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COMBINING ABILITY ANALYSIS IN MAIZE DIALLEL HYBRID POPULATIONS UNDER OPTIMUM AND DROUGHT STRESS CONDITIONS

A. AMZERI[1*], SUHARTONO[1], S. FATIMAH[1], G. PAWANA[1], and K.P.W. SUKMA[2]

[1]Faculty of Agriculture, University of Trunojoyo Madura, Indonesia
[2]Department of Agroecotechnology, Faculty of Agriculture, Universitas Islam Madura, Indonesia
*Corresponding author's email: aamzeri@gmail.com
Email addresses of co-authors: suhartono@trunojoyo.ac.id, sitifatimah@trunojoyo.ac.id,
gitapawana@trunojoyo.ac.id, keliksukma@gmail.com

SUMMARY

The latest study strategized to evaluate the maize populations by combining ability analysis under optimum and drought-stress environments to assemble the promising parental inbred lines and their hybrid populations with high productivity and resistance to drought stress. From the collection of the Trunojoyo Madura University, Indonesia, came five maize pure lines (UTM 2, UTM 7, UTM 10, UTM 19, and UTM 31) that received crossing in a complete diallel fashion to obtain 20 hybrid populations. The performance of five parental inbred lines and their 20 F1 hybrids' evaluation in crop season 2021 had a randomized complete block design with three replications under four each for optimum and drought-stress environmental conditions. Data recording ensued on grain yield and drought susceptibility index (DSI). The GCA and SCA variances revealed that grain yield had more influences from the dominant genes with maternal effects at the eight locations; hence, the parental lines have less stimulus on the hybrids' performance. The genotype UTM2 (G1) appeared resistant to drought-stress conditions based on the DSI value (0.70) and has positive GCA effects for grain yield. Therefore, it can better serve to improve drought resistance and grain yield. The results further exhibited that six maize hybrids, i.e., G3 (UTM 2 × UTM 10), G6 (UTM 7 × UTM 2), G10 (UTM 7 × UTM 31), G11 (UTM 10 × UTM 2), G22 (UTM 31 × UTM 10), and G24 (UTM 31 × UTM 19) were remarkable as commercial hybrids with high grain yield and resistance to drought stress.

Keywords: Maize (*Zea mays* L.), diallel hybrids, combining ability, additive and dominant gene action, grain yield, drought susceptibility index (DSI), drought-stress resistance, stability

Key findings: The maize inbred line UTM2 was potentially resistant to drought stress conditions with a DSI of 0.70, and it also gave positive GCA effects for grain yield; thus, it can be functional to

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assemble maize hybrids with high productivity and resistance to drought stress. Six maize hybrids G3 (UTM 2 × UTM 10), G6 (UTM 7 × UTM 2), G10 (UTM 7 × UTM 31), G11 (UTM 10 × UTM 2), G22 (UTM 31 × UTM 10), and G24 (UTM 31 × UTM 19) emerged highly recommendable as commercial hybrids with high productivity and resistance to drought stress conditions.

INTRODUCTION

Maize's low productivity in the arid zones is one of chief constraints for increased maize production in Indonesia (Asnah *et al*., 2018). The dry land area used for maize cultivation is around 24.5 million ha in Indonesia (ICALRRD, 2018). Madura Island is a dry land area of approximately 300,000 ha located in the Province of East Java, Indonesia, used for maize planting but has a low productivity of 2.15 t ha^{-1} (BPS-Statistics Indonesia, 2019). The maize planting area in Madura Island has a dominant dry climate with insufficient water due to low rainfall (less than 2,000 mm/year) and a short rainy season (3–5 months) (Mulyani and Sarwani, 2013). The average annual rainfall was around 1346.89 mm per year in the Madura Island (Suhartono *et al.,* 2020).

Drought stress is an abiotic stress that affects maize growth, development, and production. In the tropics, drought stress conditions result in maize yield decline of around 17%–60% (Sah *et al.,* 2020). During the crop lifetime, the drought stress significantly affects the maize plant growth and productivity (Song *et al.,* 2019). However, maize hybrid cultivars with high production and drought-tolerant characteristics can overcome the problem of low productivity in dryland areas (Bahtiar *et al.,* 2023). Therefore, developing high-yielding maize hybrid cultivars with drought-tolerant characteristics is possible through conventional hybridization.

In assembling superior maize hybrid cultivars, the first stage is selecting parental lines suitable for the hybridization program. The problem that often arises from selection is parental lines do not always produce superior cross combinations. Therefore, it is necessary to evaluate the combining ability of potential parent cultivars to get the best cross-combination for assembling the hybrid cultivars. Diallel crosses are appropriate methods for assessing the combining ability among potential lines (Bourgou *et al.,* 2022). The general (GCA) and specific combining ability (SCA) in diallel crosses can also help to attain information about the expected parental combinations (Abdulla *et al.,* 2022). The GCA and SCA analysis results can better determine the appropriate method for assembling maize hybrid cultivars (Adu *et al.,* 2022).

The success of producing high-yielding maize hybrid cultivars depends upon the combining ability of the parental genotypes and the gene action governing the desired characters (Temesgen, 2021). In past research, the maize hybrids produced through diallel crosses created two yellow maize hybrids with high production characteristics and resistance to drought stress (Nasser *et al.*, 2020). Badu-Apraku and Obisesan (2021) produced two other maize hybrids, which were high-yielding and resistant to drought stress conditions, and *Striga hermonthica.*

The combining ability and gene action of various characters also incur influences from environmental conditions (Chiuta and Mutengwa, 2020). The considerable influence of the environment on the genotypes and their variable appearance will make it difficult for plant breeders to carry out selection activities (Liu *et al.,* 2018). Therefore, it is necessary to carry out combining ability tests at several locations with normal environmental and drought stress conditions to improve the accuracy of the genetic variance values and the estimated values of the combining ability. Evaluating several genotypes under optimum and drought stress conditions at several locations will make it easier for plant breeders to select stable genotypes in all environments and specific to certain environments (Sewore *et al.,* 2023).

The practical biometrical analysis to determine the stability and adaptability of genotypes are the AMMI (Additive Main Effects and Multiplicative Interaction Model) analysis and GGE biplot (Genotype and Genotype-Environment Interaction) (Wang *et al.,* 2020; Khan *et al.,* 2021). AMMI analysis is a multivariate statistical method used to assess the effects of the environment on the genotypes tested in a multi-location experiment (Katsenios *et al.,* 2021). The AMMI analysis results presentation comes in graphical form, making it easy to understand and interpret. Furthermore, GGE Biplot analysis will also help plant breeders better understand complex genotype and environment interaction (GEI) in multi-location research (Olanrewaju *et al.,* 2021).

GGE biplot analysis classifies genotypic effects, which are additive in the AMMI analysis (Daemo *et al.,* 2023). GGE biplot analysis helps determine the genotypic performance under optimum and stressful environmental conditions (Wardofa *et al.,* 2019). GGE biplot analysis is more accurate and practical than AMMI analysis because it explains the middle proportion of the sum of squares of the genotype + genotype x environment (G+GxE) (Ding *et al.,* 2008). The presented research sought to evaluate the performance of maize inbred lines and their diallel hybrid populations under optimum and drought stress conditions.

