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Stability in Performance of Normal and Nutritionally Enhanced Highland Maize Hybrid Genotypes in Eastern Africa

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Abstract: Maize (*Zea mays* L.) is a major crop in Eastern Africa in terms of production, consumption and income generation. Although highland ecologies in Eastern Africa have high potential for maize production, few varieties have been developed. Breeding efforts have been also concentrated on Quality Protein Maize (QPM) as a viable and cheaper method to alleviate malnutrition. Twenty conventional and 20 QPM three-way hybrid genotypes were developed and evaluated in a randomized block design across 11 and 8 environments in Ethiopia, Kenya, Rwanda and Uganda in 2010. The objective was to identify superior and stable varieties from genotypes. Data were recorded on major agronomic traits (grain yield t ha^{-1}). Additive main effects and multiplicative interactions (AMMI) statistical model was used to assess stability in performance for grain yield. Combined analysis of variance across environments indicated highly significant differences among non-QPM and QPM genotypes. Variations due to environment and genotype×environment (GxE) were suggesting genotypes performed differently across environments. Environments of Gisozi, Holleta, Kongoni and Kapchorwa were favourable and stable while Kulumsa was favourable but unstable. Other environments were of medium to low potential. The AMMI analysis ranked 5 non-QPM genotypes were with above-average yield (6.34 t ha^{-1}) and 8 for stability performance across environments. While for QPM 3 genotypes were yielded better than best check (6.94 t ha^{-1}) and 7 genotypes were stable. Genotype 9 (7.15 t ha^{-1}) was the only non-QPM genotype with yield better than the best check across environments. The information obtained will help to streamline highland maize testing programs in the region.

Key words: Stability, highland maize, quality protein maize, AMMI

INTRODUCTION

Maize is a major staple food crop in eastern Africa comprising a significant part of the diet. It is also source of household income and used as animal feed. Maize production, processing and utilisation play a major role in the livelihoods of the majority of the population. In the region all major agro-ecological zones up to 2400 m above sea level (a.s.l) are favourable for maize cultivation (Twumasi-Afriyie *et al*., 2001). The highland zone in the region represents a very favourable maize growing environment and large quantities of maize is produced. In eastern Africa the highland maize growing agro-ecology stands second in maize production next to mid altitude. The agro-ecology is distinguished by high rainfall seasonal cool temperatures, high population density and high levels of poverty (Banziger and Diallo, 2000). Regardless of all the potentials stated above maize production in the highland agro-ecologies is categorized under low yields because of unavailability of improved varieties and extensive lack of infusion of new germplasm in the region. Although maize is an important staple food

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for many communities in the region, maize protein is deficient in two essential amino acids, lysine and tryptophan that can only be obtained from food as they cannot be metabolically synthesized (NRC, 1988). The quantity of lysine and tryptophan in Quality Protein Maize (QPM) is almost double that of conventional (normal) maize. These amino acids are essential building blocks of protein in humans and mono-gastric animals such as poultry and pigs (CIMMYT, 2000). QPM is also superior to conventional (normal) maize as an animal feed for poultry and pig, increasing animal weight gain and it provides an additional potential benefit by indirectly increasing available protein for livestock (Qi *et al.*, 2004). Thus, the utilization of QPM in the highlands of Eastern and Central Africa (ECA) region will alleviate undernourishment leading to healthy population, improved productivity and increased incomes for enhanced livelihoods.

With this background, activities were initiated in Eastern Africa to develop and release improved normal and nutritionally enhanced (QPM) varieties with higher yields, resistance to common foliar diseases and adapted to the highland ecology. The highland maize breeding program was collaboration between International Maize and Wheat Improvement Centre (CIMMYT) and National Agricultural Research Institutes (NARIs) of the eastern African countries. It comprises Burundi, Ethiopia, Kenya, Rwanda, Tanzania and Uganda under the umbrella of the previous East and Central Africa Maize and Wheat Network (ECAMAW) and now under the staple crops program of Association for Strengthening Agricultural Research in East and Central Africa (ASARECA). A regional nursery was established at Ambo, Ethiopia in 1998 to run the breeding program. Local germplasm was collected in the six countries and crossed with CIMMYT germplasm to develop improved hybrids and inbred lines for the highland ecologies of ECA. Varieties developed through this breeding programme continue to be evaluated in multi-environments across various locations (environments) in the region. Stability and wide adaptation are of these hybrid genotypes has vital importance in a region where fluctuations in growing conditions exist. Therefore, by exploiting the good adaptation and stability of yield in highland maize, it would be possible to identify high yielding and well adapted varieties.

Stability of yield is important in highland maize hybrid genotypes because varieties are developed in one country and tested in multi-environments with the expectation adapted to be released and grown across several locations over years. The most important agronomic and economic traits in maize are quantitative in nature and affected by genotype by environment interaction (Hallauer and Filho, 1981; Fan *et al.*, 2007). Genotype by environment interaction is common phenomenon in breeding and variety evaluation shown by several studies (Brancourt-Hulmel and Lecomte, 2003; Yan and Kang, 2003; Fan *et al.*, 2007). The Additive Main and Multiplicative Interaction (AMMI) model has been recommended as a better model for analysis of genotype by environment (G×E) interaction in multi-location varietal trials (Zobel *et al.*, 1988). It not only gives estimates of total GxE interaction effect of each genotype but also partitions it into interaction effects due to individual environments. It also combines conventional Analysis of Variance (ANOVA) with principal component analysis and may provide more reliable estimates of genotype performance than the mean across sites. This study was undertaken to analyze GxE interaction and evaluate the adaptability and stability of yield performance of twenty highland maize nutritionally enhanced (QPM) and normal (non-QPM) hybrid genotypes, respectively. The specific objectives were to: (1) Evaluate yield potential of highland maize hybrid genotypes in eastern Africa, (2) Determine the nature of GxE and (3) Determine stability of adapted hybrid genotypes using stability parameters.

