AJFAND ONLINE
Volume 10 No. 2
February 2010
ISSN 1684 5374
AFRICAN JOURNAL OF FOOD AGRICULTURE NUTRITION AND DEVELOPMENT

GENETIC VARIABILITY AND CORRELATION IN SINGLE CROSS HYBRIDS OF QUALITY PROTEIN MAIZE (*ZEA MAYS* L.)

Yusuf M*[1]

Mansir Yusuf

*Corresponding Author e-mail: mansiryusuf@yahoo.com

[1]Department of Plant Science, Faculty of Agriculture/ Inst. for Agric. Res., Ahmadu Bello University, Zaria, Nigeria.

ABSTRACT

Genetic variability and correlation were studied in 36 maize genotypes (15 single cross hybrids, 9 parents and 12 checks), with 26 quality protein maize genotypes among them. They were evaluated at Samaru, Northern Guinea Savanna Zone of Nigeria for two years, 2005 and 2006. The experimental design used was partial lattice design with three replications. Analysis of variance revealed significant differences for all the traits observed. Highest grain yield of 9.5t/ha was obtained from the hybrid: CML178 x CML181.The mean plant height of the genotypes ranged from 51-136cm for the inbred parent CML177 and the hybrid, CML181 x CML176.Significant differences were observed among the genotypes, indicating that they were genetically distinct with regard to the genes controlling the expression of this character. Similarly ear height ranged from 13-53cm, indicating wide variability for this character among the genotypes. Days to maturity which is a baseline for selection of early maturing genotypes ranged from 67-109 days. The inbred parent CML493 had the lowest days to maturity (67-days). This indicates that this inbred parent can be included in cross combinations for selection of early maturity. Highly significant correlation was observed between ear height and plant height ($p<0.01$). Similarly, days to silking and tasselling correlated positively and significantly at $p<0.05$. Grain yield correlated positively and significantly with one thousand seed weight ($p<0.05$). Number of leaves per plant had a significant positive correlation with ear height at $p<0.05$, indicating that these traits could be selected together for simultaneous improvement. The phenotypic coefficients of variations were higher than the genotypic coefficients of variations for all the traits studied. Thousand seed weight had the highest genotypic coefficients of variation. The highest genetic gain was obtained for plant height. Thousand seed weight and ear height also recorded high genetic gain. It is anticipated that these findings will be useful in future breeding programmes involving this very important crop.

Key words: Genetic Variability, Maize, Hybrids, Correlation

INTRODUCTION

Maize contributes 15% (more than 50 million tonnes) of protein and 19% of the calories derived from food crops in the world's diet [1]. During the period 1980 to 1997, maize production in Africa grew at an average annual rate of about two percent per annum. The average yield of the crop during this period was about one tonne per hectare [2]. Of the three major developing regions of the world, Africa is the only one in which the index of *per capita* food production has declined steadily during the last two decades [3]. As a result, the specter of hunger and malnutrition is perpetually hanging over the countries of the continent where an estimated 35 percent of the population, some 140 million people, largely children and women suffer from hunger and malnutrition [4]. In Nigeria, maize is one of the most important cereal crops, its production has progressively increased over the years with estimated national outputs reaching 7.68million tonnes in 1995 [5] and the projected production and demand by the year 2010 is put at 13.4million tonnes [6]. The bulk of maize produced in Nigeria is used directly for human consumption as well as infant nutrition in form of porridge during weaning period without any protein supplement such as egg, meat or beans, which are comparatively more costly especially in rural areas. The development of maize varieties and hybrids with high yield potential, improved nutritional quality and improved adaptation to various environments is important to increasing productivity in the diverse production environments. Useful maize inbred lines, varieties, and hybrids have been commonly selected from adapted tropical germplasm for the different growing environments in West and Central Africa [7]. Furthermore, broadening and diversifying the genetic base of adapted maize germplasm through the introduction of new genetic variation can further enhance progress for selection for both grain yield and stability of performance. Exotic germplasm has been suggested as potential source of new beneficial alleles for introgression into adapted germplasm to increase the variability in both qualitatively and quantitatively inherited traits [8, 9]. In tropical areas of West and Central Africa, landraces, temperate and introduced tropical germplasm can be potential sources of unique alleles useful for breeding programs [10].

