



BIOCHEMICAL ANALYSIS AND GRAIN YIELD CHARACTERISTICS OF QUALITY PROTEIN MAIZE (*Zea Mays Linnaeus*) IN THE SOUTHERN GUINEA SAVANNA OF NIGERIA

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Abstract- Experiments were conducted on twenty two genotypes of quality protein maize (QPM) and two local checks to assess their lysine and tryptophan levels, as well as grain yield characteristics at the Lower Niger River Basin Development Authority station, Oke-Oyi, Ilorin, Nigeria for three years (2009-2011). The results showed that the QPM genotypes and the standard checks varied from one another, with respect to crude protein, zein dry matter, zein crude, lysine and tryptophan ($P < 0.01$). The best QPM hybrids for grain yield (Dada-ba, ART98-SW5-OB, ART98-SW4-OB and TZPB-OB) had percentage lysine and tryptophan advantage of 34% compared with the local checks. These hybrids also out-yielded other genotypes with yield advantage of 10, 24 and 26% over the best inbreds, open pollinated varieties and the standard checks respectively. However, correlation studies showed that grain yield has positive association with all the characteristics except crude protein content. Kernel number per cob has maximum correlation with grain yield followed by kernel rows per cob, cob diameter and cob weight. The direct effect for crude protein was positive but the correlation was negative. Conclusively, the QPM hybrids that combined high yield with the essential amino acids could be tested in different savanna agro-ecologies to identify those that could be released to farmers, while the superior inbreds could be introgressed for further breeding programs.

Keywords- Quality protein maize, lysine, tryptophan, grain yield, inbred lines, hybrids, open pollinated varieties.

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Introduction

Maize (*Zea mays Linnaeus*) is the third most important cereal crop and major source of energy, protein and other nutrients for human and livestock in the world [33]. Maize grain accounts for about 15 to 56% of the total daily calories in diets of people in about 25 developing countries, particularly in Africa and Latin America, where animal protein is scarce and expensive [58]. In Nigeria, maize is the most available staple foods, 18.8 % in the dry savanna, 21.9% in the moist savanna and 19.8 % in the humid forest [31]. Available daily intake is generally low in tropical Africa (5g in Nigeria) compared to 46-56g for an average person and 96g for

pregnant and lactating mothers as recommended by Food and Nutrition Board of Academy of Science. A national survey revealed that an average of ₦127.20 (\$0.8) is spent per week per household on maize consumption [31]. Millions of African children and nursing mothers suffered from protein deficient inducing diseases such as stunted growth, weakened immune system and impaired intellectual development, because of poverty [58]. Few individual who could afford the right quantity and quality animal protein are skeptical for the inherent heart diseases sometimes occasioned by body accumulated cholesterol.

An adult human cannot synthesize the eight essential amino acids

(isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan and valine) and need to be supplied through foods. Absence or deficiency of any of these amino acids limits the ability of the body to make proteins, despite the presence of all other amino acids [43]. Cereal proteins contain on an average about 2% lysine, which is less than one-half of the recommended concentration for human nutrition by Food and Agriculture Organization [21]. From the human nutrition view point, lysine is the most important limiting amino acid in the maize endosperm protein, followed by tryptophan.

Quality protein maize (QPM) was developed by combining the genetic systems of the gene mutant *opaque-2* (δ^2) [44] and genetic endosperm modifiers [58,72,73]. The genetic system of the δ^2 gene is qualitative. However, because it is recessive, its effects are expressed in the endosperm when three alleles, two from female parent and one from male parent are present [52]. It increases lysine and tryptophan in endosperm by acting on the four types of storage proteins in maize endosperm: albumins, globulins, zeins and glutelins. Zeins contain low lysine with 0.1g/100g while glutelins are considerably rich in lysine with 2g/100 g or more [39]. The δ^2 mutant increases the level of lysine and tryptophan by suppressing or reducing the synthesis of zeins and increasing that of glutelins [27]. The δ^2 gene adversely affects several important agronomic traits including kernel characteristics. It adversely affects the accumulation of dry matter resulting in lower yields due to increased endosperm size. The kernel phenotype is changed in a soft, chalk and dull appearance. Kernels dry slowly following physiological maturity of the grain and have a higher incidence of ear rots. Other changes include larger germ size and low kernel density [50]. The δ^2 -endosperm genetic modifiers however are genes capable of altering the expression of other genes at different loci in the genome and alter the undesirable correlated effects of δ^2 gene [69]. The parties of the endosperm modified are vitreous and hard instead of being opaque and soft [75]. The δ^2 -modified endosperm varieties have agronomic characteristics comparable with those of normal maize. Endosperm modification of QPM is also accompanied by slight increase in total proteins and slight decrease in lysine and tryptophan [14,72]. Several conventional breeding programs that improved those agronomic shortcomings and amino acid contents through backcrossing and recurrent selection, have developed varieties with high protein value and favorable texture of QPM [58].

