Available online at www.worldscientificnews.com

World Scientific News

An International Scientific Journal

WSN 95 (2018) 75-88 EISSN 2392-2192

Yield Stability Analysis of Open Pollinated Maize (*Zea mays* L.) and their Topcross Hybrids in Uganda

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ABSTRACT

The study was aimed at determining yield stability and adaptability patterns of a set of 65 open pollinated maize genotypes evaluated across four different agro ecologies in Uganda using 5 × 13 α-lattice design replicated twice. Individual location analysis ANOVA results showed mean squares of genotype were statistically highly significant in terms of days to 50% anthesis, anthesis silking interval, grain yield and maize streak virus disease severity score for all environments tested except for grain yield in Ngetta. The highest grain yield was recorded for topcross C9/TA (ECAVL1/CML536) of 9.60 t ha^{-1} in Bulindi, for top cross C3/TA (Longe5/CML536) of 9.56 t ha^{-1} in Namulonge. However, they were quite unstable as their ranking was not consistent across environments. The genotype Ambsyn5, C4/TB, FS85 and C9/TB were showed the lowest disease score for MSV. The parent OPV SITUKA MI was with the lowest day requirement for shading pollen and hence it can be utilized in breeding for earliness. The additive main effects and multiplicative interaction (AMMI) analysis results indicated that the tested genotypes were highly influenced by genotype main effects, environment effects and genotype x environment interaction effects; the magnitude of environment and its interaction effect for grain yield was 9.8 times greater than the variation attributed to genotype main effects thus these genotypes were more affected by the environment and their interaction. Based

(Received 15 February 2018; Accepted 01 March 2018; Date of Publication 02 March 2018)

on Finlay and Wilkinson's sensitivity estimate, genotypes G40, G58, G42, G44, G56, G23, G52 and G53 were identified as the most stable and widely adaptable.

***Keywords*:** AMMI, G × E, Open pollinated varieties, Topcross, Yield stability, *Zea mays*

1. INTRODUCTION

Maize (*Zea mays* L.) is the principal cereal crop in Uganda. It remains the most important food security crop in eastern and southern Africa (ESA) predominantly grown by the resource-constrained and small-scale farmers. Newly introduced and local OPVs including their newly generated topcrosses should exhibit great yield potential and average stability over a wide range of agro-ecologies in Uganda. Stability of yield is defined as the ability of a genotype to avoid substantial fluctuations in yield over a range of environment [1]. Cultivar performance is a function of the genotype and the nature of the production environment [2]. In most cases maize productivity is function of genotype, environment and the genotype × environment interaction [3,4]. The differential response of a genotype across environments is defined as the genotype (G) × environment (E) interaction. [6,7] indicated that it is the rule to perform G × E in most quantitative characteristics. Grain yield in nature, routinely exhibits G × E interaction [8] which necessitates evaluation of cultivars in multiple environments [9,10]. 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 [11,25-28].

Existence of G × E interaction necessitates that breeders evaluate genotypes in more than one environment to obtain repeatable rankings of genotypes. In maize breeding, choice of a suitable candidate cultivar is subject to two considerations: (1) high grain yield across a wide range of environments and (2) consistent performance over environments. The performance of a genotype is determined by three factors: genotypic main effect (G), environmental main effect (E) and their interaction (G × E) [12]. Consistency of performance is dependent upon G × E interaction. Major difference in genotypes stability is due to crossover interaction effect of genotype and environment. Genotype x Environment (G × E) interaction study is an important common phenomenon in maize, especially when yield stability of varieties is going to be studied [13,14]. This study is therefore mainly intended to determine the yield stability (G × E) of the parental OPVs and their topcross hybrids in Uganda.

2. MATERIAL AND METHOD

The research was conducted at four sites: i) The National Crops Resources Research Institute (NaCRRI) Namulonge (Central Uganda) ii), National Semi-Arid Resources Research Institute (NaSARRI) Serere (Eastern Uganda) iii) Bulindi Zonal Agricultural and Development Research Institute (Western Uganda) and iv) Ngetta Zonal Agricultural and Development Research Institute, Ngetta (Northern Uganda). The description of the study sites for this study was conducted in 3 optimum sites and one site that expected random drought.

2. 1. Genetic material

The genetic materials in this section were 65 entries consisting of 19 OPVs, 38 topcrosses generated in 2015A and 8 checks. Additionally, these materials were considered to be different in their genetic back ground from where they are sourced.

2. 2. Experimental design

All 65 entries were planted under rain-fed condition and evaluated in four different agro-ecologies of Uganda. The experimental design used was 5 x 13 α-Lattice design with two replications per location. Two row plots of 5 m long were used with an inter-row spacing of 0.75 m and intra-row spacing of 0.25 m.

