



GENOTYPIC VARIABILITY AMONG MAIZE (*Zea mays* L.) GENOTYPES AND THEIR CROSSES UNDER MOISTURE STRESS IN PARTS OF BAUCHI AND PLATEAU STATES OF NIGERIA

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ABSTRACT

This study was carried out to determine the performance of hybrids from early inbred lines under moisture/drought stress and comparing yield performance of the top cross with their parental open-pollinated varieties for grain yield and yield related traits using ten (five males and five females which are known to be drought tolerant) parents. Nursery trial for the formation of initial breeding population (F_1) through a Line x Tester mating design was conducted in 2019 dry season at Lushi Irrigation Station, Bauchi. The ten parents and their resultant 25 F_1 (hybrids) were evaluated in a randomized complete block design (RCBD) with three replications at Bauchi and Jos towards the end of 2019 rainy season. Significant differences were observed among the studied genotypes, indicating that these traits were affected by location. Significant differences were also observed in the combining ability analysis in all the traits under study. The result also revealed that both additive and non-additive gene action were important in controlling drought tolerant, grain yield and other agronomic traits in maize. The parents TZEI-17, SAMMAZ-37, SAMMAZ-38, SAMMAZ-39, SAMMAZ-40 and TZEI-129 have been identified as good general combiners for earliness, drought tolerance and yield per hectare. Therefore, they can be employed in breeding programs targeted at improving certain traits. $TZEI-11 \times SAMMAZ-39$, $TZEI-129 \times SAMMAZ-40$, $\times TZEI-129 \times SAMMAZ-38$, $TZEI-16 \times SAMMAZ-37$, $TZEI-16 \times SAMMAZ-52$, $TZEI-11 \times SAMMAZ-52$, $TZEI-23 \times SAMMAZ-40$ and $TZEI-17 \times SAMMAZ-38$ was also identified as good specific combiners for earliness, drought tolerance, kernel yield and better parent heterosis in Bauchi and Jos combined locations.

Keywords: Drought, Genotypic, Maize, Moisture and Variability.

INTRODUCTION

Current maize yield growth rate combined with population growth and predicted impacts of climate change will not suffice to meet future food demand. Improving crop productivity and livelihoods of smallholders under increasing climate variability will require a multi-disciplinary approach towards crop genetic improvement (Hansen *et al.*, 2019). In terms of resource allocation, temperate maize has received much more resource over time compared to tropical maize (Andorf *et al.*, 2019). Increasing genetic gain, including a reduction in breeding cycle time, is key to providing farmers with a steady stream of improved varieties (Atlin *et al.*, 2017; Andorf *et al.*, 2019; Bailey-Serres *et al.*, 2019). Breeding of maize involves selection of varieties by breeders and farmers for their desirable characteristics such as grain yield, plant height, silking date and tolerance to biotic and abiotic stresses. Understanding the nature of drought response in maize and some major strategies used for improving drought stress-tolerant maize lines has provided opportunities for breeders to improve the breeding process.



Farmers usually have trend to grow a single cultivar in a field, this trend needs development of good level of drought/ water stress tolerance hybrids and varieties through breeding (Edmeades, 2013). A lot of work has been done to develop drought tolerance in maize and many other crops. Breeding of drought tolerant maize varieties had been recommended as a means of improving yield under stress-prone environments (Inyang *et al.*, 2021; Zandalinas *et al.*, 2018). There is need for progress on breeding drought tolerant maize varieties in SSA, as evident in the Drought Tolerant Maize for Africa, Stress Tolerant Maize for Africa, and Water Efficient Maize for Africa (WEMA) projects (ACB, 2017). Hence, introducing drought tolerance or moisture stress tolerance varieties to a moisture-stressed environment can elicit an unexpected phenotypic expression in them as environmental and genetic factors control the phenotypic expression of maize. This study was conducted to evaluate genotypic variability among maize genotypes and their crosses under moisture stress for their performance and level of drought tolerance.

