



Research Article

Identification of superior parental maize inbreds and crosses for yield traits through GGE biplot under line \times tester mating design

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Abstract

The development of high-yielding hybrid maize is an essential requirement to increase farmer's productivity. This study was conducted to gain the knowledge of combining ability effects of genotypes, to select potential parents for utilization in future breeding program and to identify the best crosses with high grain yield. Line \times tester mating was conducted with seven lines and four testers. A total of 40 genotypes (28 crosses, 11 parents and one check) were laid out in a randomized complete block design with three replications. Combining ability analysis, graphical views, and standard heterosis were calculated. The mean squares for genotypes were highly significant differences for all studied traits. The interaction of genes is a fascinating area of study, specifically when it comes to hybrid combination and their impact on grain yield and some yield-attributing traits. Line 2, Line 4 and Line 6 showed positive GCA effects for grain yield and some yield-attributing traits. T1 showed significant positive GCA effects for grain yield. The crosses; (L2 \times T1), (L6 \times T1), (L2 \times T3), (L4 \times T4), and (L4 \times T2) showed positive SCA effects and positive heterosis over nation hybrid (check), Yezin hybrid-14.

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1. Introduction

Maize demand has steadily increased in recent decades and is predicted to continue to rise, with estimated maize consumption to double by 2050 [1]. On a global scale, grain yield and its quality have been greatly increased through hybrid breeding programs [2]. The development of high-yielding hybrid maize is the essential requirement to increase farmer's income. Thus, proper breeding methodology is essential for developing high-yielding hybrids which adapt to different agroecological conditions. Among the breeding methods, the Line \times Tester mating design was technologically advanced [3], which affords the knowledge on general combining

ability effects of parents and specific combining ability effects of their hybrid combinations. The knowledge gained from line \times tester analysis can be effectively utilized to exploit maximum heterosis. In biometrical genetics, combining ability effects are reflected as the general combining ability (GCA) of parents and specific combining ability (SCA) of crosses. In combining ability estimates, GCA attributes to additive gene action while SCA attributes to non-additive gene action that contributed significantly to the inheritance of grain yield and some agronomic traits [4-6]. The information generated from line \times tester analysis is an invaluable instrument

for the assessment of genetic variability of inbred lines and their combining ability effects, selection of potential inbreds and prediction of hybrid performance [7].

The genotype and genotype \times environment (GGE) biplot method has been utilized to identify the ideal lines and testers. The author [8] who developed (GGE) biplot method to observe the combining ability effects of genotypes and interrelationships of parents based on a graphical presentation by principal component analysis, PC1 and PC2. The genetic information; GCA of parents, the SCA of crosses, groups of parents with similar inheritances, and superior combiners could be identified by the graphical presentation of GGE biplot. According to Ruswandi [9], GGE biplot graphical presentation exhibited an effective indication of GCA effects of lines and testers, SCA effects of their combinations. The combining ability effects of lines, testers and their combinations have been investigated with GGE biplot presentation by previous studies [10-12].

Heterosis, also term as hybrid vigor, is the result of the crossing of genetically diverged inbred lines revealing the superior traits over the standard or commercial variety. The significant heterosis was gained from unrelated parents rather than closely related parents [13]. The extent of heterosis is controlled by the type of gene actions whether additive or non-additive. It was limited if the trait is controlled by additive gene action, however, significant positive or negative heterosis can be attained when the trait is controlled by non-additive gene action [14]. The experiment was conducted (i) to assess general combining abilities (GCA) of parents and specific combining abilities (SCA) of the crosses for grain yield and yield attributing traits and (ii) to identify the best crosses for grain yield and yield attributing traits among the tested crosses.

2. Materials and methods

2.1 Parental materials and experimental design

Line \times tester mating design was carried out with seven lines and four testers as shown in Table 1. A total of 40 genotypes including 11 parents (seven lines and four testers), 28 hybrids, and one hybrid check (Yezin hybrid-14) were laid out in a randomized complete block design (RCBD) with three replications at Tatkon

Table 1. List of the parental inbred lines

Line Code	Inbred Code
Line1	TK-20-02
Line2	TK-20-03
Line3	TK-20-05
Line4	TK-20-20
Line5	TK-20-24
Line6	TK-20-01
Line7	Thai-10-10
Tester 1	Thai-10-04
Tester 2	YZI-14-02
Tester 3	YZCI-16-038
Tester 4	KICF-12-002

Research Farm, Department of Agricultural Research (DAR), (20 °N and 96°E at an altitude of 151.21 m above sea level), Nay Pyi Taw, Myanmar in the growing season of June to October 2023. The parental materials used in line \times tester analysis have been selected based on the phenotypic performance of newly developed homozygous inbred lines and their genetic relationships in the previous study of hybrid maize breeding programs in DAR. The best national hybrid (Yezin hybrid-14) which was released from Myanmar in 2020-21 was used as a check variety. Each plot embraced 2 rows of 5 m long with the spacing of 75 cm between rows and 25 cm between plants. Other cultural practices *viz.*, weeding and pest management were done throughout the entire growing season as the necessity.

