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A COMPARATIVE STUDY OF HERITABILITY AND COMBINING ABILITY IN MAIZE VARIETIES OF SOUTHEASTERN NIGERIA: IMPLICATIONS FOR BREEDING PROGRAMS

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Abstract

This study aims to determine heritability and combining ability estimates among seven maize (Zea mays. L) Varieties from southeastern Nigeria, comprising two local and five improved genotypes. Eight agronomic traits were evaluated using a diallel cross, and the data were analyzed using Griffing's method II and model I for fixed effects. The experiment was conducted in the late planting season of 2015 at the Center for Agricultural Research, School of Agriculture and Agricultural Technology, Federal University of Technology Owerri, Nigeria, employing a randomized complete block design (RCBD) with four replications. Findings revealed significant differences between the entries for the studied traits, with varying degrees of heritability and combining ability. These results contribute valuable information for maize breeders in southeastern Nigeria and can inform future breeding efforts to improve maize varieties in the region

1.0 Introduction

Maize (*Zea mays. L*) is one of the most important sources of carbohydrates, protein, minerals and fats for humans and animals and also a good source of raw materials for industries. The word ‘DIALLEL’ is a Greek term and implies all possible cross combinations between male and female animals or crops in set or collection. “Diallel cross” has been defined as the set of all possible mating combinations among several genotypes used as parents. Diallel cross mating methods have been widely used in breeding programs for the assessment of the genetic potential of parents ranging from inbred lines to large genetic base varieties (Hallauer and Miranda, 1988). Diallel analysis provides inferences on genetic control of the traits under investigation. As observed by Hallauer and Miranda (1988), the diallel mating designs has been used and abused more extensively than any other in maize and other plant species. However, the diallel mating designs can be very valuable if properly analyzed and interpreted (Hallauer and Miranda, 1988). Much of the abuse of diallel is due to the presence of two models for diallel analysis: a random model and a fixed model. The main

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quandary seems to arise from interpretations and inferences that can be made about estimates obtained from analysis of the diallel crosses (Hallauer and Miranda, 1988).

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 foe human and animal consumption, especially because of a low content of essential amino acids such as lysine and tryptophan (Prasanna *et al.* 2001). Quality protein maize (QPM) is nutritionally improved maize that that possesses twice the quality of lysine and tryptophan compared with non-QPM.

QPM 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). From a nutritional quality preservation point of view, little is known about the response of QPM nutritional parameters when subjected to different storage conditions as practiced by small scale farmers on their farms, as well as commercial storage conditions (Hell *et al.*, 2000). The conservation of genetic in germplasm banks and breeder conditions assumes genetic stability during storage. According to Tsugio (2001), retaining the viability of seeds during long periods of storage is the first priority of gene banks.

Xingming *et al*. (2004) evaluated combining ability and heterotic groups of yellow QPM inbreds and observed significant differences among the crosses and GCA of lines for grain yield, plant height, rows per ear, kernels per row and thousand seed weight; and nonsignificant difference in SCA mean squares for all traits.

Hadji (2004) evaluated the combining ability of 10 white QPM inbred lines and reported significant GCA mean squares for days to anthesis, ear and plan height, ears per plant, ear length, ear diameter, rows per ear, kernels per rows, kernel weight, endosperm hardness and grain yield and significant SCA mean squares for all these traits except endosperm hardness. He reported the dominance of GCA effects for most of the traits studied except for ear length, kernels per row and grain yield. Fan *et al*. (2004) analyzed the combining ability of 10 yellow QPM inbreds from CIMMYT and China, and reported significant GCA and SCA effects for grain yield and contributing traits.

As maize fills the hunger gap while other crops are still in the field, the question arises as to how to produce maize that is of high nutritional quality and in high quantity. Thus, the objectives of this work were to; Develop maize type for fresh maize production and evaluate maize genotypes for growth and yield characteristics.

2.0 Materials and Methods

The project was carried out at the Center for Agricultural Research farm of the School of Agriculture and Agricultural Technology, Federal University of Technology Owerri, Nigeria (5'27' N and 7'02'E). The location has a mean temperature of 290C, a relative humidity of 89 % during the day in the rainy season and an altitude of 50m above sea level.