MATERIAL AND METHOD

Description of Experimental Sites

The nursery trial experiment for the formation of the initial breeding population through a line \times tester mating design was conducted in 2018 dry season at the Lushi Irrigation Station, Bauchi. This area is located on latitude 10° 17' N; 9° 49' E at an altitude of 690.2 m above sea level. In 2019 raining season, the 25 F₁ (hybrids), and the ten parents were evaluated in two locations viz: Bauchi and Jos. The experiment was conducted during the 2019 late rainy season at College of Agriculture Teaching and Research farm Bauchi, Bauchi state and at Tajir village in Jos North Local Government Area of Plateau State. Bauchi state is in the northern Guinea savannah agro- ecological zone of Nigeria, located at approximately 10°17'N latitude, 9°49'E longitude and altitude of 690.3m above sea level (Kowal and Knabe, 1972). Bauchi has an average rainfall of 1095 to 1200mm per annum. Tajir Village in Jos North Local Government area of Plateau state is located at approximately 9.54'E latitude on an altitude of about 180m above mean sea level (Record of Federal Survey, 1973). The annual rainfall for the area is about 1250mm and a mean temperature of 35.50°C.

Experimental Materials

A total of five open pollinated maize varieties (OPVs) and five inbred lines were used for the study. The OPVs and the inbred lines were obtained from the Institute for Agricultural Research, Ahmadu Bello University, Zaria. The experimental material comprised of 5 drought tolerance inbred lines (TZEI-129, TZEI-11, TZEI-23, TZEI-17 and TZEI-16) and 5 open pollinated varieties (OPVs) (SAMMAZ 40, SAMMAZ 37, SAMMAZ 38, SAMMAZ 52 and SAMMAZ 39). The drought tolerance inbred lines (as male) were crossed with the OPVs (as female) to obtain 25 single cross hybrids which were later evaluated (using their parents as the checks) for their performances under drought/water stress.

Development of F₁ Population

The inbred lines and the OPVs were planted on a 2 x 3m, 4 rows plot on a spacing of 50cm x 75cm (0.50m \times 0.75m) between and within rows respectively at Lushi Irrigation Station, Bauchi Local Government Area in January of 2018. Prior to planting, land preparation was done by ploughing, followed by harrowing to produce soil with good tilt. At planting, three seeds were sown per hole and thinned to two after seedling establishment at 2 weeks after planting. Compound fertilizer NPK 15:15:15 was applied at 400kg/ha rate at 10 days after planting and later top dressed with urea 90:60:60 of nitrogen, phosphorus and potassium respectively. Weeding was done manually as required. Three percent of Carbofuran was applied into the whorls of the plants at the rate of 2kg/ha at 6 WAP to prevent stem borer's



attack. The crosses or hybrids were obtained using line \times tester mating design as described by Singh and Chaudhary, (1985) where each male in a group of five is mated to five set of females, thus making a total of 25 crosses (hybrids).

Each set of crosses were grown on a plot of 6m² in ratio of two males: two females occupying the 4 rows per plot with the males on the two side rows and the female occupying the center rows. Both the males and the females were covered with the parchment paper bags (10 \times 30 cm in size) and clipped at the base. However, during bagging date were indicated on the bag in order to assist in assessing the viability of pollen. The best time for bagging was in the morning for maximum pollen viability. The bags were checked every day for ready pollen. The bags with ready pollens were held tightly, above the point of pollen accumulation and the clip is removed to release the accumulated pollen on the females and clipped. Once the crossing is completed the bags were marked with (\times) plot or entry number of pollen parent and this completes the crossing.

The combinations provided 35 genotypes (F₁) consisting of 25 hybrid crosses, 5 inbred parents and 5 OPV parents from selfing respectively. The ears were harvested, dried and shelled manually; they were kept in a controlled environment to be used in the trials next growing season.

Data Collection

Five plants were randomly selected from each plot as samples and some quantitative characters were measured and recorded at 2 week intervals starting from 2 WAP and 4 WAP. Mean of the five plants for each entry in each replication was worked out for statistical analysis. The quantitative characters measured were; plant height, days to 50% anthesis, days to 50% silking, anthesis-silking interval, 100 seeds weight (g) and yield per hectare (t/ha).

