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RESEARCH

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

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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 13 × 10 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

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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 (Lobulu et al. 2021). 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* in the field (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 do not have access to the money required 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 study aimed to evaluate 130 tropical and sub-tropical maize germplasms in a controlled environment for their reaction to *Sh* and *Sa* infestations and for resistance breeding. This study is 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.

Materials and methods

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–April 2022, and August 2022–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 1). The germplasm from IITA/Nigeria comprised 55 inbred lines (genotypes number 1–55 in Table 1), 4 single cross hybrids (genotypes number 127–130 in Table 1), and 15 open-pollinated varieties (OPV) (genotypes number 112–126 in Table 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 56–98 in Table 1), and 1 OPV (genotype number 110 in Table 1). The NPGRC/South Africa germplasm included 5 OPVs (genotype 99–103 Table 1) and 6 hybrids (genotype 104–109 Table 1). The Nigerian accessions were tropical varieties developed for *Sh* resistance, generated from multi-parent populations (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.

Experimental design and trial management

The 130 genotypes were evaluated under two *Striga* treatments using a 13×10 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 2 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 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.

Table 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/TZLCom-pIC4S1-37-1-B*4)-4-B*4
2	TZISTR1261	IITA/Nigeria	Resistant/inbred line	(ACRSYN-W-S2-173-B*4/TZLCom-pIC4S1-37-5-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/TZLCom-pIC4S1-37-1-B*4)-28-B*4
7	TZISTR1160	IITA/Nigeria	Resistant/inbred line	(ACRSYN-W-S2-173-B*4/TZLCom-pIC4S1-37-1-B*4)-50-B*4
8	TZISTR1162	IITA/Nigeria	Resistant/inbred line	(ACRSYN-W-S2-173-B*4/TZLCom-pIC4S1-37-5-BBB)-17-B*4
9	TZISTR1165	IITA/Nigeria	Resistant/inbred line	(ACRSYN-W-S2-173-B*4/TZLCom-pIC4S1-37-1-B*4)-21-B*4
10	TZISTR1175	IITA/Nigeria	Resistant/inbred line	(ACRSYN-W-S2-173-B*4/TZLCom-pIC4S1-37-5-BBB)-3-1-1-BB
11	TZISTR1178	IITA/Nigeria	Resistant/inbred line	(ACRSYN-W-S2-173-B*4/TZLCom-pIC4S1-37-5-BBB)-56–1-1-BB
12	TZISTR1163	IITA/Nigeria	Resistant/inbred line	(ACRSYN-W-S2-173-B*4/TZLCom-pIC4S1-37-5-BBB)-25-B*4
13	TZISTR1166	IITA/Nigeria	Resistant/inbred line	(ACRSYN-W-S2-173-B*4/TZLCom-pIC4S1-37-1-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/ACR97T-ZLComp1-YS155-4-1-3-B*4)-46-1-BB-B
17	TZISTR1232	IITA/Nigeria	Resistant/inbred line	(ACR97SYN-Y-S1-79-B*4/ACR97T-ZLComp1-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/TZLCom-pIC4S1-37-1-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/ACR97T-ZLComp1-YS155-4-1-3-B*4)-14-1-BB-B

Table 1 (continued)

No°	Germplasm name/designation	Source/Origin	*Striga* resistance / genotype description	Pedigree
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
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	
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	

Table 1 (continued)

No°	Germplasm name/designation	Source/Origin	*Striga* resistance / genotype description	Pedigree
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	
84	CLHP0343	CIMMYT/Zimbabwe	Unknown/inbred line	
85	CZL1380	CIMMYT/Zimbabwe	Unknown/inbred line	
86	CLHP0326	CIMMYT/Zimbabwe	Unknown/inbred line	
87	CZL99017	CIMMYT/Zimbabwe	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	

Table 1 (continued)

