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Research Article

Genotype-by-environment interaction and yield stability of maize (*Zea Mays* L.) single cross hybrids

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Abstract
Maize (*Zea mays* L.) is one of the most important cereal crops of India in terms of production and consumption. Maize is called as Queen of cereal crops. Currently, it is produced in all the agro-ecological zones of the country. In India, 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 2019 at four locations in India to (i) determine the presence of G x E of 106single cross maize genotypes and (ii) To use the GGE biplot methodology to determine grain yield performance and stability of the genotypes evaluated across four environments. The effects of genotype and environment were significant (P < 0.01) for grain yield. Also, GxE was significant for the same trait. G44, G105, G86, G97, G65 and G76 were identified as high yielding and most stable hybrids. Therefore, these hybrids have the potential for production across the test locations. On the contrary, G26, G10, G81, G102, G96 and G22 were not only low yielding but also among the least stable genotypes.

Keywords
G x E interactions, Stability, maize.

INTRODUCTION

Maize (*Zea mays* L.) is a cereal crop with a remarkable potential for production and is the third most important grain crop after wheat and rice. The considerable genotypic variability for different traits among various maize genotypes is a key to crop improvement. Globally, maize is cultivated in an area of 183.24 m ha with a production of 1036.07 m t and productivity of 5.65 t /ha. India stands sixth among the maize producing countries in the globe with an area, production and productivity of 9.60 m ha, 27.15 m t and 2.83 t /ha, respectively .Maize is grown from below sea level to altitudes higher than 3000 m, and in areas with 250 mm to more than 5000 mm of rainfall per year and with a growing cycle ranging from 3 to 10 months. The production process of maize is highly dependent on suitable environmental factors.

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). 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 nonadditive 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, to determine the presence of GxE in 100 single cross maize hybrids and 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.

Table 1. Description of single cross maize genotypes along with checks tested across four environments in 2018

Entry Name	Entry code	Entry Name	Entry code	Entry Name	Entry code
AI-001	G1	AI-037	G37	AI-073	G73
AI-002	G2	AI-038	G38	AI-074	G74
AI-003	G3	AI-039	G39	AI-075	G75
AI-004	G4	AI-040	G40	AI-076	G76
AI-005	G5	AI-041	G41	AI-077	G77
AI-006	G6	AI-042	G42	AI-078	G78
AI-007	G7	AI-043	G43	AI-079	G79
AI-008	G8	AI-044	G44	AI-080	G80
AI-009	G9	AI-045	G45	AI-081	G81
AI-010	G10	AI-046	G46	AI-082	G82
AI-011	G11	AI-047	G47	AI-083	G83
AI-012	G12	AI-048	G48	AI-084	G84
AI-013	G13	AI-049	G49	AI-085	G85
AI-014	G14	AI-050	G50	AI-086	G86
AI-015	G15	AI-051	G51	AI-087	G87
AI-016	G16	AI-052	G52	AI-088	G88
AI-017	G17	AI-053	G53	AI-089	G89
AI-018	G18	AI-054	G54	AI-090	G90
AI-019	G19	AI-055	G55	AI-091	G91
AI-020	G20	AI-056	G56	AI-092	G92
AI-021	G21	AI-057	G57	AI-093	G93
AI-022	G22	AI-058	G58	AI-094	G94
AI-023	G23	AI-059	G59	AI-095	G95
AI-024	G24	AI-060	G60	AI-096	G96
AI-025	G25	AI-061	G61	AI-097	G97
AI-026	G26	AI-062	G62	AI-098	G98
AI-027	G27	AI-063	G63	AI-099	G99
AI-028	G28	AI-064	G64	AI-100	G100
AI-029	G29	AI-065	G65	DKC 9108	G101
AI-030	G30	AI-066	G66	DKC 9162	G102
AI-031	G31	AI-067	G67	P1844	G103
AI-032	G32	AI-068	G68	P1855	G104
AI-033	G33	AI-069	G69	P1866	G105
AI-034	G34	AI-070	G70	CO6	G106
AI-035	G35	AI-071	G71		
AI-036	G36	AI-072	G72		

MATERIALS AND METHODS

Hundred single-cross maize hybrids developed internally from Tamil Nadu Agricultural University, Coimbatore, along with six competitor hybrids (**Table 1**) were evaluated at four locations *viz.,* Bilhaur (E1), Farrukhabad (E2),