Data analysis

The data obtained were subjected to analysis of variance as described by Obi (2002). Fisher's least significant difference (F.LSD) was used to detect significant differences for mean separation among varieties. Combining ability effects are very effective genetic parameters in deciding the next phase of breeding programs. They were computed according to the line \times tester method (Singh and Chaudhary, 1985). Line \times tester analysis was performed as outlined in the format of ANOVA table given in table 1 and 2 given below.

Table 1: Anova Table for Line \times Tester Analysis including Parents and Crosses for one Location

Source of variation	Df	Ss	Ms	Expectations
Replication	(r-1) = 2	RSS		
Treatments	(g-1) = 28	GSS		
Parents	(p-1) = 8	PSS	---	
Crosses	(c-1) = 19	CSS		
Parents vs Crosses	1	---	---	
Lines	(l-1) = 4	LSS		
Testers	(t-1) = 3	TSS		$\sigma^2a + rcov (FS) - 2cov (HS) + trcov (HS)$
Line \times testers	(l-1)(t-1) = 12	LtSS		$\sigma^2a - rcov (FS) - 2cov (HS) + Lrcov (HS)$
Error	(g-1)(r-1) = 56	ESS		$\sigma^2a + rcov (FS) - 2cov (HS)$
Total				σ^2a

df: degree of freedom; Cov (FS): full-sib covariance; Cov (HS): half-sub covariance



Table 2: Form of ANOVA for Line × Tester Analysis, including Parents and Crosses for Combined Locations

SOV	Df	Ms	Expectations
Location	1		
Replicate	4		
Treatment	24		
Lines (GCA)	4	-----	
Testers (GCA)	4	-----	
Line × tester(SCA)	16		
Location × Genotype	24		
Location × Line	4		
Location × Testers	4		$\sigma^2_a + \text{rcov (FS)} - 2\text{cov (HS)} + \text{trcov (HS)}$
Location × Line × tester	16		$\sigma^2_a - \text{rcov (FS)} - 2\text{cov (HS)} + \text{Lrcov (HS)}$
Error	96		$\sigma^2_a + \text{rcov (FS)} - 2\text{cov (HS)}$
Total			σ^2_a

The statistical model for the line x tester analysis is:

$$Y_{ijk} = \mu + m_i + f_j + (m \times f)_{ij} + e_{ijk}$$

Where;

Y_{ijk} = the k^{th} observation on $I \times j^{\text{th}}$ progeny

μ = the general mean

m_i = the effect of the i^{th} male

f_j = the effect of the j^{th} female

$(m \times f)_{ij}$ = the interaction effect, and

E_{ijk} = the error associated with each observation

RESULT AND DISCUSSION

Analysis of variance and mean squares for Bauchi (Location 1)

The results of analysis of variance for combining ability, estimates of genetic variance and proportional contribution to total variance in Bauchi location are presented in Table 3 showed that the Treatment Variance (σ^2_T) estimates for all the studied traits were greater than the environmental variance (σ^2_E). It was observed that the environmental variance was low and in some cases negligible. The result indicated that there was highly significant or significant difference among the treatments for plant height at four weeks (786.4**), days to 50% silking (8.16*), cob weight (1001.84**), hundred seed weight (18.5**) and yield per hectare (1.0*). For the lines, significant difference was observed for plant height at two weeks (112.2**), plant height at four weeks (1174.77**), days to 50% tasseling (17.02*), days to 50% silking (11.35*), interval between anthesis and silking (2.41*), hundred seed weight (41.55**) and yield per hectare (1.51*). However, the result indicated that significant difference was observed only in plant height at two weeks (58.49*), plant height at four weeks (954.63**), cob weight (2004.31**), hundred seed weight (25.48*) and yield per hectare (3.44**) among the testers. All other traits did not show any significant difference among the testers. The result for the line × tester shows that plant height at two weeks, plant height at four weeks and days to 50% silking were significantly different with values of 45.83**, 647.23** and 8.32* respectively.

For the genetic components of variance, the result for the variance GCA was consistently higher than other components for plant height at two weeks (9.97), plant height at four weeks (156.34), days to 50% tasseling (1.12), days to 50% silking (1.39), interval between



anthesis and silking (0.08) and yield per hectare (0.2). The result for the variance SCA was higher for cob weight (167.06) and hundred seed weight (1.5). The result for the ($\sigma^2\text{GCA}/\sigma^2\text{SCA}$) for all the traits were more than unity except for cob weight (0.004) and hundred seed weight (0.74).

