

EVALUATION OF THE PERFORMANCE OF 21 MAIZE HYBRIDS (*Zea mays* L.) FOR YIELD AND OTHER AGRONOMIC ATTRIBUTES IN OWERRI WEST, SOUTH EASTERN NIGERIA

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Abstract: Evaluation of the performance of maize genotypes for yield and other agronomic attributes was conducted at the Centre for Agricultural Research, School of Agriculture and Agricultural Technology of Federal University of Technology, Owerri. (Lat. 5^o27' N, Long. 7^o02'E, mean temperature of 29^o C; relative humidity of 89%; and an altitude of 50-70 cm above sea level) between July and November 2016. The treatments consisted of twenty eight genotypes which comprises of seven parents and twenty one crosses derived from a partial diallel cross, laid out in randomised complete block design with four replications, the genotypes were grown in three row plots; these were tested for eighteen characters to evaluate their performance. The means sum of squares due to genotypes indicated highly significant differences ($P \leq 0.01$) for Days to 50% emergence, Days to 50% tasseling, Leaf area (cm²), Days to maturity, Plant at harvest, Days to 50% silking, Plant height (cm), Ear height (cm), Cob length (cm), Number of rows/cob, Grain weight/cob, Field weight (FWT), Number of grains/cob, Grain weight/cob, and Grain yield (t/ha) for the crosses while non-significant difference was observed in that of the parents. The significant differences observed revealed the presence of substantial variability among the genotypes. The crosses flowered and matured earlier than the parents. Furthermore, crosses involving the earliest parents; DTMA-4 and POOL 66/ACR-91 with BENDE-WHITE resulted in progenies which were earlier than the mean of the entire crosses. This suggests that they may be exploited for use in developing early maturing maize variety. OKA BENDE-WHITE recorded the highest grain yield (2.86 t/ha) while the cross between DTMA-4 X OKA BENDE-WHITE recorded the highest grain yield (3.63 t/ha), indicating that the highest yield obtained may be due to the combination of OKA BENDE-WHITE which appears as the higher yielding parent. The cross between DTMA-4 X DMR-ESRY (2.36 t/ha) had the lowest grain yield. Therefore, OKA BENDE-WHITE is recommended for use in hybridization programs in generating new improved varieties.

Keywords: Maize genotypes, Evaluation, Performance, Agronomic attributes.

Introduction

Maize (*Zea mays* L) is one of the most important sources of carbohydrates and minerals for humans and animals and also a good source of raw materials for industries. The nutritional quality of maize is very important and is mainly determined by the genotype and the growing

conditions as well as the post-harvest technology. The protein produced by normal maize is low biological quality for human and animal consumption, especially because of a low content of essential amino acids such as lysine and tryptophan. Quality protein maize cultivars have been developed by various companies in the world, to offer a nutritional solution to people who solely depend on maize as their source of protein (Salami *et al.*, 2007).

Wheat, rice and maize are the most important cereal crops in the world but maize is the most popular due to its high yielding, ease of processing, readily digested and costs less than other cereals (Jaliya *et al.*, 2008). Maize has a variety of uses as it can be used in the livestock industry to make livestock feeds, for export purposes and also used as human food and for industrial products. Between 90 and 95 percent of the crop is harvested for grain, the remaining 5-10 percent is grown for silage (Jaliya *et al.*, 2008). Maize is also a component of canned corn, baby food, mush, puddings and many more human foods. It can also be used as a major study plant for many academic disciplines such as genetics, physiology, soil fertility and biochemistry.

According to IITA (2001) report, maize contains 80 per cent carbohydrates, 10 percent protein, 3.5 percent fibre and 2 percent mineral. Iron and vitamin B are also present in maize. Africans consume maize as a starchy base in a wide variety of porridges, pastes, grits and beer.

