



COMBINING ABILITY AND GENETIC VARIATION FOR YIELD AND OTHER AGRONOMIC TRAITS IN A LINE X TESTER CROSS OF PROVITAMIN A-CARRIER MAIZE INBRED LINES ACROSS TWO CONTRASTING AGROECOLOGIES IN NIGERIA

T. M. Igyuve^{1,2}, Y. Elam², M. N. Kyat³, A. Sule², G. O. S Ojo⁴, M. A. Yusuf¹, R. S. Vangervihi¹, S. N. Mnzughul⁴, E. Ogwu¹, J. A. Akpudu¹ and P. Umeh¹

¹ Value Seeds Limited, Kaduna State, Nigeria.

² Department of Crop Science, Federal University of Agriculture, Mubi

³ Department of Soil Science, Federal University of Agriculture, Mubi

⁴ Department of Crop Production, Joseph Sarwuan Tarka University, Makurdi

⁵ Department of Plant Science, Ahmadu Bello University, Zaria

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ABSTRACT: Six maize lines × tester hybrids generated from three provitamin A-carrier maize inbred lines and two testers were evaluated across two contrasting agroecologies in Nigeria (Makurdi and Zaria) to determine combining ability and genetic variation for yield and other agronomic traits. The three inbred lines (AWSYN-Y2, BRLNTP-YC6, PVASYN13) and two testers (BR50-414, BR50-419) were crossed in a 3 × 2 design to generate six hybrids, which were evaluated alongside three commercial checks. Combined analysis of variance showed significant ($p < 0.05$ – 0.01) differences among genotypes for most agronomic traits including flowering time, leaf traits, cob weight, and 100-seed weight, while grain yield ($t\ ha^{-1}$) was not significant at the overall genotype level. Despite this, clear numerical differences were observed, with BRLNTP-YC6 × BR50-419 ($6.52\ t\ ha^{-1}$) and AWSYN-Y2 × BR50-419 ($6.38\ t\ ha^{-1}$) outperforming the best check (OBA SUPER 6, $5.51\ t\ ha^{-1}$). Combining ability analysis showed that BRLNTP-YC6 exhibited strong positive GCA effects, indicating a high frequency of favorable additive alleles for yield-related traits while AWSYN-Y2 contributed to earliness and plant architecture. Among testers, BR50-419 favored grain filling and kernel traits, whereas BR50-414 contributed to ear structural traits. Additive gene action predominated for several traits including leaf dimensions and grain yield, while non-additive effects were important for reproductive traits. Broad-sense heritability ranged from moderate to high for most traits, including grain yield ($H^2 = 65.82\%$). Correlation analysis identified cob weight, stover yield, and 100-seed weight as the strongest contributors to grain yield. The results revealed BRLNTP-YC6 × BR50-419 and AWSYN-Y2 × BR50-414 as promising hybrids, while BRLNTP-YC6 and AWSYN-Y2 emerged as valuable parental lines for developing early and high-yielding provitamin A maize adapted to Nigerian agroecologies.

Keywords: Agroecology, Biofortification, Carotenoids, Heterosis, Heritability.

INTRODUCTION

Maize (*Zea mays* L.) is a staple crop of strategic importance to food security and livelihoods in Nigeria and across sub-Saharan Africa, where it provides calories and income for millions of households

(Kamara, 2022). Despite its central role, maize productivity remains constrained by multiple abiotic and biotic stresses, including drought, low soil fertility, and pest infestations, which are further exacerbated by climate variability (Cairns *et al.*, 2013). These constraints not only limit yields but also challenge the stability of maize production across diverse agroecological zones in Nigeria.

*Corresponding Author E-mail: igyuvetm@gmail.com

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In addition to yield limitations, micronutrient malnutrition, particularly vitamin A deficiency, poses a serious public health concern in Nigeria, contributing to childhood blindness, morbidity, and mortality (WHO, 2021). Biofortification of maize with provitamin A carotenoids has emerged as a sustainable strategy to address this nutritional gap (Pixley *et al.*, 2013). However, for such biofortified maize to be widely adopted, hybrids must combine enhanced nutritional quality with high and stable yields under the variable growing conditions encountered by smallholder farmers. Developing hybrids that meet these multiple demands requires careful parental selection and an understanding of the genetic control of key agronomic traits. Line × tester analysis is a proven breeding tool for dissecting the general combining ability (GCA) of inbred parents and the specific combining ability (SCA) of their hybrids, thereby providing insight into additive and non-additive gene effects (Griffing, 1956; Kempthorne, 1957). Such information is vital for formulating breeding strategies that exploit both heterosis and stability across environments (Sprague and Tatum, 1942; Badu-Apraku *et al.*, 2020b). Although several provitamin A maize varieties have been released, many are open-pollinated and lack the yield potential and stability associated with hybrid vigor (Makinde *et al.*, 2023). Moreover, there is limited information on how newly developed provitamin A-enriched inbred lines perform in hybrid combinations across contrasting Nigerian agroecologies. Therefore, this study was undertaken to: assess the general and specific combining abilities of selected provitamin A-carrier inbred lines and testers, evaluate the relative contributions of additive

and non-additive genetic effects to key agronomic and yield traits, identify high-yielding and stable hybrids that surpass existing commercial checks across diverse agroecologies; and determine trait interrelationships that can guide selection indices.