MATERIALS AND METHODS

Plant material and research implementation

Five maize pure lines (UTM 2, UTM 7, UTM 10, UTM 19, and UTM 31), procured from the collection of Trunojoyo Madura University, Indonesia, bore crossing in a complete diallel fashion to obtain 20 hybrid populations. The promising maize research commenced in May-September 2021 (dry season) with four locations each for optimum and drought stress conditions (Table 1). This research had a randomized complete block design (RCBD) with 25 genotypes resulting from diallel crosses and three repetitions. At each test location, planting each maize genotype continued in 2 m × 5 m plots with a spacing of 70 cm × 20 cm.

The research on drought stress employed the CIMMYT method (Weber *et al.,* 2012), where drought stress instigation occurred when the plants were 50 days after planting until harvest; however, irrigation transpired with field capacity from the first day of planting to 40 days after planting at intervals of 10 days. Under optimum conditions, irrigation with field capacity ran at

Table 1. Description of the eight test locations (environments).

Location Code	Locations	Cultivation	Altitude (masl)	Mean annual rainfall (mm)	Temperature (°C)		Soil type
					Min	Max	
E1	Kamal, Bangkalan, East Java	Optimum	5 m	1741	24	34	Grumusol
E2	Kamal, Bangkalan, East Java	Drought Stress	5 m	1741	24	34	Grumusol
E3	Jrengik, Sampang, East Java	Optimum	25 m	848	28	32	Grumusol
E4	Jrengik, Sampang, East Java	Drought Stress	25 m	848	28	32	Grumusol
E5	Pademawu, Pamekasan, East Java	Optimum	7 m	2161	25	33	Alluvial
E6	Pademawu, Pamekasan, East Java	Drought Stress	7 m	2161	25	33	Alluvial
E7	Lenteng, Sumenep, East Java	Optimum	50 m	1798	20	35	Litosol
E8	Lenteng, Sumenep, East Java	Drought Stress	50 m	1798	20	35	Litosol

intervals of 10 days from the first day of planting until 80 days after planting. Both under optimum and drought stress conditions, fertilization had three stages, i.e., when the plants were seven days after planting (200 kg ha^{-1} SP-36, 100 kg ha^{-1} Urea, and 50 kg ha^{-1} KCl), 25 days after planting (100 kg ha^{-1} Urea and 50 kg ha^{-1} KCl), and 40 days after planting (100 kg ha^{-1} Urea and 50 kg ha^{-1} KCl).

Data collection and analysis

Observing grain yield per hectare happened on 50 sample plants on every test unit at the location trials. Maize crop harvesting proceeded when maize cobs ripened physiologically characterized by dry or brownish husks and when kernels hardened and contained black layers at least 50% at every line of maize kernels. The kernel moisture content has reached less than 30% in that situation. The grain yield observation on all sample plants on every test unit gained conversion to the grain yield per hectare on 15% moisture content using the following equation:

$$Y = \frac{10.000}{HA} \text{ x } \frac{100 - MC}{100 - 15} \text{ x } GW$$

Where:
Y is grain yield (kg h^{-1}),
HA is harvested area per plot (m^2),
MC is moisture content at harvest time (%), and
GW is harvested grain weight per plot (kg).

The Drought Susceptibility Index (s) measurement used the following equation (Fischer and Maurer, 1978):

$$S = \frac{(1 - (\frac{Yp}{Y})}{(1 - (\frac{Xp}{X})}$$

Where:
Yp is the mean of a genotype subjected to drought stress,
Y is the mean of a genotype not subjected to drought stress,
Xp is the mean of all genotypes subjected to drought stress, and
X is the mean of all genotypes that are drought-tolerant.

The data analysis of grain yield per hectare used the F-test and combined analysis of variance (ANOVA). If the means appear significantly different, then the HSD test (Honest Significant Difference) will proceed to determine the differences among the treatments tested. Next, the grain yield data per hectare of five pure parental lines and 20 F1 hybrids sustained the combining ability analysis using Method-I based on Eisenhart Model-II (Griffing, 1956; Singh and Chaudhary, 1985). Stability analysis continued as per the genotypes and environment interaction (GEI). A graphical multivariate stability analysis based on AMMI and GGE biplot analyses explained the GEI (Yan *et al.,* 2007). Using the what-won-where biplot helps find the superiority of the genotypes to a particular environment. Measurement of combined multivariate analysis, combining ability, AMMI, GGE biplot, and what-won-where engaged the PB-Tools program STAR.

RESULTS AND DISCUSSION

General and specific combining ability analysis

The analysis of variance for combining ability revealed that SCA and reciprocal effects significantly affected the maize grain yield at eight test locations (Table 2). The significant reciprocal effects also enunciated that the phenotypic appearance may have maternal effects affecting it. The pertinent results were analogous to the research of Zakiullah *et al.* (2019) and Suyadi *et al.* (2021), as they also observed maternal effects for grain yield in maize diallel hybrids. The GCA variance for grain yield incurred effective influences at eight locations, except at location E6.

The GCA is the average ability of the parental genotype to combine in crossing with other parental cultivars (Murtadha *et al.,* 2018). The parent cultivar with desirable GCA

Table 2. Analysis of variance for combining ability for grain yield at the eight test locations.

Source of Variation	d.f.	E1		E2		E3		E4	
		MS	F value	MS	F value	MS	F value	MS	F value
GCA	4	4.25	2.97*	1.93	2.55*	4.53	2.72*	1.74	2.39*
SCA	10	1.50	445.38**	0.79	460.56**	1.75	522.07**	0.76	403.44**
Reciprocal	10	0.27	79.64**	0.09	57.26**	1.19	59.58**	0.10	51.79**
Error	24	0.08		0.00		0.00		0.00	
Source of Variation	d.f.	E5		E6		E7		E8	
		MS	F value	MS	F value	MS	F value	MS	F value
GCA	4	5.13	3.10*	0.80	1.46^{ns}	5.07	3.18*	1.76	2.41*
SCA	10	1.74	702.09**	0.58	269.81**	1.67	1349.65**	0.77	62.84**
Reciprocal	10	0.30	122.54**	0.29	137.34**	0.22	177.88**	0.17	14.07**
Error	24	0.00		0.00		0.00		0.01	

Note: *,** = significant at 5% and 1% level of probability; d.f. = degrees of freedom.

Table 3. General combining ability effects in maize parental genotypes for grain yield at the eight test locations.

