

Full Length Research Paper

Performance of early-maturing topcross maize hybrids across multi-environments

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Maize is one of the most important cereal crops used as source of food and feed. Identification of suitable maize inbred lines and testers for the development of stable maize hybrids can be challenging. The assessments of the combining ability of selected maize inbred lines and testers, agronomic performance and yield stability of the resultant topcross hybrids would provide useful information that would guide the breeding program for optimum yield. Nine yellow maize inbred lines and two open-pollinated varieties (Early LN-Y and TZE-31DMRSRLNSYN) were crossed in a line × tester mating scheme. The resultant eighteen topcross hybrids together with two commercial hybrids and two candidate hybrids as checks were evaluated across eight locations in Nigeria. Significant differences were detected among the genotypes, lines, testers, line × tester and their interactions with the environment for most traits studied. Four inbred lines (TZEI-OR-197, TZEI-13, TZEI-17 and TZEI-ORQ-44) had significant General Combining Ability (GCA) effects for grain yield (GY), whereas TZEI-ORQ-44, TZEI-8 and TZEI-17 had significant GCA effects for earliness. Five topcrosses (TZE-31DMRSRLNSYN × TZEI-OR-197, TZE-31DMRSRLNSYN × TZEI-129, Early LN-Y × TZEI-13, TZE-31DMRSRLNSYN × TZEI-17 and Early LN-Y × TZEI-8) had significant specific combining ability effects for GY. The best eight topcross hybrids had comparable GY with the commercial checks. Four each of the eight hybrids were of either tester. Based on the GGE-biplot, TZE-31DMRSRLNSYN × ENT 13 was the most stable genotype across the test environments. The inbred lines with significant GCA effects and superior testcrosses were identified for future breeding programs.

Key words: Grain yield, inbred lines, line × tester, testers, topcross maize hybrids.

INTRODUCTION

Maize is an important and strategic cereal crop grown in diverse agroecological zones throughout the world

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(Troyer and Wellin, 2009). It is widely consumed as food, used as animal feed and raw materials for industrial products, such as corn oil, starch and bio-fuel production (Ranum et al., 2014; Eisele et al., 2021). Despite the breeding efforts made by research institutes and partner agencies in the last three decades, the grain yield of maize in sub-Saharan Africa (SSA) remains low (1.5-2.0 t ha⁻¹) (Shiferaw et al., 2011) when compared with the global average grain yield of 5 t ha⁻¹ (ICAR, 2012). The low grain yield in farmers' fields could be attributed to a combination of production constraints such as poor access to finance, low adoption of improved seeds, sub-optimal use of fertilizers, low soil fertility as well as abiotic and biotic stresses, such as drought and *Striga* infestation (Shiferaw et al., 2011; Zebire et al., 2020; Iseghohi et al., 2021). Despite the numerous challenges confronting maize production in SSA (Cairns et al., 2013), maize remains a major staple, and its cultivation is a means of livelihood for many smallholder farmers. In 2021, the demand for maize in Nigeria was approximately 15 million metric tonnes (MMT) (PWC, 2021), while production was estimated at 12.7 MMT (FAOSTAT, 2021) with a maize supply gap of over 2 MMT. To bridge this gap, there is a need to develop high-yielding, stable and affordable maize hybrids and routinely replace old varieties with improved ones for enhanced productivity. It is against this backdrop that breeders at Value Seed Limited (VSL) explored diverse early maturing maize germplasm of the International Institute of Tropical Agriculture (IITA) and International Maize and Wheat Improvement Centre (CIMMYT) for new combinations and line extraction.

Different mating schemes such as North Carolina Design (NCD I and II), diallel, half diallel and line × tester are being used to assess the relative breeding value among inbred lines and to generate hybrids. Among these mating schemes, the line × tester has become widely used in maize hybrid development (Fasahat et al., 2016). A line × tester mating design involves the crossing of several lines to a common parent (tester) (Kempthorne, 1957). It is used to estimate the general combining ability (GCA) and specific combining ability (SCA) effects of a line or tester as well as determine the gene action of traits of interest (Fasahat et al., 2016). An ideal tester combines simplicity in use with the provision of sufficient information on line performance. According to Smith (1986) and Hallauer and Miranda (1988), a line or a population with a low frequency of favourable alleles in testcross can be employed as a tester to identify lines with large frequency of favourable alleles. Information generated from a line × tester analysis is invaluable for resource allocation in breeding programs (Panhwar et al., 2008). Mostafavi et al. (2011) and Elias et al. (2016) suggested that deploying varieties for specific environments can be confounding when genotype-by-environment interaction is present since yield is an attribute of a genotype (G) and its response to the environment (E). Genotype-by-environment interaction is

environment (E). Genotype-by-environment interaction is the differential ranking of genotypes across environments, resulting in variable performance in specific environments (Crossa et al., 2002; Jandong et al., 2011; Heidari et al., 2016).

Several statistical methods have been used for the analysis and interpretation of multi-environment trial data (Crossa and Cornelius, 1997; Gauch and Zobel, 1997; Yan et al., 2000, 2007). Of these statistical tools, the two most frequently used are the additive main effects and multiplicative interaction (AMMI) model (Gauch, 1988; Zobel et al., 1988; Gauch and Zobel, 1997) and the genotype (G) main effect and Genotype by environment (E) interaction (GGE) biplot (Yan et al., 2000).

To promote the rapid adoption and commercialization of maize in Nigeria, there is a need to improve maize hybrids for the target environment and test their stability in the various agroecological zones where maize is commonly grown to ascertain their adaptability to the changing climate. Early and extra-early maturing varieties allow farmers to obtain premium prices from green maize sown at different planting dates; grow maize in shorter seasons in agroecological zones where rainfall days can be limiting, and maximize land use in mixed cropping systems (Badu-Apraku et al., 2011). Therefore, the assessment of the performance of early maturing topcross maize hybrids across diverse environments will help to ascertain the gene action of important traits among the maize parents and identify stable hybrids in specific and across locations (Amegbor et al., 2020; Badu-Apraku et al., 2023). The objectives of this study were to (i) estimate the general and specific combining ability effects for grain yield and agronomic traits of a group of early-maturing maize germplasm, (ii) determine the potential of two stress-tolerant open-pollinated varieties as testers for future use in line/variety development, and (iii) identify high-yielding and stable hybrids across major agroecological zones in Nigeria.

MATERIALS AND METHODS

Locations of experimental sites

The study was conducted at eight locations in four agroecological zones in Nigeria in the 2021 cropping season (Table 1). The agroclimatology data of the test locations varied, particularly, in the average monthly precipitation and relative humidity (Table 1). The test locations are major maize growing regions in the agroecological zones.

Genetic materials and experimental design

The germplasm used as parents comprised nine maize inbred lines of diverse genetic backgrounds with multiple stress tolerance and two low soil nitrogen tolerant Open-pollinated Varieties (OPVs) used as testers (Table 2). Eight of the nine inbred lines were obtained from the International Institute of Tropical Agriculture (IITA), Ibadan and one was obtained from the International Maize and Wheat Improvement Centre (CIMMYT), Harare, Zimbabwe.

