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Analysis of G × E interaction for identification of superior fodder cowpea genotypes

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Abstract

Estimation of G × E interaction was carried out in thirty cowpea genotype of diverse origin. The study was conducted at Pusa farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar by adopting randomized block design with three replications and spacing 45×10 cm. During *kharif* season 2019 and 2020 across six environment for days to 50% flowering trait being an important trait for fodder cowpea. All the studied genotypes showed significant interaction with environment and all thirty cowpea genotypes responded differently to evaluated environments. The analysis of GGE biplot revealed G29 (FD-2258) genotype was an ideal genotype and E1 environment as ideal environment for days to 50% flowering trait. The cowpea genotype G23 (FD-2229) was equally winner in both E3 and E6 environment; and genotype G29 (FD-2258) was winner in E1, E2, E4 and E5 for selecting superior stable fodder cowpea genotype adapted for the region.

Keywords: Fodder cowpea, rain-out shelter, 50% flowering, stability, G×E interaction

Introduction

Cowpea (*Vigna unguiculata* L. Walp) is a cheap source of quality protein which is consumed as green vegetable and used as fodder crop for feeding farm animals (Roy *et al.*, 2016) [8]. It contains 22-30% crude protein in the grain and leaves. This legume is an important part of major agricultural cropping system due to its nitrogen fixing ability which improves soil fertility (Vijayakumar *et al.*, 2020) [12]. Cowpea commonly known as *Lobia* in Hindi and also by many name *viz.*, black eye pea, southern pea, chowla. Africa is considered as primary centre of origin. In India, cowpea grown in total area 407.93 lakh ha with a production 7925.25 lakh tones and productivity 19.47 tones/ha, respectively (Kumar *et al.*, 2020) [5]. The livestock sector of India is the largest in the world level with 11.6% livestock population. Thus production of better quality feed at cheaper cost is crucial to improves farmer's income.

Our country faced severe fodder shortage during lean period. India rank's first in milk production as well as cattle population thus production of better quality feed at cheap cost is crucial to improves farmers income (Kumari *et al.*, 2017) [6]. Cowpea is a drought tolerant crop can thrives best in different adverse climatic conditions. Therefore identification of stable fodder cowpea genotype is important; so that it can contribute to the development of superior fodder cowpea variety to fulfil the fodder demand.

Genotype and environment interaction of is beneficial in the improvement of crop which helps in development of stable varieties for diverse environment (Santos *et al.*, 2015) [9]. Therefore evaluation of genotype × environment (G × E) interaction boost up plant breeder skill to develop fodder cowpea varieties which can give equal range of performance across predictable and unpredictable environment. The most widely used method to measure stability was earlier proposed (Finlay and Wilkinson, 1963) [3] and after that improved by (Eberhart and Russell, 1966) [1]. The stability defined as adaptation of varieties under different environment and the technique is used to select stable genotypes by changing environments.

GGE biplot denotes genotypes and interaction of genotype and environment, and the term first used by Yan *et al.*, (2000) [13]. In this analysis the environment main effect (E) are removed and the genotypes main effect (G) and interaction of G × E are retained and then combined. It is a graphical method and shows which genotype own where. GGE biplot elaborate the sources of variation in more details as compared to other model (Susanto *et al.*, 2015) [11]. Therefore, the present study was undertaken to identify stable fodder cowpea genotypes for days to 50% flowering trait which is inevitable for further development of superior fodder cowpea genotypes.

Material and method

The field experiment was conducted in Pusa Farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, during *Kharif* season of 2019 and 2020 to evaluate of fodder cowpea genotypes for days to 50% flowering trait under different environments.

Study area

The latitude and longitude are 25.98⁰N and 85.67⁰E, respectively. The mean altitude is 52m above mean sea level and average annual rainfall of 1234 mm. Weather prevailed during experimental period depicted in figure 1.

Treatment detail

Thirty cowpea genotype (Table 1) including one check *viz.*, Bundel lobia-1 were obtained from different research centers of the country. The genotypes were evaluated in open field irrigated condition with two date of sowing 15th July 2019 (E1) and 26th July 2019 (E2) as well as in rain shelter condition with single date of sowing 15th July 2019 (E3) in *kharif* 2019 and in *kharif* 2020 under open field irrigated condition with 15th July 2020 (E4) and 26th July 2020 (E5) as well as in rain shelter condition on 15th July 2020 (E6) installed at Pusa farm where combination of six different environment conditions named E₁, E₂, E₃, E₄, E₅ and E₆, respectively was used for stability study.