Parents	E1	E2	E3	E4	E5	E6	E7	E8
UTM 2	0.39	0.31	0.43	0.31	0.51	0.12	0.45	0.27
UTM7	-0.47	-0.43	-0.49	-0.40	-0.48	-0.31	-0.50	-0.38
UTM 10	-0.47	-0.15	-0.46	-0.19	-0.53	-0.02	-0.06	-0.20
UTM 19	-0.42	-0.33	-0.46	-0.29	-0.50	-0.06	-0.48	-0.30
UTM 31	0.96	0.60	0.98	0.57	1.01	0.41	1.04	0.60
S.E.	0.31	0.148	0.33	0.13	0.37	0.06	0.37	0.13

effects (positive/negative as based on the parameter) may have the most valued one by generally having a good combining ability. In contrast, the undesirable GCA effects (positive/negative as based on the parameter) showed that the parent cultivar has the least combining ability than other genotypes. Results revealed that parental inbred lines UTM 2 and UTM 31 have positive GCA effects at eight test locations for the grain yield (Table 3). Therefore, both parents could be the best general combiners for grain yield in maize. For inbred lines UTM 2 and UTM 31, the GCA effects ranged from 0.12 to 1.04 at eight test locations. However, the maize parental inbred lines, i.e., UTM 7, UTM 10, and UTM 19 have negative GCA effects at eight test locations. Consequently, those three parental genotypes were not better for use in hybridization in assembling the hybrid varieties. The development of hybrid varieties that use parents with low GCA values will produce hybrids with poor vigor in terms of plant characteristics (Han *et al.,* 2020).

The SCA is the value of a hybrid performance on crossing two parental genotypes, and a high SCA value generally results from the most GCA-valued parents (Bhusal and Lai, 2020; Zhang *et al.,* 2022). The findings showed that all the positive GCA-valued parents when crossed with one another will result in positive SCA in hybrid populations (Table 4). The crosses of the two maize parents (UTM 2 and UTM 31) that had positive GCA values, produced the progeny with positive SCA effects for grain yield at seven test locations (E1, E2, E3, E4, E5, E7, and E8). However, their hybrid was visible with negative SCA effects at the test location E6. According to Tokhetova *et al*. (2022), the appearance of SCA is due to influences of environmental conditions. A cross combination between negative and positive GCA-valued parents, namely, UTM 19 × UTM 31 (with negative × positive GCA), produced the progeny with the highest positive SCA effects for grain yield at eight test locations. On the other hand, the progeny with a positive SCA can result from a

Table 4. Specific combining ability effects in maize F1 diallel hybrids for grain yield at the eight test locations.

Crosses	E1		E2		E3		E4	
	SCA	REC	SCA	REC	SCA	REC	SCA	REC
UTM 2 x UTM 7	-0.50	-0.62	-0.13	-0.30	-0.04	-0.51	-0.05	-0.39
UTM 2 x UTM 10	0.47	-0.43	0.15	-0.04	0.42	-0.41	0.16	-0.08
UTM 2 x UTM 19	-0.79	-0.14	-0.58	-0.05	-0.77	-0.19	-0.53	-0.01
UTM 2 x UTM 31	1.74	0.65	0.93	0.47	1.99	0.49	0.97	0.45
UTM 7 x UTM 10	-0.07	-0.07	-0.13	-0.03	0.01	-0.01	-0.11	-0.02
UTM 7 x UTM 19	0.16	-0.06	0.07	-0.04	0.10	-0.03	0.04	-0.03
UTM 7 x UTM 31	0.01	0.37	0.09	0.29	-0.15	0.28	-0.05	0.19
UTM 10 x UTM 19	0.07	-0.12	-0.11	-0.04	0.20	-0.07	-0.12	-0.01
UTM 10 x UTM 31	-0.76	0.32	0.24	0.17	-0.77	0.33	0.22	0.20
UTM 19 x UTM 31	0.74	0.27	0.74	0.25	0.69	0.33	0.74	0.25
SE	0.40	0.06	0.21	0.02	0.47	0.04	0.20	0.02
Crosses	E5		E6		E7		E8	
	SCA	REC	SCA	REC	SCA	REC	SCA	REC
UTM 2 x UTM 7	-0.00	-0.70	0.20	-0.46	-0.03	-0.52	-0.05	-0.44
UTM 2 x UTM 10	0.37	-0.40	0.31	-0.23	0.39	-0.36	0.31	-0.04
UTM 2 x UTM 19	-0.86	-0.17	-0.40	-0.07	-0.70	-0.20	-0.58	-0.04
UTM 2 x UTM 31	1.98	0.52	-0.16	-0.94	1.91	0.64	0.88	0.47
UTM 7 x UTM 10	0.10	-0.14	-0.22	-0.07	0.04	-0.04	-0.08	-0.06
UTM 7 x UTM 19	0.12	-0.04	-0.12	-0.02	0.09	-0.04	0.05	-0.02
UTM 7 x UTM 31	-0.18	0.39	0.20	0.29	-0.24	0.27	0,20	0.51
UTM 10 x UTM 19	0.19	-0.17	-0.27	-0.06	0.06	-0.08	-0.13	-0.05
UTM 10 x UTM 31	-0.81	0.34	0.37	0.19	-0.62	0.16	0.08	0.18
UTM 19 x UTM 31	0.74	0.50	1.06	0.44	0.80	0.38	0.74	0.38
SE	0.37	0.07	0.15	0.07	0.45	0.00	0.20	0.04

couple of negative GCA-valued parents, i.e., UTM 7 × UTM 10 (at three test locations, E3, E5, and E7), UTM 7 x× UTM 19 (at seven test locations, E1, E2, E3, E4, E5, E7, and E8), and UTM 10 × UTM 19 (at four test locations, E1, E3, E5, and E7). Past studies also mentioned that the crossing of two negative GCA-valued parents produced the progeny with positive SCA effects for grain yield per hectare (Kamara *et al.*, 2020; Rani *et al.*, 2021). This phenomenon may have occurred because the beneficial genes in one genotype may have dominant effects to overcome the detrimental genes in the other genotype and also combine well.

Genetic variance

GCA variance use helps estimate the additive variance while SCA variance approximates the non-additive variance (Yadesa *et al.,* 2021). Characters with a high GCA variance will have a high additive variance, while the trait with a high SCA variance will have a high non-additive (dominant) variance. The GCA variances ranged from 0.03 to 0.35, and the SCA variances ranged from 0.34 to 1.04 for grain yield (Table 5). The GCA variances were lower than the SCA variances at eight test locations for grain yield. Therefore, the grain yield control came from non-additive genes, as indicated by a σ^2GCA/σ^2SCA ratio of less than 1 at eight locations. The results of this study aligned with those of Oliveira *et al.* (2019) and Masood and Towfiq (2022), as they reported that grain yield per hectare had a ratio of σ^2GCA/σ^2SCA less than unity. The grain yield at eight locations also has more influences from the role of a dominant gene than from the additive gene effects, which attained confirmation by the lower value of the additive variance.

Broad sense heritability for grain yield was 0.99 at all eight test sites, which also indicates that the grain yield has high criteria (Table 5). A high heritability value in the broad

Table 5. Variance components and heritability (narrow and broad sense) for grain yield at the eight test locations.