MATERIALS AND METHODS

Materials used: This study was based on the normal (non-QPM) test hybrid genotypes developed by crossing early generation germplasm from CIMMYT-Zimbabwe with Ecuador, Kitale and pool9A testers (Twumasi-Afriyie *et al.*, 2003; Gudeta *et al.*, 2012). Promising materials were subjected to successive evaluations, selections and advancements to generate the 20 elite hybrid genotypes that constituted the study materials. The 20 QPM hybrid genotypes were developed through conversion of promising elite non-QPM materials developed by highland maize research project at Ambo using CIMMYT QPM donor lines (CML144, CML159 and CML176; Twumasi-Afriyie *et al.*, 2012, 2003). Adequate seed of the two categories of hybrid genotypes was produced and two trials of three-way crosses were generated and conducted across the region.

Description of the experimental sites: The non-QPM trials were conducted in Ethiopia at Ambo (8°59'N 37°51'E), Holleta (9° 4' 0" N, 38° 30' 0" E), Kulumsa (8°02’N, 39^{O}07’E), Kokate (6°52’42”N 37^{0}48’E), Adet (11°16' 0"N, 37° 29'0" E) and Haramaya (9°36'N 41°52'E); Kenya at Kitale (1.02°N, 35°E) and Kongoni (1°16' 0.01"S 37°9' 0.00’’ E); Uganda at Kapchorwa (1.38°N, 34.52°E); Burundi at Gisozi (2°30'34"S, 30°24' 20"E) and Munanira (3°17'40"S, 29°44'26"E) both sites representing the highland environments. The QPM trials were conducted at: Ambo, Holleta, Kulumsa and Setema (8°10'0"N,36°6'0"E) in Ethiopia; Kitale and Turbo in Kenya; Kapchorwa in Uganda and Gisozi in Burundi in

2010. The lists of hybrid genotypes used for non-QPM and QPM stability in performance study including two checks are given in Annex I.

The experiments were established following a randomized complete block design, with two replications per site. Single row plots of 5.25 m long were used. The inter row spacing was 0.75 m, while the intra row spacing was 0.25 m, giving a population density of 53,333 plants per hectare. Data was recorded on grain yield (t ha^{-1}) for stability study of hybrid genotypes in performance across environments.

Data analysis: There are many statistical methods available to analyse the GxE interaction (combined ANOVA, stability analysis and multivariate analysis). Combined ANOVA is more often used to identify the existence of GxE interactions in multi-environmental experiments. However the main limitation of this analysis is the assumption of homogeneity of variance among environments required to determine genotype differences. Although, this analysis allows the determination of components of variances arising from different factors (genotype, environment and G×E interaction), it doesn't allow exploring the response of genotypes in the non-additive term; the GxE interaction (Zobel *et al.*, 1988; Gauch, 1992). AMMI is a combination for the main effects of the genotypes and the environment together with Principal Components Analysis (PCA) the genotype-environment interaction (Zobel *et al.*, 1988; Guach Jr., 1988; Gauch, 2006). The data obtained on grain yield (t ha^{-1}) was organized and subjected to general Analysis of Variance (ANOVA) using GenStat edition 3 (Wim *et al.*, 2007). Single site and across sites analysis was performed and the means were separated using the Least Significant Differences (LSD) at $p<0.05$. The additive main effects and multiplicative interactions (AMMI) model was used to compare genotype stability in performance across the various environments of the form:

$$Y_{ijl} = \mu + G_i + E_j + (\sum \lambda_k \alpha_{ik} \gamma_{jk}) + d_{ij} + e_{ijl} \qquad (1)$$

where, λ_k = kth eigenvalue, α_{ik} = principal component score for the ith genotype for the kth principal component axis, γjk = principal component score for the jth environment for the kth principal component axis, d_{ij} = residual G×E not explained by model.

AMMI estimates for performance of genotype i in the environment as:

$$E(Y_{ijl}) = \mu + G_i + E_j + (\sum \lambda_k \alpha_{ik} \gamma_{jk}) \qquad (2)$$

The AMMI Stability Value (ASV) was used to rank hybrid genotypes in terms of stability as described by Purchase (1997).

$$\text{AMMI Stability Value (ASV)} = \sqrt{\left[\frac{\text{SSIPCA1}}{\text{SSIPCA2}}(\text{IPCA1Score})\right]^2} + [\text{IPCAScore2}]^2$$

The ASV is the distance from the coordinate point to the origin in a two-dimensional interaction principal components analysis 1(IPCA1) scores against principal components analysis 2 (IPCA2) scores in the AMMI model (Purchase, 1997). Because IPCA1 score contributes more to GE interaction sum of square, a weighted value is needed. This weight is calculated for each genotype and environment according to the relative contribution of IPCA1 to IPCA2 to the interaction Sum of Square. Where:

$$\frac{\text{SSIPCA1}}{\text{SSIPCA2}}$$

is the weight given to the IPCA1 value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares.

RESULTS AND DISCUSSION

Combined analyses of variance showed high significant differences ($p<0.01$) of yield between both non-QPM and QPM hybrid genotypes (Table 1). There were also significant differences in sites ($p<0.01$ and their interactions ($p<0.01$) suggesting non-QPM and QPM hybrid genotypes performed differently across the 11 and 8 sites, respectively. This implying there was genotype by environment (G×E) interaction affecting the performance of the various hybrid genotypes.

