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Research Article

GGE biplot and AMMI model to evaluate spine gourd (*Momordica dioica* Roxb.) for genotype × environment interactionand seasonal adaptation

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Abstract

A investigation was carried out to ascertain the GEI, the yield stability and adaptability of 12 advanced spine gourd genotypes (G) in one environments over three crop years (2013, 2014 and 2015). The AMMI and GGE biplot model were used to study the nature of GEI on the fruit yield. First and second component of AMMI model totally explained more than 99% of GEI variations. G7 having maximum trait value with specific adaptation while G2 and G3 were having general adoptability. AMMI 2 biplot revealed high stability of G5 and G2 across environments. Results of GGE biplot model showed that the G4 with the environment of E3 and G7 with the environment of E1 and E2, respectively showed a special adaptability. G7 could be recommended for Northern hill zone of Chhattisgarh. Considering both graphical analysis models of AMMI and GGE biplot could be recommended. The ideal environment, according to both the models, was E2. The results indicated that AMMI and GGE biplot are facilitated visual comparison and informative methods to detect genotypes stability and in the preferential genotypes recommendations.

Key words
AMMI, GGE bioplot, Spine gourd, Stability, G X E interaction.

Introduction

Spine gourd (*Momordica dioica* Roxb., 2n = 2X = 28) belongs to family Cucurbitaceae and comes under minor cucurbits. It is a nutritionally rich summer, dioecious and perennial cucurbit having a wide range of adoptability, distributed throughout India, China, Nepal, Bangladesh, Pakistan and Shri Lanka (Rai, *et al* 2012). *Momordica dioica* climber plant commonly known as Teasle Gourd, Kakrol, Kankro, Kartoli, Kantoli, Kantola, Kantroli, Ban karola or Small bitter-gourd is a relatively small oval to ovoid vegetable. Various plant parts are consumed in a variety of ways, *viz*., immature green fruits, young twigs and leaves of this crop are used as vegetable or cooked as a Vegetable (Tiwari and Tigga, 2015). The fruit is rich in ascorbic acid and contain iodine (Rao, 2001). The fruit also contain alkaloid, flavonoids, glycosides and amino acids (Kushwaha *et al*., 2005). *Momordica dioica*as the average nutritional value per 100 g edible fruit was found to contain 84.1% moisture, 7.7 g carbohydrate, 3.1 g protein, 3.1 g fat, 3.0 g fiber and 1.1 g minerals. The plant is used, for the treatment of eye diseases, against fever, snake bite, inflammation caused by lizard; is also used as medicine for diabetes (Nadkarni, 2004). Now it has become a major vegetable in the country because of its high export potential, demand in internal market, nutritional and medicinal value. In order to meet the superior high yielding genotypes with desirable agronomic traits for diverse ecosystem is therefore a necessity. The ideal genotype should be high yielding under any environmental conditions, but as genetic effects are not independent of environmental effects, most genotypes do not perform satisfactorily in all environments (Carvalho *et al*., 1983). The development of improved genotypes, which can be adapted to a wide range of environments, is one of the final goals of researchers in plant breeding program. Varietal adaptability to environmental fluctuations is important for the stabilization of crop production over both the regions and years. An information on Genotype x Environment Interaction leads to successful evaluation of stable genotype, which could be used for general cultivation. Yield is a complex quantitative character and is greatly influenced by environmental fluctuations; hence, the selection for superior genotypes based on yield *per se* at a single location in a year may be very effective. The Additive Main Effects and Multiplicative Interaction (AMMI) and GGE biplot models can be powerful tools for effective analysis and interpretation of multi environment data structure in breeding programs (Yan *et al*. 2000; Ebdon and Gauch 2002; Samonte *et al*. 2005).The utilization of both AMMI and GGE biplot methods simultaneously in confirmation of stable genotypes with high yield conducted by many researchers. Therefore, purpose of the present study was to apply GGE biplot and AMMI techniques to study the patterns of GEI in 12 advanced spine gourd genotypes; to graphically display means, adaptability and stability, to identify suitable genotypes, to the relationship among the test environments and to compare result of GGE biplot and AMMI models.