MATERIALS AND METHODS

Study Sites and Experimental Environments

The field experiments were conducted during the 2022 and 2023 cropping seasons across two contrasting agro-ecological zones in Nigeria: Makurdi (Latitude 7°.795343”N, Longitude 8°.615679”E) in the Southern Guinea Savanna and Zaria (Latitude 11°.218846”N, Longitude 7°.777635”E), in the Northern Guinea Savanna. These sites were selected to represent distinct environmental conditions for evaluating genotype × environment interactions. Identical experimental layouts and agronomic management protocols were applied at both sites in both seasons; data from the two cropping seasons were pooled within each location prior to combined analysis, yielding two composite environments (Makurdi and Zaria) for the multi-environment ANOVA. This pooling approach is consistent with the combined analysis framework of Singh and Chaudhary (1985), which treats location-season combinations as environments only when interactions among them are significant; preliminary inspection showed no significant season × treatment interaction within either location, justifying the pooling.

Genetic Materials

The experimental materials comprised six hybrids developed through a line × tester mating design (Table 1).

Table 1. Description of parental lines, testers, and check varieties used in the study.

Genotype	Origin	Traits/Characteristics
AWSYN-Y2	IITA, Ibadan; released by IARandT, Ibadan	Fall armyworm tolerant synthetic maize
BRLNTP-YC6	IITA, Ibadan	Combines stem borer resistance and low nitrogen tolerance
PVASYN13	IITA/Nigeria	Vitamin A Orange Maize; tolerant to maize streak virus and other diseases; adapted to Northern Guinea and Sudan Savannah
BR50-419	CIMMYT Zimbabwe	Used in biofortification breeding
BR50-414	CIMMYT Zimbabwe	Used in biofortification breeding
SC510	Seed Co Ltd.	Widely adapted hybrid; used as yield standard in trials
SAMMAZ 51	IITA/IARandT, Nigeria	High-yielding, adapted to diverse ecologies in Nigeria
OBA SUPER 6	Premier Seed Nigeria Ltd.	High grain yield; adapted to Nigerian environments

The hybrids were generated from three provitamin A-carrier inbred lines (AWSYN-Y2, BRLNTP-YC6, and PVASYN13) used as female parents, and two testers (BR50-414 and BR50-419) obtained from CIMMYT Zimbabwe. The commercial checks were SC510, SAMMAZ 51, and OBA SUPER 6. The parental lines were sourced from the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, while the commercial checks were obtained from both national and private seed companies. The parental lines used (PVASYN13, BR50-414, BR50-419) have been reported in IITA and CIMMYT breeding pipelines as carriers of provitamin A alleles based on their pedigrees; however, grain carotenoid content was not quantified in this study, and future validation should confirm beta-carotene levels in superior hybrids.

Experimental Design and Field Management

The field trials were laid out in a randomized complete block design (RCBD) with three replications at each location. Each plot consisted of a single 5-m row, with inter-row spacing of 0.75 m and intra-row spacing of 0.25 m, resulting in a target plant population density of approximately 53,333 plants ha⁻¹. This 3 × 2 factorial mating design provided 6 hybrids assessed with 3 replications across 2 environments and 2 cropping seasons (pooled), yielding 36 observations per trait per location. While this sample size is modest relative to larger factorial designs (e.g., diallel crosses), it is appropriate for identifying GCA and SCA effects of the magnitude typical in quantitative breeding (Badu-Apraku *et al.* 2020b; Annor *et al.* 2019). Agronomic practices for maize production were applied uniformly across locations. NPK fertilizer (15:15:15) was applied at 60 kg N ha⁻¹ at planting, followed by top-dressing with urea (46% N) at 60 kg N ha⁻¹ at the V6 growth stage. Weed control was carried out manually as required.

Data Collection

Data were collected on eighteen agronomic and yield-related traits from five competitive plants randomly selected from the center of each plot to minimize border effects. Phenological traits included days to 50% anthesis (D50A), days to 50% silking (D50S), and days to 95% physiological maturity (D95M). Vegetative and physiological traits measured were plant height (PLHT, cm), leaf length (LL, cm), leaf

width (LW, cm), and leaf area (LA, cm²). Ear and yield component traits comprised ear diameter (ED, cm), ear length (ELNGTH, cm), number of rows per cob (RCOB), number of grains per row (GR), cob weight (CWHT, g), hundred-seed weight (HDSWT, g), and number of ears per plant (EARS). Yield traits included stover yield (SYLD, t ha⁻¹, calculated from total above-ground dry biomass minus grain, adjusted for plot size and plant population) and grain yield per plant (GYLD, g plant⁻¹). Total grain yield was later expressed as tonnes per hectare (t ha⁻¹) at 12% grain moisture content, adjusted for plot size and plant population.

Statistical Analysis

Data were analyzed using R statistical software (v4.3.0; R Core Team, 2023) and the agricolae package (de Mendiburu, 2021). A combined analysis of variance (ANOVA) across environments was performed for each trait using a linear model that included the effects of environment, replication (nested within environment), genotype, and the genotype × environment interaction. The significance of mean squares was tested at the 5% and 1% probability levels.

The line × tester analysis followed Singh and Chaudhary (1985). Data were fitted to the linear model:

$$Y_{ijkl} = \mu + E_i + R_j(E_i) + L_k + T_l + (LT)_{kl} + (EL)_{ik} + (ET)_{il} + (ELT)_{ikl} + \varepsilon_{ijkl}$$

Where; Y_{ijkl} = observation of the k^{th} line × l^{th} tester hybrid in replication j of environment i , μ = overall mean, E_i = environment effect (Makurdi or Zaria), $R_j(E_i)$ = replication within environment, L_k = line effect (**GCA for lines**), T_l = tester effect (**GCA for testers**), $(LT)_{kl}$ = line × tester interaction (**SCA**), $(EL)_{ik}$ = environment × line interaction, $(ET)_{il}$ = environment × tester interaction, $(ELT)_{ikl}$ = environment × line × tester interaction, ε_{ijkl} = experimental error. Environment and replication were random effects, while lines, testers, and their interactions were fixed.