Table 1: Combined Analysis of variance of grain yield (h^{-1}) of non-QPM and QPM hybrid genotypes over 11 and 8 sites in eastern Africa

	DF		SS		MS		VR		F probability	
Source of Variation	Non QPM	QP M	Non QPM	QP M	Non QPM	QP M	Non QPM	QP M	Non QPM	QPM
Rep	1	1	12.97	8.210	12.97	8.210	8.74	4.80		
Genotype	21	21	89.75	255.511	4.27	12.170	2.88	7.11	<0.001	<0.001
Site	10	7	3514.72	3178.330	351.47	454.050	236.79	265.43	<0.001	<0.001
Genotypex Site	210	147	452.08	373.840	2.15	2.543	1.45	1.49	0.003	0.006
Residual	241	175	357.72	299.361	1.48	1.711				
Total	483	351	4427.24	4115.248						

DF: Degree of freedom, SS: Sum of Squares, Mean Squares, VR: Variance Ratio (MS/Residual MS, QPM: Quality Protein maize

Table 2: Additive main effects and multiplicative interaction analysis of variance for grain yield of non- QPM and QPM genotypes across environments

	DF		SS		MS		F		F probability		Explained (%)	
Source of variation	Non QPM	QPM	Non QPM	QPM	Non QPM	QPM	Non QPM	QPM	Non QPM	QPM	Non QPM	QPM
Genotypes	21	21	90	256	4.27	12.17	3.46	8.90	0.00	0.00	2.0	6.2
Environment	10	7	3515	3178	351.47	454.05	45.47	46.58	0.00	0.00	79.4	77.2
Blocks within environment	11	8	85	78	8.50	9.75	6.25	7.13	0.00	0.00	1.9	1.9
Interactions	210	147	452	374	2.15	2.54	1.74	1.86	0.00	0.00	10.2	9.1
IPCA1	30	27	144	143	4.80	5.31	3.89	3.88	0.00	0.00	14.3	38.2
IPCA2	28	25	112	91	4	3.64	3.23	2.66	0.00	0.00	13.3	24.3
IPCA3	26	23	65	54	2.5	2.44	2.02	1.71	0.00	0.03	12.4	14.4
Residuals	126	72	131	86	1.04	1.19	0.84	0.87	0.86	0.74		
Error	231	351	286	230	1.24	11.72						
Total	483	168	4427	4115	9.17	1.37						

DF: Degree of freedom, SS: Sum of Squares, Mean squares, VR: Variance ratio (MS/Residual MS,QPM: Quality protein maize F: F-test

AMMI analysis of variance of grain yield for non-QPM hybrid genotypes, effects of Genotype (G), environment (E) and their interactions (G×E) were highly significant ($p<0.001$) (Table 1). The main effects of G and E accounted for 2 and 79.4%, respectively and G×E interaction accounted for 10.2% of the total variation of Sum of Squares (Table 2). QPM hybrid genotypes under 8 environments also showed that all three components of variance, Genotype (G), Environment (E) and G×E were highly significant ($p<0.0001$) (Table 2). The main effects of G and E accounted for 6.2 and 77.2%, respectively and GxE interaction accounted for 9.1% of the total Sum of Squares (Table 2). The residual contributes about 8% for non-QPM and 7% of QPM genotypes Sum of Squares of the treatments. Therefore, AMMI model gave a fit of 92% in both cases for non-QPM and QPM genotypes. A large sum of squares for environments indicated that the environments were diverse with large differences among environmental means causing the most of the variation in the grain yield. The results for QPM performance were similar to that for non-QPM genotypes showing environmental conditions accounting for most of the total variation indicating wide variations and potential of different test sites (Taye *et al*., 2000; Kaya *et al*., 2002; Alberts, 2004; Mohammadi *et al*., 2007; Admassu *et al*., 2008; Kandus *et al*., 2010).

The G×E interaction for non-QPM genotypes grain yield was partitioned Into interaction Principal Component Axis (IPCA): IPCA1, IPCA2, IPCA3 and residual effects (Table 2). Results showed that IPCA1 accounted for 32%, IPCA2 accounted for 25% and IPCA3 accounted for 14% of the G×E interaction (Table 2). The mean squares for IPCA1 and IPCA2 were highly significant ($p<0.0001$) and cumulatively contributed to 57% of the total GxE interaction. The GxE interaction for QPM genotypes grain yield indicated that IPCA1 accounted for 38%, IPCA2 accounted for 24% and IPCA3 accounted for 14% of the total interaction (Table 2). These results are in agreement with the findings that the most accurate model for AMMI can be predicted by using the first two PCAs (Gauch and Zobel, 1997; Yan *et al*., 2000; Annicchiarico, 2002; Admassu *et al*., 2008). The AMMI analysis should thus, provide an understanding of G×E, increase accuracy of yield estimates using means for multiplicative interactive effects and increase probability of identifying superior and most adapted genotypes.

Genotype by environment interaction effects of genotypes in different environments showed that non-QPM genotypes 15, 14, 18, 3, 19 and 20 had high positive interaction while genotypes 22, 13 and 10 had high negative interaction with environmental conditions (Table 3). Genotype 6 had lowest positive interaction and genotypes 21 had lowest negative interaction. While QPM genotypes 20, 12, 3, 11, 12 and 4 had high positive interaction and genotypes 17, 16, 7, 6 and 14 had high negative interaction with environmental conditions (Table 2). QPM genotypes 15 and 10 had lowest positive interaction and 22 and 5 had lowest negative interaction (Table 3). A genotype showing high positive interaction in an environment has the ability to exploit the agro-ecological condition of the specific environment and therefore, best suited to that environment (Kandus *et al*., 2010). In AMMI analysis, the IPCA scores of genotypes are an indicator of stability or adaptation over environments (Gauch and Zobel, 1996; Purchase, 1997; Alberts, 2004, Admassu *et al*., 2008). The greater the IPCA scores, the more specific adapted is the genotype to certain environments. The more IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments.