Material and Methods

In 2013, 2014 and 2015, atotal of 12 genotypes of spine gourd (Table 1) were evaluated at RMD college of Agriculture and Research Station, Ambikapur (India). The experiments were conducted in anRandomized Complete Block Design with three replications. The experimental unit consisted of 2.0 m spacing maintained between rows and between plants along with 1:8 (Male: Female) ratio in the field. All the recommended package of practices provide for good crop growth and development. Following harvest, fruit yield was determined for each plant in each test environment. Meteorological data of three crop years recorded at Ambikapur used in the experiment are given in table 2. The fruit yield data were subjected to AMMI and GGE biplots analysis. All statistical analyses were conducted by PBTools, version 1.4. 2014. Biometrics and Breeding Informatics, PBGB Division, International Rice Research Institute, Los Baños, Laguna.

Results and Discussion

Analysis of Variance of AMMI model for fruit yield, AMMI 1 and AMMI 2 score of twelve genotypes and three environments has been presented in Table 3. AMMI analysis for fruit yield revealed highly significant differences among genotypes, environments and G X E interactions. The G X E components was further portioned and explained by two interaction principal components axes (IPCA) namely IPCA I and IPCA II. The results of AMMI 1 (AMMI model with help first IPCA axis) and AMMI 2 (IPCA I and IPCA II) analysis have been presented with help of biplot in Fig 1 and 2 respectively. The first two IPCA axes explained more than 99 per cent (PC 1 = 76.9; PC 2 = 23.1) of total variation and thus AMMI was effective in explaining G X E interaction component.

To display yield stability, the main and IPCA1 effects of both G and E on fruit yield are shown in Fig. 1. Graphical analysis of IPCA1 with average fruit yield revealed that G7 had the highest trait value but G4 had the highest positive AMMI1 score. Among environments, E2 was most favorable for fruit yield but having high negative interaction with genotypes (–41.703). E3 had positive interaction with genotypes even though mean value was less than E2. As per AMMI model, genotypes having trait value greater than grand mean and IPCA score near to zero are considered to have general adaptability across environments. Thus G2 and G3 were having general adaptability. However, genotypes with high trait value and large value of IPCA score are considered to have specific adaptability to the environments. G7 and G6 were having specific adaptation (due to high trait value and large IPCA score). In AMMI model, environments that appear in a perpendicular line have similar trait value and those falling almost in a horizontal line have similar interaction pattern. In this study, all three environments were different for trait mean and interaction as suggested by AMMI1 biplot.

AMMI2 biplot (Fig. 2) does not show the additive main effects, but it is highly informative on interaction component. This graph is useful when IPCA2 is sizeable and significant. In AMMI2 biplots, if a genotype is located close to the centre of the biplot (origin); the genotype is considered more stable than those genotypes located away from the centre. G2 followed by G5 were stable genotypes as they were close to centre on biplot. E2 was most stable environment followed by E1 and E3 as suggested by AMMI2 score. G9, G11 and G12 were having positive interaction with E3. G7 and G5 had high positive interaction with E2.G2 followed by G3 and G1 had high positive interaction with E1.

According to the IPC1 *vs*IPC2 scores of genotypes and environments, when a genotype is near an environment, this indicates that the genotype is adapted to specific environment (Shafii and Price 1998). G2 were recognized as superior and stable genotype for E1 environment. In order to select appropriate environments with high ability for separating genotypes, environments should have a high IPCA1 and low IPCA2 (Mohammadi and Amir 2008). According to IPCA1, E2 environment had the most stability and the least contribution of interaction, and E1 and E3 with the most IPCA1 had the most contribution to produce GEI. It observed the least environmental IPCA2 for E3 environments and the most for E1 and E2. Ideal environment based on the more IPCA1 and the less IPCA2, was E2. AMMI stable parameters for environments have been used by several researchers (Yan *et al*. 2000;Yan and Rajcan 2002; Mohammadi *et al*. 2008) in order to preferential analyze GEI, and additionally they introduced stable and compatible genotypes to the environments. They were also able to distinguish environments with high genotype separating ability from the others.