Table 1. Agroecological zones, coordinates and the average monthly Temperature (T), Rainfall (RF) and Relative Humidity (RH) of locations where maize genotypes were evaluated in Nigeria.

Location	Code	Agroecological zone	Longitude	Latitude	Meter above sea level (M' asl)	Tmin (°C)	Tmax (°C)	RF (mm)	RH (%)
Zaria	ZA	Northern Guinea Savanna	7°46' E	11°13' N	622	20.79	32.67	89.92	47.47
Bagaddi	BAG	Northern Guinea Savanna	7°45' E	11°14' N	681	19.60	34.50	84.66	48.00
Mokwa	MOK	Southern Guinea Savanna	7°35' E	9°35' N	457	23.92	36.67	83.50	58.50
Makurdi	MAK	Southern Guinea Savanna	8°28' E	7°41' N	96	24.15	33.02	111.67	61.38
Ikole-Ekiti	EKT	Derived savanna	5°21' E	7° 48' N	556	21.52	32.29	139.30	72.53
Ibadan	IBD	Derived savanna	3°54' E	7°26' N	277	23.25	32.00	102.75	74.55
Ile-Ife	IFE	Forest zone	3°45' E	7°18' N	282	23.42	35.12	134.61	80.46
Abeokuta	AB	Forest zone	7°53' E	7°24' N	66	24.16	33.68	142.49	74.88

Tmin: Minimum temperature, Tmax: Maximum temperature.

Table 2. Description of line, tester and checks included in the study.

Genotype	Name	Pedigree	Attribute	Origin	Source
Line					
1	ENT 13	[M37W/ZM607#bF37sr-2-3sr-6- ... 1-B × CML486]-1	Drought and low N tolerant	CIMMYT	IITA1
2	TZEEIOR-197	2009 TZEE-OR1 STR	Drought tolerant and <i>Striga</i> resistance and/or tolerance	IITA1	IITA1
3	TZEI-11	TZE Comp5-Y C6 S6 Inbred 8	Tolerant to drought and low N	IITA1	IITA1
4	TZEI-129	TZE-Y Pop STR Co S6 Inbred 16-1-3	<i>Striga</i> resistant	IITA1	IITA1
5	TZEI-13	TZE-Y Pop STR Co S6 Inbred 17-2-3	<i>Striga</i> and drought tolerant	IITA1	IITA1
6	TZEI-17	TZE Comp5-Y C6- Inbred 35	<i>Striga</i> tolerant	IITA1	IITA1
7	TZEI-8	TZE-Y Pop STR Co S6 Inbred 62-3-3	Drought and <i>Striga</i> tolerant	IITA1	IITA1
8	TZEIORQ-44	2009-TZE OR2 DT STR-QPM S ₆ inb 35-2/3-3/3-4/4-1/4-1/1	Pro-Vitamin-A (PVA), Quality Protein Maize (QPM), tolerant to drought	IITA1	IITA1
9	TZEIORQ-59	2009-TZE OR2 DT STR QPM S ₆ inb 50-2/2-1/3-2/3-2/2-1/1	Pro-Vitamin-A (PVA), Quality Protein Maize (QPM), tolerant to drought and low N	IITA1	IITA1
Tester					
1	TZE-31DMRSRLNSYN	TZE31-DMRSR-LN-SYN	Resistant to downy mildew, streak and tolerant to low N	IITA2	IITA2
2	Early LN-Y	Early LN-Y	Low nitrogen tolerant	IITA2	IITA2
Check					
1	Sammaz 56	EYQH-35	Quality Protein Maize (QPM)	IITA1	IITA1
2	Ife-maizehyb-3	A0905-28	Pro-Vitamin-A (PVA)	IITA3	IITA3
3	EEPVA-12	TZdEEI 9 / TZEEI 79	Pro-Vitamin-A (PVA)	IITA1	IITA1
4	EYQH-33	TZEQI 82 / TZEQI 91	Quality Protein Maize (QPM)	IITA1	IITA1

The two OPVs were of IITA, but of a different maize breeding program as the inbred lines. All genotypes were of the early and extra-early maturing groups.

In the wet season of 2020, the genotypes were crossed in a line \times tester mating design. The inbred lines were used as females and the two OPVs as the male parents (testers). Eighteen top-cross hybrids were generated from the crossing block. The top-cross hybrids were evaluated alongside four single-cross hybrid checks, comprising two commercial hybrids (Ife-maizehyb-3 and Sammaz 56) and two candidate hybrids (EEPVA-12 and EYQH-33). All the maize genotypes included in the study were of the yellow/orange kernel type (Table 2).

The experiments were laid out in a randomized complete block design (RCBD) with three replicates in each location. Each plot was a 3 m single row with inter- and intra-row spacing of 0.75 and 0.25 m, respectively. Two seeds were sown per hill and seedlings were later thinned to one stand per hill three weeks after planting (WAP), to give a final plant population density of 53,333 plants/ha. Basal fertilizer application was done at 2WAP using NPK 15:15:15 compound fertilizer at the rate of 30 kg each of N, P and K/ha, while top-dressing was done at 6WAP using urea (46% N) fertilizer at the rate of 60 Kg N/ha, bringing the total amount of nitrogen applied to 90 Kg N/ha.

Weeds were controlled using a pre-planting spray of glyphosate (N-(phosphonomethyl) glycine) at ten days before planting. A mixture of metolachlor ([2-methoxy-1-methylethyl] amino] oxo-acetic acid) and atrazine (6-Chloro-N-ethyl-N&39;--(1-methylethyl)-1,3,5-triazine-2,4-diamine) was applied a day after planting at the rate of 1.6 kg a.i. ha⁻¹ as pre-emergence herbicides. At 4WAP, Nicosulfuron (2-[(4,6-dimethoxypyrimidin-2-yl) carbamoylsulfamoyl]-N, N-dimethylpyridine-3-carboxamide) at the rate of 160 g a.i. ha⁻¹ was applied as post-emergence herbicide.

Data collection

Data were collected on days to anthesis, days to silking, plant height, plant aspect, husk cover, stem and root lodging, ear aspect, number of ears per plant and field weight. Days to anthesis and days to silking were determined as the number of days from planting to when 50% of plants shed pollen and extruded silks. Anthesis-silking interval (ASI) was computed as the difference between days to anthesis and days to silking. Plant height was measured in centimeters (cm) on five plants of similar height as distance from the ground level to the collar of the uppermost leaf. Plant aspect was scored on a scale of 1 to 9 based on the plant overall phenotypic appeal with 1 being excellent phenotypic appeal and 9 being poor, variable and diseased plant (Badu-Apraku et al., 2012). Husk cover score was rated on a scale of 1-9 based on the tightness of the tips of the husks, where 1 represented long and tight tip, and 9 represented short and loose tip. Stem lodging was determined by counting the number of plants whose stems broke below the first ear and expressed as percentage of plant stands per plot. Root lodging was estimated by counting the number of plants that lie completely flat on the soil and/or are at angles less than 45° to the soil surface which was expressed as a percentage of plant stands per plot.

