*** |
| CML539 | 1.95ns | 1.77** | -0.18ns | -0.77ns | 0.70ns | 0.04ns | 0.44* | -0.04ns | -0.03ns | 0.54ns | -0.05ns | -19.74* |
| TZISTR1174 | 1.01ns | 1.93** | 0.92ns | 1.20ns | -0.52ns | -0.12ns | 0.41* | 0.22ns | 0.07ns | -0.49ns | 1.30ns | 20.23*** |
| TZDEEI50 | -2.59* | -1.64** | 0.95ns | 0.57ns | 0.45ns | -0.09ns | -0.47* | 0.08ns | 0.06ns | -0.21ns | 0.06ns | -7.43ns |

*, **, and *** denote significance at P < 0.05, P < 0.01 and P < 0.001, respectively, ns= non-significant, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

**Table 4.5 (continued)**

| Genotypes | DA | DS | ASI | SEC8 | SEC10 | SDR8 | SDR10 | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TZISTR1248 | -0.05ns | -1.11* | -1.07* | -1.49* | -1.82ns | 0.26ns | 0.00ns | -0.19ns | -0.10ns | 0.55ns | -0.41ns | -7.27ns |
| TZISTR10151 | .85ns | 0.78*** | -1.07* | -0.53ns | 1.90ns | -0.03ns | 0.07ns | -0.15ns | -0.04ns | 0.26ns | -1.16ns | -6.25ns |
| ***Striga* free environment** | | | | | | | | | | | | |
| **Genotypes** | **DA** | **DS** | **ASI** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** | | | | |
| CLHP0303 | 3.15*** | 3.60** | 0.72** | 0.11*** | 0.20ns | 0.99*** | -2.50*** | | | | | |
| CZL99017 | -5.04*** | -4.15** | 1.03** | 0.05ns | -0.06ns | -0.50** | 1.25*** | | | | | |
| CML440 | -4.16*** | -3.34** | 0.97** | 0.00ns | -0.04ns | 0.00ns | 0.16ns | | | | | |
| CML451 | 0.59ns | 1.41ns | 0.97** | -0.04ns | -0.02ns | 0.47** | -0.44ns | | | | | |
| CML566 | 3.90*** | 2.66* | -1.10** | 0.01ns | 0.02ns | 0.12ns | -1.08** | | | | | |
| CML540 | -1.16ns | -2.71* | -1.41** | -0.05ns | 0.02ns | -0.57** | 0.91* | | | | | |
| CLHP0343 | 1.84ns | 1.85ns | -0.41ns | -0.07ns | -0.03ns | -0.19ns | 1.32*** | | | | | |
| CML539 | 2.46* | 2.48* | -0.41ns | 0.03ns | 0.01ns | 0.18ns | -0.87* | | | | | |
| TZISTR1174 | 0.10ns | 1.23ns | 1.59*** | 0.05ns | 0.05ns | -0.16ns | 0.61ns | | | | | |
| TZDEEI50 | -0.26ns | 0.38ns | 0.90** | -0.01ns | 0.01ns | 0.76ns | -0.42ns | | | | | |
| TZISTR1248 | 0.15ns | -0.69ns | -0.82** | -0.07ns | -0.06ns | -0.25ns | 0.62ns | | | | | |
| TZISTR10150 | .26ns | -1.15ns | -2.03*** | 0.02ns | 0.00ns | -0.43ns | -0.85* | | | | | |

*, **, and *** denote significance at P < 0.05, P < 0.01 and P < 0.001, respectively, ns= non-significant, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

**Table 4.6** Specific combining ability of 30 maize crosses for agronomic and *Striga* resistance traits evaluated in *Striga asiatica*, *S. hermonthica*, and *Striga*-free environments.

| Genotypes | DA | DS | ASI | SEC8 | SEC10 | SDR8 | SDR10 | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Striga asiatica*** | | | | | | | | | | | | |
| CML451 x TZISTR1174 | -2.62** | -2.42*** | 1.52* | 0.92** | 3.94*** | -0.66*** | -1.24*** | -0.19*** | -0.17ns | -0.26*** | 0.99ns | 39.80*** |
| CML566 x TZISTR1174 | 1.26ns | 1.52ns | -2.67** | -0.20ns | -4.19*** | 1.16*** | 1.20*** | 0.00ns | -0.01ns | 1.86ns | -3.29*** | -43.11*** |
| CML540 xTZISTR1174 | -0.37ns | -3.49*** | -4.11*** | -0.39ns | -0.62ns | -0.28* | -1.18*** | 0.03ns | 0.00ns | -1.64ns | -0.10ns | 13.55*** |

*, **, and *** denote significance at P < 0.05, P < 0.01 and P < 0.001, respectively, ns= non-significant, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

**Tabe 4.6** (continued)

| Genotypes | DA | DS | ASI | SEC8 | SEC10 | SDR8 | SDR10 | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CLHP0303 x TZISTR1174 | 2.01** | 2.02** | 4.08*** | -0.20ns | 2.07*** | 0.84*** | 1.70*** | -0.16*** | -0.07ns | -1.51ns | -0.26ns | -10.17*** |
| CZL99017 x TZISTR1174 | -0.49ns | 3.39*** | 3.89*** | -0.70** | 0.50ns | -0.97*** | -0.31ns | -0.09ns | -0.03ns | 0.46*** | 0.21ns | -1.83ns |
| CML440 x TZISTR1174 | 0.89ns | 1.20ns | -0.86ns | 0.86** | -2.06*** | 0.53*** | 0.41ns | -0.10** | -0.10ns | 1.99ns | -2.19*** | -15.42*** |
| CLHP0343 x TZISTR1174 | -0.80ns | -1.67* | 1.08ns | 1.17*** | 2.75*** | -0.16ns | 0.45ns | 0.10** | 0.15* | -0.64*** | 0.87ns | 0.95ns |
| CML539 x TZISTR1174 | -0.87ns | -2.99*** | -4.42*** | -1.27*** | -1.44* | -0.72*** | -1.18*** | 0.25*** | 0.21* | -0.83** | 3.90*** | 31.52*** |
| CLHP0303 x TZDEEI50 | -0.68ns | -2.83*** | -3.30*** | -0.05ns | -0.47ns | -0.75*** | -1.54*** | -0.07ns | -0.05ns | 1.22ns | -0.79ns | 3.34ns |
| CZL99017 x TZDEEI50 | 3.82*** | -0.45ns | 0.27ns | 2.20*** | 0.72ns | 0.69*** | 0.21ns | 0.01ns | 0.00ns | 0.82** | -2.19*** | -34.69*** |
| CML440 x TZDEEI50 | -0.30ns | -0.64ns | -4.23*** | -1.48*** | -3.59*** | -0.81*** | -2.20*** | -0.01ns | 0.06ns | -0.78** | 2.28*** | 19.34*** |
| CML451 x TZDEEI50 | -0.80ns | -1.52*** | -1.61ns | -1.92*** | -0.09ns | 0.50*** | -0.23ns | 0.12** | 0.04ns | -0.53*** | 0.46ns | -5.81ns |
| CML566 x TZDEEI50 | -1.43ns | 0.17ns | 3.70*** | 0.95** | 3.53*** | -0.19ns | -0.29ns | -0.04ns | 0.01ns | -1.40ns | 0.31ns | 31.78*** |
| CML540 x TZDEEI50 | -0.05ns | 0.67ns | 3.02** | 1.77*** | 2.35*** | 0.38* | 1.34*** | -0.03ns | 0.02ns | -0.40*** | 1.99** | 17.69** |
| CLHP0343 x TZDEEI50 | 0.01ns | 1.48ns | 2.20* | -0.42ns | 0.72ns | 0.00ns | 0.96* | 0.06ns | -0.02ns | -0.15*** | 0.09ns | 13.09ns |
| CML539 x TZDEEI50 | -1.55ns | 0.67ns | -1.55* | -0.86** | -2.22*** | -0.06ns | 1.59*** | -0.19*** | -0.08ns | 0.66** | -2.01*** | -29.47*** |
| CZL99017 x TZISTR1248 | -1.82** | -2.84*** | -2.56*** | -0.68** | 0.27ns | 0.13ns | 0.54ns | 0.03ns | 0.10* | -0.56*** | 0.69ns | 18.48** |
| CML440 x TZISTR1248 | 2.06** | 2.97*** | -2.31*** | 1.13*** | -5.29*** | 0.87*** | 1.38*** | 0.04ns | -0.02ns | -0.90*** | -0.97ns | -8.12* |
| CML451 x TZISTR1248 | 3.31*** | 3.60*** | 1.31ns | -0.31ns | -2.29*** | -0.07ns | 0.60ns | 0.04ns | 0.12* | -0.15*** | -0.65ns | -18.15** |
| CML566 x TZISTR1248 | 0.94ns | -0.46ns | 2.12** | -1.18*** | 2.59*** | -0.01ns | 0.04ns | 0.16*** | -0.11* | 0.97*** | 1.44*** | -18.30** |
| CML540 x TZISTR1248 | -0.94ns | 0.54ns | 1.94* | -1.12*** | 1.40* | 0.05ns | -0.34ns | -0.13** | -0.05ns | 0.47*** | -0.87ns | -10.40* |
| CLHP0343 x TZISTR1248 | -1.88** | -1.15ns | -1.88ns | -0.81** | -0.73ns | -0.32* | -1.71*** | -0.05ns | 0.00ns | 0.72*** | 0.47ns | -4.37ns |
| CML539 x TZISTR1248 | -0.69ns | -0.21ns | 2.87*** | 2.76*** | 3.09*** | -0.13ns | -0.34ns | 0.05ns | -0.03ns | 0.03*** | -0.25ns | 25.57*** |
| CZL99017 x TZISTR1015 | -1.71** | 0.02ns | -1.71ns | -0.79** | -1.73*** | 0.40* | -0.46ns | 0.08ns | -0.06ns | -0.67*** | 1.44*** | 19.01** |
| CML440 x TZISTR1015 | 2.83*** | -3.42*** | 7.29*** | -0.47ns | 10.71*** | -0.60* | 0.38ns | 0.09ns | 0.08ns | -0.26*** | 1.03** | 5.17ns |
| CML451 x TZISTR1015 | -0.08ns | 0.46ns | -1.33ns | 1.34*** | -1.79*** | 0.21ns | 0.85* | 0.06ns | 0.04ns | 0.99* | -0.65ns | -14.86** |
| CML566 x TZISTR1015 | -0.96ns | -1.11ns | -3.27*** | 0.46ns | -2.16*** | -0.97*** | -0.96* | -0.09ns | 0.12* | -1.39ns | 1.69*** | 30.61*** |

*, **, and *** denote significance at P < 0.05, P < 0.01 and P < 0.001, respectively, ns= non-significant, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

**Table 4.6** (continued)

| Genotypes | DA | DS | ASI | SEC8 | SEC10 | SDR8 | SDR10 | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CML540 x TZISTR1015 | 1.17ns | 2.39** | -0.96ns | -0.22ns | -3.35*** | -0.16ns | 0.16ns | 0.15*** | 0.04ns | 1.61ns | -0.87ns | -19.86** |
| CLHP0343 x TZISTR1015 | 2.48*** | 1.46ns | -1.52ns | 0.09ns | -2.98*** | 0.46* | 0.29ns | -0.08ns | -0.12* | 0.11*** | -1.28*** | -8.71* |
| CML539 x TZISTR1015 | 2.92*** | 2.64*** | 2.98*** | -0.60ns | 0.34ns | 0.90*** | -0.09ns | -0.08ns | -0.08ns | 0.18*** | -1.50*** | -26.64*** |
| ***Striga hermonthica*** | | | | | | | | | | | | |
| **Genotypes** | **DA** | **DS** | **ASI** | **SEC8** | **SEC10** | **SDR8** | **SDR10** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** |
| CLHP0303 x TZISTR1174 | 0.37ns | 0.57ns | 0.21ns | -1.57** | 1.14ns | 1.12*** | 0.72** | -0.28*** | -0.23*** | -0.76** | 1.57*** | 9.71** |
| CZL99017 x TZISTR1174 | 5.62*** | 5.07*** | -0.54ns | -3.51*** | -2.36*** | 0.62** | 1.72*** | -0.13** | -0.02ns | 1.81*** | -1.43*** | -15.57*** |
| CML440 x TZISTR1174 | -3.51*** | 0.01ns | 3.52*** | -3.95*** | -6.04*** | -1.13*** | 0.16ns | 0.14** | 0.07ns | -0.13ns | 0.85* | -2.79ns |
| CML451 x TZISTR1174 | 1.43ns | -0.74ns | -2.17*** | -0.51ns | 1.89** | 0.12ns | -1.03*** | 0.04ns | -0.01ns | -1.13*** | 0.05ns | 27.56*** |
| CML566 x TZISTR1174 | -0.63ns | 0.20ns | 0.83ns | 0.12ns | -3.29*** | 0.49ns | 0.16ns | -0.21*** | -0.15** | 0.93*** | -2.74*** | -22.41*** |
| CML540 xTZISTR1174 | 3.30*** | 0.20ns | -3.11*** | 9.93*** | 5.52*** | -0.32ns | 0.22ns | -0.13** | -0.07ns | -0.26ns | -0.43ns | -12.88*** |
| CLHP0343 x TZISTR1174 | -2.51** | -3.80*** | -1.29** | -1.57** | 0.64ns | -0.32ns | -1.41*** | 0.02ns | 0.22*** | 0.49* | 0.57ns | 11.78*** |
| CML539 x TZISTR1174 | -5.07*** | -3.99*** | 1.08*** | 2.62*** | 3.89*** | -0.69ns | -0.34ns | 0.31*** | 0.04ns | -0.32* | 0.70* | 12.62*** |
| CLHP0303 x TZDEEI50 | 1.21ns | -0.87ns | -2.08*** | -0.20ns | -1.08ns | -0.91ns | -0.66** | -0.02ns | 0.11* | 1.46*** | -2.94*** | -11.68*** |
| CZL99017 x TZDEEI50 | 0.21ns | 0.14ns | -0.08ns | -0.14ns | -0.08ns | 0.09ns | 0.09ns | 0.05ns | -0.11* | 0.03ns | -0.44ns | 8.47** |
| CML440 x TZDEEI50 | -3.42*** | -5.68*** | -2.26*** | -2.32*** | -4.51*** | -1.16*** | -1.72*** | 0.06ns | 0.06ns | -1.66*** | 3.22*** | 54.13*** |
| CML451 x TZDEEI50 | 1.02ns | 1.32ns | 0.30ns | 3.12*** | -0.83ns | 0.84** | 1.84*** | -0.32*** | -0.15** | 1.09*** | -1.51*** | -14.78** |
| CML566 x TZDEEI50 | 0.46ns | -1.74* | -2.20*** | 2.99*** | 10.49*** | -0.29ns | -1.22*** | 0.21*** | 0.11* | -1.35*** | 2.88*** | 39.50*** |
| CML540 x TZDEEI50 | 0.65ns | 1.26ns | 0.61ns | -0.70ns | 0.80ns | 0.40ns | 0.84*** | 0.07ns | 0.03ns | 1.21*** | -0.94** | -24.34*** |
| CLHP0343 x TZDEEI50 | 1.09ns | 3.51*** | 2.43*** | -0.45ns | -1.83* | 0.65** | 1.47*** | -0.15** | -0.14*** | -0.29ns | -0.56ns | -29.56*** |
| CML539 x TZDEEI50 | -2.23** | -0.43ns | 1.80*** | -0.76ns | -1.58* | 0.28ns | -0.47ns | -0.14** | -0.05ns | 0.15ns | -0.56ns | -13.72** |
| CZL99017 x TZISTR1248 | -2.33** | -2.39*** | -0.06ns | 5.18*** | 2.94*** | -0.51ns | -1.13*** | 0.09ns | -0.02ns | -0.98*** | 0.91** | 8.06* |
| CML440 x TZISTR1248 | 8.80*** | 7.30*** | -1.50*** | -1.76*** | -6.25*** | 2.99*** | 1.06** | -0.2ns | -0.06ns | 1.58*** | -3.56*** | 5.22* |

*, **, and *** denote significance at P < 0.05, P < 0.01 and P < 0.001, respectively, ns= non-significant, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

**Table 4.6** (continued)

| Genotypes | DA | DS | ASI | SEC8 | SEC10 | SDR8 | SDR10 | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CML451 x TZISTR1248 | -2.52** | 0.05ns | 2.57*** | -1.07ns | 1.19ns | -1.01** | -0.63* | 0.08ns | 0.07ns | -0.67** | 2.46*** | 1.31ns |
| CML566 x TZISTR1248 | -0.08ns | 2.49*** | 2.57*** | -1.69** | -1.75** | 0.11ns | 1.31*** | 0.10** | 0.02ns | 0.89*** | -0.28ns | -16.66*** |
| CML540 x TZISTR1248 | -3.39*** | -2.76*** | 0.63ns | -3.88*** | -1.18ns | -0.45ns | -1.63*** | -0.04ns | 0.00ns | -0.80*** | 1.28*** | 8.88* |
| CLHP0343 x TZISTR1248 | 0.80ns | -0.26ns | -1.06** | 1.87*** | 3.44*** | 0.30ns | 0.75** | 0.00ns | -0.01ns | 0.20ns | 0.16ns | -23.59*** |
| CML539 x TZISTR1248 | -0.27ns | -1.95* | -1.68*** | -0.19ns | 0.19ns | -1.32*** | 0.06ns | 0.19*** | 0.16** | -0.86*** | -0.10ns | 8.75* |
| CZL99017 x TZISTR1015 | -3.72*** | -2.78** | 0.94* | -1.28* | -0.52ns | -0.23ns | -0.7ns | 0.03ns | 0.17** | -0.95*** | 1.16*** | -0.69ns |
| CML440 x TZISTR1015 | -2.10* | -1.59* | 0.51ns | 8.28*** | 16.79*** | -0.73*** | 0.49ns | 0.04ns | -0.06ns | 0.11ns | -0.31ns | -56.28*** |
| CML451 x TZISTR1015 | -0.16ns | -0.59ns | -0.43ns | -1.28* | -2.27** | 0.03ns | -0.2ns | 0.24*** | 0.12* | 0.61** | -0.80*** | -13.81** |
| CML566 x TZISTR1015 | 0.03ns | -0.91ns | -0.93* | -1.16* | -5.46*** | -0.35ns | -0.26ns | -0.05ns | 0.04ns | -0.57* | 0.34ns | -0.16ns |
| CML540 x TZISTR1015 | -0.79ns | 1.35ns | 2.13*** | -5.10*** | -5.15*** | 0.34ns | 0.55** | 0.14** | 0.06ns | -0.26ns | 0.28ns | 28.63*** |
| CLHP0343 x TZISTR1015 | 0.40ns | 0.60ns | 0.19ns | 0.41ns | -2.27** | -0.66** | -0.82*** | 0.16** | -0.05ns | -0.51* | 0.03ns | 41.66*** |
| CML539 x TZISTR1015 | 7.34*** | 6.41*** | -0.93* | -1.41* | -2.52*** | 1.71*** | 0.74** | -0.32*** | -0.12** | 0.93*** | 0.16ns | -7.38* |
| ***Striga* free environment** | | | | | | | | | | | | |
| **Genotypes** | **DA** | **DS** | **ASI** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** | | | | |
| CLHP0303 x TZISTR1174 | -1.65* | -3.23*** | -1.84*** | -0.22*** | -0.19*** | -1.34ns | -0.42ns | 8.48*** | | | | |
| CZL99017 x TZISTR1174 | 2.79*** | 4.28*** | 1.35*** | 0.10* | 0.09** | 0.16ns | -1.17*** | 0.35ns | | | | |
| CML440 x TZISTR1174 | -0.09ns | 0.96ns | 0.91ns | 0.14*** | 0.01ns | -0.09ns | 0.79* | 20.04*** | | | | |
| CML451 x TZISTR1174 | 0.16ns | -0.79ns | -1.09** | 0.08ns | 0.01ns | -1.06ns | 2.01*** | 28.73*** | | | | |
| CML566 x TZISTR1174 | -0.40ns | -1.54* | -1.28*** | -0.22*** | -0.14*** | 2.04ns | -2.22*** | -33.58*** | | | | |
| CML540 xTZISTR1174 | 0.66ns | 2.09* | 1.28*** | 0.12** | 0.04ns | 0.47ns | -0.83ns | -23.12*** | | | | |
| CLHP0343 x TZISTR1174 | -0.59ns | -0.98ns | 0.03ns | -0.10* | 0.04ns | 0.10ns | 0.51ns | -0.21ns | | | | |
| CML539 x TZISTR1174 | -2.46*** | -2.6** | 0.28ns | 0.05ns | 0.06ns | 0.78ns | 2.58*** | 31.98*** | | | | |
| CLHP0303 x TZDEEI50 | 2.01* | 1.62* | -0.65ns | 0.18*** | 0.14*** | 0.74ns | 0.23ns | -5.91** | | | | |
| CZL99017 x TZDEEI50 | 0.44ns | -1.13ns | -1.72*** | -0.17*** | -0.18*** | -0.51ns | 1.10ns | -10.66*** | | | | |
| CML440 x TZDEEI50 | -1.43ns | -2.44*** | -1.15** | -0.31*** | -0.09** | 0.99ns | -1.80*** | 3.53ns | | | | |

*, **, and *** denote significance at P < 0.05, P < 0.01 and P < 0.001, respectively, ns= non-significant, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