Variance components were estimated from the line × tester analysis, where additive genetic variance (σ^2A) was calculated as $2 \times \sigma^2GCA$, and dominance variance (σ^2D) as σ^2SCA . **Broad-sense heritability (H^2)** was computed on an entry-mean basis according

to the following expression (Falconer and Mackay, 1996):

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2/e + \sigma_\varepsilon^2/r}$$

Where; σ_g^2 = genotypic variance, σ_{ge}^2 = genotype $\times$ environment variance, σ_ε^2 = error variance, e = number of environments, and r = number of replications. Heritability values >0.75 indicate high heritability suitable for efficient selection; 0.40 – 0.75 moderate; <0.40 low.

Pearson's correlation coefficients were estimated among traits to identify yield predictors and assess interrelationships among agronomic and yield-related characters (Steel and Torrie, 1980).

RESULTS AND DISCUSSION

The mean square analysis of variance results for yield and yield-related traits of maize lines, testers, and their hybrids evaluated across Makurdi and Zaria are presented in Table 2. The combined analysis of variance revealed significant genotypic differences for most agronomic and yield-related traits, including flowering time, leaf traits, cob weight, and 100-seed weight, indicating substantial genetic variability among the evaluated materials. However, grain yield (t ha^{-1}) was not significant at the overall genotype level, despite clear numerical differences among hybrids. This agrees with Badu-Apraku et al. (2020b), who reported that in multi-environment trials of provitamin A maize, grain yield often shows high environmental sensitivity, resulting in non-significant differences even when superior hybrids are numerically evident. Similarly, Suwarno et al. (2014) observed that yield in tropical maize is strongly influenced by environment $\times$ genotype interaction, reducing statistical separation across test locations.

Significant variation among lines for flowering traits, leaf characteristics, number of ears, cob weight, and grain yield confirms that parental lines contributed differently to hybrid performance. The presence of significant line $\times$ tester interaction effects for key traits such as anthesis, silking, cob weight, and number of ears indicates the importance of non-additive gene action. This is consistent with Semagn et al. (2012), who revealed that maize hybrid performance is largely driven by interactions between parental alleles, with specific combinations outperforming others due to heterotic effects rather than general parental performance alone.

The GCA results (Table 3) showed that BRLNTP-YC6 had strong positive effects for key traits, including leaf length (5.78), number of ears (11.54), cob weight (28.38), and grain yield (0.30 t ha^{-1}), confirming its role as a good general combiner for productivity traits.

Similarly, Badu-Apraku et al. (2020b) reported that inbred lines with positive GCA effects for yield components consistently produce superior hybrids. AWSYN-Y2 contributed positively to earliness ($D50A = 2.19$, $D50S = 1.45$) and showed moderate yield contribution (0.32 t ha^{-1}), making it suitable for stress-prone environments. This supports Edmeades (2013), who showed that early flowering reduces exposure to terminal drought stress and stabilizes yield in tropical maize systems.

In contrast, PVASYN13 showed negative GCA effects for most traits, including grain yield (-0.62 t ha^{-1}) and cob weight (-57.70), indicating poor general combining ability. However, its strong negative values for flowering traits ($D50A = -4.76$, $D50S = -2.49$) confirm its contribution to earliness. This trade-off between earliness and yield has also been reported by Aboderin et al. (2024), who observed that early maturing hybrids often have reduced yield potential. Among testers, BR50-419 showed positive contributions to plant height (4.26), grain-related traits, and yield stability, while BR50-414 contributed to rows per cob (0.65) and cob structure. This aligns with Annor et al. (2019), who revealed that testers influence different yield components depending on their genetic background.

The SCA effects (Table 4) further reveal the importance of specific parental combinations. AWSYN-Y2 $\times$ BR50-419 showed positive SCA for grain yield (0.06 t ha^{-1}), cob weight (8.52), and grains per row (1.16), while AWSYN-Y2 $\times$ BR50-414 showed negative yield effects (-0.06 t ha^{-1}) despite positive ear number (2.01). Similarly, BRLNTP-YC6 $\times$ BR50-419 showed positive SCA for grain yield (0.22 t ha^{-1}) and ear length (0.31), whereas BRLNTP-YC6 $\times$ BR50-414 had negative yield effects (-0.22 t ha^{-1}) but higher cob weight (16.03). These contrasting responses confirm strong interaction between parental lines and testers, consistent with Annor et al. (2019) and Makinde et al. (2023), who showed that hybrid performance varies depending on tester background.

Table 2. Combined analysis of variance for agronomic and yield-related traits of line × tester hybrids across Makurdi and Zaria