The numerous researches reveal that the main environmental effect is of the major magnitude in stability analysis experiments, while the explained variations by the main genotype effect and GEI, which is interpretable, are low. Since the environment is not a factor that can be controlled, hence GGE biplot graphically virtualizes G plus GE of a MET in a way that facilitates visual genotypes evaluation and mega environment identification (Yan *et al*. 2000). Results of GGE biplot showed that the first two principal components (PC1 and PC2) explained 85.5% of the sum of squares with PC1 = 53%and PC2 = 32.2% of the GGE sum ofsquares. Illustration of the "whichwon-where" biplot as polygon (Fig.5) is the best way to interpret the interaction patterns between genotypes and environments and give comprehensive information (Yan and Kang 2003). According tothis analysis, ideal genotype arethose that should have high PC1scores (high mean yield) and lowPC2 scores (high stability). Also,ideal environments should havehigh PC1 scores (more power todiscriminate genotypes in terms ofthe genotypic main effect) and lowPC2 scores (more representative ofthe overall environments) (Yan *et al*. 2000; Yan and Rajcan 2002). This polygon is generated by joining the farthest genotypes from the biplot origin in a way that all other genotypes are within the polygon. The perpendicular lines to the sides of the polygon create parts of genotypes and environments (Hernandez and Crossa 2000). According to Fig. 5 the G4, G7, G9 and G10 are situated in the apex of this polygon and indicated superior genotypes and four lines divided the biplot into four parts and the environments fall into three of them and they considered as thee mega environments. In E1 and E2 environments in the first and second year is situated in a part, where G7 is located at its apexes *i.e*., G7 is the best performer under E1 and E2 environment. E3 environment in the third year has situated in a part, where G4 located at its apexes. The most important point is that there is no any environment within the parts, where G10 and G9 are located at its apex, which shows G10 and G9 are not superior in mega environment. The length of an environmental vector is an estimation of discriminating ability of the environment (Yan *et al*. 2007). Environments with longer vectors (E3 in Fig. 5) are more discriminating of the genotypes. If an environment is near to the biplot origin (E2 in Fig. 5), it means that it exhibited low interaction and all genotypes performed similarly and, therefore, it provided little or no information about the genotypic differences and therefore it is considered as nondiscriminative environment. To measure representativeness using a biplot, an average environment has to be determined and used as a criterion. The angle between the vector of an environment and the average environment axis is a measure of the representativeness of the environment. Ideal test environment, should be both discriminative and representativeness (Yan and Tinker 2006). E3 is the nearest environment to the test ideal environment. Thus, it is the most favorable environment which is most effective environment in identification of superior genotypes from other environments (Yan and Kang 2003). Correlation between environments is determined by an angle between them. In fact, the angle between vectors which are smaller than 90^o shows positive correlation between them and angle 90^o between vectors shows independent environments. Larger angle than 90^o means that there is a negative correlation between environments (Yan and Kang 2003). Because of a low angle, there is a positive and relatively high correlation between E1 and E2 indicates same response of genotypes in this environments. E2 and E3 environments possessed of close correlation to zerocaused to an independent yield of genotypes in these environments. In this research considering that E1 and E2 environments have a close correlation and with respect to these results are equally replicated duringdifferent year, can use one of these environments in order tosave and reduce costs.The mean yield and stability of genotypes areevaluated by defining an average tester coordinate(ATC) (Yan 2000; Yan and Hunt 2002). ATCX-axis or the performance of genotype passes through the biplot origin with an arrow indicating the positiveend of the axis and the average environment isindicated by a circle. The ATC Y-axis or the stabilityaxis passes through the plot origin with double arrowhead and is perpendicular to the ATC X-axis (Fig. 4).The average yield of genotypes is estimated by theprojections of their markers to the ATC X-axis. Thus,according to the Fig. 3, yield average of genotypes isin the order of G7> G2> G3> G6> G1> G4.

A longer projection to the AEC ordinate,regardless of the direction, represents a greatertendency of the GEI of a genotype, which means it ismore variable and less stable across environments (Crossa*et al*. 2002). G4 and G10 havemost instability and fluctuation of yield, because theyhave been perpendicular to horizontal axis by thelongest line compared to the other genotypes. On thecontrary, G 1, G5 and G9 with the shortest line (theleast variance) and higher yield than total average arethe most stable genotypes in all environments.An ideal genotype would be that, which has highyield average and high stability. Thus, G7 and G2are as ideal and G3, G6 and G1 are in thefollowing ranks.

In the present study, two of the well used models AMMI and GGE bioplot were employed. With respect to results of AMMI model.Regarding the two graphical analysis models of AMMI and GGE biplot, G7 can be recommended toall environments as the most stable genotypes withhigh mean yield. Thus they are recommended forcommercial cultivation to contribute forenhancing spine gourd production in northern hill zone of Chhattisgarh. Multi-environment screening is essential to evaluate quantitative traits, to quantify adoptability and stability of the germplasm since these are the complex traits and highly influenced by environment. Further, it was opined that use of both the models to evaluate multi-environment data are as effective as with the data recorded from two to five times more replications (Gauch, H.G. and Zobel 1988). The presented results indicated that AMMI and GGE biplot are facilitated visual comparison and informative methods to detect genotypes stability and in the preferential genotypes recommendations.