Quality protein maize is nutritionally superior to normal maize in that it contains the essential amino acids, lysine and tryphtophan. The low level of these essential amino acids in the diets has led to the breeding of improved varieties to improve the nutritional status of individuals who depend primarily on maize for sustenance. In order to meet with increasing demand for maize in Nigeria as human food, feed for livestock, industrial raw material, there is urgent need to increase its productivity. The aim of this research is, therefore, to determine genetic variability in some single cross hybrids of quality protein maize and to establish the relationship between key morphological traits and yield. Such information will be valuable for both maize production and breeding purposes to produce suitable varieties and synthetics for Nigeria.

MATERIALS AND METHODS

Fifteen single cross hybrids, nine parents and 12 checks were evaluated during the rainy seasons of 2005 and 2006 at the Institute For Agricultural Research Farm, Samaru (11º 11´N, 07º 38´E and 686m above sea level), located in the Northern Guinea Savanna ecological zone of Nigeria. The single cross hybrids were generated in the year 2004 rainy season at the same location using partial diallele mating design. A 6x6 partial lattice design with three replications was used to evaluate the genotypes in both years. Each plot consisted of one row of 5m long, with 0.50m intra-row and 0.75m between rows spacing respectively. Three seeds were planted per hill, drilled 3-4cm deep in the ridges and thinned to two plants per hill to give a final plant density of approximately 53,000 plants per hectare. Fertilizer was applied at a rate of 120-60-60 kg N, P_2O_5 and K_2O per hectare. Weed control was done three times manually to achieve weed control, improve soil aeration and prevent root lodging.

Data collected include days to germination, emergence count, days to 50% tassel, days to 50% silk, plant height to the tip of tassel and height to first ear from the ground level, number of leaves per plant, days to maturity, one thousand seed weight, and grain yield. The data collected were subjected to analysis of variance (ANOVA). Simple Pearson linear correlation was carried out to determine the associations between the different traits observed. The mean values of the traits were used for genetic studies to determine the genotypic coefficient of variation (GCV) [11], genetic advance (GA) [12], and phenotypic coefficient of variation (PCV) [13].

RESULTS

Mean performance combined across the two years for the different agronomic traits of the various genotypes is presented in Table 1. The result showed significant differences between the genotypes for growth, yield and yield components. The most outstanding genotypes in terms of grain yield are the hybrids, CML178 x ML181, CML178 x CML493, CML181 x CML491, CML490 x CML177, DMR-ESR-W, JO-F and JO-2 with yield ranging from 7.1-9.5t/ha. Emergence count ranged from 6-18 with the genotypes, TZEE-W and DMR-ESR-W having the highest.

Days to germination ranged between 5-7 days with a mean of 5.75. The inbred line CML178 took the longest days to germinate (7-days) (Table1). Emergence count ranged from 6-18 with a mean of 12.1. The genotype TZEE-W has the highest emergence count (17.7) (Table1).The genotypes differed significantly for days to tasselling. The range observed for this character was 44-71 with a mean of 61.27 .The inbred parents CML178 and CML493 took fewest days to Tasselling, 44 and 43 days, respectively. Days to silking varied significantly among the genotypes with a range of 45-74 and a mean of 64.06 (Table 1).The inbred parents CML181 and CML492 took the longest time to silk, with both silking 74-days after sowing (Table 1).

The mean plant height of the genotypes ranged from 51-136cm for the inbred parent CML177 and the hybrid, CML181 x CML176, respectively (Table 1). Significant differences were observed among the genotypes (Table 1). Ear height ranged from 13-53cm with a mean of 34.6cm (Table 1), indicating wide variability for this character among the genotypes, which signifies an ample opportunity for the improvement of this character. The range for number of leaves per plant recorded is 6-12, with a mean of 9.88 (Table 1). Days to maturity which is a baseline for selection of early maturing genotypes ranged from 67-109 days with a mean of 101.54(Table 1). The inbred parent CML493 took the least time to mature (67-days) (Table 1). Thousand seed weight varied from 120-220g with a mean of 169.91g (Table 1). The check, JO-F has the highest one thousand seed weight (220g).