2. 3. Data collection

Key agronomic traits were measured for entire genotypes. Grain yield (t ha^{-1}) and other selected traits were the major trait of interest in this study. Data collected at vegetative and flowering stage (Before harvest) were: Days to anthesis (AD), Anthesis-silking interval (ASI), Maize strike virus (MSV), and at harvest: Grain yield (GY).

$$GY(\text{t ha}^{-1}) = \frac{\text{F.W}\cdot(100-\text{MC})\cdot\%\,\text{S}\cdot 10}{(100-12.5)\cdot 5\text{m}\cdot 0.75\text{m}\cdot 2\text{ rows}} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots(1)$$

where: GY = grain yield, t= ton, ha^{-1} = per hectare, F.W. = Fresh weight of ear in kg at harvest, MC = Grain moisture content at harvest, S = Shelling co-efficient (0.80), moisture content required in grain at storage 12.5%, 1hectare = 10,000 m^2, net area/plot = 7.5 m^2 with 5 m long, 75 cm wide and 2 row plot.

3. STATISTICAL ANALYSIS

Analysis of variance was used to analyse differences between the 65 entries. The final grain yield was subjected to analysis of variance (ANOVA) for each site and for all the sites combined. For the combined analysis, genotype effect was assumed to be fixed and location effects as random. The linear model used for individual site analysis was:

$$\mathrm{Y_{ijk}} = \mu + \mathrm{G_i} + \mathrm{R_j} + B_{k(j)} + \varepsilon_{\mathrm{ijk}} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (2)$$

where: Y_{ijk} = the observed value of trait from the i^{th} genotype from the kth block nested in the jth replicate, μ is the overall mean, G_i = the effect of i^{th} genotype, R_j is the effect of the j^{th} replication and $B_{k(j)}$ is the effect k^{th} block nested within the j^{th} replicate and ε_{ijk} is a random error term ($\varepsilon_{ijk} \sim N(0, \sigma^2)$).

The combined analysis of variance across locations was done using ANOVA in GenStat and AMMI model was used to measure genotype stability. The Linear model used for combined analysis was:

$$\mathrm{Y_{ij}} = \mu + \mathrm{G_i} + \mathrm{E_j} + GE_{ij} + \varepsilon_{\mathrm{ij}} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (3)$$

where: μ is the overall mean; G_i, E_j and GE_{ij} represent the effect of the genotype, environment, and genotype-environment interaction, respectively; and ε_{ij} is the average of the random errors associated with the l^{th} plot that receives the i^{th} genotype in the j^{th} environment.

Finlay-Wilkinson Regression (joint regression) analysis method [15] was used for genotype stability analysis. The Linear model used for yield stability analysis was:

$$Y_{ij} = \mu + G_i + E_j \ (1 + \beta_i) + \delta_{ij} \quad \text{.....(4)}$$

where: Y_{ij} is mean of individual genotype crosses, μ is the overall mean, G_i is the effect of the i^{th} genotype (fixed effects of genotype), β_i is measures the sensitivity of genotype i over the sampled environments, E_j is the effect of j^{th} environment (random effect) and δ_{ij} is the residual (lack of fit).

4. RESULTS

4. 1. Individual location analysis

The mean squares of each trait are shown in (Table 1). Results of ANOVA for each individual location revealed statistical significant differences at ($P < 0.05$) for most traits except for grain yield in Ngetta.

Table 1. Mean squares of genotype for individual location analysis of agronomic traits evaluated for yield stability in Uganda, 2015B

SOV	AD (days)				ASI (days)				GY (t ha^{-1})				MSV (score 1-5)			
	NAM	SER	BUL	NGE	NAM	SER	BUL	NG	NAM	SER	BUL	NG	NAM	SER	BUL	NG
Genotype d.f = 64	17.2 ***	24.7 ***	20.20 ***	25.6 ***	1.1 ***	0.8 ***	0.7 ***	0.8 ***	5.4 ***	1.1 **	3.9 *	0.4 Ns	0.5 **	0.2 **	0.6 *	0.1 ***
Residual d.f = 40	0.7	0.5	0.7	0.2	0.1	0.1	0.2	0.2	1.0	0.4	1.6	0.2	0.2	0.1	0.3	0.1
LEE d.f = 40	0.9	0.5	0.7	0.2	0.1	-	0.2	0.2	1.1	0.5	2.0	0.3	0.3	0.1	0.3	-
SED	0.9	0.7	0.8	0.4	0.3	0.3	0.5	0.5	1.1	0.8	1.1	0.4	0.5	0.3	0.6	0.2
%CV	1.3	1.1	1.2	0.6	38.4	20.9	31.9	16.9	15.2	22.4	23.0	29.0	27.0	20.1	23.3	11.1
GM	72.5	65.1	69.7	64.1	0.8	1.5	1.5	2.9	7.0	3.3	6.1	1.9	1.9	1.3	2.5	1.8
Min	63.5	56.5	57.5	54.0	-1.5	-0.01	0.5	1.5	1.5	0.95	3.4	1.0	1.1	0.9	1.5	1.5
Max	86.0	76.5	77.0	72.5	2.0	3.0	3.0	4.5	9.56	4.8	9.6	3.5	3.1	2.3	3.6	2.3