2.2 Data collection and statistical analysis

Data on days to 50% anthesis (days), days to 50% silking (days), plant height (cm), ear height (cm), ear plant⁻¹, shelling%, 1000-seed weight (g), ear length (cm), row length (cm), ear diameter (cm), number of rows and kernels row⁻¹ (no.) were recorded. All the data were analyzed using Statistix version 10 software. Combining ability effects; GCA and SCA were calculated for grain yield and yield attributing traits that were significant among genotypes following line \times tester analysis using R (version 4.1.2) Software. Graphical views were also generated by using GGE biplot. Standard heterosis was calculated according to the formula by Shull [15] and its significant level was tested by critical t value [16].

3. Results and discussion

3.1 Analyses of variance (ANOVA) for grain yield and agronomic traits

Mean squares of genotypes for grain yield and agronomic traits were shown in Table 2. Analyses of variance revealed that mean squares for genotypes were significantly different for all traits indicating the existence of genetic differences among the genotypes. Mean squares of lines were significant for plant height and ear plant⁻¹. Mean squares of testers were significant for days to 50% silking, ear height, ear plant⁻¹, shelling%, and kernels row⁻¹. This result indicated the diverse nature of lines and testers. It is possible to select potential inbred lines in the maize breeding program. Mean squares of line × tester interaction was significant for days to 50% anthesis, days to 50% silking, plant height, ear height, ear plant⁻¹, 1000-seed weight, ear length, row length, ear diameter, number of kernels row⁻¹ and grain yield (t ha⁻¹). The parents and their combiners with high genetic variation could be permitted to observe their genetic potential by using combining ability analysis. This result was agreed with the previous studies of other researchers [17-20].

3.2 Contribution of lines, tester and line × tester interaction

The contribution of lines, testers, and line × tester interaction to total variances was presented in Table 3. Proportional contribution of lines showed with higher values in plant height, ear plant⁻¹ indicating that the tested lines had greater genetic variability for the improvement of those traits. The proportional contribution of testers was observed with higher values in days to 50% silking and shelling% indicating that the four testers had greater genetic variation for the improvement of those traits. The proportional contribution of line × tester interaction was identified with the greater values for days to 50% anthesis, ear height, 1000-seed weight, ear length, row length, ear diameter, number of rows, kernels row⁻¹, and grain yield, indicating that interaction of genes in hybrid combination played a major role in the manifestation of those traits.

3.3 General combining ability

General combining ability effects of parents; lines and testers were presented in Table 4. Among seven lines, L2, L4, and L6 showed positive GCA effects for grain yield while L7, L1, L3, and L5 showed negative GCA effects. The parent, L2 was observed with significant negative GCA effects for days to 50% anthesis, days to 50% silking, and positive GCA effects for ear plant⁻¹,

shelling%, ear diameter, and grain yield. Therefore, L2 should be used as a potential parental line in maize breeding programs for the improvement of early mature hybrids associated with the desired traits. L4 possessed significant positive GCA effects for ear plant⁻¹, ear length, row length, ear diameter, kernel row⁻¹, and grain yield. Therefore, L4 could also be effectively utilized in future maize breeding programs as a parental line for the development of high-yielding hybrid associated with desired traits. L6 also showed significant positive GCA effects for days to 50% anthesis, days to 50% silking, ear plant⁻¹ and grain yield. This line could also be utilized as a promising line for the development of high-yielding and late mature hybrids.

Based on the GCA estimation of testers, T2, T3, and T4 showed negative GCA effects for grain yield while T1 was observed with significant positive GCA effect for grain yield associated positive GCA effects for ear plant⁻¹, shelling%, ear diameter, kernels row⁻¹ and grain yield. Therefore, T1 could be effectively utilized as an ideal tester to identify good inbred lines in the maize breeding program of DAR. The use of testers with a high frequency of favorable alleles allows for identifying the best combiners, the ones with the highest specific combining ability with those testers [21]. The tester T1 is a common male parent for the development of Myanmar national hybrids *viz.*, Yezin hybrid-10, Yezin hybrid-11 and Yezin hybrid-14. Therefore, T1 could be effectively used as an ideal tester to identify potential inbred for the development of superior hybrids in future Myanmar maize breeding programs.