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Table 1. Mean yield of the investigated genotypes

S.No.	Genotype	Code	Mean yield (kg/ha) in all environments	IPCA I Score	IPCA II Score
1	AMBIKA 12-1	G1	7223.88	12.47	-38.61
2	AMBIKA 12-2	G2	8212.77	0.69	-8.06
3	AMBIKA 12-3	G3	7894.72	1.23	-13.53
4	AMBIKA 13-4	G4	7150.00	58.17	-17.40
5	AMBIKA 13-5	G5	5923.33	-8.77	4.74
6	AMBIKA 13-6	G6	7631.11	-14.31	-2.59
7	INDIRA KANKODA (C)	G7	8883.88	-16.22	15.34
8	NDM-2	G8	6207.50	-22.49	-5.06
9	NDM-3	G9	5035.00	9.86	13.67
10	NDM-4	G10	5786.16	-53.31	-8.86
11	RMFG-39	G11	6682.22	15.88	18.18
12	RMFG-49	G12	6681.11	18.18	33.76
		E1	6824.86	-31.621	-49.158
		E2	7155.76	-41.703	44.850
		E3	6847.30	73.324	4.308
	Mean		6942.64		

Table 2. Brief description of experimental Environments

Environments	Soil type	Altitude (m)	Annual Average Rainfall (mm)	Annual Average temp. (^{0}C)		Global position	
				Min.	Max.	Latitude	Longitude
2013	Sandy loam	623	1197.1	17.30	29.50	23°09' N	83°08'E
2014	Sandy loam	623	1209.2	16.80	29.60	23°09' N	83°08'E
2015	Sandy loam	623	1216.3	17.60	30.00	23°09' N	83°08'E

Table 3. Analysis of variance for AMMI model in fruit yield of spine gourd genotypes

Source	df	Mean square	F	ss(%)
Genotype	11	3760409.417**	21.82	87.42
Environment	2	1079556.559**	6.265	4.56
GXE	22	172306.222	0.012	8.011
IPCA1	12	16465268**	16.91	
IPCA2	10	5931838**	6.09	
Corrected total	107			