*, **, ***Statistically significant $\propto = 0.05, 0.01$ *and* 0.001 respectively, ns-statistically non-significant, SOV-source of variation, d.f-degree of freedom, AD-days to 50% anthesis, ASI-anthesis silking interval (SD-AD), GY-adjusted grain yield, Rep-replication, LEE- lattice effective error, SEM-standard error of the mean, MSV - maize streak virus, % cv-coefficient of variation, Min-minimum value, Max-Maximum value. NAM-Namulonge, SER-Serere, BUL-Bulindi, NGE-Ngett

Mean of selected genotypes (from top four and bottom four) for traits days to anthesis, anthesis silking interval, grain yield and maize streak virus in each location is indicated in

(Table 2 and Table 3) respectively. In terms of days to anthesis, the highest was recorded for OPV Ambsyn2 (85.7 days) in Namulonge, 77 days in Bulindi, 76.5 days in Serere and 72.5 days in Ngetta while the lowest was for SITUK MI (54, 56.5, 57.5 and 62.9 days) in Ngetta, Serere, Bulindi and Namulonge respectively. The highest anthesis silking interval of 4 days was recorded for topcross C14/TA (KakSyn-II/CML536) in Ngetta, 3 days for varietal hybrid check (UH5053) in Bulindi, 2.9 days for Ambsyn2 in Serere and 2 days for SUWAN in Namulonge whereas the lowest was recorded -1.5 days for topcross C1/TA (MM3/CML536) in Namulonge, 0.1 day for topcross C18/TB (SUWAN/CML202) in Serere, 0.5 days for topcross C5/TA (Longe5D/CML536) in Bulindi and 1.5 days for topcross C19/TA (VP MAX/CML536) in Ngetta.

Table 2. Mean of top and bottom four selected OPV genotypes for days to anthesis and ASI in each of 4 locations in Uganda, 2015B

Genotype	Days to anthesis (days)				Genotype	Anthesis silking interval (days)			
	Namulonge	Serere	Bulindi	Ngetta		Namulonge	Serere	Bulindi	Ngetta
SITUKA MI	62.9	56.5	57.5	54.0	C1/TA	-1.5	1.5	1.5	3.0
MM3	67.2	58.0	60.5	56.0	C17/TB	-1.5	1.0	2.0	3.5
VP MAX	68.3	57.5	66.1	57.0	C4/TA	-1.0	1.5	1.5	2.5
Longe 4	69.4	58.5	65.0	55.0	SUWAN	2.0	1.9	1.6	3.0
Longe 6H	76.3	67.0	70.5	65.5	Ambsyn2	1.0	2.9	1.6	4.4
C11/TA	76.4	67.0	73.0	66.5	C5/TA	1.0	1.5	0.5	2.5
C14/TA	76.7	72.5	75.0	71.0	UH5053	1.0	0.9	3.0	3.5
Ambsyn2	85.7	76.5	77.0	72.5	C14/TA	1.0	1.5	1.0	4.5
Mean	72.5	65.1	69.6	63.7	Mean	0.6	1.5	1.5	3.0
% CV	1.3	1.1	1.2	0.6	% CV	38.4	20.9	32.0	17.0
LSD (5 %)	2.1	1.4	1.6	0.8	LSD (5 %)	0.6	0.6	1.0	1.0

% cv-coefficient of variation, LSD- Least significant difference at 5 %, Min- minimum value, Max-Maximum value.

In terms of yield, the highest was recorded for topcross C9/TA (ECAV1/CML536) of 9.60 t ha^{-1} in Bulindi, for topcross C3/TA (Longe5/CML536) of 9.6 t ha^{-1} in Namulonge, for UH5354 (TWC) hybrid check with 4.77 t ha^{-1} in Serere and for topcross C9/TB (TMV1/CML202) with 3.47 t ha^{-1} in Ngetta while the lowest was recorded for OPV Ambsyn2 with 0.95 t ha^{-1}, 1 t ha^{-1}, 1.46 t ha^{-1} in Serere, Ngetta and Namulonge respectively. The topcross C15/TB (Ambsyn2/CML202) of 3.40 t ha^{-1} had the lowest grain yield recorded in Bulindi. Regarding the maize streak virus diseases severity score, the highest severity was recorded for topcrosses C1/TA (MM3/CML536) with value 3.56 in Bulindi, for topcross C11/TA (ECAVL2/CML536) with value 3.09 in Namulonge, for topcross C14/TA (KakSyn-II/CML536) with value 2.26 in Serere, and for UH5053 (varietal cross check) with value 2.25 in Ngetta whereas the lowest was for topcross C4/TB (Longe5/CML202) with value 0.91 in

Serere, for Ambsyn5 with value 1.12 in Namulonge, for topcross C9/TB (TMV1/CML202) with value 1.49 in Ngetta and FS85 with value 1.51 Bulindi see Table 3.