Previous studies reported lysine content of 1.80-4.5% in QPM genotypes. This value was less than the values reported by some researchers in wheat, rice, barley, oats, sorghum and normal maize [74]. Tryptophan contents of 0.94-1.06% recorded in QPM was two-fold greater than those reported for normal maize [54]. Earlier workers [45,54,71,72] suggested that QPM could assist in reducing protein deficiencies, especially in children where maize consumption dominated in their diets. The QPM is also cheaper, more affordable and easy to produce compared to animal protein [54]. Hence, breeding and production of QPM stands out as an alternative protein source for poor-resource farming communities. Against these backgrounds, evaluation of QPM yield potentials and amino acid contents in the target environment is prerequisite for adoption by the farmers. Also, Increase in land area for cultivation of QPM could increase maize productivity. Keeping in view with the aforementioned, the present study was therefore conduct-

ed to (i) evaluate some QPM, inbred lines, hybrids and open pollinated genotypes developed for acceptable level of tryptophan and lysine (ii) Assess them for grain yield characteristics in the southern Guinea savanna agro-ecology for three cropping years. It is hoped that this study will provide relevant information for future research programmes in the QPM varietal developments.

Materials and Methods

Description of Genetic Materials

Twenty two QPM genotypes and two local checks were evaluated for nutritional qualities and grain yield characteristics for three years (2009-2011) during late cropping seasons at the Lower Niger River Basin Development Authority station, Oke-Oyi, Ilorin (Latitude 8° 30'N, 8° 36'E and Longitude 4° 31'N, 4° 33'E), located in the southern Guinea savanna of Nigeria. The genetic materials comprised five OPVs, nine inbred lines and eight hybrids, while two local varieties adapted to local conditions were used as checks. The seeds of nine inbred lines and four OPVs were obtained from International Institute of Tropical Agriculture (IITA), while five hybrids from Institute of Agricultural Research and Training (IAR & T), Ibadan, Nigeria. One of the OPVs (Obatanpa) and three hybrids were obtained from the Crops Research Institute (CRI), Kumasi, Ghana (Table 1).

Table 1- Source of collection and characteristics of the QPM varieties evaluated at Ilorin

Obatanpa	CRI Ghana	White	Flint	OPV
EV8766-SR	IITA/CIMMYT	Yellow	Dent	OPV
EV8363-SR	IITA/CIMMYT	White	Dent	OPV
Pool 18-SR	IITA/CIMMYT	Yellow	Flint	OPV
Pool 19-SR	IITA/CIMMYT	White	Flint	OPV
Mama-ba	CRI Ghana	White	Flint	Hybrid
CIDA-ba	CRI Ghana	White	Dent	Hybrid
Dada-ba	CRI Ghana	White	Flint/ Dent	Hybrid
ART98-SW6-OB	IAR & T, IBADAN	White	Flint/ Dent	Hybrid
ART98-SW5-OB	IAR & T, IBADAN	White	Flint	Hybrid
ART98-SW4-OB	IAR & T, IBADAN	White	Flint	Hybrid
TZPB-OB	IAR & T, IBADAN	White	Flint	Hybrid
ILEI-OB	IAR & T, IBADAN	White	Flint	Hybrid
CML176	IITA/CIMMYT	White	Flint/ Dent	Inbred line
CML177	IITA/CIMMYT	White	Flint/ Dent	Inbred line
CML178	IITA/CIMMYT	White	Flint/ Dent	Inbred line
CML181	IITA/CIMMYT	White	Flint/ Dent	Inbred line
CML437	IITA/CIMMYT	White	Flint/ Dent	Inbred line
CML490	IITA/CIMMYT	White	Flint/ Dent	Inbred line
CML491	IITA/CIMMYT	White	Flint/ Dent	Inbred line
CML492	IITA/CIMMYT	White	Flint/ Dent	Inbred line
CML493	IITA/CIMMYT	White	Flint/ Dent	Inbred line
Oba-Super 1	LOCAL CHECK	White	Flint	Local variety
SUWAN-1-SR(DMR)	LOCAL CHECK	White	Flint	Local variety

Experimentation

The trials were established on 1st August, 2009, 29th July, 2010 and 27th July, 2011. The trials were laid out each cropping year in a randomized complete block design (RCBD) with four replications and at a planting distance of 0.75m between the rows and 0.5m within the rows. Each plot was six rows and the outer rows were used for destructive sampling, while observations were taken from the four middle rows. Seeds were treated with apron plus before planting for protection against seed borne diseases and soil borne pests. Three seeds were planted/hill but later thinned to two/hill

two weeks after planting (WAP) to provide a uniform plant population of about 53,333 plants/ha. Agronomic practices included pre-emergence application of herbicide ((a.i. 3kg/L Metolachlor, 170g/L Atrazine and 3kg/L Paraquat per hectare) to control weeds and supplemented by hoe weeding as necessary. Compound fertilizer (NPK 20:10:10) was applied as split-dosage at the rate of 80kg N/ha, 40K₂O N/ha and 40P₂O₅N/ha (3 WAP) and at anthesis (7 WAP), using the side placement method.

