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ANALYSIS OF DIVERGENCE FOR AGRONOMIC AND NUTRITIONAL DETERMINANTS OF QUALITY PROTEIN MAIZE.

[ANALISIS DE DIVERGENCIAS PARA CARACTERISTICAS AGRONOMICAS Y NUTRICIONALES DE MAIZ QPM]

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SUMMARY

Genetic diversity was evaluated among 53 Quality Protein Maize (QPM) genotypes for 12 traits in three years (1999, 2000 and 2001) using multivariate analysis (D^2 statistic). The genotypes where grouped into 11 clusters. Inter-cluster D^2 values ranged from 60.4 (between cluster 1 and VI) to 501.9 (between cluster V and IX). The following traits; plant height, days to physiological maturity, days to silk, protein content and grain yield accounted for over 70% genetic diversity among the genotypes.

Key words: Quality Protein maize, genetic diversity, D^2 analysis

RESUMEN

La diversidad genética de 53 genotipos maíz QPM fue evaluada para 12 características, en un período de 3 años (1999-2001), empleando análisis multivariado (D^2). Los genotipos fueron agrupados en 11 clusters. Los valores D^2 variarion de 60.4 (entre clusters I y VI) a 501.9 (entre clusters V y IX). Las características de altura de la planta, días a madurez fisiológica, contenido de proteína, y producción de grano contribuyeron a más del 70% de la diversidad genética entre los genotipos QPM.

Palabras clave: Diversidad génetica, maíz QPM.

INTRODUCTION

Maize has been established as staple food crop in Africa and its presence in the food basket in many west and central African countries has been increasing steadily during the last decade. About 26 million tons of maize are produced annually in Africa on about 20 million hectares of land (Byerlee and Eicher, 1997). In Nigeria; maize is grown in all the agro-ecological zones, and in northern Nigeria it is cultivated both as rainfed and under irrigation.

Maize is an important element in human diet accounting for 50% - 60% of the dietary protein especially in developing countries. The protein in ordinary or normal maize is of poor nutritional value due to limiting concentration of essential amino acids (lysine and tryptophane) that confirm the presence of opaque-2-gene. The introduction of Quality protein maize (QPM) with high concentration of lysine and trytophane content will help in alleviating the imbalance in maize protein, insufficient calorie, malnutrition, diseases and death among low income maize consuming population of developing countries including Nigeria.

Exhaustive literature relating to genetic diversity, character association, heterosis and combining ability has been generated for various crops including normal maize (Das *et al,* 1984; Thakur and Zarger, 1989; Muppidathi *et al,* 1995; Choudhary, 1997); in contrast, QPM has received scant attention in these areas. The divergence studies are necessary to understand the trend of evolutionary pattern, to asses the relative contribution of different components of yield to total divergence and to determine the nature of forces operating at inter and intra-cluster levels (Anand and Rawat, 1984; Thakur and Zarger, 1989). Such information is necessary for specific breeding objectives, thus the present study asses genetic divergence using genetic distance (D^2) analysis in introduced QPM genotypes with the goal of isolating diverse genotypes of economic importance for use in breeding programs.

MATERIAL AND METHODS

The experimental material comprised 53 QPM genotypes introduced into the Institute for Agricultural Research (IAR) Samaru, Nigeria from Mexico, Ghana and Zimbabwe. The experimental materials were sown on June 17, 1999; June 20th, 2000 and June 18, 2001, at IAR research farm (11^0 11'N; $7^0$38'E, 686m above sea level) each plot consisted of two rows of 5m length, at inter and intra row spacing of 0.75m X 0.5m (plot size = 7.5m²). The experimental design was a randomized complete block design in three replicates. All recommended agronomic practices were followed

to raise a successful crop (IAR, 1993). The genotypes were evaluated for 12 agro-nutritional traits for the three years of study. The traits included: days to tassel (DT), days to silk (DS), days to physiological maturation (DPM), plant height (PH), ear height (EH), grain yield (GY), percent protein (PRO), moisture content (MOI), carbohydrate (CHO), ash content (ASH), fibre content (FIB) and fat content (FAT).