Table 3. Mean of top six and bottom five selected genotypes for grain yield and maize streak virus in each of 4 locations in Uganda, 2015B

Genotype	Grain yield (t ha^{-1})			
	Namulonge	Serere	Bulindi	Ngetta
Ambsyn2	1.46	0.95	5.63	1.01
C9/TA	6.95	3.49	9.60	2.24
UH5354	6.97	4.77	4.41	1.96
C9/TB	7.10	3.43	6.17	3.47
C5/TA	9.23	3.49	6.79	1.84
C6/TA	9.28	4.67	6.45	2.54
C12/TA	9.42	3.52	7.71	1.73
C16/TA	9.48	3.62	8.70	2.14
C3/TA	9.56	3.50	6.74	1.94
Mean	6.86	3.27	6.14	1.96
% CV	15.18	22.35	23.02	29.14
LSD (5 %)	2.12	1.72	1.53	1.41

Table 3(continue). Mean of top six and bottom five selected genotypes for grain yield and maize streak virus in each of 4 locations in Uganda, 2015B

Genotype	Maize streak virus score (1-5)			
	Namulonge	Serere	Bulindi	Ngetta
Ambsyn5	1.12	1.39	2.52	1.51
Longe 4	1.14	1.13	2.25	1.75
FS85	1.15	1.11	1.51	1.75
C1/TA	1.41	1.47	3.56	1.5
C9/TB	1.62	1.49	2.7	1.49

UH5053	1.96	1.36	1.8	2.25
C14/TA	2.48	2.26	3.53	1.75
C4/TB	2.58	0.91	1.72	2
C11/TA	3.09	1.55	2.76	1.51
Mean	1.94	1.34	2.52	1.80
% CV	27.00	20.06	23.3	11.10
LSD (5 %)	1.15	0.56	0.58	0.38

% cv-coefficient of variation, LSD- Least significant difference at 5 %, Min- minimum value, Max-Maximum value.

4. 2. Combined analysis of variance for G x E

The combined analysis of variance (ANOVA) of the 65 entries evaluated across 4 locations according to the Additive Main effects and Multiplicative Interaction (AMMI) model is presented in (Table 4). AMMI analysis indicated highly significant differences ($P < 0.001$) for environments (E), genotypes (G) and GxE interaction effects for all selected traits except which were non-significant for anthesis silking interval and maize streak virus. The first two interaction principle components (IPCA1 and IPCA2) were also highly significant ($P < 0.001$).

The highest significant percentage of the total explained variation (51.44%) due to environment effect was observed for grain yield. The first two IPCA axes explained 71.65 % of the GxE interaction for days to anthesis, 74.90 % for anthesis silking interval, 91.57 % for grain yield and 89.48 % for maize streak virus.

The first four AMMI selections per environment is summarized in Table 5. The first two genotypes (G14 and G52) required the highest days to shade pollen in all environments. The genotypes G6, G16, G18 and G30 were well performed genotypes in terms of yield in more than two environments. The highest mean yield was observed for G3, G6, G12 and G16 in Namulonge and G9, G10 and G35 in Bulindi. Similar results were also observed when G x E was analyzed using GGE biplot (result not shown).

The genotype sensitivity estimates for days to anthesis, anthesis silking interval, grain yield and MSV was shown in Table 6. G28 and G65 were observed with the highest and the lowest sensitivity estimate (0.89 and 0.49) for days to anthesis, G12 and G24 with sensitivity (0.29 and 0.75) for anthesis silking interval, genotype 45 and 53 with (0.32 and 0.85) and genotype 51 and 18 with (0.75 and –0.09) respectively.

5. DISCUSSION

5. 1. Individual location analysis

Determination of yield stability of genotypes evaluated in different agro ecologies is an important goal for breeder to facilitate maize breeding and yield improvement efforts. For

most traits measured, except for grain yield in Ngetta indicated that there exists genetic potential difference between the tested genotypes in each environment. These differences can help the breeder to decide his breeding strategy to the specific environment for better yield.

Statistical analysis revealed significant differences among the tested maize genotypes for days to anthesis. The OPV Ambsyn2 took maximum number of days for pollen shedding (85.7 days) in Namulonge, 77 days in Bulindi, 76.5 days in Serere and 72.5 days in Ngetta while the minimum date was for SITUK MI (54, 56.5, 57.5 and 62.9 days) in Ngetta, Serere, Bulindi and Namulonge respectively indicated the existence of genotype by environment interaction effect. Therefore, OPV Ambsyn2 and SITUKA MI were grouped under the highest and lowest days to anthesis respectively. These contrasting ranges of days for flowering can help breeders to breed these varieties in different maturity groups for tested environments. The newly introduced genotype SITUKA MI noted to be quite the earliest OPV among the genotypes evaluated and could be used as germplasm source in developing varieties with early maturity. Previously, [16,17] have also reported significant amount of variability for days to anthesis among different open pollinated maize genotypes.

