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GGE biplot and AMMI analysis of maize hybrids assessed for stability across environments

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Abstract
Maize is a versatile crop with wider genetic variability and is able to grow successfully in tropical, sub tropical and temperate agro-climatic conditions. Determining stable genotypes across environments is essential for realizing improved yields. A study was conducted in which fifty six yellow maize hybrids were evaluated for grain yield stability across four diversified environments of Andhra Pradesh *viz.*, Vizianagaram, Peddapuram, Garikapadu, Reddipalli representing different agro ecological zones of Andhra Pradesh, India. Combined analysis of variance did show show highly significant differences for genotypes, environments and genotype by environment interactions based on AMMI analysis. Environments have significantly affected grain yields of hybrid maize which accounted for 64.7 per cent of the total variation in yield while the genotype by environment interaction accounted for 26.6 per cent. GGE was partitioned through GGE Biplot which depicted first two interaction principal component axes (IPCA) contributing about 84.0 percent (48.4% and 35.6% by IPCA1 and IPCA2 respectively) of the grain yield variation due to genotype and genotype by environment interaction (GGE). Contribution of 8.7 percent by the genotypes indicates least contribution of genotypes to the total variation in the multi environment trials. The mean grain yield over environments ranged from 5747 kg/ha (CAH163) to 3628 kg/ha (CAH1542) with a grand mean of 4710 kg/ha. Out of fifty six hybrids, 29 hybrids had above the mean average yields. The present study revealed Peddapuram and Vizianagaram are the most discriminating environments among the four and most representative due to their longest distance from the origin of the biplot. Genetic differentiation of experimental hybrids is best demonstrated in the representative environments.

Keywords: Climate change, AMMI, stability, GGE, biplot

Introduction
Maize (*Zea mays* L.) is one of the three most important cereals in India including rice and wheat. This cereal provides food, feed, fodder, fuel and has been serving as a important source of basic raw material for a number of industrial products *viz.,* starch, oil, protein, alcoholic beverages, food sweeteners, cosmetics and bio-fuel etc. The physiological efficiency of Maize is based on the fact that it belongs to C_4 lineage because of which it can produce higher grain yield and have wider adaptation over wide range of environmental conditions (Pandey *et al.* 2017) [11]. The significant increase in demand for maize is because of increased use in poultry and livestock industries. Maize is a genetically divergent crop and is being grown in different agro ecological zones (Saleem abid and Saleem Zahid, 2018) [12]. Newly developed hybrids should possess characteristics of adaptability across a diverse range of different environments (CIMMYT, 1991) [5]. Improved hybrids perform best in the environments where they are found adaptable. Profitable cultivation of any crop involves growing of selected genotypes of particular crop most suitable for certain agro-ecological zones of the region.

Under changing climate scenario cultivation of genotypes un-adapted to the cultivation region greatly influences yield. Adaptability and stability of genotypes will determine their superiority which can be best assessed by evaluation of cultivars in different environments and ecological regions. Stability can be defined as the ability of a genotype to produce uniform yield regardless of environmental effects and adaptability may be defined as the ability of a cultivar to provide stable and high yield under varied environmental conditions (Hill *et al.* 1998) [8]. The performance of a stable genotype does not change or show a least change regardless of changes in the environmental conditions (Baker and Leon, 1988) [3]. Identification of promising maize hybrids for their adaptability and stability help in choosing superior maize hybrids for production which depends on the extent of presence of genotype × environment interaction (GEI). There are several stability statistics that can be used to partition GEI which include regression analysis, multivariate analysis, cluster analysis, genotype main effect plus genotype × environment (GGE) biplot and additive main effect and multiplicative interaction (AMMI).

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AMMI Model is the most commonly used statistical analysis for the interpretation of GEI based on the use of biplots. Evaluation of hybrids across different environments and assessment of those using GGE biplot and AMMI analysis helps in identification of stable hybrids across cultivation ecologies. Genotype × Environment studies allow identifying the ideal location to each genotype, which would maximize the grain yield potential and reduce production costs (Oyekunleet al. 2017) [10].

Materials and Methods
Newly developed maize hybrids were evaluated across different locations of Andhra Pradesh *viz*, Vizianagaram, Peddapuram, Garikapadu and Reddipalli representing different agro ecological maize growing regions of Andhra Pradesh, India. Location wise information on climate was presented in Table1.