The mean grain yield ranged from 3-9t/ha with a mean of 5.46t/ha. (Table 1). The single cross hybrid, CML178 x CML181 recorded the highest yield (9.5t/ha). It out yielded the highest yielding check, DMR-ESR-W. All the hybrids out yielded their parents (Table 1) indicating heterosis for yield in the single cross hybrids. The wide variability observed for yield as a quantitatively inherited character among the genotypes means there is ample opportunity for selection among the genotypes for improvement of this important economic character. The differences in performance among the genotypes are an indication of variability which could be heritable and can be exploited in the overall process of selection in breeding programs.

The results presented in Table (2) showed that days to silking and tasselling correlated positively and significantly at $P<0.05$. Highly significant correlation was observed between ear height and plant height ($P<0.01$) (Table 2). Number of leaves per plant had a significant positive correlation with ear height at $P<0.05$. Also one thousand seed weight correlated positively and significantly with ear height ($P<0.05$). Grain yield correlated positively and significantly with one thousand seed weight (Table 2). These positive and significant associations between these characters signified that they can be selected simultaneously for improvement. There were no significant negative correlations observed in this study. Estimates of genotypic and phenotypic variances as well as coefficients of genotypic and phenotypic variations, and genetic advance are shown in Table 3. The value for genotypic variances ranged from 0.1198 for days to germination (indicating the least genotypic variation for the trait) to 605.6453 for plant height, (the highest genotypic variation), while the phenotypic variances per plant ranged from 0.6056 to 1052.4841 for the same traits, respectively.

DISCUSSION

Studies on the coefficients of variations revealed that the phenotypic coefficients of variations (PCV) were higher than the genotypic coefficients of variations (GCV) for all the traits studied. Thousand seed weight had the highest GCV of 169.2 and the trait days to silk had the highest PCV of 252.9 (Table 3). The highest genetic gain of 2073.8% was obtained for plant height and the lowest genetic gain of 0.04% was recorded for the trait number of leaves per plant. This suggests broader genetic base for plant height and narrower genetic base for number of leaves per plant among the genotypes studied.

The high PCV values observed in this study may indicate significant genotype x environment interactions for the traits. It is, therefore, suggested that the populations used in this study showed greater range of genetic variability. The high genetic gain recorded for plant height, thousand seed weight and ear height may indicate that there is a better scope for their selection for genetic improvement of this crop. The low genetic gain recorded for number of leaves per plant, days to, days to germination and emergence count signifies that there is no significant variability in these traits and hence may not be so useful in breeding program involving this crop.

CONCLUSION

The results presented in this study are exploratory in nature and could be useful in suggesting associations and variances that could be exploited in quality protein maize breeding programs, to facilitate its genetic improvement. The results from correlation study indicate that some traits could be selected and improved simultaneously. For example, improvement in one thousand seed weight could lead to improvement in grain yield. Also, increase in number of leaves per plant could lead to increase in ear height. Similarly, the characters days to silking and tasselling could be selected and improved simultaneously for breeding for early maturity, and ear height and plant height could be selected together for short stature. The overall mean performance of the genotypes signifies that there is substantial variability within the germplasm which could be used in quality protein maize breeding programs to develop suitable hybrids and varieties. The high genetic gain observed for thousand seed weight indicated that there is opportunity for improvement of this trait and consequently yield due to its positive association with it.

Table 1: Mean Performance for agronomic traits of some Quality Protein Maize Genotypes Evaluated in 2005 and 2006 at Samaru

