

Gene Action for Grain Yield and Agronomic Traits in Selected Maize Inbred Lines with Resistance to *Striga Hermonthica* in Uganda

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Abstract Combining ability of inbred lines is crucial information in maize hybrid breeding programs incorporating materials from various germplasm sources. This study was conducted to assess the gene action for grain yield and other agronomic traits for germplasm having varying resistance to *Striga hermonthica* and genetic. In a half diallel cross of ten parents, general and specific combining abilities for grain yield, plant and ear height, plant and ear aspect, ears and plants harvested, ear rot, husk cover, moisture and resistance to *Striga hermonthica* were determined. The grain yields of the single crosses were significantly higher for 1368STR x TZISTR1198, TZISTR1132 x CML442, TZISTR1174 x TZISTR1198 and TZISTR1199 x TZISTR1174. The importance of both GCA (50%) and SCA (50%) for grain yield, ear rot, ear texture and ears harvested were observed, but a preponderance of GCA was existed for AUSNPC, whereas plant and ear height, plant and ear aspect, and moisture content exhibited preponderant SCA. TZISTR1174, TZISTR1162, TZISTR1192, and CML442 were good general combiners for grain yield showing highly significant positive GCA effects of 0.40, 0.2, 0.17, and 0.22, respectively while lines TZISTR1199, TZISTR1192, TZISTR1174 and TZISTR1162 were good general combiners for resistance to *Striga* showing highly significant negative GCA effects of -646.99, -428.21, -338.00, and -76.51. These inbred lines could be exploited in hybrid breeding to develop high yielding *Striga* resistant maize varieties. Hybrids such as TZISTR1174 x CML312, TZISTR1192 x CML442 and TZISTR1174 x 1368STR had significant positive SCA effects for grain yield whereas crosses like TZISTR1162 x TZISTR1198, TZISTR1199 x TZISTR1181, TZISTR1192 x 1368STR had highest negative significant SCA effects of -1453.19, -1058.28, and -808.252 for AUSNPC which can be used for direct production as single cross hybrids or developed further as three way cross hybrids.

Keywords: gene action, combining ability

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1. Introduction

Maize has a remarkable place among cereals and it is used as human food, animal feeding and industry [1,2]. The identification of parental inbred lines that perform superior hybrids is the most costly and time consuming phase in maize hybrid development [3]. Maize breeding programmes designed for specific-end uses, improved maize genotypes tolerant to pests/disease, and development of commercial maize hybrids usually require a good knowledge of combining ability of the breeding materials to be used. Hence, the relevance of combining ability studies for successful maize breeding [4]. Many breeders have used combining ability to solve many maize agronomic problems. These include breeding for higher grain yield and adaptation to tropical Africa [5],

selecting for high heterosis and adaptation to different agro-ecologies [6], developing maize varieties with good ear height and uniform flowering days [7], and identifying suitable maize inbred lines for higher grain yield and improved agronomic traits [8]. Plant breeders and geneticists often use diallel mating designs to obtain genetic information about a trait of interest from a fixed or randomly chosen set of parental lines [9]. The diallel analysis is an important method to know gene actions and it is frequently used by crop breeders to choose the parents with a high general combining ability (GCA) and hybrids with high specific combining ability (SCA) effects [10]. Large genotype × environment effects tend to be viewed as problematic in breeding because the lack of a predictable response hinders progress from selection [11], and influence the environment and interaction between genotype and environment [12]. Breeders still contend, however, that dominance effects caused by genes with

over dominant gene action are also important [13]. Most of the literature about maize, one of the most extensively studied plant species, suggests that additive effects of genes with partial to complete dominance are more important than dominance effects in determining grain yield [14]. The objective of this study was therefore to evaluate ten inbred lines and their crosses using a diallel to identify type of gene action controlling the inheritance for studied traits, estimate of combining ability effects for the inbred lines and identify superior crosses and inbred lines to improve the yielding ability in maize breeding programs.