Table 1: Climatic information of test sites

Location	Latitude	Longitude	Altitude (m)	Soil type	Mean temp	Rainfall (mm)
Vizianagaram	18.11^{0}N	83.40^{0}E	68.1	Red sandy	27.4	1097.0
Peddapuram	17.07^{0}N	82.14^{0}E	46.2	Sandy loam	27.3	988.6
Garikapadu	16.33^{0}N	79.70^{0}E	84.0	Black	28.5	1043.0
Reddipalli	18.01^{0}N	83.34^{0}E	137.0	Shallow red	29.1	753.0

A total of 56 hybrids were evaluated in the above locations. The experiment was designed in alpha lattice with two replications during 2017 Rainy season. The four environments were subjected to combined analysis of variance and genotype by environment interaction was performed according to additive main effects and multiplicative interactions (AMMI) model of Gauch and Zobel, 1997 [7]. The pooling of principal component analysis (PCA) of the G x E interaction with the analysis of variance for the genotype and environment main effects is possible through additive main effects and multiplicative interactions analysis (Kilic, 2014) [9]. The model equation is:

$$Y_{ij} = \mu + G_i + E_j + (\Sigma_k \lambda_k \alpha_{ik} Y_{jk}) + e_{ijl}$$

where Y_{ij} is the maize yield of ith genotype in j^{th} environment; G_i and E_j are the genotype and environment deviations from the grand mean, respectively; μ is the grand mean; α_{ik} is the eigenvalue of the principal component analysis axis k; and are the genotype and environment principal component scores for axis k; λ_k is the singular value of the kth axis in the PCA; Y_{jk} is is the eigen vector of Jth environment for the kth axis; e_{ij} is the average of the corresponding random error; n is the number of principal components retained in the model and is the error term. The GGE biplot and AMMI analysis were carried out using GEA-R software (CIMMYT, 2015) [6].

Results and Discussion
The relative expression of hybrid changes with type of growing environment which is depicted in the rank wise performance of the hybrid over environments (Saleem abid and Saleem Zahid, 2018) [12]. The hybrids with high mean performance are generally retained in a breeding program as selection of hybrids on the basis of their performance in specific environments is rarely practiced. The mean grain yields for fifty six maize hybrids and mean performance over four environments were illustrated in Table 2.

Table 2: List of hybrids and Mean performance of grain yield (kg/ha) for 56 maize hybrids and their combined means across environments

Sl No	Genotype	Vizianagaram	Peddapuram	Garikapadu	Reddipalli	Mean
1	CAH1514	7382	5803	4088	3940	5303
2	CAH158	5410	6814	3472	2776	4618
3	CAH1452	6118	5914	4164	4056	5063
4	CAH1547	6215	5487	3096	3952	4687
5	CAH1538	5670	4707	2356	4584	4329
6	CAH1422	6090	6108	3340	4952	5123
7	CAH1544	5889	5409	2648	4072	4504
8	CAH1423	5040	5058	2972	3912	4246
9	CAH1542	4309	4802	3264	2136	3628
10	CAH1428	5281	6153	2552	3448	4359
11	CAH1424	4508	7986	3244	4008	4937
12	CAH169	6254	5840	3256	3956	4827
13	CAH1532	5070	4540	3812	4568	4498
14	CAH142	5690	5725	2668	5508	4898
15	CAH1584	5916	5633	3264	4160	4743
16	CAH1639	4814	5215	3228	3516	4193
17	CAH163	6092	7036	4696	5164	5747
18	CAH1620	6305	6159	3104	4300	4967
19	CAH1521	5918	5705	3688	7080	5598
20	CAH1592	5774	5027	3048	3200	4262
21	CAH15107	5556	5550	2644	3480	4308
22	CAH1515	4362	6779	3644	4684	4867
23	CAH1458	4571	6464	3812	4744	4898
24	CAH162	4539	4909	3644	5116	4552
25	CAH1626	6103	4852	4080	4510	4886
26	CAH1449	5400	7366	3380	3112	4814
27	CAH1530	4019	5906	3076	3808	4202
28	CAH1421	5286	6045	3284	5064	4920

29	CAH1526	5094	4765	2696	4548	4276
30	CAH1548	4580	5264	3372	4876	4523
31	CAH1543	5373	6070	3312	5460	5054
32	CAH1414	6524	5561	3344	4620	5012
33	CAH1446	6015	5232	2612	4324	4546
34	CAH15110	3332	4711	2592	5076	3928
35	CAH15104	5017	5462	3168	4832	4620
36	CAH1437	5862	5748	2072	5164	4712
37	CAH147	5349	6745	4148	3880	5030
38	CAH1628	5357	5729	2896	3836	4455
39	CAH165	6890	5113	3256	3236	4624
40	CAH166	5102	6094	3220	4008	4606
41	CAH148	4474	5410	3080	5324	4572
42	CAH15112	6807	5736	3196	3880	4905
43	CAH1555	6653	5789	3620	4032	5023
44	CAH1448	5258	5969	3440	5120	4947
45	CAH1436	6540	5198	3460	4548	4937
46	CAH1630	5728	6664	3216	3972	4895
47	CAH1540	5043	6735	2816	5596	5047
48	CAH167	5099	6006	3228	3328	4415
49	CAH1535	6221	4755	2344	5204	4631
50	CAH1638	5440	4683	4256	4364	4686
51	900MGold	5398	6945	2872	3828	4761
52	DKC8101	5386	7283	3804	3660	5033
53	CP838	6817	5002	3120	4320	4815
54	P3396	5411	6555	2860	4512	4834
55	HTMH5101	4360	5761	2896	4744	4440
56	NK6240	4003	6674	3928	3140	4436