The result for the proportional contribution of tester to the total variance was higher than that of line \times tester in cob weight (55.57) and yield per hectare (25.25). On the other hand, the result for line \times tester contribution to total variance was higher than that of tester in plant height at two weeks (51.79), plant height at four weeks (54.87), days to 50% tasseling (61.23), days to 50% silking (67.98), interval between anthesis and silking (56.03) and hundred seed weight (39.62).

Analysis of variance and mean squares for Location 2 (Jos location)

The results of analysis of variance for combining ability, estimates of genetic variance and proportional contribution to total variance in Jos location are presented in Table 4. The Treatment Variance ($\sigma^2\text{T}$) estimates for all the studied traits were greater than the environmental variance ($\sigma^2\text{E}$). It was observed that the environmental variance was low and in some cases negligible. The result indicated that there was highly significant or significant difference among all the traits under study. For the lines, significant difference was observed for all the traits except days to 50% silking (3.7). However, the result also indicated that significant difference was observed in all the traits under study among the testers. The result for the line \times tester shows that plant height at two weeks, plant height at four weeks, days to 50% tasseling, days to 50% silking, anthesis – silking interval and cob weight were significantly different with values of 30.7**, 556.5**, 11.3**, 5.1**, 2.7** and 789.7** respectively.

For the genetic components of variance, the result for the variance GCA was consistently lower than other components for all the traits under study. On the other hand, the result for the variance SCA was higher for all the traits under study. The result for the ($\sigma^2\text{GCA}/\sigma^2\text{SCA}$) for all the traits were less than unity except for hundred seed weight (1.0) and yield per hectare (9.5).

The result for the proportional contribution of lines to the total variance was lesser than that of line \times tester in all the traits under study except yield per hectare (18.9). On the other hand, the result for line \times tester contribution to total variance was higher than that of lines in plant height at two weeks (36.4), plant height at four weeks (64.2), days to 50% tasseling (47.5), days to 50% silking (40.7), interval between anthesis and silking (73.9), cob weight (54.2) and hundred seed weight (36.8).

Analysis of variance and mean squares for combined Location (Bauchi and Jos location)

The results of analysis of variance for combining ability, estimates of genetic variance and proportional contribution to total variance across location presented in Table 5 below indicated that there was highly significant difference in locations (Bauchi and Jos combined) for plant height at two weeks (205.34**), plant height at four weeks (3082.67**), interval between anthesis and silking (10.67**) and cob weight (2440.17**). However, all other traits did not show any significant difference across location. The result also indicated the existence of highly significant or significant difference in all the traits under study for the treatments except hundred seed weight (27.72). For the lines, significant difference was observed in all the traits except hundred seed weight (59.18). On the other hand, the result shows that there was highly significant or significant difference among the testers in plant height at two weeks (184.98**), plant height at four weeks (1303.52**), days to 50% tasseling (30.97**), days to 50% silking (24.76**), cob weight (1281.44**) and yield per hectare. Line \times tester shows



highly significant or significant difference in all the traits under study except hundred seed weight (15.12) and yield per hectare (0.5).

For the genetic components of variance, the Treatment Variance (σ^2T) estimates for all the studied traits were greater than the environmental variance (σ^2E). It was observed that the environmental variance was very low and in some cases negligible. The result for the variance GCA was higher than other components only for cob weight (99.5), hundred seed weight (1.26) and yield per hectare (0.17). The result for the variance SCA indicated higher component for plant height at two weeks (7.69), plant height at four weeks (152.67), days to 50% tasseling, days to 50% silking (1.21) and interval between anthesis and silking (0.35). The result for the (σ^2GCA/σ^2SCA) was more than unity for cob weight (1.26) and yield per hectare (17.0). The result for the proportional contribution of lines to the total variance was higher than that of line \times tester only in cob weight (40.31) and yield per hectare (22.03). On the other hand, the result for line \times tester contribution to total variance was higher than that of lines in plant height at two weeks (39.18), plant height at four weeks (57.29), days to 50% tasseling (53.94), days to 50% silking (52.2), interval between anthesis and silking (66.7) and hundred seed weight (36.36) in Bauchi and Jos location combined.