Genotype	Days To Germ	Emergence Count	Days To Tassel	Days To Silk	Plant Height(cm)	Ear Height (cm)	No. of Leaves/Plt	Days To Maturity	1000 S.D. Wt.(g)	Grain Yield (t/ha)
CML176 x CML490	5.0	14.3	61.3	62.3	113.8	39.5	12.3	107.8	158.3	5.4
CML177 x CML178	5.3	10.7	57.3	63.0	118.0	48.5	11.0	101.0	181.3	6.7
CML178 x CML181	5.7	12.0	59.7	63.7	127.0	52.6	11.0	101.7	180.3	9.5
CML178 x CML493	6.0	11.7	64.0	65.3	118.0	42.0	10.3	103.3	190.3	7.1
CML181 x CML176	5.0	12.3	61.7	62.0	135.7	40.9	10.3	103.7	182.7	6.7
CML181 x CML437	6.0	11.3	61.0	65.3	111.2	37.9	9.3	103.3	190.3	6.8
CML181x CML490	5.3	16.0	62.7	68.0	114.4	41.2	10.7	104.0	175.0	6.3
CML181 x CML491	5.0	13.7	60.7	62.3	122.1	48.3	11.0	104.0	187.3	8.5
CML437 x CML490	4.7	12.0	57.3	61.0	111.6	43.6	10.7	101.3	173.3	7.4
CML490 x CML177	6.0	13.7	60.6	63.7	116.0	47.4	10.3	103.3	192.7	8.1
CML490 x CML492	5.7	9.7	61.0	63.0	90.1	32.3	11.0	104.7	152.7	7.7
CML491 x CML490	6.0	14.3	63.7	66.3	108.3	37.3	11.0	102.0	160.0	6.8
CML492 x CML490	6.3	14.7	64.0	65.0	91.9	31.8	10.7	102.0	183.3	6.7
CML493 x CML490	5.0	12.0	59.3	62.7	113.1	52.4	10.3	101.3	210.0	7.4
CML493 x CML492	6.0	14.3	62.0	64.3	101.4	28.3	10.3	103.0	179.7	5.6
CML176	6.3	7.3	70.3	72.7	76.5	13.2	9.3	104.0	145.7	3.4
CML177	6.3	11.7	65.0	67.3	51.4	16.3	9.3	102.7	130.0	3.5
CML178	7.0	5.7	44.3	45.3	87.5	24.7	7.3	109.0	155.3	3.6
CML181	6.3	7.7	69.7	74.5	80.6	24.1	6.7	104.7	158.0	4.3
CML437	5.7	8.7	64.0	65.0	54.3	17.4	6.3	100.3	168.0	3.4
CML490	6.0	8.7	71.0	73.3	61.2	21.3	9.3	105.1	150.0	4.3
CML491	6.0	12.0	44.3	46.7	53.7	13.1	7.3	105.7	173.7	3.7
CML492	6.0	11.0	70.7	74.0	59.9	30.5	9.3	100.7	128.0	3.7
CML493	6.3	11.0	43.3	45.3	64.1	18.5	8.7	66.7	125.0	5.3
New Kaduna	5.7	12.0	62.7	65.0	106.1	38.3	10.3	106.0	160.0	6.8
Oba-98(QPM)	6.0	11.7	61.0	64.7	113.2	45.3	7.3	103.0	206.3	4.8
Oba-Super 1	6.0	12.3	62.7	65.3	66.8	33.2	11.0	103.0	180.0	6.8
Oba-Super 2	5.0	10.7	62.3	66.7	116.1	44.9	10.3	104.7	163.3	4.8
DMR-LSR-W	5.7	11.3	62.3	63.7	115.5	38.4	10.0	101.7	206.3	6.7
TZEE-W	5.3	17.7	58.0	62.3	82.5	25.5	8.7	100.0	150.3	4.8
DMR-ESR-W	6.0	17.7	61.3	63.3	111.9	39.7	10.3	105.0	219.7	8.9
SUWAN-1-SR(DMR)	5.7	15.7	62.0	63.0	115.5	43.1	11.3	103.7	149.3	3.5

Obatanpa-Prem.QPM	6.0	15.3	65.0	67.7	114.7	40.3	11.0	104.0	120.3	6.8
JO-F	6.0	9.7	62.7	67.3	101.1	31.3	10.7	69.3	220.0	8.8
JO-1	6.0	9.7	64.0	69.7	101.1	37.1	10.7	106.7	150.3	4.8
JO-2	4.7	15.0	62.7	65.3	76.3	26.2	10.3	103.0	160.0	8.3
Mean	5.75	12.09	61.27	64.06	97.20	34.62	9.88	101.54	169.91	5.96
S.E.±	0.09	0.46	1.04	1.09	3.93	1.84	0.23	1.42	4.26	0.30
CV (%)	9.1	22.8	10.2	10.2	24.3	31.9	14.2	8.4	15.0	30.2
Range	5-7	6-18	44.3-71	45.3-74	51-136	13-53	6-12	67-109	120-220	3-9

Table 2: Combined Correlation matrix for growth parameters and yield in quality protein maize genotypes evaluated at Samaru