Data Collection and Analyses

Data were collected on grain yield and yield characteristics. All ears harvested from each plot were weighed to determine grain yield per plot (assuming 80% shelling percentage) and was later converted to tones per hectare (t/ha⁻¹) after adjusting to 15% moisture content. One thousand grain samples were collected from each plot at harvest for the determination of harvest moisture. The samples were first weighed to obtain initial weight followed by drying to a constant weight in the oven at 80°C in the laboratory and the difference between the two weights recorded as moisture at harvest. Additional data were also collected on yield components viz: cob length (cm), cob diameter (cm), cob weight, kernel number per cob, kernel rows per cob, kernel row number, kernel depth (cm) and 1000 kernel weight (gm). Kernel-rows per cob were counted from five cobs from each entry. The weight of sun dried 1000-grain samples drawn at randomly in each plot were recorded in grams at 15 per cent moisture content through electronic balance. Length of the ear was measured in centimeters (from the base to the tip of the cob) and recorded as cob length. Number of kernel rows per cob was counted and recorded. Number of kernels per row was counted and average was recorded as number of kernels per row.

Laboratory Analyses

The laboratory studies involved the determination of proximate composition of QPM and the local maize genotypes. Five ears were randomly selected in each plot at harvest, followed by careful removal of the grains by hand. From each genotype, equal number of grains were selected from each plot, mixed together to form a balanced bulk and then subjected to proximate analyses in the laboratory. The grains obtained were grounded to form a fine powder and each sample was oven dried to a constant weight at 80°C to obtain grain moisture content. Three replicates determinations were analyzed for each genotype and the mean recorded for each sample. Crude protein determination was estimated using standard micro-Kjeldahl procedure (AOAC, 2006).

The amino acid was determined using the procedure as described by Sentayehu (2008). Maize flour samples of 0.5 gm were weighed in tarred scoop and transferred to boiling tubes. A catalyst tablet, selenium was dropped into each tube and about 25ml of concentrated sulfuric acid was added. The tubes then placed in an automatic controlled heater set at 200°C. The mixtures were heated until the color changes to light blue. For samples which have digest color of light brown or yellow, the digestions were repeated two or more times. Thirty milliliter of distilled water was added into the digestion tube carefully. During these events, the organic matter of QPM flour is oxidized and the nitrogen in the protein is converted to ammonium by sulfuric acid as described by Aykroyd, et al. (1964) and Purseglove, et al. (1968).

Ammonium in the digestion mixture was determined by distillation and titration [9]. The digestion tube was placed on to the Tecator steam distillation apparatus. The distiller was set, the digestion tube inserted in the system and 150 ml ammonia was collected in the receiver flask containing 50 ml 4% boric acid solution. Then ammonia was titrated against a standard acid (0.1N 10%HCl). Since 1 ml of 0.1 N HCl equivalents to 1.401 mg N, calculation is made to arrive at the nitrogen content of the sample.

$$\%N = \frac{(m1HCl\text{-ml black}) \times \text{normality} \times 14.007 \times 100}{\text{mg sample}}$$

$$\% \text{ Protein} = \%N \times 6.25$$

Because of the simplicity of the estimation of the tryptophan, its content has been used as a criterion for screening materials with superior protein quality. For estimation of tryptophan of opaque-2 maize materials, papain hydrolysis method was used (Hornandez and Bates, 1969).

A single step papain hydrolysis is utilized for protein solubilization. The iron ions oxidise acetic acid to glyoxylic acid in the presence of sulphuric acid. The indole ring of free tryptophan as well as that bound in soluble proteins reacts with glyoxylic acid and a violet-purple compound is produced. The intensity of the violet-purple color is measured at 545- nanometer with spectrophotometer. By drawing a standard curve of optical density vs. tryptophan concentration, percent tryptophan in sample is recorded.

$$\% \text{ tryptophan in protein} = \frac{\% \text{ tryptophan in sample}}{\% \text{ protein in sample}}$$

Because of the relationship observed by various researchers [18, 28,44] between tryptophan and lysine in the maize endosperm protein and that the tryptophan could be used as a single parameter for protein quality evaluation, the value of tryptophan was increase by 4 times to obtain the value of lysine [66]. However, Zein dry matter percentage was estimated by the formula suggested by Drochioiu, et al. (2002) given as:

$$\% \text{ Zein in dry matter} = \% \text{ crude protein} \times 0.386\text{-}2.22.$$

Statistical Analyses

Data collected from the field experiments and laboratory samples were statistically analyzed using PROC GLM model of SAS [67] to compute mean square for each parameter at P<0.01. Analysis of variance (ANOVA) on individual year basis was first computed before a combined ANOVA across years. Genotypic correlation coefficients were estimated from the mean squares and mean across products as suggested by Mode and Robinson (1959). The correlation coefficients were partitioned into direct and indirect effects using the path coefficient analysis according to Dewey and Lu (1959). Pertinent means were separated by the use of least significance difference [68]. The degree of variation was estimated using percentage coefficient variation, all at P<0.05.

Results and Discussion

Biochemical Analyses

Biochemical analyses of the QPM genotypes showed that mean square values of crude protein, zein dry matter, zein in crude form, lysine and tryptophan were significantly different among the QPM genotypes at $P < 0.01$ (Table 2).