**Table 4.6** (continued)

| Genotypes | DA | DS | ASI | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|
| CML451 x TZDEEI50 | -0.18ns | 0.06ns | 0.10ns | -0.06ns | 0.02ns | -0.11ns | 0.17ns | -13.04*** |
| CML566 x TZDEEI50 | -1.49ns | -0.44ns | 0.91ns | -0.04ns | 0.07ns | -1.64ns | 1.84*** | 26.78*** |
| CML540 x TZDEEI50 | -3.43*** | -1.32ns | 1.97*** | 0.10* | 0.00ns | -0.95ns | 2.20*** | 31.62*** |
| CLHP0343 x TZDEEI50 | 1.07ns | 1.37ns | 0.72ns | 0.20*** | -0.02ns | 0.18ns | -0.33ns | -0.35ns |
| CML539 x TZDEEI50 | 1.44ns | 0.49ns | -0.53ns | 0.04ns | -0.04ns | 0.80ns | -2.15*** | 0.71ns |
| CML451 x TZDEEI50 | -0.18ns | 0.06ns | 0.10ns | -0.06ns | 0.02ns | -0.11ns | 0.17ns | -13.04*** |
| CML566 x TZDEEI50 | -1.49ns | -0.44ns | 0.91ns | -0.04ns | 0.07ns | -1.64ns | 1.84*** | 26.78*** |
| CML540 x TZDEEI50 | -3.43*** | -1.32ns | 1.97*** | 0.10* | 0.00ns | -0.95ns | 2.20*** | 31.62*** |
| CLHP0343 x TZDEEI50 | 1.07ns | 1.37ns | 0.72ns | 0.20*** | -0.02ns | 0.18ns | -0.33ns | -0.35ns |
| CML539 x TZDEEI50 | 1.44ns | 0.49ns | -0.53ns | 0.04ns | -0.04ns | 0.80ns | -2.15*** | 0.71ns |
| CZL99017 x TZISTR1248 | -1.82** | -2.84*** | -2.56*** | -0.68** | 0.27ns | 0.13ns | 0.54ns | 0.03ns |
| CML440 x TZISTR1248 | 2.06** | 2.97*** | -2.31*** | 1.13*** | -5.29*** | 0.87*** | 1.38*** | 0.04ns |
| CML451 x TZISTR1248 | 3.31*** | 3.60*** | 1.31ns | -0.31ns | -2.29*** | -0.07ns | 0.60ns | 0.04ns |
| CML566 x TZISTR1248 | 0.94ns | -0.46ns | 2.12** | -1.18*** | 2.59*** | -0.01ns | 0.04ns | 0.16*** |
| CML540 x TZISTR1248 | -0.94ns | 0.54ns | 1.94* | -1.12*** | 1.40* | 0.05ns | -0.34ns | -0.13** |
| CLHP0343 x TZISTR1248 | -1.88** | -1.15ns | -1.88ns | -0.81** | -0.73ns | -0.32* | -1.71*** | -0.05ns |
| CML539 x TZISTR1248 | -0.69ns | -0.21ns | 2.87*** | 2.76*** | 3.09*** | -0.13ns | -0.34ns | 0.05ns |
| CZL99017 x TZISTR1015 | -1.71** | 0.02ns | -1.71ns | -0.79** | -1.73*** | 0.40* | -0.46ns | 0.08ns |
| CML440 x TZISTR1015 | 2.83*** | -3.42*** | 7.29*** | -0.47ns | 10.71*** | -0.60* | 0.38ns | 0.09ns |
| CML451 x TZISTR1015 | -0.08ns | 0.46ns | -1.33ns | 1.34*** | -1.79*** | 0.21ns | 0.85* | 0.06ns |
| CML566 x TZISTR1015 | -0.96ns | -1.11ns | -3.27*** | 0.46ns | -2.16*** | -0.97*** | -0.96* | -0.09ns |
| CML540 x TZISTR1015 | 1.17ns | 2.39** | -0.96ns | -0.22ns | -3.35*** | -0.16ns | 0.16ns | 0.15*** |
| CLHP0343 x TZISTR1015 | 2.48*** | 1.46ns | -1.52ns | 0.09ns | -2.98*** | 0.46* | 0.29ns | -0.08ns |
| CML539 x TZISTR1015 | 2.92*** | 2.64*** | 2.98*** | -0.60ns | 0.34ns | 0.90*** | -0.09ns | -0.08ns |
| CZL99017 x TZISTR1015 | -1.71** | 0.02ns | -1.71ns | -0.79** | -1.73*** | 0.40* | -0.46ns | 0.08ns |

*, **, and *** denote significance at P < 0.05, P < 0.01 and P < 0.001, respectively, ns= non-significant, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

4.3.3.2 **Specific combining ability effects**

***Striga asiatica* environment:** The following families exhibited significant and positive SCA effect for GY: CML451 x TZISTR1174, CML540 xTZISTR1174, CML539 x TZISTR1174, CML440 x TZDEEI50, CML566 x TZDEEI50, CML540 x TZDEEI50, CZL99017 x TZISTR1248, CML539 x TZISTR1248, CZL99017 x TZISTR1015, and CML566 x TZISTR1015 (Table 4.6). Among these families, CML540 x TZISTR1174, CML539 x TZISTR1174, and CML440 x TZDEEI50 showed negative and significant SCA effects for *Striga* parameters ASI, SEC8, SEC10, SDR8, and SDR10 which is the desirable direction. Family CML451 x TZISTR1174 only had significant and negative SCA effects for SDR8 and SDR10, whereas CZL99017 x TZISTR1248 showed significant and negative SCA effects for SEC8. The family CZL99017 x TZISTR1015 showed the same trend for SEC8 and SEC10 while the same trend was observed for SDR8 for family CML566 x TZISTR1015. Only family CML539 x TZISTR1174 exhibited a positive and significant SCA effect for PLHT and EHT. Negative and significant SCA effects were recorded for EASP for the families CML451 x TZISTR1174, CML539 x TZISTR1174, CML440 x TZDEEI50, CML540 x TZDEEI50, CZL99017 x TZISTR1248, and CZL99017 x TZISTR1015. Significant SCA was observed for CL for CML539 x TZISTR1174, CML440 x TZDEEI50, CML540 x TZDEEI50, and CZL99017 x TZISTR1015 in the desirable direction.

***Striga hermonthica* environment**: Several crosses showed positive and significant SCA effects for GY: these are CLHP0303 x TZISTR1174, CML451 x TZISTR1174, CLHP0343 x TZISTR1174, CML539 x TZISTR1174, CZL99017 x TZDEEI50, CML440 x TZDEEI50, CML566 x TZDEEI50, CZL99017 x TZISTR1248, CML440 x TZISTR1248, CML540 x TZISTR1248, CML539 x TZISTR1248, CML540 x TZISTR1015, CLHP0343 x TZISTR1015, and CML539 x TZISTR1015 (Table 4.6). From this list, CML440 x TZDEEI50 showed a significant SCA effect for SEC8, SEC10, SDR8, SDR10, EASP, and CL in the desirable direction. CLHP0303 x TZISTR1174 showed significant SCA for SEC8 and SDR8 whereas CLHP0343 x TZISTR1174 showed the same trend for SEC8 and SDR10. The same trend was observed for CML566 x TZDEEI50 for SDR10, CML440 x TZISTR1248 for SEC8, SEC10 and SDR8, CML540 x TZISTR1248 for SEC8, SEC10 and SDR10, CML540 x TZISTR1015 for SEC8 and SEC10, CML540 x TZISTR1015 for SEC10, SDR8, and SDR10, and CML451 x TZISTR1174 for SDR10. CML539 x TZISTR1174, CML566 x TZDEEI50, CML539 x TZISTR1248, CML540 x TZISTR1015, and CLHP0343 x TZISTR1015, exhibited

a significant and positive SCA for PLHT whereas CLHP0303 x TZISTR1174, CML451 x TZISTR1174, CML539 x TZISTR1174, CML440 x TZDEEI50, CML566 x TZDEEI50, CZL99017 x TZISTR1248, CML540 x TZISTR1248, CML539 x TZISTR1248, and CLHP0343 x TZISTR1015 exhibited significant SCA effect for EASP. CLHP0303 x TZISTR1174, CML539 x TZISTR1174, CML440 x TZDEEI50, CML566 x TZDEEI50, CZL99017 x TZISTR1248, and CML540 x TZISTR1248 showed positive and significant SCA effect for CL.

***Striga*-free environment:** The following crosses exhibited significant and positive SCA effect for GY: CLHP0303 x TZISTR1174, CML440 x TZISTR1174, CML451 x TZISTR1174, CML539 x TZISTR1174, CML566 x TZDEEI50, CML540 x TZDEEI50, CZL99017 x TZISTR1248, CML540 x TZISTR1248, CLHP0343 x TZISTR1248, CML451 x TZISTR1015, and CML566 x TZISTR1015 (Table 4.6). Among these crosses, CLHP0303 x TZISTR1174, CML451 x TZISTR1174, and CML540 x TZISTR1248 showed negative and significant SCA for ASI in the desirable direction, while CML540 x TZDEEI50 showed a significant and positive SCA effect for PLHT and CL. CLHP0303 x TZISTR1174 and CML451 x TZISTR1174 showed negative SCA effect for EASP in favourable direction but not significant, whereas CML451 x TZISTR1174, CML539 x TZISTR1174, CML566 x TZDEEI50 and CML540 x TZDEEI50 exhibited positive and significant SCA effect for CL.

#### 4.3.3.3 **Heterosis for agronomic traits and *Striga* parameters**

Table 4.7 presents the standard heterosis of the crosses under *Sa, Sh,* and *Striga*-free environments, respectively. In a *Striga*-free environment, heterosis for GY ranged from -54.56% (for CML540 x TZISTR1248) to 59.39% (CLHP0303 x TZDEEI50) with a mean of 9.64%. Positive and high heterosis values were also recorded for GY by the following crosses: CZL99017 x TZISTR1248 (58.60%), CZL99017 x TZISTR1174 (41.30%), CML440 x TZISTR1174 (45.21%), CML539 x TZISTR1174 (48.74%), CML540 x TZDEEI50 (41.46%), and CZL99017 x TZISTR1015 (32.57%) (Table 4.7). Crosses CML540 x TZISTR1248, CML566 x TZISTR1015, and CZL99017 x TZISTR1248 exhibited the lowest heterosis for ASI in a desirable direction, while the desirable heterosis values for PLHT were only exhibited by CZL99017 x TZISTR1174 and CML440 x TZISTR1174. It is worth noting that the highest heterosis value for PLHT was exhibited by cross CLHP0303 x TZDEEI50, which showed the lowest heterosis value for GY. CML540 x TZDEEI50 exhibited the highest heterosis for CL

(31.37%), followed by CML539 x TZISTR1174 (28.29%) and CML451 x TZISTR1174 (27.32%), respectively.

In *Sa* environment, heterosis for GY ranges from -83.53 to 51.45% with a mean of -1.44% (Table 4.7). The highest and lowest heterosis values were exhibited by CLHP0343 x TZDEEI50 (51.45%) and CML566 x TZISTR1174 (-83.53%). Most of the crosses' heterosis values for GY were influenced by *Sa* infestation except for CML539 x TZISTR1174 and CML540 x TZDEEI50, which kept their high heterosis from control to *Sa*-infested environments. The following crosses also had high and positive heterosis values for GY under *Sa* conditions: CML451 x TZISTR1174, CML540 x TZISTR1174, CLHP0343 x TZISTR1174, CLHP0343 x TZDEEI50, CLHP0343 x TZISTR1248, and CML539 x TZISTR1248. Only CML539 x TZISTR1174, CLHP0343 x TZISTR1174, and CML540 x TZISTR1174 showed high and positive heterosis for PLHT while CML539 x TZISTR1174 had the highest heterosis for CL followed by CLHP0343 x TZISTR1174, CLHP0343 x TZDEEI50, CML540 x TZDEEI50, and CLHP0343 x TZISTR1248.

In *Sh* environment, heterosis ranged from -44.44% (for CML540 xTZISTR1174) to 73.66% (for CML440 x TZDEEI50) (Table 4.7). The heterosis of most crosses was affected by *Sh* infestation except for CML440 x TZISTR1174, CZL99017 x TZISTR1248, and CZL99017 x TZISTR1015 which maintained their high heterosis from *Striga* free to *Sh* infested environment. The following crosses had high and positive heterosis in *Sh* environment: CML440 x TZISTR1174, CML451 x TZISTR1174, CML440 x TZDEEI50, CML566 x TZDEEI50, CZL99017 x TZISTR1248, CML440 x TZISTR1248, CML540 x TZISTR1248, CZL99017 x TZISTR1015, CML540 x TZISTR1015, and CLHP0343 x TZISTR1015. CML451 x TZISTR1174 had the lowest ASI heterosis, followed by CML540 x TZISTR1015 while only CML540 x TZISTR1015 had a positive heterosis for PLHT. None of the crosses showed high heterosis in the desirable direction for EASP and CL. Only cross CML451 x TZISTR1174 showed high and positive heterosis for GY and other economic traits in the two *Striga*-infested environments.

**Table 4.7** Standard heterosis (%) for agronomic traits among single crosses of maize evaluated in *Striga asiatica*, *S. hermonthica*, and *Striga*-free environment.

| Genotypes | DA | DS | ASI | SEC8 | SEC10 | SDR8 | SDR10 | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Striga asiatica*** | | | | | | | | | | | | |
| CLHP0303 x TZISTR1174 | 15.30 | 20.27 | -2.32 | -50.00 | -53.85 | 200.00 | 108.33 | 12.21 | 21.33 | 116.67 | 0.00 | -45.95 |
| CZL99017 x TZISTR1174 | 4.63 | 15.12 | -6.89 | -41.67 | -73.08 | 20.00 | 41.67 | 1.74 | 13.33 | 175.33 | 10.64 | -1.16 |
| CML440 x TZISTR1174 | 8.90 | 8.59 | -4.89 | -8.33 | -61.54 | 180.00 | 79.33 | -13.37 | 2.67 | 233.33 | -14.89 | -15.76 |
| CML451 x TZISTR1174 | 2.85 | 6.19 | -0.93 | 41.67 | -7.69 | 20.00 | 0.00 | -9.30 | -1.33 | 100.00 | 14.89 | 50.87 |
| CML566 x TZISTR1174 | 19.93 | 17.87 | -16.07 | -41.67 | -84.62 | 220.00 | 100.00 | 3.49 | 36.00 | 350.00 | -44.68 | -83.53 |
| CML540 x TZISTR1174 | 3.91 | -1.03 | -2.35 | -66.67 | -76.92 | 40.00 | -41.67 | 11.05 | 26.67 | 16.67 | 4.26 | 32.08 |
| CLHP0343 x TZISTR1174 | 12.46 | 12.03 | -7.50 | -33.33 | -38.46 | 60.00 | 50.00 | 12.79 | 54.67 | 50.00 | 29.79 | 35.26 |
| CML539 x TZISTR1174 | 9.25 | 7.22 | -3.50 | -41.67 | -53.85 | 0.00 | -8.33 | 15.12 | 62.67 | 83.33 | 36.17 | 37.28 |
| CLHP0303 x TZDEEI50 | 7.12 | 8.93 | -9.48 | -16.67 | -80.77 | 0.00 | -41.67 | 9.30 | 9.33 | 300.00 | -7.49 | -28.17 |
| CZL99017 x TZDEEI50 | 6.41 | 5.15 | -13.76 | 83.33 | -57.69 | 80.00 | 16.67 | -0.58 | 4.00 | 200.00 | -12.77 | -36.99 |
| CML440 x TZDEEI50 | 2.85 | 1.37 | -11.48 | -58.33 | -73.08 | 0.00 | -50.00 | -15.70 | 8.00 | 50.00 | 20.17 | 26.59 |
| CML451 x TZDEEI50 | 1.07 | 2.75 | 3.38 | -25.00 | -57.69 | 40.00 | -8.33 | 1.16 | 12.00 | 83.33 | 7.40 | 0.29 |
| CML566 x TZDEEI50 | 11.74 | 11.34 | -10.91 | 25.00 | 46.15 | 40.00 | 8.33 | -6.40 | 22.67 | 133.33 | -17.02 | 5.20 |
| CML540 x TZDEEI50 | 0.00 | 0.00 | -4.05 | 33.33 | -19.23 | 20.00 | 0.00 | -0.58 | 13.33 | 100.00 | 19.15 | 39.02 |
| CLHP0343 x TZDEEI50 | 9.25 | 11.68 | -7.18 | -58.33 | -57.69 | 0.00 | 25.00 | 2.33 | 17.33 | 83.33 | 20.17 | 51.45 |
| CML539 x TZDEEI50 | 3.91 | 7.56 | -7.46 | 0.00 | -53.85 | -20.00 | 41.67 | -18.02 | 8.00 | 183.33 | -17.02 | -31.06 |
| CZL99017 x TZISTR1248 | 0.36 | 1.03 | -11.75 | 0.00 | -57.69 | 40.00 | 50.00 | -9.88 | 6.67 | 50.00 | 19.15 | 29.19 |
| CML440 x TZISTR1248 | 8.19 | 5.50 | -8.32 | 41.67 | -92.31 | 160.00 | 91.67 | -23.26 | -10.67 | -16.67 | 0.00 | -0.43 |
| CML451 x TZISTR1248 | 8.19 | 5.50 | -8.32 | 41.67 | -92.31 | 160.00 | 91.67 | -23.26 | -10.67 | -16.67 | 0.00 | -0.43 |
| CML566 x TZISTR1248 | 17.08 | 9.62 | -12.28 | -33.33 | 38.46 | 80.00 | 41.67 | -5.23 | -2.67 | 233.33 | 0.00 | -47.98 |
| CML540 x TZISTR1248 | 0.71 | -1.03 | -8.85 | -50.00 | -26.92 | 20.00 | -33.33 | -16.86 | -5.33 | 100.00 | 2.13 | 11.27 |
| CLHP0343 x TZISTR1248 | 8.54 | 7.22 | -2.27 | -58.33 | -73.08 | 0.00 | -41.67 | -14.53 | 9.33 | 83.33 | 30.81 | 35.99 |
| CML539 x TZISTR1248 | 7.12 | 5.50 | -1.13 | 133.33 | 34.62 | 0.00 | 0.00 | -15.12 | 5.33 | 83.33 | 5.28 | 37.28 |

DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

**Table 4.7** (continued)

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CZL99017 x TZISTR1015 | 4.98 | 8.93 | 4.58 | -75.00 | -61.54 | 120.00 | 25.00 | -5.23 | -14.67 | 116.67 | -5.36 | 1.29 |
| CML440 x TZISTR1015 | 5.69 | 0.69 | -5.99 | -83.33 | 180.77 | 80.00 | 66.67 | -19.19 | 1.33 | 100.00 | -13.87 | -13.58 |
| CML451 x TZISTR1015 | 8.54 | 8.59 | 0.58 | 25.00 | -50.00 | 80.00 | 58.33 | -11.05 | 1.33 | 200.00 | -25.53 | -33.95 |
| CML566 x TZISTR1015 | 18.86 | 12.71 | -10.28 | -50.00 | -7.69 | 40.00 | 16.67 | -18.60 | 26.67 | 150.00 | -28.77 | -19.94 |
| CML540 x TZISTR1015 | 8.19 | 5.50 | -3.13 | -91.67 | -73.08 | 40.00 | -8.33 | 0.58 | 5.33 | 250.00 | -28.77 | -28.17 |
| CLHP0343 x TZISTR1015 | 19.22 | 14.777 | 3.155 | -100 | -80.77 | 100 | 33.33 | -14.54 | -6.67 | 116.67 | -14.89 | 2.46 |
| CML539 x TZISTR1015 | 16.73 | 13.40 | -0.56 | -50.00 | 19.23 | 120.00 | 16.67 | -20.93 | -2.67 | 166.67 | -36.17 | -51.58 |
| Minimum | 0.00 | -1.03 | -16.07 | -100.00 | -92.31 | -20.00 | -50.00 | -23.26 | -14.67 | -16.67 | -44.68 | -83.53 |
| Maximum | 19.93 | 20.27 | 4.58 | 133.33 | 180.77 | 220.00 | 108.33 | 15.12 | 62.67 | 350.00 | 36.17 | 51.45 |
| Mean | 8.40 | 7.77 | -5.67 | -20.28 | -38.21 | 64.67 | 24.31 | -6.40 | 10.44 | 129.18 | -1.57 | -1.44 |
| ***Striga hermonthica*** | | | | | | | | | | | | |
| **Genotypes** | **DA** | **DS** | **ASI** | **SEC8** | **SEC10** | **SDR8** | **SDR10** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** |
| CLHP0303 x TZISTR1174 | 14.29 | 20.85 | 32.20 | -100.00 | -57.89 | 160.00 | 100.00 | 30.13 | 43.06 | 0.00 | 0.00 | -60.00 |
| CZL99017 x TZISTR1174 | -12.50 | -17.25 | -24.36 | 0.00 | 137.50 | -61.54 | -50.00 | -23.15 | -30.10 | 150.00 | -16.56 | 19.03 |
| CML440 x TZISTR1174 | -1.25 | -5.85 | -20.51 | 0.00 | -37.50 | -46.15 | 5.56 | -11.82 | -7.77 | 225.00 | -21.28 | 25.85 |
| CML451 x TZISTR1174 | -7.50 | -7.31 | -1.28 | 0.00 | -25.00 | -61.54 | 0.00 | -14.29 | -12.62 | 200.00 | -21.28 | 27.87 |
| CML566 x TZISTR1174 | -2.81 | -6.73 | -17.95 | 0.00 | 37.50 | -15.38 | -5.56 | -12.81 | -19.42 | 225.00 | -30.42 | 8.94 |
| CML540 xTZISTR1174 | 0.00 | -2.05 | -8.97 | 0.00 | -62.50 | -30.77 | 5.56 | -15.27 | -16.50 | 375.00 | -45.72 | -44.44 |
| CLHP0343 x TZISTR1174 | -0.31 | -10.53 | -44.87 | 0.00 | 412.50 | -69.23 | -27.78 | -14.29 | -19.42 | 100.00 | -18.89 | 17.01 |
| CML539 x TZISTR1174 | -5.00 | -10.23 | -24.36 | 0.00 | 25.00 | -46.15 | -33.33 | -9.85 | 15.53 | 275.00 | -11.02 | 13.28 |
| CLHP0303 x TZDEEI50 | -6.88 | -9.06 | -11.54 | 0.00 | 312.50 | -61.54 | -5.56 | 3.94 | -7.77 | 225.00 | -16.56 | 14.53 |
| CZL99017 x TZDEEI50 | -3.44 | -5.85 | -11.54 | 0.00 | -62.50 | -61.54 | -50.00 | 5.91 | 31.07 | 250.00 | -36.27 | -8.59 |
| CML440 x TZDEEI50 | -12.50 | -15.79 | -17.95 | 0.00 | 125.00 | -61.54 | -50.00 | -9.85 | -17.48 | 75.00 | -22.85 | 73.66 |
| CML451 x TZDEEI50 | -7.81 | -8.48 | -5.13 | 0.00 | -50.00 | 7.69 | 38.89 | -37.44 | -34.95 | 475.00 | -48.05 | -25.66 |
| CML566 x TZDEEI50 | -3.13 | -8.48 | -24.36 | 0.00 | 675.00 | -53.85 | -44.44 | -1.97 | 6.80 | 175.00 | -18.14 | 50.38 |
| CML540 x TZDEEI50 | -8.13 | -13.45 | -25.64 | 0.00 | 225.00 | -46.15 | -33.33 | -11.33 | -10.68 | 275.00 | -29.97 | 20.73 |
| CLHP0343 x TZDEEI50 | -5.00 | -5.85 | -5.13 | 0.00 | -50.00 | -15.38 | 11.11 | -25.62 | -20.39 | 225.00 | -26.01 | -20.09 |
| CML539 x TZDEEI50 | -7.81 | -9.06 | -7.69 | 0.00 | 87.50 | -30.77 | -27.78 | -24.63 | -17.48 | 300.00 | -32.30 | -0.22 |
| CZL99017 x TZISTR1248 | -12.50 | -18.13 | -28.21 | 0.00 | 162.50 | -69.23 | -66.67 | -20.69 | -24.27 | 50.00 | -17.38 | 67.60 |

DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

**Table 4.7** (continued)

| Genotypes | DA | DS | ASI | SEC8 | SEC10 | SDR8 | SDR10 | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CML440 x TZISTR1248 | 6.56 | -2.34 | -37.18 | 0.00 | -100.00 | 76.92 | 11.11 | -50.25 | -42.72 | 475.00 | -59.82 | 50.22 |
| CML451 x TZISTR1248 | -9.06 | -9.36 | -3.85 | 0.00 | -62.50 | -38.46 | -5.56 | -31.03 | -28.16 | 375.00 | -26.01 | -11.24 |
| CML566 x TZISTR1248 | -0.63 | -2.92 | -10.26 | 0.00 | -50.00 | -30.77 | 22.22 | -19.70 | -16.50 | 475.00 | -40.99 | -24.89 |
| CML540 x TZISTR1248 | -10.00 | -17.54 | -35.90 | 0.00 | 12.50 | -61.54 | -77.78 | -29.56 | -28.16 | 150.00 | -18.95 | 56.42 |
| CLHP0343 x TZISTR1248 | -2.19 | -9.65 | -33.33 | 0.00 | 100.00 | -15.38 | 5.56 | -31.03 | -23.30 | 350.00 | -24.43 | -18.22 |
| CML539 x TZISTR1248 | -2.19 | -10.23 | -35.90 | 0.00 | 62.50 | -69.23 | -5.56 | -21.18 | -12.62 | 275.00 | -32.30 | 22.12 |
| CZL99017 x TZISTR1015 | -11.88 | -16.37 | -23.08 | 0.00 | 175.00 | -69.23 | -55.56 | -22.17 | 0.97 | 25.00 | -20.53 | 44.63 |
| CML440 x TZISTR1015 | -4.69 | -10.53 | -26.92 | 0.00 | 1237.50 | -46.15 | 0.00 | -36.95 | -35.92 | 300.00 | -44.08 | -38.24 |
| CML451 x TZISTR1015 | -3.75 | -7.89 | -19.23 | 0.00 | -50.00 | -15.38 | 5.56 | -21.18 | -17.48 | 475.00 | -51.20 | -42.11 |
| CML566 x TZISTR1015 | 1.88 | -4.68 | -28.21 | 0.00 | -50.00 | -53.85 | -11.11 | -25.62 | -8.74 | 300.00 | -41.75 | -16.51 |
| CML540 x TZISTR1015 | 9.29 | 8.13 | -5.08 | -90.00 | -57.89 | 40.00 | 44.44 | 5.13 | 19.44 | 10.00 | -16.08 | 41.84 |
| CLHP0343 x TZISTR1015 | -0.31 | -6.43 | -26.92 | 0.00 | 0.00 | -53.85 | -27.78 | -21.18 | -21.36 | 250.00 | -29.97 | 50.69 |
| CML539 x TZISTR1015 | 0.00 | 0.00 | -0.02 | 0.00 | 0.56 | 0.05 | 0.02 | -0.22 | -0.33 | 4.25 | -0.02 | 0.00 |
| Minimum | -12.50 | -18.13 | -44.87 | -100.00 | -100.00 | -69.23 | -77.78 | -50.25 | -42.72 | 0.00 | -59.82 | 60.00 |
| Maximum | 14.29 | 20.85 | 32.20 | 0.00 | 1237.50 | 160.00 | 100.00 | 30.13 | 43.06 | 475.00 | 0.00 | 73.66 |
| Mean | -3.64 | -7.44 | -17.77 | -6.33 | 102.41 | -30.00 | -10.93 | -16.60 | -11.91 | 235.48 | -27.29 | 9.82 |
| ***Striga* free environment** | | | | | | | | | | | | |
| **Genotypes** | **DA** | **DS** | **ASI** | **PLHT** | **EHT** | **EASP** | **CL** | **GY** | | | | |
| CLHP0303 x TZISTR1174 | 6.10 | 8.59 | 17.50 | -4.21 | -6.60 | 25.00 | -9.05 | -27.20 | | | | |
| CZL99017 x TZISTR1174 | 1.02 | 8.25 | 52.50 | 10.00 | -4.72 | 25.00 | 15.20 | 41.30 | | | | |
| CML440 x TZISTR1174 | -1.69 | 4.81 | 47.50 | 9.47 | -10.38 | 50.00 | 22.23 | 45.21 | | | | |
| CML451 x TZISTR1174 | 5.08 | 8.93 | 27.50 | 4.21 | -8.49 | 0.00 | 27.32 | 21.15 | | | | |
| CML566 x TZISTR1174 | 8.81 | 9.62 | 5.00 | -8.95 | -18.87 | 275.00 | -12.13 | -21.07 | | | | |
| CML540 x TZISTR1174 | 3.39 | 7.22 | 27.50 | 5.79 | -1.89 | 50.00 | 15.20 | 15.86 | | | | |
| CLHP0343 x TZISTR1174 | 5.76 | 9.28 | 25.00 | -6.32 | -6.60 | 50.00 | 29.35 | 6.97 | | | | |
| CML539 x TZISTR1174 | 4.07 | 7.90 | 27.50 | 6.32 | -0.94 | 0.00 | 28.29 | 48.74 | | | | |

DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

**Table 4.7** (continued)

| Genotypes | DA | DS | ASI | PLHT | EHT | EASP | CL | GY |
|---|---|---|---|---|---|---|---|---|
| CLHP0303 x TZDEEI50 | 10.85 | 14.09 | 22.50 | 13.68 | 20.75 | 325.00 | -12.13 | -54.56 |
| CZL99017 x TZDEEI50 | -2.37 | -0.34 | 15.00 | -7.89 | -33.96 | 50.00 | 25.30 | 16.48 |
| CML440 x TZDEEI50 | -3.73 | -1.03 | 20.00 | -17.37 | -22.64 | 250.00 | -7.03 | 16.17 |
| CML566 x TZDEEI50 | 7.12 | 9.97 | 20.00 | -3.16 | -1.89 | 0.00 | 12.37 | 8.81 |
| CML540 x TZDEEI50 | -2.37 | 1.37 | 27.50 | 1.58 | -8.49 | 0.00 | 31.37 | 41.46 |
| CLHP0343 x TZDEEI50 | 7.80 | 11.34 | 25.00 | 5.79 | -15.09 | 150.00 | 14.15 | -9.50 |
| CML539 x TZDEEI50 | 9.15 | 11.00 | 12.50 | 2.11 | -13.21 | 250.00 | -18.19 | 8.43 |
| CZL99017 x TZISTR1248 | -3.50 | -2.50 | 1.00 | -0.06 | -0.19 | 0.00 | 2.88 | 58.60 |
| CML440 x TZISTR1248 | 1.69 | 2.41 | 5.00 | 4.21 | -14.15 | 0.00 | 21.26 | 14.10 |
| CML451 x TZISTR1248 | 7.12 | 9.97 | 20.00 | -11.58 | -21.70 | 250.00 | -2.99 | -36.17 |
| CML566 x TZISTR1248 | 10.17 | 12.03 | 12.50 | 0.00 | -16.04 | 25.00 | 2.26 | -19.54 |
| CML540 x TZISTR1248 | 4.41 | 1.37 | -22.50 | -6.84 | -16.04 | 0.00 | 20.21 | 59.39 |
| CLHP0343 x TZISTR1248 | 4.07 | 5.15 | 7.50 | -7.89 | -16.04 | 0.00 | 30.32 | 26.44 |
| CML539 x TZISTR1248 | 8.14 | 10.65 | 17.50 | -4.74 | -19.81 | 75.00 | 8.08 | 7.89 |
| CZL99017 x TZISTR1015 | -4.41 | -1.72 | 20.00 | 8.42 | -13.21 | 25.00 | 15.20 | 32.57 |
| CML440 x TZISTR1015 | -2.03 | 1.03 | 22.50 | 1.58 | -15.09 | 0.00 | 7.11 | 15.17 |
| CML451 x TZISTR1015 | 3.39 | 5.50 | 15.00 | 3.68 | -12.26 | 50.00 | -4.04 | 10.04 |
| CML566 x TZISTR1015 | 11.86 | 8.59 | -25.00 | 11.05 | -0.94 | 50.00 | 1.05 | 21.69 |
| CML540 x TZISTR1015 | 5.08 | 0.69 | -32.50 | -13.16 | -12.26 | 25.00 | 1.05 | -11.11 |
| CLHP0343 x TZISTR1015 | 9.15 | 9.97 | 5.00 | -8.42 | -19.81 | 25.00 | 7.11 | -24.14 |
| CML539 x TZISTR1015 | 8.81 | 9.62 | 5.00 | 0.00 | -8.49 | 50.00 | -8.00 | 3.14 |
| Minimum | -4.41 | -2.50 | -32.50 | -17.37 | -33.96 | 0.00 | -18.19 | -54.56 |
| Maximum | 11.86 | 14.09 | 52.50 | 13.68 | 20.75 | 325.00 | 31.37 | 59.39 |
| Mean | 4.25 | 6.42 | 15.20 | -0.63 | -11.01 | 75.43 | 8.93 | 9.64 |

DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, SEC8 = *Striga* emergence counts eight weeks after sowing, SEC10 = *Striga* emergence counts ten weeks after sowing, SDR8 = *Striga* damage rating eight weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height, EHT = ear height, EASP = ear aspect, CL = cob length, and GY = grain yield.

## 4.4 **Discussion**

In SSA, maize production is severely affected by the scourge of *S. hermonthica* and *S. asiatica* infestations, leading to lost productivity, food insecurity, and poverty. Deploying *Striga*-resistant and locally adapted improved varieties is a cost-effective and environmentally friendly approach to limit the yield gap and impact of *Striga* infestation in the region. The present study examined genetically complementary inbred lines and derived hybrids for combining ability for yield and *Striga* resistance traits in *S. asiatica*, *S. hermonthica*, and *Striga*-free environments over two locations. The combined ANOVA for each treatment (Table 4.2) indicated the significant effects of genotypes and locations for most assessed traits. The findings suggest the existence of an appreciable genetic variability among the experimental material, including the lines, testers, and F1 hybrids. Related results were reported on maize inbred lines and hybrids in *Striga* infestation and *Striga*-free environments (Okunlola et al., 2023b; Zebire et al., 2020). The genotype x location interaction effect was significant for GY and SDR8 under both *Striga*-infested environments (Table 4.2). The results show that GY loss and higher *Striga* damage scores were predominantly higher under *Striga* infestation than the other traits. The current findings corroborate the reports of Akaogu et al. (2020) and Makinde et al. (2023), who also reported a significant effect of genotype x location interaction on GY and *Striga* parameters in maize.

### 4.4.1 Mean performance of the test genotypes

The highly variable mean values of test genotypes (appendices 4.1, 4.2, and 4.3) indicated a marked effect of *Striga* infestation on yield and *Striga* parameters. The current study identified unique lines, testers, and F1 crosses that showed a high level of *Striga* resistance compared to others. The variable phenotypic responses observed among the lines, testers, and $F_1$ hybrids allow targeted selection of better-performing genotypes after evaluation in multiple environments. Lines CZL99017 and CML540 and tester TZISTR1015 had the highest yield performance and lowest *Striga* parameters scores in the *Sa* environment (Table 4.3). The selected lines and testers are useful to develop *Striga*-resistant varieties for cultivation in *Sa*-infested environments. The line CLM540 was also relatively high-yielding (5.11 t/ha) under *Sh* environment (Table 4.3). Line CLM540 and tester TZISTR1015 were the 10 best-performing genotypes in *Sa* environment in a previous study by Dossa et al. (2024). CIMMYT also reported CML540 as a high-yielding genotype adapted to tropical and sub-tropical

environments (https://www.cimmyt.org/news/cimmyt-releases-22-new-maize-inbred-lines-for-the-tropics-and-subtropics/).

Under the three test environments, most of the F1 hybrids outperformed their respective parental line and testers (Table 4.3). The parents contributed to desirable genes for high GY and *Striga* resistance to their progenies in the prevailing environments. The following $F_1$ hybrids exhibited relatively higher grain yields and low levels of *Striga* damage scores than all their respective parental lines and testers in *Sa* environment: CML451 x TZISTR1174, CML540 x TZISTR1174, CLHP0343 x TZISTR1174, CML539 x TZISTR1174, CML540 x TZDEEI50, CML440 x TZDEEI50, CML540 x TZDEEI50, CZL99017 x TZISTR1248, CLHP0343 x TZISTR1248, and CML539 x TZISTR1248. These could be valuable hybrid sources for *Sa* resistance breeding.

Crosses CZL99017 x TZISTR1174, CML440 x TZISTR1174, CZL99017 x TZDEEI50, CML440 x TZDEEI50, CML566 x TZDEEI50, CZL99017 x TZISTR1248, CML540 x TZISTR1248, CML440 x TZISTR1248, CZL99017 x TZISTR1015, CML540 x TZISTR1015, and CLHP0343 x TZISTR1015 exhibited high GY and relatively low level of *Striga* damage scores in *Sh* environments. The best families were CML440 x TZDEEI50, CML540 x TZISTR1015 and CZL99017 x TZISTR1248. These findings suggest that the $F_1$ hybrids possess desirable genetic combinations buffering *Sa* and *Sh*-resistance. The parental lines CML540 and CZL99017 and testers TZISTR1174 and TZDEEI50 showed the best performances in hybrid combinations in the two *Striga* environments (Table 4.3). The lines are a source of genes for *Sa* and *Sh* resistance breeding programs in developing high-yielding $F_1$ hybrids. Abimiku et al. (2020) and Okunlola et al. (2023b) reported comparable results for yield and yield components and *Striga* resistance traits in maize.

### 4.4.2 Combining Ability Effects

The test genotypes GCA and SCA effects were influenced by *Striga* conditions agreeing with previous studies (Akhtar et al., 2023). Under both *Sa* and *Sh* infestation conditions, mean squares due to lines and testers revealed significant differences for most traits (Table 4.4). These indicate the presence of genetic divergence among the lines and testers. Higher GCA effects were recorded for most assessed traits, revealing the contribution of additive genetic effect (Shams et al., 2010). The mean square due to line-by-tester was significant for all the

studied traits except for SDR8, PLHT, and EHT in *Sa* environment and DS and EHT in *Sh* environment, indicating variable performance among testers. This implies the presence of nonadditive gene effects in controlling the traits. This finding corroborates with Mrema et al. (2019), Okunlola et al. (2023b), and Makinde et al. (2023), who reported that *Striga* resistance is governed by additive and non-additive effects.

In *Sa* environment, lines CML540 and CLHP0343 were good general combiners for GY, ASI, SEC8, SEC10, SDR8, and SDR10, and CLHP0343 for GY, ASI, SEC8, and CL (Table 4.5). Among the testers, TZISTR1248 was a good general combiner for GY, ASI, SDR8, and CL. In the *Sh* environment, the good general combiners were CZL99017, CML566, CML540, CLHP0343, and tester TZISTR1174, for the following traits: GY, SDR8, SDR10, and EASP. Line CML540 was the best for GY, SDR8, SDR10, and EASP. Whereas lines CML566, CLHP0343, and tester TZISTR1174 were good combiners only for GY. High general combining ability effects are associated with additive genetic effects, and best-performing genotypes can be selected through a recurrent selection method (Abd-Elaziz et al., 2021; Çetin and Çopur, 2022). Parents with higher GCA effects are ideal for developing superior hybrids for high grain yield and low levels of *Striga* damage for *Sa* and *Sh* resistance. Additive genetic variance is associated with a higher response to selection (Akhtar et al., 2023). The significant contribution of both lines and testers to GY, SEC8, SEC10, SDR8, and SDR10 indicated that additive gene effects were important for these traits, guaranteeing successful selections. Comparable results on the predominance of additive gene action in controlling GY and *Striga* resistance parameters in maize were reported by Afolabi et al. (2021) and Zebire et al. (2020). The involvement of additive and non-additive gene action in controlling *Striga* resistance in sorghum has been reported (Mrema et al., 2019). Contrary to the current finding, studies have shown the predominance of non-additive gene action in controlling yield and *Striga* parameters in millet (Balami et al., 2022; Rouamba et al., 2024).

In *Sa* environment, crosses CML451 x TZISTR1174, CML540 x TZISTR1174, CML539 x TZISTR1174, CML440 x TZDEEI50, CML566 x TZDEEI50, CML540 x TZDEEI50, CZL99017 x TZISTR1248, CML539 x TZISTR1248, CZL99017 x TZISTR1015, and CML566 x TZISTR1015 were identified as the best specific combiners for GY (Table 4.6). Crosses CML540 x TZISTR1174, CML539 x TZISTR1174, and CML440 x TZDEEI50 were the best specific combiners for GY, ASI, and all *Striga* resistance parameters. Whereas in *Sh* environment, crosses CLHP0303 x TZISTR1174, CML451 x TZISTR1174, CLHP0343 x TZISTR1174, CML539 x TZISTR1174, CZL99017 x TZDEEI50, CML440 x TZDEEI50,

CML566 x TZDEEI50, CZL99017 x TZISTR1248, CML440 x TZISTR1248, CML540 x TZISTR1248, CML539 x TZISTR1248, CML540 x TZISTR1015, CLHP0343 x TZISTR1015, and CML539 x TZISTR1015 were the best specific combiners for GY (Table 4.6). Under both *Sa* and *Sh* infestation conditions, crosses CML440 x TZDEEI50, CML451 x TZISTR1174, CML539 x TZISTR1174, CML566 x TZDEEI50, CZL99017 x TZISTR1248, and CML539 x TZISTR1248 were the best specific combiners for GY. CML440 x TZDEEI50 was the best specific combiner for GY, ASI, all the *Striga* resistance parameters, EASP, and CL (Table 4.6). These crosses are good *Striga*-resistant hybrid candidates for the two *Striga* species and procet dual-infestations. The results demonstrated that non-additive gene effects were expressed under both *Sa* and *Sh* infestation conditions. The findings agree with Mrema et al. (2019), who reported related findings in sorghum, and Abimiku et al. (2020) and Badu-Apraku et al. (2021) in maize.

High specific combining ability indicates the importance of the non-additive gene effect (Mogesse et al., 2020). The $F_1$ crosses selected from the present study can be further evaluated to confirm the repeatability of their performance in *Striga*-infested environments for commercialization. The GCA/SCA ratio of <1.00 for all the studied traits under all the test environments indicates the predominance of non-additive gene effect of the traits, which can be exploited in hybrid breeding programs. Similar findings were reported by Amusan (2010) and Adu et al. (2022), where non-additive gene action controlled the inheritance of grain yield and other agronomic traits and *Striga* resistance traits in maize. However, the ratio was less than 0.50 for SDR8 in the *Sa*-infested environment and SEC8, SEC10, EHT, and GY in *Sh*-infested environments, indicating that the additive gene effect of these traits might be higher than the non-additive gene effect. Low GCA/SCA ratios were reported by Sangaré et al. (2018) and Makinde et al. (2023).

### 4.4.3 Heterosis and Heritability Estimates

Heterosis plays a significant role in enhancing hybrid performance in maize, particularly in terms of grain yield (Li et al., 2021). Single-cross varieties of maize have substantially contributed to the improvement of maize productivity in the past decades (Hochholdinger and Baldauf, 2018). In this study, standard heterosis estimates over the best standard check (CML540) were computed for grain yield and yield-related traits. In *Sa* environment, the highest heterosis for GY was recorded for CLHP0343 x TZDEEI50, followed by CML539 x

TZISTR1174, CML540 x TZDEEI50, CML451 x TZISTR1174, CML540 x TZISTR1174, CLHP0343 x TZISTR1174, CLHP0343 x TZISTR1248, and CML539 x TZISTR1248 (Table 4.7), suggesting that these crosses possess *Sa* resistant genes. In *Sh* environment, CML440 x TZDEEI50, CML440 x TZISTR1174, CML451 x TZISTR1174, CML440 x TZDEEI50, CML566 x TZDEEI50, CZL99017 x TZISTR1248, CML440 x TZISTR1248, CML540 x TZISTR1248, CZL99017 x TZISTR1015, CML540 x TZISTR1015, and CLHP0343 x TZISTR1015 had the highest standard heterosis (Table 4.7), indicating their outperformance over the standard check. In addition, CML451 x TZISTR1174 had high and positive heterosis for GY and other economic traits in the two *Striga*-infested environments, indicating the unique potential of the hybrid and its parental lines to suppress both *Striga* species during dual-infestation. The new families with higher grain yield than the standard checks are desirable for improving maize grain yield by exploiting maximum heterosis (Li et al., 2021; Mogesse and Zeleke, 2022). Under both *Sa* and *Sh* infestation conditions, moderate to high broad and narrow sense heritability values were recorded for the studied traits. This indicates a minor environmental and a more significant genetic effect, suggesting a higher selection response (Yar et al., 2020). Badu-Apraku et al. (2012), Badu-Apraku and Fakorede (2013), and Kimutai et al. (2024) reported moderate to high broad and narrow sense heritabilities for *Striga* resistance and agronomic traits in maize. Similar findings were reported in millets by Rouamba et al. (2024) and Balami and Izge (2024).

## 4.5 **Conclusions**

Significant genetic variation was observed for grain yield, yield-related, and *Striga* resistance traits for the assessed lines, testers, and $F_1$ crosses. Both additive and non-additive gene actions conditioned the inheritance of *S. asiatica* and *S. hermonthica* resistance with a predominance of non-additive gene effect, signifying the value of hybrid breeding. The best general combiner tester was TZISTR1248 in the *Sa*-infested environment, while tester TZISTR1174 was noteworthy under *Sh* environment. Lines CML540 and CLHP0343 were the best combiners in *Sa* environment, while CZL99017, CML566, CML540, and CLHP0343 were promising in *Sh* environment, and CML540 was the best general combiner in all test environments. Under *Sa*-infested conditions, crosses CML540 x TZISTR1174, CML539 x TZISTR1174, and CML540 x TZDEEI50 exhibited high grain yield and relatively high specific combining ability and heterosis. In contrast, cross CML440 x TZDEEI50 in *Sh* environment had the best specific combining ability and heterosis for GY. Most of the crosses exhibited good specific combining

ability for grain yield only or *Striga* parameters, which can be useful in *Striga* resistance breeding programs. Substantial standard heterosis was recorded in the developed hybrids in both *Sa* and *Sh*-infested environments. Under both *Sa* and *Sh*-infested conditions, the highest heterosis for GY and *Striga* parameters was recorded for cross CML451 x TZISTR1174. None of the F1 hybrids showed high performance simultaneously in both *Striga*-infested environments, even though some crosses in this study showed good specific combining ability in the two *Striga*-infested environments. Therefore, there is a need for a rigorous evaluation of the new crosses across multiple environments to confirm their dual resistance. However, it is more prudent to breed for *S. asiatica* and *S. hermonthica* resistance separately, as the present results showed a significant difference in performance among the genotypes across the two *Striga* species. The selected parental lines and testers could be valuable genetic resources for developing high-yielding and *Striga*-resistant maize cultivars. The best-perfoming experimental single-cross hybrids are recommended for direct production or in developing three-way or double-cross hybrids in *Striga*-prone agroecologies. The study selected parental lines and single crosses with high combining ability for *Striga* parameters, yield, and yield-related traits under *Sa* and *Sh* infestation.