Parameter	DG	EC	DT	DS	PH	EH	LP	DM	TSW	GY
DG	1.00									
EC	-0.38	1.00								
DT	-0.10	-0.05	1.00							
DS	-0.16	0.22	0.46*	1.00						
PH	-0.41	0.21	0.05	0.24	1.00					
EH	-0.28	0.13	0.09	0.20	0.84**	1.00				
LP	-0.39	0.27	0.13	0.16	0.36	0.45*	1.00			
DM	-0.11	-0.06	0.27	0.10	0.26	0.22	0.23	1.00		
TSW	-0.31	0.14	0.04	0.24	0.37	0.41*	0.28	-0.02	1.00	
GY	-0.08	0.04	-0.11	0.05	0.21	0.27	0.02	-0.17	0.50*	1.00

Key: DG= Days to germination

*Significant at P<0.05
**Significant at P<0.01

EC= Emergence count
DT= Days to Tasselling
DS= Days to silking
PH= Plant height
EH= Ear height
LP= Number of leaves per plant
DM= Days to maturity
TSW= Thousand (1000) seed weight
GY= Grain yield

Table 3: Estimates of genotypic (δ^2g) and phenotypic (δ^2p) variances, coefficients of genetic variability and genetic advance in ten characters of single cross hybrids of quality protein maize studied

Character	δ^2g	δ^2p	GCV	PCV	GA (%)
Days to germination	0.1	0.6	14.4	32.5	0.8
Emergence count	3.4	16.3	52.9	115.1	11.1
Days to tassel	32.6	155.3	72.1	159.2	23.0
Days to silk	10.3	409.7	16.1	252.9	0.8
Plant height	605.6	1052.5	125.4	551.4	2073.8
Ear height	121.9	1052.5	125.4	212.9	152.2
Number of leaves per plant	0.1	11.1	12.2	106.1	0.0
Days to maturity	2.6	211.1	15.1	144.2	0.1
Thousand seed weight	486.7	644.1	169.2	194.7	445.8
Grain yield	3.0	3.4	71.5	75.1	95.1

Where
δ^2g = Genotypic variance
δ^2p = Phenotypic variance
GCV= Genotypic coefficient of variation
PCV= Phenotypic coefficient of variation
GA= Genetic advance

REFERENCES

1. **CIMMYT.** People and partnership: Medium term plan of the International Maize and Wheat Improvement Centre. 2000-2002. Mexico, D.F., CIMMYT, 1999; 76.

2. **FAO.** (Food and Agriculture Organization). Agrostat data. Rome, Italy, FAO, 1999.

3. **Abalu GI** The role of regional organizations in achieving food security and sustainable development in Africa. Invited paper presented at the workshop on Regional Cooperation and Trade in the Greater Horn of Africa, Nairobi, Kenya, 1998; February 18-19.

4. **IFPRI.** (International Food Policy Research Institute), 2020 vision for food, agriculture, and the environment, the vision, challenge and recommended action. Washington, D.C., IFPRI. 1995.

5. **Edache OA** Maize production and utilization in Nigeria: Problems and Prospects. In: Proceedings of National Workshop on Maize Production, Kaduna, Nigeria, 1996; 3-8.

6. **FMANR.** Federal Ministry of Agriculture and Natural Resources, Nigeria. National Agricultural Research Strategic Plan (1996-2010), 1995; **1**: 140-142.

7. **IITA.** Sustainable food production in sub-Saharan Africa 1. IITA^{s} contributions. IITA, 1992, Ibadan, Nigeria.

8. **Echandi CR and AR Halluer** Evaluation of US Corn Belt and adapted tropical maize cultivars and their diallele crosses. Maydica, 1996; **41**: 317-324.

9. **Goodman MN** Exotic maize germplasm status, prospects and remedies. Iowa state J.Res, 1985; **59**: 497-527.

10. **Efron Y** Use of temperate and tropical germplasm for maize breeding in the tropical areas of Africa. In: Brandolini A. Salamini F (eds). Breeding strategies for maize production improvement in the tropics. FAO and Instituto Agronomico per L oltremare. Florence. Italy, 1985; 105-131.

11. **Burton GW** Quantitative inheritance in grasses. Proceedings of the 6th International Grassland Conference, 1952; **1**: 227-283.

12. **Johns HW, Robinson HF and RE Comstock** Estimate of genetic and environmental variability in Soybean. Agron J., 1958; **47**: 318.

13. **Uguru MI** Crop genetics and breeding Onitsha: The Conic printers, 1998; 113-116.