Mean performance of parental lines and testers across location (Bauchi and Jos)

The mean performance in traits of lines and testers across location during 2019 rainy season presented in Table 6 indicated that significant differences were found in all traits among the testers except cob weight and hundred seed weight, while hundred seed weight showed no significant difference among the testers. The result shows that SAMMAZ-40, SAMMAZ-52 and SAMMAZ-39 had the highest days to 50% tasseling with value of 57 among the testers, while TZEI-11, TZEI-17 and TZEI-16 had the highest days to 50% tasseling (56) among the lines. The least number of days to 50% tasseling were obtained from tester SAMMAZ-37 (52), SAMMAZ-38, (52) and tester TZEI-23 (51). The result for lines on the other hand shows that TZEI-11, TZEI-17 and TZEI-16 had the highest days to 50% silking (59). The result for interval between anthesis and silking indicated that the tester SAMMAZ-40 and SAMMAZ-16 were low (3). The lowest anthesis – silk interval among the lines were TZEI-11 and TZEI-17 with 3 days. Among the testers, SAMMAZ-37 and SAMMAZ-36 were the heaviest in terms of weight (73.5g) while TZEI-11 was the heaviest among the lines with (78.17g). SAMMAZ-37, SAMMAZ-38, SAMMAZ-52 and SAMMAZ-39 were the heaviest among the parents in terms of 100 seeds weight with 24g followed by TZEI-11 with 23.83g. The result further indicated that SAMMAZ-7, SAMMAZ-38 and TZEI-23 were the best yielder among the parents with 3.18 and 3.07t/ha respectively under combined result.



Table 3: Analysis of variance for combining ability, estimates of genetic variance and proportional contribution to total variance in Bauchi location

Source of variation	Df	PHT2(cm)	PHT4(cm)	TSL	SLK	ASI	CWG(g)	HSW(g)	YH(t/ha)
Replication	2	14.2	1201.3**	23.2*	17.6*	1.2	1930.8**	13.1	1.6
Treatment	24	59.0	786.4**	10.0	8.2*	1.2	1001.9**	18.5**	1.0*
Line	4	58.5*	954.6**	6.2	4.3	0.9	2004.3**	25.5	3.4**
Tester	4	112.2**	1174.8**	17.0*	11.4*	2.4*	3340.7	41.6**	1.5*
Line × Tester	16	45.8**	647.2**	9.2	8.3*	1.0	166.5	11.0	0.3
Error	48	15.9	178.2**	5.8	4.2	0.8	303.5	7.7	0.6
Genetic components of variance									
σ^2 Treatment		472.0	6291.1	79.8	65.3	9.9	8014.9	148.0	8.0
σ^2 Line		0.8	20.5	0.0	0.0	0.0	122.5	1.0	0.2
σ^2 Tester		4.4	35.2	0.5	0.2	0.1	211.6	2.0	0.1
σ^2 GCA		10.0	156.3	1.1	1.4	0.1	0.7	1.1	0.2
σ^2 SCA		2.6	27.8	0.2	0.4	0.0	167.1	1.5	0.2
GCA:SCA		3.8	5.6	7.0	3.5	2.0	0.0	0.7	1.3
σ^2 A		10.5	111.3	0.7	0.0	0.2	668.3	6.0	0.6
σ^2 D		39.9	625.4	4.5	5.6	0.3	0.0	4.4	0.0
σ^2 E		5.3	59.4	1.9	1.4	0.3	101.2	2.6	0.2
Proportional contribution to total variance									
Line		16.5	20.2	10.3	8.8	11.4	33.3	23.0	57.4
Tester		31.7	24.9	28.4	23.2	32.6	55.7	37.4	25.3
Line × Tester		51.8	54.9	61.2	68.0	56.0	11.1	39.6	17.3

2019 Rainy Season

KEYS:

PHT2 = Plant height at 2 weeks
 PHT4 = Plant height at 4 weeks
 TSL = Days to 50% tasseling
 SLK = Days to 50% silking