Data analysis

Stability analysis was done by using INDOSTAT software. GGE Biplot was utilized to determine the main and genotype-environment interaction effect for days to 50% flowering as proposed by Yan (1999)^[14] and Yan *et al.*, (2000)^[13]. The GGE biplot analysis was done using PBTools software version 1.4 (PBTools, 2014).

Results and Discussion

Combined analysis of variance for thirty cowpea genotype is shown in Table 2; where highly significant interaction of environment and genotype was found. The studied environmental effect revealed existence of highly significant variance. The joint regression analysis of variance is depicted in Table 3. The linear component of cowpea genotype interaction with environment i.e. (G × E) linear was smaller in amount as compared to calculated value of [E + (G×E)] mean squares although both the value were highly significant. So, it implies that tested 30 genotypes were acted differently to tested environments. All studied trait were found as influenced by environmental combination as noted as environment (E) linear component were highly significant. The results of our study is also appeared to be in harmony with those obtained by (Patel and Jain 2012)^[7] and (El-Shaieny *et al.*, 2015)^[2].

Mean performance and stability parameters of thirty cowpea genotypes based on pooled data over six different environment is depicted in Table.4. The mean ranges from 69.4063 (FD-2258) to 45.8644 (PL-2). On the basis of three stability parameters (\bar{x} , b_i and S^2d_i) the results shows that G29 was highly responsive most suitable for favorable environment with higher mean value. Ten genotypes (RL-4, IVTC-10, FD-2230, FD-2229, FD-2233, FD-2242, FD-2260, FD-2262, FD-2258, and Bundel lobia-1) were evaluated as stable for favourable environment and three genotypes (EC 390216, IVCT-8 and IVCT-1) were found suitable for poor environment with higher mean value than population mean (μ).

Kabir *et al.* (2009)^[4] studied wheat variety and recommended that variety which were sensitive to environmental changes can be incorporate in cultivation for favourable condition. The results of our study is also in parallel with results from cowpea (Singh *et al.* 2020)^[10]. The higher mean value with regression coefficient less than unity for seed yield per plant trait in cowpea were suggested as suitable for favourable environment (Patel and Jain 2012)^[7].

Ranking of genotypes based on relative to the ideal genotypes

GGE biplot helps in visualization and finding of the most stable genotypes (Susanto *et al.*, 2015)^[11]. Ranking of genotypes relative to ideal genotype is shown in figure.1. The ideal cowpea genotypes located in the center of concentric circles to be a point on average environmental axis (AEA) in the positive direction and cowpea genotypes located closer to the ideal genotypes are more preferable than the others. Hence, the graphical picture of GGE biplot shown that G29 was an ideal genotype, followed by other genotypes like G25, G18, G23 are desirable genotypes as they are closer to the ideal genotype.

What-won-where pattern of GGE biplot based on 30 cowpea genotype studied in six different environment

The polygon view of GGE biplot indicates the best genotypes for each environment and group of environments (Yan *et al.*, 2002)^[15]. Here, polygon is produced by joining the signs of the genotypes that are situated farthest away from the biplot origin, such that all other genotypes are retained in the polygon. In this situation, all the furthestmost genotypes are connected by polygon and perpendicular lines divide the polygon into many sectors. This sectors indicate the mega environments. The winning genotype are located at the vertex in each sector.

The polygon view of thirty cowpea genotypes under different environment is shown in figure 2. The cowpea genotypes G4, G19 G12, G26, G29, G23 and G3 are located at the top of the polygon. These genotypes were the best or the poorest genotype in some or all the environment, as they are located at the maximum distance from the biplot origin. In E1, E4, E5 and E2 the genotype G29 had late flowering and in E3 the cowpea genotype G23 perform best. The sequence of environment in biplot advice that presence of mega environment.

In this results the generated biplot based on standard singular value decomposition model of untransformed days to 50% flowering data exhibited 96.2% (PC 1 = 91.6%, PC 2 = 4.6%) of total GGE variation, that strongly explained environment centered data and power of model to ascertain the stability of genotype across environment.

The discrimination and representatives view of the GGE biplot

Ranking of test environments relative to the ideal environments by the discrimination and representative's view of the GGE biplot is shown in Figure 3. The ideal test environments for classifying generally adapted genotypes within a single mega-environment, the need is most discriminating or informative ideal test environment. Ideal test environment is the center of the concentric circles. The studied results shows that E1 is nearest to this point and that's why it was consider best environment, whereas E4, E5 and E2 were poorest for selecting cowpea genotype adapted to the region.

