Assessment of Genotype by Environment interactions and Grain Yield Performance of Extra-Early Maize (*Zea Mays* L.) Hybrids

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Abstract

Maize (*Zea mays* L.) is one of the most important cereal crops of Ghana in terms of production and consumption. Currently, it is produced in all the agro-ecological zones of the country. In Ghana, Genotype by Environment interactions (GxE) effects on maize grain yield is usually significant due to the diverse environmental conditions at growing sites. A proper understanding of the effects of GxE on variety evaluation and cultivar recommendations is vital. The study was conducted in 2011 at three locations in Ghana to (i) determine the presence of GxE of 100 extra-early maize genotypes and (ii) To use the GGE biplot methodology to determine grain yield performance and stability of the genotypes evaluated across three environments. The effects of genotype and environment were significant (P < 0.01) for grain yield. However, GxE was not significant for the same trait. TZEEI 8 x TZEEI 51, TZEEI 5 x TZEEI 53, TZEEI 21 x TZEEI 39, TZEEI 27 x TZEEI 36 and TZEEI 4 x TZEEI 6 were identified as high yielding and most stable hybrids. Therefore, these hybrids have the potential for production across the test locations as well as others within the same agro-ecological zones. On the contrary, DODZI, TZEEI 23 x TZEEI 6, TZEEI 19 x TZEEI 24, TZEEI 11 x TZEEI 24 and TZEEI 20 x TZEEI 39 were not only low yielding but also among the least stable genotypes.

Keywords: Zea mays, single-cross, stability, multiple environments, GxE

1. Introduction

Maize (*Zea mays* L.) is produced in all the agro-ecological zones of Ghana and its highest production is in the transition zone. Maize yields in Ghana are well below their attainable levels; averaging approximately 0.5 metric tons per hectare. However, yields as high as 5.5 metric tons per hectare have been realized by farmers using improved seeds, fertilizer, mechanization and irrigation (MiDA 2010). Lower yields have been attributed to the use of low-yielding varieties, use of self produced seed, poor soil fertility and limited use of fertilizers, low plant population, and inappropriate weed control methods. Moreover, significant potential improvements in yields could be achieved through the use of hybrid maize varieties.

Crop breeders have been striving to develop genotypes with superior grain yield, quality and other desirable characteristics over a wide range of different environmental conditions. Genotype by environment interaction (GxE) makes it difficult to select the best performing and most stable genotypes. GxE refers to the differential ranking of genotype among locations or years. It is an important consideration in plant breeding programmes because it impedes progress from selection in any given environment (Yau 1995). In West and Central Africa, GxE interaction effects have been reported in maize cultivars (Fakorede & Adeyemo 1986; Badu-Apraku *et al*. 2007; 2008). Various studies have been conducted to study the effects of genotype by environment interaction in Sub-Saharan Africa and on Ghanaian maize varieties. However, the changing environmental conditions, the expansion of maize into new agro-ecologies, coupled with inadequate maize varieties available for the different environments necessitate a rigorous and continuous study of GxE interaction effects for a dynamic crop improvement programme.

There are many statistical methods available to analyse GxE: for example, combined ANOVA, stability analysis and multivariate methods. Combined analysis of variance (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 the components of variance arising from different factors (genotype, environment and the GxE), it does not allow exploring the response of the genotypes in the non-

additive term: the GxE (Zobel *et al.* 1988). Among the statistical analyses proposed for the interpretation of the GxE based on the use of biplots, the AMMI (additive main effect and multiplicative interaction) model stands out due to the largest group of technical interpretations available (Duarte & Vencovsky 1999). AMMI analysis interprets the effect of the genotype (G) and sites (E) as additive effects plus the GxE as a multiplicative component and submits it to principal component analysis. Yan *et al.* (2000) proposed a modification of the conventional AMMI analysis called GGE that has been used for GxE analysis. The GGE analysis pools genotype effect (G) with GE (multiplicative effect) and submits these effects to principal component analysis. This biplot is identified as a GGE biplot. The GGE biplot has been recognized as an innovative methodology in biplot graphic analysis to be applied in plant breeding. Fan *et al.* (2007) showed that the GGE biplot methodology was a useful tool for identifying locations that optimized hybrid genotypes performance and for making better use of limited resources available for the maize testing programmes.