At harvest, ear aspect was rated per plot, based on the size, neatness, uniformity of ears and grain fill on the cobs on a scale of 1-9 (Badu-Apraku et al., 2012), with 1 representing clean and well-filled ears, and 9 representing ears with scanty and rotten or damaged kernels. The number of ears per plant was estimated as the number of harvested ears divided by the number of plants per plot at harvest. Field weight was measured in kg as the weight of the de-husked maize cobs per plot at harvest. Grain moisture content was determined by testing threshed grains with Dickey-John® moisture meter. Grain yield was calculated from the field weight and adjusted to 14% moisture content, assuming a shelling

percentage of 80%. The formula was used for the computation:

$$\text{Grain yield Kg}^{-\text{ha}} = \text{Field weight (Kg)/area (m}^2) \times (100 - \text{moisture})/86 \times (10,000 \times 0.80).$$

Statistical analysis

A combined Analysis of Variance (ANOVA) was done for grain yield (GY) and other agronomic traits across environments using the PROC GLM procedures in SAS 9.2 package (SAS Institute, Cary, NC) following a linear model:

$$Y_{ijk} = \mu + r(e_k) + e_k + l_i + t_j + (l \times t)_{ij} + (l \times e)_{ik} + [(t \times e)_{jk} + (l \times t \times e)_{sijk}] + e_{ijk}$$

where Y_{ijk} is the measured trait of the genotype of i^{th} line crossed to j^{th} tester evaluated in r replications across k environments; μ is the grand mean; $r(e_k)$ is the effect of replication nested within the k environments; l and t represent average effects of lines and of testers, respectively, which is equivalent to GCA effects of lines and testers, respectively; $l \times t$ = line \times tester interaction effects that is equivalent to the SCA effects of the crosses; e is the environmental main effects; $l \times e$, $t \times e$ and $l \times t \times e$ are the interactions of the lines, testers and the lines \times testers with the environments, and e_{ijk} is the random experimental error.

The hybrid component of variation was divided into variation attributable to line (female), tester (male) and line \times tester interaction. General and specific combining abilities for the studied traits were estimated according to Singh and Chaudhary (1985). The GEA-R version 4.1 was used for the stability and GGE biplot analyses (Pacheco et al., 2015). The singular value decomposition (SVD) of the first two principal components was used to fit the GGE biplot model according to the following equation:

$$Y_{ij} = \mu + \beta_j + \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

where Y_{ij} is the trait mean for genotype i in environment j ; μ is the grand mean; β_j is the main effect of environment j ; $\mu + \beta_j$ is the mean yield across all genotypes in environment j ; λ_1 and λ_2 are the singular values (SV) for the first and second principal components (PC1 and PC2), respectively; ξ_{i1} and ξ_{i2} are the Eigen vectors of genotype i for PC1 and PC2, respectively; η_{j1} and η_{j2} are the Eigen vectors of environment j for PC1 and PC2; and ε_{ij} is the residual associated with genotype i in environment j . In GGE biplot analysis, scores of PC1 were plotted against PC2 (Yan et al., 2007). The GGE biplot analysis was also used to generate graphs for the (i) mean performance and stability of the genotypes, (ii) which-won-where pattern, and (iii) the relationship among the test locations (Yan and Tinker, 2006).

RESULTS AND DISCUSSION

The genetic analysis of maize inbred lines in a predetermined mating design is important to elucidate the gene action of traits and to identify genotypes with good general and specific combining abilities in maize breeding programs. In the present study, eighteen topcross maize hybrids generated from a line \times tester mating scheme of nine early and extra-early maize inbred lines and two testers together with four checks were evaluated in eight

environments in Nigeria. The mean squares from the combined analysis of variance of the topcrosses revealed that the environmental effect was significant ($p < 0.05$ - $p < 0.01$) for the eleven traits measured, indicating that the eight locations differed. This may have been due to the differences in agro-climatic and edaphic conditions associated with the various locations of study (Iseghohi et al., 2020). Also, the genotype, line, tester and line \times tester effects were significant for grain yield and most of the traits studied. This suggests that the lines and testers used in the present study were diverse and belonged to different genetic backgrounds and thus, selection can be made among them. In addition, the broad genetic background of the tester was effective in discriminating among the inbred lines. The significant line \times tester effect for most traits indicated that the topcross hybrids differed for grain yield and most agronomic traits measured, and therefore could facilitate selection for trait improvement. Furthermore, the significant line, tester, and line \times tester effects signified the presence of additive and non-additive gene actions in the inheritance of GYLD, DPOLL, DYSK, SL, RL, PASP and EASP, which are consistent with previous studies (Badu-Apraku et al., 2013; Diribu, et al., 2019; Iseghohi et al., 2020). The knowledge of gene action helps in the selection of parents for use in varietal development and also in the choice of appropriate breeding procedures for the genetic improvement of various characters (Fasoula and Fasoula, 1997). The presence of both additive and non-additive gene effects indicates the possibility of exploiting recurrent selection techniques for increased GCA and the use of heterosis breeding to maximize the SCA effect. The interaction effect of the environment with genotype, line, tester and line \times tester was significant for GYLD and most agronomic traits, signifying that the genotypes were greatly influenced by the environments for most of the traits measured. Previous studies (Beyene et al., 2011; Murtadha et al., 2018; Abenezer et al., 2020) reported significant genotype \times environment (G \times E) interaction effect for yield and secondary traits in maize and noted the presence of wide variability among tested genotypes and environments. Genotype by Environment Interaction (GEI) effect is an important factor in breeding programs and sometimes confounds the genetic potential of a candidate variety. Therefore, the strategic deployment of hybrids in specific environments is important for maximizing the benefit of such hybrids. These results corroborate earlier reports of Chandel and Mankotia (2014) and Mosa (2010) who reported significant interaction of line \times environment, tester \times environment and line \times tester \times environment for grain yield and other agronomic traits.