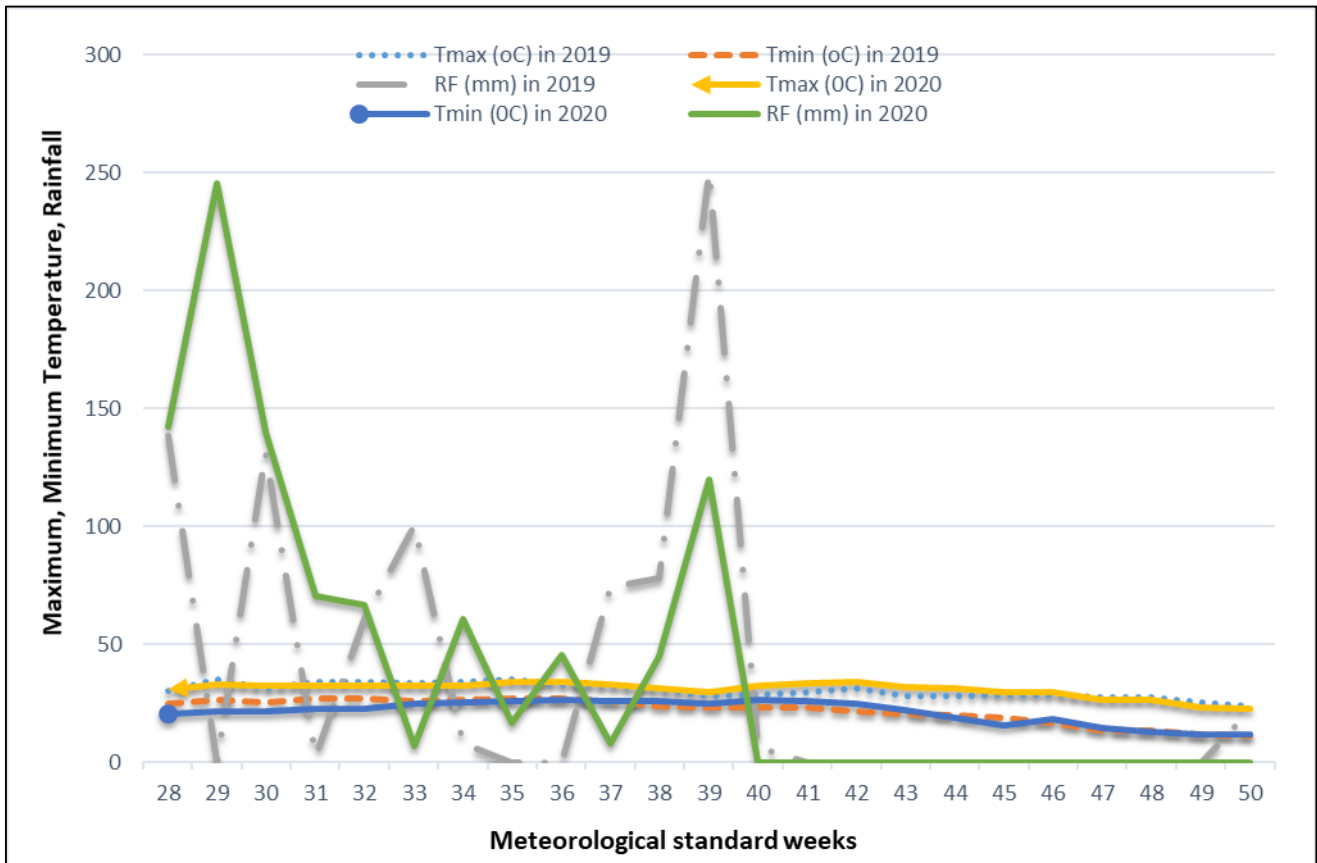


Fig 1: Weather prevailed during experiment period of kharif 2019 and 2020