SOV	Df	D50A	D50S	PLHT (cm)	LL (cm)	LW (cm)	ED (cm)	ELNGTH (cm)	RCOB	GR	EARS	D95M	SYLD (t/ha)	HSDSWT (g)	GYLD (t/ha)
Env.	1	691.94**	432.93**	37765.84**	531.35*	58.78*	16.54**	2.42	353.79**	3997.11**	1424.60**	1756.74**	925.29**	664.51*	110.40**
Rep(Env)	4	1.67	18.22	44.78	44.44	3.05	0.03	0.43	4.12	1.66	5.55	38.1	2.23	35.7	0.75
Gen	8	69.50**	33.53*	395.87	136.28**	3.31	0.16	1.92	8.52**	62.79	437.70**	31.37	72.20**	40.64*	3.31
Lines (L)	2	204.45**	56.48*	400.8	312.02**	3.42	0.45	2.13	2.77	38.56	1253.69**	21.18	132.38**	37.31	3.43
Testers (T)	1	36.40**	26.69	652.46	1.44	0.78	0.00	1.24	15.08**	0.68	11.88	9.20	6.38	12.19	0.09
L × T	2	24.29**	6.33	285.74	23.61	2.88	0.05	3.41	18.72**	12.02	86.13*	21.88	26.82**	56.57*	0.81
Checks	2	28.73**	42.71	8.29	136.33*	5.82	0.11	0.42	4.45	32.55	96.55	23.4	40.26**	3.63	1.59
Crosses vs Checks	1	4.65	30.51	1124.82*	144.84*	1.47	0.06	2.22	1.23	335.42**	617.00**	108.8	172.34**	117.92**	14.72**
G × E	8	2.33	13.25	444.82*	97.72**	10.76**	0.16	1.84	1.68	10.31	9.39	30.97	16.07**	30.59	0.17
L × E	2	4.31	11.66	268.55	121.87*	4.08	0.45	0.64	2.29	19.58	18.21	17.81	28.82**	46.27	0.28
T × E	1	2.15	2.89	0.24	104.35	10.55*	0.00	0.06	1.80	5.66	2.12	14.69	1.53	18.19	0.00
(L × T) × E	2	0.62	0.54	350.26	114.16*	10.23*	0.05	5.41	1.17	12.38	3.92	32.84	0.86	30.31	0.07
Checks × E	2	2.77	35.89	8.29	15.73	9.89*	0.11	0.14	1.98	5.58	1.35	63.32	14.13*	15.61	0.10
(Cr vs Ck)×E	1	1.12	6.95	2304.09**	173.86*	27.09**	0.06	2.31	0.74	1.75	26.09	5.16	39.42**	42.13	0.42
Error	32	4.15	11.59	186.47	25.99	2.52	0.21	2.33	1.51	34.23	21.87	22.24	2.92	14.95	1.57

* = significant at $p < 0.05$; ** = significant at $p < 0.01$., **Env.** = Environment; **Rep** = Replication; **Cr** = Crosses; **Ck** = Checks **D50A** = Days to 50% anthesis; **PLHT** = Plant height (cm); **LL** = Leaf length (cm); **LW** = Leaf width (cm); **D50S** = Days to 50% silking; **D95M** = Days to 95% maturity; **ED** = Ear diameter; **ELNGTH** = Ear length; **RCOB** = Number of rows per cob; **GR** = Number of grains per row; **SYLD** = Stover yield (t ha⁻¹); **EARS** = Number of ears per plant; **HSDSWT** = Hundred-seed weight (g); **GYLD** = Grain yield (t ha⁻¹).

Table 3. General combining ability (GCA) effects of lines and testers for agronomic and yield-related traits across environments.

Line	D50A	D50S	PLHT (cm)	LL (cm)	LW (cm)	ED (cm)	ELNGTH (cm)	RCOB	GR	EARS	CWHT (g)	D95M	SYLD (t/ha)	HSDSWT (g)	GYLD (t/ha)
AWSYN-Y2	2.19**	1.45	4.39	-1.93	-0.47	-0.19	-0.48	-0.06	1.49	-3.63*	29.31**	1.49	1.24**	-0.22	0.32
BRLNTP-YC6	2.57**	1.05	2.16	5.78**	0.58	-0.01	0.3	0.51	0.5	11.54**	28.38**	-1.05	2.52**	1.86	0.30
PVASYN13	-4.76**	-2.49*	-6.55	-3.85*	-0.11	0.2	0.18	-0.45	-1.99	-7.91**	-57.70**	-0.45	-3.76**	-1.64	-0.62
S.E.	0.69	1.07	3.22	1.58	0.42	0.13	0.5	0.35	1.86	1.28	6.06	1.37	0.38	1.09	0.35
GM	72.43	78.98	174	51.5	7.86	5.77	10.07	15.27	35.62	25.68	263.24	108.32	9.42	29.72	6.05
Tester															
BR50-414	-1.01	-0.86	-4.26	-0.2	0.15	0.00	-0.19	0.65*	-0.14	0.57	3.99	-0.51	0.42	0.58	0.05
BR50-419	1.01	0.86	4.26	0.2	-0.15	0.00	0.19	-0.65*	0.14	-0.57	-3.99	0.51	-0.42	-0.58	-0.05
S.E.	0.57	0.87	2.63	1.29	0.34	0.11	0.4	0.28	1.52	1.05	4.95	1.12	0.31	0.89	0.28
GM	72.43	78.98	174	51.5	7.86	5.77	10.08	15.27	35.62	25.68	263.24	108.32	9.42	29.72	6.05

GCA = general combining ability; * = significant at $p < 0.05$; **GM** = Grand Mean; **SE (±)** = values are standard errors for testing GCA effects, **D50A** = Days to 50% anthesis; **PLHT** = Plant height (cm); **LL** = Leaf length (cm); **LW** = Leaf width (cm); **D50S** = Days to 50% silking; **D95M** = Days to 95% maturity; **ED** = Ear diameter; **ELNGTH** = Ear length; **RCOB** = Number of rows per cob; **GR** = Number of grains per row; **SYLD** = Stover yield (t ha⁻¹); **EARS** = Number of ears per plant; **CWHT** = Cob weight (g); **HSDSWT** = Hundred-seed weight (g); **GYLD** = Grain yield (t ha⁻¹).