Three years mean trait performances were used in statistical computation. The genetic divergence of the 53 QPM genotypes was estimated using Mahalanobis' D^2 statistics (Mahalanobis, 1936). The D^2 values for 'K' traits between i^{th} and j^{th} genotypes was computed as:

$$D^2 = (Y_{it} - Y_{jt})^2$$

D^2 significance was tested using chi-square (χ^2) values at 't' degrees of freedom at 0.05 level of significance where 't' is the number of traits evaluated. Tocher's method described by Rao (1952) was used in grouping the QPM genotypes into clusters with the aid of D^2 being treated as the square of the generalized distance. Each trait evaluated was ranked on the basis of $d_i = y_l - y_{ki}$ values, rank one (1) was given to the highest mean difference. Percentage contribution of each was computed thus:

Percent contribution (x) = (Nx/PC) 100;

Nx is number of genotype combination which were ranked first for a trait and,
 PC is possible combination= n (n-1)/2 =1378.

RESULTS AND DISCUSSION

Cluster grouping and mean values for 12 agro-nutritional traits of Quality protein maize are presented in Table 1. Cluster II has the largest genotypes, accommodating 12 QPM genotypes followed by cluster IV (7 genotypes), V and VIII (6 genotypes each). The superior clusters with respect to grain yield are VIII (4.8t/ha), III (4.7t/ha), VII, XI and V yielded equal or above 4.0t/ha. In term of percent protein content, cluster VI, XI, I, IV, XI, III, VII and V had above or equal to 8% protein content. Genotypes of cluster VIII, in addition to being high yielders, exhibited other desirable traits such as medium to late maturity (99 DPM), earlier days to tassel and silk (62 and 68). However, they had some undesirable traits such as high fibre content (2.8%), high moisture and fat content (6.5% and 2.4% respectively). Genotypes in cluster V showed lower grain yield than those in cluster VIII but they had some desirable traits such as plant height (190cm) high percent protein (12.1%), low moisture content (4.8%), low ash, fibre and fat content (1.0%, 1.8% and 1.9% respectively). Thus, intercrossing genotypes from these two clusters and other genotypes from cluster III, VII and XI may create wider variability which is expected to produce high-yielding transgressive segregants in maize population improvement programs.

The 53 genotypes grouped into 11 clusters, inter and intra cluster genetic distance (D^2) are present in Table 2. High range of inter-cluster D^2 values ranged from 60.4 (between cluster I and VII) to 501.9 (between cluster V and IX), therefore, over 80% inter-cluster variability was present. The intra-cluster distance was also variable ranging from 0 to 37.2. The wide range of D^2 values obtained revealed that enormous diversity could be created through hybridization. The inter cluster proximity was minimum between cluster I and VI, thereby indicating that they are closely related. These results are in conformity to those reported in chickpea (Anilkumar et al., 1993); Muppidathi et al., (1995) and Chungui et al., (1996) in sunflower and Quendeba et al., (1995) in African pearl Millet.

Table 1. Cluster mean values for 12 agro-nutritional traits of QPM

Cluster number		DT	DS	DPM	PH	EH	GY	PRO	MOI	CHO	ASH	FIB	FAT
I.	(2)*	56	61	89	146	58	2.8	9.3	6.3	78.5	1.3	2.1	3.3
II.	(12)	59	65	94	180	67	3.6	7.5	1.5	81.0	1.1	2.0	2.8
III.	(2)	65	69	99	201	80	4.7	10.7	7.0	76.2	1.1	1.9	2.1
IV.	(7)	61	66	96	181	69	3.4	9.4	5.5	75.1	1.6	2.0	2.9
V.	(6)	66	70	100	190	79	4.0	12.1	4.8	80.6	1.0	1.8	1.9
VI.	(3)	55	61	90	148	58	2.2	8.0	8.4	79.2	1.4	1.7	3.4
VII.	(5)	69	71	100	201	83	4.2	11.6	6.1	78.1	1.6	2.2	2.0
VIII.	(6)	62	68	99	200	80	4.8	10.4	6.5	78.2	1.4	2.8	2.4
IX.	(3)	62	67	96	179	65	3.3	7.8	9.1	80.6	1.7	1.9	3.3
X.	(4)	56	60	87	146	56	2.5	8.1	9.3	75.2	1.7	2.1	2.8
XI.	(3)	69	70	101	199	81	4.2	9.4	6.4	76.3	1.5	2.1	2.9