Means of top eleven genotype ranking for anthesis-silking interval shown in (Table 4) reveal significant amount of variation for ASI in each locations. The means of anthesis silking interval that exhibited among the topcrosses (C8/TA, C17/TA, C19/TA) in Namulonge were having 0.5 days i.e. both the pollen shedding and silking were well synchronized. This synchronization helps to carry out successful pollination so as to produce better yield. At the same time, the Genotypes (C1/TA, C17/TB, C10/TB, C4/TA, FS85, ECAVL1, ECAVL18) gave negative ASI values ranging from -1.5 to -1 days in Namulonge. The observed negative sign of ASI shows that the silking was earlier than pollen shedding (female flowered first) indicating that there exists the possibility to develop improved drought tolerant open pollinated maize varieties with better synchronization in anthesis and silking parameters while positive sign of ASI indicates that pollen shedding was earlier than silking. Similarly, genotypes C18/TB with (0.1 days) and TMV (0.5 days) in Serere, C5/TA, C15/TA, VP MAX and C13/TA with (0.5 days) in Bulindi and C19/TA (1.5 days) in Ngetta were with the lowest value of ASI. Therefore, these genotypes showed potential to breed for specific environment with better pollen shading and silking time synchronizations. [18] observed considerable genotypic variability among various maize genotypes for different traits.

Genotype ranking using mean grain yield is shown in (Table 5). Highly significant ($p < 0.001$) variability in grain yield among the genotypes evaluated in 4 location indicated difference in responses for each genotype in the different environment. The highest grain yield was recorded for topcross C9/TA (TMV1/CML536) of 9.60 t ha^{-1} in Bulindi and for topcross C3/TA (Longe4/CML536) of 9.56 t ha^{-1} in Namulonge. Similarly, the topcrosses: C16/TA (9.48 t ha^{-1}), C12/TA (9.42 t ha^{-1}), C6/TA (9.28 t ha^{-1}) and C5/TA (9.23 t ha^{-1}) selected as high yielders. However, they were quite unstable as their ranking was not consistent across environments. As it was observed from the result, better responses were noted for topcrosses than parental OPVs and the checks indicating future possibilities to breed for specific environment with higher yield. Souza *et al.*, (2008) reported that different genotypes have different performance in each region that can be capitalized to maximize productivity.

Regarding the MSV diseases severity on a scale (1-5), the highest severity was recorded for topcross C1/TA (MM3/CML536) with value 3.56 in Bulindi, for topcross C11/TA (ECAVL2/CML536) with value 3.09 in Namulonge, for topcross C14/TA (KakSyn-

II/CML536) with value 2.26 in Serere, and for UH5053 (varietal cross check) with value 2.25 in Ngetta whereas the lowest was for topcross C4/TB (Longe5/CML202) with value 0.91 in Serere, for Ambsyn5 with value 1.12 in Namulonge, for topcross C9/TB (TMV1/CML202) with value 1.49 in Ngetta and FS85 with value 1.51 Bulindi indicating that the presence of the promising genotypes resistance to MSV. [20] on six foliar disease based on severity score has explained the variation among tested genotypes which can help researchers to develop disease resistant varieties.

Table 4. ANOVA results based on the AMMI model of days to anthesis, anthesis silking interval, grain yield and maize streak virus for maize genotypes tested in four locations showing the total sum of squares and the portion of the total sum of squares explained by G, E, IPC1 and IPC2

		Total variation explained by each component (%)			
Trait	TSS	Genotype	Environment	IPCA 1	IPCA2
AD	11742.0	39.32 ***	51.44 ***	3.22 ***	2.25 ***
ASI	556.3	10.57 ns	53.33 ***	11.94 ***	9.04 ***
GY	3238.0	8.26 ***	68.01 ***	6.45 ***	5.02 ***
MSV	228.6	10.71 ns	39.07 ***	14.70 ***	10.08 ***

*, **, ***Statistically significant $\propto = 0.05, 0.01$ and 0.001 respectively, ns - statistically non-significant, E - Environment; G × E - genotype by Environment; Rep - replication; df - degrees of freedom; SS- Sum of square; MS - Mean square; IPCA - Interaction principal component axis, TSS - total sum of squares

Table 5. The first four AMMI selections per environment for 65 tested maize OPV genotypes in Uganda, 2015B.