3.4 Specific combining ability

The specific combining ability effects of 28 crosses are presented in Table 5. Among all crosses, (L4 × T1), (L5 × T3) and (L2 × T2) possessed significant negative SCA effects for grain yield. The crosses; (L4 × T2), (L6 × T2), (L5 × T4), (L2 × T1), (L6 × T1), (L2 × T3), and (L1 × T1) showed high SCA effects for grain yield. Among them, the cross (L6 × T1) showed a significant negative SCA effect for earliness associated with a positive SCA effect for grain yield, and it was observed as a promising cross to develop an early mature hybrid. The cross (L4 × T4) showed significant positive SCA effects for ear diameter and grain yield. This cross also showed positive SCA effects for some yield

Table 2. Analyses of variance for grain yield and agronomic traits in crosses and their parents

SV	Df	DA	DS	PH	EH	EPP	SH	TSW
Replications	2	2.33	0.62	11.17	2.59	0.017	0.35833	633.01
Genotypes	38	34.37**	30.89**	1126.39**	240.13**	0.079**	53.10**	3159.36**
Parents (P)	10	20.02**	21.74**	786.04**	188.46**	0.07**	118.35**	6762.47**
P vs. C	1	886.48**	791.01**	25606.34**	4334.14**	0.09**	255.153**	10641.33**
Crosses (C)	27	8.12**	6.13**	345.78**	107.64**	0.08**	21.44**	1547.77**
Lines (L)	6	11.15	7.77381	672.86**	119.6126	0.21**	16.02	2493.07
Testers (T)	3	20	21.28**	798.52	329.02*	0.15**	84.35**	468.30
L × T	18	5.13**	3.06**	161.30**	66.76**	0.03**	12.76	1412.58**
Error	76	1.11	0.69	31.03	25.42	0.008	10.30	576.50

** , * = Significant at 1% and 5% level, respectively. Df =degree of freedom, DA = days to 50% anthesis, DS = days to 50% silking, PH = plant height, EH = Ear height, EPP = ear plant⁻¹, SH = shelling%, TSW = 1000-seed weight, EL = ear length, RL = row length, ED = ear diameter, RPE = number of rows, KER = kernels row⁻¹, GY = grain yield (t ha⁻¹)

Table 2. (Continued)

SV	Df	EL	RL	ED	RPE	KER	GY
Replications	2	5.01	4.17	0.003	0.1	1.46	0.11
Genotypes	38	8.46**	7.28**	0.60**	3.48**	68.06**	16.18**
Parents (P)	10	3.75*	3.89**	0.38**	5.99**	86.16**	4.63**
P vs. C	1	158.51**	136.23**	13.01**	23.08**	1437.36**	409.64**
Crosses (C)	27	4.64**	3.76**	0.22**	1.82	10.64**	5.89**
Lines (L)	6	3.95	4.96	0.20	1.41	9.8	8.18
Testers (T)	3	10.20	5.72	0.47	3.43	37.60**	12.02
L × T	18	3.95**	3.04**	0.19**	1.69	6.43**	4.10**
Error	76	1.68	1.28	0.01	1.19	1.38	1.69

** , * = Significant at 1% and 5% level, respectively. Df =degree of freedom, DA = days to 50% anthesis, DS = days to 50% silking, PH = plant height, EH = Ear height, EPP = ear plant⁻¹, SH = shelling%, TSW = 1000-seed weight, EL = ear length, RL = row length, ED = ear diameter, RPE = number of rows, KER = kernels row⁻¹, GY = grain yield (t ha⁻¹)

Table 3. Proportional contribution (%) to total variance for grain yield and agronomic traits

Genotypes	DA	DS	PH	EH	EPP	SH	TSW	EL	RL	ED	CD	RPE	KER	GY
Lines	30.52	28.17	43.24	24.69	55.71	16.61	35.79	18.91	29.31	19.68	31.00	17.25	20.46	30.86
Tester	27.37	38.56	25.66	33.96	20.52	43.72	3.36	24.41	16.89	23.55	14.90	20.93	39.25	22.68
L × T	42.12	33.26	31.10	41.34	23.78	39.67	60.84	56.68	53.80	56.78	54.09	61.82	40.29	46.46

DA = days to 50% anthesis, DS = days to 50% silking, PH = plant height, EH = Ear height, EPP = ear plant⁻¹, SH = shelling%, TSW = 1000-seed weight, EL = ear length, RL = row length, ED = ear diameter, RPE = number of rows, KER = kernels row⁻¹, GY = grain yield (t ha⁻¹)

attributing traits *viz.*, ear plant⁻¹, ear length, row length, number of rows, and kernels row⁻¹. The cross (L5 × T2) showed significant positive SCA effects for ear diameter, kernels row⁻¹, and grain yield. This cross also showed positive SCA effects for some yield attributing traits *viz.*, 1000-seed weight, ear length, and row length. These two crosses could also be effectively utilized to develop high-yielding hybrids. The SCA effect was to be more appreciated than the GCA effect to produce hybrids with high grain yield [22, 23].