2. Materials and Methods

2.1. Plant Materials

Fifty six inbred lines were evaluated in farmers' abandoned naturally *Striga* infested fields in Nakyere, Namutumba district of Eastern Uganda during 2016 B growing season using a 7×8 alpha lattice design with two replications. Ten inbred lines Table 1 of varying resistance to *Striga hermonthica* were selected from the preceding study of 2016B and all possible crosses were made among the inbred lines using 10 × 10 half diallel to generate 45 single-crosses during 2017A growing season.

Table 1. List of parental inbred lines used

Name	Source	Response to <i>Striga</i>	Estimated yield (t ha ⁻¹)
CML442	CIMMYT	Susceptible	0.5
CML312	CIMMYT	Susceptible	0.2
1368STR	IITA	Resistant	0.9
TZISTR1181	IITA	Resistant	1
TZISTR1162	IITA	Resistant	0.8
TZISTR1192	IITA	Resistant	1.1
TZISTR1174	IITA	Resistant	1.2
TZISTR1198	IITA	Resistant	0.9
TZISTR1199	IITA	Resistant	1.2
TZISTR1132	IITA	Resistant	0.9

Source: Experiment in 2016B growing season.

2.2. Evaluation of Single Crosses

Seed of the successful crosses were harvested and single crosses were evaluated in a 9×5 alpha lattice replicated two times in three farmers' abandoned naturally *Striga* infested fields at Nakyeere in Namutumba district; Ngerekyomu in Tororo district (Eastern Uganda) and Kinyamaseka in Kasese district (western Uganda) during 2017 B growing season. The hybrids were planted in two row plots measuring 5m in length. Planting was done at a spacing of 75cm by 25cm at the rate of two seeds per hole. 8 g of Diammonium Phosphate (DAP) were banded below the maize seed. The maize seedlings were thinned to one per stand at 14days after crop establishment. Low fertilizer dosage (50kg/ha NPK 20-10-10) was applied by broadcast to minimize the likelihood of nitrogen (N) suppressing *Striga* emergence [15]. Hand weeding was

done to remove all other weeds other than *Striga*. Cypermethrine was applied to control fall army worm and stem borer infestation.

2.3. Data Collection

Maize plant and ear heights were measured at maturity by measuring five plants selected randomly in each plot using a graduated measuring stick. Husk cover was scored for when ears were fully developed using a score rating of 1 to 5, where 1: husk tightly arranged and protracted beyond the tip of the ear and 5: ear tips fully exposed as described by CIMMYT [16] while that of ear rot was rated on the scale of 1 to 5 as described by CIMMYT [16], where; 1: little or no visible ear rot, and 5: extensive visible ear rot. Plants and ears harvested included the total number of respective plants and ears harvested per plot. Ear aspect scored on a scale of 1 to 5, where 1: best, 3: average, and 5: poorest ear aspect. Certain factors such as ear size, insect damage, grain filling, and uniformity of cob size, grain colour and texture were also considered while scoring. At physiological maturity the ears were harvested, dehusked and weighed for each genotype to determine the field weights. Furthermore, each genotype was sampled to obtain grain used for estimation of the moisture content (%). Grain yield (t ha⁻¹) was calculated for each genotype as follows:

$$\text{Grain yield (t ha}^{-1}\text{)} = \left\{ \frac{[(\text{Grain weight (kg / plot)}) \times 10 \times (100 - MC)]}{(100 - 12.5)(\text{Plot area})} \right\} \times \text{Shelling percentage}$$

Where MC = grain moisture content (%).

Striga related traits assessed included *Striga* count/m² at 8,10, and 12 weeks after crop emergence, *Striga* vigour (using a scale of 0-9), where 0= no emerged *Striga* plants and 9= very vigorous *Striga* plants (average height >40cm with >10 branches) [17], plant damage scores (using a scale of 0-9), where 1=Normal plant growth, no visible symptoms and 9 = Complete leaf scorching of all leaves, causing premature death or collapse of host plant and no ear formation [18], area under *Striga* number progress curve (AUSNPC) and area under *Striga* severity progress curve (AUSVPC) [19]. The AUSNPC was calculated as follows;

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

where n is the number of *Striga* assessment dates, Y_i the *Striga* number at the ith assessment date, t_i the days after planting at the ith assessment date, t is 0, and Y is 0.