No°	Germplasm name/designation	Source/Origin	*Striga* resistance / genotype description	Pedigree
110	ZM1423	CIMMYT/Zimbabwe	Unknown/local OPV	
111	ZM1421	CIMMYT/Zimbabwe	Unknown/local hybrid	
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	Z. Diplo.BC4C3-W-DT C1	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/WhiteDT-STRSYN) 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

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 1–5, 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 1–9, 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

A

B

C

D

E

◂**Fig. 1** Photographs showing the experimental setup with artificial infestations of maize with *Striga asiatica* (**A**–**C**), and *S. hermonthica* (**D**, **E**) in the African Center for Crop Improvement greenhouse at the University of Kwazulu-Natal, South Africa

of host plant damage 8 and 10 weeks after planting, designated as SDR8 and SDR10, was done using a visual rating score of 1–9 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).

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:

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

where $\sigma^2 g, \sigma^2 s, \sigma^2 r, \sigma^2 b,$ and σ^2_ε 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).

Results

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) 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.

Mean performance and statistical summary

Under Sa-infested conditions

Table S1 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 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 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 to 214.00 g/plant for Hickory/1421 and N.Choice/1421, respectively for the hybrid checks, and from 35.00 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 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

Table 2 Analysis of variance for yield components and *Striga* parameters of 126 maize genotypes evaluated under *Sa* and *Sh* infestation conditions

Source of variation	df	DA	DS	ASI	EPP	PLHT	EHT	HUSK	CL	EASP	GY	SEC8	SEC10	SDR8	SDR10
S. asiatica															
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 × 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 × 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															
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 × 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 × 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 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 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 (1–5)	CL (cm)	EASP (1–9)	GY (g/plant)	SEC8	SEC10	SDR8 (1–9)	SDR10 (1–9)
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*TZECOM-P3DT/WhiteDT-STRSYN) 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

Table 3 (continued)

Genotype	DA	DS	ASI	EPP	PLHT (m)	EHT (m)	HUSK (1–5)	CL (cm)	EASP (1–9)	GY (g/plant)	SEC8	SEC10	SDR8 (1–9)	SDR10 (1–9)
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

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).

Under Sh-infested conditions

Table S2 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 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

Table 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 (1–5)	CL (cm)	EASP (1–9)	GY (g/plant)	SEC8	SEC10	SDR8 (1–9)	SDR10 (1–9)
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

yield ranged from 10.05 to 151 g/plant, with a mean of 63.83 g/plant for the inbred lines, from 34.75 to 133.25 g/plant with a mean of 79.79 g/plant for the hybrids, and 33.60 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 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).

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 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 made the highest contributions 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,

Table 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 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

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.

Biplots based on principal components are presented to decipher the performance of the maize germplasm with *Sa* and *Sh* infestations using Figs. 2 and 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 (Fig. 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).

Under *Sh*-infested conditions (Fig. 3), GY had a strong correlation with EHT, PLHT, and EPP and