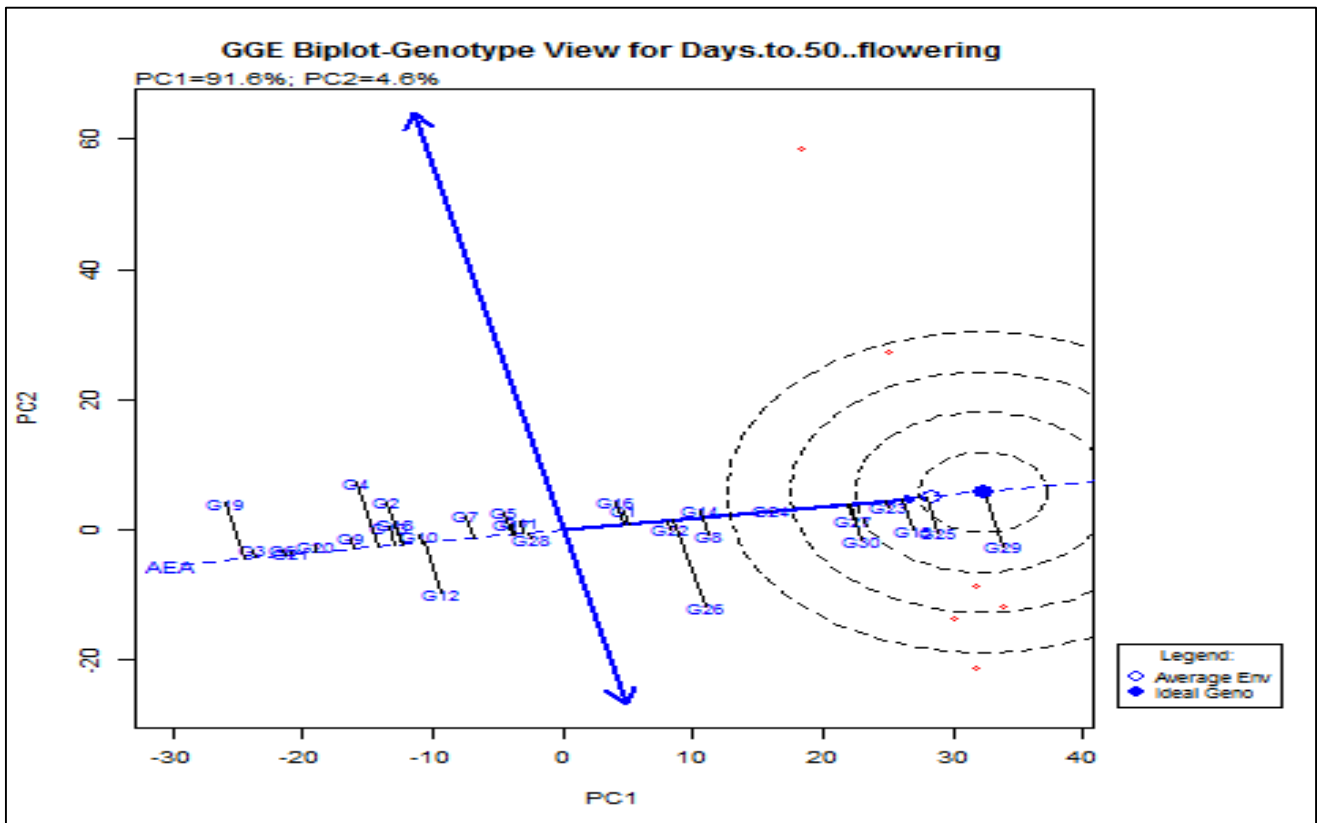


Fig 2: The average-environment coordination view to rank genotypes relative to an ideal genotype