Table 4. Specific combining ability (SCA) effects of line×tester hybrids for agronomic and yield-related traits across environments

SCA	D50A	D50S	PLHT (cm)	LL (cm)	LW (cm)	ED (cm)	ELNGTH (cm)	RCOB	GR	EARS	CWHT (g)	D95M	SYLD (t/ha)	HDSDWT (g)	GYLD (t/ha)
AWSYN-Y2 X BR50-414	0.62	0.27	0.67	1.27	-0.46	-0.07	0.62	-1.4	-1.16	2.01	-8.52	1.52	-0.46	-2.25	-0.06
AWSYN-Y2 X BR50-419	-0.62	-0.27	-0.67	-1.27	0.46	0.07	-0.62	1.4	1.16	-2.01	8.52	-1.52	0.46	2.25	0.06
BRLNTP-YC6 X BR50-414	1.01	0.55	-5.18	-1.51	0.52	0.05	-0.31	1.01	0.54	1.03	16.03	-1.05	1.67	0.18	-0.22
BRLNTP-YC6 X BR50-419	-1.01	-0.55	5.18	1.51	-0.52	-0.05	0.31	-1.01	-0.54	-1.03	-16.03	1.05	-1.67	-0.18	0.22
PVASYN13 X BR50-414	-1.63	-0.82	4.51	0.24	-0.06	0.03	-0.3	0.39	0.61	-3.04	-7.51	-0.47	-1.21	2.08	0.29
PVASYN13 X BR50-419	1.63	0.82	-4.51	-0.24	0.06	-0.03	0.3	-0.39	-0.61	3.04	7.51	0.47	1.21	-2.08	-0.29
S.E.	0.98	1.51	4.55	2.24	0.59	0.19	0.7	0.49	2.63	1.82	8.57	1.94	0.54	1.54	0.49
GM	72.43	78.98	174	51.5	7.86	5.77	10.08	15.27	35.62	25.68	263.24	108.32	9.42	29.72	6.05

GM = Grand Mean; **SE (±)** = values are standard errors; **D50A** = Days to 50% anthesis; **PLHT** = Plant height (cm); **LL** = Leaf length (cm); **LW** = Leaf width (cm); **D50S** = Days to 50% silking; **D95M** = Days to 95% maturity; **ED** = Ear diameter; **ELNGTH** = Ear length; **RCOB** = Number of rows per cob; **GR** = Number of grains per row; **SYLD** = Stover yield (t ha⁻¹); **EARS** = Number of ears per plant; **CWHT** = Cob weight (g); **HDSDWT** = Hundred-seed weight (g); **GYLD** = Grain yield (t ha⁻¹).

Table 5. Genetic variance components for measured traits across Makurdi and Zaria environment

Traits	Mean	σ^2_g	σ^2_p	GCV	PCV	H ² bs (%)	GA	GAM (%)
D50A	72.43	11.19	11.89	4.62	4.76	94.19	6.70	9.25
D50S	78.98	3.38	5.59	2.33	2.99	60.48	2.95	3.73
PLHT	174.00	7.41	74.14	1.56	4.95	10.00	1.76	1.01
LL	51.50	6.43	22.71	4.92	9.25	28.29	2.78	5.40
LW	7.86	0.18	1.79	5.40	17.02	10.06	0.28	3.56
ED	5.77	0.003	0.03	0.95	3.22	10.00	0.04	0.69
ELNGTH	10.08	0.01	0.40	0.99	6.30	2.50	0.04	0.44
RCOB	15.27	1.14	1.42	6.99	7.81	80.29	1.97	12.93
GR	35.62	8.75	14.45	8.30	10.67	60.55	4.75	13.33
EARS	25.68	71.38	75.03	32.90	33.73	95.14	17.00	66.20
CWHT	263.24	1819.07	1975.38	16.20	16.88	92.09	84.44	32.08
D95M	108.32	0.07	5.23	0.24	2.11	1.34	0.06	0.05
SYLD	9.42	9.36	12.03	32.47	36.83	77.80	5.56	59.07
HDSDWT	29.72	1.68	6.77	4.35	8.76	24.82	1.33	4.47
GYLD	6.05	0.52	0.79	11.96	14.65	65.82	1.22	20.16

GCV: Genotypic Coefficient of Variation, **PCV:** Phenotypic Coefficient of Variation σ^2_g = Genotypic variance; σ^2_p = Phenotypic variance; **H²bs** = broad-sense heritability on entry-mean basis. **GA:** Genetic Advance, **PLHT** = Plant height (cm); **LL** = Leaf length (cm); **LW** = Leaf width (cm); **D50S** = Days to 50% silking; **D95M** = Days to 95% maturity; **ED** = Ear diameter; **ELNGTH** = Ear length; **RCOB** = Number of rows per cob; **GR** = Number of grains per row; **SYLD** = Stover yield (t ha⁻¹); **EARS** = Number of ears per plant; **CWHT** = Cob weight (g); **HDSDWT** = Hundred-seed weight (g); **GYLD** = Grain yield (t ha⁻¹).

Broad-sense heritability estimates were high for several traits, including number of ears per plant (0.95), cob weight (0.92), and rows per cob (0.80), indicating strong genetic control. Grain yield exhibited moderate heritability (65.82%), indicating that both genetic and environmental factors contributed substantially to phenotypic expression. This pattern is consistent with Ma et al. (2024b), who reported moderate heritability for grain yield due to environmental variability. Evaluation of hybrid performance (Figure 1) further confirmed the superiority of BRLNTP-YC6 × BR50-419 (6.52 t ha⁻¹) and AWSYN-Y2 × BR50-419 (6.38 t ha⁻¹), both exceeding SC510 (4.46 t ha⁻¹), SAMMAZ 51 (4.79 t ha⁻¹), and OBA SUPER 6 (5.51 t ha⁻¹). Although these differences were not statistically significant, they represent meaningful yield advantages under field conditions. Similar observations were made by Aboderin et al. (2024), where improved hybrids outperformed checks numerically across environments. PVASYN13-based hybrids were consistently earlier, with anthesis as low as 49.00

days, compared to 54.50 days in other hybrids and checks. However, their grain yield ranged from 5.10 t ha⁻¹ downward, confirming that earliness did not translate into superior yield. This agrees with Aboderin et al. (2024), who emphasized that early maturity must be complemented with strong yield components.