**, * and ns significant at the 0.01 and 0.05 probability level, respectively and non-significant.

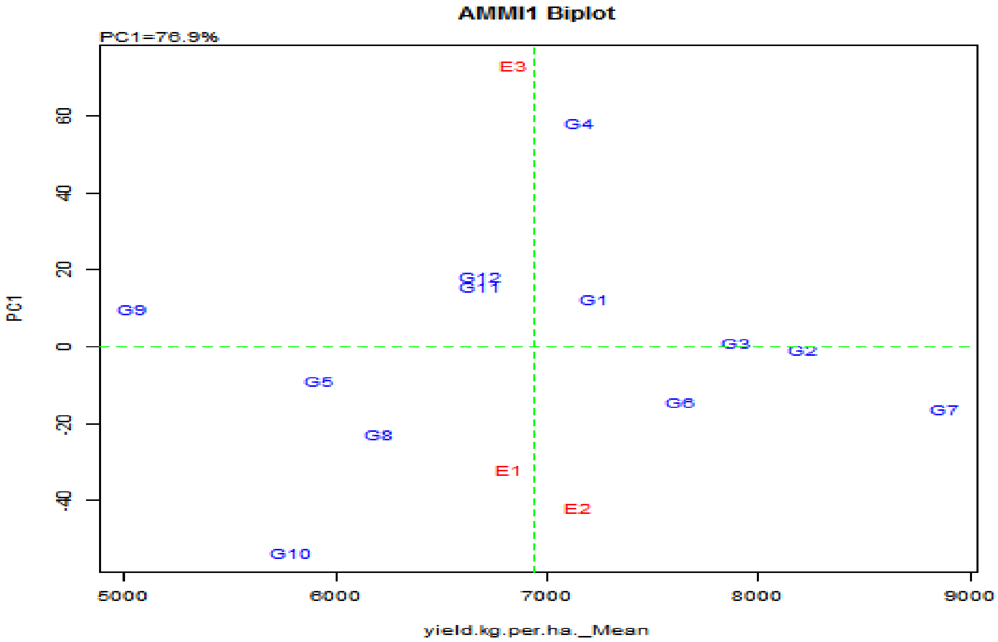


Fig. 1. AMMI 1 bioplot showing IPCA 1 *vs.* main effect

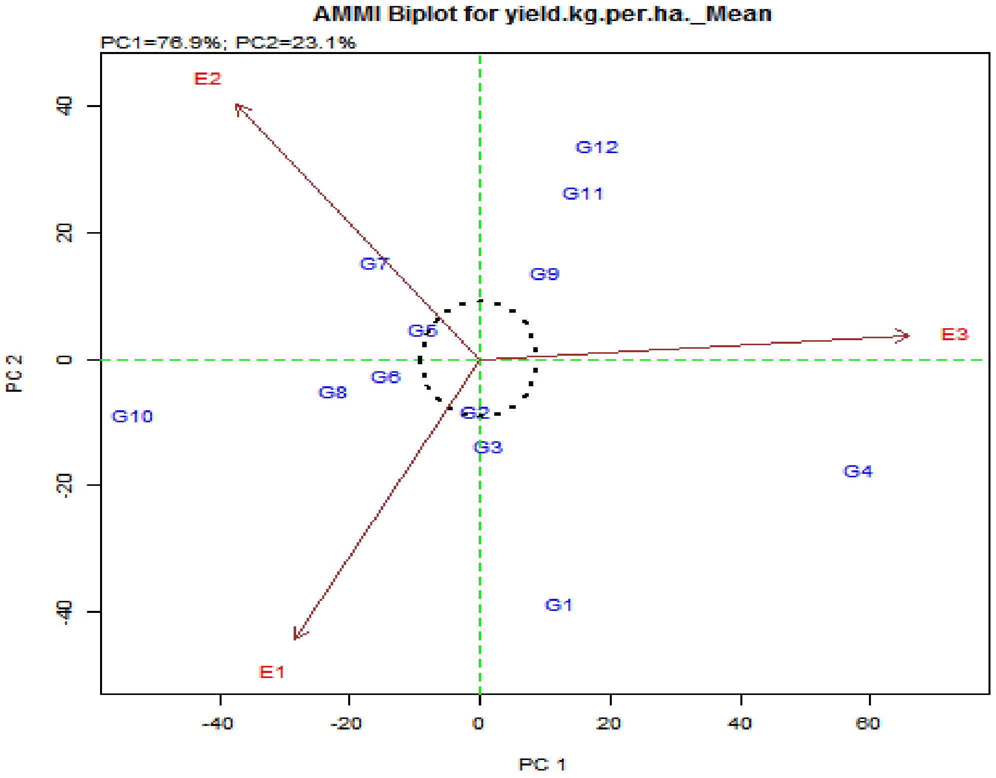


Fig. 2.Bioplot of IPCA 1 with IPCA 2