ASI = Anthesis – Silking interval
 CWG = Cob weight
 HSW = 100 seeds weight
 YH = Yield per hectare



Table 4: Analysis of variance for combining ability, estimates of genetic variance and proportional contribution to total variance in Jos location

Source of variation	Df	PHT2(cm)	PHT4(cm)	TSL	SLK	ASI	CWG(g)	HSW(g)	YH(t/ha)
Replication	2	14.7	174.4*	0.6	0.1	1.3	38.5	2.3	0.3
Treatment	24	56.3**	578.0**	15.9**	8.4**	2.4**	982.4**	11.5**	1.3**
Line	4	65.2**	683.3**	10.7**	3.7	2.4**	1039.1**	20.1**	1.5**
Tester	4	149.8**	558.8**	39.3**	26.2**	1.5*	1660.5**	23.5**	4.9*
Line × Tester	16	30.7**	556.5**	11.3**	5.1**	2.7**	789.7**	6.3	0.3
Error	48	6.9	52.5	2.3	2.0	0.4	96.6	3.3	0.3
Genetic components of variance									
σ^2 Treatment		450.4	462.4	126.9	67.1	19.4	7858.9	92.0	10.4
σ^2 Line		2.3	8.5	0.0	0.0	0.0	16.0	0.9	0.1
σ^2 Tester		7.9	0.2	1.9	1.4	0.0	57.5	1.2	0.3
σ^2 GCA		5.1	4.3	0.9	0.7	0.1	36.7	1.0	0.2
σ^2 SCA		7.9	168.0	3.0	1.0	0.8	234.0	1.0	0.0
GCA:SCA		0.7	0.1	0.3	0.6	0.1	0.2	1.0	9.5
σ^2 A		20.5	17.2	3.7	2.6	0.0	147.0	4.1	0.8
σ^2 D		31.7	672.1	11.9	4.1	3.0	936.1	4.0	0.1
σ^2 E		2.3	17.5	0.8	0.	0.1	32.2	1.1	0.1
Proportional contribution to total variance									
Line		19.3	19.7	11.2	7.3	16.2	17.6	29.2	18.9
Tester		44.3	16.1	41.3	52.0	10.0	28.2	34.1	63.6
Line × Tester		36.4	64.2	47.5	40.7	73.9	54.2	36.8	17.5

2019 Rainy Season

Keys:

PHT2 = Plant height at 2 weeks
 PHT4 = Plant height at 4 weeks
 TSL = Days to 50% tasseling
 SLK = Days to 50% silking

ASI = Anthesis- Silking interval
 CWG = Cob weight
 HSW = 100 seeds weight



Table 5: Analysis of variance for combining ability, estimates of genetic variance and proportional contribution to total variance evaluated across location (Bauchi and Jos), 2019 rainy season

Source of variation	Df	PHT2(cm)	PHT4(cm)	TSL	SLK	ASI	CWG(g)	HSW(g)	YH(t/ha)
Location	1	205.34**	3082.67**	8.17	4.17	10.67**	2440.17	35.53	0.56
Replication	4	14.45	687.85	11.89*	8.83*	1.27	984.67	7.67	0.92
Treatment	24	97.9	1200.25**	20.33**	13.21**	2.74	1668.05	27.72	2.18*
Line	4	172.25*	1772.53**	25.22**	13.12**	4.21**	4034.53**	59.18	2.88*
Tester	4	184.98*	1303.52**	30.97**	24.76**	1.26	3281.44*	46.67	8.22**
Line × Tester	16	57.54	1031.36	16.45**	10.34**	2.74**	673.09	15.12	0.5
Error	96	11.42	115.34	4.07	3.1	0.62	200.08	5.51	0.42
Genetic components of variance									
σ^2 Treatment		391.59	4801	81.34	52.83	10.95	6672.22	110.89	8.73
σ^2 Line		3.82	24.71	0.29	0.09	0.05	112.05	1.47	0.08
σ^2 Tester		4.25	9.07	0.48	0.48	0.0	86.95	1.05	0.26
σ^2 GCA		4.04	16.89	0.39	0.29	0.0	99.5	1.26	0.17
σ^2 SCA		7.69	152.67	2.06	1.21	0.35	78.84	1.6	0.01
GCA:SCA		0.53	0.11	0.19	0.24	0.0	1.26	0.79	17.0
σ^2 A		16.14	67.56	1.55	1.15	0.0	397.99	5.04	0.67
σ^2 D		30.74	610.68	8.25	4.83	1.41	315.34	6.41	0.05
σ^2 E		4.9	43.62	1.39	0.63	0.25	91.39	0.92	0.07
Proportional contribution to total variance									
Line		29.33	24.61	20.67	16.56	25.63	40.31	35.58	22.03
Tester		31.49	18.1	25.39	31.24	7.67	32.79	28.06	62.8
Line × Tester		39.18	57.29	53.94	52.2	66.7	26.9	36.36	15.17