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**Appendix 4.1** Mean response for 10 traits of eight lines and four testers and 30 $F_1$ hybrids of maize evaluated in *Striga*-free environment.

| Genotypes | DA | DS | ASI (days) | PLHT (cm) | EHT (cm) | EPP | HUSK | EASP | CL (cm) | GY (tons/ha) |
|---|---|---|---|---|---|---|---|---|---|---|
| **Parental lines** | | | | | | | | | | |
| CLHP0303 | 84.75 | 84.75 | 11.00 | 155.00 | 66.00 | 1.00 | 1.00 | 7.50 | 9.62 | 2.49 |
| CZL99017 | 78.25 | 79.00 | 11.75 | 138.00 | 56.00 | 1.00 | 1.00 | 3.50 | 11.25 | 4.05 |
| CML440 | 84.50 | 83.25 | 9.75 | 135.00 | 76.00 | 1.00 | 1.00 | 7.25 | 8.25 | 2.70 |
| CML451 | 75.75 | 77.75 | 13.00 | 118.00 | 61.00 | 1.00 | 1.00 | 3.50 | 10.50 | 2.72 |
| CML566 | 82.50 | 85.50 | 14.00 | 169.00 | 86.00 | 1.00 | 1.00 | 4.00 | 12.25 | 5.56 |
| CML540 | 73.75 | 72.75 | 10.00 | 190.00 | 106.00 | 1.00 | 1.00 | 1.00 | 12.37 | 6.96 |
| CLHP0343 | 81.75 | 80.75 | 10.00 | 139.00 | 79.00 | 1.00 | 1.00 | 2.50 | 13.25 | 3.43 |
| CML539 | 79.75 | 77.00 | 8.25 | 168.00 | 94.00 | 1.00 | 1.00 | 2.25 | 13.50 | 5.58 |
| TZISTR1174 | 80.25 | 80.00 | 10.75 | 135.00 | 80.00 | 1.00 | 1.00 | 1.50 | 10.12 | 5.21 |
| TZDEEI50 | 85.75 | 89.50 | 14.75 | 120.00 | 97.00 | 1.00 | 1.00 | 7.75 | 11.00 | 1.31 |
| TZISTR1248 | 81.00 | 77.25 | 7.25 | 116.00 | 72.00 | 1.00 | 1.00 | 2.75 | 11.87 | 4.83 |
| TZISTR1015 | 82.25 | 80.50 | 9.25 | 127.00 | 73.00 | 1.00 | 1.00 | 2.75 | 7.50 | 3.58 |
| **Parental lines statistics** | | | | | | | | | | |
| Minimum | 73.75 | 72.75 | 7.25 | 116.00 | 56.00 | 1.00 | 1.00 | 1.00 | 7.50 | 1.31 |
| Maximum | 85.75 | 89.50 | 14.75 | 190.00 | 106.00 | 1.00 | 1.00 | 7.75 | 13.50 | 6.96 |
| Mean | 80.85 | 80.67 | 10.81 | 143.00 | 79.00 | 1.00 | 1.00 | 3.85 | 10.96 | 4.04 |
| **F1 hybrids** | | | | | | | | | | |
| CLHP0303 x TZISTR1174 | 78.25 | 79.00 | 11.75 | 182.00 | 99.00 | 1.00 | 1.00 | 1.25 | 11.25 | 5.07 |
| CZL99017 x TZISTR1174 | 74.50 | 78.75 | 15.25 | 209.00 | 101.00 | 1.00 | 1.00 | 1.25 | 14.25 | 9.83 |
| CML440 x TZISTR1174 | 72.50 | 76.25 | 14.75 | 208.00 | 95.00 | 1.00 | 1.00 | 1.50 | 15.12 | 10.11 |
| CML451 x TZISTR1174 | 77.50 | 79.25 | 12.75 | 198.00 | 97.00 | 1.00 | 1.00 | 1.00 | 15.75 | 8.43 |
| CML566 x TZISTR1174 | 80.25 | 79.75 | 10.50 | 173.00 | 86.00 | 1.00 | 1.00 | 3.75 | 10.87 | 5.49 |
| CML540 xTZISTR1174 | 76.25 | 78.00 | 12.75 | 201.00 | 104.00 | 1.00 | 1.00 | 1.50 | 14.25 | 8.06 |
| CLHP0343 x TZISTR1174 | 78.00 | 79.50 | 12.50 | 178.00 | 99.00 | 1.00 | 1.00 | 1.50 | 16.00 | 7.45 |
| CML539 x TZISTR1174 | 76.75 | 78.50 | 12.75 | 202.00 | 105.00 | 1.00 | 1.00 | 1.00 | 15.87 | 10.35 |
| CLHP0303 x TZDEEI50 | 81.75 | 83.00 | 12.25 | 216.00 | 128.00 | 1.00 | 1.00 | 4.25 | 10.87 | 3.16 |
| CZL99017 x TZDEEI50 | 72.00 | 72.50 | 11.50 | 175.00 | 70.00 | 1.00 | 1.00 | 1.50 | 15.50 | 8.11 |
| CML440 x TZDEEI50 | 71.00 | 72.00 | 12.00 | 157.00 | 82.00 | 1.00 | 1.00 | 3.50 | 11.50 | 8.09 |
| CML451 x TZDEEI50 | 77.00 | 79.25 | 13.25 | 178.00 | 94.00 | 1.00 | 1.00 | 2.88 | 12.87 | 5.07 |
| CML566 x TZDEEI50 | 79.00 | 80.00 | 12.00 | 184.00 | 104.00 | 1.00 | 1.00 | 1.00 | 13.90 | 7.57 |
| CML540 x TZDEEI50 | 72.00 | 73.75 | 12.75 | 193.00 | 97.00 | 1.00 | 1.00 | 1.00 | 16.25 | 9.85 |
| CLHP0343 x TZDEEI50 | 79.50 | 81.00 | 12.50 | 201.00 | 90.00 | 1.00 | 1.00 | 2.50 | 14.12 | 6.30 |
| CML539 x TZDEEI50 | 80.50 | 80.75 | 11.25 | 194.00 | 92.00 | 1.00 | 1.00 | 3.50 | 10.12 | 7.55 |
| CZL99017 x TZISTR1248 | 70.25 | 70.25 | 11.00 | 184.00 | 87.00 | 1.00 | 1.00 | 1.00 | 15.25 | 10.09 |
| CML440 x TZISTR1248 | 75.00 | 74.50 | 10.50 | 198.00 | 91.00 | 1.00 | 1.00 | 1.00 | 15.00 | 7.94 |
| CML451 x TZISTR1248 | 79.00 | 80.00 | 12.00 | 168.00 | 83.00 | 1.00 | 1.00 | 3.50 | 12.00 | 4.44 |
| CML566 x TZISTR1248 | 81.25 | 81.50 | 11.25 | 190.00 | 89.00 | 1.00 | 1.00 | 1.25 | 12.65 | 5.60 |
| CML540 x TZISTR1248 | 77.00 | 73.75 | 7.75 | 177.00 | 89.00 | 1.00 | 1.00 | 1.00 | 14.87 | 11.09 |
| CLHP0343 x TZISTR1248 | 76.75 | 76.50 | 10.75 | 175.00 | 89.00 | 1.00 | 1.00 | 1.00 | 16.12 | 8.80 |
| CML539 x TZISTR1248 | 79.75 | 80.50 | 11.75 | 181.00 | 85.00 | 1.00 | 1.00 | 1.75 | 13.37 | 7.51 |
| CZL99017 x TZISTR1015 | 70.50 | 71.50 | 12.00 | 206.00 | 92.00 | 1.00 | 1.00 | 1.25 | 14.25 | 9.23 |
| CML440 x TZISTR1015 | 72.25 | 73.50 | 12.25 | 193.00 | 90.00 | 1.00 | 1.00 | 1.00 | 13.25 | 8.02 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, LSD= least significant difference, SEM= standard error of mean, %CV= coefficient of variation, cm= centimeter, ha= hectare.

## Appendix 4.1 (continued)

| Genotypes | DA | DS | ASI (days) | PLHT (cm) | EHT (cm) | EPP | HUSK | EASP | CL (cm) | GY (tons/ha) |
|---|---|---|---|---|---|---|---|---|---|---|
| CML451 x TZISTR1015 | 76.25 | 76.75 | 11.50 | 197.00 | 93.00 | 1.00 | 1.00 | 1.50 | 11.87 | 7.66 |
| CML566 x TZISTR1015 | 82.50 | 79.00 | 7.50 | 211.00 | 105.00 | 1.00 | 1.00 | 1.50 | 12.50 | 8.47 |
| CML540 x TZISTR1015 | 77.50 | 73.25 | 6.75 | 165.00 | 93.00 | 1.00 | 1.00 | 1.25 | 12.50 | 6.19 |
| CLHP0343 x TZISTR1015 | 80.50 | 80.00 | 10.50 | 174.00 | 85.00 | 1.00 | 1.00 | 1.25 | 13.25 | 5.28 |
| CML539 x TZISTR1015 | 80.25 | 79.75 | 10.50 | 190.00 | 97.00 | 1.00 | 1.00 | 1.50 | 11.38 | 7.18 |
| **Hybrids Statistics** | | | | | | | | | | |
| Minimum | 70.25 | 70.25 | 6.75 | 157.00 | 70.00 | 1.00 | 1.00 | 1.00 | 10.12 | 3.16 |
| Maximum | 82.50 | 83.00 | 15.25 | 216.00 | 128.00 | 1.00 | 1.00 | 4.25 | 16.25 | 11.09 |
| Mean | 76.85 | 77.40 | 11.55 | 189.00 | 94.00 | 1.00 | 1.00 | 1.75 | 13.56 | 7.60 |
| **Trial statistics** | | | | | | | | | | |
| LSD | 5.32 | 5.18 | 4.71 | 0.43 | 0.22 | 2.41 | 3.23 | 69.17 | 5.32 | 5.18 |
| SEM | 2.68 | 2.61 | 2.37 | 0.22 | 0.11 | 1.21 | 1.63 | 34.88 | 2.68 | 2.61 |
| CV% | 4.86 | 4.72 | 29.61 | 0.43 | 17.20 | 72.94 | 17.95 | 39.98 | 4.86 | 4.72 |
| Broad sense heritability | 0.64 | 0.70 | 0.31 | 0.61 | 0.75 | 0.55 | 0.68 | 0.57 | 0.64 | 0.70 |
| Narrow-sense heritability | 0.53 | 0.45 | 0.13 | 0.00 | 0.09 | 0.05 | 0.30 | 0.21 | 0.53 | 0.45 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, LSD= least significant difference, SEM= standard error of mean, %CV= coefficient of variation, cm= centimeter, ha= hectare.

**Appendix 4.2** Mean response for 14 traits of eight lines and four testers and 30 $F_1$ hybrids of maize evaluated in *Striga-asiatica* environment.

| Genotypes | DA | DS | ASI (days) | SEC8 | SEC10 | SDR8 | SDR10 | PLHT (cm) | EHT (cm) | EASP | CL (cm) | GY (tons/ha) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Parental lines** | | | | | | | | | | | | |
| CLHP0303 | 82.25 | 80.50 | 10.25 | 2.25 | 6.50 | 5.00 | 6.50 | 136.00 | 86.00 | 5.25 | 8.75 | 1.98 |
| CZL99017 | 79.00 | 77.50 | 10.50 | 3.25 | 4.25 | 4.00 | 5.50 | 130.00 | 46.00 | 2.50 | 12.87 | 4.79 |
| CML440 | 83.25 | 82.50 | 11.25 | 0.00 | 1.25 | 1.25 | 4.00 | 156.00 | 91.00 | 3.00 | 11.62 | 4.36 |
| CML451 | 73.50 | 77.25 | 15.75 | 3.50 | 5.25 | 5.25 | 7.25 | 124.00 | 58.00 | 3.00 | 12.00 | 4.55 |
| CML566 | 84.75 | 85.00 | 12.25 | 2.75 | 7.00 | 4.25 | 6.25 | 174.00 | 73.00 | 4.50 | 9.37 | 4.08 |
| CML540 | 70.25 | 72.75 | 14.50 | 3.00 | 6.50 | 1.25 | 3.00 | 172.00 | 75.00 | 1.50 | 11.75 | 4.61 |
| CLHP0343 | 80.75 | 81.75 | 13.00 | 3.50 | 5.75 | 2.25 | 4.50 | 159.00 | 70.00 | 3.50 | 11.62 | 2.39 |
| CML539 | 73.75 | 71.75 | 10.00 | 1.75 | 1.25 | 1.75 | 4.75 | 116.00 | 80.00 | 2.25 | 8.75 | 3.09 |
| TZISTR1174 | 83.50 | 82.50 | 11.00 | 1.00 | 1.00 | 4.25 | 6.25 | 145.00 | 69.00 | 4.25 | 10.00 | 2.62 |
| TZDEEI50 | 81.50 | 83.75 | 14.25 | 2.00 | 0.75 | 2.50 | 6.50 | 152.00 | 84.00 | 6.00 | 7.00 | 1.17 |
| TZISTR1248 | 80.00 | 79.75 | 11.75 | 0.38 | 1.25 | 2.75 | 6.00 | 110.00 | 65.00 | 6.13 | 10.25 | 2.45 |
| TZISTR1015 | 82.75 | 84.00 | 13.25 | 2.00 | 2.50 | 3.75 | 7.00 | 136.00 | 70.00 | 5.50 | 6.00 | 6.39 |
| **Parental lines statistic** | | | | | | | | | | | | |
| Minimum | 70.25 | 71.75 | 10.00 | 0.00 | 1.25 | 1.25 | 3.00 | 116.00 | 46.00 | 1.50 | 8.75 | 1.17 |
| Maximum | 84.75 | 85.00 | 15.75 | 3.50 | 7.00 | 5.25 | 7.25 | 174.00 | 91.00 | 5.25 | 12.87 | 6.39 |
| Mean | 78.44 | 78.58 | 12.31 | 2.35 | 4.60 | 3.15 | 5.20 | 146.00 | 72.00 | 3.23 | 10.84 | 3.54 |
| **$F_1$ hybrids** | | | | | | | | | | | | |
| CLHP0303 x TZISTR1174 | 81.00 | 87.50 | 18.50 | 1.50 | 3.00 | 3.75 | 6.25 | 193.00 | 91.00 | 3.25 | 11.75 | 2.49 |
| CZL99017 x TZISTR1174 | 73.50 | 83.75 | 22.25 | 1.75 | 1.75 | 1.50 | 4.25 | 175.00 | 85.00 | 4.13 | 13.00 | 4.56 |
| CML440 x TZISTR1174 | 76.50 | 79.00 | 14.50 | 2.75 | 2.50 | 3.50 | 5.38 | 149.00 | 77.00 | 5.00 | 10.00 | 3.89 |
| CML451 x TZISTR1174 | 72.25 | 77.25 | 17.00 | 4.25 | 6.00 | 1.50 | 3.00 | 156.00 | 74.00 | 3.00 | 13.50 | 6.96 |
| CML566 x TZISTR1174 | 84.25 | 85.75 | 13.50 | 1.75 | 1.00 | 4.00 | 6.00 | 178.00 | 102.00 | 6.75 | 6.50 | 0.76 |
| CML540 xTZISTR1174 | 73.00 | 72.00 | 11.00 | 1.00 | 1.50 | 1.75 | 1.75 | 191.00 | 95.00 | 1.75 | 12.25 | 7.16 |
| CLHP0343 x TZISTR1174 | 79.00 | 81.50 | 14.50 | 2.00 | 4.00 | 2.00 | 4.50 | 194.00 | 116.00 | 2.25 | 15.25 | 6.24 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, cm= centimeter, ha= hectare.

## Appendix 4.2 (continued)

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CML539 x TZISTR1174 | **76.75** | **78.00** | **13.25** | **1.75** | **3.00** | **1.25** | **2.75** | **198.00** | **122.00** | **2.75** | **16.00** | **6.33** |
| CLHP0303 x TZDEEI50 | 75.25 | 79.25 | 16.00 | 2.50 | 1.25 | 1.25 | 1.75 | 188.00 | 82.00 | 6.00 | 10.87 | 3.31 |
| CZL99017 x TZDEEI50 | 74.75 | 76.50 | 13.75 | 5.50 | 2.75 | 2.25 | 3.50 | 171.00 | 78.00 | 4.50 | 10.25 | 2.91 |
| CML440 x TZDEEI50 | 72.25 | 73.75 | 13.50 | 1.25 | 1.75 | 1.25 | 1.50 | 145.00 | 81.00 | 2.25 | 14.12 | 5.84 |
| CML451 x TZDEEI50 | 71.00 | 74.75 | 15.75 | 2.25 | 2.75 | 1.75 | 2.75 | 174.00 | 84.00 | 2.75 | 12.62 | 4.63 |
| CML566 x TZDEEI50 | 78.50 | 81.00 | 14.50 | 3.75 | 9.50 | 1.75 | 3.25 | 161.00 | 92.00 | 3.50 | 9.75 | 4.85 |
| CML540 x TZDEEI50 | 70.25 | 72.75 | 14.50 | 4.00 | 5.25 | 1.50 | 3.00 | 171.00 | 85.00 | 3.00 | 14.00 | 7.00 |
| CLHP0343 x TZDEEI50 | 76.75 | 81.25 | 16.50 | 1.25 | 2.75 | 1.25 | 3.75 | 176.00 | 88.00 | 2.75 | 14.12 | 6.99 |
| CML539 x TZDEEI50 | 73.00 | 78.25 | 17.25 | 3.00 | 3.00 | 1.00 | 4.25 | 141.00 | 81.00 | 4.25 | 9.75 | 3.18 |
| CZL99017 x TZISTR1248 | 70.50 | 73.50 | 15.00 | 3.00 | 2.75 | 1.75 | 4.50 | 155.00 | 80.00 | 2.25 | 14.00 | 5.96 |
| CML440 x TZISTR1248 | 76.00 | 76.75 | 12.75 | 4.25 | 0.50 | 3.25 | 5.75 | 132.00 | 67.00 | 1.25 | 11.75 | 4.59 |
| CML451 x TZISTR1248 | 76.50 | 79.25 | 14.75 | 4.25 | 1.00 | 1.50 | 4.25 | 148.00 | 84.00 | 2.25 | 12.37 | 4.19 |
| CML566 x TZISTR1248 | 82.25 | 79.75 | 9.50 | 2.00 | 9.00 | 2.25 | 4.25 | 163.00 | 73.00 | 5.00 | 11.75 | 2.40 |
| CML540 x TZISTR1248 | 70.75 | 72.00 | 13.25 | 1.50 | 4.75 | 1.50 | 2.00 | 143.00 | 71.00 | 3.00 | 12.00 | 5.13 |
| CLHP0343 x TZISTR1248 | 76.25 | 78.00 | 13.75 | 1.25 | 1.75 | 1.25 | 1.75 | 147.00 | 82.00 | 2.75 | 15.37 | 6.27 |
| CML539 x TZISTR1248 | 75.25 | 76.75 | 13.50 | 7.00 | 8.75 | 1.25 | 3.00 | 146.00 | 79.00 | 2.75 | 12.37 | 6.33 |
| CZL99017 x TZISTR1015 | 73.75 | 79.25 | 17.50 | 0.75 | 2.50 | 2.75 | 3.75 | 163.00 | 64.00 | 3.25 | 11.12 | 4.67 |
| CML440 x TZISTR1015 | 74.25 | 73.25 | 11.00 | 0.50 | 18.25 | 2.25 | 5.00 | 139.00 | 76.00 | 3.00 | 10.12 | 3.99 |
| CML451 x TZISTR1015 | 76.25 | 79.00 | 14.75 | 3.75 | 3.25 | 2.25 | 4.75 | 153.00 | 76.00 | 4.50 | 8.75 | 3.05 |
| CML566 x TZISTR1015 | 83.50 | 82.00 | 10.50 | 1.50 | 6.00 | 1.75 | 3.50 | 140.00 | 95.00 | 3.75 | 8.37 | 3.69 |
| CML540 x TZISTR1015 | 76.00 | 76.75 | 12.75 | 0.25 | 1.75 | 1.75 | 2.75 | 173.00 | 79.00 | 5.25 | 8.37 | 3.31 |
| CLHP0343 x TZISTR1015 | 83.75 | 83.50 | 11.75 | 0.00 | 1.25 | 2.50 | 4.00 | 147.00 | 70.00 | 3.25 | 10.00 | 4.73 |
| CML539 x TZISTR1015 | 82.00 | 82.50 | 12.50 | 1.50 | 7.75 | 2.75 | 3.50 | 136.00 | 73.00 | 4.00 | 7.50 | 2.23 |
| **Hybrids statistics** | | | | | | | | | | | | |
| Minimum | 70.25 | 72.00 | 9.50 | 0.00 | 0.50 | 1.00 | 1.50 | 132.00 | 64.00 | 1.25 | 6.50 | 0.76 |
| Maximum | 84.75 | 87.50 | 22.25 | 7.00 | 18.25 | 5.25 | 7.25 | 198.00 | 122.00 | 6.75 | 16.00 | 7.16 |
| Mean | 77.19 | 78.86 | 14.32 | 2.29 | 3.94 | 2.40 | 4.30 | 155.00 | 80.00 | 3.59 | 11.11 | 4.59 |
| **Trial statistics** | | | | | | | | | | | | |
| LSD | 5.69 | 7.13 | 13.99 | 5.32 | 10.27 | 2.36 | 3.15 | 0.47 | 0.24 | 2.96 | 2.97 | 53.66 |
| SEM | 2.87 | 3.59 | 9.93 | 2.68 | 5.18 | 1.19 | 1.59 | 0.23 | 0.12 | 1.49 | 1.49 | 27.06 |
| CV% | 4.06 | 5.06 | 12.00 | 164.31 | 187.39 | 72.12 | 53.21 | 21.69 | 22.06 | 58.65 | 19.04 | 48.02 |
| Broad sense heritability | 0.85 | 0.76 | 0.45 | 0.56 | 0.39 | 0.25 | 0.56 | 0.59 | 0.66 | 0.61 | 0.90 | 0.76 |
| Narrow-sense heritability | 0.66 | 0.51 | 0.18 | 0.28 | 0.20 | 0.25 | 0.24 | 0.31 | 0.33 | 0.02 | 0.25 | 0.15 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, cm= centimeter, ha= hectare.