Recent breeding efforts in the west and central Africa (WCA) sub region have focused on improvement of maize grain quality characteristic or organoleptic and nutritional properties. Genetic improvement for sweet corn (*Zea mays* Saccharata) for grain yield has been limited primarily because of its narrow genetic base, the lack of defined heterotic group and the greater effort devoted to improving yield in field corn (Tracy, 1990).

Consequently, the focus in field corn X sweet corn crosses is the exploitation of hybrid vigour in the improvement of sweet corn varieties for grain yield, adaptation and genetic diversity (Tracy, 1990). Transfer of mutant genes (Su1, Su2, bt2 wx and O²) from sweet corn into field corn, on the other hand, is for the improvement in nutritional contents (Protein, lysine, soluble sugar, sucrose, reducing sugar, albumin, globulin and glutelin) of the grains, which has also been accompanied by a corresponding reduction in starch and Ze in either in the varieties per se (Li and Liu, 1994). Although characters associated with organoleptic and quality characters in maize is well documented (Olaoye *et al.*, 2001; Akande and Lamidi

2006; Gupta *et al.*, 2009), there is limit on the effects of transferring the mutant genes from sweet corn to field corn especially on endosperm attributes of the resulting populations.

Olaoye *et al.*, (2008) reported improvement in the flavour and grain texture characteristics of F₁ hybrids derived through the transfer of mutant Su² genes from sweet corn into three field corn varieties without adverse consequence on grain yield potential of the resulting hybrids.

The success of crop improvement programme does not only depend on the amount of genetic variability present in the population but rather on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection (Najeeb *et al.*, 2009).

Thus, evaluating the genotypes to study genetic variability for agronomic characters is a key component of breeding programmes for broadening the gene pool of crops (Ahmed *et al.*, 2011). Therefore, present study was conducted to evaluate maize genotypes and identify appropriate germplasm for development of maize hybrid for production in South-eastern Nigeria.

Materials and Methods

Experimental Site

The research was carried out at the Centre for Agricultural Research, School of Agriculture and Agricultural Technology of the Federal University of Technology Owerri, Imo State, (Lat. 5^o27' N, Long. 7^o02'E, mean temperature of 29^o C; relative humidity of 89%; and an altitude of 50-70 cm above sea level) between July and November 2016.

Description of genotypes used for the study:

The material consisted of 28 genotypes, 7 of which were parents and the remaining 21 were crosses as shown in the table below;

Table 1: Evaluated Genotypes

S/N	ENTRIES	EXPERIMENTAL CODE	STATUS
1	DTMA-4	V1	PARENT
2	DMR-ESRY (POOL 18-SR)	V2	PARENT
3	PVA SYM 8 F2 (PRO VIT A)	V3	PARENT
4	POOL 66/ACR-91 SUWAN – 1- SR (QPM)	V4	PARENT
5	DTMA – W	V5	PARENT
6	Oka Mbaise	V6	PARENT
7	Oka Bende-white	V7	PARENT
8	DTMA-4 X DMR-ESRY (POOL 18-SR)	v1v2	HYBRID
9	DTMA-4 X PVA SYM 8 F2 (PRO VIT A)	v1v3	HYBRID
10	DTMA-4 X POOL 66/ACR-91 SUWAN – 1- SR (QPM)	v1v4	HYBRID
11	DTMA-4 X DTMA – W	v1v5	HYBRID
12	DTMA-4 X Oka Mbaise	v1v6	HYBRID
13	DTMA-4 Oka Bende-white	v1v7	HYBRID
14	DMR-ESRY (POOL 18-SR) X PVA SYM 8 F2 (PRO VIT A)	v2v3	HYBRID
15	DMR-ESRY (POOL 18-SR) X POOL 66/ACR-91 SUWAN – 1- SR (QPM)	v2v4	HYBRID
16	DMR-ESRY (POOL 18-SR) X DTMA – W	v2v5	HYBRID