According to the AMMI Stability Value (ASV) non-QPM genotypes 8 followed by 7 then 1, 20 and 9 were stable and genotypes 22, 15, 12, 13 and 10 were least stable (Table 3). Only genotype 9 (7.2 t ha^{-1}) had average yield better than the best check (6.9 t ha^{-1}) across the eleven environments but only hybrids 2, 13 and 20 had yields less than mean of checks (6.2 t ha^{-1}). For QPM genotypes 15 followed by 1 then 13, 9 and 18 were

Table 3: AMMI adjusted mean grain yield (t ha^{-1}), IPCA scores and AMMI stability value (ASV) of 22 QPM and 22 non-QPM hybrid genotypes tested across 8 and 11 environments, respectively

QPM Genotypes	Mean yield (t ha^{-1})	IPCA1	IPCA2	ASV	Non-QPM genotypes	Mean yield (t ha^{-1})	IPCA1	IPCA2	IPCA3	ASV
G1	7.527	0.257	-0.088	0.421	G1	6.522	0.295	0.384	-0.305	0.490
G2	6.548	-0.629	1.071	1.469	G2	5.702	-0.363	-0.472	0.382	0.608
G3	6.950	0.879	0.711	1.576	G3	6.522	0.549	0.713	-0.039	0.714
G4	7.210	0.442	0.555	0.899	G4	5.761	-0.448	-0.583	0.291	0.651
G5	5.909	-0.227	0.669	0.761	G5	6.682	0.241	0.313	0.533	0.618
G6	7.235	-0.678	0.434	1.168	G6	6.507	0.035	0.045	-0.928	0.929
G7	7.256	-0.855	-0.069	1.369	G7	6.568	-0.248	-0.322	0.216	0.387
G8	7.215	0.104	0.655	0.675	G8	6.335	-0.257	-0.334	0.086	0.345
G9	7.842	0.302	-0.296	0.566	G9	7.155	-0.370	-0.481	-0.235	0.536
G10	8.757	0.022	-0.769	0.770	G10	5.982	-0.605	-0.786	1.005	1.276
G11	6.887	0.586	0.229	0.964	G11	6.899	-0.337	-0.439	0.319	0.542
G12	8.938	0.988	-0.694	1.727	G12	6.619	-0.259	-0.336	-0.477	0.584
G13	6.773	0.315	0.149	0.526	G13	5.942	-1.012	-1.316	-0.239	1.338
G14	7.974	-0.673	-0.428	1.158	G14	6.217	0.886	1.152	-0.364	1.208
G15	7.304	0.009	-0.310	0.310	G15	6.233	1.138	1.479	0.069	1.481
G16	6.750	-0.874	0.468	1.474	G16	6.787	0.424	0.551	-0.815	0.984
G17	6.952	-0.910	0.018	1.457	G17	5.920	0.273	0.355	0.783	0.859
G18	8.083	0.260	-0.424	0.593	G18	6.016	0.857	1.114	-0.464	1.206
G19	9.219	-0.608	-1.026	1.414	G19	6.294	0.483	0.628	-0.051	0.630
G20	7.081	1.308	0.291	2.113	G20	6.442	0.407	0.529	-0.045	0.531
G21	8.716	0.189	-0.598	0.670	G21	5.420	-0.139	-0.181	1.330	1.342
G22	8.601	-0.207	-0.549	0.642	G22	6.944	-1.547	-2.012	-1.050	2.269

QPM: Quality protein maize, ASV: AMMI stability value

Table 4a: Mean yield (t ha^{-1}) of 22 non-QPM hybrid genotypes (G1 to G22) tested at 11 sites in eastern Africa in 2010

	Ethiopia						Burundi		Uganda	Kenya		
Genotypes	Adet	Alemaya	Ambo	Holetta	Kokate	Kulumsa	Gisozi	Munanira	Kapchorwa	Kitale	Kongoni	Mean
1	5.95	6.73	5.91	7.39	4.09	8.86	10.15	3.00	11.53	2.39	5.73	6.52
2	6.13	5.18	5.68	7.30	3.54	10.11	6.86	2.80	9.48	1.49	4.15	5.70
3	6.70	6.55	6.46	8.18	4.59	8.37	8.72	3.57	10.11	1.71	6.77	6.52
4	4.47	6.36	6.59	7.37	2.87	9.43	6.69	3.61	10.52	1.25	4.21	5.76
5	6.98	6.25	5.75	9.24	3.51	9.06	7.81	4.00	13.38	1.61	5.92	6.68
6	4.99	7.20	7.18	9.00	1.87	9.38	0.48	3.26	10.10	1.82	6.30	6.51
7	6.56	7.36	6.56	8.46	3.09	8.89	8.90	4.30	13.79	0.54	3.81	6.57
8	6.51	7.58	6.13	8.25	2.92	9.01	8.39	3.65	11.84	1.51	3.88	6.33
9	6.59	6.49	8.61	9.46	3.64	10.58	0.10	2.80	13.49	2.05	4.88	7.15
10	5.70	6.25	7.36	7.21	2.08	10.40	5.46	3.02	12.25	0.98	5.08	5.98
11	7.22	5.43	7.94	7.18	4.63	11.54	9.37	3.05	12.05	1.74	5.74	6.90
12	5.64	7.63	7.57	11.46	4.04	8.97	7.90	3.05	10.83	0.88	4.83	6.62
13	5.56	7.78	6.83	8.40	3.23	10.60	7.28	2.64	8.55	1.59	2.90	5.94
14	6.19	5.21	7.27	8.44	3.86	6.80	9.40	3.16	10.30	1.94	5.81	6.22
15	6.68	5.22	6.34	8.39	3.03	6.82	8.53	3.09	11.15	2.01	7.31	6.23
16	5.52	6.13	7.45	9.29	4.51	8.72	10.60	2.99	10.51	2.84	6.09	6.79
17	6.56	5.05	5.68	7.38	3.55	9.06	6.25	3.66	10.21	1.64	6.08	5.92
18	6.15	5.21	5.65	8.80	3.68	6.78	9.37	2.77	10.22	2.37	5.18	6.29
19	7.20	6.25	7.46	8.21	2.92	7.83	8.66	2.48	10.71	1.74	5.78	6.44
20	6.80	5.60	6.91	8.27	4.33	8.56	8.97	3.45	10.52	1.75	5.69	5.42
21	7.01	4.76	6.37	5.51	3.43	9.00	4.91	2.91	10.30	1.49	3.92	5.42
22	5.15	7.74	7.39	9.58	4.24	13.68	10.93	2.40	10.50	0.97	3.81	6.94
Mean	6.19	6.27	6.78	8.31	3.53	9.20	8.44	3.17	11.02	1.65	5.18	6.34
LSD (5%)	2.56	2.91	2.11	2.02	1.76	2.86	2.84	0.85	3.36	1.76	1.75	2.40
CV (%)	19.80	22.30	3.60	11.70	24.00	15.00	16.20	12.90	14.70	24.00	16.20	19.20

stable while hybrids 20, 12, 3, 16 and 2 were unstable. QPM hybrids 19 (9.2 t ha^{-1}) and 12 (8.9 t ha^{-1}) had the highest yield across 8 locations (Table 3).