Kannauj (E3) and Lucknow (E4) from, February 2018 to June 2018 spring season. The evaluation sites are in the northern part of India (**Table 2**). A standard protocol was adopted at each site during the period of evaluation. Evaluations were done under irrigated conditions. The genotypes were planted in a randomized complete block design with two replications. Each plot consisted 2-rows of 4 m long, an interrow spacing of 60 cm and an intra-row spacing of 20 cm. Two seeds were sown per hill and seedlings later thinned to one after emergence and seedling establishment. Other agronomic management practices were done according to the recommendations of the specific areas. Data recorded include days to anthesis, days to silking, plant and ear heights, 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. 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 2. Description of the test locations used in the study

Location/ Parameter	Bilhaur	Farrukhabad	Kannauj	Lucknow
Latitude	26° 50' N	27° 23' N	27° 3' N	26° 51' N
Longitude	80° 3' E	79° 35'E	79° 55' E	80° 56' E
Avg temp ^{0}C(Max)	32.72	31.52	32.43	32.78
Avg temp ^{0}C(Min)	18.85	18.18	18.57	18.82

The data were analysed separately for each location, and then combined and analysed across locations for grain yield with PB tools 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 four environments. The GGE biplots were constructed using the first two principal components (PC1 and PC2) that were derived from subjecting environment cantered trait means for each environment to singular value decomposition. The data were not transformed (Transform = 0), standardized (Scale = 1), and were environment-cantered (Centring = 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 R STUDIO. 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:

Yj is the average yield across all genotypes in environment **j**; ë1 and ë2 are the singular values for **PC1** and **PC2**, respectively; îi1 and îi2 are the **PC1** and **PC2** scores, respectively, for genotype i; çj1 and çj2 are the **PC1** and **PC2** scores, respectively, for environment j; and åij is the residual of the model associated with the genotype i in environment j.

RESULTS AND DISCUSSION

i.Analysis of variance:The combined ANOVA showed differences among environments (E) and genotypes (G) to be significant indicating that they were diverse. Also genotype by environment interactions for grain yield was alsosignificant. The proportions of the total variance in grain yield attributable to the environments were the highest (185.73) while genotypes and G x E contributed 10.44 and 3.85, respectively **(Table 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 significant GxE mean square for grain yield indicated that the expression of this trait will not be consistent across the test environments. Mean grain yield of all the entries evaluated at the three locations was 6.505 t/ha (**Table 3**). The grain yields recorded for 53 of the genotypes were above the average yield (**Fig. 1**).

ii. GGE biplot analysis of grain yield response and stability of the 100 single cross maize hybrids along with six checks.The biplots in **Fig. 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 35.1 % of total variation; while PC2 explained 29.9 %. Thus, these two axes accounted for 65 % of the G+G×E variation for grain yield (**Fig. 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.

Table 3. Mean square values from the combined analyses of variance of grain yield (t/ha) of 100single cross maize hybrids along with six checks evaluated across four environments in India

Source of Variation	DF	Mean square
Environment	3	185.73***
Reps (Environment)	1	3.95
Blocks (Environment*Reps)	105	4.11***
Genotype	3	10.44***
Environment*Genotype	315	3.85***
Error	420	1.38
Mean		6.505
CV (%)		21.3

Signif.codes:0'***'0.001'**'0.01'*'0.05'.'0.1' ' 1
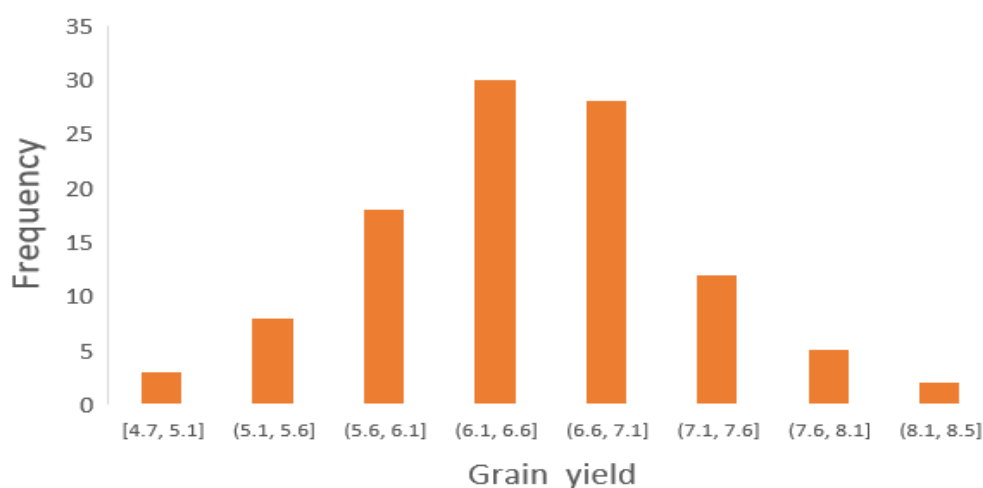
Fig. 1. The frequency distribution of grain yield (t/ha) of the 100 single cross maize hybrids along with six checks evaluated across four environments in India

iii. 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 **Fig. 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 G101 was the vertex genotype where E1 fell while entry G44 is good at E1 and E2; G26 and G46 are good at E4; G46 is good at E3. Genotypes within the polygon, particularly those located near entries G10, G68, G72, and many other genotypes were less responsive than the vertex genotypes.