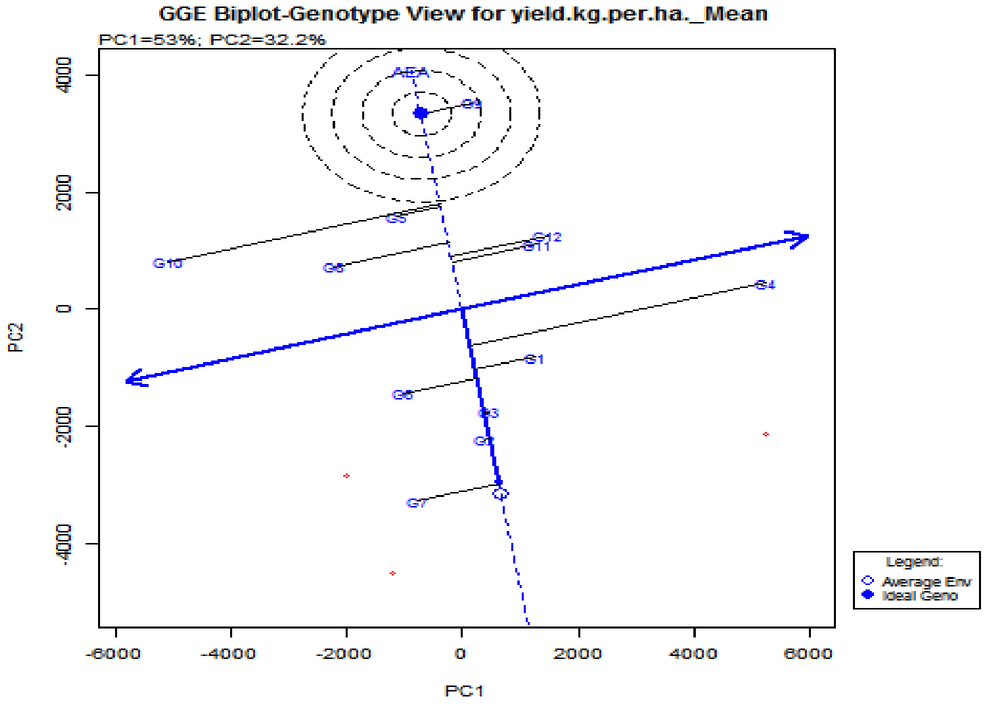


Fig. 3. Yield average and stability of genotypes.

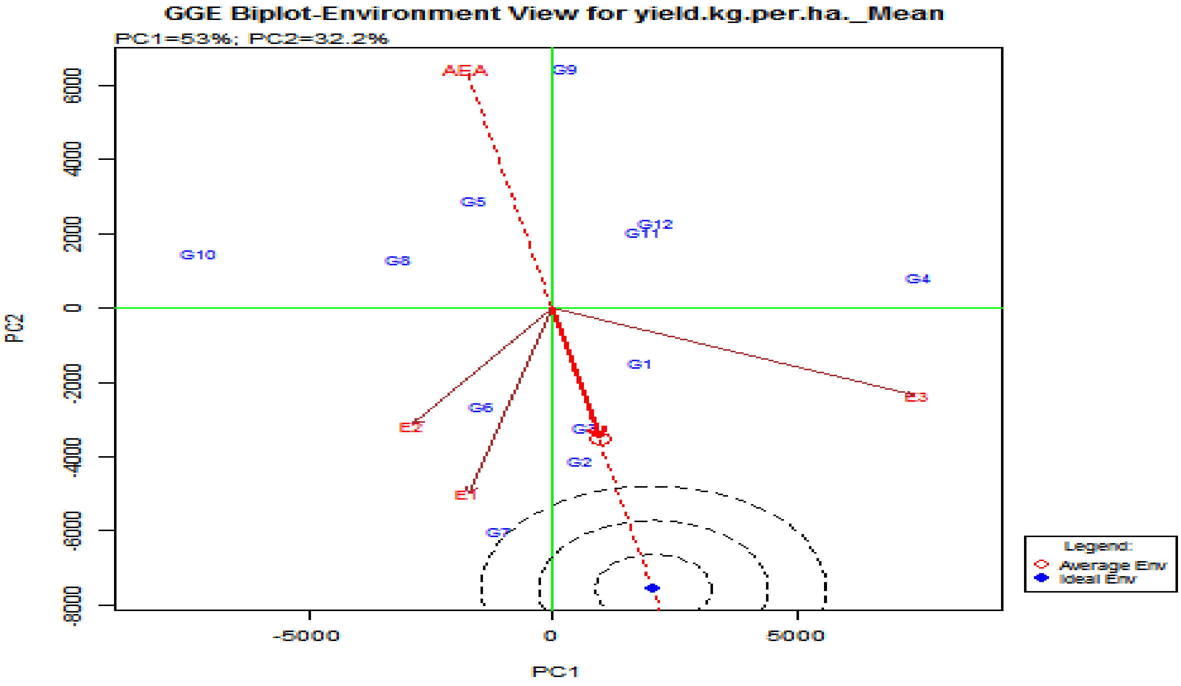


Fig. 4. Average environment coordination (AEC) view of the GGE biplot based on environment-focused scaling for the means performance and stability of genotypes