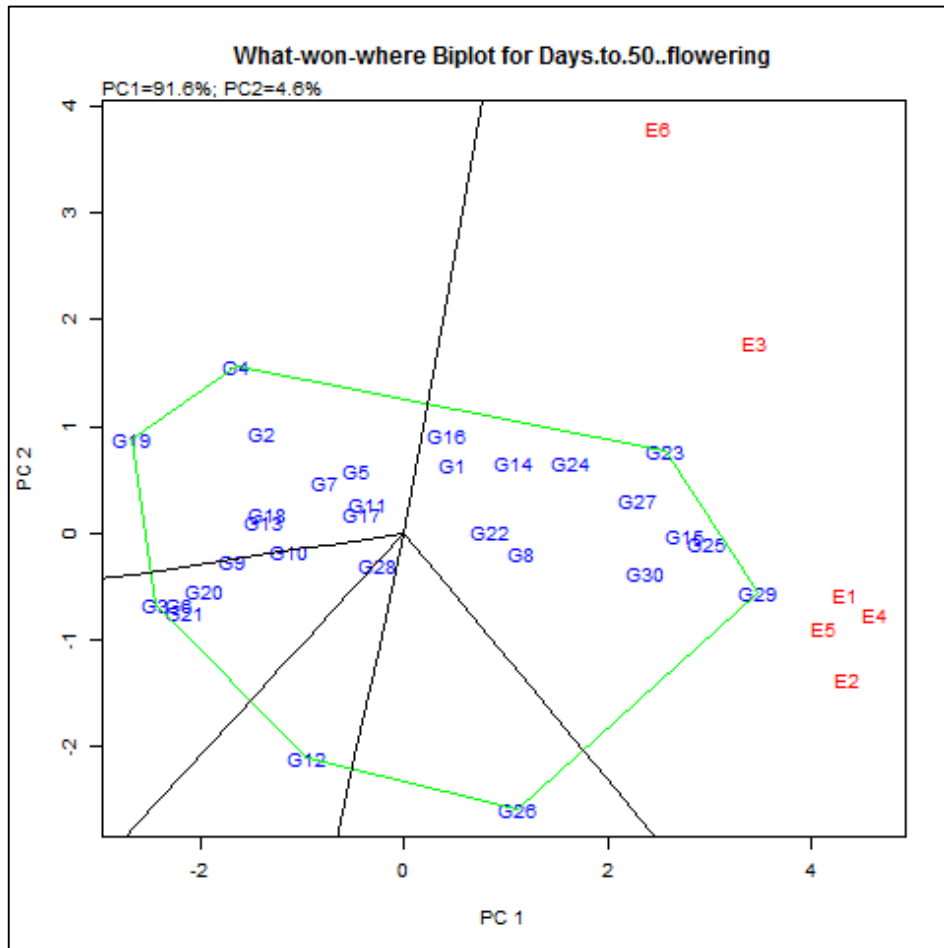


Fig 3: What-won-where pattern of GGE biplot for days to 50% flowering of 30 cowpea genotypes

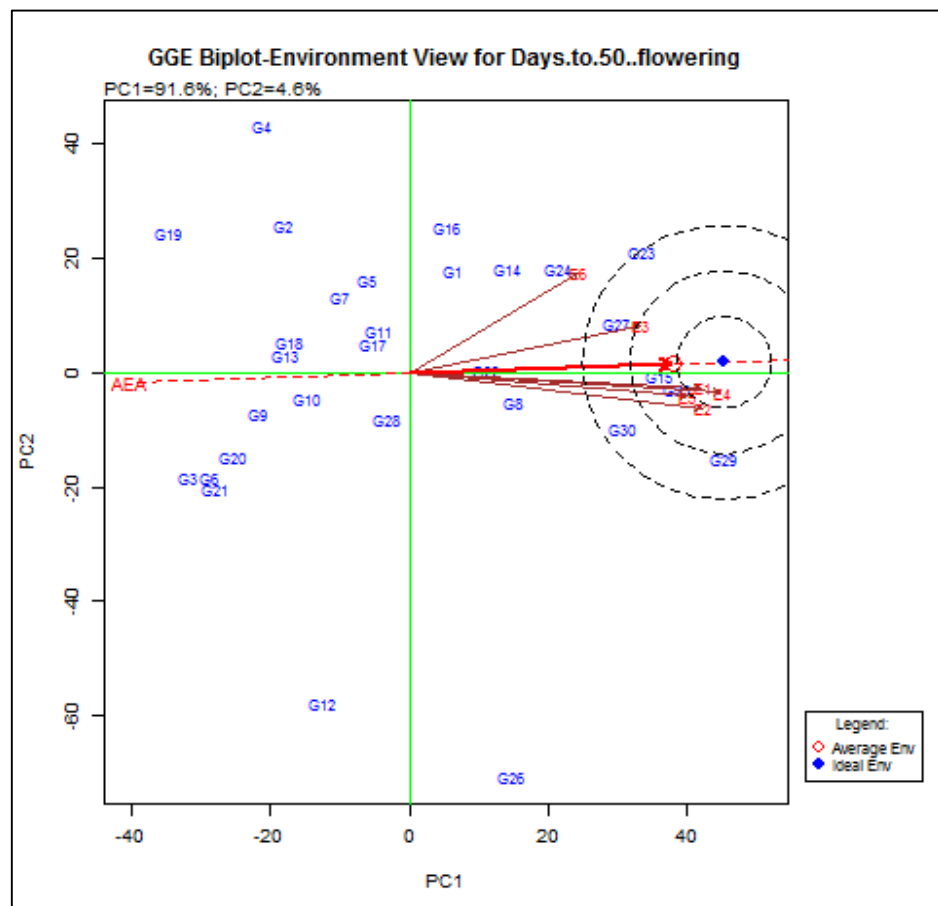


Fig 4: The discrimination and representatives view of the GGE biplot to rank test environments relative to the ideal environments