General combining ability effects

The presence of significant GCA effects for most traits, indicative of additive genes shows that early-generation

testing of the maize inbred lines will be effective and that selection of superior hybrids will be successful based on the prediction from GCA effects (Badu-Apraku et al., 2013; Iseghohi et al., 2020). The GCA effects of lines for grain yield and secondary traits across test environments show that lines TZEIOR-197, TZEI-13, TZEI-17, and TZEIORQ-44 had significant positive GCA effects for grain yield, whereas lines TZEI-11, TZEI-8 and TZEIORQ-59 had significant negative GCA effects for grain yield (Table 4). Consequently, the lines with significant positive GCA effects could be selected as good combiners for grain yield improvement and could serve as testers for new lines developed in breeding programs or for testing introduced lines of similar product profiles. Of the two testers, Early LN-Y had significant positive GCA effect for grain yield, whereas TZE-31DMRSRLNSYN had significant negative GCA effect for the trait (Table 4), indicating that testers of opposite heterotic orientation for grain yield were included in the study, consistent with earlier findings (Ahmad and Saleem, 2003; Pswarayi and Vivek, 2008; Legesse et al., 2009; Mosa, 2010; Zeleke and Tuna, 2010; Diribu et al., 2019). Based on the assumption of Castellanos et al. (1998), Early LN-Y was a better combiner with the lines for grain yield than TZE-31DMRSRLNSYN due to its significant positive GCA effect for GY. Three lines (TZEIOR-197, TZEI-129 and TZEI-8) had significant negative GCA effects for flowering traits (Table 4), suggesting that they could be used for developing early maturing genotypes. The importance of significant negative GCA effect for days to 50% anthesis and silking has previously been suggested for the development of early maturing maize varieties (Sundararajan and Kumar, 2011; Abenezer et al., 2020).

Lines TZEI-8, TZEI-13 and TZEI-17 had significant negative GCA effects for plant height, a GCA considered desirable as shorter genotypes do not easily lodge (Ji et al., 2006). Line TZEI-13 combined a significant negative GCA effect for PHT with significant negative GCA effect for root and stem lodging, whereas four lines (TZEIOR-197, TZEI-129, TZEI-17 and TZEI-8) had significant positive GCA effects for stem lodge, which is undesirable. Girma et al. (2015) and Abenezer et al. (2020) in their study suggested that inbred lines with negative GCA effects for plant height often produce hybrids of smaller stature. Two maize inbred lines (TZEI-129 and TZEI-17) had significant negative (desirable) effects for husk cover score, while two other maize inbred lines (TZEI-13 and TZEI-8) had significant positive GCA effects for the trait. Tight husk leaves protect the developing ear against birds and insects and also reduce ear rot incidence by preventing excess moisture into the tip of the developing ear. Inbred lines TZEIOR-197 and TZEIORQ-44 had negative and significant GCA effects for plant and ear aspect scores, while TZEI-8 was the only line with positive and significant GCA for these two traits. Inbred lines ENT 13, TZEIOR-197, TZEI-8 and TZEI-17 and TZEI-8 had significant positive GCA effects for ears per

plant, a measure of prolificacy and an important trait in selection targeted at biotic stress tolerance. Of the two OPVs used as testers, Early LN-Y had desirable GCA effects for flowering traits (DPOLL, DYSK, ASI) and RL, whereas TZE-31DMRSRLNSYN had desirable GCA effects for PLHT, EPP, HUSK, PASP, SL, and EASP. The two testers had different GCA effects for different traits, suggesting that they contributed differently in influencing the mean performance of their crosses and can be used to improve early maize germplasm for these specific traits.

Specific combining ability effects

The SCA effect which is a measure of the nonadditive gene effect is important for heterosis breeding (Melchinger, 1999). In the present study, five hybrids (TZE-31DMRSRLNSYN × TZEI-197, TZE-31DMRSRLNSYN × TZEI-129, Early LN-Y × TZEI-13, TZE-31DMRSRLNSYN × TZEI-17, and Early LN-Y × TZEI-8) had significant positive SCA effects for grain yield, while five other hybrids (Early LN-Y × TZEI-197, Early LN-Y × TZEI-129, TZE-31DMRSRLNSYN × TZEI-13, Early LN-Y × TZEI-17 and TZE-31DMRSRLNSYN × TZEI-8) had significant negative SCA effects for the trait (Table 5). This suggests that the maize inbred lines had specific heterotic affinities with the testers for grain yield. For most of the topcrosses, positive SCA effects for grain yield were associated with negative SCA effect for plant aspect score, and vice versa. It suggests that a strong relationship exists between both traits, as desirable plant aspect characterized by uniform plants and luxuriant plant architecture tend to produce more grain yields than poor plant aspect. Nevertheless, the SCA effects for other traits did not follow a definite pattern with the SCA effect for grain yield (Table 5).

Significant GCA effect for grain yield of some parent lines did not necessarily translate to significant SCA effect of their crosses for the trait. For example, the cross of the inbred line (TZEI-197) which had a significant positive GCA effect with the tester (Early LN-Y) resulted in a significant negative SCA effect for grain yield (Table 5). However, the cross of the inbred line (TZEI-8) with a low GCA effect and the tester (Early LN-Y) with a high GCA effect resulted in a significant positive SCA effect for grain yield. The inbred line TZEI-13, which ranked 4th in GCA (0.11) for grain yield when crossed with Early LN-Y (0.06) (higher GCA tester), resulted in a hybrid that had the highest SCA effect (0.38) for grain yield. The SCA estimates of the topcrosses show irregular patterns, thus indicating the complexity in predicting a cross' SCA effect from GCA estimates of its parents. Abenezer et al. (2020), Dey et al. (2014); Talukder et al. (2016) and Zhang et al. (2015) suggested that hybrids with high SCA effects from parents with low GCA effects might be due to non-additive gene action, that is, dominance gene effect

and epistasis. Results from the study revealed that in three of four instances, crosses between parents with high GCA effect for grain yield resulted in hybrids with low SCA effect for grain yield which could be attributed to lack of complementarity of additive gene action in some of the crosses. Although, Fasahat et al. (2016), alluded that GCA effect is the main effect, while SCA is an interactive effect, it is however very important in exploiting heterosis in commercial maize hybrid production (Melchinger, 1999). The negative SCA effects for GY arising from some of the inbred lines with significant positive GCA effect for the trait highlights the effects of loci interactions in determining the direction and magnitude of gene products. The high SCA effects derived from crosses including good × poor general combiner parents may be attributed to favourable additive effects of the good general combiner parent and epistatic effects of poor general combiner (Dey et al., 2014), while the high SCA effects manifested by low × low crosses may be due to dominance × dominance type of non-allelic gene interaction producing over dominance thus being non-fixable (Wassimi et al., 1986). A good *per se* performance of a line may not necessarily produce better hybrid when used in crossing (Shukla and Pandey, 2008). It suggests that worst parent can weaken the high combining ability effect of an excellent parent (Bao et al., 2009), and vice versa. Furthermore, limited number of testers used in this study may have also restricted the combining options of the maize inbred, howbeit Hallauer and Miraander (1988) suggested the use of large number of testers for effective dissection of the genetic potentials of inbred lines.