iv. Performance of genotypes and their stability across environments. In the entry/tester view of the GGE biplot of grain yield of the 100 single cross maize hybrids along with six checks evaluated in four environments in India (**Fig. 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 aboveaverage 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 G44, G105, G86, G97, G65 and G76 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 G44, G105, G86, G97, G65 and G76 were closest to the ideal genotype and may be considered as best genotypes. These Six hybrids are suitable for production in E1, E2, E3 and E4 locations. Entries G101, G89, G21, G104 were the least stable highest yielding hybrids. On the contrary, entries G13, G2, G45, G3, G24and G79were lowest yielding but very stable hybrids. However, G26, G10, G81, G102, G96 and G22 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.
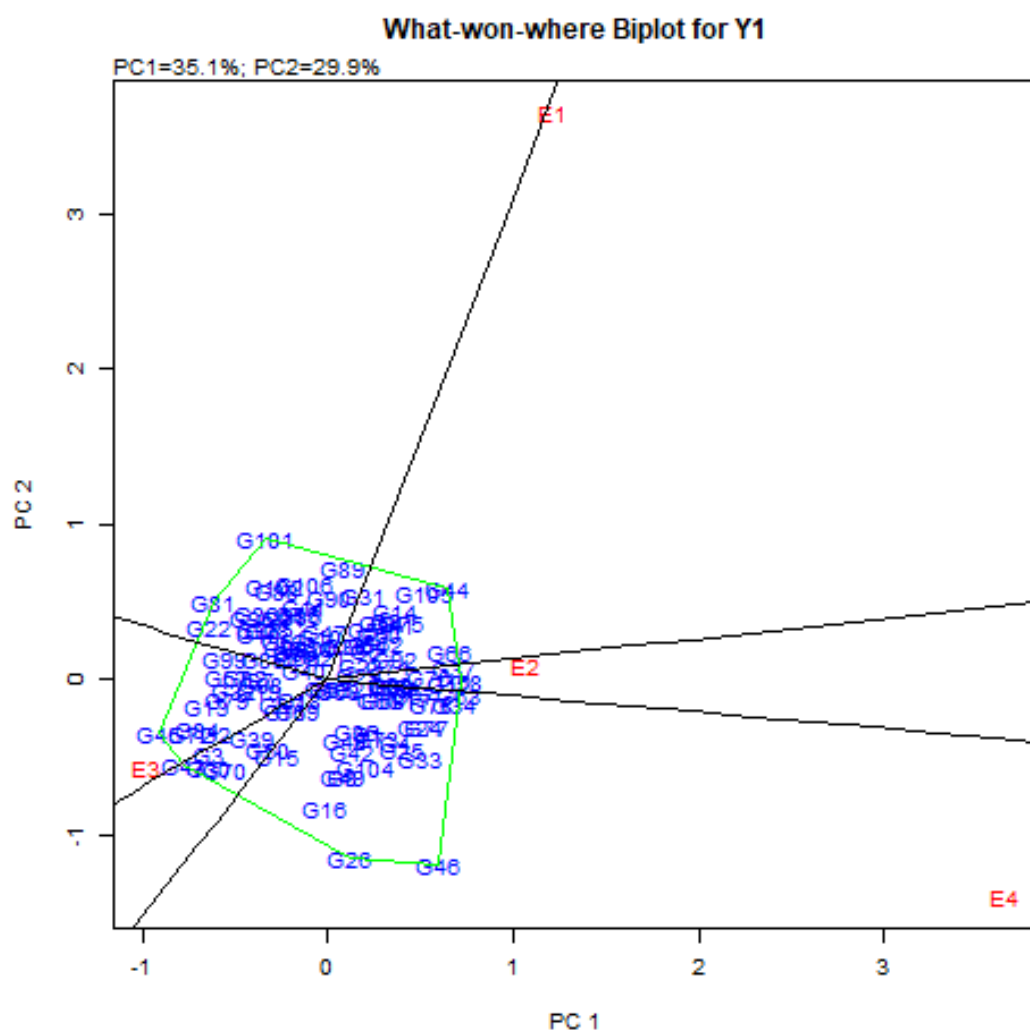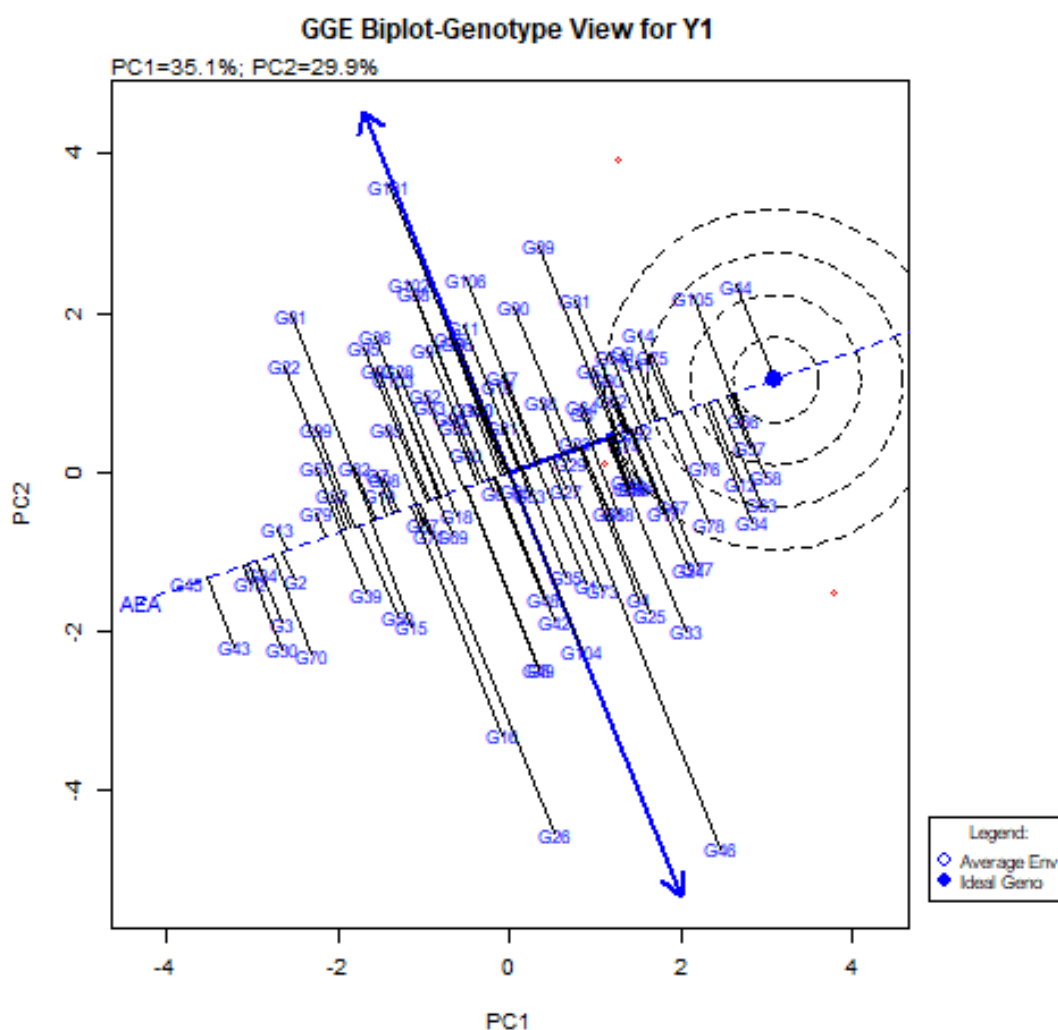