Variance Components	E1	E2	E3	E4	E5	E6	E7	E8
σ^2GCA	0.28	0.12	0.29	0.10	0.35	0.03	0.35	0.10
σ^2SCA	0.89	0.47	1.04	0.45	1.03	0.34	0.99	0.45
σ^2GCA/ σ^2SCA	0.31	0.26	0.28	0.22	0.34	0.09	0.35	0.22
σ^2A	1.13	0.47	1.14	0.41	1.39	0.10	1.39	0.41
σ^2D	3.56	1.89	4.14	1.81	4.13	1.37	3.98	1,80
h^2_{ns}	0.24	0.19	0.21	0.18	0.25	0.07	0.26	0.18
h^2_{bs}	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99
h^2_{ns}/ h^2_{bs}	0.24	0.19	0.21	0.18	0.25	0.07	0.26	0.18
Dominance ratio	2.51	2.83	2.69	2.99	2.44	5.20	2.39	2.96

sense of a character implies that the character has more control from non-additive gene action (Rachman *et al.,* 2022). Narrow sense heritability at eight test sites ranged from 0.07 to 0.25 (low to moderate). The narrow sense heritability was in the extremely low category at four test locations (E2, E4, E6, and E8), while the narrow sense heritability was moderate at the other four test locations (E1, E3, E5, and E7). The contribution of additive variance in determining the genetic variance of a character can be measured from the h^2_{ns}/h^2_{bs} ratio (Badami *et al.,* 2020). The value of the ratio h2ns/h2bs was close to unity, indicating the total genetic variance of the grain yield was more due to a non-additive variance. The h^2_{ns}/h^2_{bs} ratios at eight locations ranged from 0.07 to 0.25, implying that the grain yield gained more control from the dominant genes than from additive genes.

Drought tolerance indices

Drought stress caused the 20 maize hybrids to decrease the mean grain yield value (1.90 t ha^{-1}) (Table 6). The hybrids that experienced the maximum decrease in grain yield were G5 (UTM2 × UTM31) at 4.24 t ha^{-1}, whereas the lowest occurred in G23 (UTM31 × UTM10) at 0.92 t ha^{-1}. The drought sensitivity index (DSI) can assess a decrease in yield caused by a suboptimal environment compared to an optimum environment (Akbar *et al.,* 2018). A low DSI value indicates that the genotype tested under suboptimal conditions did not show a significant decrease, meaning the genotype is stable and tolerant. The drought stress test results revealed that nine hybrids showed moderate tolerance, i.e., G1, G3, G6, G10, G11, G15, G20, G23, and G24. Furthermore, the drought stress results revealed that 16 hybrids proved as drought-sensitive, namely, G2, G4, G5, G7, G8, G9, G12, G13, G14, G16, G17, G18, G19, G21, G22, and G25.

Genotype by environment interaction (GEI) effects

Pooled analysis of variance (ANOVA) of 25 maize genotypes (five parental genotypes + 20 F1 hybrids) for grain yield at eight test locations showed that genotypes, environments, and genotype by environment interactions were highly influential ($p < 0.01$) (Table 7). The result of combined ANOVA shows that genotypes, environments, and their interaction were the main determinants of grain yield. However, past studies revealed that genotypes were more influential than environments and their interaction (GEI) because the breeding material evaluated has a diverse genetic background (D’Aguillo *et al.,* 2022).

The genotypes’ significance for grain yield revealed genetic differences among genotypes tested in eight test locations, hence an opportunity to select the preferred maize genotypes. The importance of the environments for grain yield showed that eight testing locations were visibly useful in determining adaptive genotypes at specific locations and all test locations (Karimizadeh *et al.,* 2023). The significant genotype and environment interaction (GEI) for grain yield at optimum and drought stress conditions

Table 6. Grain yield and drought tolerance indices under normal and stress conditions of the maize genotypes.

Genotypes	Optimum	Drought stress	ΔY	S
G1 (UTM2xUTM2)	3.21	2.09	1.12	0.70 (MT)
G2 (UTM2xUTM7)	3.17	1.41	1.76	1.12 (DS)
G3 (UTM2xUTM10)	3.79	2.19	1.60	0.85 (MT)
G4 (UTM2xUTM19)	2.86	1.35	1.51	1.06 (DS)
G5 (UTM2xUTM31)	7.75	3.51	4.24	1.10 (DS)
G6 (UTM7xUTM2)	4.34	2.21	2.13	0.99 (MT)
G7 (UTM7xUTM7)	2.89	1.21	1.68	1.17 (DS)
G8 (UTM7xUTM10)	2.81	1.25	1.56	1.12 (DS)
G9 (UTM7xUTM19)	2.95	1.26	1.69	1.15 (DS)
G10 (UTM7xUTM31)	4.53	2.53	2.00	0.89 (MT)
G11 (UTM10xUTM2)	4.59	2.39	2.20	0.97 (MT)
G12 (UTM10xUTM7)	2.93	1.33	1.60	1.10 (DS)
G13 (UTM10xUTM10)	3.03	1.49	1.54	1.02 (DS)
G14 (UTM10xUTM19)	2.89	1.33	1.56	1.09 (DS)
G15 (UTM10xUTM31)	3.88	2.51	1.37	0.71 (MT)
G16 (UTM19xUTM2)	3.20	1.44	1.76	1.11 (DS)
G17 (UTM19xUTM7)	3.03	1.32	1.71	1.14 (DS)
G18 (UTM19xUTM10)	3.11	1.41	1.70	1.10 (DS)
G19 (UTM19xUTM19)	2.69	1.23	1.46	1.09 (DS)
G20 (UTM19xUTM31)	5.48	3.36	2.12	0.78 (MT)
G21 (UTM31xUTM2)	6.60	3.28	3.32	1.01 (DS)
G22 (UTM31xUTM7)	3.88	1.90	1.98	1.03 (DS)
G23 (UTM31xUTM10)	3.31	2.39	0.92	0.56 (MT)
G24 (UTM31xUTM19)	4.71	2.69	2.02	0.86 (MT)
G25 (UTM31xUTM31)	4.06	1.22	2.84	1.41 (DS)
Mean	3.83	1.93	1.90	

Note: MT = Moderately tolerant; DS = Drought sensitive; ΔY = optimum grain yield value minus drought stress grain yield; S = Drought sensitivity index.

Table 7. Combined analysis of variance for grain yield at the eight test locations.

Source of variance	d.f.	SS	MS	F Value
Block	1	0.01	0.01	1.97^{ns}
Genotype (G)	24	362.83	15.12	2030.45**
Environment (E)	7	358.27	51.18	6874.06**
G × E	168	63.21	0.38	50.53**
Error	199	1.48	0.01	
Total	399	785.80		

Note: ** = significant at the ɑ level of < 0.01; ns = non significant; df = degrees of freedom; SS = Sum of squares; MS = mean squares.

exhibited that the genotypes tested have different responses to varying environments. Hence, it needs to continuously test the genotypes at the optimum and drought stress locations to find the high-quality hybrid cultivars for commercial release.