Regarding non-QPM genotypes performance across eleven different environments, genotypes above grand mean (6.34 t ha^{-1}) were 1,3,5,6,7, 9,11,12,16 and 22 rated best while genotypes closer to grand mean 8, 14,13, 15, 18 and 19 exhibited an average yield performance and genotypes below the grand mean 2,4,10, 17,20 and 21 exhibited poor performance across sites (Table 4a). However, the hybrids combining both high yield and stability across environments were genotypes 1, 5, 6, 7, 8, 11 and 12 (Table 4a). For QPM genotypes performance across

Table 4b: Mean yield (t ha^{-1}) of 22 QPM hybrid genotypes (G1 to G22) tested at 8 sites in east Africa in 2010

	Ethiopia				Burundi	Kenya		Uganda	
Genotypes	Ambo	Holleta	Jimma	Kulumsa	Gisozi	Kitale	Turbo	Kapchorwa	Mean
1	6.45	9.97	3.57	9.35	2.41	7.26	13.74	7.47	7.53
2	6.22	5.79	2.18	7.15	3.16	8.00	12.62	7.27	6.55
3	6.92	8.66	2.34	8.19	3.02	4.88	12.69	8.89	6.95
4	6.26	8.55	3.16	9.38	3.64	5.90	12.44	8.35	7.21
5	5.74	6.91	2.75	6.10	3.14	6.62	9.38	6.62	5.91
6	5.52	7.44	3.20	9.01	3.30	8.90	12.82	7.67	7.23
7	5.39	8.29	1.95	9.59	2.89	9.84	13.51	6.58	7.26
8	6.31	7.82	3.14	8.31	2.77	7.09	12.82	9.46	7.22
9	7.23	10.79	2.97	9.76	3.32	7.95	12.15	8.57	7.84
10	6.83	11.97	6.12	10.95	3.00	9.38	12.62	9.18	8.76
11	5.78	9.27	2.48	8.49	2.55	5.76	12.60	8.16	6.89
12	9.89	13.68	3.53	9.58	3.18	8.32	12.97	10.34	8.94
13	7.35	8.88	3.31	7.71	1.94	6.40	11.95	6.65	6.77
14	6.67	9.07	3.50	11.20	2.74	0.14	12.31	8.17	7.97
15	5.00	10.09	3.66	9.41	2.41	7.63	13.33	6.89	7.30
16	5.38	6.95	2.93	7.90	2.96	8.98	12.47	6.44	6.75
17	6.89	6.95	3.36	9.15	2.61	9.57	9.39	7.70	6.95
18	8.18	10.67	3.26	10.37	2.56	8.33	12.72	8.59	8.08
19	7.99	12.04	4.86	11.25	3.07	12.12	13.15	9.26	9.22
20	6.97	9.60	2.28	10.09	2.89	3.83	12.22	8.78	7.08
21	7.47	11.56	4.77	12.18	3.59	8.59	13.45	8.11	8.72
22	6.98	10.44	2.97	11.26	2.37	10.28	13.51	10.99	8.60
Mean	6.70	9.34	3.29	9.38	2.89	7.99	12.49	8.19	7.53
LSD (5%)	1.72	1.78	1.32	2.28	1.31	3.42	3.54	2.88	2.58
CV (%)	12.40	9.20	19.30	11.70	21.80	20.60	13.60	16.90	17.40

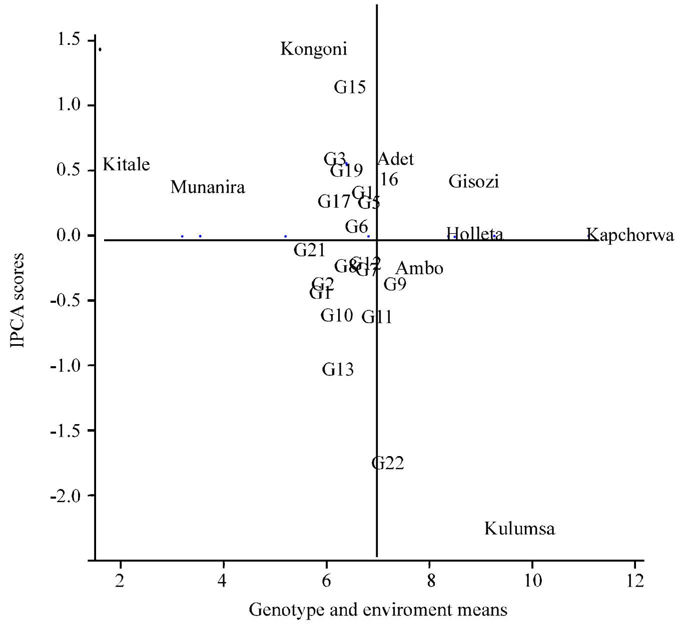

Fig. 1: AMMI1 showing interaction of genotype x environments for non-Quality protein Maize (QPM) hybrids

8 environments, genotypes above grand mean (7.53 t ha^{-1}) were 9, 10, 12, 14, 18, 19, 21 and 22 rated best and closer to grand mean 1, 4, 6, 7, 8, 15 and 20 exhibited average yield performance and below grand mean 2, 3, 11, 13, 16 and 17 exhibited poor performance across sites (Table 4b). AMMI analysis was also helpful in identifying the first best performing four genotypes for each environment for both non-QPM and QPM genotypes (Table 5).