3.5 Identification of the best lines, testers, and their crosses by GGE biplots

The ideal tester could be effectively identified based on the yield performance of line × tester combinations shown in Fig. 1. The average tester coordinate (ATC), which is presented as a small circle, signifies the location of the average tester and the line passing over the average tester and origin of biplot, with an arrow indicating to the average tester is called average tester axis (ATA) [8]. Among the four testers; T1 and T3 were observed as the beneficial testers because they showed the highest projection on the average tester coordinate (ATC) which is well-defined by the average PC1 and PC2 scores. T2 and T4 were also observed as useful testers because they also possessed

Table 4. General combining ability effects (GCA) for grain yield and agronomic traits

GCA effect	DA	DS	PH	EH	EPP	SH	TSW	EL	RL	ED	RPE	KER	GY
L1	0.18	0.20	-10.52**	-3.56*	-0.11**	-1.19	11.33	0.33	-0.53	0.03	-0.05	-0.11	-0.60
L2	-0.68*	-0.63*	11.04**	5.64**	0.16**	1.96*	8.68	-1.02*	-0.77*	0.13**	-0.21	0.39	1.12*
L3	-0.76*	-1.05**	-2.12	-2.87*	-0.07*	0.03	-26.81**	-0.46	-0.61	-0.11**	0.62*	0.73	-0.54
L4	-0.76*	-0.21	7.09**	1.29	0.06*	1.07	9.37	0.73*	0.93*	0.21**	-0.05	1.23**	0.93*
L5	-0.35	-0.38	-2.57	-1.23	-0.01	-0.21	-2.93	0.21	0.50	-0.10**	-0.21	-0.11	-0.31
L6	1.57**	0.95**	2.93	1.72	0.15**	-0.53	-10.48	0.00	0.21	-0.11**	-0.38	-0.61	0.43
L7	1.16**	1.12**	-5.84**	-0.99	-0.19**	-1.13	10.84	0.20	0.28	-0.05	0.29	-1.52**	-1.02*
SE (gca for line)	0.30	0.24	1.61	1.46	0.03	0.93	6.93	0.37	0.33	0.03	0.31	0.34	0.38
T1	-0.43	-0.46*	-6.04**	-3.18*	0.09*	2.26*	-4.67	0.37	0.44	0.17**	0.29	1.35**	1.09*
T2	-1.00*	-1.08**	0.11	1.20	0.01	0.74	0.43	-0.53	-0.3	-0.11*	-0.57*	-0.37	-0.51
T3	1.29**	1.25**	8.44**	5.08**	-0.12**	-2.47*	6.36	0.80*	0.46	0.07	0.01	0.73*	-0.06
T4	0.14	0.30	-2.51	-3.10*	0.01	-0.54	-2.12	-0.64	-0.55	-0.14**	0.29	-1.70**	-0.52
SE (gca for tester)	0.23	0.18	1.22	1.10	0.02	0.70	5.24	0.28	0.25	0.03	0.24	0.26	0.28

** , * = Significant at 1% and 5% level, respectively. SE = Standard error. T1 = Tester-1, T2 = Tester-2, T3 = Tester-3, L1 = Line-1, L2 = Line-2, L3 = Line-3, L4 = Line-4, L5 = Line-5, L6 = Line-6, L7 = Line-7. DA = days to 50% anthesis, DS = days to 50% silking, PH = plant height, EH = Ear height, EPP = ear plant⁻¹, SH = shelling%, TSW = 1000-seed weight, EL = ear length, RL = row length, ED = ear diameter, RPE = number of rows, KER = kernels row⁻¹, GY = grain yield (t ha⁻¹).

Table 5. Specific combining ability effects of line × tester cross for grain yield and agronomic traits