Table 2- Mean square for crude protein and essential amino acids of the QPM genotypes

Source of variation	Crude protein %	Zein dry matter %	Zein crude ml/ μ g	Lysine %	Tryptophan %
Replicate	0.31	0.00045	3.99	0.0067	0.0018
Variety	4.35**	1872.6**	0.75**	0.072**	0.0007**
Error	0.09	0.68	0.005	0.005	0.00006

** Significant at $P < 0.01$

Tryptophan had the highest mean square value (1872.6) followed by crude protein (4.35), while lowest value of 0.072 was recorded for lysine. Obi (1982) and Olakojo, et al. (2011) made similar observations when lysine content of some QPM genotypes tested varied significantly at $P < 0.05$. However, the QPM genotypes and the standard checks varied significantly from one another with respect to crude protein and other amino acids (Table 3).

Table 3- Character means of some essential amino acids and crude protein in QPM and local varieties

Variety	Crude protein (%)	Zein dry matter %	Zein crude ml/ μ g	Lysine %	Tryptophan %
OPVs					
Obatanpa	7.21	0.56	140.13	3.53	0.67
EV8766-SR	7.1	0.30	143.87	3.49	0.66
EV8363-SR	7.34	0.63	147.38	3.47	0.75
Pool 18-SR	7.23	0.45	141.42	3.56	0.7
Pool 19-SR	6.89	0.45	134.72	3.48	0.62
Hybrids					
Mama-ba	8.14	0.76	163.85	3.66	0.7
CIDA-ba	7.57	0.83	159.67	3.59	0.71
Dada-ba	8.23	0.77	157.45	3.59	0.71
ART98-SW6-OB	6.34	0.68	194.78	3.68	0.78
ART98-SW5-OB	8.34	0.82	158.34	3.83	0.82
ART98-SW4-OB	8.33	0.81	159.67	3.59	0.72
TZPB-OB	8.12	0.75	129.78	3.67	0.67
ILEI-OB	6.02	0.63	126.83	3.36	0.64
Inbreds					
CML176	7.34	0.65	156.93	3.18	0.6
CML177	7.57	0.55	148.83	3.16	0.79
CML178	8.23	0.56	151.78	3.27	0.63
CML181	7.34	0.60	157.73	3.01	0.71
CML437	7.34	0.53	157.21	3.08	0.63
CML490	8.03	0.65	146.98	3.29	0.52
CML491	7.14	0.48	153.58	3.29	0.56
CML492	8.13	0.66	152.39	3.15	0.67
CML493	6.79	0.60	132.65	3.26	0.46
Local checks					
Oba-Super 1	4.35	0.29	131.48	2.78	0.44
SUWAN-1-SR (DMR)	3.23	0.26	124.64	1.55	0.31
Mean	7.74	0.55		3.35	0.72
CV (%)	3.05	9.04	25.85	2.56	12.05
LSD (0.05)	0.89*	0.04*	1.97*	1.34*	0.04*

This probably suggests high variability that exists in maize genotypes with respect to these biochemical parameters. Plant breeder could therefore find this attribute useful in genetic manipulation

and cultivar development for enhanced protein biochemical parameters. Crude protein and other amino acids were very high among the hybrids followed by inbreds, open pollinated varieties and the checks in that order (Table 3).

Hybrid ART98-SW5-OB generally yielded the highest amount of crude protein and amino acids compared with other genotypes. Hussein, et al. (2006) reported that while crude protein content in QPM hybrids is slightly improved, their lysine contents improved by 82 to 98% of the normal hybrids. The authors further observed that on the relative basis of the grain yield, the QPM hybrids have almost doubled the amount of lysine content. Across the inbreds, crude protein ranged from 6.79% (CML493) to 8.23% (CML178), while in open pollinated varieties (OPVs), it ranged between 6.89% (Pool 19-SR) and 7.34% (EV8363-SR). The trend was comparable to that of zein with a range of 0.63% (ILEI-OB) to 0.82% (ART98-SW5-OB), 0.46 (CML491) to 0.66 (CML492) and 0.30 (EV8766-SR) to 0.63 (EV8363-SR) in the hybrids, inbreds, OPVs respectively. Percentage zein content of the two local checks, Oba-Super 1 (0.29) and SUWAN-1-SR (0.26) were the lowest compared with the other genotypes. Hybrid ART98-SW5-OB had a yield advantage of 60% for zein content over SUWAN-1-SR (Check). Similarly, ART98-SW5-OB had the highest amount of zein crude (ml/ μ g) with yield advantages of 19, 24 and 32% over the best inbreds, OPVs and checks respectively.

Correlation Coefficients Analysis of Biochemical Parameters

Pearson correlation (r) among various biochemical parameters of the QPM genotypes in this trial revealed that Crude protein was highly significantly positively correlated with tryptophan ($r = 0.78^{**}$), but correlated negatively with zein dry matter, zein crude form and lysine with coefficient of $r = -0.58$, -0.91^{**} and 0.93^{**} respectively (Table 4). Pixley and Bjarnason (1993) earlier reported the need for monitoring protein content, tryptophan and lysine while breeding or selecting for QPM genotypes. Lysine was positive and highly significantly associated with tryptophan ($r = 0.90^{**}$), zein dry matter ($r = 0.71^{**}$) and zein crude form ($r = 0.79^{**}$). Similarly, zein dry matter was positive but not significantly correlated with zein crude. Tryptophan on the other hand was negatively correlated with zein dry matter and zein crude.