Plotting the environments and the genotypes on the same graph, the relations between the genotype and environments can be clearly described (Fig. 1 and 2).

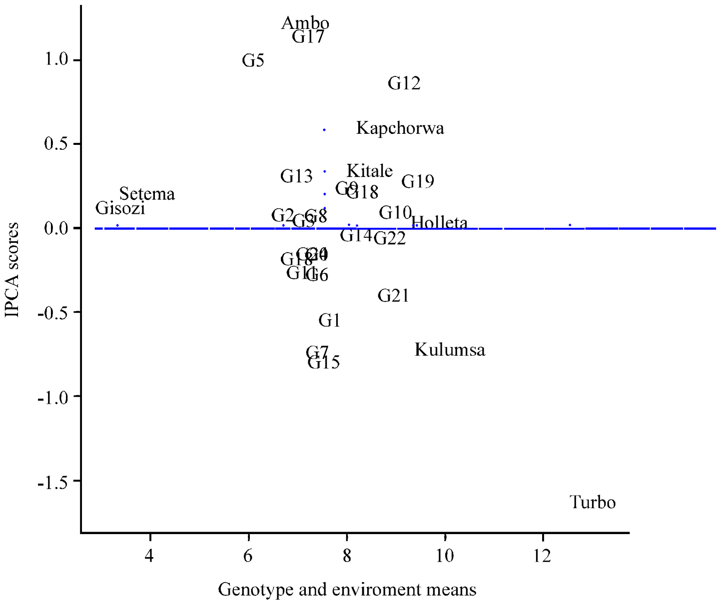

Fig. 2: AMMI3 showing interaction of genotype x environments of Quality Protein Maize (QPM) hybrid genotypes

Table 5: First best four non-QPM and QPM hybrid genotypes for each site as per AMMI analysis

Non-QPM Genotypes

Environment	Mean	Score	1st	2nd	3rd	4th
Kongoni	5.18	1.41	G15	G3	G14	G16
Kitale	1.65	0.56	G3	G16	G11	G20
Adet	6.20	0.54	G5	G11	G17	G15
Gisozi	8.44	0.42	G16	G6	G22	G9
Munanira	3.17	0.22	G5	G9	G11	G7
Awassa	3.53	0.19	G11	G16	G3	G22
Kapcho	1.02	0.01	G7	G5	G9	G10
Holleta	8.31	0.00	G22	G9	G6	G16
Ambo	6.78	-0.32	G22	G9	G11	G16
Alemaya	6.27	-0.81	G22	G9	G7	G12
Kulumsa	9.20	-2.21	G22	G13	G11	G9

QPM Genotypes

Environment	Mean	Score	1st	2nd	3rd	4th
Holleta	9.34	1.33	G12	G19	G10	G21
Kapchrowa	8.19	0.66	G12	G19	G10	G21
Ambo	6.70	0.62	G12	G19	G10	G18
Turbo	2.49	0.18	G21	G1	G15	G22
Kulumsa	9.38	-0.03	G19	G21	G10	G22
Gisozi	2.89	-0.12	G2	G8	G4	G6
Jimma	3.29	-0.23	G19	G12	G10	G22
Kitale	7.99	-2.40	G19	G14	G17	G22

Results from additive main effects and multiplicative interactions (AMMI) analysis of non-QPM genotypes indicated that Kulumsa, Gisozi, Holleta and Kapchorwa fall under high yielding environments; Alemaya, Ambo, Adet and Kongoni fall under medium yielding environments; while Kitale, Munanira and Kokate are under low yielding environments (Fig. 1). For QPM hybrids Ambo, Holetta, Kitale and Kapchorwa were high yielding and stable environments. Environment Kulumsa was found high yielding and unstable and Setema and Gisozi low yielding and stable (Fig. 2).

CONCLUSION

The analysis of variance for AMMI model of grain yield of both non-QPM and QPM hybrid genotypes revealed that genotypes, environments, G×E interaction were significant. According to AMMI stability value hybrids of non-QPM 8, 7, 1 and 20 and QPM 15, 1, 13, 9 and 18 were found stable. The best performing varieties from stability study will be further evaluated in performance trials across the region. Following across locations and years evaluation of the hybrids they can be released regionally those which had stable performance and to a specific country based on specific environment adaptation.

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Annex I: List of Genotypes used for the experiment