The objectives of this study were (i) to determine the presence of GxE of 100 extra-early maize genotypes and (ii) to use the Genotype main effect plus Genotype by Environment interaction (GGE) biplot methodology to determine grain yield performance and stability of the genotypes evaluated across three environments.

2. Materials and Methods

2.1 Field evaluations

Ninety-eight single-cross maize hybrids, one local three-way hybrid (Akposoe) and an open pollinated variety (Dodzi) (Table 1) were evaluated at Fumesua, Ejura and Kpeve from April, 2011 to July, 2011 major season. The evaluation sites are located in the deciduous forest, transition and coastal Savannah zones of Ghana, respectively (Table 2). The hybrids were developed from 61 extra-early maturing white and yellow endosperm inbred lines developed for grain yield, drought and Striga hermonthica tolerance. A standard protocol was adopted at each site during the period of evaluation. Evaluations were done under rain fed conditions and fields were planted when the rains at each experimental site had become fully established. The genotypes were planted in an incomplete block design (10 x 10) with two replications. Each plot consisted 2-rows of 5 m long, an inter-row spacing of 75 cm and an intra-row spacing of 40 cm. Three seeds were sown per hill and seedlings later thinned to two after emergence and seedling establishment. Pre-emergence chemical weed control was practised and comprised an application of a combination of Pendimethalin [N-(1-ethylpropyl)-3, 4-dimethyl-2, 6-dinitrobenzenamine] and Gesaprim [2-chloro-4-(ethylamino)-6-(isopropylamino)-s-triazine] at 1.5 Lha^{-1} and 1.0 Lha^{-1} active ingredient, respectively at planting. Hand weeding was also done when necessary to control weeds during the growing period. NPK 15-15-15 fertilizer was applied at the rate of 30 kg N ha^{-1} and 60 kg P$_2$O$_5$ ha^{-1} as basal fertilizer at 1-2 weeks after planting and top-dressed with additional N at 60 kg N ha^{-1} at four weeks after planting. Other management practices were done according to the recommendations of the specific areas.

2.2 Collection of agronomic data

Data recorded include days to anthesis, days to silking, plant and ear heights, root lodging (number of plants leaning more than 300 from vertical), stalk lodging (stalks broken at or below highest ear node), ear aspect, number of plants harvested, number of ears harvested and percent moisture in the grains. Days to anthesis and days to silking were calculated as the number of days from planting to when 50 % of the plants had shed pollen and had emerged silks, respectively. Anthesis-silking interval was determined as the difference between days to silking and days to anthesis. Plant and ear heights were measured as the distance from the base of the plant to the height of the flag leaf and the node bearing the upper ear, respectively. Husk cover was rated on a scale of 1 to 5, where 1= husk tightly arranged and extended beyond the ear tip and 5 = ear tips exposed. Ear aspect was based on a scale of 1 to 5, where 1= clean, uniform, large, and well-filled ears and 5 = ears with undesirable features. Number of ears per plant was obtained by dividing the total number of ears per plot by the number of plants harvested. The grain yield in kilograms per plot recorded was converted to grain yield in tons per hectare at 15 % grain moisture based on 80% shelling percentage. Even though data were collected on several traits, only those on the most important trait in the study are presented in the results.

Table 1. Description of extra-early maturing maize genotypes tested across three environments in 2011