Table 4- Correlation coefficient (r) of amino acids and crude proteins of the QPM and local varieties

	Crude Protein	Lysine %	Tryptophan %	Zein dry matter %	Zein crude ml/ μ g
Crude protein	-	-	-	-	-
Lysine %	-0.93**	-	-	-	-
Tryptophan %	0.78**	0.90**	-	-	-
Zein dry matter %	-0.58	0.71*	-0.72*	-	-
Zein crude ml/ μ g	-0.91**	0.79**	-0.31	0.32	-

Grain Yield and Related Attributes

Grain yield in maize is a complex character and is the result of correlation between yield and yield components and between yield components themselves. Therefore, it is very imperative to examine the contribution of each of the various components in order to attract the attention to which one has the greatest influence on grain yield. This however is prerequisite to planning and evaluating meaningful breeding programs. Means for the interac-

tive effect of genotype by year (GxY) was significant for grain yield among the QPM genotypes and the standard checks (Table 5). The QPM genotypes and checks had the lowest grain yield in the year 2010 compared with 2009 and 2011 (Fig. 1). Rainfall distribution that was higher and consistent throughout the flowering/grain filling periods of July to September in 2009 and 2011 and a significant drop in rainfall in August, 2010 could contribute to significant differences among the genotypes for grain yield (Fig. 1).

Table 5- Performance of QPM and local varieties for grain yield evaluated in 2009 - 2011 cropping seasons at Ilorin, Nigeria

Genotype	2009	2010	2011
OPVs			
Obatanpa	3.5	3.3	3.7
EV8766-SR	3.6	3.4	3.7
EV8363-SR	3.6	3.4	3.8
Pool 18-SR	3.7	3.7	3.9
Pool 19-SR	3.9	3.3	4
Hybrids			
Mama-ba	4.1	4	4.3
CIDA-ba	4.2	3.8	4
Dada-ba	4.8	4.4	4.9
ART98-SW6-OB	3.8	3.6	4.5
ART98-SW5-OB	5	4.5	5.1
ART98-SW4-OB	4.8	4.5	5
TZPB-OB	4.5	4.4	5.2
ILEI-OB	4.2	4	4.4
Inbred lines			
CML176	4.2	3.8	4.4
CML177	4.1	3.9	4.2
CML178	4.5	4.3	4.7
CML181	4.6	4.2	4.6
CML437	4.3	3.9	4.5
CML490	4.1	4.1	4.3
CML491	4.2	3.8	4.4
CML492	4.2	3.8	4.4
CML493	3.6	3.4	3.8
Local checks			
Oba-Super 1	3.8	3.4	3.9
SUWAN-1-SR (DMR)	3.6	3	3.8
Mean	4		
LSD (0.05)	0.45*		

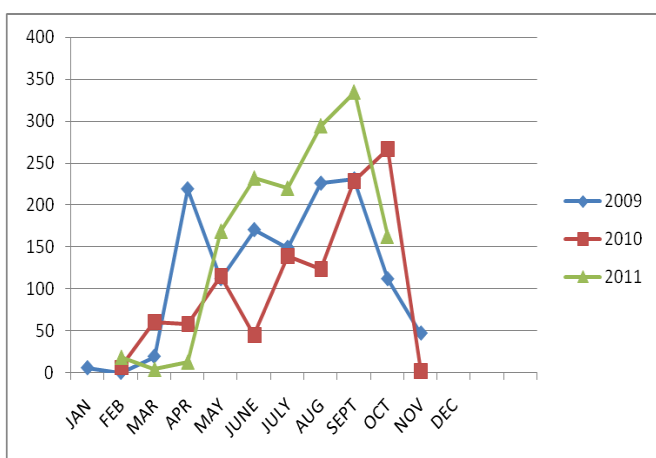


Fig. 1- Monthly rainfall distribution pattern (3 years) at Ilorin from 2009 to 2011

This relatively better rainfall pattern could favour accumulation and translocation of photo-assimilates in the genotypes with corresponding larger ear size, subsequently higher grain yield [13]. This favorable condition is often encouraged by high moisture during the growing period [4,54]. In the present study, the hybrids were superior for grain yield irrespective of the cropping years followed by inbreds, OPVs and local varieties. Hybrids ART98-SW5-OB, ART98-SW4-OB, TZPB-OB and Dada-ba had the highest grain yield of 5.0 t/ha with yield advantage of 10, 24 and 26% over the best inbreds, OPVs and checks respectively. The two local checks (Oba-Super 1 and SUWAN-1-SR) demonstrated instability of performance for grain yield with a difference of 14.7% and 21% yield loss in 2010 compared to 2009 and 2011 respectively. All the QPM genotypes had stable grain yield except CML493 (inbred) and Pool 19-SR (OPV). Hussein, et al. (2006) earlier reported that the hybrids had better yield potential than the local checks. The authors therefore suggested that QPM hybrids should be released to farmers for adoption not only for higher QPM grain yield but also superior protein quality and amino acids contents.