Two of the seven maize genotypes used in this study were local varieties; Oka Mbise and Oka Bende White collected from Imo State and Abia State respectively, while the rest are improved varieties collected from International Institute for Tropical Agriculture (IITA) (Table 1). The improved genotypes from IITA have emphases for; protein, sugar, vitamin A contents as well as taste and softness whereas the local ones are the leading cultivars in different parts of Southeast Nigeria. The crosses made from these seven genotypes were evaluated using randomized complete block design (RCBD) with four replications using 3 m row plots with inter row spacing distance of 0.75m and intra row spacing distance of 0.25m. Data collected were subjected to analysis of variance (ANOVA) and those that were found significant (P = 0.05) were subjected genetic analysis using Griffing's method II and model I for fixed effects.

Table 1: Genotype code, name of the genotype and collection site for the local openpollinated and improved maize genotypes evaluated for developing maize for fresh maize production

Genotype code	Name of genotype	Collection site IITA,
GEN1	DTMA-4	Ibadan
GEN2	DMR-ESRY (POOL 18-SR)	IITA, Ibadan
GEN3	PVA SYM 8 F2 (PRO VIT A)	IITA, Ibadan
GEN4	POOL 66/ACR-91 SUWAN – 1- SR (QPM)	IITA, Ibadan
GEN5	DTMA – W	IITA, Ibadan
GEN6	Oka Mbaise,	Mbaise, Imo State
GEN7	Oka Bende-white	Umuahia,Abia State

2.1 Cultural Practices

Two seeds were planted per hill and later thinned to one. Weeding was done manually using hand hoe as at required. Inorganic fertilizer, NPK 15:15:15, was applied at the rate of 400 kg/ha split, first at planting and later at anthesis. Furadan 3 % granular formulation of carbofuran (insecticides) was dropped into the funnel of the young seedlings three weeks after planting to control stem borers.

2.2 Data Collection

Data were collected on some agronomic characteristics such as:

i. Days to 50 % emergence: This is the number of days it took half of the plants in a plot to emerge.

ii. Days to maturity: determined by calculating the days from planting to "physiological maturity" or black layer formation.

iii. Ear height (cm). iv. Cob length: This was measured using measuring tape.

v. Number of row/cob: measured by counting. vi. Number of grain/cob: measured by counting. vii. Grain weight/cob: The weight in g of deshelled cob. viii. Field weight (FWT): The weight in kg of all the dehusked ears in each plot.

ix. Grain yield (t/ha) adjusted to 15% moisture and based on 80% shelling percentage was calculated as;

$$\text{Grain yield} = \frac{\text{FWT}}{1000} \text{ X } \frac{(100 - \text{Moisture }\%) \text{ x Plot size}}{85 \text{ x } 10000}$$

2.0 Results and Discussion

Genotypes were significantly different (P = 0.05) in all the traits studied (Table 1). Furthermore, 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, DMRESRY 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 BENDEWHITE and OKA MBAISE X OKA BENDE-WHITE emerged at 5 days after planting (Table 2). 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). Highest 1000 dry seed weight was recorded in the cross between OKA MBAISE X OKA BENDE-WHITE (606.90g) and least was recorded in the cross between PVA SYM 8 F2 X DTMA – W (430.40 g). The cross between DTMA-4 X DMR-ESRY (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 (3.15t/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.

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.

Table 2: Mean performance of maize genotypes

Genotypes	Days to 50% emergence	Days to maturity	Ear height (cm)	Cob length (cm)	Number of row per cob	Number of grain per cob	Grain weight per cob(kg)	Field weight (kg)	1000 seed weight (g)	Grain yield(t ha^{-1})
DTMA-4	4.23	88.91	108.26	10.23	12.33	187	0.37	109.92	445	2.42
DMR-ESRY	3.98	102.41	97.06	8.86	8.83	73.8	0.37	92.42	363	2.02
PVA SYM 8	3.98	104.11	110.06	9.73	9.58	92.8	0.36	79.92	395	1.74
POOL 66	3.73	91.11	111.86	9.99	10.58	100.8	0.37	77.42	333	1.68
DTMA–W	3.98	60.41	52.86	5.39	5.08	81.1	0.32	54.92	180	1.18
Oka Mbaise	4.73	145.11	103.06	9.99	12.33	102.8	0.38	112.42	358	2.47
Oka Bende	3.5	101.91	119.26	12.99	12.58	293.8	0.37	129.92	395	2.86
Gen1 x Gen2	4.5	98.5	108	10.5	12.5	247	0.34	139.5	449.1	2.36
Gen1 x Gen3	3.75	104.8	134.3	11.8	13	278	1.24	138.2	448.6	2.67
Gen1 x Gen4	4.25	89.5	121.3	11.25	10.75	231	1.41	137.2	467.1	2.53
Gen1 x Gen5	5.5	103	118.5	12.75	10	180	0.91	111.8	431.1	2.87
Gen1 x Gen6	5	129.3	124.8	15.13	14.25	257	1.56	138.2	484.1	3.4
Gen1 x Gen7	4	98.25	133.8	16.12	13	210	1.46	158	546.3	3.63
Gen2 x Gen3	4	114.5	114.8	11.78	10.75	165	1.22	119.8	487.9	2.65
Gen2 x Gen4	4.25	102.5	110.8	12.25	12.25	227	0.74	127.2	473.1	2.76
Gen2 x Gen5	5	113.3	114	13.13	12.25	151	0.65	125.8	461	2.95