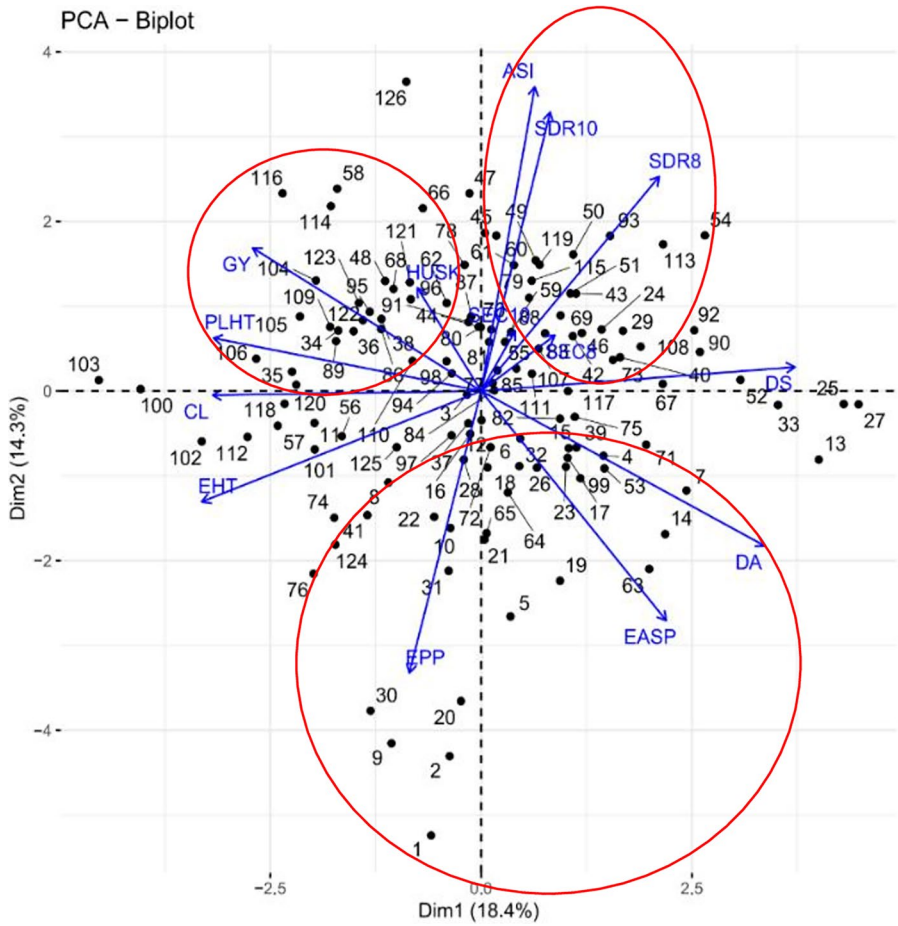

Fig. 2 Principal component of 126 maize population under *Sa*-infested condition. Genotypes are coded with numbers as recorded in Table S1. Dim = dimension, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, EPP = ear per plant, PLHT = Plant height, EHT = ear height, HUSK = husk cover, CL = cob length, EASP = ear aspect, GY = grain yield, SEC8 = *Striga* emergence counts 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