17	DMR-ESRY (POOL 18-SR) X Oka Mbaise	v2v6	HYBRID
18	DMR-ESRY (POOL 18-SR) X Oka Bende-white	v2v7	HYBRID
19	PVA SYM 8 F2 (PRO VIT A) XPOOL 66/ACR-91 SUWAN – 1- SR (QPM)	v3v4	HYBRID
20	PVA SYM 8 F2 (PRO VIT A) X DTMA – W	v3v5	HYBRID
21	PVA SYM 8 F2 (PRO VIT A) X Oka Mbaise	v3v6	HYBRID
22	PVA SYM 8 F2 (PRO VIT A) X Oka Bende-white	v3v7	HYBRID
23	POOL 66/ACR-91 SUWAN – 1- SR (QPM) X DTMA – W	v4v5	HYBRID
24	POOL 66/ACR-91 SUWAN – 1- SR (QPM) X Oka Mbaise	v4v6	HYBRID
25	POOL 66/ACR-91 SUWAN – 1- SR (QPM) X Oka Bende-white	v4v7	HYBRID
26	DTMA – W X Oka Mbaise	v5v6	HYBRID
27	DTMA – W X Oka Bende-white	v5v7	HYBRID
28	Oka Mbaise X Oka Bende-white	v6v7	HYBRID

Experimental Design

The diallel was generated during the second maize planting season of August, 2015 at the Centre for Agricultural Research, School of Agriculture and Agricultural Technology Teaching and Research Farm of Federal University of Technology Owerri. Half-diallel mating method involving the parents and excluding the reciprocals (that is, 21 crosses) in the first filial was used for the study. NPK 15:15:15 was applied at equivalent rate of 300kg/ha two weeks after planting and also at tasseling. The field was also treated with furadan 3% granular formulation of carbofuran to minimize stem borer and termite attack.

The maize genotypes were planted on sandy clay loam. The experimental design was randomised complete block design with four replications. The genotypes were grown in three row plots. The experimental area measures 12 m x 12 m. The whole area was divided into four blocks with spacing of 1m between each block. Each block contains twenty eight treatments with an inter row spacing distance of 0.75 m and intra row spacing distance of 0.25 m with the row 3 m long. The maize genotypes were planted under rain-fed conditions. After harvesting, the seeds were dried to 15% moisture.

Data Collection

Data were collected for, Days to 50% emergence, Days to 50% tasseling, Leaf area (cm²), Days to maturity, Plant at harvest, Days to 50% silking, Plant height (cm), Ear height (cm), Cob length (cm), Number of rows/cob, Grain weight/cob, Field weight (FWT), Number of grains/cob, Grain weight/cob, and Grain yield (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.

Results and Discussion

Analysis of Variance

Analysis of variance (ANOVA) for growth agronomic attributes of the F₁ genotypes (Table 2) showed that the mean square for crosses were highly significant ($P = 0.05$) for days to 50% emergence, leaf area, stem girth, plant height, days to 50% tasselling, days to 50% silking and days to maturity.

The ANOVA revealed that general combining ability (GCA) is highly significant ($P = 0.01$) for all the growth agronomic traits studied except for days to maturity that is significant ($P = 0.01$). The specific combining ability (SCA) is highly significant ($P = 0.01$) for all the growth parameters measured except for days to 50% emergence that was not significant (NS) and leaf area that was significant ($P = 0.05$). The block, however, showed no significant difference among the studied traits.

ANOVA also showed that mean squares of the crosses were highly significant ($P = 0.01$) for plant stand, ear heights, field weight, cob length, number of row per cob, grain number per cob, grain weight per cob, 1000 dry seed weight and grain yield (Table 3). GCA for all the yield parameters were highly significant ($P = 0.01$) except for cob length that is not significant. The SCA for the yield attributes were highly significant except for plant stand and grain yield that were significant ($P = 0.05$).