The correlation analysis (Figure 2) provided further insight into yield determination. Days to anthesis and silking showed a very strong positive correlation ($r = 0.97$), confirming tight synchronization of flowering processes, as also reported by Adu et al. (2019). Grain yield showed the strongest positive correlations with cob weight ($r = 0.73$), stover yield ($r = 0.72$), and 100-seed weight ($r = 0.52$), indicating that these traits are the main drivers of yield in the studied materials. Similar findings were reported by Annor et al. (2019), who identified cob weight and kernel weight as primary determinants of yield, and by Tufa et al. (2023a), who showed that yield components contribute indirectly to grain yield through biomass accumulation.

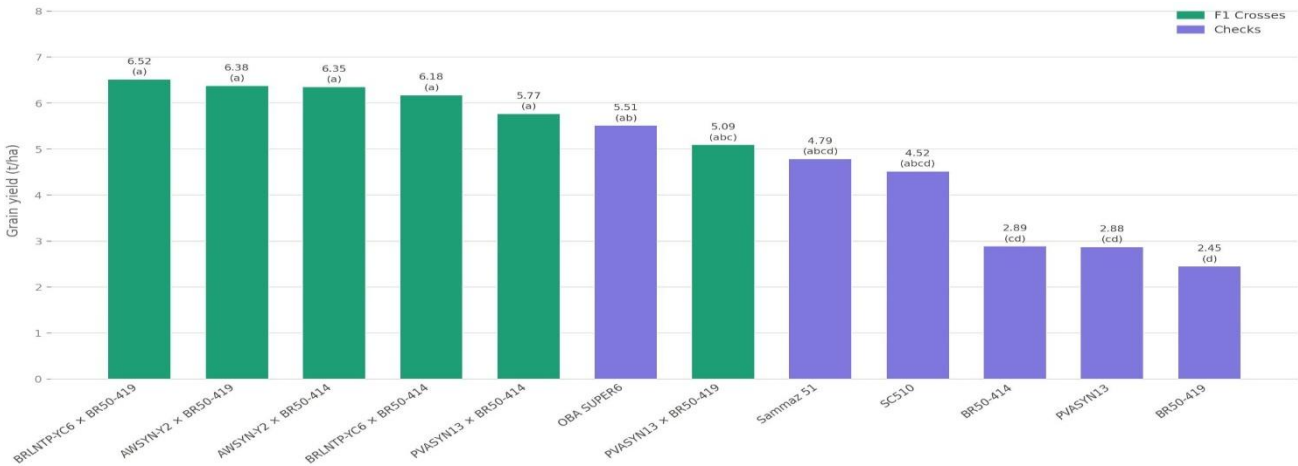


Figure 1. Mean performance of line × tester hybrids and commercial checks across environments for grain yield

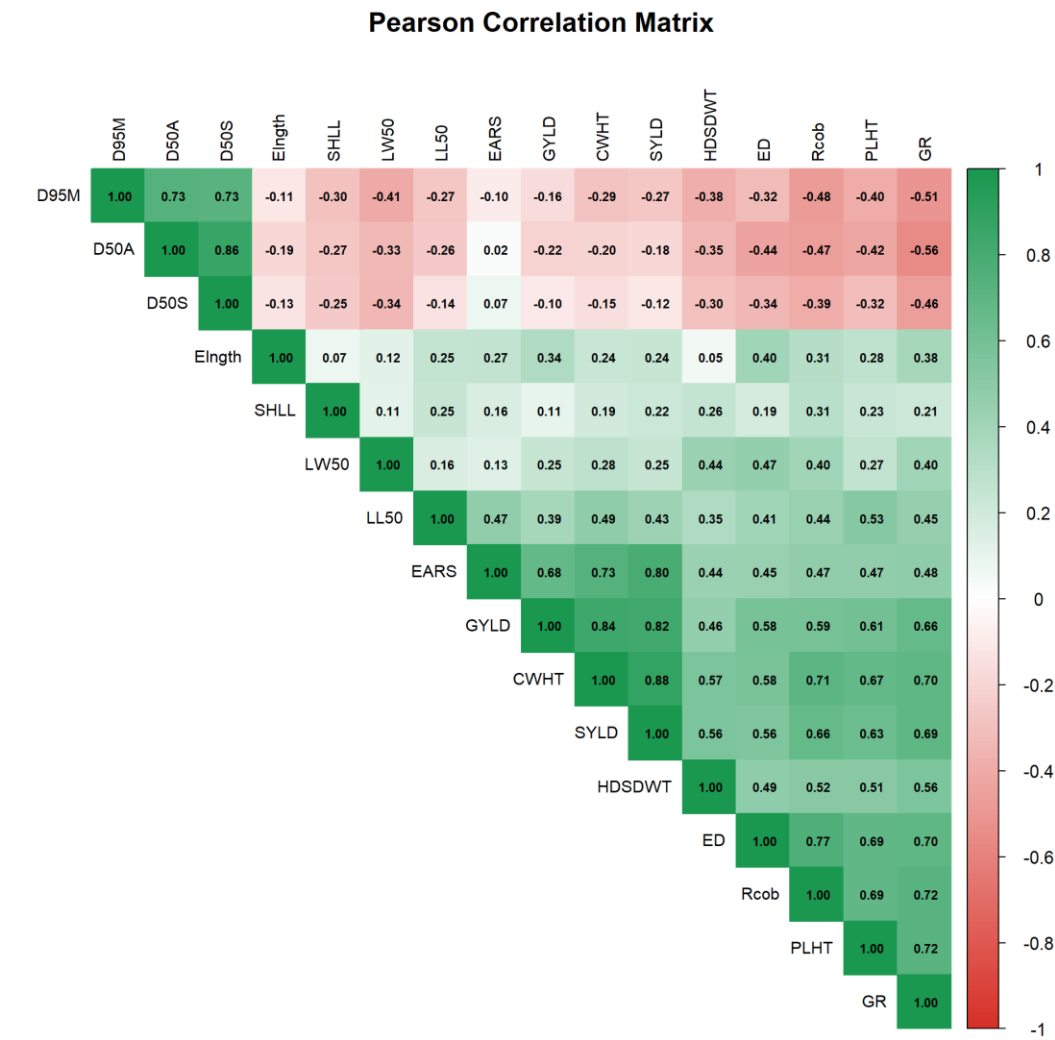


Figure 2. Pearson correlation matrix showing pairwise relationships among agronomic and phenological traits in maize lines