2.4. Data Analysis

The analysis of variance (ANOVA) for all traits under study was carried out using Genstat release 14.1 statistical package [20]. The 10×10 half-diallel analysis was executed to estimate general combining ability (GCA) and

specific combining ability (SCA) effects using Griffing's diallel analyses, Model 1 (fixed genotype effects), Method IV (Crosses only) [21], according to model; $Y_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$, where; Y_{ijk} : Observed measurement for the ij_{th} cross in the k_{th} replication/environment combination, μ : Overall mean, g_i and g_j : GCA effects for the i_{th} and j_{th} parents respectively, s_{ij} : SCA effects for the i_{th} and j_{th} parents, e_{ijk} : Error term associated with the ij_{th} cross evaluated in the k_{th} replication/environment combination. The interaction terms were used to test for the significance of the corresponding main effect [22]. The environments and replications within environments were considered random and therefore tested against the residual error term. Mean squares of parents were estimated from the GCA effects while that of single-crosses were obtained from the SCA effects of the diallel analysis. These were further used to estimate GCA: SCA ratios [23,24].

3. Results and Discussion

3.1. Analysis of Variance

Table 2 presents the combined analyses of variance. The observed significant mean squares of location and genotypes for *Striga* and maize agronomic traits indicated that the three environments were distinct and that there were genetic variations among the single-cross hybrids, suggesting that selection of such traits for further improvement was feasible. Similar findings were reported by Badu-Apraku *et al.*, [25]. The significant G×E interaction for *Striga* and maize agronomic traits suggested differences in expression of traits of the set of hybrid genotypes across the locations. The expression of almost all traits was influenced by the environmental differences further suggesting the need to develop specific varieties for specific environments to take into account the high influence of the environment on the expression of traits. Similar results were reported by Olakojo *et al.*, [15] when they assessed the performance of newly developed *Striga lutea* (Lour)

tolerant maize genotypes including seven *Striga* tolerant open pollinated maize varieties. The significant mean square estimates of GCA observed indicated the important role of additive genes in the inheritance of such traits. Derera *et al.*, [26] and Vivek *et al.*, [27] reported that resistance to phaeosphaeria leaf spot (PLS) was predominately additive.

The traits with significant mean squares for SCA indicated that the non-additive gene effect contributed significantly to the inheritance of such traits and thus, selection of such traits for further improvement could be achieved through recurrent selection, and backcrossing methods. There were significant differences among GCA and SCA effects for grain yield; both GCA (50%) and SCA (50%) were equally important for this trait. The association of both GCA and SCA with grain yield concurs with other findings [28,29,30]. Vivek *et al.*, [27] also reported that in addition to GCA, SCA was also very important in the inheritance of resistance to PLS in maize. Badu-Apraku *et al.*, [31] further observed significant mean square of GCA and SCA for maize agronomic traits which suggested presence of additive and non-additive gene actions and proposed the use of hybridization, backcrossing and recurrent selection methods to develop synthetics, populations and hybrid varieties. The observed significant mean square of GCA×E interaction indicated variations in the combining abilities of the inbred lines and emphasized the need for testing the inbred lines under different environments with the view to assess performance and stability. Similar observations were made by Menkir *et al.*, [32] and Badu-Apraku *et al.*, [33] in a similar study. The observation that GCA x location interaction was highly significant and greater than SCA x location interaction also agreed with other authors [28,34,35]. The lack of significant mean square estimates of SCA×E interaction for some traits suggested that expressions of such traits among the single cross hybrids were consistent across environments and therefore, good selection progress for improvement of such traits was feasible under any environment as similarly observed by Machado *et al.*, [29].