**Appendix 4.3.** Mean response for 14 traits of eight lines and four testers and 30 $F_1$ hybrids of maize evaluated in *S. hermonthica*-infested environment.

| Genotypes | DA | DS | ASI (days) | SEC8 | SEC10 | SDR8 | SDR10 | PLHT (cm) | EHT (cm) | EPP | HUSK | EASP | CL (cm) | GY (tons/ha) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CLHP0303 | 81.25 | 82.25 | 15.00 | 1.75 | 5.75 | 2.00 | 6.00 | 119.00 | 72.00 | 1.00 | 1.50 | 7.25 | 8.87 | 2.28 |
| CZL99017 | 75.25 | 74.50 | 13.25 | 4.00 | 5.25 | 2.75 | 5.50 | 144.00 | 50.00 | 1.00 | 1.25 | 3.00 | 11.75 | 4.19 |
| CML440 | 85.25 | 84.00 | 12.75 | 0.00 | 1.25 | 1.25 | 4.25 | 116.00 | 88.00 | 1.00 | 1.25 | 4.75 | 11.75 | 2.75 |
| CML451 | 75.25 | 77.25 | 16.00 | 4.00 | 2.00 | 1.75 | 4.25 | 109.00 | 54.00 | 1.00 | 1.00 | 4.50 | 9.38 | 2.66 |
| CML566 | 83.75 | 82.75 | 13.00 | 1.25 | 9.50 | 1.75 | 4.75 | 145.00 | 70.00 | 1.25 | 1.00 | 4.38 | 12.00 | 3.71 |
| CML540 | 70.00 | 70.75 | 14.75 | 7.50 | 4.75 | 1.25 | 2.25 | 156.00 | 72.00 | 1.00 | 1.00 | 2.50 | 13.25 | 5.11 |
| CLHP0343 | 83.25 | 80.25 | 11.00 | 1.00 | 6.75 | 3.25 | 5.75 | 116.00 | 57.00 | 1.00 | 1.00 | 3.25 | 10.50 | 3.25 |
| CML539 | 76.00 | 75.00 | 13.00 | 1.50 | 1.75 | 3.25 | 5.25 | 138.00 | 82.00 | 1.00 | 1.00 | 3.50 | 11.00 | 4.35 |
| TZISTR1174 | 82.25 | 84.00 | 15.75 | 0.75 | 2.25 | 4.00 | 5.50 | 119.00 | 63.00 | 1.00 | 1.00 | 4.25 | 7.75 | 1.76 |
| TZDEEI50 | 76.50 | 77.50 | 15.00 | 0.75 | 1.00 | 3.75 | 5.00 | 137.00 | 77.00 | 1.00 | 1.00 | 6.75 | 8.00 | 1.49 |
| TZISTR1248 | 81.75 | 80.25 | 12.50 | 0.00 | 1.25 | 3.75 | 6.00 | 106.00 | 64.00 | 1.00 | 1.00 | 6.25 | 8.25 | 2.17 |
| TZISTR1015 | 82.25 | 76.50 | 8.25 | 0.75 | 0.75 | 4.75 | 7.25 | 128.00 | 62.00 | 1.00 | 1.00 | 3.25 | 5.75 | 3.23 |
| **Parental lines statistic** | | | | | | | | | | | | | | |
| Minimum | 70.00 | 70.75 | 8.25 | 0.00 | 0.75 | 1.25 | 2.25 | 106.00 | 50.00 | 1.00 | 1.00 | 2.50 | 5.75 | 1.49 |
| Maximum | 85.25 | 84.00 | 16.00 | 7.50 | 9.50 | 4.75 | 7.25 | 156.00 | 88.00 | 1.25 | 1.50 | 7.25 | 13.25 | 5.11 |
| Mean | 79.40 | 78.75 | 13.35 | 1.94 | 3.52 | 2.79 | 5.15 | 128.00 | 68.00 | 1.02 | 1.08 | 4.47 | 9.85 | 3.08 |
| **$F_1$ hybrids** | | | | | | | | | | | | | | |
| CLHP0303 x TZISTR1174 | 80.00 | 85.50 | 19.50 | 0.00 | 2.00 | 3.25 | 4.50 | 203.00 | 103.00 | 1.00 | 1.00 | 1.00 | 15.88 | 4.30 |
| CZL99017 x TZISTR1174 | 79.00 | 80.50 | 15.50 | 2.75 | 1.25 | 1.75 | 4.75 | 179.00 | 95.00 | 1.00 | 1.00 | 3.25 | 12.50 | 5.41 |
| CML440 x TZISTR1174 | 74.00 | 79.25 | 19.25 | 0.50 | 1.50 | 1.25 | 4.50 | 174.00 | 90.00 | 1.00 | 1.00 | 3.00 | 12.50 | 5.49 |
| CML451 x TZISTR1174 | 77.75 | 79.75 | 16.00 | 4.75 | 2.75 | 2.75 | 4.25 | 177.00 | 83.00 | 1.00 | 1.00 | 3.25 | 11.05 | 4.68 |
| CML566 x TZISTR1174 | 80.00 | 83.75 | 17.75 | 4.50 | 0.75 | 2.25 | 4.75 | 172.00 | 86.00 | 1.00 | 1.00 | 4.75 | 8.62 | 2.39 |
| CML540 x TZISTR1174 | 79.75 | 76.50 | 10.75 | 17.50 | 10.25 | 1.00 | 3.25 | 174.00 | 83.00 | 1.00 | 1.00 | 2.00 | 12.88 | 5.03 |
| CLHP0343 x TZISTR1174 | 76.00 | 76.75 | 14.75 | 0.75 | 2.50 | 1.75 | 3.00 | 183.00 | 119.00 | 1.00 | 1.00 | 3.75 | 14.13 | 4.87 |
| CML539 x TZISTR1174 | 74.50 | 77.75 | 17.25 | 6.50 | 8.25 | 1.25 | 4.25 | 211.00 | 95.00 | 1.00 | 1.00 | 3.25 | 13.25 | 4.92 |
| CLHP0303 x TZDEEI50 | 77.25 | 80.50 | 17.25 | 0.75 | 0.75 | 1.25 | 2.25 | 215.00 | 135.00 | 1.00 | 1.25 | 3.50 | 10.12 | 3.93 |
| CZL99017 x TZDEEI50 | 70.00 | 72.00 | 16.00 | 5.50 | 4.50 | 1.25 | 2.25 | 183.00 | 85.00 | 1.00 | 1.00 | 1.75 | 12.25 | 7.46 |
| CML440 x TZDEEI50 | 70.50 | 70.00 | 13.50 | 1.50 | 4.00 | 1.25 | 1.75 | 152.00 | 88.00 | 1.00 | 1.00 | 1.75 | 13.62 | 9.30 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, cm= centimeter, ha= hectare.

**Appendix 4.3 (continued)**

| Genotypes | DA | DS | ASI (days) | SEC8 | SEC10 | SDR8 | SDR10 | PLHT (cm) | EHT (cm) | EPP | HUSK | EASP | CL (cm) | GY (tons/ha) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CML451 x TZDEEI50 | 73.75 | 78.25 | 18.50 | 7.75 | 1.00 | 3.50 | 6.25 | 127.00 | 67.00 | 1.00 | 1.25 | 5.75 | 8.25 | 3.19 |
| CML566 x TZDEEI50 | 77.50 | 78.25 | 14.75 | 6.75 | 15.50 | 1.50 | 2.50 | 199.00 | 110.00 | 1.00 | 1.00 | 2.75 | 13.00 | 6.46 |
| CML540 x TZDEEI50 | 73.50 | 74.00 | 14.50 | 6.25 | 6.50 | 1.75 | 3.00 | 180.00 | 92.00 | 1.00 | 1.00 | 3.75 | 11.12 | 5.19 |
| CLHP0343 x TZDEEI50 | 76.00 | 80.50 | 18.50 | 1.25 | 1.00 | 2.75 | 5.00 | 151.00 | 82.00 | 1.00 | 1.00 | 3.25 | 11.75 | 3.43 |
| CML539 x TZDEEI50 | 73.75 | 77.75 | 18.00 | 2.50 | 3.75 | 2.25 | 3.25 | 153.00 | 85.00 | 1.00 | 1.00 | 4.00 | 10.75 | 4.29 |
| CZL99017 x TZISTR1248 | 70.00 | 70.00 | 14.00 | 8.75 | 5.25 | 1.00 | 1.50 | 161.00 | 78.00 | 1.00 | 1.00 | 1.50 | 13.12 | 7.20 |
| CML440 x TZISTR1248 | 85.25 | 83.50 | 12.25 | 0.00 | 0.00 | 5.75 | 5.00 | 101.00 | 59.00 | 1.00 | 1.00 | 5.75 | 6.38 | 6.45 |
| CML451 x TZISTR1248 | 72.75 | 77.50 | 18.75 | 1.50 | 0.75 | 2.00 | 4.25 | 140.00 | 74.00 | 1.00 | 1.75 | 4.75 | 11.75 | 3.81 |
| CML566 x TZISTR1248 | 79.50 | 83.00 | 17.50 | 0.00 | 1.00 | 2.25 | 5.50 | 163.00 | 86.00 | 1.00 | 1.25 | 5.75 | 9.37 | 3.23 |
| CML540 x TZISTR1248 | 72.00 | 70.50 | 12.50 | 1.00 | 2.25 | 1.25 | 1.00 | 143.00 | 74.00 | 1.00 | 1.00 | 2.50 | 12.87 | 6.72 |
| CLHP0343 x TZISTR1248 | 78.25 | 77.25 | 13.00 | 1.50 | 4.00 | 2.75 | 4.75 | 140.00 | 79.00 | 1.00 | 1.25 | 4.50 | 12.00 | 3.51 |
| CML539 x TZISTR1248 | 78.25 | 76.75 | 12.50 | 1.00 | 3.25 | 1.00 | 4.25 | 160.00 | 90.00 | 1.00 | 1.00 | 3.75 | 10.75 | 5.25 |
| CZL99017 x TZISTR1015 | 70.50 | 71.50 | 15.00 | 3.25 | 5.50 | 1.00 | 2.00 | 158.00 | 104.00 | 1.00 | 1.25 | 1.25 | 12.62 | 6.21 |
| CML440 x TZISTR1015 | 76.25 | 76.50 | 14.25 | 11.00 | 26.75 | 1.75 | 4.50 | 128.00 | 66.00 | 1.00 | 1.00 | 4.00 | 8.88 | 2.65 |
| CML451 x TZISTR1015 | 77.00 | 78.75 | 15.75 | 2.25 | 1.00 | 2.75 | 4.75 | 160.00 | 85.00 | 1.00 | 1.00 | 5.75 | 7.75 | 2.49 |
| CML566 x TZISTR1015 | 81.50 | 81.50 | 14.00 | 1.50 | 1.00 | 1.50 | 4.00 | 151.00 | 94.00 | 1.00 | 1.00 | 4.00 | 9.25 | 3.59 |
| CML540 x TZISTR1015 | 76.50 | 76.50 | 14.00 | 0.75 | 2.00 | 1.75 | 3.25 | 164.00 | 86.00 | 1.00 | 1.00 | 2.75 | 11.12 | 7.25 |
| CLHP0343 x TZISTR1015 | 79.75 | 80.00 | 14.25 | 1.00 | 2.00 | 1.50 | 3.25 | 160.00 | 81.00 | 1.00 | 1.00 | 3.50 | 11.12 | 6.47 |
| CML539 x TZISTR1015 | 87.75 | 87.00 | 13.25 | 0.75 | 4.25 | 3.75 | 5.00 | 112.00 | 68.00 | 1.00 | 1.00 | 5.25 | 10.25 | 3.87 |
| **Hybrids statistics** | | | | | | | | | | | | | | |
| Minimum | 70.00 | 70.00 | 10.75 | 0.00 | 0.00 | 1.00 | 1.00 | 101.00 | 59.00 | 1.00 | 1.00 | 1.00 | 6.38 | 2.39 |
| Maximum | 87.75 | 87.00 | 19.50 | 17.50 | 26.75 | 5.75 | 6.25 | 215.00 | 135.00 | 1.00 | 1.75 | 5.75 | 15.88 | 9.30 |
| Mean | 76.62 | 78.04 | 15.43 | 3.46 | 4.18 | 2.03 | 3.75 | 162.00 | 87.00 | 1.00 | 1.07 | 3.53 | 11.30 | 4.97 |
| **Trial statistics** | | | | | | | | | | | | | | |
| LSD | 5.84 | 7.41 | 7.06 | 8.89 | 13.48 | 2.43 | 3.07 | 0.45 | 0.29 | 0.11 | 0.45 | 2.90 | 4.26 | 59.04 |
| SEM | 2.94 | 3.74 | 3.56 | 4.48 | 6.80 | 1.22 | 1.55 | 0.23 | 0.15 | 0.05 | 0.23 | 1.46 | 2.15 | 29.78 |
| CV% | 5.38 | 6.76 | 33.97 | 209.71 | 241.13 | 77.25 | 52.76 | 21.08 | 25.67 | 7.67 | 30.09 | 54.55 | 27.91 | 50.72 |
| Broad sense heritability | 0.93 | 0.69 | 0.80 | 0.28 | 0.40 | 0.75 | 0.60 | 0.72 | 0.63 | 0.47 | 0.66 | 0.68 | 0.93 | 0.69 |
| Narrow-sense heritability | 0.11 | 0.25 | 0.15 | 0.00 | 0.00 | 0.00 | 0.10 | 0.36 | 0.44 | 0.45 | 0.09 | 0.15 | 0.11 | 0.25 |

DA= days to 50% anthesis, DS= days to 50% silking, ASI= anthesis-silking interval, EPP = ear per plant, PLHT= plant height, EHT= ear height, HUSK= husk cover, CL= cob length, EASP= ear aspect, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, cm= centimeter, ha= hectare.

## Chapter 5: Genome-wide association analysis of grain yield and *Striga hermonthica* and *S. asiatica* resistance in tropical and sub-tropical maize populations


### Abstract

**Background:** Genetic improvement for *Striga hermonthica* (*Sh*) and *S. asiatica* (*Sa*) resistance is the most economical and effective control method to enhance the productivity of maize and other major cereal crops. Hence, identification of quantitative trait loci (QTL) associated with *Striga* resistance and economic traits will guide the pace and precision of resistance breeding in maize. The objective of this study was to undertake a genome-wide association analysis of grain yield and *Sh and Sa* resistance among tropical and sub-tropical maize populations to identify putative genetic markers and genes for resistance breeding. 130 maize genotypes were evaluated under controlled environment conditions using artificial infestation of *Sh* and *Sa*. The test genotypes were profiled for grain yield (GY), *Striga* emergence counts at 8 (SEC8) and 10 (SEC10) weeks after planting, and *Striga* damage rate scores at 8 (SDR8) and 10 (SDR10) weeks after planting. Population structure analysis and genome-wide association mapping were undertaken based on 16000 single nucleotide polymorphism (SNP) markers.

**Results**: A linkage disequilibrium (LD) analysis in 798,675 marker pairs revealed that 21.52% of pairs were in significant linkage ($P < 0.001$). Across the chromosomes, the LD between SNPs decayed below a critical level ($r^2=0.1$) at a map distance of 0.19 Mbp. The genome-wide association study identified 50 significant loci associated with *Sh* resistance and 22 significant loci linked to *Sa* resistance, corresponding to 39 and 19 candidate genes, respectively.

**Conclusion**: The study found no significant loci associated with resistance to the two examined *Striga* species. Some of the detected genes reportedly conditioned insect and pathogen resistance, plant cell development, variable senescence, and pollen fertility. The markers reported in the present study for *Sa* resistance are novel. The gene Zm00001eb219710 was pleiotropic, and conditioned GY and SEC10, while Zm00001eb165170 affected SDR8 and SDR10, and Zm00001eb112030 conditioned SDR8 and SDR10 associated with *Sh* resistance. The candidate genes may facilitate simultaneous selection for *Sh* and *Sa* resistance and grain yield in maize after further validation and introgression in breeding pipelines. Overall, we recommend breeding maize resistant to *Sh* and *Sa* on separate genetic backgrounds.



**Keywords**: Grain yield, GWAS, maize**,** resistance breeding, *Striga* resistance.

## 5.1 **Introduction**

Maize (*Zea mays* L., 2n = 2x = 20) is the global food, feed, and industrial cereal. In sub-Saharan Africa (SSA), the per capita consumption of maize is > 330g/person/day [1]. The productivity of maize in SSA has remained stagnant and low (<3 t/ha) compared to the potential productivity reaching 5 to 10 t/ha [2]. The parasitic weeds, *Striga hermonthica* (Del.) Benth *and S. asiatica* (L.) Kuntze are among the leading causes of low productivity of maize, especially in communal and small-scale maize production systems with low agricultural inputs [3,4].

*Striga hermonthica* (*Sh*) and *S. asiatica* (*Sa*) are cosmopolitan parasitic weeds and destructive species affecting major cereals crops, including maize in SSA [3,5,6]. The parasite damages the host species by extracting its photoassimilates, diminishing its growth and productivity, especially under moisture stress and sub-optimal soil nutrient conditions, which are common in marginal maize production areas of SSA [7]. Under severe *Striga* infestation, yield loss reaching 100% has been recorded in susceptible maize varieties [8]. Hence, there is a need for genetic improvement for *Striga* resistance and grain yield to enhance the productivity of maize and other major cereal crops in SSA.

Various *Striga* control strategies have been recommended, such as cultural practices (e.g., crop rotation, intercropping, catch-cropping, trap-cropping, and the application of organic and inorganic fertilizers), chemical and bio-herbicides. The control practices are used solo or in combination, which is referred to as integrated *Striga* management [9,10]. Most of the described control options have limited application, and some are inaccessible and unaffordable to many smallholder farmers [8,11,12]. *Striga*-resistant varieties are the most economical and environmentally friendly option to control the parasitic weed under low-input farming systems [13,14].

Several *Striga*-resistant varieties have been developed by the International Institute of Tropical Agriculture (IITA) in West Africa, where *Sh* is prevalent. However, only partial to moderate *Striga* resistance has been attained so far [15,16], due to the low heritability of *Striga* resistance traits [8]. Low heritable traits are subject to genotype, environment, and genotype x environment interaction effects [17]. Molecular marker-assisted breeding tools could improve selection gains for *Striga* resistance and low heritable traits. Molecular markers can identify, locate, and map genes conditioning economic traits and *Striga* resistance. Linkage mapping has successfully identified quantitative trait loci (QTL) for complex traits using bi-parental populations [18]. However, detecting recombination events within pedigree and families is

minimal in linkage mapping, leading to low mapping resolution of genetic markers and genes. Genome-wide association study (GWAS) is a cost-effective tool for discerning marker-trait association and dissecting the genetic architecture of complex quantitative traits, which can provide a high-resolution and high allelic richness. GWAS saves time in genetic analysis compared to linkage mapping for identifying QTL [19]. Various populations can be used in association mapping, including elite cultivars, landraces, wild relatives, and introductions [20,21]. Limited studies documented QTL mapping associated with *Striga* resistance, yield, and yield component traits.

The first QTL associated with *Striga* resistance in maize were reported by Amusan [22]. The authors reported two QTL mapped on chromosome 6 using an $F_2$ mapping population involving a cross between a susceptible (5057) and a resistant (ZD05) maize inbred lines. The two QTL accounted for 55% of observed phenotypic variation for incompatible responses to *Sh* infestation on host roots. Adewale, et al. [13] used GWAS and reported three markers located close to the putative genes GRMZM2G164743 (bin 10.05), GRMZM2G060216 (bin 3.06), and GRMZM2G103085 (bin 5.07), linked to grain yield, the number of ears per plant, and *Striga* damage under *Striga* infestation. The three QTL explained 9 to 42% of the phenotypic variance for the incompatible response of *Sh* on the agronomic traits. Further, using QTL mapping, Badu-Apraku et al. (2020a) identified 12 QTL associated with *Sh* resistance traits from an $F_{2:3}$ population. The authors further identified 14 other QTL and 154 candidate genes associated with *Striga* resistance/tolerance traits using QTL mapping [23]. Gowda, *et al.* [24] identified 57 SNPs significantly associated with *Sh* resistance indicator traits and grain yield, pin-pointing 32 candidate genes near the significant SNPs using GWAS. Recently, 22 SNP markers associated with grain yield, *Striga* damage, number of emerged *Striga* plants after planting, and ear aspect were reported by Okunlola, *et al.* [25] using GWAS. So far, only one study [8] reported on QTL associated with *Sa* resistance. The authors identified 3 SNP markers on chromosome numbers 5, 6, and 7 for total *Sa* plants that emerged. There is a need to identify QTL associated with *Striga* resistance and economic traits to guide the pace and precision of resistance breeding in maize aiming *Sh* and *Sa*.

Thus far, QTL associated with *Striga*-resistance has been detected using a bi-parental population, which may have low mapping resolution due to the small number of accumulated recombination events [26]. The quantitative trait loci intervals found are extended over several centimorgans (cM). Compared with *Sh*, there is a dearth of information on major QTL for *Sa* resistance. Hence, this study will be the first attempt to report QTL associated with both *Sa* and

*Sh* resistance for *Striga* resistance breeding. The two species are the most devastating parasitic weed populations occurring in tandem over space and time in SSA, especially in East Africa. Therefore, the objective of this part of the study was to undertake a genome-wide association analysis of grain yield and *Striga* resistance among 130 tropical and subtropical maize genotypes to identify genetic markers linked to resistance to *Sh* and *Sa*. The QTL associated with resistance to both parasites will be useful in developing *Striga*-resistant maize with wide adaptability across the SSA region.

## 5.2 **Materials and Methods**

### **5.2.1 Plant material and phenotyping**

The current study used a panel of 130 maize germplasm. Of these, 74 were acquired from the *Striga*-resistant pool developed and released by IITA/Nigeria, 45 were locally adapted varieties from the International Maize and Wheat Improvement Centre (CIMMYT)/Zimbabwe, and 11 were from the National Plant Genetic Resources Centre, South Africa (NPGRC)/South Africa (Appendix 5.1). The germplasm included tropical and sub-tropical inbred lines, open-pollinated varieties (OPVs), and top-cross hybrids, as described in [27]. The 130 genotypes were rigorously phenotyped under *Sa* and *Sh*-infested conditions separately at the University of KwaZulu-Natal Controlled Environment Facilities (UKZN-CEF)/South Africa in two cropping seasons, from December 2021 to April 2022, and from August 2022 to December 2022. The average maximum temperature during those seasons is between 26 and 28°C, while the minimum is 10°C. Each of the experiments was arranged in a 13 X 10 alpha lattice design with two replications. The UKZN-CEF is situated at the UKZN College of Agriculture, Engineering, and Science (29.62° S, 30.40° E). Two weeks before planting, each pot was infested with a scoop of sand mixed with 0.03 g of 2-year-old *Sa* or *Sh* seed containing approximately 3000 *Striga* seeds.

Grain yield and *Striga* resistance parameters were collected. The GY (expressed in g/plant) was determined as the weight of the grain from the ears of an individual plant after shelling, adjusted to 12.5% moisture content. *Striga* parameters comprised the number of emerged *Sa* and *Sh* plants 8 and 10 weeks after planting, denoted as SEC8 and SEC10. A rating of host plant damage 8 and 10 weeks after planting, designated as SDR8 and SDR10, was done using

a visual score of 1 to 9, where 1 = no damage, indicating normal plant growth and a high level of tolerance, and 9 = complete collapse or death of the maize plant, i.e., highly susceptible [28].

### 5.2.2 Genotyping

Following the plant DNA extraction protocol for DArT, genomic DNA was extracted from fresh leaves of 129 genotypes at the three-leaf stage [29]. The quality and purity of the extracted DNA were rigorously assessed using the NanoDrop 2000 spectrophotometer (ND-2000 V3.5, NanoDrop Technologies Inc) [30]. Each genotype provided a 20 µl DNA sample with concentrations between 50 and 100 ng and absorbance values ranging from 1.75 to 2.05. These samples were sent to Sequential Art (SEQAT) in Kenya (https://www.seqart.net/) for high-throughput genotyping using the DArTseq protocol. The genotyping yielded 70,197 SNPs, of which 16,000 informative SNPs were selected for further analysis after filtering out DArT loci with unknown chromosomal positions and markers with more than 20% missing data.