Number of ears per plant also showed a meaningful positive correlation with yield ($r = 0.47$), confirming the role of prolificacy in yield improvement. In contrast, shelling percentage showed a weak correlation ($r = 0.09$), indicating limited influence on yield variation. Leaf traits such as leaf length, width, and area were strongly inter-correlated ($r = 0.73$ – 0.88), but showed weak direct correlations with yield ($r = 0.13$ – 0.38). This suggests that while leaf development contributes to photosynthetic capacity, its effect on yield depends on assimilate partitioning. This agrees with Sultan et al. (2022a), who reported that leaf area contributes indirectly to yield through biomass production rather than direct grain formation. Stover yield (SYLD) was a key trait, showing a strong positive correlation with grain yield ($r = 0.72$) and high genetic variability. It recorded high GCV (32.47%), heritability (77.80%), and GAM (59.07%), indicating strong additive gene action and high selection potential, consistent with Mallaiah et al. (2024) who reported high heritability and genetic advance for biomass-related traits in maize. BRLNTP-YC6 had the highest GCA effect (2.52 t ha^{-1}), and its hybrid with BR50-419 combined high grain and stover yield.

The predominance of additive effects suggests effective improvement through selection, aligning with Sanfo et al. (2023) and Mabhaudhi et al. (2023) who reported that high biomass production and improved fodder traits are critical for enhancing livestock productivity and resilience in mixed farming systems. Stover remains essential in sub-Saharan Africa, contributing up to 39% of feed in Tanzania and 34% in Kenya (Herrero et al., 2015), while also supporting soil health under climate stress (Amole et al., 2024). Thus, improving stover yield enables a dual-purpose breeding strategy for both grain and biomass.

REFERENCES

Aboderin, O. S., Bankole, F. A., Oyekunle, M., and Olaoye, G. (2024). Yield performance and stability of maize hybrids of different maturity groups in multiple environments in Nigeria. *Thai Journal of Agricultural Science*, 57(3):164-180

Conclusion

This study reveals the presence of substantial genetic variability among provitamin A maize lines and their hybrids across contrasting agroecologies. Both additive and non-additive gene actions played important roles, with additive effects influencing key traits such as leaf characteristics and grain yield, while dominance effects were more relevant for reproductive and kernel traits. BRLNTP-YC6 was identified as the most effective parent for yield and vegetative traits, while AWSYN-Y2 contributed to earliness and acceptable yield performance. Among testers, BR50-419 enhanced grain filling and kernel weight, whereas BR50-414 contributed to ear structural traits. Nevertheless, BRLNTP-YC6 $\times$ BR50-419 and AWSYN-Y2 $\times$ BR50-414 consistently exhibited higher numerical grain yield across environments, suggesting potential performance advantages that require confirmation under expanded multi-environment trials with greater statistical resolution. PVASYN13-based hybrids were consistently early, making them suitable for short-duration environments despite their lower yield performance. Cob weight, stover yield, and 100-seed weight were identified as key traits associated with grain yield and can serve as reliable selection criteria. The strong additive genetic control of stover yield and superior performance of BRLNTP-YC6 shows the feasibility of developing dual-purpose maize hybrids that simultaneously meet grain production and livestock feeding demands a critical necessity in mixed crop–livestock systems where stover serves as essential dry-season fodder. The moderate to high heritability observed for most traits supports the effectiveness of selection in breeding programs. BRLNTP-YC6 and AWSYN-Y2 are promising parental lines, while the identified superior hybrids provide a strong basis for advancing provitamin A maize breeding in Nigeria. Future work should include direct quantification of carotenoid content to confirm the nutritional value of these materials.

Adu, G. B., Badu-Apraku, B., Akromah, R., Garcia-Oliveira, A. L., Awuku, F. J., and Gedil, M. (2019). Genetic diversity and population structure of early-maturing tropical maize inbred lines using SNP markers. *PLOS ONE*, 14(4): e0214810. <https://doi.org/10.1371/journal.pone.0214810>