Crosses	DA	DS	PH	EH	EPP	SH	TSW	EL	RL	ED	ROW	KER	GY
L1 × T1	1.18*	0.46	3.37	3.03	-0.03	1.09	-26.45*	-0.14	0.62	0.19**	1.38*	1.16*	1.19
L1 × T2	0.75	0.75	-4.41	-3.68	-0.13**	-2.32	-7.66	1.00	0.86	-0.20**	0.24	-0.131	-1.20
L1 × T3	-0.54	-0.25	1.82	-3.30	0.08	-0.64	25.94*	0.34	-0.91	0.12*	-0.33	-2.23**	0.30
L1 × T4	-1.39*	-0.96*	-0.79	3.95	0.07	1.87	8.18	-1.20	-0.57	-0.10	-1.27*	1.20*	-0.29
L2 × T1	-0.66	-0.04	-6.32*	-3.34	-0.08	-2.82	23.96*	0.65	0.46	0.08	0.21	0.99	0.95
L2 × T2	0.58	-0.42	-3.30	-3.55	0.02	-1.83	6.98	0.25	0.27	-0.31**	-0.26	-2.30**	-1.43*
L2 × T3	0.63	0.92*	11.60**	10.07**	0.05	3.13	2.43	0.36	0.53	0.38**	-0.17	0.94	1.13
L2 × T4	-0.56	-0.46	-1.98	-3.18	0.02	1.52	-33.37*	-1.25	-1.26*	-0.14*	0.21	0.37	-0.66
L3 × T1	0.76	0.38	8.16**	6.14*	0.09*	-0.83	-24.28*	0.48	0.63	0.02	0.05	-0.35	0.12
L3 × T2	-0.67	-0.67	-0.12	2.73	-0.01	3.61*	-9.36	-0.36	-0.55	-0.07	-0.43	1.04	-0.51
L3 × T3	-0.95	-1.00*	-5.12*	-2.13	-0.04	-0.54	27.35*	-1.11	-0.53	0.05	0.33	-1.06	0.67
L3 × T4	0.86	1.29**	-2.93	-6.74*	-0.03	-2.24	6.30	0.99	0.45	0.00	0.05	0.37	-0.28
L4 × T1	0.76	0.21	-1.20	-1.65	-0.14**	1.05	-13.08	-0.17	-0.21	-0.47**	-0.62	-0.85	-2.13**
L4 × T2	0.67	0.17	-7.59*	-2.12	0.20**	-0.40	3.90	-1.21	-0.96	0.28**	0.91	-0.46	0.76
L4 × T3	-0.95	-0.83*	9.28**	0.93	-0.13**	0.58	11.82	0.37	0.37	-0.07	-0.33	0.77	0.01
L4 × T4	-0.48	0.45	-0.49	2.84	0.07	-1.23	-2.64	1.01	0.81	0.25**	0.05	0.54	1.36*
L5 × T1	0.35	-0.29	0.48	-1.90	0.08	0.90	14.56	0.65	0.16	-0.16*	-0.45	-1.85**	-0.59
L5 × T2	0.25	1.00*	0.97	2.16	-0.02	-0.19	7.24	0.41	0.24	0.22**	-0.26	1.87**	1.30*
L5 × T3	-1.37*	-0.67	-4.70	-0.73	0.01	-2.32	-31.61*	-0.41	-0.07	-0.26**	-0.17	-0.56	-1.59*
L5 × T4	0.77	-0.05	3.26	0.46	-0.06	1.61	9.82	-0.65	-0.33	0.19**	0.89	0.54	0.88
L6 × T1	-2.57**	-1.62**	7.46*	3.59	0.11*	-0.81	31.35*	1.12	0.87	0.35**	0.38	1.66*	0.98
L6 × T2	-1.00	-0.67	3.37	2.04	0.01	1.36	-3.71	-0.21	0.06	0.07	-0.10	0.04	0.86
L6 × T3	3.05**	2.33**	-10.89**	-5.51*	0.01	1.26	-21.20	-1.14	-0.68	-0.25**	-0.67	0.61	-0.77
L6 × T4	0.52	-0.05	0.06	-0.12	-0.12*	-1.81	-6.44	0.23	-0.25	-0.17*	0.38	-2.30**	-1.07
L7 × T8	0.18	0.88*	-11.95**	-5.87*	-0.02	1.42	-6.05	-2.58**	-2.53**	-0.01	-0.95	-0.76	-0.52
L7 × T2	-0.58	-0.17	11.07**	2.42	-0.07	-0.23	2.61	0.12	0.09	0.01	-0.10	-0.05	0.22
L7 × T3	0.13	-0.50	-1.99	0.67	0.04	-1.47	-14.72	1.60*	1.28*	0.03	1.33*	1.52*	0.24
L7 × T4	0.27	-0.21	2.86	2.79	0.05	0.28	18.17	0.86	1.16*	-0.03	-0.29	-0.71	0.06

Table 5. (Continued)

Crosses	DA	DS	PH	EH	EPP	SH	TSW	EL	RL	ED	ROW	KER	GY
SE	0.61	0.48	3.22	2.91	0.05	1.85	13.86	0.75	0.65	0.07	0.63	0.68	0.75

(sca for crosses)

**,* = Significant at 1% and 5% level, respectively. SE = Standard error. DA = days to 50% anthesis, DS = days to 50% silking, PH = plant height, EH = Ear height, EPP = ear plant⁻¹, SH = shelling%, TSW = 1000-seed weight, EL = ear length, RL = row length, ED = ear diameter, RPE = number of rows, KER = kernels row⁻¹, GY = grain yield (t ha⁻¹)

similar conditions of tester T1 and T3. Even though T1 showed significant positive GCA effects in line × tester analysis, all four testers were observed as the qualified testers on the graphical view because they could be identified as the best lines viz., L2 and L4 for grain yield.

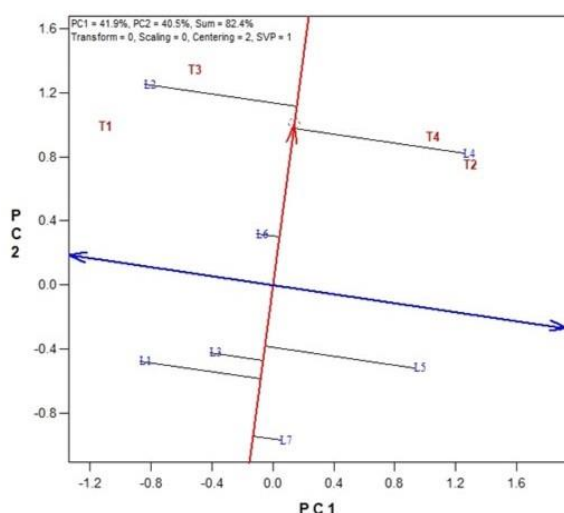


Figure 1. GGE biplot for grain yield presenting average tester coordinate view. The arrow symbolizes the average tester.