### 5.2.3 Grain yield and *Striga* parameters data analysis

Data collected on GY and *Striga* parameters were subjected to Bartlet's homogeneity of variance test before analysis of variance (ANOVA) using a lattice procedure, using the Deltagen platform. Genotypes mean comparison was done at the 5% significance level using Fisher's least significance difference (LSD). Broad sense heritability ($H^2$) was computed using DeltaGen with the following formula:

$$(H^2)= \frac{\sigma^2 g}{\sigma^2 g+\frac{\sigma^2 s}{ns}+\frac{\sigma^2 r}{nr}+\frac{\sigma^2 b}{nb}+\frac{\sigma_\varepsilon^2}{ns+nr+nb}}$$

where $\sigma^2 g, \sigma^2 s, \sigma^2 r, \sigma^2 b,$ and $\sigma_\varepsilon^2$ are the variance components for genotype, season, replication, block, and the pooled error, respectively, while ns, nr, and nb are the number of seasons, replications, and blocks, in that order. The linear mixed model was best-fit by the restricted maximum likelihood and used for phenotypic data analysis.

### 5.2.4 Genome-wide analysis to decipher marker-trait associations

The initial 70197 SNPs were imputed by removing SNPs with >20% missing data and < 5% minor allele frequency (MAF) on the KDCompute server (https://kdcompute.seqart.net/). A

filtered set of 16000 highly informative SNP markers was used for GWAS. The 130 maize genotypes were assessed for kinship using the software Structure [31]. The parameters of the analysis were set at 10000 burn-in periods, with 10000 Markov chain–Monte Carlo (MCMC) repetitions after burn-in. Five iterations were run for population number (K) values of 1 to 10 to allow the selection of the replication with the highest mean value of ln likelihood. The optimum K value was determined by the *ad-hoc* delta K method [32]. The linkage disequilibrium (LD) decay was estimated using the LD function in TASSEL software version 5.2.92 [33], and plotted with R version 4.3.0 (R Core Team, 2022) as described by Remington, *et al.* [34]. To identify the possible number of loci that are associated with *Striga* resistance in maize, pairwise LD of the populations was estimated using squared allele frequency correlations ($r^2$) for the DArTseq SNPs markers [30,35]. This was achieved using the LD measure, $r^2$ program (Version 2.1) within the KDCompute plugin system. The $r^2$ was estimated by an LD sliding window size of 50 and a threshold of $r^2$ set at 0.1, such that any SNP that was below 0.1 was considered to have a weak LD [36]. The SNPs significantly associated with *Striga* resistance were compared with the rest of the SNPs within the linkage group. The distribution pattern for the whole genome LD was visualized using graphs generated as LD heatmap from TASSEL v5.2.5. The inter-chromosomal LD among the SNPs was achieved by examining the LD data to determine whether some SNPs had an $r^2$ equal to or above 0.1. SNPs significantly associated with the traits of interest were recorded for each chromosome pair. Analysis for the genomic regions associated with *Striga* resistance and grain yield, probability values, and percentage of the effect of the markers were computed using the genome association and prediction integrated tool (GAPIT) package via the KDCompute interface (https://kdcompute.seqart.net/).

The associations between Single Nucleotide Polymorphisms (SNPs) and phenotypic traits were analyzed using the Compressed Mixed Linear Model (CMLM) implemented in the GAPIT software, as outlined by Yu et al. (2006). In this model, SNP markers were treated as fixed effects and were assessed individually. The model can be expressed as: $Y = X\beta + W\alpha + Qv + Zu + \varepsilon$, where Y is the observed vector for the phenotypic records of the traits; β is the fixed-effect vector ($p \times 1$) other than the molecular marker effects and the population structure; α is the fixed-effect vector of the molecular markers; v is the fixed-effect vector from the population structure; u is the random-effect vector from the polygenic background effect; X, W, Q, and Z are the incidence matrixes from the associated β, α, v, and u parameters; and ε is the residual effect vector, in that order [37]. The P values and false discovery rate thresholds were set at $P < 1 \times 10^{-4}$ and $-\log(p) = 3$ respectively. The kinship matrix was calculated from the 16000

markers, and the quantile-quantile (QQ) and Manhattan plots were generated using the log10 (p) value distributions of the GAPIT function in KDCompute.

The SNP(s) above the threshold value were used to indicate the genomic region associated with *Striga* resistance and grain yield traits. Further, the QQ plot was used to evaluate how well the model used in GWAS for this study accounted for population structure. The significant markers identified for each trait were blasted on Ensemble based on the maize genome version B73_V4.0. assembly to identify candidate genes associated with the markers using the maizeGDB (https://www.maizegdb.org/) platform.

## 5.3 **Results**

### **5.3.1 Phenotyping for grain yield response and *Striga* parameters**

Analysis of variance indicated significant genotypic variation (P< 0.05) for grain yield and *Striga* parameters in both *Sa* and *Sh*-infested environments (Table 5.1). Testing seasons had significant effects (P<0.001) on GY and *Striga* parameters under both *Striga*-infested conditions except for SEC10 under *Sa*-infested conditions. Also, significant effects of replications in seasons were noted for the assessed traits under the two conditions except for SDR8 and SDR10 under *Sa* conditions. Significant differences were also attributed to the block nested into replication-by-season interaction effect under both *Sa* and *Sh*-infested environments except for GY under *Sa*-infested conditions, and SDR10 under *Sh*-infested conditions.

**Table 5.1** Analysis of variance and significance tests for grain yield and *Striga* parameters of 130 maize genotypes evaluated under *Striga asiatica* and *S. hermonthica* infested conditions.

| | | ***S. asiatica*** | | | | |
|---|---|---|---|---|---|---|
| **Source of variation** | **Df** | **GY (g/plant)** | **SEC8** | **SEC10** | **SDR8** | **SDR10** |
| **Genotypes (G)** | 125 | 1205.52*** | 0.32*** | 52.94*** | 0.78*** | 0.55*** |
| **Seasons (S)** | 1 | 268.64*** | 6.55** | 0.70 | 53.50*** | 0.26* |
| **G x S** | 125 | 0.00 | 0.45 | 0.00 | 0.00 | 0.00 |
| **Replications in seasons** | 1 | 58.37*** | 2.22*** | 34.96*** | 0.40 | 0.04 |
| **Block/(replication x season)** | 13 | 0.00 | 0.79*** | 2.69** | 0.32*** | 0.73*** |
| **Error** | 238 | 924.67 | 0.95 | 100.66 | 1.54 | 1.47 |
| | | ***S. hermonthica*** | | | | |
| **Source of variation** | **Df** | **GY** | **SEC8** | **SEC10** | **SDR8** | **SDR10** |
| **Genotypes (G)** | 125 | 579.51*** | 4.29*** | 1.75*** | 0.88*** | 0.93*** |
| **Seasons (S)** | 1 | 460.89*** | 8.43*** | 1.73*** | 1.88*** | 0.44*** |
| **G x S** | 125 | 152.51 | 0.00 | 0.46 | 0.00 | 0.00 |
| **Replications in seasons** | 1 | 270.00*** | 2.27*** | 1.47*** | 1.97*** | 0.92*** |
| **Block/(replication x season)** | 13 | 41.39** | 0.61* | 0.33** | 2.44** | 0.03 |
| **Error** | 233 | 1126.63 | 5.84 | 4.83 | 2.21 | 1.28 |

*, **, and *** denote significance at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively, Df = degrees of freedom, GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing.

Low broad-sense heritability values were recorded for SDR8 (< 0.10) and SDR10 (0.11) in *Sa*-infested conditions. In contrast, a high heritability value was recorded for SEC8, SEC10, SDR8, and SDR10 ($H^2$ >0.50) but low for GY ($H^2$=0.02) under *Sh*-infested conditions (Table 5.2).

**Table 5.2** Broad sense heritability estimates for grain yield and *Striga* resistance traits of 130 maize genotypes evaluated over two seasons, under two *Striga*-infested conditions and two replications.

| | ***S. asiatica*** | | | | | ***S. hermonthica*** | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Parameter** | GY (g/plant) | SEC8 | SEC10 | SDR8 | SDR10 | GY | SEC8 | SEC10 | SDR8 | SDR10 |
| **Broad sense heritability** | 0.96 | 0.88 | 0.34 | 0.01 | 0.11 | 0.02 | 0.88 | 0.87 | 0.92 | 0.82 |
| **LSD (5%)** | 1.93 | 37.73 | 1.87 | 12.44 | 1.64 | 1.39 | 34.87 | 34.87 | 2.37 | 1.62 |

GY= grain yield, SEC8= *Striga* emergence counts eight weeks after sowing, SEC10= *Striga* emergence counts ten weeks after sowing, SDR8= *Striga* damage rating eight weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing, LSD= least significant difference.

### 5.3.2 Population structure and linkage disequilibrium

After removing markers with>20% missing values and a marker frequency (MAF) <5%, 16000 SNP markers were found polymorphic and were used for GWAS. The 16000 markers were distributed on the 10 chromosomes of the maize genome, with the highest and lowest marker densities observed on chromosome 8 (1272 SNPs) and chromosome 4 (835 SNPs), respectively. A population structure was constructed to reveal genetic relationships and aid genotype selection using the software Structure. The highest value for ΔK occurred at K= 8, showing that the genotypes could be clustered into eight sub-populations (Figure 5.1A and 5.1B). The minimum coefficient for membership to a particular sub-population was 0.70. A similar trend was also observed using the Kinship analysis, where eight clusters were identified (Figure 5.2).

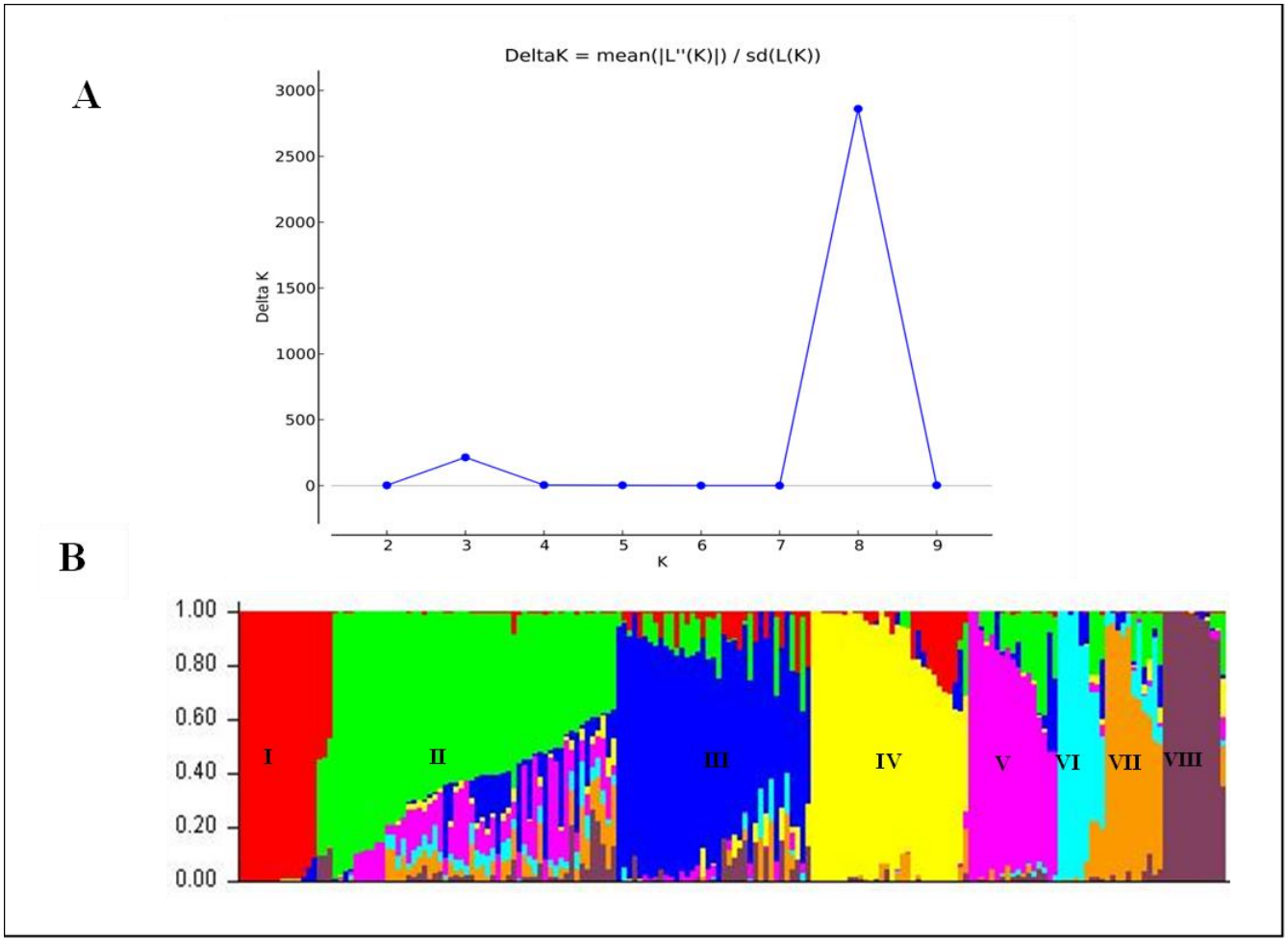


**Figure 5.1** The population structure ΔK (A) and the eight populations (B) of 130 maize genotypes resolved by the Evanno method based on 16000 SNP markers.

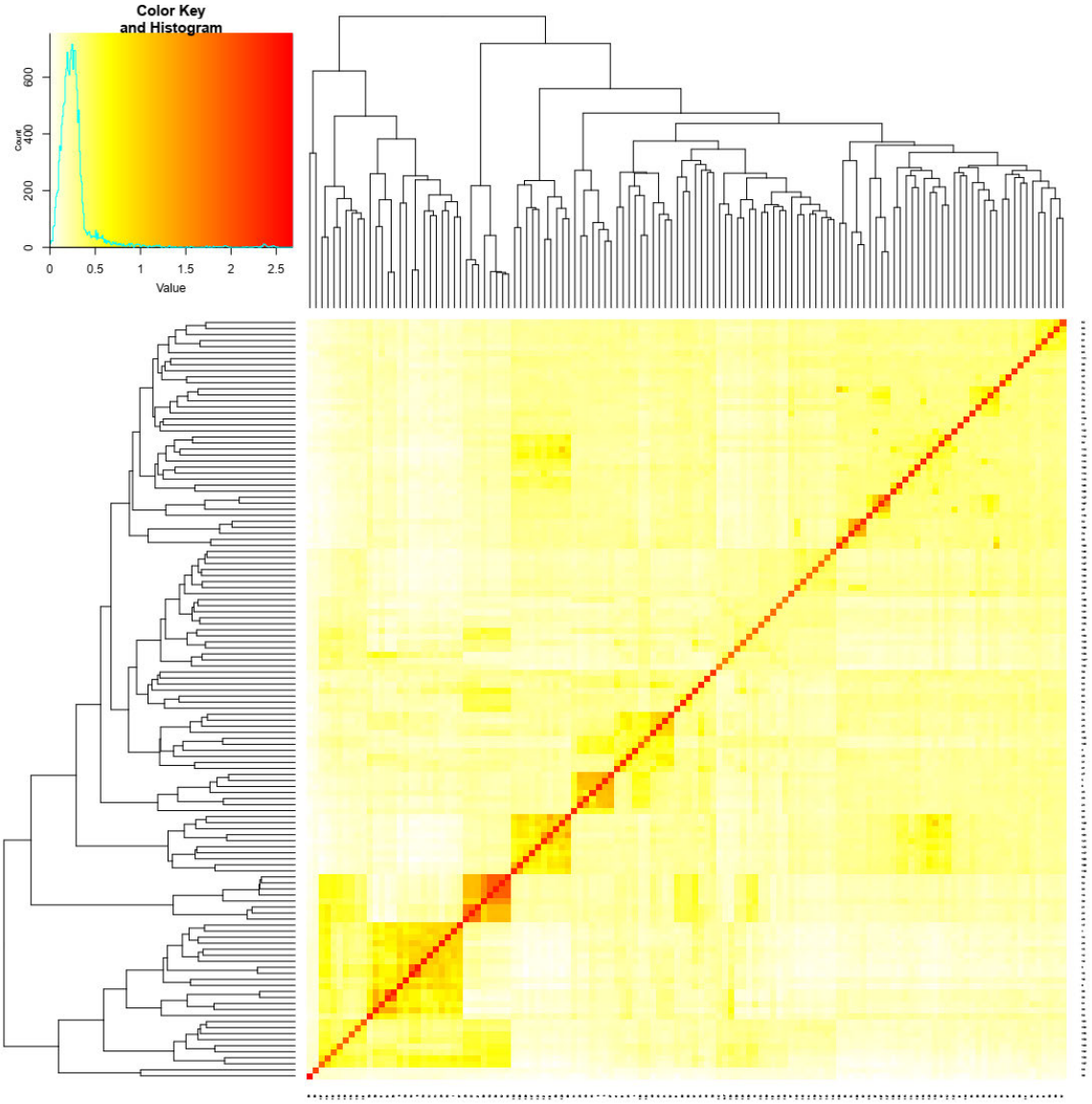


**Figure 5.2** Kinship heatmap showing the phylogenetic relationship among 130 maize genotypes using 16000 SNP markers. Red small squares indicate genetic relatedness, dark orange colours represent high kinship relations, while lighter colours (yellow) represent weaker relations. The dendrogram out of the matrix indicated the resulting clusters.

The LD was estimated by calculating the squared correlation coefficient ($r^2$) for all the 16000 SNPs. Pairwise LD analysis between 16000 SNP markers generated 798,675 comparisons within a physical distance extending up to 40,000,000 bp and was found to decay rapidly with the genetic distance. It was observed that LD varied along the chromosomes, with regions of high LD interspersed with regions of low LD (Figure 5.3A). About 353,719 (21.52%) loci pairs were in significant LD ($P < 0.001$). Further, 78157 (9.78%) were in complete LD ($r^{2 =} 1$), while 0.19% were at completely no LD ($r^2 = 0$). A critical value of $r^2$ was calculated from inter-

chromosomal LD analysis and is estimated to be 0.1, beyond which LD is assumed to be caused by genetic linkage. The point at which the locally estimated scatterplot smoothing (LOESS) curve intercepts the critical $r^2$ is determined as the average LD decay of the population. Based on these criteria, the intra-chromosomal LD decayed at 0.19 Mb for the whole genome (Figure 5.3B). The significant intra-chromosomal LD ($P < 0.001$) ranged from 0.00 to 1.00 with an average of 0.11 Mb for the whole panel.

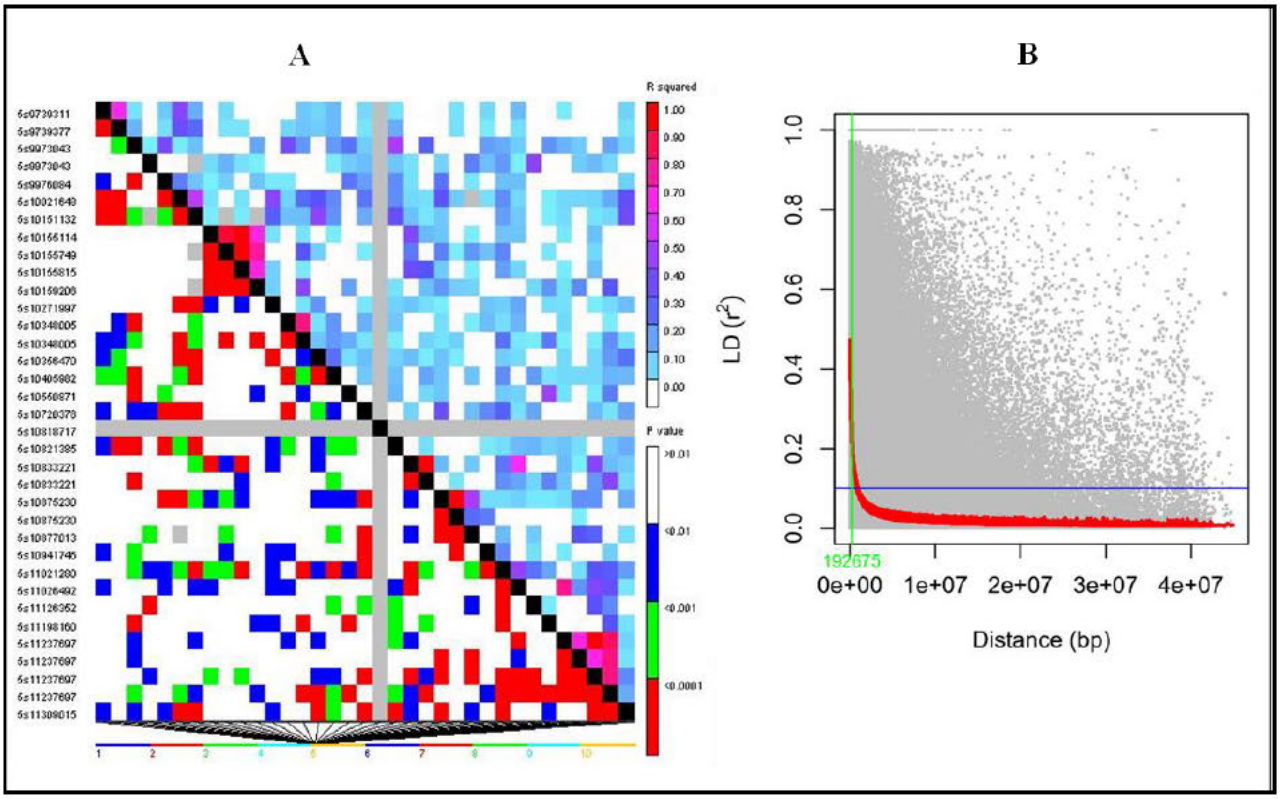


**Figure 5.3** Plots showing linkage disequilibrium (LD) heatmap (A) and intra-chromosomal LD decay (B) for 130 maize genotypes using 16000 SNP markers. Note: in Figure A the triangle on the right diagonal revealed the squared correlation coefficients ($r^2$), while the P values are shown on the lower diagonal of the triangle for each marker pair. In Figure B, the horizontal blue line indicates the 95$^{th}$ percentile distribution of unlinked $r^2$, while the red cover shows the locally estimated scatterplot smoothing (LOESS) illustrating the LD decay.

