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Full Length Research Paper

Genetic analysis of single cross Quality Protein Maize (QPM) hybrids

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Correlation coefficients and stability of grain yield were determined using 6 extra-early quality protein maize (QPM) parental inbred lines and their F1 (15) single crosses evaluated in selected ecological zones of Ghana. The objectives were; to estimate the genetic correlation between grain yield and other agronomic traits and to determine the stability of the single cross hybrids across four locations. Randomized Complete Block Design (RCBD) with three replications was used for each location. Estimates of correlation coefficients and stability analysis of grain yield was done using Genstat 9.2 and additive main effects and multiplicative interaction (AMMI) statistical model (MATMODEL 2.0). Results from phenotypic correlation of grain yield showed highly positive correlation with thousand grain weight (TGW) and number of kernels per row (NKR) across all locations suggesting that selection efficiency could be improved through indirect selection. AMMI analysis revealed non-significant genotype by environment interaction (GEI) for grain yield whilst genotypic and environmental main effects were highly significant. However, the contribution of the environment was higher which suggests that anyone of the locations used in this study can be used for subsequent evaluations in order to manage the limited resources available for the testing program.

Key words: Correlation, stability, grain yield.

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important cereals cultivated in the world and a primary staple food in many developing countries. In most maize breeding programs, among all the agronomic traits, a particular attention is paid to grain yield. The knowledge of correlation between yield and its component characters and among the component characters is essential for yield improvement programmes (Vidya and Oommen, 2002). Correlation measures the degree of association between two or more characters and is measured by a correlation coefficient (Hallauer and Miranda, 1988). This could be influenced by genetic or environmental (non-genetic) effects. Genetic correlation is associated with the breeding values of two characters (Falconer, 1989) and their measurements can be identified directly in a number of individuals in a population (Hallauer and Miranda, 1988).

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Table 1. List of parental inbred lines and pedigrees.

Name	Pedigree	Designation
TZEEQI 1	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (18) 2-5-1-1	P_1
TZEEQI 2	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (3/4) 3-7-3-7	P_2
TZEEQI 7	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (7) 4-10-1-1	P_3
TZEEQI 6	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (7) 1-10-1-10	P_4
TZEEQI 8	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (7) 6-10-4-5	P_5
TZEEQI 12	TZEE-W Pop x 1368 STR S7 Inb 40 x Pool 15 SR QPM BC1S5 (7) 10-10-10-10	P_6

Table 2. List of genotypes evaluated in the study.

S/N	Genotype	S/No	Genotype
1	P1xP1*	12	P3xP3*
2	P1xP2	13	P3xP4
3	P1xP3	14	P3xP5
4	P1xP4	15	P3xP6
5	P1xP5	16	P4xP4*
6	P1xP6	17	P4xP5
7	P2xP2*	18	P4xP6
8	P2xP3	19	P5xP5
9	P2xP4	20	P5xP6
10	P2xP5	21	P6xP6*
11	P2xP6	22	Check (GH110)

*Parental lines.

Yield is a complex trait determined by several component characters. Therefore, there is the need to consider other contributing traits when selecting for yield.

Grain yield in nature, routinely exhibits GXE Interaction (Khalil et al., 2011) which necessitates evaluation of cultivars in multiple environments (Kang, 2004; Fan et al., 2007). Crop cultivars are grown in diverse environments of different soil types, soil fertility levels, moisture levels, temperatures and cultural practices. During production, all these cumulated conditions constitute the growing environment for the crop varieties (Abdulai et al., 2007). This poses a serious challenge to plant breeders in the identification and selection of appropriate genotypes to perform consistently in multiple environments (Ngaboyisonga, 2008). Selection is therefore, usually ineffective since genotypes may fail to exhibit the same relative performance in varied environments (Knight, 1970). It has also been shown by Comstock and Moll (1963) that correlation between phenotypic and genotypic values was significantly reduced by GEI affecting progress of selection. This is because, relative rankings for major traits often varies across multiple environments hence possibility of identifying single superior genotype poses difficulties if not impossible (Khalil et al., 2011; Abdulai et al., 2007). Stability analysis defines the true performance of a cultivar when reproduced at distinct environments (Brown and Caligari, 2008). As indicated by Khalil et al. (2011), several stability statistic studies have been done to partition GEI which includes regression analysis (Gauch, 1988), multivariate analysis (Westcoff, 1987), cluster analysis (Crossa et al., 1991), additive main effect and multiplicative interaction (AMMI) model (Gauch, 1992) and GGE-biplot (Yan, 1999).

The information on genetic correlation and stability analysis could be beneficial for making breeding strategies as well as to manage available funds, resources and time to achieve the desired research goal. Therefore the objectives of this study were; to estimate the genetic correlation between grain yield and other agronomic traits and to determine the stability of the genotypes across various locations.

MATERIALS AND METHODS

Six extra-early quality protein maize (QPM) F_6 inbred lines were obtained from International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria (Table 1). These were crossed in the major season of the year 2011 in partial diallel mating design to form 15 F_1 hybrids using hand-pollination (Table 2). These single cross hybrids were produced and evaluated in the major season of 2012 at Crops Research Institute (CRI) – Fumesua in the forest ecological zone of Ghana with coarse sandy-loam soil. The field evaluation was replicated at Ejura in the forest transition zone with fine coarse

Table 3. Phenotypic correlation matrix of measured traits across all the locations.