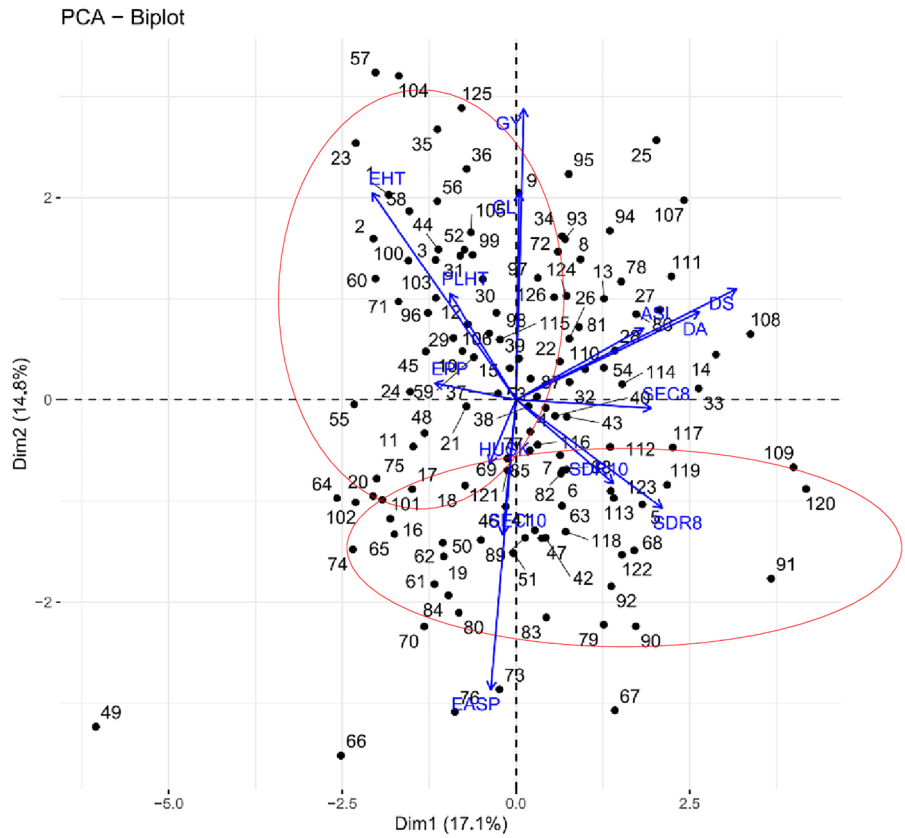

Fig. 3 Principal component of 126 maize population under *Sh*-infested condition. Genotypes are coded with numbers as recorded in Table S2. Dim = dimension, DA = days to 50% anthesis, DS = days to 50% silking, ASI = anthesis-silking interval, EPP = ear per plant, PLHT = Plant height, EHT = ear height, HUSK = husk cover, CL = cob length, EASP = ear aspect, GY = grain yield, SEC8 = *Striga* emergence counts 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

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.

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 Fig. 4A, B, respectively**.** Under *Sa* conditions (Fig. 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

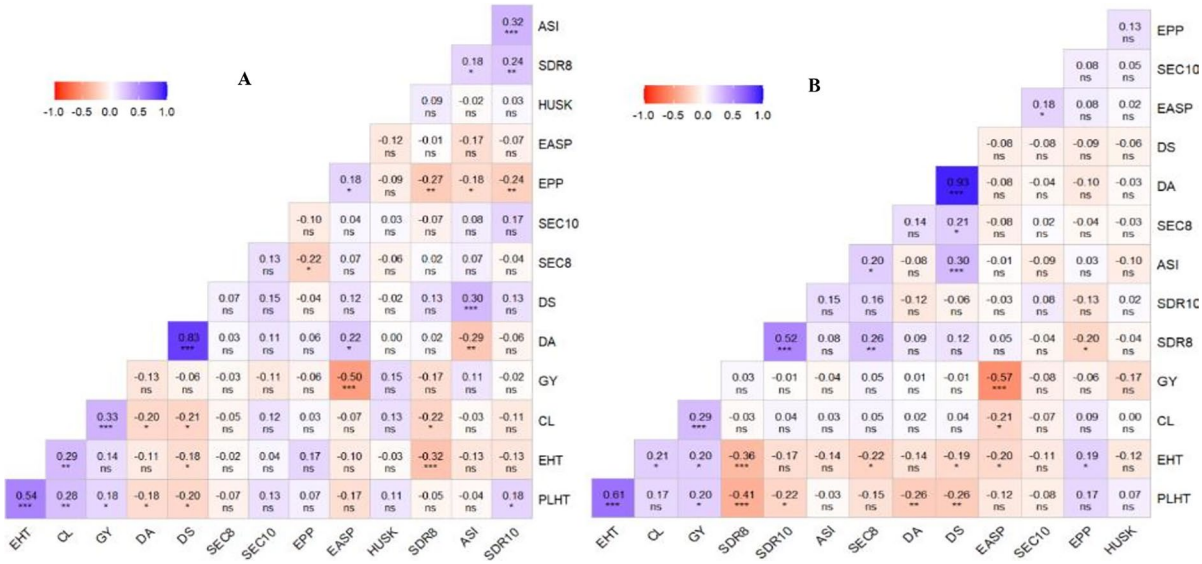

Fig. 4 Correlation matrix plot between yield components and *Striga* parameters in a population of 126 maize genotypes *under Sa* (**A**) and *Sh* (**B**) infestation. The colour variation indicates the magnitude of correlations; traits with deep blue are strongly and positively correlated, while deep 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 8 weeks after sowing, SEC10 = *Striga* emergence counts 10 weeks after sowing, EPP = ear per plant, EASP = ear aspect, HUSK = husk cover, SDR8 = *Striga* damage rating 8 weeks after sowing, ASI = anthesis-silking interval, SDR10 = *Striga* damage rating 10 weeks after sowing, PLHT = plant height

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).