### 5.3.3 Marker-trait association (MTAs) under *S. asiatica* and *S. hermonthica*-infested conditions

Grain yield and *Striga* parameters (SEC8, SEC10, SDR8, and SDR10) were subjected to GWAS using 16000 SNP markers. The traits SDR8 under *Sa*-infested conditions and GY under *Sh*-infested conditions were not included in the GWAS due to their low heritability ($H^2 < 0.1$). The GWAS results across environments are shown in Manhattan plots and Q-Q plots of P

values comparing the expected −log10 p values to the observed −log10 p values in Figures 5.4 and 5.5 for *Sa* and *Sh* environments, respectively. A total of 72 MTAs were identified at $P \leq 1 \times 10^{-4}$ (Tables 5.3 and 5.4). Two MTAs were detected for GY under *Sa* (Table 5.3 and Figure 5.4), while seven significant MTAs were associated with the same trait under *Sh*-infested conditions (Table 5.4 and Figure 5.5). There were two, seven, and eleven MTAs for SEC8, SEC10, and SDR10, respectively, under *Sa*-infested conditions (Table 5.3 and Figure 5.4), while twelve, fourteen, seventeen, and seven MTAs were detected for the same traits, respectively under *Sh* conditions (Table 5.4 and Figure 5.5).

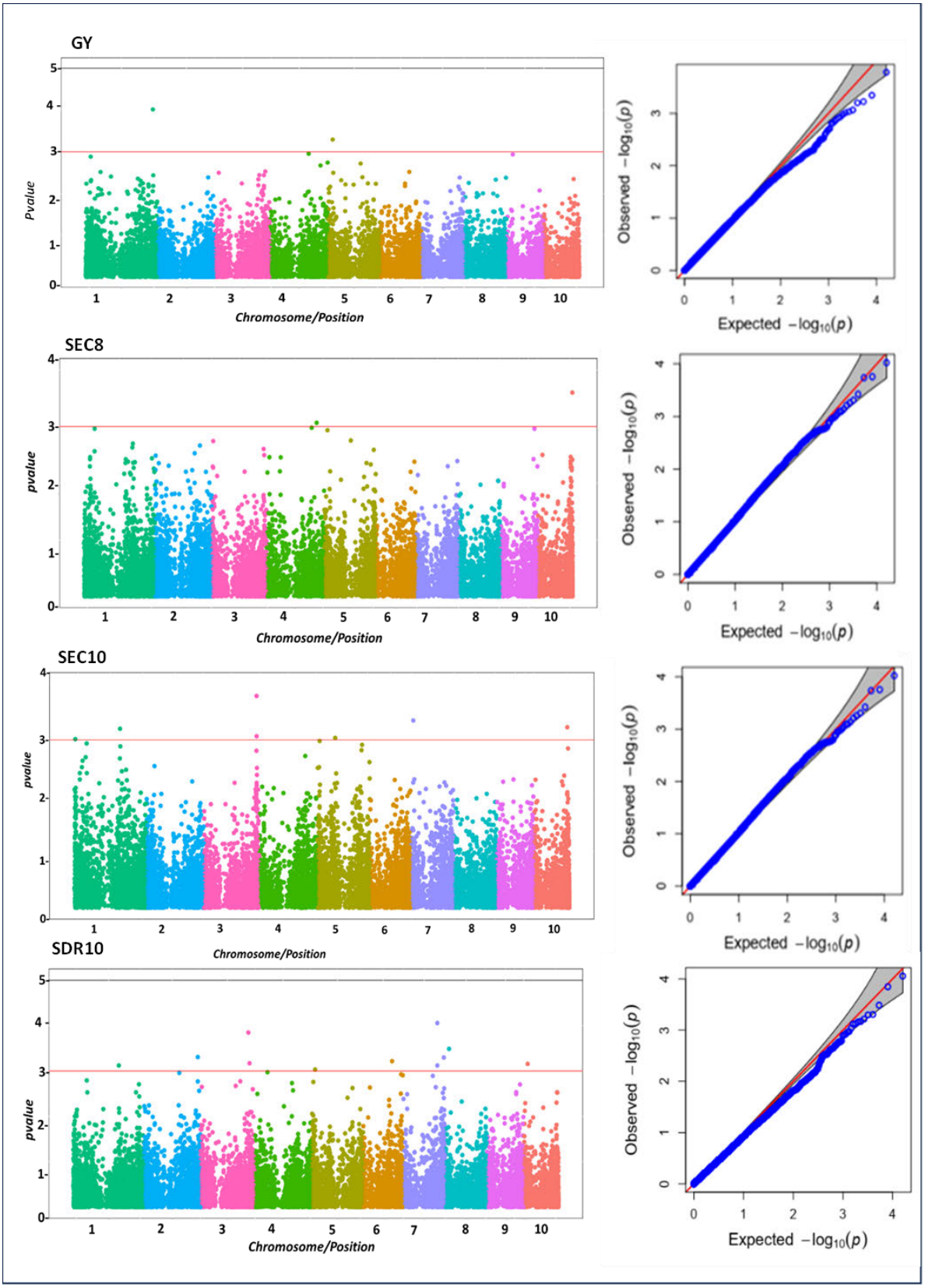


**Figure 5.4** Manhattan (right) and quantile-quantile (Q-Q) (left) plots showing SNPs associated with grain yield and *Striga* parameters in assessing 130 maize genotypes under *Striga asiatica*-infested conditions and 16000 SNP markers. The plots were drawn using the compressed mixed linear model at P <0.001. GY= grain yield, SEC8= *Striga* emergence counts 8 weeks after sowing, SEC10= *Striga* emergence counts 10 weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing

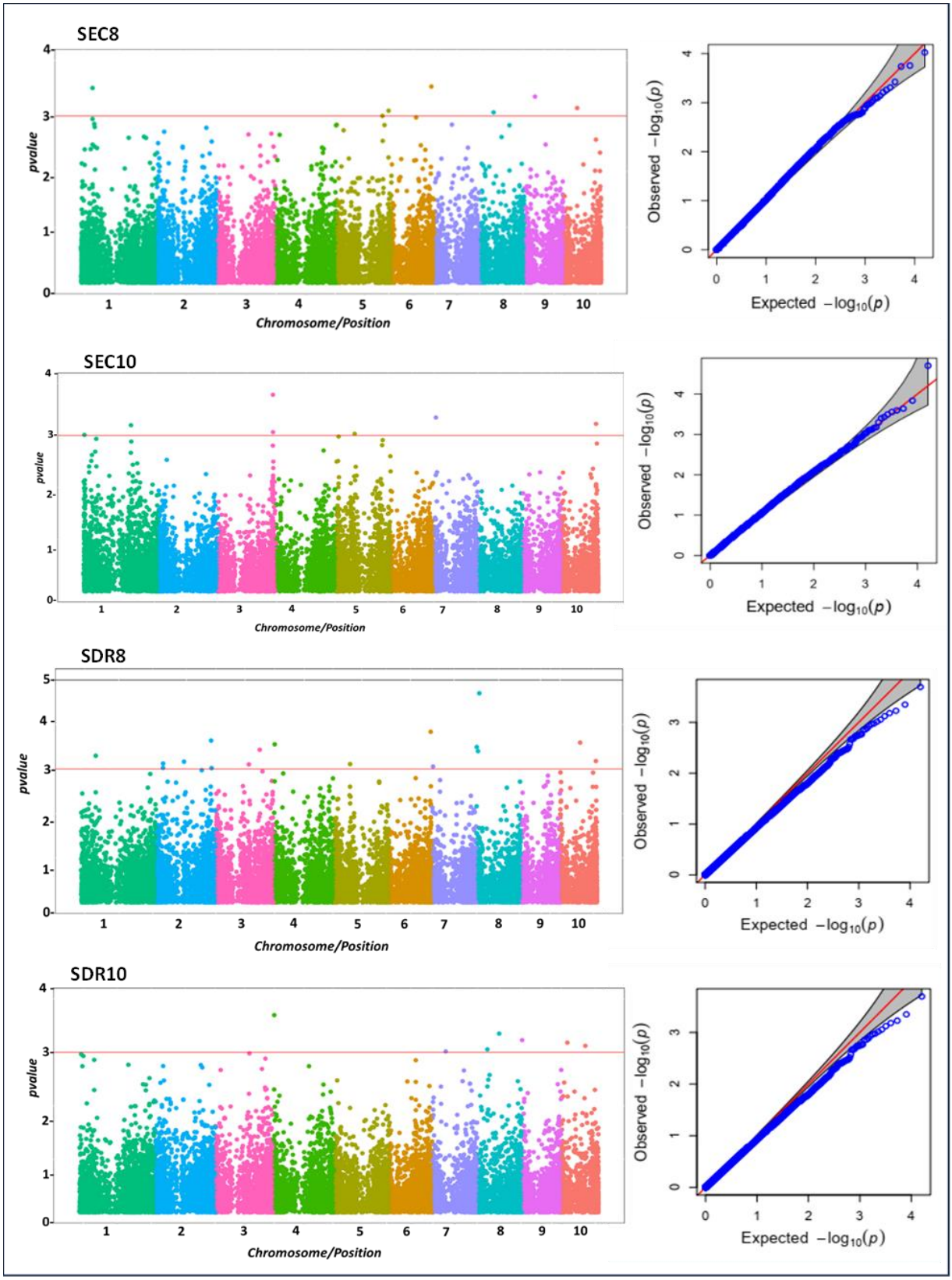


**Figure 5.5** Manhattan (right) and quantile-quantile (Q-Q) (left) plots showing SNPs associated with grain yield and *Striga* parameters in assessing 130 maize genotypes under *Striga hermonthica*-infested conditions and 16000 SNP markers. The plots were drawn using the compressed mixed linear model at P <0.001. SEC8= *Striga* emergence counts 8 weeks after sowing, SEC10= *Striga* emergence counts 10 weeks after sowing, SDR8= *Striga* damage rating 8 weeks after sowing, and SDR10= *Striga* damage rating 10 weeks after sowing.

**Table 5.3** *Striga asiatica* resistance-associated SNP markers and candidate genes identified in the association mapping panel of 130 maize genotypes.

| Traits | Marker codes | Chr | Position | p value | MAF | $R^2$ | Allelic effect | Gene ID | Annotation |
|---|---|---|---|---|---|---|---|---|---|
| GY | 2459912 | chr1 | 2.87E+08 | $9.67 \times 10^{-6}$ | 0.15 | 0.25 | 2.86 | | |
| | 100065851 | chr5 | 19528687 | $5.10 \times 10^{-5}$ | 0.10 | 0.22 | 0.47 | | |
| SEC8 | 100034001 | chr10 | 1.49E+08 | $2.50 \times 10^{-5}$ | 0.12 | 0.16 | 0.59 | Zm00001eb432870 | Putative oligouridylate binding protein |
| | 100096602 | chr4 | 2.15E+08 | $8.60 \times 10^{-5}$ | 0.13 | 0.14 | -0.54 | | |
| SEC10 | 2567877 | chr3 | 2.23E+08 | $1.60 \times 10^{-6}$ | 0.11 | 0.20 | 5.89 | Zm00001eb159960 | Transcription factor bHLH87 |
| | 100070348 | chr7 | 9877800 | $4.50 \times 10^{-6}$ | 0.35 | 0.19 | 4.03 | Zm00001eb301250 | Ethylene-overproduction protein 1 |
| | 4771900 | chr10 | 1.41E+08 | $5.90 \times 10^{-6}$ | 0.39 | 0.18 | 3.19 | Zm00001eb430230 | UBC core domain-containing protein |
| | 4590609 | chr1 | 1.94E+08 | $6.30 \times 10^{-6}$ | 0.16 | 0.18 | -4.88 | Zm00001eb036050 | Ras-related protein ARA-4 |
| | 4774001 | chr3 | 2.23E+08 | $8.60 \times 10^{-6}$ | 0.26 | 0.18 | 3.54 | Zm00001eb160080 | HSF transcription factor |
| | 100047118 | chr5 | 74829144 | $9.20 \times 10^{-6}$ | 0.42 | 0.17 | -2.70 | Zm00001eb230770 | tRNA (guanine(26)-N(2))-dimethyltransferase |
| | 4584680 | chr1 | 4146000 | $9.70 \times 10^{-6}$ | 0.38 | 0.17 | -3.54 | Zm00001eb001400 | NADH ubiquinone oxidoreductase B14 subunit |
| SDR10 | 4579420 | chr7 | 1.48E+08 | $8.70 \times 10^{-5}$ | 0.22 | 0.21 | 0.87 | Zm00001eb319510 | Oxidoreductase-like domain-containing protein |
| | 4582405 | chr3 | 2.08E+08 | $1.42 \times 10^{-6}$ | 0.25 | 0.20 | 0.054 | | |
| | 4770550 | chr8 | 16558612 | $3.20 \times 10^{-6}$ | 0.22 | 0.19 | 0.63 | | |
| | 100092893 | chr2 | 2.33E+08 | $4.90 \times 10^{-6}$ | 0.13 | 0.19 | 0.66 | Zm00001eb336310 | Myosin-binding protein 7; GTD-binding domain-containing protein |
| | 100048286 | chr7 | 1.76E+08 | $5.05 \times 10^{-6}$ | 0.19 | 0.18 | 0.85 | Zm00001eb114280 | PCI domain-containing protein; Uncharacterized protein |
| | 2464091 | chr6 | 1.25E+08 | $6.09 \times 10^{-6}$ | 0.27 | 0.18 | 0.52 | | |
| | 4773089 | chr3 | 2.13E+08 | $6.76 \times 10^{-6}$ | 0.28 | 0.18 | 0.56 | Zm00001eb156390 | Uncharacterized protein |
| | 7060947 | chr10 | 16779790 | $6.97 \times 10^{-6}$ | 0.25 | 0.18 | 0.62 | Zm00001eb409270 | Ureide permease 5 |
| | 2431593 | chr1 | 1.98E+08 | $7.50 \times 10^{-6}$ | 0.21 | 0.18 | 0.36 | | |
| | 100056350 | chr5 | 15102289 | $9.20 \times 10^{-6}$ | 0.30 | 0.18 | 0.54 | Zm00001eb217880 | Protein CDC73-like protein |

GY= grain yield, SEC8= *Striga* emergence counts 8 weeks after sowing, SEC10= *Striga* emergence counts 10 weeks after sowing, SDR10= *Striga* damage rating 10 weeks after sowing, MAF= minor allele frequency, and $R^2$ = squared correlation coefficient, Gene ID = gene identity.

**Table 5.4** *Striga hermonthica* resistance-associated SNP markers and their candidate genes identified in the association mapping panel of 130 maize genotypes.

| Traits | Marker codes | Chr | Position | p value | MAF | $R^2$ | Allelic effect | Gene ID | Annotation |
|---|---|---|---|---|---|---|---|---|---|
| **SEC8** | 100083158 | chr2 | 2.27E+08 | $9.5 \times 10^{-6}$ | 0.25 | 0.41 | 0.42 | | |
| | 4773476 | chr7 | 1.22E+08 | $1.75 \times 10^{-6}$ | 0.18 | 0.41 | 0.42 | | |
| | 100095995 | chr6 | 1.46E+08 | $1.84 \times 10^{-6}$ | 0.29 | 0.41 | 0.45 | Zm00001eb313080 | protein_coding |
| | 4582578 | chr5 | 2.06E+08 | $3.77 \times 10^{-6}$ | 0.21 | 0.40 | 0.54 | | |
| | 100085103 | chr9 | 1.28E+08 | $4.92 \times 10^{-6}$ | 0.16 | 0.39 | 0.42 | | |
| | 2375758 | chr5 | 2.13E+08 | $5.51 \times 10^{-6}$ | 0.19 | 0.39 | -0.05 | | |
| | 100077767 | chr5 | 4211185 | $6.16 \times 10^{-4}$ | 0.20 | 0.39 | 0.14 | Zm00001eb253620 | Sadenosylmethionine carrier 1 |
| | 4775335 | chr6 | 88822670 | $7.25 \times 10^{-4}$ | 0.15 | 0.39 | 0.59 | | |
| | 100072527 | Chr10 | 1.39E+08 | $7.99 \times 10^{-4}$ | 0.13 | 0.39 | 0.41 | | |
| | 100081160 | chr3 | 2.33E+08 | $8.01 \times 10^{-4}$ | 0.35 | 0.39 | 0.50 | Zm00001eb163250 | Clathrin heavy chain |
| | 2443196 | chr1 | 2.91E+08 | $8.98 \times 10^{-4}$ | 0.19 | 0.39 | 0.49 | Zm00001eb060090 | Nuclear pore complex protein NUP1 |
| | 4772592 | chr10 | 1.33E+08 | $9.96 \times 10^{-4}$ | 0.14 | 0.39 | 0.42 | Zm00001eb427110 | Serine/arginine repetitive matrix protein 2 |
| **SEC10** | 4771611 | chr3 | 27066610 | $2.7 \times 10^{-6}$ | 0.12 | 0.32 | 1.65 | Zm00001eb126130 | protein_coding |
| | 2378993 | chr3 | 27133911 | $4.9 \times 10^{-5}$ | 0.15 | 0.31 | 1.59 | Zm00001eb428830 | Dof zinc finger protein DOF4.6 |
| | 5583989 | chr10 | 1.28E+08 | $6.92 \times 10^{-5}$ | 0.09 | 0.30 | 1.79 | | |
| | 2447143 | chr5 | 66769956 | $1.1 \times 10^{-4}$ | 0.25 | 0.30 | 1.06 | | |
| | 4773342 | chr10 | 20619497 | $1.35 \times 10^{-4}$ | 0.18 | 0.29 | 1.18 | Zm00001eb409850 | Phosphoglucan |
| | 2429588 | chr6 | 1.33E+08 | $3.29 \times 10^{-4}$ | 0.36 | 0.28 | 0.84 | Zm00001eb281590 | proline-rich receptor-like protein kinase PERK8 |
| | 2448259 | chr5 | 76338383 | $3.30 \times 10^{-4}$ | 0.24 | 0.28 | 1.17 | | |
| | 2404041 | chr10 | 1.38E+08 | $3.37 \times 10^{-6}$ | 0.22 | 0.28 | 1.20 | Zm00001eb428830 | Dof zinc finger protein DOF4.6 |
| | 2543649 | chr8 | 1.68E+08 | $4.06 \times 10^{-4}$ | 0.15 | 0.28 | 1.30 | | |
| | 4770876 | chr5 | 20571879 | $4.78 \times 10^{-6}$ | 0.31 | 0.28 | 0.93 | Zm00001eb219710 | Terpene cyclase/mutase family member |
| | 4586050 | chr7 | 20584385 | $6.16 \times 10^{-6}$ | 0.30 | 0.27 | 0.95 | Zm00001eb303380 | Eukaryotic translation initiation factor 3 subunit E |
| | 2485365 | chr1 | 4403200 | $6.2 \times 10^{-6}$ | 0.17 | 0.27 | -0.13 | | |
| | 2468459 | chr10 | 1.22E+08 | $6.51 \times 10^{-4}$ | 0.30 | 0.27 | 0.80 | Zm00001eb001470 | Transcription factor TFIIIC |
| | 2463944 | chr1 | 2.37E+08 | $7.57 \times 10^{-4}$ | 0.22 | 0.27 | 1.13 | Zm00001eb046220 | Protein kinase domain-containing protein |

SEC8= *Striga* emergence counts 8 weeks after sowing, SEC10= *Striga* emergence counts 10 weeks after sowing, SDR8= *Striga* damage rating 8 weeks after sowing, SDR10= *Striga* damage rating 10 weeks after sowing, MAF= minor allele frequency, and $R^2$ = squared correlation coefficient, Gene ID = gene identity.

**Table 5.4** (continued)

| Traits | Marker codes | Chr | Position | p value | MAF | $R^2$ | Allelic effect | Gene ID | Annotation |
|---|---|---|---|---|---|---|---|---|---|
| **SDR8** | 4764587 | chr8 | 11275425 | $1.99 \times 10^{-6}$ | 0.18 | 0.20 | 1.01 | Zm00001eb334960 | Actin-interacting protein 1-2 |
| | 4772065 | chr6 | 1.68E+08 | $1.46 \times 10^{-6}$ | 0.46 | 0.16 | -0.46 | Zm00001eb295600 | Golgin candidate 5 |
| | 9681009 | chr2 | 2.23E+08 | $2.30 \times 10^{-6}$ | 0.45 | 0.16 | 0.42 | Zm00001eb112030 | Sister chromatid cohesion protein DCC1 |
| | 100068489 | chr10 | 81558128 | $2.55 \times 10^{-5}$ | 0.18 | 0.15 | 0.70 | | |
| | 2512743 | chr4 | 2964998 | $2.79 \times 10^{-5}$ | 0.37 | 0.15 | 0.97 | Zm00001eb165170 | protein_coding |
| | 2554932 | chr8 | 822625 | $3.20 \times 10^{-5}$ | 0.28 | 0.15 | 0.47 | Zm00001eb332250 | protein_coding |
| | 2447891 | chr3 | 1.77E+08 | $3.7 \times 10^{-5}$ | 0.23 | 0.15 | -0.08 | Zm00001eb145870 | LigB domain-containing protein |
| | 4778435 | chr8 | 5857145 | $3.90 \times 10^{-6}$ | 0.33 | 0.15 | 0.52 | | |
| | 4774228 | chr1 | 60226359 | $5.04 \times 10^{-4}$ | 0.21 | 0.14 | 0.54 | Zm00001eb016900 | protein_coding |
| | 2434422 | chr10 | 1.46E+08 | $6.63 \times 10^{-4}$ | 0.35 | 0.14 | 0.41 | | |
| | 4774905 | chr2 | 1.13E+08 | $6.85 \times 10^{-4}$ | 0.18 | 0.14 | -0.01 | | |
| | 2469044 | chr2 | 27774525 | $7.5 \times 10^{-4}$ | 0.19 | 0.14 | 0.16 | Zm00001eb076570 | Tubulin-folding cofactor B |
| | 100020060 | chr5 | 63352656 | $7.77 \times 10^{-4}$ | 0.13 | 0.14 | -0.63 | | |
| | 2539015 | chr3 | 1.33E+08 | $7.89 \times 10^{-4}$ | 0.31 | 0.14 | 0.49 | Zm00001eb137350 | ATP10 protein expressed |
| | 4775714 | chr7 | 4773701 | $8.87 \times 10^{-4}$ | 0.15 | 0.13 | 0.59 | Zm00001eb299670 | GYF domain-containing protein |
| | 5585130 | chr2 | 27502516 | $9.44 \times 10^{-4}$ | 0.21 | 0.13 | 0.47 | Zm00001eb112030 | Sister chromatid cohesion protein DCC1 |
| **SDR10** | 2512743 | chr4 | 2964998 | $2.01 \times 10^{-6}$ | 0.37 | 0.14 | 0.94 | Zm00001eb165170 | protein_coding |
| | 2620744 | chr8 | 88538381 | $4.47 \times 10^{-6}$ | 0.37 | 0.14 | 0.52 | Zm00001eb346540 | protein_coding |
| | 7049807 | chr9 | 328756 | $5.92 \times 10^{-5}$ | 0.19 | 0.14 | 0.79 | Zm00001eb371500 | microtubule-associated protein 70-2 isoform X2 |
| | 2520511 | chr10 | 24263900 | $6.58 \times 10^{-5}$ | 0.20 | 0.13 | 0.50 | Zm00001eb410250 | Kinesin-like protein KIN-14Q |
| | 4582343 | chr10 | 96965850 | $7.56 \times 10^{-5}$ | 0.25 | 0.13 | -0.53 | Zm00001eb419180 | Receptor kinase |
| | 4770996 | chr8 | 40631480 | $8.81 \times 10^{-5}$ | 0.46 | 0.13 | 0.41 | Zm00001eb340640 | Polygalacturonase |
| | 4590802 | chr7 | 54060484 | $9.64 \times 10^{-5}$ | 0.25 | 0.12 | 0.43 | Zm00001eb307490 | Phytocyanin domain-containing protein |

SEC8= *Striga* emergence counts 8 weeks after sowing, SEC10= *Striga* emergence counts 10 weeks after sowing, SDR8= *Striga* damage rating 8 weeks after sowing, SDR10= *Striga* damage rating 10 weeks after sowing, MAF= minor allele frequency, and $R^2$ = squared correlation coefficient, Gene ID = gene identity.