2019 Rainy Season

Keys:

PHT2 = Plant height at 2 weeks
 PHT4 = Plant height at 4weeks
 TSL = Days to 50% tasseling
 SLK = Days to 50% silking

ASI = Anthesis – Silking interval
 CWG = Cob weight
 HSW = 100 seeds weight
 YH = Yield per hectare



Table 6: Mean performance of maize parental lines for eight traits at Bauchi and Jos combined location, 2019 rainy season

Parents	PHT2(cm)	PHT4(cm)	TSL	SLK	ASI	CWG(g)	HSW(g)	YH(t/ha)
Lines								
TZEI-129	26.17**	73.17**	53*	57*	5**	62.33	18.5	2.17*
TZEI-11	18.5	38.83	56	59	3	78.17**	23.83	2.77
TZEI-23	30.67**	78.67**	52*	57*	5**	60.5	22.67	3.07
TZEI-17	16.67	55.0	56	59	3	28.5	18.83	1.4**
TZEI-16	20.0	47.67*	56	60**	4	66.17**	20.0	2.38*
Mean	22.4	58.67	54	59	4	59.13	20.77	2.36
CV (%)	18.4	6.3	10.0	10.9	8.9	11.3	21.8	12.8
Testers								
SAMMAZ-40	23.33**	44.17*	57**	60**	3**	67.17	20.83	2.27*
SAMMAZ-37	31.17	96.83a	52	56	4	73.5	24.0	3.18**
SAMMAZ-38	31.17	96.83a	52	56	4	73.5	24.0	3.18**
SAMMAZ-52	28.5	81.67a	53*	57*	4	62.67	24.0	2.4*
SAMMAZ-39	17.33*	56.83**	57**	60**	3**	58.33	24.0	2.02*
Mean	26.3	75.27	54	58	4	67.03	23.37	2.61
CV (%)	11.20	5.90	2.9	0.0	10.1	9.2	23.7	13.4

2019 Rainy Season

* = Significant at 5% level of probability

** = Significant at 1% level of probability

KEYS:

PHT2 = Plant height at 2 weeks

PHT4 = Plant height at 4weeks

TSL = Days to 50% tasseling

SLK = Days to 50% silking

ASI = Anthesis- Silking interval

CWG = Cob weight

HSW = 100 seeds weight

YH = Yield per hectare



CONCLUSION AND RECOMMENDATIONS

The significant difference among the genotypes for most of the traits studied in separate locations and from combined results as shown by the ANOVA indicates the presence of significant variations among the genotypes, which is the backbone for any crop improvement programs. The observed significance in the hybrid is as a result of the gene actions which are important for the characters observed across locations (Bauchi and Jos). Falconer (1981) pointed out the amount of improvement that can be achieved by selection among a number of crosses is dependent on the amount of variation between the crosses and the intensity of the selection, since selection is ultimately applied to the crosses.

Genetic recombination and improvement of grain yield can be achieved, as depicted by high variability among the genotypes studied. This study also showed that both additive and non-additive gene action were important in controlling the interval between anthesis and silking, seed yield and other agronomic traits in maize. The female parent SAMMAZ-52 was identified as good parent in terms of drought tolerant. TZEI-11 and TZEI-17 as male were regarded as the best parents for drought tolerant. On the other hand, the female parents SAMMAZ-37 and SAMMAZ-38 were identified as a good parent with the best yield per hectare, TZEI-17 as male is regarded as the best parent for yield across location.

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