Under *Sh* conditions (Fig. 4B), GY was positively correlated with EHT (r = 0.20), CL (r = 0.29), and PLHT (0.20), whereas with EASP and CL, GY exhibited a negative correlation with 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).

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* (Fig. 5 and Table S3) and *Sh*-infested environments (Fig. 6 and Table S4). 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 an *Sa*-infested environment, the heatmap revealed six clusters (Fig. 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

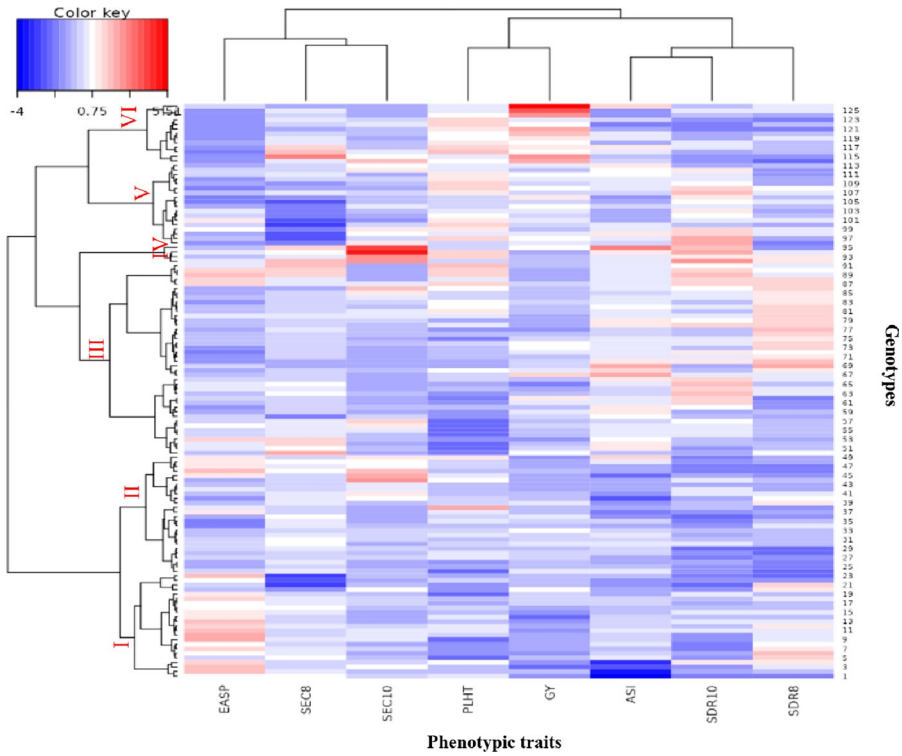

Fig. 5 Six clusters (I–VI) heatmap plot showing a colour pattern of 126 maize genotypes based on 4 maize yield components and 4 *Striga* parameters recorded in *Sa*-infested environment. Blue: lowest performance; red: highest performance. The numbers at the right represent the genotype numbers as coded in Table S1. EASP = ear aspect, SEC8 = *Striga* emergence counts 8 weeks after sowing, SEC10 = *Striga* emergence counts 10 weeks after sowing, PLHT = Plant height, GY = grain yield, ASI = anthesis-silking interval, SDR10 = *Striga* damage rating 10 weeks after sowing, SDR8 = *Striga* damage rating 8 weeks after sowing