The two MTAs recorded for GY under *Sa*-infested conditions were located on chromosomes 1 and 5 (Table 5.3). For SEC8, the 14 MTAs were identified on chromosomes 1 (one marker), 2 (one marker), 3 (one marker), 5 (three markers), 6 (two markers), 7 (one marker), 9 (one marker), and 10 (two markers) for *Sh*-infested conditions and chromosomes 10 (one marker) and 4 (one marker) for *Sa*-infested conditions. The 21 MTAs observed for SEC10 were on chromosomes 1 (two markers), 3 (two markers), 5 (three markers), 6 (one marker), 7 (one

marker), 8 (one marker), and 10 (four markers) for *Sh*-infested conditions and on chromosomes 1 (two markers), 3 (two markers), 5 (one marker), seven (one marker), and 10 (ten markers) for *Sa*-infested conditions. SDR8 had 15 MTAs from chromosomes 1 (one marker), 2 (five markers), 3 (one marker), 4 (one marker), 5 (one marker), 6 (one marker), 7 (one marker), 8 (two markers), and 10 (two markers) in *Sh*-infested environment. MTAS for SDR10 were identified on chromosomes 4 (one marker), 8 (two markers), 9 (one marker), 10 (two markers), and 7 (one marker) under *Sh*-infested conditions and on chromosomes 1 (one marker), 2 (one marker), 3 (two markers), 5 (one marker), 6 (one marker), 7 (three markers), 8 (one marker), and 10 (one marker) for *Sa*-infested environment. Ten of the significant MTAs showed a negative allelic effect under *Sa*-infested conditions (Table 5.3), and six had a negative allelic effect under *Sh*-infested conditions (Table 5.4). One pleiotropic MTA was identified for SDR8 and SDR10 on chromosome 4 under *Sh*-infested conditions (Table 5.4).

### 5.3.4 Candidate genes associated with grain yield and *Striga* resistance traits

Based on SNP genome-wide association mapping, 33 and 14 candidate genes were identified for *Sh* and *Sa* resistance, respectively. The significant SNPs associated with GY under *Sh* were linked to six candidate genes Zm00001eb288770, Zm00001eb014030, Zm00001eb014020, Zm00001eb381210, Zm00001eb412710, and Zm00001eb219710. However, no candidate genes were associated with GY under *Sa*-infested conditions. Five of the markers linked to SEC8 under *Sh*-infested environment flanked the regions overlapping the candidate genes Zm00001eb313080, Zm00001eb253620, Zm00001eb272670, Zm00001eb163250, and Zm00001eb060090 on chromosome 1, 5, 6, and 10. In *Sa*-infested environment, only one candidate gene, Zm00001eb432870, was associated with SEC8. Eight and seven putative candidate genes were detected for SEC10 under *Sh* and *Sa*-infested conditions, respectively. These genes were located on chromosomes 5, 6, 7, 8, and 10, under *Sa* conditions, and 1, 5, 6, 7, 8, and 10 under *Sh*-conditions. Under *Sa*-conditions, the genes associated with SEC10 were located on chromosomes 1, 3, 5, 7, and 10. Twelve genes were identified for SDR8 under *Sh*-infested conditions and were located on chromosomes 1, 2, 3, 4, 5, 6, 7, and 8. The significant SNPs involved in SDR10 under *Sh*-infested conditions were localized within the following candidate genes: Zm00001eb165170, Zm00001eb346540, Zm00001eb371500, Zm00001eb410250, Zm00001eb419180, Zm00001eb340640, and Zm00001eb307490. Out of the 12 MTAs for SDR10 in *Sa*-infested environment, nine were found in regions covering the

following genes: Zm00001eb319510, Zm00001eb336310, Zm00001eb114280, Zm00001eb329320, Zm00001eb156390, Zm00001eb409270, and Zm00001eb217880 on chromosomes 2, 3, 5, 7, and 10.

## 5.4 **Discussion**

### 5.4.1 Phenotyping

The parasitic weeds *Sh* and *Sa* have been recognized as major constraints to maize production in SSA. *Striga* resistance is a polygenic trait and is subject to genotype-environment interaction effects needing accurate selection strategies. Agronomic management options (e.g. crop rotation, intercropping, catch-cropping, and trap-cropping) are often insufficient. There is a need for integrated *Striga* management spearheaded by resistance breeding programmes. Breeding for *Striga* resistance is the most economical approach to minimize yield loss of major cereal crops caused by *Striga* infestation in SSA. Hence, genetic markers associated with *Striga* resistance need to be identified to guide the pace and precision of resistance breeding in maize [38,39]. Integrating marker-assisted and conventional breeding techniques will accelerate the breeding and genetic gain of maize for *Striga* resistance [40]. In this study, a GWAS was conducted based on a panel of genetically diverse maize populations comprising 98 inbred lines, 21 OPVs, and 11 top cross hybrids to discern genetic loci associated with resistance to the two dominant *Striga* species (Appendix 5.1).

The phenotypic evaluation revealed significant variability for both *Sa* and *Sh* resistance among the tested maize genotypes, thus confirming the availability of relevant alleles for future breeding and genetic improvement (Table 5.1). The broad sense heritability observed for *Striga* damage under *Sa*-infested conditions was low (SDR8= 0.01 and SDR10= 0.11) compared to *Sh* resistance (SDR8= 0.92 and SDR10= 0.82) (Table 5.2). This suggests that the genotypic variance of the *Sa* resistance traits was low compared to the phenotypic variance, making direct selection difficult for *Sa* resistance. This confirms that *Sh* resistance has been the focus of more research that yielded higher genetic variation than *Sa* in maize. The high heritability of *Sh* resistance suggests that the genotypic variance was relatively higher supporting phenotypic selection. Hence, *Sh* traits can be relatively quickly selected (Table 5.2). The present results agree with Olakojo and Olaoye [41], who reported low heritability of some *Striga* parameters and high heritability on other associated traits when assessing maize agronomic traits for yield improvement and *Sa* tolerance. However, the high heritability values obtained here could suggest the involvement of high nonadditive genetic variance and the confounding effects of the test environments, as *Striga* resistance traits are known low heritable. This implies the need to test the population across multiple growing environments to reduce the confounding effect of the test environments and genotype-by-environment interaction effect.

### 5.4.2 Population structure and linkage disequilibrium

Estimating population structure and within-group familial relatedness in maize genomic association studies is important to reduce the risks of false positives [42]. The Structure and Kinship analyses revealed population stratifications and admixtures, suggesting the need to use a robust statistical model in association analysis to control spurious MTAs [43]. The present analyses suggested eight sub-groups in the assessed tropical and sub-tropical maize population (Figure 5.1), and the clustering was mainly based on genotype and geographic origin. This was expected, given that the genetic material used in the study was from diverse sources. The kinship heatmap showed different genetic relatedness in each group (Figure 5.2). Hybrids and OPVs from IITA/Nigeria, NPGRC/South Africa, and CIMMYT/Zimbabwe form a distinct cluster from inbred lines from IITA/Nigeria and CIMMYT/Zimbabwe. Some clusters consisted of inbred lines from IITA (Clusters VI, VII, and VIII) or inbred lines from CIMMYT (Cluster V) (Figures 5.1 and 5.2). The genetic distinctness of tropical inbred lines from CIMMYT lines suggests that crosses could be explored to achieve high heterosis and *Striga* resistance with broader adaptation.

Based on pairwise LD analysis involving 16000 DArTSeq SNP markers, a low number of markers (9.78%) were in perfect LD ($r^2$=1), which are more likely to be inherited across the whole genome. This reveals that this marker population was ideal for association mapping, as SNP markers in a strong LD provide redundant genotyping information during association analysis [44]. Furthermore, the rapid LD decay points to the high genetic diversity of the present panel and its usefulness for GWAS with a genetic mapping resolution (Figure 5.3). The high genetic diversity is also associated with the genetic material that is composed of tropical and sub-tropical populations. The rapid LD decay is in agreement with previous studies in maize [45,46] and other crops [47-49].

### 5.4.3 Marker-trait association for *Striga* resistance

For GWAS analysis, the study used CMLM model in GAPIT. The CMLM model of GAPIT was demonstrated to be more powerful and effective in association studies and can provide accurate predictions with less computing time [50]. Also, the method significantly reduces false positives [51]. The QQ plots revealed that the population structure and the phenotypic data were well distributed in both *Striga*-infested conditions, as the expected P-values were close to

the observed P-values (Figures 5.4 and 5.5). The plots revealed a good fit of the model. The kinship deviation at the top of the null hypothesis diagonal points to a great association between the markers and the traits (Figures 5.4 and 5.5). The present study identified 22 MTAs for grain yield and *Striga* resistance traits under *Sa* infestations. The MTAs comprised of 2 MTAs conditioning GY, 2 MTAs conditioning SEC8, 7 MTAs conditioning SEC10, and 11 MTAs conditioning SDR10 (Table 5.3 and Figure 5.4). Fifty-seven MTAs were found for GY (7), SEC8 (12), SEC10 (14), SDR8 (17), and SDR10 (7) under *Sh* infestation (Table 5.4 and Figure 5.5). The marker 2512743 was pleiotropic for SDR8 and SDR10 for *Sh* resistance (Table 5.4) and could be useful for simultaneous selection. The SNPs were distributed across almost all chromosomes for all the assessed traits in the present study. The variable chromosome suggests that *Striga* resistance is a complex trait governed by polygenes. The significant markers identified in the current populations were located on chromosomes previously reported to harbour genes linked to *Striga* resistance traits including *Striga* emergence counts and *Striga* damage rating scores [13,24,52]. The significant markers for GY were located on chromosomes 1, 5, 6, 8, 9, and 10 and were associated with *Sh* resistance, and on chromosomes 1 and 5, they were associated with *Sa* resistance. These results corroborate previous studies that highlighted the importance of chromosome 10 [13], chromosome 6 [24], and chromosome 9 [52] for GY response under *Sh* conditions. In the present study, MTAs for *Striga* emergence counts were recorded on chromosome 5, previously reported to have a significant association with the same trait using the marker GRMZM2G018508 by [24], and GRMZM2G129543 and GRMZM5G823157 [52] in tropical maize lines. The same authors reported the ten chromosomes harbouring genes for *Sh* host damage in agreement with the present study. The markers reported in the present study for *Sa* resistance are novel except for the three SNPs reported by Pfunye, et al. [8] on chromosomes 5, 6, and 7 for total *Striga* plants emerged. There is a knowledge gap in QTL analysis associated with *Sa* resistance. The results revealed that different genomic regions are involved in *Striga* resistance (Tables 5.3 and 5.4). None of the genetic markers were associated with dual resistance of both *Sa* and *Sh*, suggesting that different genomics regions govern resistance for the two *Striga* species. Further association studies should be done using different populations to search for markers and genes controlling GY and *Striga* resistance traits under *Sa* and *Sh* infestation, as the two *Striga* species occur in tandem, especially in East Africa.

Seven of the significant markers had a negative allelic effect under *Sh*-infested conditions and four significant MTAs showed a negative allelic effect under *Sa*-infested conditions (Tables

5.3 and 5.4). This implies that these genetic markers are linked with *Striga* resistance proper for introgression into desirable parents. A negative allelic effect indicates that the allele is associated with a more resistant phenotype in a desirable direction. On the other hand, a positive effect indicates the opposite [53]. Stably expressing SNPs are useful for maize breeders to introduce target QTL in pipeline breeding materials. In this study, markers 4772065 and 2447891 are more stable for SDR8 under *Sh*-infested conditions.

Forty-one and 23 candidate functional genes were identified for *Striga* resistance under *Sh* and *Sa*-infested environments, respectively (Tables 5.3 and 5.4). Most detected genes are involved in various cellular and metabolic processes, plant defense, and cell development. The candidate gene Zm00001eb319510 is significantly associated with SDR10 under *Sa*-infested conditions and encodes Oxidoreductase-like domain-containing protein. Other candidate genes, such as Zm00001eb163250, Zm00001eb295600, Zm00001eb165170, and Zm00001eb165170 associated with SEC8, SDR8, and SDR10 under *Sh*-infested conditions, encode Clathrin heavy chain, Golgin candidate 5, and AAA+ ATPase domain-containing protein respectively. The candidate gene Zm00001eb288770 associated with GY under *Sh*-conditions on chromosome 6 encodes for Coronatine-insensitive protein 1. Zm00001eb288770 is linked with jasmonate production, which regulates defense against insects and pathogens, wound healing, and pollen fertility [54]. The results show the involvement of Zm00001eb288770 in maize's tolerance response to *Striga*. Another putative gene Zm00001eb253620, encodes for S-adenosylmethionine carrier 1 chloroplastic/mitochondrial that acts as a precursor of ethylene (a senescence inducer) and polyamines (antisenescence molecules) and controls the regulation of senescence in plants [55]. One of the main symptoms of *Striga* infestation is rapid senescence. This suggests that the gene Zm00001eb253620 is vital to unlocking *Striga* resistance breeding. Zm00001eb409850 encodes CBM20 domain-containing protein is implicated in both glycogen metabolism and autophagy [56]. The gene model Zm00001eb219710 associated with GY under *Sh*-infested conditions on chromosome 8 is associated with SEC10 under the same conditions on chromosome 7. Zm00001eb165170 and Zm00001eb112030 are linked with SDR8 and SDR10 under *Sh*-infested conditions.

## 5.5 **Conclusion and recommendation**

The present study is the first attempt to identify genomic regions associated with the dual resistance of maize to *Sa* and *Sh*. A population of 130 maize germplasm was used, comprising tropical and sub-tropical inbred lines, OPVs, and hybrids. The study identified 72 SNPs

associated with grain yield and *Striga* resistance parameters under *Sa* and *Sh*-infested conditions. However, markers 4772065 and 2447891 are considered more stable for SDR8 under *Sh*-infested conditions. No marker was linked with dual resistance to *Sh* and *Sa*. Fifty significant markers were associated with *Sh* resistance and 22 were linked to *Sa* resistance. Significant SNPs were found flanking 47 protein-coding putative genes, of which one was associated with GY, while six, sixteen, eleven, and thirteen genes linked to SEC8, SEC10, SDR8, and SDR10 were associated with *Sh* and *Sa* resistance. Some of the detected genes reportedly conditioned insect and pathogen resistance, plant cell development, variable senescence, and pollen fertility. The gene Zm00001eb219710 was pleiotropic, and conditioned GY and SEC10, while Zm00001eb165170 affected SDR8 and SDR10, and Zm00001eb112030 conditioned SDR8 and SDR10 associated with *Sh* resistance. The candidate markers may facilitate simultaneous selection for *Sh* and *Sa* resistance and grain yield in maize after further evaluation and introgression in breeding pipelines. We recommend resistance breeding of maize on separate genetic backgrounds for *Sa* and *Sh* resistance. This will allow to separately appreciate the economic importance of the two major *Striga* species. The genetic markers associated with *Striga* resistance detected in this study can be utilized in breeding programs using strategies including marker-assisted selection, gene editing technology, and gene pyramiding. The results concluded that novel markers and genes controlling *Sa* and *Sh* in maize are detected using GWAS in genetically diverse tropical and sub-tropical maize populations.

## 5.6 **References**


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## Introduction and objectives of the thesis

Maize (*Zea mays* L., 2n = 2x = 20) is a commodity cereal crop serving diverse value chains worldwide. It is the leading food staple in sub-Saharan Africa (SSA), sustaining the livelihood of more than 900 people. The grain yield of maize in SSA is < 3 t/ha due to various production challenges. The low productivity of maize in the region is attributable to an array of abiotic and biotic stresses with parasitic weeds of the genus *Striga,* mainly *Striga hermonthica* (*Sh*) and *S. asiatica* (*Sa*) being the leading yield-limiting factors, with 10 to 100% yield losses under severe infestation. *Striga*-resistant varieties are the most economical and environmentally friendly control method, which can be adopted for sustainable use by small-holder maize producers. However, most available resistant varieties have been bred for *Sh* resistance, while both *Sh* and *Sa* are challenging for maize production in the same or different fields in the region. There is a need to bolster the genetic resistance of maize against *Sa* and *Sh* by harnessing genetic diversity and identifying markers and genes for breeding. Detailed information on the genetic diversity of the available tropical and sub-tropical genetic resources, their genetic interrelationships, heterotic patterns, quantitative trait loci (QTL), and combining ability and gene action of parents and derived hybrids are prerequisites in *Striga* resistance breeding programs. Unique *Sa* and *Sh* resistance genes or QTL that confer durable resistance to maize can be deciphered using a genome-wide association study (GWAS). This chapter highlights the study objectives, major outcomes, and implications.

The objectives of this study were:

6) To undertake a meta-analysis and provide a detailed comparison of the *Striga* control methods in the production of maize, sorghum, and the major millets as a guide to effective *Striga* management.
7) To assess the response of 130 tropical and sub-tropical African maize germplasm to *Sh* and *Sa* resistance and desirable agronomic traits and select promising genotypes.
8) To determine the genetic diversity of 130 tropical and sub-tropical maize inbred lines, hybrids, and open-pollinated varieties using phenotypic traits and single nucleotide polymorphism (SNP) markers to select *Striga*-resistant and complementary genotypes for breeding.

9) To determine the combining ability and gene action controlling grain yield and *Striga* resistance among single crosses of maize to select desirable hybrids with *Sh* and *Sa* resistance and promising agronomic traits.
10) To undertake a genome-wide association analysis of grain yield and *Sh* and *Sa* resistance among tropical and sub-tropical maize populations to identify putative genetic markers and genes for marker-assisted resistance breeding and gene pyramiding.

The major findings were that maize and sorghum varieties with *Striga*-resistant genes showed higher grain yields and lower *Striga* damage than other non-genetic control methods. *Striga* damage rating score (SDR) was found to be the best selection criterion for improving grain yield (GY) performance in maize, while *Striga* emergence count (SEC) and SDR are the parameters of choice in sorghum selection programs for better GY under *Striga* infestation. The results from the meta-analysis demonstrate that not all the recommendations on *Striga* control methods in Africa were fully implemented and supported. The analysi revealed that the integrated *Striga* management (ISM) recommended by most research institutions is yet to be explored and optimised by rigorous agronomic and socio-economic data. This advancement underscores the need for further research on optimal ISM combinations and multi-environment evaluations to enhance *Striga* resistance and cereal production in *Striga*-infested regions. Host resistance emerged as the most effective control method, highlighting the need for further research on optimal ISM combinations for cereal production under *Striga* infestation in Africa. Few studies have investigated *Striga* control methods in pearl millet and finger millet, which limits the ability to make comprehensive comparisons. The limited research on *Striga* control methods in millets shows that research must focus on millets production under *Striga* infestation. Addressing this research deficiency is crucial for advancing *Striga* control and improving yields in regions where pearl millet and finger millet are staple crops. These new insights are important in advancing *Striga* research in SSA.

One hundred and thirty tropical and sub-tropical maize germplasms were evaluated, identifying several genotypes with dual resistance to both *Striga* species. Significant genetic diversity and phenotypic variation were revealed among the assessed tropical and sub-tropical maize inbred lines, hybrids, and open-pollinated varieties germplasm when assessed using phenotypic traits and single nucleotide polymorphism markers. This offers various clusters of genetically distant, high-yielding and *Striga*-resistant tropical and sub-tropical genotypes that can be used to breed durable *Striga*-resistant maize varieties in SSA.

Hybrid breeding using specific testers and lines demonstrated high yields and *Striga* resistance, with several promising crosses identified. Finally, a genome-wide association study (GWAS) identified significant loci and candidate genes associated with *Sh* and *Sa* resistance, with markers for *Sa* resistance reported for the first time. These results provide new insights for *Striga* research advancement by emphasizing the importance of developing and utilizing *Striga*-resistant crop varieties to improve maize yield. The identification of dual-resistant genotypes and significant loci offers valuable resources for breeding programs. The findings also highlight the potential for simultaneous selection for *Sh* and *Sa* resistance and grain yield, paving the way for more effective and targeted breeding strategies.

**Implications of the study for future maize breeding with enhanced yield and *Striga asiatica* and *S. hermonthica* resistance in sub-Saharan Africa**.

The overall implications of the present study are described below.

- The meta-analysis indicated that host resistance is the most effective method for controlling *Striga* infestation and boosting GY in maize and sorghum. There is an ongoing need for research into the best combinations of the reported control methods as a sound basis for recommending an ISM package across target production environments of common cereals in Africa.
- The following tropical and sub-tropical genotypes have dual resistance to *Sa* and *Sh*: CML440, CML566, CML540, CML539, CLHP0343, CLHP0326, TZISTR1248, TZSTRI115, TZISTR25, TZISTR1205, TZSTRI113, TZISTR1119, TZISTR1174 and the OPVs B.King/1421, Shesha/1421, ZM1421, DTSTR-W SYN13, DTSTR-Y SYN14, and 2*TZECOMP3DT/WhiteDTSTRSYN) C2. The identified genotypes are suitable for use as parents in developing high-performing maize varieties with *Striga* resistance and improved grain yield.
- Considerable genetic variation was available in the panel of maize evaluated in this study using phenotypic traits and SNP markers. The following genetically distant inbred lines were selected, displaying good agronomic performance and *Sa* and *Sh* resistance: CML540, TZISTR25, TZISTR1248, CLHP0303, TZISTR1174, TZSTRI113, TZDEEI50, TZSTRI115, CML539, TZISTR1015, CZL99017, CML451, CML566, CLHP0343 and CML440.

- Parental lines and single crosses with high combining ability for *Striga* parameters, yield, and yield-related traits were selected. The selected lines and testers and the new experimental hybrids are recommended for multi-environment evaluation in *Sa* and *Sh*-prone agro-ecologies to enhance grain yield and *Striga* resistance.
- Fifty significant loci associated with *Sh* resistance, and 22 significant loci linked to *Sa* resistance were identified, corresponding to 39 and 19 candidate genes, respectively.
- Breeding maize specifically for resistance to each *Striga* species using germplasm adapted to the endemic region of each parasite is paramount with gene pyramiding in productive hybrid cultivars.

Overall, the results from all chapters support the initial hypothesis of this thesis: Considerable genetic variation was available in the panel of maize evaluated, and novel genetic markers and genes were identified associated with *Sa* and *Sh* resistance and high grain yield useful in *Striga* resistance breeding programs in SSA.