Table 2. Analysis of variance for *Striga* and maize agronomic characters

Source of variation	D.f	<i>Striga hermonthica</i> traits				Plant agronomic traits							
		SC/m ² (8wap)	SC/m ² (10wap)	SC/m ² (12wap)	AUSNPC (m ²)	GY (t ha ⁻¹)	PH (cm)	EH (cm)	EP (%)	PA (1-5)	HC (1-5)	MC (%)	HC (1-5)
Location (E)	2	1632.5**	13583.6***	42447.7*	38387312***	23.1**	11574.9**	0.002*	2152.5**	9.4**	0.0**	2.1*	0.0**
REP	3	2686.9***	21980.3***	30989.0**	61056577**	5.9**	976.6*	500.7	32.7	6.3*	0.5	27.8	0.5
Cross(G)	44	477.0	1751.8	1398.1***	4097567*	1.3**	1823.8**	461.3**	94.1**	1.4**	0.2*	34.8**	0.2*
GCA	9	895.5	3476.6*	2628.4*	8367264*	2.5**	1392.5**	460.2**	98.0*	1.0*	0.1*	34.8**	0.1*
SCA	35	401.4	1419.5	1081.7***	3179240	1.2**	2097.1**	505.7**	98.7**	1.5**	0.2**	37.2*	0.2**
GXE	88	354.0	1781.2*	1126.6*	3641193	1.3**	321.1**	81.1**	26.2**	0.4**	0.0	19.3**	0.0
E×GCA	18	504.4	2340.2*	1774.2*	5120955*	1.6***	147.6**	92.3	33.1**	0.3**	0.0	22.9***	0.0
E×SCA	70	348.1	1774.8	960.1	3487003	1.3**	403.2**	86.1*	26.4*	0.4*	0.0**	20.1**	0.0**
Residual	108	309.0	1631.1	814.4	3168332	1.4	598.4	183.9	45.3	0.8	0.1	22.4	0.1
GCA: SCA (%)		79.2	61.4	58.4	79.6	0.0	7.6	10.7	12.3	3.8	6.8	10.5	6.8

PH: Plant height, EH: Ear height, EP: Percentage ear position, PA: Plant aspect, HC: Husk cover, GY: Grain yield, ER: Ear rots, and MC: Moisture content, E: Location, G: Genotype SC: *Striga* count, AUSNPC: Area under *Striga* progressive curve, wap: weeks after planting.

Table 3. Estimates of GCA effects for *Striga* and maize agronomic traits

Parents	Striga hermonthica traits				Plant agronomic traits								
	SC/m ² (8wap)	SC/m ² (10wap)	SC/m ² (12wap)	AUSNPC (m ²)	PH (cm)	EH (cm)	EP (%)	PA (1-5)	HC (1-5)	GY (t ha ⁻¹)	ER (%)	MC (%)	EA (1-5)
TZISTR1199	-7.02***	-11.36**	-13.04***	-646.99**	10.17**	4.10**	-0.38	-0.34**	-0.04*	0.001**	-0.12	0.04	-0.07
TZISTR1192	-3.41*	-8.77*	-7.87*	-428.21*	-0.5	-1.79	-0.67	-0.07	-0.01	-0.13	0.17*	1.56**	-0.07
TZISTR1132	0.15	3.34	3.20	155.87	-1.92	-0.38	1.39*	0.07	-0.04*	-0.04	-0.15	-1.40	0.06
TZISTR1174	-4.10*	-7.17*	-4.79*	-338.00*	4.13*	2.04	-1.59*	-0.03	0.02	0.40**	-0.53	-0.80*	-0.22*
1368STR	2.16	13.74**	9.31**	580.57**	3.96	1.07	-0.26	0.00	0.05*	-0.13	0.15	0.29	0.10
TZISTR1162	-1.70	-0.34	-2.51	-76.51	3.23	4.52**	2.56**	-0.01	0.05*	0.20	0.11	0.84*	0.01
TZISTR1181	5.48**	7.16*	7.60*	408.66*	-4.74*	-2.22	0.10	0.11	0.02	0.17**	0.29	-0.81*	0.14
TZISTR1198	6.56**	6.57	8.03**	420.57*	-4.80*	-4.93**	-1.43*	0.19*	-0.08**	0.04	0.35*	0.16	0.04
CML312	2.92	5.30	2.51	225.34	-7.88*	-3.23	-1.37*	0.09	-0.04	-0.40*	-0.32	-0.04	0.24**
CML442	-1.03	-8.48	-2.44	301.30*	-1.66	0.82	1.66*	-0.01	0.08**	0.22*	0.05	0.16	-0.23*