Variables	GY	DTA	DTS	ASI	PHT	EHT	TGW	CL	CD	NRC	NKR	SL
GY	-											
DTA	-0.27***	-										
DTS	-0.3***	0.94***	-									
ASI	-0.15*	0.04	0.39***	-								
PHT	0.56***	-0.43***	-0.44***	-0.12	-							
EHT	0.33***	-0.39***	-0.38***	-0.08	0.74***	-						
TGW	0.61***	0.01	-0.01	-0.07	0.38***	0.05	-					
CL	0.47***	-0.15*	-0.16	-0.08	0.49***	0.43***	0.15**	-				
CD	0.68***	-0.27***	-0.3***	-0.17**	0.47***	0.34***	0.42***	0.55***	-			
NRC	0.34***	-0.2**	-0.17**	0.04	0.3***	0.26***	0.12**	0.31***	0.55***	-		
NKR	0.39***	0.01	0	-0.02	0.27***	0.16**	0.16**	0.54***	0.36***	0.34***	-	
SL	0.04	-0.16**	-0.17**	-0.06	0.05	0.14**	-0.16**	0.07*	0.25***	0.17**	-0.19**	-
RL	0.02	0.13**	0.17**	0.13*	-0.23**	-0.18**	0.01	-0.07	0.02	0.06	0.19**	-0.14*

GY; Grain yield; DTA; days to 50% anthesis; DTS, days to 50% silking; ASI, anthesis-silking interval; PHT, plant height; EHT, ear height; TGW, thousand grain weight; CL, cob length; CD, diameter; NRC, number of rows per cob; NKR, number of kernels per row; SL, stem; RL, root lodging. *, Significant ($P<0.05$); **, high significant ($P<0.01$); ***, highly significant ($P<0.001$).

sandy-loam soil, Pokuase and Akomadan in the coastal savannah and semi-deciduous forest ecological zones respectively with coarse sandy-loam soil for both locations (Sallah et al., 2004).

Randomized complete block design (RCBD) with three replications and two-row plot of 5 m long each with planting interval of 75 cm × 40 cm was used. Three seeds were sown per hill and later thinned to two plants per hill at three weeks after planting (WAP) to obtain a final planting density of approximately 66,000 plants ha^{-1} in each trial. Normal field management practices such as fertilization, weeding, pest and disease control were used for each location.

Data collection and analysis

For each plot, five plants were randomly sampled for data on agronomic and morphological characters. Border plants on each row as well as non-competitive plants were excluded. Days to 50% anthesis and full emergence of silks were also recorded and designated as Anthesis (AD) and silking (SD), respectively. Anthesis–silking interval (ASI) was calculated as the difference between number of days to 50% silking and anthesis (SD–AD). A measuring pole was used to measure from the ground level to the node bearing the uppermost ear and flag leaf node and was considered as ear and plant heights respectively. At physiological maturity, root and stem lodging parameters were taken as the percentage of plants leaning at an angle greater than 45° from the vertical and percentage of plants with broken stalks at or below the main ear at maturity respectively. After harvesting, grain weight was obtained using weighing scale. Thousand (1000) kernel weights were determined for each plot. Cob diameter was measured at mid-portion along the cob (n=5) whilst cob length was measured as length of the cob (n=5) from the base to the tip using callipers. The kernel number per row and number of rows per cob were counted and averages recorded for each plot. Estimates of correlation coefficients were determined to show the degree of association between yield and its components, and among yield components using Genstat version 9.2. The genetic (r_G) and phenotypic correlations (r_P) between two characters, X and Y, were estimated according to Akhtar et al. (2011):

$$r_G = \frac{COV_{G(XY)}}{\sqrt{V_{G(X)} . V_{G(Y)}}}$$

Where, $COV_{G\ (XY)}$ = Genetic covariance among trait X and Y; $V_{G(X)}$ and $V_{G(Y)}$ = Genetic variance for trait X and Y, respectively.

$$r_P = \frac{COV_{P(XY)}}{\sqrt{V_{P(X)} . V_{P(Y)}}}$$

Where, $COV_{P\ (XY)}$ = Phenotypic covariance among traits X and Y; $V_{P(X)}$ and $V_{P(Y)}$ = Phenotypic variance for traits X and Y, respectively.

The grain yield of individual genotypes was analysed using additive main effects and multiplicative interactions (AMMI) statistical model (MATMODEL 2.0 (Gauch, 1993) to obtain analysis of variance and mean estimates of AMMI.

RESULTS

Results from phenotypic correlation showed that grain yield had a highly positive correlation ($P<0.001$) with plant height, ear height, cob length, cob diameter and number of rows per cob at Ejura and Akomadan (Data not shown). Grain yield showed highly positive correlation with thousand grain weight and number of kernels per row across all locations (Table 3). At flowering there was a highly significant ($P<0.001$) positive association between days to 50% anthesis and silking across locations. However, DTS and DTA correlated negatively ($P<0.05$) with plant height, ear height, cob length, cob diameter, and stem lodging. There was no association between days to silking and number of kernels per row. Plant height and ear height showed positive and highly significant ($P<0.001$) correlation, and both had similar

Table 4. AMMI Analysis of grain yield.