The variances due to genotypes and test locations managed and highly affected the maize grain yield (Figure 1). Grain yield variance at test locations showed that a low variance was evident at location E4 (Sampang District with drought stress), while the high variance at location E5 (Pamekasan District with optimum condition) (Figure 1a). The grain yield variance based on the tested genotypes revealed that the low variance for grain yield emerged in genotype G23 and the high variance in genotype G5 (Figure 1b). The grain

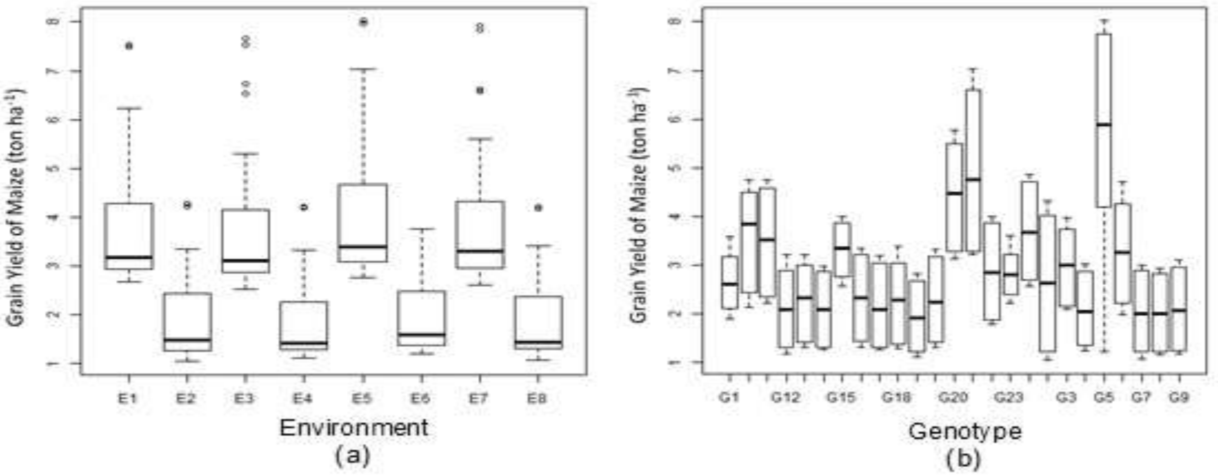


Figure 1. (a) Data distribution of grain yield (t ha^{-1}) based on environment. (b) Data distribution of grain yield (t ha^{-1}) based on genotype.

yield variance based on the tested genotypes was higher than the tested locations' variance, i.e., 46.17% and 45.59%, respectively (Table 7). The differences in grain yield at eight locations gained intense effects from the maize genotype's adaptability toward the environments (Matongera *et al.,* 2023). However, a well-adapted and stable genotype of maize and other field crops will show a low level of variance (Evans *et al.,* 2017; Amzeri *et al.,* 2020).

At the four locations with optimum conditions, the mean grain yield per hectare was 3.83 t ha^{-1} while at four locations with drought stress conditions, the mean grain yield was 1.93 t ha^{-1} (Table 8). At optimum locations, the hybrid G5 showed a higher mean grain yield per hectare than other hybrids at four locations with optimum conditions. Hybrid G8 gave the lowest mean grain yield at Location E1 (Bangkalan with optimum condition), while hybrid G19 enunciated the minimum mean grain yield at locations, E3, E5, and E7 (Sampang, Pamekasan, and Sumenep with optimum conditions). Under drought stress conditions, the hybrid G5 displayed the highest mean grain yield per hectare at three locations, i.e., E2, E6, and E8 (Bangkalan, Pamekasan, and Sumenep with drought stress conditions), while hybrid G20 demonstrated the highest mean grain yield at the location E4 (Sampang with drought stress condition). The hybrid G25 showed the lowest mean grain yield per hectare at three locations. i.e., E2, E4, and E8, and hybrid G19 exhibited the bottommost mean grain yield at the location E6.

AMMI analysis

AMMI analysis of variance results of 25 maize genotypes (five parental inbred lines + 20 F1 hybrids) manifested that variance components of the genotypes (G), locations (E), and genotype and environment interactions (GEI) significantly ($p < 0.01$) affected the grain yield per hectare (Table 9). The contribution of genotypes, locations, and the genotype by environment interactions for grain yield per hectare was 46.17%, 45.59%, and 8.04%, respectively. Genotypes and locations were the main contributors to grain yield variance, revealing maize genotypes and the locations used for the maize planting primarily affected grain yield. The highest genotype percentage and locations for grain yield showed that maize genotypes and test locations' variations were broad (Alam *et al.,* 2022). The location conditions for maize growth may cause differences in plant expression; thus, the same genotype will provide different responses at locations to grain yield (Li *et al*., 2018).

Table 8. The mean values of grain yield for maize genotypes at the eight test locations.