Gen2 x Gen6	4.75	132.3	120.8	14.25	14.5	270	1.53	145.5	509.4	3.21
Gen2 x Gen7	4	100.8	125.8	13.38	14	320	1.18	177.8	526.5	3.01
Gen3 x Gen4	4.25	96.75	120.8	14.38	10.75	177	0.66	115.8	504.5	3.23
Gen3 x Gen5	5.25	103.5	120.3	13.75	11.75	150	1.09	116.2	430.4	3.09
Gen3 x Gen6	5	130.5	113	14	13.25	215	1.09	150.5	506.9	3.15
Gen3 x Gen7	3.75	96	125.8	13.75	14.25	205	1.47	181.4	508	3.09
Gen4 x Gen5	5	111.8	114.8	14.5	12.25	237	1.18	112.5	439.4	3.26
Gen4 x Gen6	5	136	127.3	15.25	12.75	251	1.27	142	519.3	3.43
Gen4 x Gen7	4.25	98.25	127	12.88	12.75	345	1.58	133.8	541.4	2.9
Gen5 x Gen6	5.25	132	121.5	11.25	12.25	216	1.21	130	482.6	2.53
Gen5 x Gen7	5	105.5	128.3	11.38	13.5	243	1.52	147.5	467.1	2.56
Gen6 x Gen7	5	129	135	14	15.25	347	1.62	156.5	606.9	3.15
LSD(P=0.05)	0.67	7.64	13.48	2.42	1.879	69.5	0.55	20.14	76.1	0.544
CV%	10.4	5	8.1	13.7	10.9	23	43.3	11	11.6	13.7

The variance components, genotypic coefficient of variation and phenotypic coefficient of variation are presented in Table 3. Genotypic variance (σ^2G) estimates for the studied traits were generally greater than the environmental variances except for percentage emergence, plant stand and ear height.

Generally, the environmental variances were very low and in some cases negligible. The phenotypic variances (σ^2ph) of all the traits were higher than the genotypic variances (σ^2G); similarly, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV).

The highest PCV was recorded for grain weight per cob and grain yield which were 80.14 and 36.90% respectively, the GCV ranged from 7.93% (ear height) to 67.44% (grain weight per cob).

Table 3: Variance components, genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) estimates of some agronomic attributes of seven (7) maize genotypes

Source of variation	σ^2G	σ^2e	σ^2ph	GCV(%)	PCV(%)
Days to 50 % Emergence	0.34	0.22	0.57	12.76	16.48
Days to maturity	252.39	28.87	281.9	14.49	15.31
Ear height (cm)	88.57	91.79	180.36	7.93	11.32
Field weight (kg)	574.39	195.39	776.83	18.41	21.41
Cob length (cm)	3.12	2.89	6.07	14.07	19.62
Number of row per cob	2.18	1.74	3.96	12.08	16.3
Grain number per					

cob	4598.91	2440.28	7039.19	31.56	39.04
Grain weight per cob	0.37	0.15	0.53	67.44	80.14
1000 dry seed weight	3117.3	2885.25	6042.63	11.96	16.65
Grain yield (t ha^{-1})	0.72	19.3	1.09	23.73	36.9

The heritability of these traits showed that days to maturity (89.53%), field weight (73.94%), grain weight per cob (70.80%), and grain yield (62.84%) had high (> 60%) heritability estimates and Days to 50% emergence (59.90%), number of row per cob (54.95%), 1000 dry seed weight (51.59%), cob length (51.45%) and ear height (49.11%) had moderate heritability (35 – 59%) (Table 4).

The coefficients of variation obtained showed that most of the traits had less than 25% CV estimates except for grain weight per cob that had moderate (43.30%) CV estimate (CV% = 25 –59%) while the GCA – SCA ratio was less than unity (Table 4).

Table 4: Components of general combining ability (GCA), specific combining ability (SCA), grand mean, heritability and coefficient of variation estimates of some agronomic attributes of seven (7) maize genotypes.