Source	DF	SS	MS	F	F_prob	% of total $_{ss}$
Total	263	155797429	592386			
Treatments	87	89778856	1031941	2.74	0.001	
Genotypes	21	16206650	771745	2.05	0.01	10.40
Environment	3	55432532	18477511	52.75	0.00000	35.78
Block	8	2802021	350253	0.93	0.49257	
Interaction	63	18139674	287931	0.77	0.88866	
IPCA1	23	10621260	461794	1.23	0.22806	
IPCA2	21	4462626	212506	0.56	0.93696	
Residual	19	3055787	160831	0.43	0.98307	
Error	168	63216552	376289			

SS, Sum of squares; MS, Mean square; DF, Degree of freedom, and F-test used to measure significant at 0.01 F probability level.

association with cob length, cob diameter, number of rows per cob and number of kernels per row. On the other hand, plant height and ear height had negative and highly significant (P<0.01) correlation with root lodging. Thousand grain weight significantly (P<0.01) correlated positively with plant height, cob length, cob diameter, number of rows per cob and number of kernels per row across all the locations. It was however observed to have negative and highly significant (P<0.01) correlation with stem lodging. The association between cob length and cob diameter was significant (P<0.001) positive.

In the additive main effects and multiplicative interaction (AMMI) analysis of stability and adaptability for grain yield (Table 4), two principal component (PC) axes were generated to decompose genotype × environment interaction and both were not significant. By principle, AMMI analysis is used when genotype by environment interaction (GEI) is significant however this was done to identify the relative importance of these factors. The main effects of genotype and environment were significant at (P<0.01) and (P<0.001), respectively but the contribution of environment (35.8%) was higher than genotypes (10.4%).

DISCUSSION

Genetic correlation analysis is an important tool for estimating the value and association of various characters with grain yield (Edmeades et al., 1997). The genetic association among traits plays a vital role in improving selection efficiency in plant breeding programs. In selection programs, grain yield and some yield components (such as number of rows per cob, cob length and diameter) are among the most economic traits usually targeted by plant breeders. The studies on relationships among yield and related characters could be important strategy for crop improvement. Therefore, special preferences should be given to these parameters when formulating indirect selection indices for grain yield improvement in maize. The corroborative reports of significant positive correlation between grain yield and other yield components suggests that any one of the traits could be used to select indirectly for grain yield. For instance, Yousuf and Saleem (2001), affirmed the opportunity to select plant height, number of kernels per row cob length (Ali et al., 2010) thousand-grain weight, cob diameter, and number of rows per cob (Rafiq et al., 2010) indirectly for grain yield. On the other hand, the strong positive correlation between traits (days to anthesis and silking; plant height and ear height) suggests that each of two pairs of traits may either be controlled by the same or similar genes or by genes with pleiotropic effect on these traits or may be controlled by closely linked genes (Brown and Caligari, 2008). However, both days to anthesis and silking exhibited negative significant correlation with grain yield, plant height, ear height, cob diameter and stem lodging. Hence, flowering days seems undesirable for indirect selection for these traits. The negative significant association between days to flowering and grain yield agrees with Jayakumar et al. (2007). Depending on the breeder’s objectives, the strong positive association between plant height and ear height as well as their relationship with other traits (thousand-grain weight, cob length, cob diameter, number of rows per cob, number of kernels per row and root lodging) can play a major role in formulating selection indices. The positive correlation among some yield components (thousand-grain weight, cob length, cob diameter, number of rows per cob and number of kernels per row) suggests their usefulness for indirect selection.

The magnitude and nature of genotype by environment (GE) effect displayed by additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield in the main effects showed higher environmental effects than the genotypic effects. According to Easwari and Sheela (1998), and Cach et al. (2006) as cited by Ssemakula et al. (2007), the predominance of environmental effect over genotypic effect was because yield is a polygenic trait and, therefore, subject to much influence from the environment. As observed in the AMMI analysis, the non-significant GE interaction implies that the genotypes had similar responses across the environments in which they were evaluated and that all the genotypes can reliably be assessed under anyone of the locations used for this study in future or advance evaluation trials (Yan and Tinker, 2006). In other words, it is unnecessary to assess these genotypes simultaneously in the multi-environments used for the study in subsequent evaluations, thereby offering an opportunity to manage the limited resources available for the testing program (Tonk et al., 2011).

Conclusion

The correlation among studied traits especially the positive association between grain yield and other essential yield components (such as thousand-grain weight, cob length, cob diameter, number of rows per cob and number of kernels per row) gives a positive indication that these traits could be considered in developing selection indices in maize improvement programs. The non-significant genotype × environment interaction revealed by AMMI suggests that the relative performance of the genotypes in grain yield did not change across all environments hence anyone of the locations used in this study can be used for subsequent evaluations.

Conflict of Interest

The authors have not declared any conflict of interest.

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