Mean performance of topcrosses

The mean performance of topcrosses and standard checks across eight environments for grain yield are presented in Table 6. The mean values ranged from 4.72 t/ha to 6.09 t/ha. Four topcross hybrids [Early LN-Y × TZEI-13 (5.81 t/ha), TZE-31DMRSRLN × TZEI-197 (5.63 t/ha), Early LN-Y × TZEI-17 (5.48 t/ha) and Early LN-Y × TZEI-8 (5.46 t/ha)] had higher grain yield than three of the four standard checks, while the fourth check (Ife-MaizeHyb-3) (6.09 t/ha) was the highest yielding hybrid (Table 6). Ten genotypes yielded higher than the hybrid mean and were not significantly different from the highest-yielding genotype (Ife Maize-Hybrid 3). These top 10 hybrids also did not differ significantly for days to silking, ASI and ear aspect score. Among these ten hybrids, crosses of TZEI-197, TZEI-17 and TZEI-13 to both testers were inclusive.

The significant genotype × environment interaction for grain yield necessitated the use of Genotype by Genotype × Environment (GGE) biplot analysis to identify high-yielding and stable hybrids across the test environments (Table 3). According to Yan and Tinker (2006), genotypes at the corners of the polygons in a

Table 3. Mean squares from the analysis of variance of agronomic traits of eighteen topcross hybrids evaluated in eight environments in Nigeria in 2021.

Source of variation	Df	DPOLL	DYSK	ASI	PLHT	HUSK	RL	SL	EPP	EASP	PASP	GYLD (t/ha)
Env.	7	926.27**	904.92**	8.49**	19731.39**	10.12*	10.07**	283.9**	0.13**	67.76**	107.18**	25.65**
REP(Env.)	16	49.82	53.98	2.77	1533.26	1.04	1.37	1.36	0.1	3.18	2.57	6.72
GENOTYPES	17	12.67**	16.07**	1.12**	1380.32**	1.36**	1.12**	1.82**	0.03 ^{ns}	1.46**	1.11**	1.68**
LINE	8	15.41**	20.98**	1.74*	2683.68**	0.52 ^{ns}	1.19**	2.23**	0.04 ^{ns}	2.08**	1.80**	1.85**
TESTER	1	42.63**	52.48**	0.37 ^{ns}	13.38 ^{ns}	0.46 ^{ns}	0.78*	1.52**	0.01 ^{ns}	0.49*	0.49*	1.43*
LINExTESTER	8	6.33**	6.62**	0.65 ^{ns}	250.02**	2.30**	1.11**	1.43**	0.03 ^{ns}	0.93**	0.48*	1.53*
Env.xGENOTYPES	119	5.89*	5.93**	1.89**	302.70**	1.36**	1.15**	1.47**	0.06**	0.73*	0.66*	2.27**
Env.xLINE	56	5.37*	6.32**	2.27**	339.98**	1.90**	0.76*	1.50**	0.06**	0.65*	0.78**	2.56**
Env.xTESTER	7	15.56**	12.45**	1.70**	435.06**	0.46 ^{ns}	0.94*	1.08*	0.09**	0.91**	0.42 ^{ns}	2.06**
Env.xLINExTESTER	56	5.19*	4.73 ^{ns}	1.53**	248.88**	0.93*	1.56**	1.50**	0.06*	0.79**	0.58*	2.01**
Error	263	6.1	5.85	1.29	178.52	1.11	0.95	1.15	0.06	0.78	0.68	1.58

**, *Significance at 0.05 and 0.01, probability levels, respectively; SE = standard error, DPOLL = days to 50% pollen shed, DYSK = days to 50% silking, PLHT = plant height, PASP = plant aspect, HUSK = husk cover, RL = root lodging, SL = stalk lodging, EASP = ear aspect, EPP = ears per plant, GYLD = grain yield.

Table 4. Estimates of general combining ability (GCA) effects of the nine lines and two testers for agronomic traits measured in eight environments in Nigeria in 2021

Parent genotypes	DPOLL	DYSK	ASI	PLHT	HUSK	RL	SL	EPP	EASP	PASP	GYLD (t/ha)
Lines											
ENT 13	0.09 ^{ns}	0.15 ^{ns}	0.06 ^{ns}	7.08*	-0.03 ^{ns}	0.39**	-0.19*	0.02*	-0.23**	-0.02 ^{ns}	-0.02 ^{ns}
TZEEIOR-197	-0.51*	-0.44*	0.08 ^{ns}	7.53**	0.04 ^{ns}	-0.08 ^{ns}	0.20*	0.03*	-0.28**	-0.20**	0.28**
TZEI-11	0.67**	0.99**	0.28**	-3.08 ^{ns}	-0.10 ^{ns}	-0.10 ^{ns}	-0.32**	-0.05**	0.03 ^{ns}	-0.08 ^{ns}	-0.22**
TZEI-129	-0.74**	-0.71**	0.04 ^{ns}	7.09**	-0.08*	0.01 ^{ns}	0.26*	-0.03**	0.20*	-0.24**	0.00 ^{ns}
TZEI-13	0.23 ^{ns}	0.43*	0.21**	-8.37**	0.12**	-0.24**	-0.45**	-0.02*	-0.04 ^{ns}	0.02 ^{ns}	0.11*
TZEI-17	0.24 ^{ns}	-0.08 ^{ns}	-0.32**	-4.69*	-0.15**	-0.14*	0.23*	0.03*	0.06 ^{ns}	0.02 ^{ns}	0.14*
TZEI-8	-0.85**	-1.02**	-0.17*	-12.73**	0.23**	-0.04 ^{ns}	0.25*	0.03**	0.45**	0.46**	-0.31**
TZEIORQ-44	-0.20 ^{ns}	-0.27 ^{ns}	-0.07 ^{ns}	-0.11 ^{ns}	0.00 ^{ns}	-0.04 ^{ns}	0.11 ^{ns}	0.00 ^{ns}	-0.20*	-0.19*	0.17*
TZEIORQ-59	0.61**	0.56*	-0.04 ^{ns}	5.12*	-0.01 ^{ns}	0.26**	-0.05 ^{ns}	0.01 ^{ns}	-0.04 ^{ns}	0.18*	-0.15*
S.E	0.54	0.63	0.18	7.13	0.11	0.19	0.26	0.03	0.21	0.20	0.19
Testers											
TZE-31DMRSRLNSYN	0.24*	0.29*	0.05**	-0.48**	-0.03*	0.05*	-0.08**	0.005*	-0.04**	-0.03*	-0.06**
Early LN-Y	-0.34**	-0.38**	-0.03**	0.00 ^{ns}	0.04*	-0.05*	0.09**	-0.004*	0.03*	0.02*	0.06**
S.E	0.32	0.35	0.03	0.18	0.04	0.05	0.08	0.03	0.04	0.04	0.06

**, *Significance at 0.05 and 0.01, probability levels, respectively; SE = standard error; DPOLL = days to 50% pollen shed, DYSK = days to 50% silking, PLHT = plant height, PASP = plant aspect, HUSK = husk cover, RL = root lodging, SL = stalk lodging, EASP = ear aspect, EPP = ears per plant, GYLD = grain yield.

Table 5. Estimates of specific combining ability (SCA) effects of top-crosses evaluated for yield and agronomic traits at eight locations in 2021.