PH: Plant height, EH: Ear height, EP: Percentage ear position, PA: Plant aspect, HC: Husk cover, GY: Grain yield, ER: Ear rots, and MC: Moisture content, E: Location, G: Genotype SC: *Striga* count, AUSNPC: Area under *Striga* progressive curve, wap: weeks after planting.

3.2. Estimates of GCA Effects

Table 3 presents the GCA effects. The observed significant positive and negative GCA effects for GY for the inbred lines TZISTR1199, TZISTR1174, TZISTR1181 and CML312 indicated the possibility of transmitting favorable alleles from the parental lines to their hybrid combinations for improved GY [36,37]. Badu-Apraku *et al.*, [38] observed preponderance of GCA effect over SCA effect and suggested that the additive gene action was more important than the non-additive gene action in modulating the expression of GY and other agronomic traits. Similar observations were also made by Xingming *et al.*, [39]. Parents TZISTR1199, TZISTR1174 and TZISTR1162 were considered as best general combiners for PHT and EHT due to their respective significant positive GCA effects and could be selected for increasing yield in their hybrid combinations. Tall maize genotypes with high ear positioning or placement might offer opportunity for more ears to develop on the nodes below and ultimately increasing final yield [40,41] even though they may be susceptible to lodging [42,43]. Number of ears per plant is an indicator for increased grain yield while genotypes with long tipped off husk covers of maize cob provide maximum protection of the ear against birds' damage, fungal infection and early germination of kernel when moisture and conditions suitable for germination occurred in the field. Similar results were reported by Abbrha *et al.*, [44].

Parents TZISTR1181, TZISTR1198, CML312, 1368STR and TZISTR1132 had very high GCA effects for area under *Striga* number progressive curve indicating susceptibility [45,46], while TZISTR1199, TZISTR1192, TZISTR1174 and TZISTR1162 had low GCA effects indicating good resistance to *Striga hermonthica*. Similarly, GCA effect for area under *Striga* severity progressive curve and *Striga* vigor were generally low. The least values were recorded in TZISTR1199, TZISTR1192, TZISTR1174 and TZISTR1162 indicating good resistance to *Striga hermonthica*, hence higher resistance level in the parents confirming its near immunity status [47]. Kim [18] reported low GCA effects for *Striga hermonthica* emergence and host-plant response for most resistant

maize inbred lines and high GCA effects for the susceptible. Omanyia *et al.*, [48] and Hausmann *et al.*, [49] reported strong genetic control for AUSNPC in the field. They observed that the parameter was a useful measure of progressive *Striga* development in the field. However, Hausmann *et al.*, [50] additionally found that individual *Striga* emergence count was also under genetic control from experiments conducted in pots.