Environment	Days to anthesis (days)					Environment	Anthesis silking interval (days)				
	Mean	1st	2nd	3rd	4th		Mean	1st	2nd	3rd	4th
Ngetta	64.1	G52	G14	G45	G65	Namulonge	0.8	G39	G55	G63	G56
Bulindi	69.7	G52	G14	G45	G65	Ngetta	2.9	G52	G14	G63	G2
Serere	65.1	G52	G14	G45	G65	Serere	1.5	G52	G14	G3	G10
Namulonge	72.5	G52	G14	G11	G64	Bulindi	1.5	G3	G62	G21	G57
Environment	Grain yield (days)					Environment	Maize streak virus (score 1-5)				
	Mean	1st	2nd	3rd	4th		Mean	1st	2nd	3rd	4th
Namulonge	6.97	G12	G16	G6	G3	Bulindi	2.5	G14	G1	G10	G64

Serere	3.26	G18	G30	G6	G19	Ngetta	1.8	G14	G7	G57	G32
Ngetta	1.91	G18	G28	G30	G11	Serere	1.3	G14	G4	G32	G9
Bulindi	6.11	G9	G35	G16	G10	Namulonge	1.9	G11	G10	G22	G14

G - genotype; AMMI - interaction additive main - effect and multiplicative interaction

Table 6. Finlay and Wilkinson modified joint regression analysis sorted sensitivity estimates eight least sensitive (most stable) genotypes.

AD (days)					ASI (days)				
G	β	SE	Mean	MS dev.	G	β	SE	Mean	MS dev.
65	0.49	0.21	71.84	5.69	24	0.28	0.37	1.53	0.09
34	0.54	0.21	67.40	2.46	21	0.38	0.37	1.76	0.46
45	0.56	0.21	72.86	2.06	19	0.38	0.37	1.26	0.21
51	0.57	0.21	67.69	1.39	51	0.40	0.37	1.70	0.15
8	0.64	0.21	70.10	6.22	54	0.45	0.37	1.46	0.30
14	0.64	0.21	73.81	0.14	7	0.46	0.37	1.53	0.01
49	0.88	0.21	70.19	0.72	40	0.74	0.37	1.50	0.07
28	0.89	0.21	66.95	0.12	12	0.75	0.37	1.51	0.09
GY (t ha^{-1})					MSV (score 1-5)				
G	β	SE	Mean	MS dev.	G	β	SE	Mean	MS dev.
53	0.31	0.23	2.78	5.15	18	–0.08	0.46	1.88	0.01
52	0.48	0.23	2.26	5.61	35	–0.06	0.46	1.61	0.04
40	0.56	0.23	3.61	0.06	57	–0.02	0.46	1.79	0.02
58	0.56	0.23	3.70	0.88	33	0.23	0.46	1.73	0.11
42	0.57	0.23	3.63	1.86	62	0.25	0.46	1.84	0.18
44	0.60	0.23	3.57	1.09	58	0.26	0.46	1.38	0.11
56	0.63	0.23	4.16	0.93	4	0.29	0.46	2.16	0.18
45	0.85	0.23	3.76	0.68	51	0.75	0.46	1.86	0.06

AD - days to anthesis; ASI - anthesis silkig interval; G - genotype; β - genotype sensitivity estimate; SE - standard error; MS dev. - mean square of deviation.

5. 2. Combined analysis of Variance for GxE by AMMI model

The interaction between genotypes and environment that produces a phenotype is referred as genotype x environment interaction. AMMI analysis result for G × E showed statistically highly significant effect of environments, genotypes and genotypes x environment interaction on days to anthesis, anthesis-silking interval, grain yield and reaction to maize streak virus disease. The observed performance of the tested maize genotypes indicated their potential to respond and adapt the environment either broadly or specifically. The variation due to environment and G × E was 1.5 time more than variation attributed to genotype main effect for days to anthesis, 7.7 times more for anthesis silking interval, 9.8 times more for grain yield and 6.2 time more for maize streak virus disease severity scores indicating the importance of G × E interaction.

The occurrence of a statistically significant G × E interaction effect indicated inconsistent phenotypic performance of the tested genotypes across locations, which may cause selections made in one environment to perform poorly in another environment. In agreement with this study, [21] reported the higher contribution of environmental variance than both genotypic variance and G × E interaction in terms of grain yield for wheat cultivars tested in 3 different locations. However, [22] in contrast reported that variation due to genotype was higher than both the environment variance and G × E interaction for 30 maize hybrids tested across locations in Kenya. The significant contribution of environment to the differences in genotype expression across locations would remain a serious challenge in both crop management and breeding for varieties with little variation (stable) or improved performance due to environmental changes. Large contribution of the environment component to grain production in maize has been similarly reported by many works [23,24]. Therefore, differences in the amount of variation accounted for by the environment, the values obtained were important implications to emphasize the necessity of description of environments for the ultimate interest of driving the direction of plant breeding for stable or positive response.

Regarding the genotype stability, AMMI analysis result showed the occurrence of a statistically significant G × E interaction effect. As a result, inconsistent performance of the tested genotypes across locations was observed. However, according to [15] genotype sensitivity estimate, the genotypes with the lowest sensitivity were the most stable and widely adaptable. Therefore, in terms of days to anthesis (G65, G34, G45 and G51), anthesis silking interval (G24, G21, G19 and G51), Grain yield (G40, G58, G42, G44, G56 G23 G52, G53) and maize streak disease score (G18, G33, G35, G57, G62) were most stable and wider adaptable.