Grain yield was significantly higher in 2009 and 2011 by 0.8 t/ha compared to 2010, representing 22.2% yield increase (Table 6). The differences in performance among the genotypes for this character indicate variability which could be heritable and can be exploited in the overall process of selection in breeding programs. Similar results were reported by Ahmed, et al. (2000), Souza, et al. (2002) and Hussein, et al. (2011) who evaluated and identified high yielding maize varieties among different genotypes tested. McCutcheon, et al. (2001) and Akbar, et al. (2009) also reported significant differences among maize cultivars for grain yield. The hybrids ranked best for grain yield in this study followed by inbred lines, OPVs and standard checks. The range was from 4.0-4.7, 4.0-4.4 and 3.4-3.7t/ha of the hybrids, inbreds and OPVS values respectively. It is worthy to note that most of the hybrids and some inbred lines out-yielded the OPVs and local checks with yield advantage of about 38% over the best OPVs and local varieties. The local varieties as poorest yielders may be due to genetic constitution of the genotypes. It has also been reported by many researchers that QPM varieties widely grown in many African countries produce higher grain yield compared with the currently released normal maize varieties for most grain yield characters [54,64,72]. Among the genotypes tested, highest grain yield of 4.7 t/ha from ART98-SW5-OB was recorded within the hybrids, 4.4 t/ha (CML178 and CML181), 3.7 t/ha in the OPVs and 3.3 t/ha (SUWAN-1-SR (DMR)) among the checks. However, hybrid ART98-SW5-OB which ranked first for grain yield out-yielded the OPV checks by more than 44%. The genotypes also differed significant for yield contributing characteristics among all the genotypes with inbred lines ranked the highest followed by hybrids, OPVs and the local checks on average values. The cob weight ranged from 39-48gm in the inbreds and between 39 and 45gm in both hybrids and OPVs. The checks also had the least cob weight range of 39-40gm.

Correlation Coefficients Analysis of Grain Characteristics

Genotypic correlation coefficients between grain characteristics showed that kernel number per cob has the most positive correlation ($r=0.671^{**}$) with grain yield followed by kernel rows per cob (r

= 0.556**), cob diameter ($r = 0.543^{**}$) and cob weight ($r = 0.452^{**}$) (Table 7). Crude protein content recorded negative non-significant association with all the traits studied including grain yield except cob weight and kernel rows per cob. Between 1000-kernel weight and cob weight was positive and significant correlation ($r=0.571^{**}$). It seems that by increasing cob weight due to more absorption of photo assimilates, the most portion of assimilates remobilizes to grains, so the grain weight will increase. Number of kernels per row was positively correlated with grain yield. One thousand kernel weight positively that was correlated with grain yield was in confirmation with the findings of Dwivedi and Godawat (1997), Jin and Wang (1997), Gautam, et al (1999), Prakash, et al. (2006) and Golam, et al., 2011). Khayatnezhad, et al. (2010) also reported that 500-grain weight had the most positive correlation with grain yield. Kernel rows per cob and kernel number per cob that were positively correlated with grain yield was also confirmed by Saha (1985) and You, et al. (1998). Numbers of kernels per row and kernel rows per cob have a positive genetic correlation with grain yield in this study was also observed by previous workers [35,79,81]. The high correlation of grain yield with the number of rows per cob recorded in this study was also reported by other researchers [48]. A highly significant and positive correlation exists between grain yield and cob length was also noticed by Rafiq, et al. (2010). In this study the correlation between grain yield and kernel depth was not significant. This suggests that cob length is a more important yield component than kernel depth in contributing to final grain yield in maize. Correlation of grain yield with grain number per row noticed in this study was also reported by Marefatzadeh, et al. (2010) and Khodarahmpour and Hamidi (2012). The results of significant correlations between yield and number of rows per cob, number of kernel per row and 1000-grain weight, number of kernel per row and number of rows per cob observed by earlier researchers [36,49,60,80] agreed with the present study. Orlyan, et al. (1999), Khazaei, et al. (2010) and Zirehzadeh, et al. (2011) also suggested that most important traits influencing grain yield are number of kernel per row. Cob length that showed positive and significant correlation with kernel number per row in this study indicates that increase in cob length will increase the kernel number per row. Ultimately as a result of increase kernel number per row, kernel number per cob will increase invariably, therefore increasing the grain yield. A positive correlation between cob length and cob weight recorded in this study is in accordance with Amin, et al. (2003), Sadek, et al. (2006) and Abou-Deif (2007). Result of this study therefore showed that, kernel number per cob, kernel number per row, kernel row per cob, kernel depth, cob weight, cob diameter, cob length and 1000-kernel weight could be used as important traits for prediction of grain yield. This finding was also in agreement with the results of earlier researchers [12,13,15,25,32,48,78]. Actually, yield components have effect on each other in positive way, which may due to same genes controlling these traits.