Mean Performance

The mean performance for growth agronomic characters of the F₁ presented in Table 4 showed that there were significant differences among the genotypes in terms of vegetative attributes. The cross between DTMA-4 X PVA SYM 8 F₂ (3.75) and PVA SYM 8 F₂ X OKA BENDE-WHITE (3.75) were earliest in emergence at 3 days after planting, while DTMA-4 X DMR-ESRY, DTMA-4 X POOL 66/ACR-91, DTMA-4 X OKA BENDE-WHITE, DMR-ESRY X PVA SYM 8 F₂, DMR-ESRY X POOL 66/ACR-91, DMR-ESRY X OKA MBAISE, DMR-ESRY X OKA BENDE-WHITE, PVA SYM 8 F₂ X POOL 66/ACR-91, POOL 66/ACR-91 X OKA BENDE-WHITE emerged at 4 days after planting and DTMA-4 X DTMA – W, DTMA-4 X OKA MBAISE, DMR-ESRY X DTMA – W, PVA SYM 8 F₂ X DTMA – W, PVA SYM 8 F₂ X OKA MBAISE, POOL 66/ACR-91 X DTMA – W, POOL 66/ACR-91 X OKA MBAISE, DTMA – W X OKA MBAISE, DTMA – W X OKA BENDE-WHITE and OKA MBAISE X OKA BENDE-WHITE emerged at 5 days after planting. The percentage emergence ranges from DTMA-4 X DMR-ESRY (63.50) to DMR-ESRY X POOL 66/ACR-91 (96.61). The cross between OKA MBAISE X OKA BENDE-

WHITE (24.50), PVA SYM 8 F2 X OKA BENDE-WHITE (24.50), DMR-ESRY X OKA BENDE-WHITE (24.25) and DTMA-4 X POOL 66/ACR-91 (24.00) had the highest plant stand while DMR-ESRY X POOL 66/ACR-91 (18.75), DMR-ESRY X DTMA – W (18.00), and DTMA-4 X DTMA – W (18.00) had the lowest plant stand.

Days to 50% tasseling and silking ranges from POOL 66/ACR-91 X OKA BENDE-WHITE (41.00) to DMR-ESRY X OKA MBAISE (61.75) and PVA SYM 8 F2 X OKA BENDE-WHITE to DMR-ESRY X DTMA – W (67.75) respectively.

The highest leaf area was recorded in the cross between OKA MBAISE X OKA BENDE-WHITE (101.20 cm²) while DMR-ESRY X DTMA – W (32.70 cm²) had the smallest leaf area. Highest plant height was recorded in OKA MBAISE X OKA BENDE-WHITE (247.20 cm) while the shortest height was recorded in the cross between DTMA-4 X DTMA – W (97.20 cm). The stem girth ranges from PVA SYM 8 F2 X DTMA – W (0.50 cm) to DTMA – W X OKA BENDE-WHITE (1.33 cm).

Table 5 showed the mean performance for yield characteristics of the F1 genotypes which all had significant difference (P = 0.05).

The crosses between DTMA-4 X POOL 66/ACR-91 (89.50), PVA SYM 8 F2 X Oka Bende-white (96.00), PVA SYM 8 F2 X POOL 66/ACR-91 (96.75), DTMA-4 X Oka Bende-white (98.25) and DTMA-4 X DMR-ESRY (98.50) were the earliest in maturity while DTMA – W X OKA MBAISE (132), PVA SYM 8 F2 X OKA MBAISE (130.50), DMR-ESRY X OKA MBAISE (132.30), DTMA-4 X Oka Mbaise (129.30) and OKA MBAISE x OKA BENDE-WHITE (129.00) were late maturing. The cross between DTMA-4 X OKA BENDE-WHITE had the highest plant at harvest (17) while DMR-ESRY X PVA SYM 8 F2 had the least plant at harvest (9.50). Ear height ranges from DTMA-4 X DMR-ESRY (108.00) to OKA MBAISE X OKA BENDE-WHITE (135.00) among the cross. The highest cob length was recorded in the crosses between DTMA-4 X OKA BENDE-WHITE (16.12), DTMA-4 X OKA MBAISE (15.13), POOL 66/ACR-91 X DTMA – W (14.50), DMR-ESRY X OKA MBAISE (14.25), OKA MBAISE X OKA BENDE-WHITE (14.00) and the least recorded in the cross between DTMA-4 X DMR-ESRY (10.50).