6. CONCLUSIONS

Individual location analysis showed highly significant differences among the genotypes evaluated. The topcrosses showed quite better response than the OPVs and the check in grain yield. The results of AMMI analysis indicated that the genotype performance of maize parental OPVs and topcrosses were highly influenced by genotype main effects, environment effects and genotype x environment interaction effects; the magnitude of environment and its interaction effect for grain yield was 9.8 times that of variation attributed due to genotype main effects indicating that the importance of genotype by environment (the tested genotypes were affected by G × E). Those genotypes with lower sensitivity estimate were most stable

and wide adapters they can give appropriate mean yield when grown in different agro ecologies of Uganda. In general, high variability exists among the tested genotypes. The presence of this phenotypic and genotypic variability among the local and introduce OPVs indicates that the genotypes could be used in future maize breeding programs for further manipulation to develop breeding lines with improved attributes. The promising topcrosses: C3/TA, C5/TA, C6/TA, C9/TA, C12/TA, C9/TA, C9/TB, C11/TA, C15/TA and C16/TA due to their superiority in grain yield and Ambsyn5, C4/TB, FS85 and C9/TB because of their resistance to MSV can be incorporated in breeding program for specific locations. The parent SITUKA MI due to its the lowest day requirement for shading pollen can be utilized in breeding for earliness. Stable genotypes (i.e. wider adaptable across locations) in terms of days to anthesis (G65, G34, G45 and G51), anthesis silking interval (G24, G21, G19 and G51), grain yield (G40, G58, G42, G44, G56 G23 G52, G53) and maize streak disease score (G18, G33, G35, G57, G62) can be included in the breeding programme targeting those traits. In general genotypes with superior characters are recommended to be incorporated in maize breeding program. However, this study was carried out only in 4 locations for one season and due highly significant genotype by environment interaction for an effective stability determination it is important to consider testing these genotypes in many locations and more than two seasons.

Acknowledgement

The author is grateful to all authors for their professional help. Department of maize breeding program at NaCRRI, Namulonge for their technical supports. The author is also grateful to AGRA (Alliance for Green revolution in Africa), for the fellowship during both the course and research work.

Reference

[1] M.S. Kang, Using Genotype by Environment Interaction for Crop Cultivar Development. *Adv. Agron.* 62 (1998) 199–246.

[2] M. Cooper, D.E. Byth, Understanding plant adaptation to achieve systematic applied crop improvement- A fundamental challenge in Plant adaptation and crop improvement, CAB Int. IRRI, UK. (1996) 5–23.

[3] H. Namorato, G.V. Miranda, L.V. De Souza, L.R. Oliveira, R.O. Delima, Comparing Biplot Multivariate Analyses with Eberhart and Russell ' Method for Genotype x Environment Interaction, *Biotechnology* 9 (2009) 299–307. doi:10.12702/1984-7033.v09n04a03.

[4] A. Deitos, E. Arnhold, F. Mora, G.V. Miranda, Yield and Combining Ability of Maize Cultivars under Different Ecogeographic Conditions. *Crop Breed. Appl. Biotechnol.* 6 (2006) 222–227.

[5] Y. Beyene, S. Mugo, K. Pillay, T. Tefera, S. Ajanga, S. Njoka, H. Karaya, J. Gakunga, Testcross Performance of Doubled Haploid Maize Lines Derived from Tropical Adapted Backcross Populations, *Maydica* 56 (2011) 351–358.

[6] Y. Beyene, S. Mugo, C. Mutinda, T. Tefera, H. Karaya, S. Ajanga, J. Shuma, R. Tende, V. Kega, Genotype by Environment interactions and Yield Stability of Stem Borer Resistant Maize Hybrids in Kenya, *African J. Biotechnol.* 10 (2011) 4752–4758.

[7] J.M. Bernardo, R. Rueda, Bayesian hypothesis testing: A reference approach. *Int. Stat. Rev.* 70 (2002) 351–372. doi:10.1111/j.1751-5823.2002.tb00175.x.

[8] I.A. Khalil, H.U.R. Rahman, M. Arif, I.H. Khalil, M. Iqbal, K. Afridi, M. Sajjad, M. Ishaq, Evaluation of Maize Hybrids for Grain Yield Stability in North-West of Pakistan. *Sarhad J. Agric.* 27 (2011) 213–218.

[9] X. Fan, M.S. Kang, H. Chen, Y. Zhang, J. Tan, C. Xu, Yield Stability of Maize Hybrids Evaluated in Multi-Environment Trials in Yunnan, China. *Am. Soc. Agron.* 99 (2007) 220–228. doi:10.2134/agronj2006.0144.