Entry	Entry name	Entry	Entry name	Entry	Entry name
1	TZEEI 1 x TZEEI 2	34	TZEEI 9 x TZEEI 58	67	TZEEI 20 x TZEEI 22
2	TZEEI 1 x TZEEI 4	35	TZEEI 9 x TZEEI 59	68	TZEEI 20 x TZEEI 24
3	TZEEI 1 x TZEEI 5	36	TZEEI 9 x TZEEI 60	69	TZEEI 20 x TZEEI 39
4	TZEEI 1 x TZEEI 13	37	TZEEI 10 x TZEEI 22	70	TZEEI 21xTZEEI 20
5	TZEEI 1 x TZEEI 14	38	TZEEI 11 x TZEEI 8	71	TZEEI 21 x TZEEI 24
6	TZEEI 1 x TZEEI 22	39	TZEEI 11 x TZEEI 22	72	TZEEI 21 x TZEEI 39
7	TZEEI 1 x TZEEI 23	40	TZEEI 11 x TZEEI 24	73	TZEEI 22 x TZEEI 6
8	TZEEI 1 x TZEEI 50	41	TZEEI 12 x TZEEI 19	74	TZEEI 22 x TZEEI 24
9	TZEEI 2 x TZEEI 1	42	TZEEI 13 x TZEEI 1	75	TZEEI 22 x TZEEI 36
10	TZEEI 2 x TZEEI 11	43	TZEEI 13 x TZEEI 6	76	TZEEI 22 x TZEEI 51
11	TZEEI 2 x TZEEI 14	44	TZEEI 13 x TZEEI 12	77	TZEEI 23 x TZEEI 4
12	TZEEI 2 x TZEEI 24	45	TZEEI 13 x TZEEI 22	78	TZEEI 23 x TZEEI 5
13	TZEEI 4 x TZEEI 6	46	TZEEI 14 x TZEEI 4	79	TZEEI 23 x TZEEI 6
14	TZEEI 4 x TZEEI 7	47	TZEEI 14 x TZEEI 6	80	TZEEI 23 x TZEEI 36
15	TZEEI 4 x TZEEI 24	48	TZEEI 14 x TZEEI 22	81	TZEEI 23 x TZEEI 39
16	TZEEI 4 x TZEEI 39	49	TZEEI 14 x TZEEI 39	82	TZEEI 23 x TZEEI 40
17	TZEEI 4 x TZEEI 51	50	TZEEI 14 x TZEEI 49	83	TZEEI 23 x TZEEI 50
18	TZEEI 4 x TZEEI 90	51	TZEEI 14 x TZEEI 90	84	TZEEI 23 x TZEEI 90
19	TZEEI 5 x TZEEI 4	52	TZEEI 15 x TZEEI 6	85	TZEEI 24 x TZEEI 51
20	TZEEI 5 x TZEEI 23	53	TZEEI 1 x TZEEI 8	86	TZEEI 26 x TZEEI 24
21	TZEEI 5 x TZEEI 39	54	TZEEI 15 x TZEEI 19	87	TZEEI26 x TZEEI 51
22	TZEEI 5 x TZEEI 40	55	TZEEI 15 x TZEEI 21	88	TZEEI 26 x TZEEI 53
23	TZEEI 5xTZEEI 50	56	TZEEI 15 x TZEEI 22	89	TZEEI 27 x TZEEI 36
24	TZEEI 5 x TZEEI 53	57	TZEEI 15 x TZEEI 24	90	TZEEI 27 x TZEEI 51
25	TZEEI 6 x TZEEI 4	58	TZEEI 15 x TZEEI 39	91	TZEEI 29 x TZEEI 26
26	TZEEI 6 x TZEEI 5	59	TZEEI 19 x TZEEI 6	92	TZEEI 29 x TZEEI 33
27	TZEEI 6 x TZEEI 23	60	TZEEI 19 x TZEEI 8	93	TZEEI 29 x TZEEI 36
28	TZEEI 6 x TZEEI 36	61	TZEEI 19 x TZEEI 21	94	TZEEI 30 x TZEEI 4
29	TZEEI 6 x TZEEI 39	62	TZEEI 19 x TZEEI 22	95	TZEEI 30 x TZEEI 23
30	TZEEI 6 x TZEEI 40	63	TZEEI 19 x TZEEI 24	96	TZEEI 30 x TZEEI 36
31	TZEEI 6 x TZEEI 90	64	TZEEI 20 x TZEEI 8	97	TZEEI 30 x TZEEI 39
32	TZEEI 8 x TZEEI 24	65	TZEEI 20 x TZEEI 19	98	TZEEI 31 x TZEEI 8
33	TZEEI 8 x TZEEI 51	66	TZEEI 20 x TZEEI 21		
Check					
99	AKPOSOE (Three-way)	100	DODZI (OPV)		