3.3. Estimates of SCA Effects

Table 4 presents the SCA effects. The significant positive effects of SCA for GY for TZISTR1192 x 1368STR, TZISTR1192 x CML442, TZISTR1132 x CML442, TZISTR1174 x CML312 and 1368STR x TZISTR1198 across research locations suggested that the parents contributed favorable alleles to these single-cross hybrids. GCA effects of GY for some inbred lines were low and negative but resulted in increased SCA effects which meant that it was feasible to identify such inbred lines to develop hybrids with high yielding abilities, test and select based on increased SCA effects, even if GCA was more important in identifying potential inbred lines [51]. The hybrid TZISTR1199 x TZISTR1174 showing a good SCA effect for GY was identified as single-cross tester based on assumptions described by Vivek and Pixley [52]. Tall maize genotypes are important not only for increase grain yield but also for high biomass production for silage production [53,54]. Hybrids 1368STR x TZISTR1181, 1368STR x CML442, TZISTR1162 x CML312, CML442, TZISTR1174 x CML312, TZISTR1174 x TZISTR1198, TZISTR1132 x TZISTR1174, TZISTR1192 x 1368STR and TZISTR1199 x CML442 showed good specific combining ability for plant height and could be released for silage production in intensive livestock production agro-systems. Hybrids with large number of ears per plant and long husk cover off the tip of the cob are desirable for increased yield and cob protection from several diseases and pests. Therefore hybrids such as TZISTR1199 x TZISTR1181 and TZISTR1199 x TZISTR1162 which had significantly high positive SCA effects could be considered as best combiners for ears per plant and husk cover, respectively.

Significant SCA effects recorded for some *Striga* related characters indicated differential response of the crosses to these *Striga* traits. Non-additive gene action played significant role in the inheritance of resistance to *Striga* in most of the crosses. Inbred lines TZISTR1199, TZISTR1192, TZISTR1174 and TZISTR1162 were identified as good combiners whose crosses had the lowest SCA making them useful in resistance to *Striga* breeding of maize. Kim [55] reported that the highest level of resistance to *Striga hermonthica* was obtained from crosses involving two resistant parents. The results also suggested that the genes for resistance might be recessive since *Striga hermonthica* resistance appeared more

common in resistant x resistant crosses compared with resistant x susceptible crosses. Related results were reported by [56] when studying genetic analysis of resistance to MSV in dwarf maize germplasm. Hung and Holland [57] also reported similar findings in their diallel analysis of resistance to Fusarium ear rot and Fumonisin contamination in maize. Kim [18] reported a negative SCA effect of -1.0 for *Striga* tolerant rating while studying the genetics of *S. hermonthica* tolerance in maize. Storey and Howland [58] also observed that heterozygotes between resistant and susceptible lines reacted to infection in a manner intermediate between the parents where neither allelomorph was fully dominant.