Path Analysis of Grain Characteristics

Since, significant of simple correlation among yield parameters cannot give enough reasons for cause/effect phenomenon, path coefficient analysis for determination of direct and indirect effects is very essential [13]. This is because the characteristics that are interrelated do not exist by themselves, but are linked to other

yield attributes. The path coefficient analysis not only specify the effective measure of direct and indirect causes of association, but also depicts the relative importance of each factor involved in contributing to the final product of yield. In the present study, cob length has a maximum positive direct effect on grain yield (13.067) followed, kernel rows per cob (3.154) and crude protein (0.823) (Table 8). Positive and highly significant direct effect of cob length for grain yield was reported by other workers [51,65]. Selvaraj and Nagarajan (2011) also noticed favorable influence of kernel rows per cob on grain yield. Direct effect of crude protein on grain yield was reported by Baheeruddin, et al. (1999). In this study, kernel number per cob, kernel number per row, kernel depth, cob diameter, cob weight and 1000 kernel weight recorded negative direct effect on grain yield even though genotypic correlation coefficients on grain yield were positive, as previously reported by Manivannan (1998) and Selvaraj and Nagarajan (2011) (Table 6).

The indirect effect of kernel number per row through kernel rows per cob and crude protein content were positive and through kernel number per cob, kernel number per row, kernel depth, cob length, cob diameter, cob weight and 1000 kernel weight were negative (Table 7).

Table 7- Genotypic correlation coefficients between grain yield, other yield characteristics and crude protein in QPM genotypes

Parameters	Grain Yield (t/ha)	Kernel number per cob (no)	Kernel number per row (no)	Kernel rows per cob (no)	Kernel depth (cm)	Cob length (cm)	Cob diameter (cm)	Cob weight (gm)	1000 kernel weight (gm)	Crude protein %
Grain Yield (t/ha)	-									
Kernel number per cob (no)	0.671**	-								
Kernel number per row (no)	0.124	0.798**	-							
Kernel rows per cob (no)	0.556**	0.673**	-0.157	-						
Kernel depth (cm)	0.065	-0.541**	-0.413	-0.174	-					
Cob length (cm)	0.235	0.765**	0.641**	0.007	-0.089	-				
Cob diameter (cm)	0.543**	0.114	-0.312	0.651**	0.276	0.121	-			
Cob weight (gm)	0.452**	0.032	-0.231	0.63*	0.431**	0.234	0.879**	-		
1000 kernel weight (gm)	0.067	-0.53**	-0.653**	0.177	0.751**	-0.125	0.567**	0.571**	-	
Crude protein %	-0.031	-0.0086	-0.064	0.091	-0.0097	-0.098	-0.0076	0.056	-0.076	-

Negative indirect effect of kernel number per cob on grain yield was noticed on all the characteristics studied except via crude protein. Positive indirect effect of cob length on grain yield was noticed for kernel number per cob, kernel number per row and 1000 kernel weight but it was negative through kernel rows per cob, kernel depth, cob diameter, cob weight and crude protein. A highly significant and positive direct effect of cob length on grain yield was indicated by previous researchers [24,51,65]. Cob length due to involve direct and indirect effects through kernel total number has high correlation with kernel yield in this study. Ross and Hallauer (2003) earlier suggested that cob length is a

basic component effecting on kernel yield, therefore, genetically control recognition of ear length and additional trait correlate to kernel yield can be of help to heredity and diversity recognition of kernel yield. The authors further stressed that kernel numbers in ear have a best direct effect with kernel yield, therefore maize breeders must allowed importance for kernel and row number as select indicators for yield breeding. The authors also suggested that kernel numbers per cob is greatest of trait affected on kernel yield. In the present study, positive indirect effect of cob weight on grain yield was recorded through kernel number per cob, kernel number per row, cob length and 1000 kernel weight; it was negative through the remaining parameters. Whilst indirect influence of crude protein on grain yield via kernel rows per cob was only positive, through other parameters were negative.

Table 8- Path coefficient analysis showing the direct and indirect effects of traits on yield of QPM genotypes

Trait	Kernel number per cob (no)	Kernel number per row (no)	Kernel rows per cob (no)	Kernel depth (cm)	Cob length (cm)	Cob diameter (cm)	Cob weight (gm)	1000 kernel weight (gm)	Crude protein %
Kernel number per cob (no)	-5.142	-4.366	-1.957	-2.312	-4.952	-4.584	-3.541	-2.871	0.076
Kernel number per row (no)	-2.758	-4.641	0.095	-1.461	-3.675	-1.572	-2.712	-1.978	0.175
Kernel rows per cob (no)	0.579	-0.597	3.154	-0.357	-0.654	0.414	-0.571	-0.487	0.265
Kernel depth (cm)	-0.672	-0.076	-0.045	-0.56	-5.842	-0.561	-0.095	-0.047	-0.431
Cob length (cm)	11.076	12.432	-3.175	-0.169	13.067	-0.671	-0.573	10.112	-2.672
Cob diameter (cm)	-0.842	-0.712	-0.153	-1.831	0.879	-1.087	-1.946	-0.895	0.198
Cob weight (gm)	6.573	8.679	-2.679	-0.352	10.071	-0.345	-0.572	9.451	-0.045
1000 kernel weight (gm)	-2.637	-1.963	0.632	-1.739	-3.452	-3.453	-4.621	-4.105	0.117
Crude protein %	-0.009	-0.065	0.085	-0.038	-0.075	-0.214	-0.456	-0.045	0.823
Genotypic	0.046	0.745	0.387	0.078	0.163	0.543	0.034	0.456	0.084