Source of variation	GCA	SCA	GCASCA ratio	Grand mean	h^2 bs(%)	CV%
Days to 50 % Emergence	0.16	0.02	7.5	4.58	59.9	10.4
Days to maturity	114.89	22.6	5.08	109.65	89.53	5
Field weight (kg)	83.41	407.57	0.2	130.2	73.94	11
Cob length (cm)	0.09	2.94	0.03	12.56	51.45	13.7
Number of row per cob	0.4	1.37	0.3	12.21	54.95	10.9
Grain number per cob	974.4	2650.11	0.37	214.9	65.33	23
Grain weight per cob	0.01	0.35	0.03	0.91	70.8	43.3
1000 dry seed weight	381.93	2353.44	0.16	466.8	51.59	11.6
Grain yield (t ha^{-1})	0.03	2363.44	0.66	2.83	62.84	13.7

Linear correlation coefficient (r) values between the traits are presented in Table 5. The results showed significant (P = 0.05) positive correlation between days to 50% emergence and days to maturity (r = 0.55**). There was very significant correlation (P = 0.01) between cob length and grain yield (r = 1.00*). There was also a high significant positive correlation between 1000 dry seed weight and number of row per cob (r = 0.57**), number of grain per cob (r = 0.58**) and field weight (r = 0.59**).

Table 5: Correlation matrix of agronomic characteristics of the maize genotypes

	Days to 50% emergence	*Days to maturity*	*Ear height (cm)*	*Cob length (cm)*	*Number of row per cob*	*Number of grain per cob*	*Grain weight per cob(kg)*	*Field weight (kg)*	*1000weight (kg) seed*	*Grain yield(t ha-1)*
Days to 50% emergence										
Days to maturity	0.55**									
Ear height (cm)	-0.22	0.04								
Cob length (cm)	0.09	0.3	0.33							
Number of row per cob	-0.07	0.41	0.46	0.33						
Number of grain per cob	-0.18	0.15	0.50*	0.02	0.64**					
Grain weight per cob(kg)	-0.07	0.25	0.72**	0.31	0.51*	0.48				
Field weight (kg)	-0.42	0.01	0.47	0.18	0.75**	0.48	0.43			
1000 dry seed weight	-0.24	0.27	0.54*	0.44	0.57**	0.58**	0.49	0.59**		
Grain yield(t ha-1)	0.09	0.3	0.33	1.00**	0.33	0.02	0.31	0.18	0.43	

*** =** Correlation is significant (P=0.05), ** = Correlation is highly significant (P=0.01)

The genetic constitution of crops does not change in different environments with respect to qualitative traits. Correlation is also an important measurement indicating that traits which should be given importance to increase yield. In this experiment, one association showed positive significant with yield, that is, cob length/grain yield. Positive significant correlation between cob length and grain yield per plant had also been recorded by salami *et al.* (2007). The positive and significant correlation between traits suggested additive genetic model thereby less affected by environmental fluctuation.

Heritability estimates is of tremendous significance to the breeder, as its magnitude indicates the accuracy with which a genotype can be recognized by its phenotypic expression. Most of the traits studied showed high heritability.

The assessment of the agronomic attributes of the parents and crosses indicated that the variety crosses are superior to the parents in most of the traits. The significant differences observed between the parents and the crosses is suggestive of the occurrence of heterosis in the following attributes; days to 50% emergence, ear height, field weight, cob length, and grain yield. Genotype DTMA-4 showed outstanding trait for earliness, it was not only the earliest but nearly all the hybrids involving it were earlier than the mid – parent. This shows that DTMA-4 will contribute in any breeding effort to develop early maturing maize variety.

4.0 Conclusion

Considering the results of the study, it was observed that the crosses between DTMA-4 X OKA BENDE-WHITE, OKA MBAISE X OKA BENDE-WHITE, PVA SYM 8 F2 X OKA BENDE-WHITE, POOL 66/ACR-91 X OKA BENDE-WHITE and DMR-ESRY X OKA

BENDE-WHITE had very good performances in terms of the yield parameters studied. Since the improved genotypes from IITA namely; DTMA-4, DMR-ESRY, PVA SYM 8 F (PRO VIT A), SUWAN – 1- SR (QPM) 2 and DTMA – W were bred essentially for high quality protein, high sugar content and pro-vitamin A (carotinoids) and Oka Mbaise and Oka Bende White are well adapted to southeastern Nigeria, these developed genotypes will improve the nutritional status of the region and generally the standard of living of farmers in the area. However, the chemical and nutritional contents of these developed genotypes should be studied and fine-tuned.

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