Genotypes	Optimum conditions				Mean	Stress conditions				Means	Mean of Optimum and Stress
	E1	E3	E5	E7		E2	E4	E6	E8		
G1 (UTM2xUTM2)	3.18 ^{g}	2.98 ^{hijkl}	3.51 ^{g}	3.17 ^{jkl}	3.21	2.20 ^{efg}	1.98 ^{ef}	2.23 ^{fgh}	1.95 ^{gh}	2.09	2.65
G2 (UTM2xUTM7)	3.02 ^{ghij}	3.11 ^{hi}	3.30 ^{ghi}	3.25 ^{jk}	3.17	1.39 ^{hi}	1.39 ^{g}	1.49 ^{jk}	1.37 ^{i}	1.41	2.29
G3 (UTM2xUTM10)	3.72 ^{f}	3.70 ^{g}	3.92 ^{f}	3.81 ^{gh}	3.79	2.21 ^{efg}	2.12 ^{def}	2.12 ^{gh}	2.31 ^{ef}	2.19	2.99
G4 (UTM2xUTM19)	2.81 ^{hijk}	2.73 ^{lm}	2.96 ^{jk}	2.92 ^{lmn}	2.86	1.29 ^{hi}	1.39 ^{g}	1.41 ^{jk}	1.32 ^{i}	1.35	2.11
G5 (UTM2xUTM31)	7.51 ^{a}	7.60 ^{a}	8.00 ^{a}	7.89 ^{a}	7.75	4.25 ^{a}	4.20 ^{a}	1.38 ^{k}	4.19 ^{a}	3.51	5.63
G6 (UTM7xUTM2)	4.26 ^{e}	4.12 ^{ef}	4.70 ^{d}	4.28 ^{ef}	4.34	2.00 ^{fg}	2.16 ^{de}	2.41 ^{efg}	2.26 ^{fg}	2.21	3.28
G7 (UTM7xUTM7)	2.78 ^{ijk}	2.81 ^{ijklm}	2.98 ^{ijk}	2.98 ^{klm}	2.89	1.19 ^{hi}	1.28 ^{g}	1.27 ^{k}	1.10 ^{i}	1.21	2.05
G8 (UTM7xUTM10)	2.69 ^{k}	2.77 ^{klm}	2.93 ^{jk}	2.83 ^{mn}	2.81	1.21 ^{hi}	1.20 ^{g}	1.32 ^{k}	1.25 ^{i}	1.25	2.03
G9 (UTM7xUTM19)	2.98 ^{ghijk}	2.84 ^{hijklm}	3.07 ^{hijk}	2.92 ^{lmn}	2.95	1.21 ^{hi}	1.23 ^{g}	1.29 ^{k}	1.31 ^{i}	1.26	2.11
G10 (UTM7xUTM31)	4.64 ^{d}	4.33 ^{de}	4.72 ^{d}	4.42 ^{e}	4.53	2.49 ^{cde}	2.20 ^{de}	2.53 ^{def}	2.90 ^{c}	2.53	3.53
G11 (UTM10xUTM2)	4.59 ^{d}	4.52 ^{d}	4.73 ^{d}	4.53 ^{de}	4.59	2.28 ^{ef}	2.28 ^{de}	2.58 ^{de}	2.40 ^{def}	2.39	3.49
G12 (UTM10xUTM7)	2.83 ^{hijk}	2.78 ^{jklm}	3.20 ^{ghij}	2.91 ^{lmn}	2.93	1.26 ^{hi}	1.23 ^{g}	1.45 ^{jk}	1.37 ^{i}	1.33	2.13
G13 (UTM10xUTM10)	3.12 ^{gh}	2.93 ^{hijkl}	3.08 ^{hijk}	2.97 ^{klm}	3.03	1.48 ^{h}	1.37 ^{g}	1.71 ^{ij}	1.39 ^{i}	1.49	2.26
G14 (UTM10xUTM19)	2.83 ^{hijk}	2.93 ^{hijkl}	2.97 ^{jk}	2.83 ^{mn}	2.89	1.30 ^{hi}	1.31 ^{g}	1.40 ^{jk}	1.29 ^{i}	1.33	2.11
G15 (UTM10xUTM31)	3.82 ^{f}	3.80 ^{fg}	3.99 ^{ef}	3.92 ^{g}	3.88	2.80 ^{c}	2.71 ^{c}	2.90 ^{c}	1.63 ^{cd}	2.51	3.20
G16 (UTM19xUTM2)	3.09 ^{ghi}	3.10 ^{hij}	3.30 ^{ghi}	3.32 ^{ij}	3.20	1.39 ^{hi}	1.41 ^{g}	1.54 ^{jk}	1.40 ^{i}	1.44	2.32
G17 (UTM19xUTM7)	3.10 ^{gh}	2.89 ^{hijklm}	3.14 ^{hij}	3.00 ^{jklm}	3.03	1.29 ^{hi}	1.28 ^{g}	1.33 ^{k}	1.36 ^{i}	1.32	2.18
G18 (UTM19xUTM10)	3.07 ^{ghi}	3.06 ^{hijk}	3.30 ^{gh}	3.00 ^{jklm}	3.11	1.39 ^{hi}	1.32 ^{g}	1.52 ^{jk}	1.39 ^{i}	1.41	2.26
G19 (UTM19xUTM19)	2.73 ^{jk}	2.58 ^{m}	2.79 ^{k}	2.64 ^{n}	2.69	1.16 ^{i}	1.20 ^{g}	1.28 ^{k}	1.28 ^{i}	1.23	1.96
G20 (UTM19xUTM31)	5.32 ^{c}	5.26 ^{c}	5.73 ^{c}	5.59 ^{c}	5.48	3.20 ^{b}	3.17 ^{b}	3.66 ^{a}	3.39 ^{b}	3.36	4.42
G21 (UTM31xUTM2)	6.20 ^{b}	6.63 ^{b}	6.96 ^{b}	6.60 ^{b}	6.60	3.31 ^{b}	3.31 ^{b}	3.25 ^{b}	3.26 ^{b}	3.28	4.94
G22 (UTM31xUTM7)	3.91 ^{f}	3.78 ^{g}	3.93 ^{f}	3.88 ^{gh}	3.88	1.92 ^{g}	1.83 ^{f}	1.95 ^{hi}	1.88 ^{h}	1.90	2.89
G23 (UTM31xUTM10)	3.18 ^{g}	3.14 ^{h}	3.31 ^{gh}	3.60 ^{hi}	3.31	2.46 ^{de}	2.31 ^{d}	2.51 ^{def}	2.28 ^{f}	2.39	2.85
G24 (UTM31xUTM19)	4.70 ^{d}	4.59 ^{d}	4.73 ^{d}	4.83 ^{d}	4.71	2.69 ^{cd}	2.68 ^{c}	2.78 ^{cd}	2.62 ^{cde}	2.69	3.70
G25 (UTM31xUTM31)	3.97 ^{ef}	3.92 ^{fg}	4.28 ^{e}	4.08 ^{fg}	4.06	1.14 ^{i}	1.17 ^{g}	1.30 ^{k}	1.26 ^{i}	1.22	2.64
Means	3.76	3.72	3.98	3.85	3.83	1.94	1.91	1.94	1.93	1.93	2.88

Note: Numbers in one column followed by the same letter show no significant difference based on the HSD test at the level of ɑ = 5%.

Table 9. AMMI analysis of variance for maize grain yield.

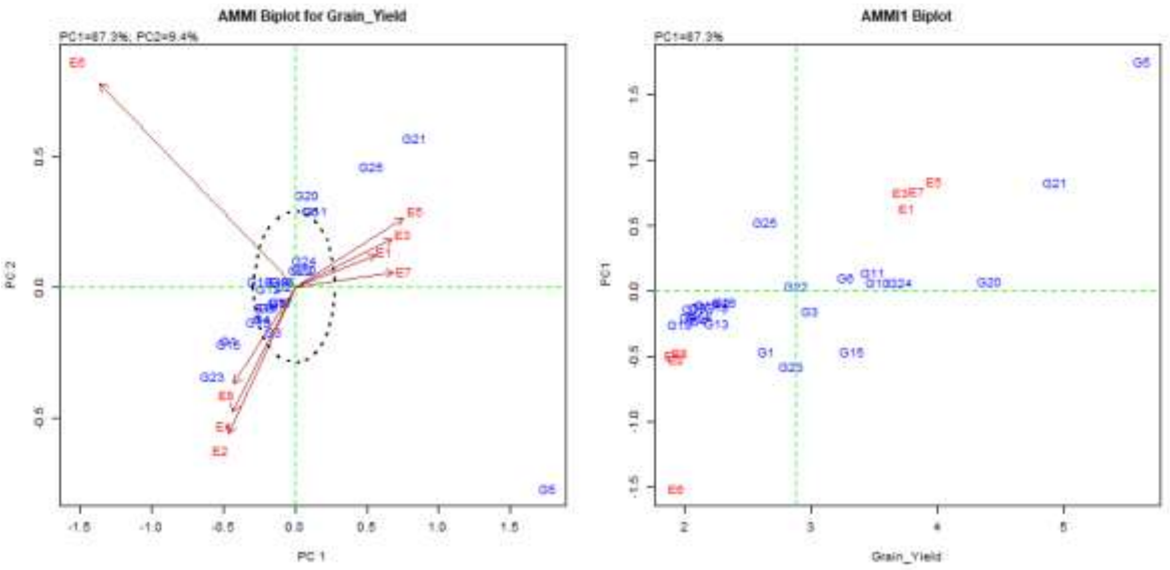
Source of Variance	d.f.	SS	MS	F-Value	Variance (%)	Accumulation
Block	1	0.01	0.01	1.97^{ns}	0.00	-
Genotype (G)	24	362.83	15.12	2030.45**	46.17	-
Location (E)	7	358.27	51.18	6874.06**	45.59	-
G × E	168	63.21	0.38	50.53**	8.04	-
IPCA 1	30	27.58	0.92	92.00**	87.30	87.30
IPCA 2	28	2.96	0.11	10.56**	9.40	96.70
IPCA 3	26	0.48	0.02	1.85^{ns}	1.50	98.20
IPCA 4	24	0.24	0.01	0.98^{ns}	0.80	99.00
IPCA 5	22	0.17	0.01	0.76^{ns}	0.50	99.50
IPCA 6	20	0.10	0.00	0.49^{ns}	0.30	99.80
IPCA 7	18	0.09	0.00	0.48^{ns}	0.30	100.00
IPCA 8	16	0.00	0.00	0.00^{ns}	0.00	100.00
Error	199	1.48	0.01	-	-	-
Total	399	785.80	-	-	-	-

Note: E = Environment (location); IPCA = Interaction Principal Component Analysis; ** = significant at the α level of < 0.01; ns = nonsignificant; df = degrees of freedom; SS = Sum of squares; MS = mean squares.