The number of row per cob and number of grains per cob ranges amongst the crosses from DTMA-4 X DTMA – W (10.00) to OKA MBAISE X Oka Bende-white (15.25) and DTMA-4 X DTMA – W (180.00) to OKA MBAISE X OKA BENDE-WHITE (347.00) respectively. The highest grain weight per cob was recorded in the cross between OKA MBAISE X OKA BENDE-WHITE (1.62 Kg) and the least between DTMA-4 X DMR-ESRY (0.34 Kg). The

highest field weight was recorded in the cross between PVA SYM 8 F2 X OKA BENDE-WHITE (181.40 kg) followed by DMR-ESRY X Oka Bende-white (177.80 kg) and OKA MBAISE X OKA BENDE-WHITE (156.50 kg). The least field weight of 111.80 kg was recorded in the cross between DTMA-4 X DTMA – W.

Highest 1000 dry seed weight was recorded in the cross between OKA MBAISE X OKA BENDE-WHITE (606.90 kg) and least was recorded in the cross between PVA SYM 8 F2 X DTMA – W (430.40 kg). The cross between DTMA-4 X OKA BENDE-WHITE (3.63 t/ha) had the highest grain yield, followed by POOL 66/ACR-91 X OKA MBAISE (3.43 t/ha), DTMA-4 X OKA MBAISE (3.40 t/ha), POOL 66/ACR-91 X DTMA – W (3.26 t/ha), PVA SYM 8 F2 X POOL 66/ACR-91 (3.23 t/ha), DMR-ESRY X OKA MBAISE (3.21 t/ha), OKA MBAISE X OKA BENDE-WHITE (3.15 t/ha) and PVA SYM 8 F2 X OKA MBAISE (3.15 t/ha). The cross between DTMA-4 X DMR-ESRY (2.36 t/ha) had the lowest grain yield.

Table 2: Combined analysis of variance for growth agronomic attributes of the F1 genotypes of the seven maize genotypes

Source of Variation	Df	Days to 50 % Emergence	Percentage emergence	Leaf area	Stem girth	Plant height (cm)	Days to 50% tasselling	Days to 50% silking	Days to maturity
Block	3	0.08 ^{NS}	51.21 ^{NS}	64.74 ^{NS}	0.01 ^{NS}	235.37 ^{NS}	1.10 ^{NS}	12.56 ^{NS}	11.41 ^{NS}
Cross	27	1.58 ^{**}	248.46 ^{**}	2161.34 ^{**}	0.16 ^{**}	4953.02 ^{**}	294.56 ^{**}	189.33 ^{**}	1018.97 ^{**}
GCA	6	5.99 ^{**}	623.60 ^{**}	8395.61 [*]	0.62 ^{**}	18480.30 ^{**}	930.40 [*]	414.07 ^{**}	4165.64 [*]
SCA	21	0.31 ^{NS}	141.28 ^{**}	380.12 [*]	0.03 ^{**}	1088.09 ^{**}	112.90 [*]	125.12 ^{**}	119.92 ^{**}
Error	81	0.23	59.22	187.91	0.02	211.99	9.02	11.97	29.52

*, ** = Significant at P = 0.05 and 0.01, respectively. NS = Non significant

Table 3: Combined analysis of variance for agronomic characteristics of the F1 genotypes of the seven maize genotypes