Table 2. Description of the test environments used in the study

Location	Latitude	Longitude	Altitude (m ASL)	Mean Seasonal Rainfall *(mm)	Agro-ecological zone	Soil Type
Ejura	7° 38'N	1° 37'E	228.7	599.7	Transition	Forest/savannah ochrosols
Fumesua	6° 43'N	1° 36'W	228	626.86	Deciduous forest	Ferric acrisols
Kpeve	3° 20'N	0° 17'E	69	519.11	Coastal savannah	Savannah achrosols

*: mean rainfall during April to July, 2011

2.3 Statistical analysis

The data were analyzed separately for each location, and then combined and analyzed across locations for grain yield with PROC GLM in SAS using a RANDOM statement with the TEST option (SAS 2001) to determine if GxE interaction effects were significant. In the combined analysis of variance, genotypes were considered as fixed effects, while environments, replications, genotype by environment interaction and all other sources of variation were considered as random effects. Means were separated using the LSD at P < 0.05. Subsequently, the data on the grain yield were subjected to GGE biplot analysis to determine grain yield stability and the pattern of response of genotypes evaluated across the three environments. The GGE biplots were constructed using the first two principal components (PC1 and PC2) that were derived from subjecting environment centered trait means for each environment to singular value decomposition. The data were not transformed (Transform = 0), standardized (Scale = 1), and were environment-centered (Centering = 2). This provided information on the cultivars that were suitable for the different environments and investigation of stability of genotypes in the various environments. The analyses were done and biplots generated using the GGEbiplot software (Version 6.5). The GGE biplot Model 3 equation used is as follows:

$$Y_{ij} - Y_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where:

Y_j is the average yield across all genotypes in environment **j**; λ_1 and λ_2 are the singular values for PC1 and PC2, respectively; ξ_{i1} and ξ_{i2} are the PC1 and PC2 scores, respectively, for genotype i; η_{j1} and η_{j2} are the PC1 and PC2 scores, respectively, for environment j; and ε_{ij} is the residual of the model associated with the genotype i in environment j.

3. Results and Discussion

3.1 Analysis of variance

The combined ANOVA showed differences among environments (E) and genotypes (G) to be significant indicating that they were diverse. However, genotype by environment interactions for grain yield was not significant. The proportions of the total variance in grain yield attributable to the environments were the highest (87.27 %) while genotypes and GxE contributed 5.45 % and 0.84 %, respectively (Tables 3). This result is similar to the findings of Badu-Apraku *et al*. (1995; 2003) and Mohammadi *et al*. (2009), who reported that the largest proportion of total variation in multi-environment trials is attributed to locations, whereas G and G×E sources of variation are relatively smaller. The lack of significant GxE mean square for grain yield indicated that the expression of this trait would be consistent across the test environments. Mean grain yield of all the entries evaluated at the three locations was 5.21 t/ha (Table 3). The grain yields recorded for 54 of the genotypes were above the average yield (Figure 1).

Table 3. Mean square values from the combined analyses of variance of grain yield (t/ha) of 100 extra-early maturing maize genotypes evaluated across three environments in Ghana

Source of variation	DF	Mean square
Environment	2	87.27^{**}
Reps(Environment)	3	12.47^{**}
Blocks (Environment*Reps)	54	1.96^{**}
Genotype	99	5.45^{**}
Environment*Genotype	198	0.84^{ns}
Error	243	0.75
Mean		5.2
CV%		16.65