AMMI analysis helped recognize the genotype and environment interaction (GEI) and the stability of the tested maize genotypes at some locations (Yamamoto *et al.,* 2021). AMMI analysis of variance results showed a significant interaction between genotypes and environments; thus, it can progress using AMMI analysis. AMMI variance analysis for grain yield displayed that the interaction between IPCA1 and IPCA2 was highly significant ($p < 0.01$), while IPCA3 to IPCA48 had nonsignificant interactions. AMMI analysis of variance revealed that the GEI effects could be illustrative of the following: contribution of G × E interaction effect for each component IPCA1 and IPCA2 was 87.30% and 9.40%. The contribution values denoted that the IPCA1 and IPCA2 components have a dominant role in explaining the effect of interaction (96.70%).

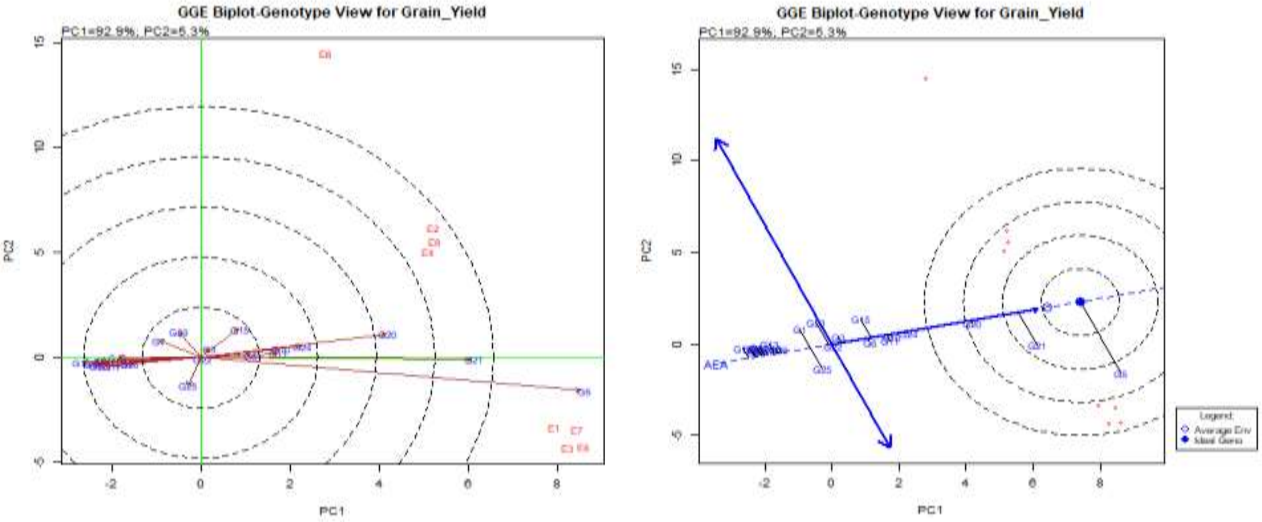
Biplot PC1 vs. PC2 provided stable genotypes either at all the test locations or at the specific location for grain yield (Figure 2a). The genotype near the environment line showed that a genotype can grow well at that location, and a genotype near the coordinate point (coordinate 0.0) signified that the genotype can grow well at all the test locations and has a stability level at all test locations. In the AMMI analysis results, biplot PC1 vs. PC2 revealed 18 genotypes near the coordinate point, i.e., G2, G3, G4, G6, G7, G8, G9, G10, G11, G12, G13, G14, G16, G17, G18, G19, G22, and G24, with those genotypes classified as stable and widely adapted maize genotypes. However, the genotypes G1, G5, G15, G20, G21, G23, and G25 that grow well at specific locations had narrow adaptability.

AMMI biplot analysis for the mean of grain yield vs. PC1 showed that the main effects were the same if the genotype and environment points were parallel to the vertical axis. Interaction effects were the same if the genotypes and environments' points were parallel to the flat axis. Genotypes G1 and G2 were parallel to the vertical axis; hence, these genotypes gave the same effect toward grain yield (2.65 t ha^{-1}) at all test locations. However, the two genotypes' interaction with the environment differed (Figure 2b). The optimum test location with the highest mean grain yield was E5 (3.98 t ha^{-1}), whereas the test under drought stress was lowest at E4 (1.91 t ha^{-1}). The genotype with the highest mean value was G5 (7.75 t ha^{-1}), while the lowest was G19 (1.23 t ha^{-1}). The genotypes with a low interaction with the environment have PC1 values close to zero. The environment with a PC1 value close to zero showed a low interaction with genotypes. Genotypes with a low interaction factor were G10, G20, G22, and G24, and the test locations with low interaction factor were E1 and E8.



(a) (b)

Figure 2. AMMI biplot for grain yield in the maize hybrids. (a) AMMI biplot PCI vs PC2 and (b) AMMI biplot for the mean grain yield vs. PC1.



(a) (b)

Figure 3. GGE biplot for grain yield in maize hybrids. (a) The genotype view of the maize hybrids in the GGE plot. (b) The ideal genotype plot for maize hybrids in the GGE biplot.

GGE Biplot analysis

GGE biplot displayed the mean values of 25 maize genotypes evaluated for grain yield (Figure 3a). The vector length of a genotype showed the difference of the genotype itself on the mean value of the genotype, where a genotype near a biplot coordinate point has a low genotype effect and GEI. The genotype with a close vector distance from the origin point of the biplot is stable (Daemo *et al.,* 2023). The longer the environmental vector, the greater the effect of the genotypes, environments, and their interaction effects on various traits (Enyew *et al.,* 2021). According to the GGE biplot, the stable maize genotypes were G1, G3, G6, G15, G22, G23, and G25, while the genotype G5 has the lengthiest vector with the grain yield.

The results on hybrids' stability appear in Figure 3b. Based on the findings of Memon *et al*. (2023), an average environment axis (AEA = X axis) shows an average result of grain yield in each hybrid. A Y axis is the perpendicular line toward the AEA axis reflecting a grain yield stability of the tested genotypes. The genotype on the right side of the Y axis has a higher grain yield than the grain yield average of all the genotypes, and a genotype on the left side of the Y axis has a lower grain yield. In addition, a genotype has an unstable indication if it moves further away from the X-axis. Genotype G5 manifested with the highest grain yield but was unstable since the genetic distance was far from the X-axis. Genotypes G6, G10, G11, G20, and G24 emerged as stable genotypes since their genetic distance was close to the X-axis.