The mean of grain yield of maize hybrids across the environments showed significant variations in ranks among the hybrids, which demonstrate high hybrid and location interactions (Baker, 1988) [2]. The real value of a Hybrid is determined by grain yield which is one of the most important parameter in almost all breeding programs. Partitioning of overall variability in to additive main effects due to environment (E), genotype (G) and non-additive genotype ×

environment interaction (GE) is done by analysis of variance (ANOVA). Significant statistical differences were detected among the hybrids for mean grain yield over all the four environments under study. Highly significant differences for environments, genotypes by environment interactions was revealed by combined analysis of variance based on AMMI analysis (Table 3).

Table 3: AMMI analysis of variance for grain yield over four environments

Source	df	Sum of squares	MSS	Total variance explained	G×E explained (%)	F_{cal}
Environments (E)	3	451290688	150430229	64.7		160.63**
Genotypes (G)	55	60206321	1094660	8.6		1.45*
G×E	165	185666936	1125254	26.6		1.36*
IPC1	57			48.4	48.4	2.52**
IPC2	55			35.6	84.1	1.85**
IPC3	53			15.8		1.24ns
IPC4	51			0		0.68ns
Error	223					

Environment significantly affected grain yields of hybrid maize genotypes as explained by contribution of 64.7 percent of total variation by environment followed by genotype by environment interaction which revealed 26.6 percent of the total yield variation. Partitioning of GGE through GGE Biplot analysis showed the first two interaction principal component axes (IPCA) revealed about 84.0 percent (48.4% and 35.6% by IPCA1 and IPCA2 respectively) of the grain yield variation due to genotype and genotype by environment interaction (GGE). Contribution of 8.6 percent by the genotypes indicates least contribution of genotypes to the overall variation in the multi environment trials.

The first two IPCA axes are highly significant and explained 64.2% of the G x E interaction. Commercialization of maize hybrids is determined by the level of average yield but also by the stability (Babic *et al*. 2006) [1]. Significant difference between the reaction of genotype to various ecological conditions for factors under study was revealed by AMMI analysis. High quantum of overall interaction was revealed by

the first PC1 axis, which signifies the importance of genotype in both overall variation and overall interaction. More complex pattern of GE interaction was seen in the studies of Balestre *et al.,* 2009 [4] who evaluated genotypes at locations within the same state but different sites in terms of soil and climatic features.