Source of Variation	of	Df	plant sand	Field weight (kg)	Cob length (cm)	Number of row per cob	Grain per cob	no Grain weight per cob	1000 seed weight	dry weight	Grain yield (t ha ⁻¹)
Block		3	4.54 ^{NS}	5.08 ^{NS}	1.22 ^{NS}	0.67 ^{NS}	11461.60 ^{**}	0.01 ^{NS}	1802.84 ^{NS}		1.69 [*]
Parents		6	144.32 ^{**}	2590.50 ^{**}	20.33 ^{**}	28.91 ^{**}	33844.00 ^{**}	0.002 ^{NS}	29324.00 ^{**}		1.31 ^{**}
Crosses		27	20.36 ^{**}	2137.73 ^{**}	12.83 ^{**}	9.27 ^{**}	18480.27 ^{**}	1.34 ^{**}	13302.60 ^{**}		1.71 ^{**}
GCA		6	40.94 ^{**}	3205.23 ^{**}	6.27 ^{NS}	16.33 ^{**}	37518.74 ^{**}	0.53 ^{**}	16674.90 ^{**}		2.56 ^{**}
SCA		21	14.47 [*]	1832.73 ^{**}	14.71 ^{**}	7.26 ^{**}	13040.71 ^{**}	1.57 ^{**}	12339.10 ^{**}		1.47 [*]
Parents x Crosses	x	1	28.3 ^{NS}	0.6 ^{NS}	158.54 ^{**}	13.32 ^{NS}	44.30 ^{NS}	11.12 ^{NS}	134.32 ^{NS}		0.83 [*]
Error		81	8.29	202.44	2.94	1.783	2440.28	0.15	2925.33		0.16

*, ** = Significant at P = 0.05 and 0.01, respectively. NS = Non significant

Table 4: Mean values for growth agronomic attributes of seven open pollinated maize genotypes and their F₁ progenies

Genotypes	Days to 50% emergence	to Percentage emergence	Plant stand	Days to 50% tasseling	Days to 50% silking	Leaf area (cm ²)	Plant height (cm)	Stem girth (cm)	Ear height (cm)
DTMA-4	4.23	59.98	34.22	39.71	50.77	46.14	114.60	0.88	108.26
DMR-ESRY	3.98	84.83	31.97	39.46	56.27	31.34	111.60	0.93	97.06
PVA SYM 8	3.98	62.88	26.72	53.46	64.52	43.24	121.10	0.85	110.06
POOL 66	3.73	64.98	31.97	37.21	2.52	37.94	122.90	0.95	111.86
DTMA-W	3.98	85.01	16.47	54.46	67.27	30.84	106.90	0.85	52.86
Oka Mbaise	4.73	76.23	30.97	59.46	64.77	70.74	218.40	0.98	103.06
Oka Bende	3.50	81.56	35.72	37.21	57.77	73.74	168.70	1.05	119.26
v1v2	4.50	63.50	19.25	50.00	62.50	42.30	122.50	0.70	108
v1v3	3.75	91.15	23.25	58.75	67.25	44.20	110.50	0.70	134.3
v1v4	4.25	94.82	24.00	51.75	63.75	45.20	116.80	0.95	121.3
v1v5	5.50	76.07	18.00	59.75	65.00	40.30	97.20	0.68	118.5
v1v6	5.00	76.50	23.25	61.25	67.50	71.30	182.20	1.13	124.8
v1v7	4.00	86.92	25.00	42.25	53.50	86.20	178.50	0.98	133.8
v2v3	4.00	93.57	17.50	55.50	65.50	48.80	115.20	0.58	114.8
v2v4	4.25	96.61	18.75	47.50	58.75	42.20	120.00	0.78	110.8
v2v5	5.00	82.52	18.00	61.25	67.75	32.70	105.20	0.55	114
v2v6	4.75	77.68	24.75	61.75	66.75	79.30	149.20	0.80	120.8
v2v7	4.00	85.28	24.25	48.25	56.75	78.50	135.50	0.75	125.8
v3v4	4.25	91.12	21.00	50.75	62.25	48.90	124.00	0.78	120.8
v3v5	5.25	83.54	20.25	60.25	67.00	41.50	101.80	0.50	120.3
v3v6	5.00	79.88	23.25	59.50	62.50	92.00	134.20	0.80	113
v3v7	3.75	92.50	24.50	43.00	47.75	91.00	134.50	0.75	125.8
v4v5	5.00	81.96	19.50	60.50	65.00	52.70	115.80	0.80	114.8
v4v6	5.00	85.92	20.75	60.25	60.50	84.40	160.80	1.18	127.3
v4v7	4.25	94.00	21.75	41.00	49.50	86.50	165.50	1.03	127
v5v6	5.25	80.10	23.00	60.75	64.50	87.80	126.80	0.70	121.5
v5v7	5.00	88.73	23.25	59.75	65.25	89.10	139.80	0.73	128.3
v6v7	5.00	92.32	24.50	58.75	64.75	101.20	247.20	1.33	135
Mean Parent	4.02	73.64	29.72	45.85	51.98	47.71	137.74	0.93	100.35
Mean crosses	4.61	86.56	21.93	55.13	62.08	67.19	138.04	0.83	128.04
SED (0.05) Parent	0.59	7.71	5.39	4.59	5.75	23.77	32.85	NS	37.27
SED (0.05) crosses	0.67	10.83	4.05	4.23	4.87	19.29	20.48	0.20	13.48
SED (0.05) P vs C	0.32	NS	0.44	0.11	NS	NS	7.46	NS	NS