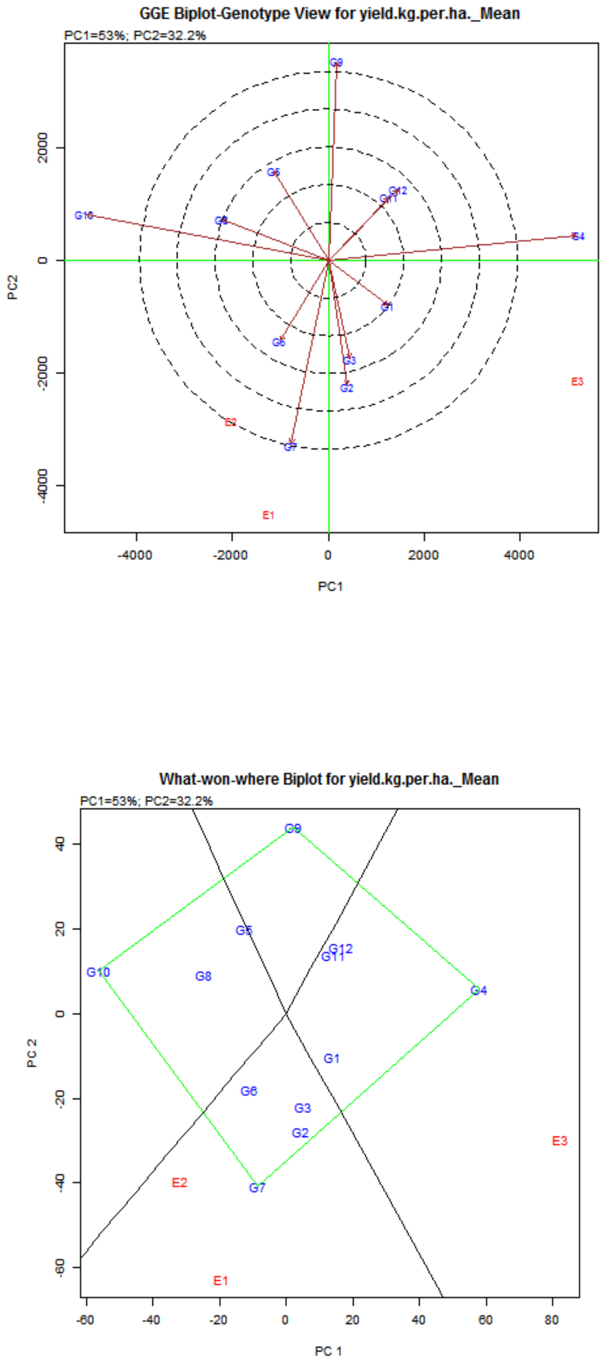
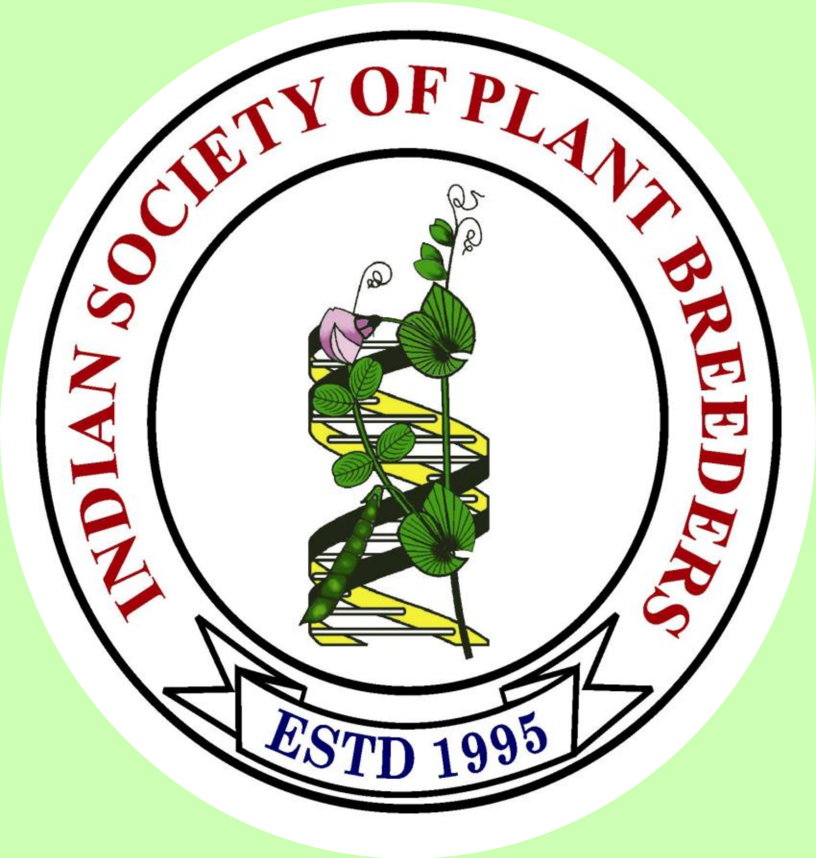


Fig. 5. The polygon for determining mega-environments and the best genotypes for each environment



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