$^{*} = P \leq 0.05$, $^{**} = P \leq 0.01$, ^{ns} = not significant, respectively
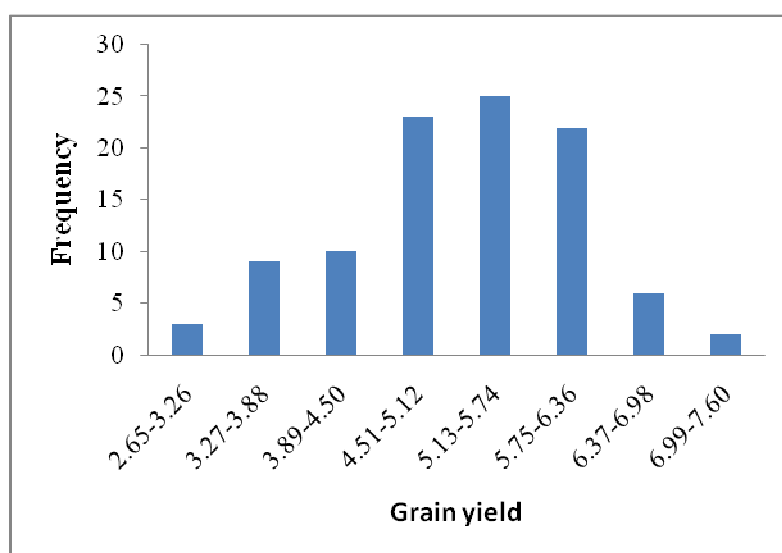
Figure 1. The frequency distribution of grain yield (t/ha) of the 100 extra-early maturing maize genotypes evaluated across three environments in Ghana

3.2 GGE biplot analysis of grain yield response and stability of the 100 extra-early maturing maize genotypes
The biplots in Figure 2 and 4 were based on genotype-focused singular value partitioning (SVP = 2) and is therefore appropriate for visualizing the relationships among environments. Also, the biplot in Figure 3 was based on environment focused-singular value partitioning (SVP = 1) and is therefore appropriate for visualizing the relationships among genotypes. The principal component (PC) axis 1 explained 74.4 % of total variation; while PC2 explained 17 %. Thus, these two axes accounted for 91.4 % of the G+G×E variation for grain yield (Figure 2, 3 and 4). The entry names of entries used in this section are shown in Table 1. The results are presented as three sections. Section one presents the results of "which won-where" to identify the best genotypes for each environment. Section two; the results of hybrids' performance and their stability; section three gives the discriminating power and representativeness of the test environments.

i.   The "which-won-where" patterns
The GGE biplot is an invaluable statistical tool for examining the performance of genotypes tested in different environments. The polygon view of the GGE biplot in Figure 2 indicated the best genotype in each environment. The presence of two or more environments within a sector indicates that a single genotype has the highest yield in those environments. If environments fall into different sectors, it means that different genotypes won in different environments (Yan *et al*. 2005; 2010). Based on the above information, entry 25 was the vertex genotype where Ejura and Fumesua fell while entry 78 was the highest yielding genotype at Kpeve. No

environment fell into the sector where entries 100, 44, 86, 79 and 70 were the vertex genotypes, indicating that these genotypes were the lowest-yielding genotypes at all or some locations. Genotypes within the polygon, particularly those located near entries 87, 77, 33, 90, 95, 80, 70, 90, 96 and 48 were less responsive than the vertex genotypes.
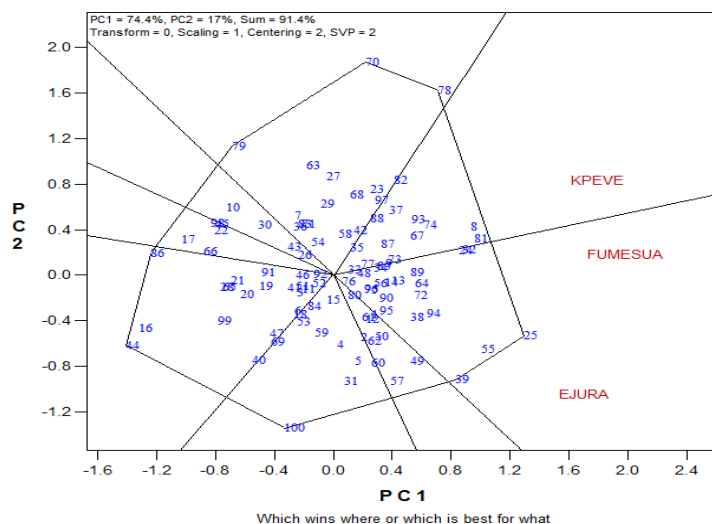