No.	Non QPM Hybrid Genotypes	QPM Hybrid Genotypes
1	[ECU/SNSYN[SC/ETO]]c1F1-##(GLS=1.5)-3-2-1-2-#-#-#-#/[POOL9Ac7-SR(BC2)]FS68-2SR-1-1-3-1-#-1-1-#//[POOL9Ac7-SR(BC2)]FS59-4-1-2-1-1-1-#-#-#-#	[POOL9Ac7-SR(BC2)]FS170-2-1-3-1-#/CML176(BC2)-28-1-1/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-21-2-1-#/CML176BC1F1-1-1-1//SADVLA/CML176 BC2F6-8-3-B
2	[ECU/SNSYN[SC/ETO]]c1F1-##(GLS=1.5)-3-2-1-2-#-#-#-#/[POOL9Ac7-SR(BC2)] FS68-2SR-1-1-3-1-#-1-1-#//[POOL9Ac7-SR(BC2)]FS67-1-2-3-1-#-#-#-#-#	[POOL9Ac7-SR(BC2)]FS170-2-1-3-1-#/CML176(BC2)-28-1-1/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-21-2-1-#/CML176BC1F1-1-1-1//SADVLA/CML176 BC2F6-8-5-B
3	[ECU/SNSYN[SC/ETO]]c1F1-##(GLS=1.5)-3-2-1-2-#-#-#-#/[POOL9Ac7-SR(BC2)]FS68-2SR-1-1-3-1-#-1-1-#//[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-23-3-3-1-1-#	[POOL9Ac7-SR(BC2)]FS170-2-1-3-1-#/CML176(BC2)-28-1-1/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-21-2-1-#/CML176BC1F1-1-1-1//SADVLA/CML176 BC2F6-8-12-B
4	[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-1-2-1-2-1-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-32-2-2-1-1-#-#//B.T.Z.T.V.C -43-B -2-1 -3-2-#-#	[POOL9Ac7-SR(BC2)]FS170-2-1-3-1-#/CML176(BC2)-28-1-1/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-21-2-1-#/CML176BC1F1-1-1-1//CML159
5	[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-1-2-1-2-1-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-32-2-2-1-1-#-#//{POOL 9AXMISSOU-MO17)-57X12-1)-1/POOL 9A C6 MHM 3-1-3-1-1-2p-3p-4p-1-1-1-B-B)-1-1-1-1	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-3-1-1//SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-48-1-1-#/CML176(BC2)-11-2-1-1-1-#
6	[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-1-2-1-2-1-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-32-2-2-1-1-#-#//{G9AC7HS 41-2/POOL 9A C6 MHM 3-1-3-1-1-2p-3p-4p-1-1-1-B-B)-1-1-1-1	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-3-1-1//[POOL9Ac7-SR(BC2)]FS60-2-1-1-1-#/CML176BC1F1-5-3-1-2-1
7	[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-1-2-1-2-1-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-32-2-2-1-1-#-#//SINT T.SR.B.T.Z.T.8P-1P-1-5P-1P-1P-1-3-#-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-3-1-1//CML144
8	[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-1-2-1-2-1-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-32-2-2-1-1-#-#//POOL 9A C6 R.L6-1P-1P-1P-2P-1P-2P-B-1-1-3-#-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-3-1-1//CML159
9	[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-1-2-1-2-1-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-32-2-2-1-1-#-#//[POOL9Ac7-SR(BC2)]FS59-4-1-2-1-1-1-#-#-#-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-3-1-1//CML491
10	[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-1-2-1-2-1-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-32-2-2-1-1-#-#//[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-21-2-3-1-1-1-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-3-1-1//142-1-eQ
11	SRSYN95[KIT//N3/TUX]F1-##(GLS=2)-22-2-2-2-2-#-#-#-#/SRSYN95[ECU//SC/ETO]F1-##(GLS=3)-43-1-2-1-1-#-#//[POOL9Ac7-SR(BC2)]FS67-1-2-3-1-#-#-#-#-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-3-1-1//F7215Q
12	[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-21-2-3-1-1-1-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-32-2-2-1-1//B.T.Z.T.V.C -43-B -2-3 -3-2-#-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-48-3-1-#/CML176(BC2)-3-1-1/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2.5)-32-1-1-#/CML176BC1F1-12-1-1//TUX/CML159 BC2F41-4-6-B
13	[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=1)-21-2-3-1-1-1-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-32-2-2-1-1//{POOL 9AXMISSOU-MO17)-35x12-1/G9AC7HS15-3}-2-1-2-2	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-48-3-1-#/CML176(BC2)-3-1-1/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2.5)-32-1-1-#/CML176BC1F1-12-1-1//[POOL9Ac7-SR(BC2)]FS67-1-2-3-1-#/CML144(BC2)-10-11-2-4-1-2
14	[POOL9Ac7-SR(BC2)]FS59-4-1-2-1-1-1-#-#-#-#/[POOL9Ac7-SR(BC2)]FS67-1-2-3-1-#-#-#-#-#//B.T.Z.T.V.C -43-B -2-2 -2-1-#-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-48-3-1-#/CML176(BC2)-3-1-1/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2.5)-32-1-1-#/CML176BC1F1-12-1-1//[POOL9Ac7-SR(BC2)]FS60-2-1-1-1-#/CML176BC1F1-5-3-1-2-1
15	[POOL9Ac7-SR(BC2)]FS59-4-1-2-1-1-1-#-#-#-#/[POOL9Ac7-SR(BC2)]FS67-1-2-3-1-#-#-#-#-#//{G9AC7HS 93-3/POOL 9A C6 MHM 3-1-3-1-1-2p-3p-4p-1-1-1-B-B)-1-1-1-1	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-48-3-1-#/CML176(BC2)-3-1-1/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2.5)-32-1-1-#/CML176BC1F1-12-1-1//CML159
16	[POOL9Ac7-SR(BC2)]FS59-4-1-2-1-1-1-#-#-#-#/[POOL9Ac7-SR(BC2)]FS67-1-2-3-1-#-#-#-#-#//[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-23-3-3-1-1-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-14-1-1//SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-48-1-1-#/CML176(BC2)-11-2-1-1-1-#
17	[POOL9Ac7-SR(BC2)]FS59-4-1-2-1-1-1-#-#-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-23-3-3-1-1-#//[POOL9Ac7-SR(BC2)]FS68-1-1-1-3-1-1-#-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-14-1-1//[POOL9Ac7-SR(BC2)]FS60-2-1-1-1-#/CML176BC1F1-5-3-1-2-1
18	[POOL9Ac7-SR(BC2)]FS59-4-1-2-1-1-1-#-#-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-23-3-3-1-1-#//B.T.Z.T.V.C -43-B -2-3 -3-2-#-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-14-1-1//CML491
19	[POOL9Ac7-SR(BC2)]FS59-4-1-2-1-1-1-#-#-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-23-3-3-1-1-#//{POOL 9AXMISSOU-MO17)-35x12-1/G9AC7HS15-3}-2-1-2-2	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-14-1-1//142-1-eQ
20	[POOL9Ac7-SR(BC2)]FS59-4-1-2-1-1-1-#-#-#-#/[KIT/SNSYN[N3/TUX]]c1F1-##(GLS=2)-23-3-3-1-1-#//[POOL9Ac7-SR(BC2)]FS67-1-2-3-1-#-#-#-#-#	SRSYN95[ECU//SC/ETO]F1-##(GLS=3.5)-20-2-1-#/CML176(BC2)-4-1-2/[POOL9Ac7-SR(BC2)]FS89-2SR-1-2-1-#/CML176(BC2)-14-1-1//F7215Q
21	WENCHI	AMH760Q
22	BH660	BH660

REFERENCES

Admassu, S., M. Nigussie and H. Zelleke, 2008. Genotype-environment interaction and stability analysis for grain yield of maize (*Zea mays* L.) in Ethiopia. Asian J. Plant Sci., 7: 163-169.