Table 4. Estimates of SCA effects for *Striga* and maize agronomic traits

Single crosses	<i>Striga hermonthica</i> traits				Plant agronomic traits							
	SC/m ² (8wap)	SC/m ² (10wap)	SC/m ² (12wap)	AUSNPC (m ²)	PH (cm)	EH (cm)	EP (%)	PA (1-5)	HC (1-5)	GY (t ha ⁻¹)	ER (%)	MC (%)
TZISTR1199 x TZISTR1192	2.28	2.08	7.39	170.91	-13.78	2.84	6.82**	0.14	-0.15*	-0.43	5.77	0.92
TZISTR1199 x TZISTR1132	0.96	-6.21	-8.06	-295.06	-12.47	-6.56	-0.61	0.50	-0.12	0.24	-10.16	1.89
TZISTR1199 x TZISTR1174	-2.36	17.93	6.35	666.33	-19.59	-5.82	5.16*	0.81*	0.07	0.24	-9.98	-0.91
TZISTR1199 x 1368STR	7.58	23.18	10.94	961.67	-0.76	0.57	-0.26	0.14	0.04	-0.14	-10.90	-0.93
TZISTR1199 x TZISTR1162	6.16	-7.42	-5.91	-236.10	3.49	-0.54	-2.37	-0.30	0.29**	-0.12	-0.47	-0.84
TZISTR1199 x TZISTR1181	-7.45	-26.61*	-12.58	-1058.28	16.11	5.67	-3.30	-0.84*	0.07	0.49	-17.70	-0.43
TZISTR1199 x TZISTR1198	-1.20	2.45	3.35	104.66	7.46	-6.27	-5.87*	0.64*	-0.09	-0.14	34.77*	-1.43
TZISTR1199 x CML312	-2.10	-10.72	-1.26	-391.69	0.15	0.31	0.81	-0.23	-0.12	0.09	11.59	3.76*
TZISTR1199 x CML442	-3.86	5.32	-0.22	77.56	19.38*	9.80*	-0.39	-0.86**	0.01	-0.21	-2.94	-2.02
TZISTR1192 x TZISTR1132	9.86	5.95	-12.34	170.77	9.14	3.27	-1.22	0.32	-0.15*	-0.21	9.14	0.52
TZISTR1192 x TZISTR1174	-7.34	-7.04	-5.58	-4100.00	-4.94*	-1.84	1.51	-0.36	0.04	-0.33	-15.30	-3.58*
TZISTR1192 x 1368STR	-8.79	-23.72	-13.13	-1053.57	18.94*	4.65	-4.89*	-0.67*	-0.24**	0.66*	31.96*	-2.48
TZISTR1192 x TZISTR1162	-1.53	-7.28	4.40	-171.39	13.76	2.25	-5.71*	-0.45	0.26**	0.39	-20.86	-0.46
TZISTR1192 x TZISTR1181	-3.44	-4.43	-10.64	-375.22	-10.25	-4.92	0.49	0.82*	0.04	-0.03	-11.61	-1.69
TZISTR1192 x TZISTR1198	12.00*	14.82	2.31	648.83	7.13	0.90	-3.04	-0.23	0.13	-0.56	66.40**	-0.38
TZISTR1192 x CML312	-8.65	5.80	12.03	233.93	-26.59**	-14.62*	1.71	0.30	-0.15*	0.00	-35.66	4.46*
TZISTR1192 x CML442	5.61	13.82	15.56	785.74	6.58	7.46	4.33*	0.12	0.23**	0.51*	-29.83	2.69
TZISTR1132 x TZISTR1174	-2.77	-18.19	-16.09	-842.02	14.93*	5.63	-1.96	-0.28	0.32**	-0.19	14.57	1.34
TZISTR1132 x 1368STR	-5.09	3.80	14.11	215.41	-15.58*	-2.78	3.40	0.25	0.04	-0.95*	7.90	-0.58*
TZISTR1132 x TZISTR1162	2.66	18.18	3.89	684.60	7.56	3.09	-1.74	-0.13	0.04	0.16	3.74	-3.87
TZISTR1132 x TZISTR1181	-1.90	9.63	7.61	341.71	8.31	2.07	-0.98	-0.32	0.07	0.49	-9.17	0.75
TZISTR1132 x TZISTR1198	12.78*	14.83	25.80*	1012.09	-15.71*	-6.23	1.70	-0.12	-0.09	0.10	-27.46	-0.44
TZISTR1132 x CML312	-10.71*	-18.08	-15.8	-968.50	5.17	2.53*	0.13	0.05	-0.12	-0.46	13.56	-0.34