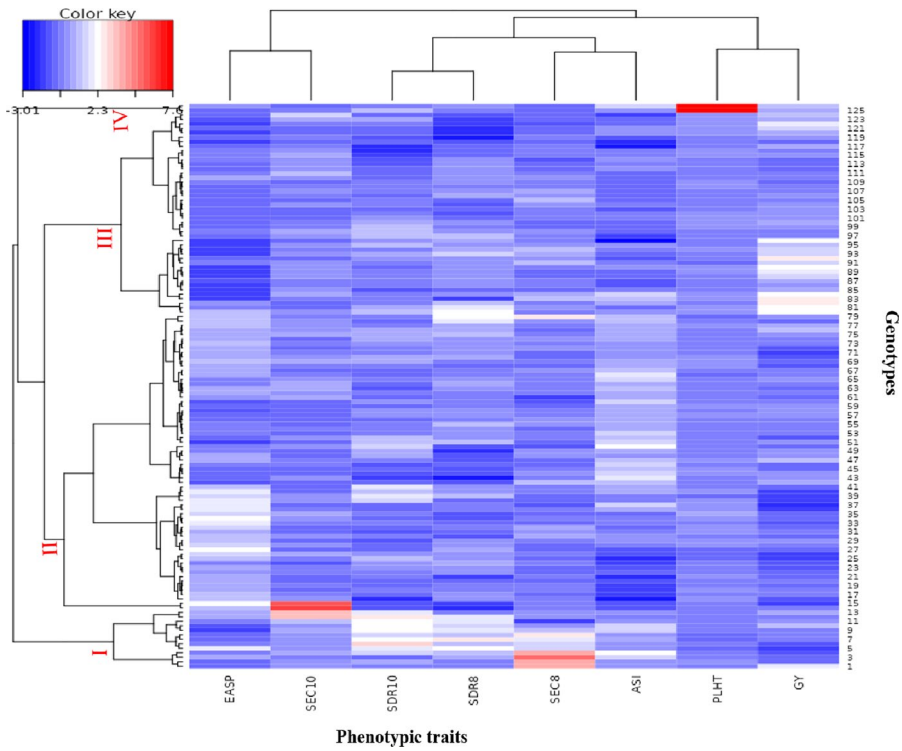

Fig. 6 Four clusters (I–IV) heatmap plot showing a colour pattern of 126 maize genotypes based on 4 maize yield components and 4 *Striga* parameters recorded in *Sh*-infested environment. Blue: lowest performance; red: highest performance. The numbers at the right represent the genotype numbers as coded in Table S2. EASP = ear aspect, SEC10 = *Striga* emergence counts 10 weeks after sowing, SDR10 = *Striga* damage rating 10 weeks after sowing, SDR8 = *Striga* damage rating 8 weeks after sowing, SEC8 = *Striga* emergence counts 8 weeks after sowing, ASI = anthesis-silking interval, PLHT = plant height, GY = grain yield

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 CIMMYT CML304, which showed a high SEC10 number, was clustered in that cluster together with the IITA OPVs (2*TZECOM-P3DT/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.

Under *Sh*-infested conditions (Fig. 6 and Supplemental Table 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, which were characterized by low GY, low 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 *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.

Discussion

Breeding highly *Striga*-resistant maize genotypes adaptable to wide agro-ecological areas in SSA would be a sustainable solution to manage *Striga* infestations in maize crop. 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 −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 traits 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 × 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 an *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 in a previous study low heritability values 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 to *Sa*. These results indicate that these OPVs that have been bred for *Sh* resistance are not resistant to *Sa*. 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 *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 heterosis breeding in *Striga* resistance breeding programs.

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.

Supplementary Materials

The following supporting information can be downloaded: Table S1: Mean values for 10 yield components and 4 *Striga* parameters measured for 126 maize genotypes evaluated under *Sa* infestation. Table S2. Mean values for 10 yield components and 4 *Striga* parameters measured for 126 maize genotypes evaluated under *Sh* infestation. Table S3. Clusters and their member genotypes of 126 maize genotypes evaluated under *Sa* infestation. Table S4: Clusters and their member genotypes of 126 maize genotypes evaluated under *Sh* infestation.

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Declarations

Conflict of interest The authors declare that they have no competing financial interests or personal relationships that could have appeared to influence this work.

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