Conclusion

From the present study, QPM genotypes evaluated are generally of considerable lysine and tryptophan contents. The QPM hybrids seem superior for the essential amino acid contents followed by inbreds and OPVs, with the local checks most inferior. This phenomenon is of the same trend for grain yield. The best QPM hybrids for grain yield (Dada-ba, ART98-SW5-OB, ART98-SW4-OB and TZPB-OB) had percentage lysine and tryptophan advantage of 34% compared with the local checks. Similarly, these hybrids out-yielded other genotypes with yield advantage of 10, 24 and 26% over the best inbreds, OPVs and checks respectively. Most of the QPM hybrids and inbred lines evaluated have superior performance for grain yield compared with open pollinated and local varieties. The QPM hybrids that combined high yield performance and essential amino acids (especially hybrids Dada-ba, ART98-SW5-OB, ART98-SW4-OB and TZPB-OB) could be assessed in different agro-ecologies to identify those that could either be release to farmers in each environment. The inbreds (especially CML 178 and CML 181) that were superior for grain yield, lysine and tryptophan contents could also be introgressed for further breeding programs. However, correlation studies showed that

grain yield having positive association with all the yield attributes except for crude protein content which was negatively correlated. Kernel number per cob has maximum correlation with grain yield followed by kernel rows per cob, cob diameter and cob weight. Direct selection of these characteristics might be rewarding for yield improvement since they revealed true relationship with grain yield. The direct effect for crude protein was positive but the correlation was negative, in such a situation direct selection for this parameter should be practiced to reduce the undesirable indirect effect.

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Table 6: Mean performance for grain yield characteristics of QPM and local varieties evaluated in 2009-2011 cropping seasons at Ilorin, Nigeria

Genotype	Grain Yield (t/ha)	Kernel number per cob (no)	Kernel number per row (no)	Kernel rows per cob (no) OPVs	Kernel depth (cm)	Cob length (cm)	Cob diameter (cm)	Cob weight (gm)	1000 kernel weight (gm)
Obatanpa	3.5	300	23	18	18.5	6.3	15.3	0.45	295.5
EV8766-SR	3.6	302	21	17	20.3	5.9	16.4	0.39	282.4
EV8363-SR	3.6	312	22	19	19.7	6	15.2	0.4	297.4
Pool 18-SR	3.8	298	20	20	16.8	5.8	16.1	0.42	267.4
Pool 19-SR	3.7	302	19	16	19.8	6.2	16	0.39	298.6
Hybrids									
Mama-ba	4.1	299	25	18	19.4	6	16	0.44	289.6
CIDA-ba	4	306	24	19	21.5	5.7	15.9	0.45	296.2
Dada-ba	4.7	301	25	17	18.9	5.9	16.2	0.44	289.1
ART98-SW6-OB	4	304	23	17	17.7	6.1	15.9	0.45	299.5
ART98-SW5-OB	4.9	307	26	18	16.8	6.3	15.3	0.39	278.4
ART98-SW4-OB	4.8	304	23	17	19.8	6.2	16.3	0.41	287.6
TZPB-OB	4.7	300	25	19	19.7	5.8	15.5	0.45	297.4
ILEI-OB	4.1	301	24	19	17.4	6.1	16.1	0.39	295.6
Inbred lines									
CML176	4.1	300	19	20	19.5	5.7	15.4	0.39	289.9
CML177	4.1	299	23	16	19.4	6.1	16.1	0.38	296.9
CML178	4.5	302	25	17	16.8	5.9	15.7	0.43	300.3
CML181	4.5	298	24	18	17.7	6	16	0.45	275
CML437	4.2	301	20	19	17.7	5.9	15.8	0.39	302.4
CML490	4.2	304	23	19	17.4	6.2	15.9	0.4	297.6
CML491	4.2	297	22	17	17.5	5.9	15.4	0.43	267
CML492	4.2	303	23	16	16.5	5.9	15.2	0.39	298.6
CML493	3.6	302	24	17	19.7	6	15.7	0.48	300.9
Local checks									
Oba-Super 1	3.7	278	19	19	18.8	6.2	14.7	0.39	286.2
SUWAN-1-SR(DMR)	3.5	262	18	19	19.2	5.8	15.4	0.4	256.3
Mean	4.1	299	23	18	18.6	6	15.7	0.42	289.4
CV %	11.6	2.05	0.11	5.73	3.04	0.07	0.01	11.98	0.11
LSD (0.05)	0.45*	10.04*	3.07*	1.26*	1.11*	0.09*	0.94*	1.03*	12.24*