Crosses	DPOLL	DYSK	ASI	PLHT	HUSK	RL	SL	EPP	EASP	PASP	GYLD (t/ha)
TZE-31DMRSRLNSYN x ENT 13	-0.05 ^{ns}	-0.12 ^{ns}	-0.07*	-1.55*	0.31**	0.25**	-0.15*	0.02*	-0.13*	0.00 ^{ns}	0.08 ^{ns}
EARLY LN-Y x ENT 13	0.15 ^{ns}	0.21*	0.05 ^{ns}	2.03*	-0.31**	-0.25**	0.14*	-0.02*	0.14**	0.01 ^{ns}	-0.08 ^{ns}
TZE-31DMRSRLNSYN x TZEI-197	-0.28*	-0.46**	-0.18**	1.81*	-0.43**	-0.09 ^{ns}	-0.24**	-0.02*	-0.04 ^{ns}	-0.13**	0.14*
EARLY LN-Y x TZEI-197	0.38**	0.55**	0.16**	-1.33*	0.42**	0.09 ^{ns}	0.23**	0.02*	0.05 ^{ns}	0.15**	-0.14*
TZE-31DMRSRLNSYN x TZEI-11	0.38**	0.45**	0.04 ^{ns}	0.57 ^{ns}	-0.01 ^{ns}	-0.07 ^{ns}	-0.15*	0.04**	0.05 ^{ns}	0.13**	-0.05 ^{ns}
EARLY LN-Y x TZEI-11	-0.28*	-0.37*	-0.06 ^{ns}	-0.09 ^{ns}	0.01 ^{ns}	0.07 ^{ns}	0.14*	-0.04**	-0.04 ^{ns}	-0.12**	0.05 ^{ns}
TZE-31DMRSRLNSYN x TZEI-129	0.66**	0.64**	-0.01 ^{ns}	-0.40 ^{ns}	-0.13 ^{ns}	-0.10*	0.20*	0.00 ^{ns}	-0.23**	-0.12**	0.20**
EARLY LN-Y x TZEI-129	-0.55**	-0.56**	-0.01 ^{ns}	0.88 ^{ns}	0.13 ^{ns}	0.10 ^{ns}	-0.21*	0.00 ^{ns}	0.24**	0.13**	-0.20**
TZE-31DMRSRLNSYN x TZEI-13	0.15 ^{ns}	0.18 ^{ns}	0.03 ^{ns}	-1.70*	-0.23*	-0.12*	-0.15*	-0.01 ^{ns}	-0.04 ^{ns}	0.21**	-0.38**
EARLY LN-Y x TZEI-13	-0.05 ^{ns}	-0.09 ^{ns}	-0.05 ^{ns}	2.18*	0.23*	0.12*	0.14*	0.01 ^{ns}	0.05 ^{ns}	-0.20**	0.38**
TZE-31DMRSRLNSYN x TZEI-17	-0.11 ^{ns}	-0.19 ^{ns}	-0.07 [†]	5.50**	0.19*	0.11*	0.16*	0.03**	0.09*	-0.07*	0.10*
EARLY LN-Y x TZEI-17	0.22*	0.28*	0.06 ^{ns}	-5.02**	-0.19*	-0.11*	-0.17*	-0.03**	-0.08 ^{ns}	0.09*	-0.10*
TZE-31DMRSRLNSYN x TZEI-8	-0.58**	-0.28*	0.30**	0.01 ^{ns}	0.27**	-0.12*	-0.12*	-0.03**	0.31**	0.01 ^{ns}	-0.17**
EARLY LN-Y x TZEI-8	0.68**	0.36**	-0.32**	0.47 ^{ns}	-0.27**	0.12*	0.11 ^{ns}	0.03**	-0.29**	0.00 ^{ns}	0.17**
TZE-31DMRSRLNSYN x TZEIORQ-44	-0.09 ^{ns}	-0.17 ^{ns}	-0.07**	-2.25**	-0.19*	0.35**	0.41**	0.01 ^{ns}	0.11*	0.02 ^{ns}	0.02 ^{ns}
EARLY LN-Y x TZEIORQ-44	0.20*	0.26*	0.06 ^{ns}	2.73**	0.19*	-0.35**	-0.42**	-0.01 ^{ns}	-0.10*	-0.01 ^{ns}	-0.02 ^{ns}
TZE-31DMRSRLNSYN x TZEIORQ-59	0.39**	0.33*	-0.05 ^{ns}	0.16 ^{ns}	0.21*	-0.22**	-0.02 ^{ns}	-0.03**	-0.07 ^{ns}	0.01 ^{ns}	0.07 ^{ns}
EARLY LN-Y x TZEIORQ-59	-0.28*	-0.24*	0.03 ^{ns}	0.32 ^{ns}	-0.22*	0.22**	0.01 ^{ns}	0.03**	0.08 ^{ns}	0.00 ^{ns}	-0.07 ^{ns}
S.E	0.34	0.35	0.11	2.18	0.24	0.18	0.21	0.03	0.14	0.10	0.17

** , *Significance at 0.05 and 0.01, probability levels, respectively; SE = standard error, DPOLL = days to 50% pollen shed, DYSK = days to 50% silking, PLHT= plant height, PASP = plant aspect, HUSK= husk cover, RL = root lodging, SL = stalk lodging, EASP = ear aspect, EPP = ears per plant, GYLD = grain yield.

“which-won-where” polygon are the outstanding genotypes in the environment. Therefore, the polygon view (Figure 1) of the GGE biplot for grain yield of eighteen maize hybrids and four checks across eight environments in Nigeria shows that Ife-MaizeHyb-3 (CK2) was the highest yielding variety in Ekiti (EK), Zaria (ZA), and Abeokuta (AB), while Early LN-Y x TZEI-197 (HB14) was the best yielding variety in Ife. Topcross hybrid Early LN-Y x TZEI-129 (HB2) was the apex variety in Ibadan (IBD); while TZE-31DMRSRLNSYN x TZEI-197 (HB9) was the Highest yielding in Bagaddi (BAG). These topcrosses can be adapted and grown for

optimum yield in these locations.

The single-arrow of the Average Tester Coordinate (ATC) abscissa of a GGE biplot points in the direction of increasing mean performance for grain yield across locations (Yan and Tinker, 2006). In the present study, the mean-stability view of the GGE biplot (Figure 2) shows that the ATC abscissa categorizes the genotypes into high-yielding (those on the right) and low-yielding (those on the left) genotypes. Meanwhile, the stability of the genotypes is measured by their projections from the ATC in the directions of the double arrows (Yan and Tinker, 2006). The greater the absolute length of the projection the

less stable the genotype. Based on the aforementioned, Ife-MaizeHyb-3 (CK2) was the furthest in the direction of increasing yield performance and thus the highest-yielding hybrid across the eight environments. Eight maize hybrids (EARLY LN-Y x TZEI-8, EARLY LN-Y x TZEI-13, TZE-31DMRSRLNSYN x TZEI-197, TZE-31DMRSRLNSYN x ENT 13, TZE-31DMRSRLNSYN x TZEIORQ-44, EARLY LN-Y x TZEIORQ-44, TZE-31DMRSRLNSYN x TZEI-11 and EARLY LN-Y x TZEI-197) and the four checks were grouped in the high-yielding category. Of the high-yielding hybrids, TZE-31DMRSRLNSYN x ENT 13 (HB7) had the

Table 6. The mean performance of eighteen Topcross maize hybrids and five checks evaluated in eight environments in Nigeria.