The GCA values of Kempthorne’s and GGE biplot analysis are completely related. Conversely, GGE biplots help the breeders to understand clearly the identification of potential parents and their combinations based on its graphical view [8]. Polygon of GGE biplot provides the greatest manner to interpret the results of the performance of lines, testers and their combinations [24]. According to the polygon view of the biplot, interaction patterns of lines and testers could be observed definitely (Fig. 2). According to the result, biplot was separated into five sections based on the performance of genotypes for grain yield. The two testers; T1 and T3 clearly fell in sector 1 while the L2 was positioned at the vertex of the polygon. Based on the result, L2 was observed as the best combiner with T1 and T3. The testers; T2 and T4 were allocated in sector 2 while the L4 was

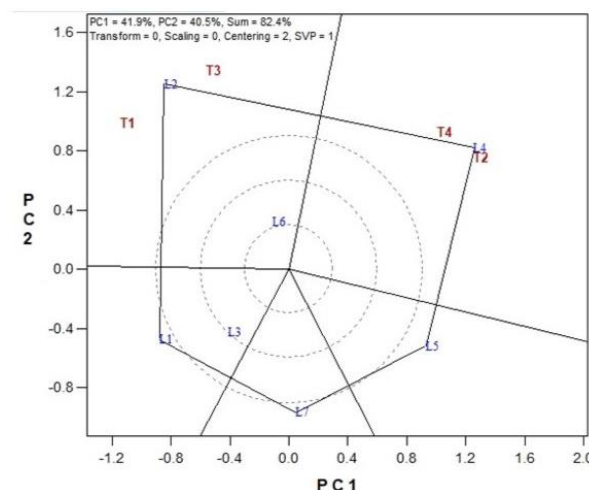


Figure 2. GGE biplot for grain yield presenting polygon view

positioned at the vertex of the polygon. In that case, L4 was identified as the best partner with T2 and T4. Based on this finding, the breeders can easily identify the crosses as (L2 × T1) and (L2 × T3) were heterotic groups with (L4 × T2) and (L4 × T4). There was no tester in sections L1, L5 and L7 indicating that these three lines were the best combiners for any of the testers and were identified as the poorest-mating partners with all four testers. Therefore, GGE biplot well presents to identify the best combiners among the genotypes by directing in a polygon view.

3.6 Mean performance

The mean performance of the 28 crosses and one check hybrid (Yezin hybrid-14) for grain yield and yield-attributing traits are presented in Table 6. Mean values of crosses for ear plant⁻¹ ranged from 1.06 to 1.67, the 11 crosses were significantly higher compared with Yezin hybrid-14. Regarding shelling%, crosses ranged from 74.17% to 83.63% and the two crosses were significantly higher over Yezin hybrid-14. For 1000-seed weight, the crosses ranged from 249.09 to 348.48 (g) and the eight crosses showed higher values over the check. For ear length, the crosses range from 15.27 to 20.27 (cm) and the four

Table 6. Mean performance of 28 crosses and check (Yezin hybrid-14) for grain yield and yield-attributing traits

Crosses	EPP	SH	TSW	EL	RL	ED	RPE	KER	GY
L1 × T1	1.27	81.42	285.06	18.73	17.73	4.83	16	36	11.24
L2 × T1	1.50	80.64	332.83	18.17	17.33	4.83	14	36	12.72
L3 × T1	1.43	80.7	249.09	18.57	17.67	4.53	14	35	10.23
L4 × T1	1.33	83.63	296.47	19.1	18.37	4.37	14	35	9.45
L5 × T1	1.47	82.2	311.81	19.4	18.30	4.37	12	33	9.75
L6 × T1	1.67	80.17	321.05	19.67	18.73	4.87	14	36	12.07
L7 × T1	1.43	80.70	304.97	18.57	17.67	4.60	14	32	10.23
L1 × T2	1.10	76.47	308.95	18.97	17.20	4.17	14	33	7.24
L2 × T2	1.51	80.11	320.94	16.87	16.37	4.17	12	31	8.74
L3 × T2	1.25	83.61	269.10	16.83	15.70	4.17	14	35	8.00
L4 × T2	1.59	80.65	318.55	17.17	16.83	4.83	14	34	10.74
L5 × T2	1.29	79.58	309.59	18.27	17.60	4.47	12	35	10.04
L6 × T2	1.49	80.81	291.09	17.43	17.13	4.30	12	32	10.35
L7 × T2	1.08	78.62	318.73	17.97	17.23	4.30	14	31	8.24
L1 × T3	1.18	74.95	348.48	19.63	16.23	4.67	14	32	9.20
L2 × T3	1.41	81.87	322.32	18.3	17.43	5.03	14	35	11.75
L3 × T3	1.10	76.26	311.74	17.4	16.53	4.47	14	34	9.64
L4 × T3	1.14	78.42	332.4	20.07	18.97	4.67	14	36	10.44
L5 × T3	1.20	74.24	276.67	18.77	18.10	4.17	14	33	7.60
L6 × T3	1.35	77.50	279.53	17.83	17.20	4.17	12	34	9.17
L7 × T3	1.06	74.17	307.33	20.77	19.23	4.50	16	34	8.73
L1 × T4	1.29	79.38	322.24	16.67	15.57	4.23	12	33	8.16
L2 × T4	1.51	82.19	278.05	15.27	14.63	4.30	14	32	9.50
L3 × T4	1.24	76.49	282.22	18.07	16.50	4.20	14	33	8.23
L4 × T4	1.47	78.55	309.46	19.27	18.40	4.77	14	33	11.33
L5 × T4	1.25	80.11	309.62	17.1	16.83	4.40	14	32	9.61
L6 × T4	1.37	76.37	285.81	17.77	16.63	4.03	14	29	8.41
L7 × T4	1.20	77.85	331.74	18.6	18.10	4.23	14	29	8.08
HY#14 (Check)	1.25	79.00	320.3	19.33	18.63	4.30	14	35	10.01
Mean	1.30	78.71	302.73	17.53	16.67	4.31	14	32	9.04
Manimum	1.06	74.17	249.09	15.27	14.63	4.03	12	29	7.24
Maximum	1.67	83.63	348.48	20.27	19.23	5.03	16	36	12.72
F test	**	**	**	**	**	**	ns	**	**
LSD (0.05)	0.14	3.71	32.44	2.13	1.77	0.19	1.77	1.57	1.86
CV	6.35	2.88	6.48	7.16	6.28	2.58	7.88	2.89	11.9