NS = non-significant

Table 5: Mean values for yield agronomic attributes of seven open pollinated maize genotypes and their F₁ progenies

Genotypes	Days to maturity	Plant at harvest	Cob length (cm)	Number of row per cob	Number of grain per cob	Grain weight per cob(kg)	Field weight (kg)	1000weight (g) seed	Grain yield (t ha ⁻¹)
DTMA-4	88.91	28.18	10.23	12.33	187.00	0.37	109.92	445.00	2.42
DMR-ESRY	102.41	25.93	8.86	8.83	73.80	0.37	92.42	363.00	2.02
PVA SYM 8	104.11	20.68	9.73	9.58	92.80	0.36	79.92	395.00	1.74
POOL 66	91.11	25.93	9.99	10.58	100.80	0.37	77.42	333.00	1.68
DTMA-W	60.41	10.43	5.39	5.08	81.10	0.32	54.92	180.00	1.18
Oka Mbaise	145.11	24.93	9.99	12.33	102.80	0.38	112.42	358.00	2.47
Oka Bende	101.91	29.68	12.99	12.58	293.80	0.37	129.92	395.00	2.86
v1v2	98.50	11.25	10.50	12.5	247.00	0.34	139.50	449.10	2.36
v1v3	104.80	15.25	11.80	13	278.00	1.24	138.20	448.60	2.67
v1v4	89.50	16.00	11.25	10.75	231.00	1.41	137.20	467.10	2.53
v1v5	103.00	10.00	12.75	10	180.00	0.91	111.80	431.10	2.87
v1v6	129.30	15.25	15.13	14.25	257.00	1.56	138.20	484.10	3.4
v1v7	98.25	17.00	16.12	13	210.00	1.46	158.00	546.30	3.63
v2v3	114.50	9.50	11.78	10.75	165.00	1.22	119.80	487.90	2.65
v2v4	102.50	10.75	12.25	12.25	227.00	0.74	127.20	473.10	2.76
v2v5	113.30	10.00	13.13	12.25	151.00	0.65	125.80	461.00	2.95
v2v6	132.30	16.75	14.25	14.5	270.00	1.53	145.50	509.40	3.21
v2v7	100.80	16.25	13.38	14	320.00	1.18	177.80	526.50	3.01
v3v4	96.75	13.00	14.38	10.75	177.00	0.66	115.80	504.50	3.23
v3v5	103.50	12.25	13.75	11.75	150.00	1.09	116.20	430.40	3.09
v3v6	130.50	15.25	14.00	13.25	215.00	1.09	150.50	506.90	3.15
v3v7	96.00	16.50	13.75	14.25	205.00	1.47	181.40	508.00	3.09
v4v5	111.80	11.50	14.50	12.25	237.00	1.18	112.50	439.40	3.26
v4v6	136.00	12.75	15.25	12.75	251.00	1.27	142.00	519.30	3.43
v4v7	98.25	13.75	12.88	12.75	345.00	1.58	133.80	541.40	2.9
v5v6	132.00	15.00	11.25	12.25	216.00	1.21	130.00	482.60	2.53
v5v7	105.50	15.25	11.38	13.5	243.00	1.52	147.50	467.10	2.56
v6v7	129.00	16.50	14.00	15.25	347.00	1.62	156.50	606.90	3.15
Mean Parent	99.14	23.68	9.60	10.19	133.16	0.36	93.85	352.71	2.053
Mean crosses	116.30	14.49	13.87	13.30	246.10	1.25	145.26	514.54	3.12
SED (0.05) Parent	38.81	5.41	3.81	3.54	71.52	NS	46.15	137.6	1.04
SED (0.05) crosses	7.64	4.05	2.42	1.879	69.50	0.55	20.14	76.1	0.544
SED (0.05) P vs C	0.52	NS	0.01	0.02	NS	NS	0.05	0.08	0.06