[10] T. Bacha, Genotype X Environment Interaction and Yield Stabliity of Breade Wheat (*Triticum eastivum* L .) Genotype in Ethiopia using the Ammi Analisis. *J. Biol. Agric. Healthc.* 5 (2015) 129–140.

[11] M.S. Abdulai, P.Y.K. Sallah, O. Safo-Kantanka, Maize Grain Yield Stability Analysis in Full Season Lowland Maize in Ghana. *Int. J. Agric. Biol.* 9 (2007) 41–45.

[12] W. Yan, M.S. Kang, B. Ma, S. Woods, P.L. Cornelius, GGE Biplot vs AMMI Analysis of Genotype-by-Environment Data, *Crop Sci.* 47 (2007) 641–653. doi:10.2135/cropsci2006.06.0374.

[13] W. Abera, V. Rensburg, M. Labuschagne, H. Maartens, Genotype-Environment Interactions and Phenotypic Stability Analyses of Linseed in Ethiopia, *S. Afri. J. Plant Soil.* 71 (2004) 66–71.

[14] M. Shahryarinasab, R. Chogan, Stability Analysis of Maize Yield by using Unvariate Statistical Method, *Biol. Forum – An Int. J.* 7 (2015) 394–399.

[15] K.W. Finlay, G.N. Wilkinson, The Analysis of Adaptation in a Plant-Breeding Programme, *Aust. J. Agric. Res.* 14 (1963) 742–754.

[16] H.- Rahman, I. Khalil, I. Hussain, F. Afzal, Diversity for Morphological and Maturity Traits in Maize Populations From Upper Dir, 24 (2008).

[17] A.E. Idris, A.I. Abuali, Genetic variability for vegetative and yield traits in maize (*Zea mays* L) genotypes, *Int. Res. J. Agric. Sci. Soil Sci.* 1 (2011) 408–411.

[18] F. Ali, I. Nawaz, M. Munir, H. Ullah, Genetic Analysis of Mmaturity and Morphological Traits under Maydis Leaf Blight (MLB) Epiphytoticsin Maize (Zea mays L.), *ARPN J. Agric. Biol. Sci.* 6 (2011) 13–19.

[19] M.F.M. De Souza, R. Rodrigues, A.T. Do Amaral, C.P. Sudré, Resistance to Xanthomonas spp. in Tomato: Diallel analysis and gene effects estimative in a breeding programme carried out in Brazil, *J. Phytopathol.* 156 (2008) 660–667. doi:10.1111/j.1439-0434.2008.01474.x.

[20] X. Wang, Y. Zhang, X. Xu, H. Li, X. Wu, S. Zhang, X. Li, Evaluation of maize inbred lines currently used in Chinese breeding programs for resistance to six foliar diseases, *Crop J.* 2 (2014) 213–222. doi:10.1016/j.cj.2014.04.004.

[21] K. Koutis, Multienvironmental evaluation of wheat landraces by GGE Biplot Analysis for organic breeding, *Agric. Sci.* 03 (2012) 66–74. doi:10.4236/as.2012.31009.

[22] Y. Beyene, S. Mugo, T. Tefera, J. Gethi, J. Gakunga, H. Karaya, R. Musila, W. Muasya, R. Tende, S. Njoka, Yield Stability of Stem Borer Resistant Maize Hybrids Evaluated in Regional Trials in East Africa, *African J. Plant Sci.* 6 (2012) 77–83. doi:10.5897/AJPS11.262.

[23] A.L. Nassir, O.J. Ariyo, Genotype x environment interaction and yield-stability analyses of rice grown in tropical inland swamp, *Not. Bot. Horti Agrobot. Cluj-Napoca.* 39 (2011) 220–225.

[24] M. Kandus, D. Almorza, R.B. Ronceros, J. Salerno, Statistical Models for Evaluating the Genotype-Environment Interaction in Maize (*Zea mays* L), *Int. J. Exp. Bot.* 79 (2010) 39–46.

[25] Duru Chidi Edbert, Duru Ijeoma Akunna, Adsorption Capacity of Maize Biomass Parts in the Remediation of Cu^{2+} Ion Polluted Water. *World News of Natural Sciences* 12 (2017) 51-62

[26] Yallew Mazengia. Smallholders commercialization of maize production in Guangua district, northwestern Ethiopia. *World Scientific News* 58 (2016) 65-83

[27] P. I. Akwaji, E. J. Umana, E. I. Okon. Phytochemical and Antifungal Activity of Leaf Extracts of Corchorus olitorius and Gongronema latifolium on Fungi Associated with Post-Harvest Deterioration of Maize (*Zea mays*) Seeds in Oban Community, Nigeria. *World Scientific News* 53(3) (2016) 157-177

[28] Musefa Redi, Wubayehu Gebremedhin, Fitsum Merkeb, Mohamed Yimam. Critical Level of Extractable Phosphorus for Maize (*Zea mays* L.) at Metekel Zone, Northwestern Ethiopia. *World Scientific News* 54 (2016) 14-26