The degree of interaction of the genotypes in different environments is indicated by their distances from the origin. Angle between the vectors represents genotype and environment interaction. Genotypes close to particular environment on IPC1 *vs* IPC2 biplot show specific adaptation those environments. Genotypes falling near the center of the biplot may have broader adaptation. Based on the biplot analysis between IPC1 and grain yield, genotype 35 (CAH15104) may be considered as most adaptable to all the environments (Fig. 1). The first two IPC scores (PC1 *vs* PC2) derived upon GGE biplot analysis based on AMMI model were presented in Fig. 2 which shows the association between different environments.
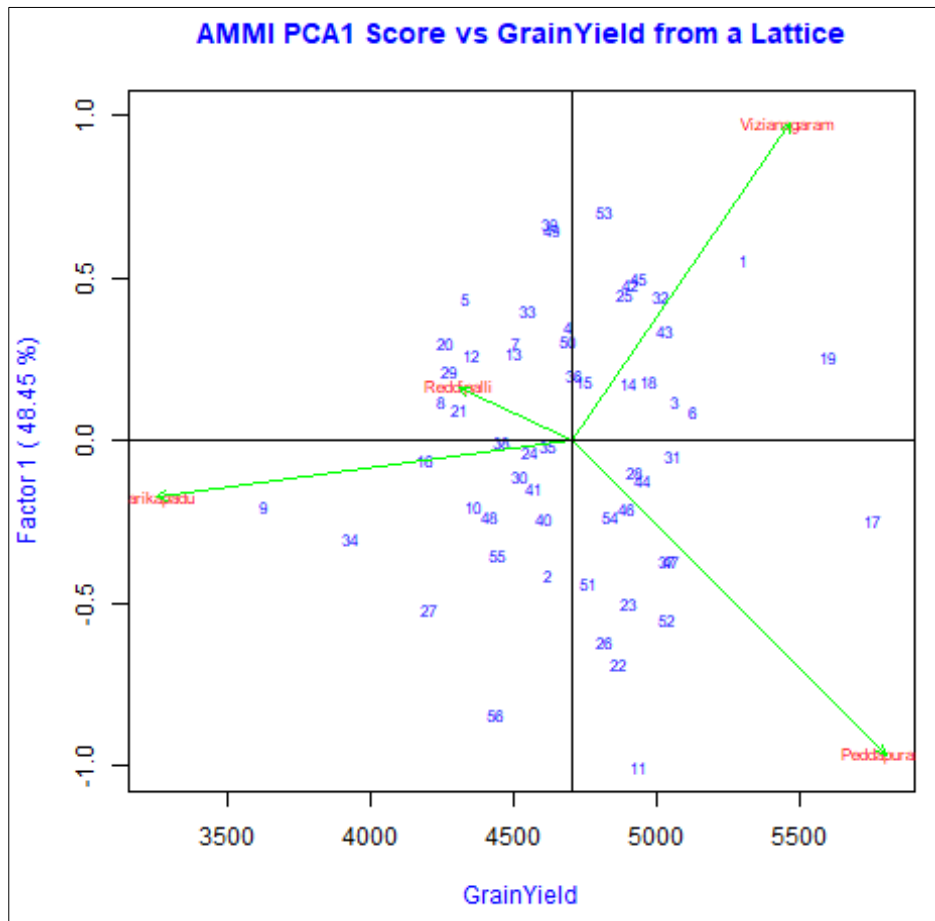
Fig 1: Biplot analysis of genotype × environment interaction for IPC1 and grain yield of maize hybrids
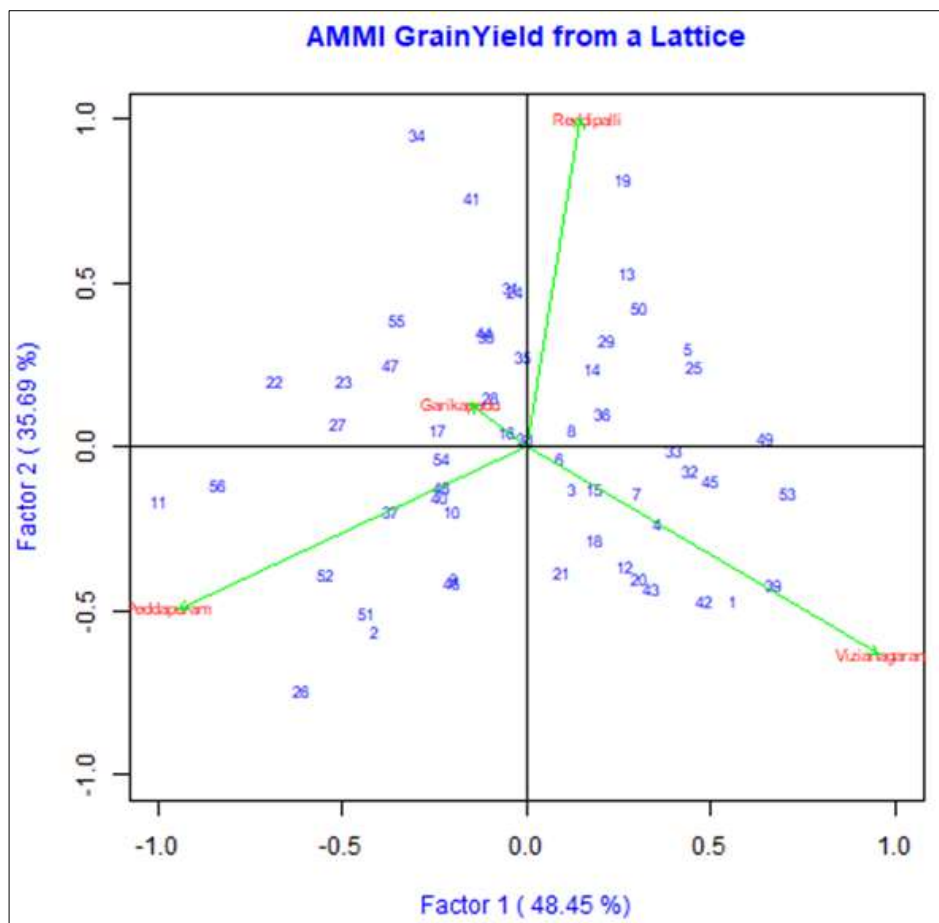
Fig 2: Biplot analysis of genotype × environment interaction for first two IPC scores (PC1 vs PC2)

The present study revealed locations *viz.*, Peddapuram and Vizianagaram as most discriminating environments among the four and most representative due to their longest distance from the origin of the biplot. In conclusion, identified hybrid CAH15104 can be further promoted in State and National Varietal Testing Network and farmer adaptive trials. The most discriminating environments will be used for testing of hybrids in future and it will help in trial cost cutting.

Acknowledgement

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