Figure 2. 'which-won-where' or 'which is best for what' based on a genotype x environment yield data of the 100 extra-early maturing maize genotypes evaluated in three environments in Ghana during the 2011 growing season

ii.   Performance of genotypes and their stability across environments

In the entry/tester view of the GGE biplot of grain yield of the 100 extra-early maturing maize genotypes evaluated in three environments in Ghana (Figure 3). The genotypes were ranked along the average-tester axis (ATC abscissa), with an arrow pointing to a greater value based on their mean performance across all environments. The double-arrowed line separates entries with below-average means from those with above-average means. The average yield of the genotypes is approximated by the projections of their markers on the average-tester axis.   In the GGE biplot analysis, the average-tester coordinate (ATC) approximates the genotypes' contributions to G×E, which is a measure of their instability. The stability of the genotypes is measured by their projections onto the double-arrow line (average-tester coordinate [ATC] y axis). The greater the absolute length of the projection of a genotype, the less stable it is (Yan *et al*. 2000; 2010). Based on this, entries 32, 24, 72, 89 and 13 were the most stable with an above average performance. Since they were located away from the ATC abscissa and had a near zero projection onto the ATC coordinate. This implies that their rankings were highly consistent across locations. For selection for broad adaptation in maize production, an ideal genotype should have both high mean performance and high stability (Badu-Apraku *et al*. 2011). Therefore, entries 32, 24, 72, 89 and 13 were closest to the ideal genotype and may be considered as best genotypes. These five hybrids are suitable for production in Ejura, Fumesua and Kpeve. On the other hand, ideal genotypes for specific environments are those that have high mean yield and respond best to the particular environments. Thus, entries 25 and 78 are especially suitable for production at Ejura and Fumesua, and Kpeve, respectively. Entries 70, 78, 23, 83, 57, 49 and 39 were the least stable highest yielding hybrids. On the contrary, entries 86, 17, 66, 28, 19 and 91 were lowest yielding but very stable hybrids. However, 100, 79, 63, 40, 69, 47, 27, 16 and 44 were not only low yielding but also among the least stable genotypes. Thus, they may not be good candidates for commercial production across these environments.
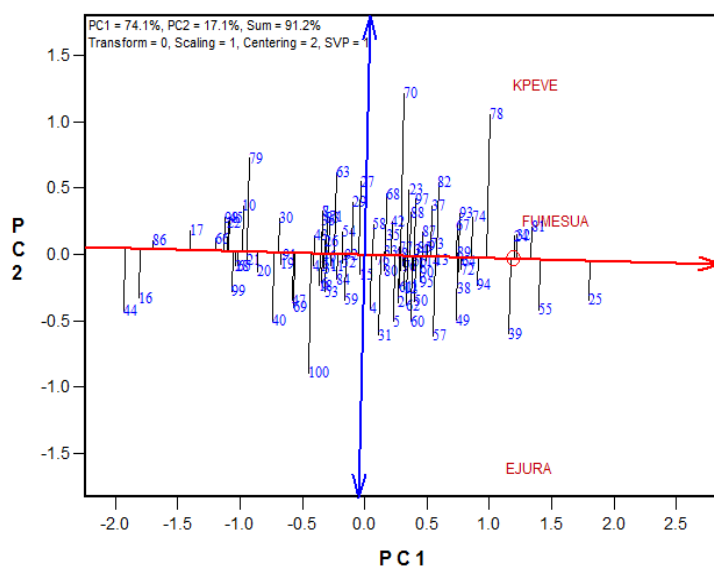
Figure 3. The 'mean vs. stability' view of the GGE biplot based on a genotype x environment yield data of the 100 extra-early maturing maize genotypes evaluated in three environments in Ghana during the 2011 growing season