* - Number of genotypes for each cluster in parenthesis.
Table 2. Inter - and intra – cluster (bold) D^2 values among 11 clusters of QPM

Cluster Number	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I.	**8.1**	78.6	120.7	129.9	66.5	60.4	207.1	411.5	91.3	77.1	280.2
II.		**0.0**	106.5	95.0	79.2	110.5	200.3	326.1	100.6	85.6	341.3
III.			**0.0**	71.7	63.9	100.2	96.5	229.8	214.7	69.4	141.8
IV.				**12.1**	100.4	85.5	115.4	106.6	315.6	100.7	322.1
V.					**3.9**	72.7	88.5	120.3	501.9	81.5	122.4
VI.						**0.0**	95.1	81.7	120.6	91.9	107.5
VII.							**0.0**	113.2	160.5	85.9	213.3
VIII.								**0.0**	130.7	116.7	339.6
IX.									**0.0**	99.1	240.8
X.										**37.2**	178.4
XI.											**0.0**

The analysis for estimating the contribution of each trait towards the expression of genetic divergence measured by D^2 values revealed that, the highest contributor was plant height (33.8%) followed by days to physiological maturity (16.2%), days to silk (8.4%), protein content (7.7%) and ear height (6.9%) as seen in Table 3. These traits could be used in selecting desired genotypes for further selection and choice of parents for hybridization and creation of more variability. The present study clearly indicated that progenies expected from crossing diverse parents would reveal greater diversity for crop improvement. These results are in good agreement with the finding of Thakur and Zarger, (1989); Alagaswamy and Chandra, (1998).

High *per se* performance of genotypes with high D^2 values along with maximum inter-cluster distance among genotypes should be considered while choosing genotypes as parents for hybridization. However, low *per se* performance and low genetic divergence between two or more genotypes when crossed, are not likely to produce high-yielding, high protein and any exceptionally high heterotic effect of any practical value. Based on results of D^2 analysis in this study, good parental combinations should have high yielding ability along with desired traits and moderates to high D^2 value.

Table 4 revealed the number of clusters and the corresponding QPM genotypes in them. Therefore QPM genotypes; PMG011M, PMG001L, PMGO1OL and PMG023L included in cluster VIII, PMG019E and PMG007 of cluster V and PMG028E of cluster III were high-yielding; they exhibited other desirable traits like high protein content, carbohydrate content, low ash, fibre and fat content. Among these genotypes are early, medium and late maturing, tall and short plants. Therefore, these desirable and divergent QPM genotypes could be used for crop improvement.

Table 3. Degree of contribution of each trait to divergence

Trait	percent contribution	Rank
Days to tassel	4.7	9
Days to silk	8.4	3
Days to physiological maturity	16.2	2
Plant height (cm)	33.8	1
Ear height (cm)	6.9	5
Grain yield (t/ha)	6.0	6
Protein content (%)	7.7	4
Moisture content (%)	5.4	8
Carbohydrate (%)	1.3	11
Ash content (%)	5.9	7
Fibre content (%)	2.8	10
Fat content (%)	0.9	12

Table 4. Clusters formed and corresponding QPM genotypes

Cluster	No. of QPM genotype	QPM Genotype
I	2	PMG012E & 014E
II	12	PMG001L, 002L, 003L, 005L, 008L, 009L, 015E, 016E, 017E, 018E, 021M & 023M
III	2	PMG009E & 028E
IV	7	PMG001M, 002M, 005M, 008M, 012M, 009E & 003L
V	6	PMG005E, 007E, 008E, 019E, 001M, & 002M
VI	3	PMG004L, 008L & 009M
VII	5	PMG009E, 010E, 011E, 020E & 022M
VIII	6	PMG006M, 007M, 011M, 007L, 010L & 023L
IX	3	PMG014M, 015M & 002E
X	4	PMG012M, 013M, 020E & 021E
XI	3	PMG019L, 020L & 020M

CONCLUSIONS

This investigation revealed that intercrossing genotypes in clusters VIII, V, III, VII and XI would create wider variability for exploitation in crop improvement program. Five traits viz; plant height, days to physiological maturity, days to silk, protein content and grain yield contributed most towards genetic divergence of the genotypes. Seven QPM genotypes with desirable traits from three clusters were identified for further crop improvement.

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