Single crosses	<i>Striga hermonthica</i> traits				Plant agronomic traits							
	SC/m ² (8wap)	SC/m ² (10wap)	SC/m ² (12wap)	AUSNPC (m ²)	PH (cm)	EH (cm)	EP (%)	PA (1-5)	HC (1-5)	GY (t ha ⁻¹)	ER (%)	MC (%)
TZISTR1132 x CML442	-5.79	-9.90	0.87	-319.00	-1.36	-1.01	1.28	-0.28	0.01	0.83*	-2.11	0.74
TZISTR1174 x 1368STR	12.33*	16.86	18.87*	1000.14	-22.85*	-9.40*	2.98	0.04	-0.02	0.26	-6.22	0.08
TZISTR1174 x TZISTR1162	-0.47	-9.01	-7.37	-414.02	-10.69	-5.72	1.38	0.37	-0.27**	-0.44	16.24	-0.06
TZISTR1174 x TZISTR1181	-5.09	0.36	5.80	3.53510	-11.97	-2.67	3.65	0.26	-0.24**	-0.39	53.14*	1.79
TZISTR1174 x TZISTR1198	-5.86	-14.35	-18.18*	-808.25	16.69*	2.52	-4.96*	-0.60*	0.10	0.29	-32.64*	0.84
TZISTR1174 x CML312	10.32	20.55	25.47*	1179.60*	19.74*	11.70	-6.12*	-0.20	0.07	0.86*	-15.11	-0.29
TZISTR1174 x CML442	1.24	-7.12	-9.27	-375.31	18.69*	5.59	-1.65	-0.03	-0.06	-0.30	-4.69	0.78
1368STR x TZISTR1162	-3.18	-6.78	-4.12	-318.94	-24.42**	-8.42*	4.71*	0.85**	-0.31**	-0.32	9.83	-0.67
1368STR x TZISTR1181	-3.75	-8.17	-17.21*	-507.23	30.24**	9.37*	-5.11*	-0.55*	0.23**	0.23	-20.52	-0.16*
1368STR x TZISTR1198	0.93	11.29	-3.01	352.70	8.04	6.55	2.35	-0.05	0.07	0.65*	-37.91*	7.84
1368STR x CML312	3.35	-5.95	4.42	-83.26	-25.98**	-17.53*	-2.31	0.59*	0.04	-0.21	6.77	-2.45
1368STR x CML442	-3.36	-10.50	-10.89	-566.94	32.37**	16.98**	-0.88	-0.61*	0.16**	-0.19	19.10	-0.66
TZISTR1162 x TZISTR1181	-0.34	12.76	21.24*	669.54	-2.70	-1.99	1.26	-0.19	-0.27	-0.11	-4.54	1.99
TZISTR1162 x TZISTR1198	-18.15**	-29.41*	-19.13*	-1453.19*	-11.34	-6.77	-1.00	0.25	0.07	0.05	-13.70	-1.06
TZISTR1162 x CML312	11.69*	30.55*	7.58	1228.73*	34.76**	17.92**	-0.38	-0.78*	0.29**	0.64*	-6.52	3.59*
TZISTR1162 x CML442	3.16	-1.58	-0.59	10.76	-10.41	0.18	3.84	0.39	-0.09	-0.26	16.29	1.37
TZISTR1181 x TZISTR1198	16.27*	6.72	13.39	653.90	6.37	11.60*	6.65	-0.09	0.10	-0.03	9.47	-0.38
TZISTR1181 x CML312	2.30	0.81	-10.35	-40.24	-0.50	2.18	6.05*	0.20	0.07	-0.60	-2.79	-2.31
TZISTR1181 x CML442	3.40	8.93	2.75	312.27	-35.61**	-21.30	-8.72*	0.72*	-0.06	-0.05	3.73	0.44
TZISTR1198 x CML312	-11.28*	-15.17	-14.22	-872.11	2.12	6.45	1.05	-0.14	-0.09	-0.18	14.40	-4.04*
TZISTR1198 x CML442	-5.48	8.82	9.68	361.36	-20.76*	-8.76*	3.12	0.34	-0.21*	-0.19	-13.32	-0.94
CML312 x CML442	5.09	-7.79	-7.89	-286.45	-8.87	-8.95*	-0.94	0.21	0.01	-0.14	13.77	-2.39

PH: Plant height, EH: Ear height, EP: Percentage ear position, PA: Plant aspect, HC: Husk cover, GY: Grain yield, ER: Ear rots, and MC: Moisture content, E: Location, G: Genotype SC: *Striga* count, AUSNPC: Area under *Striga* progressive curve, wap: weeks after.

4. Conclusion

The additive gene action was important in controlling *Striga* resistance indicating that resistance could be effectively improved through selection. There was significant genetic control for PH, EH, EHS, and EA with preponderance of additive genetic effects indicating that improvement could be achieved through selection. Maize parental lines TZISTR1199, TZISTR1192, TZISTR1174 and TZISTR1162 displayed negative GCA effects for resistance to *Striga* hence could be used as sources of resistance genes to *Striga* and could be used to introgress resistance to popular susceptible maize varieties. The parental lines TZISTR1174, TZISTR1162, TZISTR1192, TZISTR1132 and CML442 could be used as sources of genes for grain yield increment in a breeding programme.

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