iii.   Discriminating power and representativeness of the test environments

The three test environments used in this study were Ejura, Fumesua and Kpeve representing the transition, deciduous forest and coastal savannah zones of Ghana. The purpose of test-environment evaluation is to identify environments that effectively identify superior genotypes in a group of environments. The representativeness and discriminating power view of GGE biplot analysis are presented in Figure 4. Ejura had the longest vectors followed by Kpeve while Fumesua had the shortest vector. Fumesua was at the smallest angle to the average-environment axis (AEA) followed by Kpeve while Ejura was at the largest angles to it (Figure 4). Since the AEC abscissa is the average--environment axis, test environments at smaller angles to the AEA are more representative of the group of environments than those at larger angles to it. Therefore, the cosine of the angle between any environment vector and the average-environment axis approximates the correlation coefficient between the genotype values in that environment and the genotype means across the environments (Yan *et al*. 2007). The small circle is the average-environment and the arrow pointing to it is used to indicate the direction of the AEA (Yan & Tinker 2005). The absolute length of the projection from the marker of an environment onto the AEA is a measure of its representativeness: the shorter the projection, the more representative the environment. In contrast, the absolute length of the projection from the marker of an environment onto the AEA is a measure of its discriminative ability: the longer the projection, the more discriminative the environment. Based on these requirements, Ejura was highly discriminating but least representative of the test environments. Kpeve was most representative and discriminating of the test environments. On the other hand, Fumesua was the least discriminating but most representatives of the test environments. An ideal test environment should effectively discriminate genotypes and represent the environments (Yan & Rajcan 2002). This indicated that amongst the three locations, Kpeve located in the coastal savannah zone, represented the ideal testing environment for these set of genotypes. This location would therefore be the most appropriate for selecting superior genotypes. Similar result was reported by Abdulai *et al*. (2007).
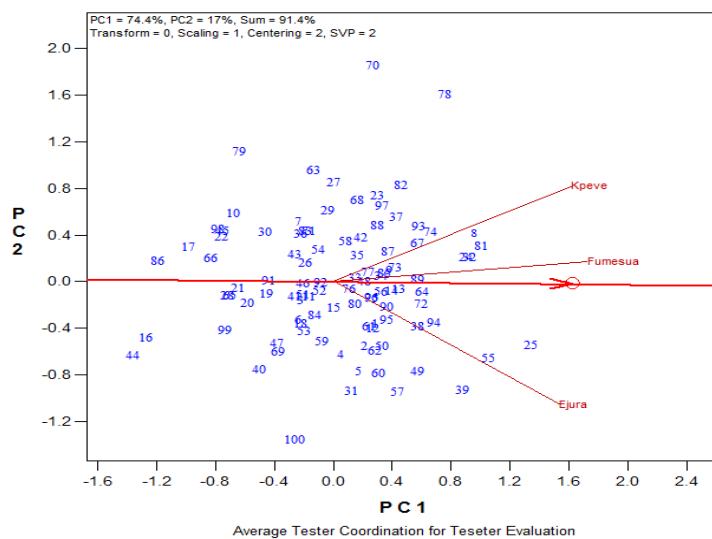
Figure 4. The 'discriminating power and representativeness' view of GGE biplot based on a genotype x environment yield data of the 100 extra-early maturing maize genotypes evaluated in three environments in Ghana during the 2011 growing season

4. Conclusion

The non significant GxE interaction effects for grain yield suggests that a promising genotype selected in one of these locations will also be suitable for production in the other locations in the same agro-ecological zone. Environments were found to contribute greatly to the variations in performance of genotypes. This indicates that, unpredictable environmental conditions are one of the major constraints to selecting superior and widely adapted maize varieties. The use of GGE biplot analyses provided clear bases for determining stability and performance of the 100 extra-early maize genotypes. Based on the analyses, entries 32, 24, 72, 89 and 13 were the highest yielding and most stable hybrids. They were the closest to the ideal genotype and may be considered as the best hybrids. These five hybrids have the potential for production in Ejura, Fumesua and Kpeve and other locations within the same agro-ecological zones. Entries 86, 17, 66, 28, 19 and 91 were lowest yielding but stable. Thus, the performance of these genotypes would be predictable in less favourable environments. Entry 25 was identified as the most promising for production in Ejura and Fumesua, and entry 78 in Kpeve. Kpeve located in the coastal savannah zone, was identified as the ideal testing environment for this set of genotypes.

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