Crosses	DPOLL	DYSK	ASI	PLHT	HUSK	RL	SL	EPP	EASP	PASP	GYLD (t/ha)
TZE-31DMRSRLNSYN x ENT 13	54.7	56.2	1.6	155.0	2.90	1.25	1.67	0.96	3.48	4.00	5.27
EARLY LN-Y x ENT 13	54.0	55.7	1.6	157.8	2.39	0.65	2.22	0.91	3.79	4.10	5.22
TZE-31DMRSRLNSYN x TZEI-197	53.6	55.1	1.5	157.54	2.28	0.48	2.07	0.93	3.48	3.71	5.63
EARLY LN-Y x TZEI-197	53.7	55.4	1.8	154.88	3.19	0.55	2.70	0.98	3.64	4.05	5.46
TZE-31DMRSRLNSYN x TZEI-11	55.8	57.8	1.9	145.36	2.56	0.45	1.57	0.91	3.88	4.10	4.93
EARLY LN-Y x TZEI-11	54.1	55.8	1.7	147.37	2.67	0.47	1.98	0.81	4.01	4.15	5.16
TZE-31DMRSRLNSYN x TZEI-129	54.3	55.9	1.6	154.90	2.44	0.38	2.50	0.89	3.76	3.71	5.41
EARLY LN-Y x TZEI-129	52.5	54.0	1.5	156.65	2.78	0.63	2.30	0.89	4.31	4.00	5.13
TZE-31DMRSRLNSYN x TZEI-13	55.1	56.9	1.8	138.11	2.53	0.20	1.42	0.89	3.71	4.33	4.95
EARLY LN-Y x TZEI-13	54.1	55.8	1.7	141.67	3.12	0.35	1.87	0.90	3.89	3.96	5.81
TZE-31DMRSRLNSYN x TZEI-17	54.5	55.7	1.2	149.02	2.69	0.28	2.08	0.96	3.95	4.00	5.44
EARLY LN-Y x TZEI-17	54.3	55.5	1.3	138.98	2.39	0.15	2.35	0.91	3.86	4.21	5.37
TZE-31DMRSRLNSYN x TZEI-8	53.2	54.8	1.6	135.19	3.14	0.40	2.18	0.92	4.55	4.48	4.72
EARLY LN-Y x TZEI-8	53.6	54.7	1.1	136.88	2.69	0.53	2.58	0.98	4.02	4.56	5.18
TZE-31DMRSRLNSYN x TZEIORQ-44	54.1	55.5	1.5	145.85	2.47	1.00	2.87	0.93	3.71	3.88	5.39
EARLY LN-Y x TZEIORQ-44	53.8	55.3	1.5	151.30	2.92	0.07	1.72	0.91	3.57	3.90	5.48
TZE-31DMRSRLNSYN x TZEIORQ-59	55.4	56.9	1.5	153.49	2.86	0.63	1.80	0.90	3.69	4.24	5.13
EARLY LN-Y x TZEIORQ-59	54.1	55.6	1.5	154.12	2.50	1.11	2.10	0.96	3.90	4.29	5.11
Checks											
Sammaz 56 (QPM)	54.5	56.0	1.5	145.06	2.28	0.07	1.55	1.19	3.62	3.38	5.45
Ife-MaizeHyb-3	55.4	56.8	1.4	151.62	1.67	0.13	1.45	0.93	3.62	3.67	6.09
EEPVA-12	53.9	54.4	0.5	153.87	2.11	0.45	2.72	0.8	3.97	4.34	4.76
EYQH-33	56.0	58.7	2.7	140.56	1.96	0.3	1.83	1.01	3.77	4.05	5.22
Grand Mean	54.29	55.83	1.54	148.42	2.57	0.48	2.07	0.93	3.83	4.05	5.28
CV (%)	2.01	2.03	22.49	4.08	14.87	76.09	23.47	13.38	9.40	10.36	9.14
LSD <i>0.05</i>	1.78	1.87	0.57	9.96	0.63	0.6	0.8	0.21	0.59	0.69	0.79

CV= Coefficient of variation, LSD = Least significant difference, DPOLL = days to 50% pollen shed, DYSK = days to 50% silking, PLHT= plant height, PASP = plant aspect, HUSK= husk cover, RL = root lodging, SL = stalk lodging, EASP = ear aspect, EPP = ears per plant, GYLD = grain yield.

shortest projection from the abscissa and was thus the most stable across contrasting environments, followed by EARLY LN-Y x TZEI-8 and EARLY LN-Y x TZEI-13. The check varieties Sammaz 56 and EYQH-33 were equally stable across environments.

Conclusion

The genetic variability observed among the lines and testers for grain yield and other agronomic traits indicates the potential of the genetic materials for the development of improved hybrids

targeted for specific and diverse environments in SSA. The top 50% of the topcross hybrids in this study were not significantly different from the two commercial checks in terms of grain yield and agronomic performance. Inbred lines TZEI-197, TZEI-13, TZEI-17, and TZEIORQ-44 exhibited