EPP = ear per plant, SH = shelling%, TSW = 1000-seed weight, EL = ear length, RL = row length, ED = ear diameter, RPE = number of kernel rows, KER = number of kernels per row, GY = grain yield (t ha⁻¹)

crosses showed higher values over check hybrid. Regarding the row length, the crosses ranged from 14.63 to 19.23 (cm) and the four crosses were observed with higher values over check hybrid. In the ear diameter, the crosses ranged from 4.03 to 5.03 (cm) and the 13 crosses were significantly higher over Yezin hybrid-14. In the number of kernel rows, the crosses ranged from 12 to 16 and the two crosses were significantly higher over check hybrid. In the number of kernels per row, the crosses ranged from 29 to 36 and four crosses were higher over check hybrid.

Regarding the grain yield, the crosses ranged from 7.24 to 12.72 (t ha⁻¹), the grain yield of eight crosses *viz.*, (L5 × T2), (L7 × T1), (L3 × T1), (L6 × T2), (L4 × T3), (L4 × T2), (L1 × T1) and (L4 × T4) were higher over Yezin hybrid-14 while the two crosses *viz.*, (L2 × T3) (L6 × T1) and (L2 × T1) shown significantly higher over Yezin Hybrid-14. The crosses possessing higher grain yield compared with check hybrid could be tested for their performance in different agroecological conditions for their adaptability.

Table 7. Estimates of heterosis over Yezin hybrid-14 for grain yield and yield- attributing traits