What-won-where biplot for grain yield is available in Figure 4. This biplot polygon formation resulted from the farthest genotype vector collection from zero intersection on the X and Y axis, where each farthest genotype vector has a straight line connection forming a polygon. A genotype best performs if it has a location in the environmental gathering sector; however, the best genotype should exactly plot on this sector's straight line. Meanwhile, a genotype performs less if outside the environmental gathering sector, and the worst genotype plots at the exact straight line. The divided polygon into three sectors appears in Figure 4. Sector-I is the environmental gathering sector where E2, E4, E6, and E8 (stress condition) plot at the top right sector. Meantime, environments E1, E3, E5, and E7 (with optimum conditions) plot at the bottom right sector. Genotypes G1, G3, G6, G10, G11, G15, G20, G23, and G24 appeared in sector-I located at the top right sector with G15, G20 and G23, as the best genotypes. The G5 and G21 plot at the bottom right part of sector-I with genotype G5 as the best genotype. Genotypes in the sector-I were characteristics of the highest mean grain yield (Table 7). Sector-II and sector-III were not the environmental gathering sectors; hence, the maize genotypes in these sectors performed poorly. Genotypes G2, G4, G7, G8, G9, G12, G13, G14, G16, G17, G18, G19, G22, and G25 were notably with the low grain yield, with genotype G19 having the lowest grain yield.

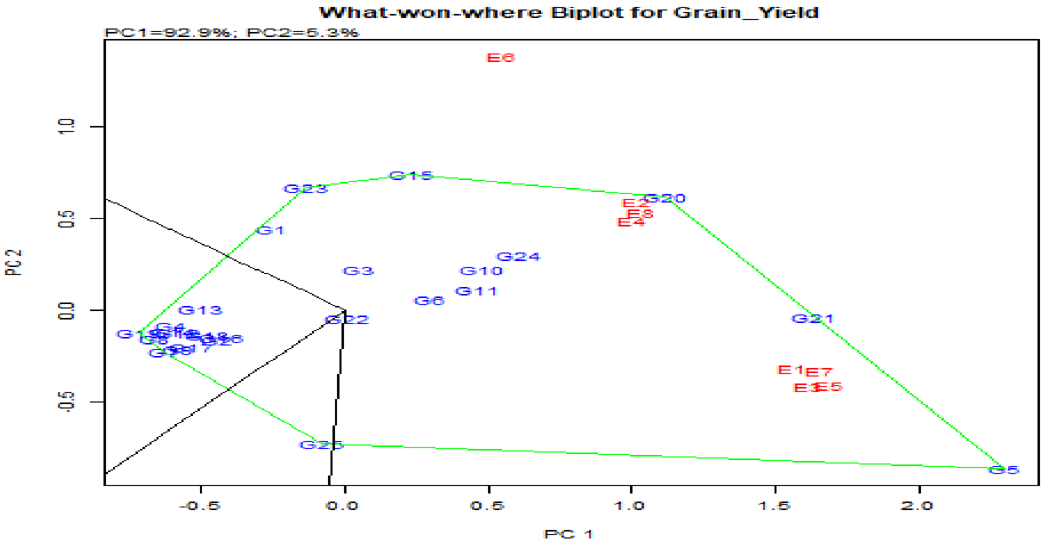


Figure 4. What-won-where biplot for grain yield depicting the grouping of environments and maize genotypes based on their G × E interactions.

Selection of promising parental genotypes and F1 hybrids

Plant breeders often used diallel crossing to get hybrid populations through the direct and maternal effects of the parental genotypes. The result showed the real influence on reciprocals; thus, the pure line determination as male and female parents was distinct for grain yield in the resulting maize hybrids (Eze *et al.,* 2020). Furthermore, a diallel cross is beneficial to determining the gene action in a crossing, easing plant breeders' selection of what breeding method to use to assemble the hybrid cultivars. The GCA and SCA predictions also showed that grain yield at eight tested locations incurred more influences from the dominant genes than by additive gene effects; hence, the maize pure lines (parents) have lesser effects on the hybrid performance (Yu *et al.,* 2020).

The presented research aimed to get the maize hybrid cultivars with high grain yield and resistance to drought stress conditions. Determining the hybrid with high production and drought tolerance depended on the drought susceptibility index test and AMMI and GGE biplot analyses. The average grain yield at optimum and stress environments for 25 genotypes was 2.88 t ha^{-1}; therefore, the maize hybrids with a higher grain yield than the above mean value of grain yield require selection. The testing outcome of 25 maize genotypes in eight locations resulted in genotype G5 having the highest grain yield (5.63 t ha^{-1}). However, this genotype was drought intolerant (DSI = 1.10). The DSI test showed eight genotypes as drought stress tolerant with a grain yield above the mean value, namely, G1, G3, G6, G10, G11, G15, G20, G23, and G24. The genotype G1 (UTM2I was drought tolerant with a DSI of 0.70 and positive GCA values for grain yield. Hence, the genotype UTM2 can benefit as a parental genotype to assemble the maize hybrid cultivars with high production and drought-stress resistance.

Evaluating 25 maize genotypes at eight locations determined the adaptation level and genotype stability when tested in several environments. The test results can serve as the base to determine the genotype for release as a commercial hybrid cultivar. The multivariate statistics (AMMI and GGE biplot) helped categorize the tested maize genotypes into three groups. Group I had a very stable genotype with high-yielding potential, i.e., G3, G6, G10, G11, G22, and G24. Group II contained the maize genotypes with low stability. However, they gave the highest grain yield, i.e., G5, G15, G20, and G21. Group III comprised the genotypes with high stability but low grain yield, i.e., G2, G4, G7, G8, G9, G12, G13, G14, G16, G17, G18, and G19. Group I consisted of the maize genotypes with a good performance in all the test locations and notably as ideal genotypes with the highest stability and grain yield. Therefore, the pertinent research recommended six maize hybrids for commercial cultivation with high productivity and drought stress resistance.

CONCLUSIONS

The GCA and SCA predictions showed that maize genotypes' grain yield at eight test locations received more influences from the dominant gene effects than the additive genes. Hence, the parental inbred lines have lesser effects on the hybrid performance. The Drought Susceptibility Index (DSI) test showed that nine maize genotypes (G1, G3, G6, G10, G11, G15, G20, G23, and G24) emerged as drought tolerant with the highest average grain yield (2.88 t ha^{-1}). The genotype G1 (UTM2) was notably drought tolerant with a DSI value of 0.70 and also has desirable and positive GCA effects for grain yield. Thus, the said parental genotype and hybrid populations can better serve in assembling the highest-yielding and drought-tolerant maize hybrid cultivars. Based on the AMMI and GGE biplot analyses, six maize hybrids (G3, G6, G10, G11, G22, and G24) were also suitable for commercial cultivation with high productivity and drought stress resistance.

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