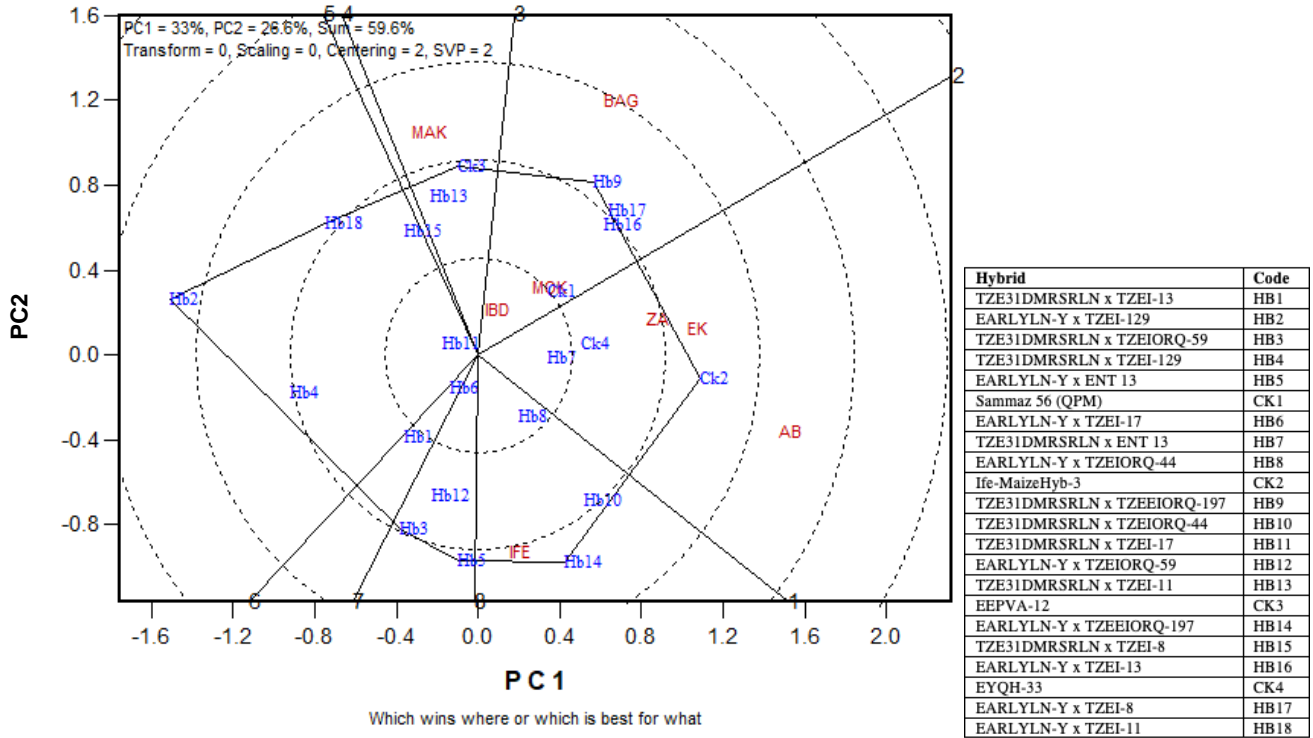


Figure 1. The which-wins-where view of the genotype and genotype by environment biplot of eighteen maize topcross hybrids and four hybrid checks evaluated across eight environments in Nigeria. AB= Abeokuta, EK= Ekiti, IFE= Ife, MOK= Mokwa, BAG= Bagaddi, IBD= Ibadan, MKD= Makurdi, ZA= Zaria.

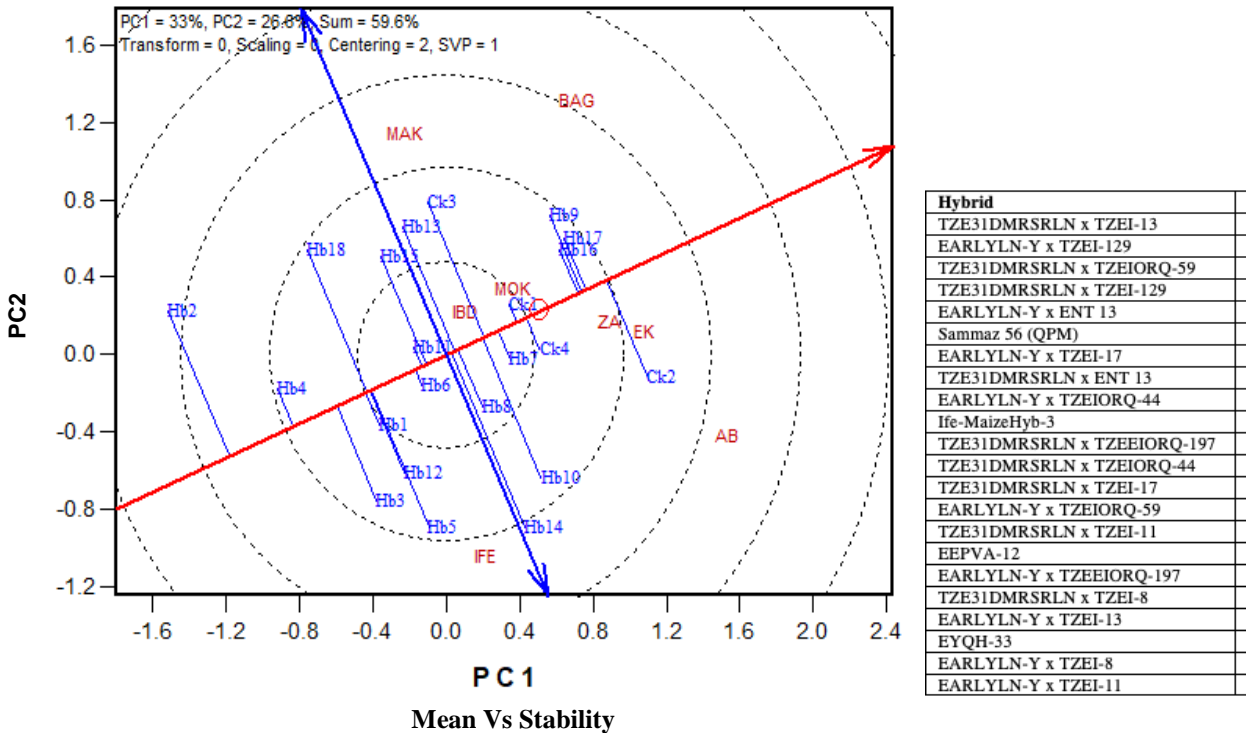


Figure 2. A Mean Vs Stability view of the genotype and genotype by environment biplot of eighteen maize topcross hybrids and four hybrid checks evaluated across eight environments in Nigeria. AB= Abeokuta, EK= Ekiti, IFE= Ife, MOK= Mokwa, BAG= Bagaddi, IBD= Ibadan, MKD= Makurdi, ZA= Zaria.

significant positive GCA effects for grain yield. The topcrosses TZE-31DMRSRLNSYN × TZEEIOR-197, TZE-31DMRSRLNSYN × TZEI-129, Early LN-Y × TZEI-13 and TZE-31DMRSRLNSYN × TZEI-17 were among the highest yielding topcrosses and had significant positive SCA effects for grain yield. On average, the grain yields of most topcrosses were above the hybrid mean, suggesting that these OPVs could serve as sources for line extraction for the development of high-yielding single crosses in combination with the inbred lines included in this study. In addition, the study highlights an alternative approach for the development of high-performing hybrids by combining germplasm across breeding programs of different product profiles of similar maturity groups. Results from this study could guide line conversion efforts for short-term gains for specific product profiles. For example, nutrient-dense varieties (PVA or/ QPM) of the two testers can be created for eventual development of PVA or QPM hybrids with TZEEIOR-197 or TZEIORQ-44, or *Striga* resistance and drought tolerance can be introgressed into same testers by recurrent backcrossing with TZEI 8 or TZEI 13. This study identified genotypes that are uniquely adapted to specific and diverse environments. The commercial hybrid check Ife-Maizehyb-3 was the highest yielding genotype in four of the eight environments while TZE-31DMRSRLNSYN × ENT 13 was the most stable across environments.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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