Crosses	EPP	SH	TSW	EL	RL	ED	RPE	KER	GY
L1 × T1	1.96	1.78	-11.00*	-3.09	-4.66	12.40**	14.29*	1.90*	12.27
L2 × T1	19.53**	0.80	3.91	-6.02	-6.81	12.40**	0.00	2.86	27.03**
L3 × T1	14.06**	0.88	-22.23**	-3.95	-5.02	5.43**	0.00	0.00	2.19
L4 × T1	6.25	4.53*	-7.44	-1.19	-1.25	1.55	0.00	0.00	-5.64
L5 × T1	17.19**	2.75	-2.65	0.36	-1.61	1.55	-14.29*	-6.67**	-2.62
L6 × T1	32.81**	0.21	0.23	1.74	0.72	13.18**	0.00	1.90	20.54*
L7 × T1	14.51**	0.88	-4.79	-3.95	-5.02	6.98**	0.00	-8.57**	2.19
L1 × T2	-12.16*	-4.42	-3.54	-1.88	-7.53	-3.10	0.00	-6.67	-27.65**
L2 × T2	20.78**	0.13	0.20	-12.74*	-12.01**	-3.10	-14.29*	-11.43	-12.70
L3 × T2	0.39	4.51*	-15.98**	-12.92*	-15.59**	-3.10	0.00	-0.95	-20.09*
L4 × T2	27.06**	0.82	-0.55	-11.19*	-9.50*	12.40**	0.00	-3.81	7.25
L5 × T2	3.53	-0.53	-3.34	-5.50	-5.38	3.88*	-14.29*	-0.95	0.27
L6 × T2	19.22**	1.02	-9.12	-9.81*	-7.89*	0.00	-14.29*	-8.57**	3.35
L7 × T2	-13.73*	-1.72	-0.49	-7.05	-7.35	0.00	0.00	-10.48**	-17.65*
L1 × T3	-5.88	-6.32*	8.80*	1.57	-12.72**	8.53**	0.00	-9.52**	-8.04
L2 × T3	12.94*	2.33	0.63	-5.33	-6.27	17.05**	0.00	0.95	17.42*
L3 × T3	-12.16*	-4.68	-2.67	-9.98*	-11.11*	3.88*	0.00	-3.81	-3.66
L4 × T3	-9.02	-1.98	3.78	3.81	1.97	8.53**	0.00	2.86	4.34
L5 × T3	-4.31	-7.20*	-13.62**	-2.91	-2.69	-3.10	0.00	-4.76	-24.03**
L6 × T3	8.24	-3.12	-12.73**	-7.74	-7.53	-3.10	-14.29*	-2.86	-8.40
L7 × T3	-15.29**	-7.29*	-4.05	7.43	3.41	4.65*	14.29*	-2.86	-12.83
L1 × T4	3.53	-0.78	0.61	-13.78**	-16.31**	-1.55	-14.29*	-6.67**	-18.51*
L2 × T4	20.78**	2.73	-13.19**	-21.02**	-21.33**	0.00	0.00	-7.62**	-5.05
L3 × T4	-1.18	-4.38	-11.89*	-6.54	-11.29*	-2.33	0.00	-6.67**	-17.78*
L4 × T4	17.65**	-1.81	-3.38	-0.33	-1.08	10.85**	0.00	-4.76	13.15
L5 × T4	0.39	0.14	-3.33	-11.54*	-9.50*	2.33	0.00	-8.57**	-4.00
L6 × T4	9.80*	-4.54	-10.77*	-8.09	-10.57*	-6.20**	0.00	-18.10**	-16.02*
L7 × T4	-4.31	-2.69	3.57	-3.78	-2.69	-1.55	0.00	-16.19**	-19.26*
SE(d)	0.07	0.02	16.19	1.07	0.88	0.09	0.88	0.79	0.93

** , * = Significant at 1% and 5% level, respectively. SE = Standard Error. EPP = ear plant⁻¹, SH = shelling%, TSW = 1000-seed weight, EL = ear length, RL = row length, ED = ear diameter, RPE = number of rows, KER = kernels row⁻¹, GY = grain yield (t ha⁻¹)

3.7 Heterosis

The standard heterosis was observed by comparing with Yezin hybrid-14 for grain yield and yield attributing traits revealed in Table 7. Among the 28 crosses, eight crosses viz., (L1 × T2), (L5 × T3), (L7 × T4), (L1 × T4), (L3 × T4), (L7 × T2) and (L6 × T4) showed significant negative heterosis for grain yield. The three crosses; (L4 × T4), (L1 × T1) and (L4 × T2) had greater positive heterosis. The positive or negative direction of standard heterosis is mainly determined by the breeding objectives and the type of traits employed [14]. The cross (L2 × T1) showed highly significant positive heterosis for grain yield associated with yield attributing traits viz., ear plant⁻¹, shelling%, seed weight, ear diameter, number of rows and kernels row⁻¹. The cross (L6 × T1) showed significant positive connections with yield attributing traits viz.,

ear plant⁻¹, shelling%, seed weight, ear length, row length, ear diameter and kernels row⁻¹. The cross (L2 × T3) also showed significant positive heterosis linked with yield attributing traits viz., ear plant⁻¹, shelling%, seed weight, ear diameter and kernels row⁻¹. This result pointed out that the superior grain yield of some crosses was higher over Yezin hybrid-14. Based on this finding, the crosses with higher yield over Yezin hybrid-14 could be tested for their performance in different agroecological conditions for their adaptability.

4. Conclusions

Line × tester analysis effectively identified the potential lines viz., L2 (TK.20.03), L4 (TK.20.20) and L6 (TK20.01) which were good general combiners for grain yield and yield attributing traits. Therefore,

these 3 lines could be effectively utilized as a genetic material in future breeding programs to develop high-yielding hybrids. The crosses; (L2 × T1), (L2 × T3), (L4 × T4), (L4 × T2) and (L6 × T1) showed positive SCA effects and positive heterosis and GGE biplot presented superior parental maize inbred lines and crosses related to grain yield. Therefore, the yield adaptation of these five crosses should be carried out in different agroecosystems of Myanmar. The line × tester analysis provided detailed genetic information of lines, testers and their combinations while GGE biplot approach provided the breeders with an effective way to identify potential parents and crosses by presenting its graphical view.

Authors' contributions

Execution of the experiment and data collection, N.A.; Manuscript preparation N.A., M.A.; Data analysis and interpretation, K.M., M.A., N.M.H.; Designing of the experiment and conceptualization of experimental results, N.M.H.; All draft of manuscript revision, N.A., M.A.; Final draft of the manuscript revision, N.A., N.M.H., SW.

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Availability of data and materials

All data will be made available on request according to the journal policy

Conflicts of interest

The authors declare no conflict of interest

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