NS: non-significant

Discussion

Knowledge about germplasm diversity and relationships among diverse germplasm is useful for plant breeders because it assists them to select suitable parents for crossing (Dwivedi *et al.*, 2001). In the development of maize for fresh maize production, two factors are considered important; characteristics of the inbred line itself and behavior of the inbred line in a particular hybrid combination.

The highly significant genotype effect obtained for the agronomic parameters indicated that enough variability exists to allow identification of local germplasm with reasonable levels of desirable agronomic characteristics. This observation supports the earlier report by Ngwuta *et al.* (2001) that locally available germplasm can serve as sources of hybrid maize development.

The genotypes are morphologically differentiated and identified using morphological traits. The significant difference recorded in days to 50% emergence could be as a result of the differences in the thickness of seed coat and tissue layer, which agrees with the earlier report on maize (Prasanna *et al.* 2001). The differences observed on the number of days to 50% tasseling and silking were mainly due to varietal differences among the examined genotypes. However, the ANOVA suggested presence of ample genetic variability amongst the genotypes. Shahrokhi and khorsani (2013) also observed significant variation amongst maize genotypes for stem girth, plant height, ear height, days to maturity, number of grain per cob and grain yield. Ahmed (2013) also observed significant variation among maize genotypes for days to 50% emergence, days to 50% tasseling, days to 50% silking, days to maturity, plant height, ear height, cob length, 1000 grain weight and grain yield.

The ultimate goal of a plant breeding program is higher grain yield. The result from this study showed significant variation amongst maize genotypes for grain yield.

Similar results for grain yield suggesting heterotic effects in different cross combinations of maize hybrid have been reported by Venugopal *et al.* (2002), and Joshi *et al.* (2002).

The assessment of the agronomic attributes of the parents and the crosses indicated that the variety crosses are superior to the parents in most of the traits studied. The significant differences observed between the parents and the crosses are suggestive of the occurrence of heterosis in most of the agronomic attributes.

In terms of flowering and maturity, the crosses flowered and matured earlier than the parents. Furthermore, crosses involving the earliest parents; DTMA-4 and POOL 66/ACR-91 with BENDE-WHITE resulted in progenies which were earlier than the mean of the entire crosses.

This suggests that they may be exploited for use in developing early maturing maize variety. Early maturing maize can be very useful in areas where rainfall regime is short and unpredictable in order to escape short duration drought.

Conclusion and Recommendation

The means sum of squares due to genotypes from the present study indicated highly significant differences ($P = 0.01$) for yield and other agronomic characters studied, thus revealed the presences of substantial genetic variability among the evaluated genotypes.

It was observed that the cross between DTMA-4 X OKA BENDE-WHITE and POOL 66/ACR-91 X OKA MBAISE are higher yielding genotypes with 3.63 t/ha and 3.43 t/ha respectively.

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