Fig. 2. 'which-won-where' or 'which is best for what' based on a genotype x environment yield data of the 100 single cross maize hybrids along with six checks evaluated in Four environments in India during the 2018 growing season

v.Discriminating power and representativeness of the test environments. The four test environments used in this study were Bilhaur (E1), Farrukhabad(E2), kannauj (E3) and Lucknow (E4) representing the spring corn locations in India. 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 **Fig. 4**. Kannauj(E3) had the longest vectors followed by Bilhaur (E1), later followed by Lucknow (E4) while Farrukhabad (E2) had the shortest vector. Farrukhabad(E2) was at the smallest angle to the

averageenvironment axis (AEA) followed by Lucknow (E4), followed by Bilhaur (E1) while Kannauj (E3) was at the largest angles to it (**Fig. 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, Kannauj (E3) was highly discriminating but least representative of the test environments. Lucknow (E4) followed by Bilhaur(E1) was most representative and discriminating of the test environments. On the other hand, Farrukhabad (E2) 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 four locations, Lucknow(E4) followed by Bilhaur (E1) 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).

Fig. 3. The 'mean vs. stability' view of the GGE biplot based on a genotype x environment yield data of the100singlecross maize hybrids along with six checks evaluated in four environments in India during the 2018 growingseason.
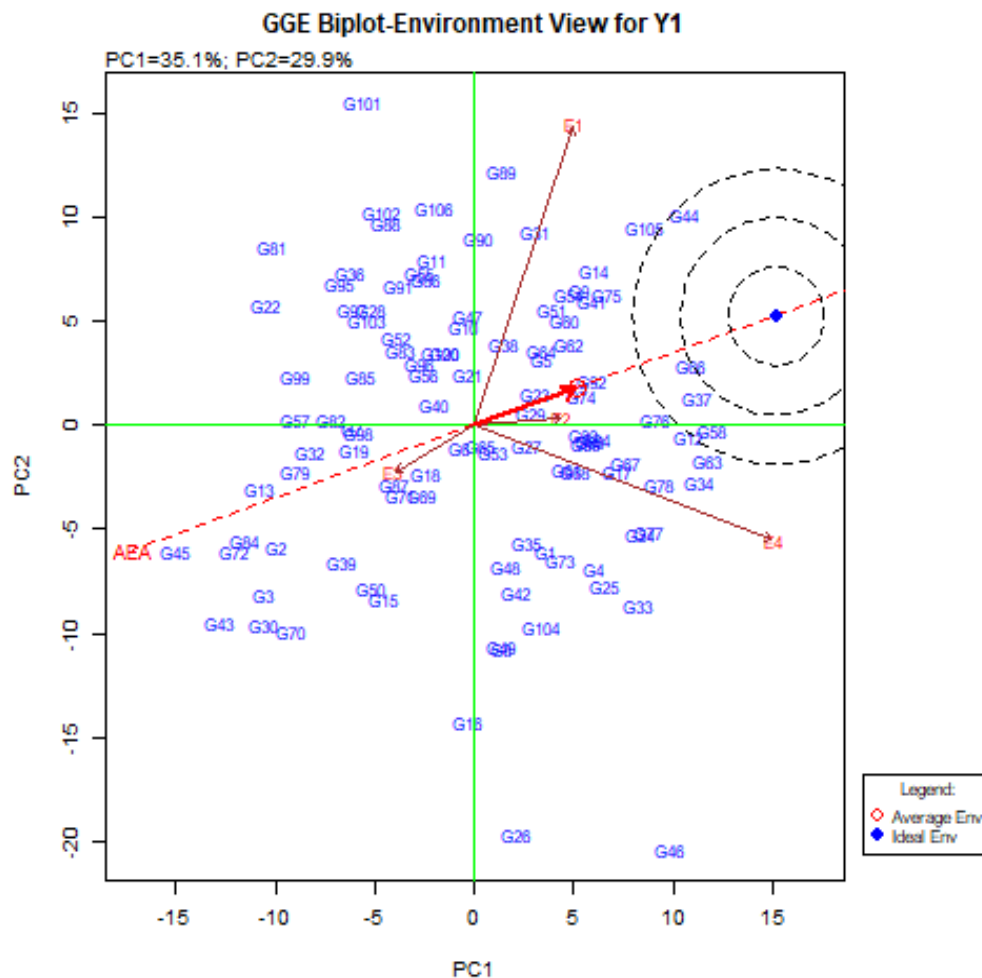
Fig. 4. The 'discriminating power and representativeness' view of GGE biplot based on a genotype x environment yield data of the 106single cross maturing maize genotypes evaluated in four environmentsin India during the 2018 growing season

The significant GxE interaction effects for grain yield suggests thatgenotypes perform differently across different environments, this suggest that selection of genotype should be specific to the environments. 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 106single cross maize genotypes. Based on the analyses, entries G44, G105, G86, G97,

G65 and G76 were higher yielding and most stable hybrids. They were the closest to the ideal genotype and may be considered as good hybrids. These six hybrids have the potential for production in Bilhaur(E1), Farrukhabad(E2), Kannauj(E4) and Lucknow(E4). Entries G13, G2, G45, G3, G24 and G79 were lower yielding but stable. Thus, the performance of these genotypes would be predictable in less favourable environments. Entry G101 at E1, while entry G44 at E1 and E2; G26 and G46 at E4; G46 at E3 were performed good respectively. Lucknow (E4) followed by Bilhaur (E1) were identified as the ideal testing environment for this set of genotypes.

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