Alberts, M.J.A., 2004. A comparison of statistical methods to describe genotype x environment interaction and yield stability in multi-location maize trials. M.Sc. Thesis, University of Free State, South Africa.

Annicchiarico, P., 2002. Genotype environment interactions-challenges and opportunities for plant breeding and cultivar recommendation. Food and Agriculture Organization (FAO), Rome.

Banziger, M. and A.O. Diallo, 2000. Stress tolerant maize for farmers in Sub-Saharan Africa. Maize Research Highlights, pp: 1-8.

Brancourt-Hulmel, M. and C. Lecomte, 2003. Effect of environmental variates on genotype X environment interaction of winter wheat: A comparison of biadditive factorial regression to AMMI. Crop. Sci., 43: 608-617.

CIMMYT, 2000. CIMMYT Annual Report in 1999-2000. Science and Sustenance, International Maize and Wheat Improvement Center, Mexico, pp: 6-7.

Fan, X.M., M.S. Kang, H. Chen, Y. Zhang, J. Tan and C. Xu, 2007. Yield stability of maize hybrids evaluated in multi-environment trials in Yunnan, China, Agron. J., 99: 220-228.

Guach Jr., H.G., 1988. Model selection and validation for yield trials with interactin. Biometrics, 44: 705-715.

Gauch, H.G., 1992. Statistical Analysis of Regional Yield Trials: Ammi Analysis of Factorial Designs. Elsevier, Amsterdam, The Netherlands, ISBN-13: 9780444892409, Pages: 278.

Gauch, H.G. and R.W. Zobel, 1996. AMMI Analysis of Yield Trials. In: Genotype-by-Environment Interaction, Kang, M.S. and H.G. Gauch (Eds.). CRC Press, Boca Raton, FL., USA., pp: 85-122.

Gauch Jr., H.G. and R.W. Zobel, 1997. Identifying mega-environments and targeting genotypes. Crop Sci., 37: 311-326.

Gauch, H.G., 2006. Statistical analysis of yield trials by AMMI and GGE. Crop Sci., 46: 1488-1500.

Gudeta, N., S. Twumasi-Afriyie, A.K. Demissew, A. Baysisa and N. Demewoz *et al*., 2012. Development of improved maize germplasm for Highland Agro-ecologies of Ethiopia. Proceedings of the 3rd National Maize Workshop of Ethiopia, April 18-20, 2011, Addis Ababa, Ethiopia, pp: 43-46.

Hallauer, A.R., J.B.M. Filho, 1981. Quantitative Genetics in Maize Breeding. 1st Edn., Iowa State University Press, Ames.

Kandus, M., D. Almora, R.B. Ronceros and J.C. Salenro, 2010. Statistical models for evaluating the genotype-environment interaction in maize (*Zea mays* L.). Phyton, 79: 39-46.

Kaya, Y., C. Palta and S. Taner, 2002. Additive main effects and multiplicative interactions analysis of yield performance in bread wheat genotypes a cross environments. Turk. J. Agric., 26: 275-279.

Mohammadi, R., M. Armion, A. Shabani and A. Daryaei, 2007. Identification of stability and adaptability in advanced durum wheat genotypes using AMMI analysis. Asian J. Plant Sci., 6: 1261-1268.

NRC, 1988. Quality Protein Maize. National Academic Press, Washington, DC., USA.

Purchase, J.L., 1997. Parametric analysis to describe genotype X environment interaction and yield stability in winter wheat. Ph.D Thesis, University of the Orange Free State, Bloemfontein, South Africa.

Qi, G.H., Q.Y. Diao, Y. Tu, S.G. Wu and S.H. Zhang, 2004. Nutritional evaluation and utilization of Quality Protein Maize (QPM) in animal feed. Protein Sources for Animal Feed Industry, Nutritional Evaluation and Utilization of Quality Protein Maize in Animal Feed, pp: 185-198.

Taye, G., T. Getachew and G. Bejiga, 2000. AMMI adjustment for yield estimate and classification of genotypes and environments in field pea (*Pisum sativum* L.). J. Genet. Breed., 54: 183-191.

Twumasi-Afriyie, S., H. Zelleke, K. Yihun, B. Asefa and S. Tariku, 2001. Development and improvement of highland maize in Ethiopia. Proceedings of the 2nd National Maize workshop of Ethiopa, November 12-16, 2001, Addis Ababa, Ethiopia, pp: 31-37.

Twumasi-Afriyie, S., A.K. Demissew, B. Gezahegn, A. Wonde and N. Gudeta *et al*., 2012. A decade of quality protein maize research progress in Ethiopia (2001-2011). Proceedings of the 3rd National Maize Workshop of Ethiopia, April 18-20, 2011, Addis Ababa, Ethiopia, pp: 47-57.

Twumasi-Afriyie, S., Y. Kassa and N. Gudeta, 2003. Exploitation of heterosis and combining ability to develop highland maize cultivars for Eastern Africa. Proceedings of the Hallauer International Plant Breeding Symposium, August 17-23 2003, Mexico, pp: 282-283.

Wim, B., S. Roger, C. Rice and M. Crispin, 2007. GenStat Discovery Edition 3 for Everyday Use. ICRAF Nairobi, Kenya, pp: 117.

Yan, W., L.A. Hunt, Q. Sheng and Z. Szlavnics, 2000. Cultivar evaluation and mega environment investigation based on GGE biplot. Crop Sci., 40: 597-605.

Yan, W. and M.S. Kang, 2003. GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists and Agronomists. 1st Edn., CRC Press, Boca Roton, FL., USA., Pages: 271.

Zobel, R.W., M.J. Wright and H.G. Gauch, 1988. Statistical analysis of yield trial. Agron. J., 80: 388-393.