- Amole, T., Ayantunde, A., Balehegn, M., and Adesogan, A. T. (2024). Livestock feed resources in the West African Sahel. *Agronomy Journal*, 114(7): 26–45. <https://doi.org/10.1002/agj2.20955>
- Annor, B., Badu-Apraku, B., Nyadanu, D., Akromah, R., and Fakorede, M. A. B. (2019). Testcross performance and combining ability of early-maturing maize inbreds under stress and optimal conditions. *Scientific Reports*, 9: 13809. <https://doi.org/10.1038/s41598-019-50345-3>
- Badu-Apraku, B., Fakorede, M. A. B., Talabi, A. O., Oyekunle, M., Aderounmu, M., Lum, A. F., Ribeiro, P. F., Adu, G. B., and Toyinbo, J. O. (2020b). Genetic studies of extra-early provitamin-A maize inbred lines and their hybrids in multiple environments. *Crop Science*, 60(3): 1325–1345. <https://doi.org/10.1002/csc2.20071>
- Cairns, J. E., Hellin, J., Sonder, K., Araus, J. L., MacRobert, J. F., Thierfelder, C., and Prasanna, B. M. (2013). Adapting maize production to climate change in sub-Saharan Africa. *Food Security*, 5(3): 345–360.
- de Mendiburu, F. (2021). *agricolae: Statistical Procedures for Agricultural Research*. R package version 1.3-5.
- Edmeades, G. O. (2013). Progress in achieving and delivering drought tolerance in maize – An update. In C. James (Ed.), *Global status of commercialized biotech/GM crops: 2012* (ISAAA Brief No. 44, pp. 239–272). International Service for the Acquisition of Ag-biotech Applications (ISAAA).
- Falconer, D. S., and Mackay, T. F. C. (1996). *Introduction to quantitative genetics* (4th ed.). Longman.
- Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences*, 9(4): 463–493.
- Herrero, M., Ramirez-Villegas, J., Aruévelo, A., Flores-Renteria, D., Silván, M. I., and Thornton, P. K. (2015). Climate smart agriculture and livestock systems. In *Climate smart agriculture: Enhancing adaptive capacity of farming communities to climate change* (pp. 43–76). Springer, Cham.
- Kamara, A. Y., Kamai, N., Omoigui, L. O., Togola, A., Ekeleme, F., and Onyibe, J. E. (2022). *Guide to maize production in Northern Nigeria*. International Institute of Tropical Agriculture. (pp. 1–44).
- Kempthorne, O. (1957). *An Introduction to Genetic Statistics*. John Wiley and Sons, New York. Pp. 545.
- Ma, C., Liu, C., and Ye, Z. (2024b). Influence of Genotype × Environment Interaction on Yield Stability of Maize Hybrids with AMMI Model and GGE Biplot. *Agronomy*, 14(5): 1000. <https://doi.org/10.3390/agronomy14051000>
- Mabhaudhi, T., Chibarabada, T. P., and Sikka, A. (2023). Status of integrated crop-livestock research in the mixed farming systems of the Global South: A scoping study. *Frontiers in Sustainable Food Systems*, 7: 1241675. <https://doi.org/10.3389/fsufs.2023.1241675>
- Makinde, S. A., Badu-Apraku, B., Ariyo, O. J., and Porbeni, J. B. (2023). Combining ability of extra-early maturing provitamin A maize inbred lines and performance of derived hybrids under *Striga hermonthica* infestation and low soil nitrogen. *PLOS ONE*, 18(2): e0280814. <https://doi.org/10.1371/journal.pone.0280814>
- Mallaiah, B., Naga Brahma Reddy, K., Hemalatha, V., Yathish, K. R., and Kadhyayani, N. (2024). Study of genetic variability, heritability and genetic advance in maize (*Zea mays* L.) inbred lines. *Journal of Experimental Agriculture International*, 46(8):595–601. <https://doi.org/10.9734/jeai/2024/v46i82741>
- Ndoro, O., Magorokosho, C., Setimela, P. S., and Labuschagne, M. T. (2024). Performance of tropical and subtropical maize inbred lines under well-watered and drought-stressed environments. *Euphytica*, 220: 178. <https://doi.org/10.1007/s10681-024-03395-2>
- Pixley, K., Palacios-Rojas, N., Babu, R., Mutale, R., Surles, R., and Simpungwe, E. (2013). Biofortification of maize with provitamin A carotenoids. In *Carotenoids and Human Health* (pp. 271–292).
- R Core Team. (2023). *R: A language and environment for statistical computing*. R Foundation for Statistical Computing, Vienna, Austria. <https://www.R-project.org/>
- Sanfo, A., Zampaligré, N., Kulo, A. E., Somé, S., Traoé, K., Rios, E. F., Dubeux, J. C. B., Boote, K. J., and Adesogan, A. (2023). Performance of food–feed maize and cowpea cultivars under monoculture and intercropping systems: Grain yield, fodder biomass, and nutritive value. *Frontiers in Animal Science*, 3: 998012, 1–14. <https://doi.org/10.3389/fanim.2022.998012>

- Semagn, K., Magorokosho, C., Vivek, B. S., Makumbi, D., Beyene, Y., Mugo, S., Prasanna, B. M., and Warburton, M. L. (2012). Molecular characterization of diverse CIMMYT maize inbred lines from eastern and southern Africa using single nucleotide polymorphic markers. *BMC Genomics*, 13:113. <https://doi.org/10.1186/1471-2164-13-113>
- Singh, R. K., and Chaudhary, B. D. (1985). *Biometrical Methods in Quantitative Genetic Analysis* (3rd ed.). Kalyani Publishers, New Delhi, Pp 1-318.
- Sprague, G. F., and Tatum, L. A. (1942). General vs. specific combining ability in single crosses of corn. *Agronomy Journal*, 34(10):923–932. <https://doi.org/10.2134/agronj1942.00021962003400100008x>
- Steel, R. G. D., and Torrie, J. H. (1980). *Principles and Procedures of Statistics: A Biometrical Approach* (2nd ed.). McGraw-Hill, New York, 1-633
- Sultan, M., Abdalh, N., Liu, G., Hassouna, M. S., and Li, J. (2022). Physiological determinants of maize yield and their relationships with drought and lodging stress. *Journal of Crop Science and Biotechnology*, 25, 521–534. <https://doi.org/10.1007/s12892-022-00148-2>
- Suwarno, W. B., Pixley, K. V., Palacios-Rojas, N., Kaeppler, S. M., and Babu, R. (2014). Formation of heterotic groups and understanding genetic effects in a provitamin A biofortified maize breeding program. *Crop Science*, 54(1):4–24. <https://doi.org/10.2135/cropsci2013.02.0113>
- Tufa, A., Habte, J., and Abebe, F. (2023a). Correlation and path coefficient analysis of yield and yield-related traits in maize (*Zea mays* L.). *Heliyon*, 9(8): e19076. <https://doi.org/10.1016/j.heliyon.2023.e19076>
- World Health Organization. (2021). *Vitamin A deficiency* (Fact Sheet No. 124). World Health Organization. <https://www.who.int/data/nutrition/nlis/info/vitamin-a-deficiency>

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