Table 1: List of thirty cowpea genotypes

Genotype code	Genotype	Source	Genotype code	Genotype	Source
G1	EC 390216	IIVR, Varanasi	G16	IVTC-1	IGFRI, Jhansi
G2	Kashigauri		G17	EC 97738	IIVR, Varanasi
G3	EC 390268		G18	EC 9736	
G4	Kashikanchan		G19	PL-2	GBPUA & T, Pantnagar
G5	RL-1	G20	PL-5		
G6	RL-2	G21	PL-3		
G7	RL-3	Local collection (Pusa, farmer's field)	G22	FD-2230	TNAU, Coimbatore
G8	RL-4		G23	FD-2229	
G9	RL-5		G24	FD-2233	
G10	RL-6		G25	FD-2242	
G11	PL-4	GBPUA & T, Pantnagar	G26	FD-2260	
G12	EC 97306	IIVR, Varanasi	G27	FD-2262	
G13	EC 390252		G28	FD-2272	
G14	IVTC-8	IGFRI, Jhansi	G29	FD-2258	
G15	IVTC-10		G30	Bundel Lobia-1 (check)	IGFRI, Jhansi (National Check)

Table 2: Combined analysis of variances for days to 50% flowering of thirty cowpea genotypes under different environment

Sources of variation	Degree of freedom	Sum of squares	Mean sum of squares
Environments	5	6797.23293	1359.44659**
Replication within Environments	12	37.75653	3.14638
Genotypes (G)	29	8676.26609	299.18159**
GxE	145	1111.01405	7.66217**
Error	348	1026.46010	2.94960

*Significant at $P < 0.05$; **highly significant at $P < 0.01$

Table 3: The joint regression analysis of variance for days to 50% flowering of thirty cowpea genotypes

Sources of variation	Degree of freedom	Sum of squares	Mean squares
Genotypes (G)	29	8676.26609	299.18159**
E.+ (G × E)	150	7908.24698	52.72165**
E (Linear)	1	6797.23293	6797.23293**
G × E (Linear)	29	682.43716	23.53232**
Pooled Deviation	120	428.57690	3.57147
Pooled Error	348	1026.46010	2.94960

*Significant at $P < 0.05$; **highly significant at $P < 0.01$

Table 4: Mean performance and stability parameters of thirty cowpea genotypes

Genotype no	Mean	b_i	S^2d_i
G1	58.1211	0.844	-2.1340
G2	50.9103	0.589*	-0.1876
G3	46.1913	0.955	-1.3181
G4	50.1043	0.277**	-1.6277
G5	54.4134	0.759*	-2.1129
G6	47.0717	0.951	0.4276
G7	53.1331	0.757**	-2.3609
G8	60.4600	1.231	-0.7231
G9	49.3114	0.874	-1.5776
G10	51.5381	0.911	-2.3177
G11	54.7239	0.866*	-2.7272
G12	51.5917	1.589**	0.3096
G13	50.6617	0.775	-0.9343
G14	60.4526	0.930	-1.2725
G15	66.8444	1.292*	-1.0786
G16	57.9264	0.788	-0.5206
G17	54.4433	0.889*	-2.8005
G18	50.8917	0.771*	-1.6198
G19	45.8644	0.493*	4.3362*
G20	48.1861	0.994	2.4344
G21	47.3702	0.991	-0.0454
G22	59.4047	1.082	2.0598
G23	66.2683	1.081	0.0936
G24	62.5961	1.015	-0.5908
G25	67.5494	1.333*	0.2268

G26	59.4957	1.738	32.9561**
G27	65.0567	1.184	0.3760
G28	54.8840	1.036	4.7584*
G29	69.4063	1.588**	-2.5015
G30	65.1137	1.417*	-1.0682
Mean	55.9995	1.0000	
Std. Err.	0.8452	0.1256	

Conclusion

The magnitude of G×E (linear) component was higher than pooled deviation (non-linear) sources of variation; which suggested that genotype performance can be predicted but with caution and should be based on both regression and deviation from regression value. The three parameter model of stability suggested G23 (FD-2229) as highly responsive suitable for favourable environment. On the basis of GGE biploids G29 (FD-2258) was ideal and this genotype was equally winner in environment E1, E2, E4 and E5. The environment E1 was also suggested as ideal environment.

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