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EVALUATION OF FODDER COWPEA GENOTYPES UNDER DIVERSE ENVIRONMENTS FOR G × E INTERACTION BASED ON GGE BIPLOT ANALYSIS

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SUMMARY

Thirty cowpea genotypes was evaluated for interaction of genotype and environment (G×E) over six different environments *viz.*, four environment under open field irrigated condition and two under rain-out shelter, during *kharif* season of 2019 and 2020 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. Based on G×E interaction study the sources of variation for genotype (G), environment (E) and G×E interaction was found highly significant. In GGE biplot analysis ('What won where' biplot) indicated G4 (Kashikanchan) genotype was winner equally in both E_3 and E_6 environment; and genotype G3 (EC 390268) was ideal as well as highest seed yielder. For days to maturity genotype G29 was winner in both E4 and E5 followed by E_1 and E_2 and genotype G30 (Bundel Lobia-1) was found ideal genotype for days to maturity. GGE biplot graphical evaluation for seed yield per plant and days to maturity revealed E_1 was best environment followed by E_2 and E_4 for selecting stable fodder cowpea genotype adapted for the region.

Key words : Fodder cowpea, rain-out shelter, seed yield, GGE biplot, GxE interaction

Cowpea (Vigna unguiculata) is an herbaceous self-pollinated (2n=22) legume belongs to family Fabaceae which originated in West Africa and grown as fodder crop for livestock and nutritious vegetable for man (Roy *et al.,* 2016). It is locally known as lobia, chowli, southern pea or black eye pea (Gupta *et al.,* 2017). Cowpea is a quick growing short duration, multicut, nitrogen fixing fodder crop and well known being tolerant to shade, drought (Vu *et al.,* 2017; Ngoc *et al.,* 2019). It is also highly nutritive having crude protein content approximately 22 to 30% in the grain and leaves (Praveena *et al.,* 2019). This legume is more nutritious than lablab and provides feeds in areas where rainfall situation is erratic and irregular (Atumo, 2018). The crop cutting for fodder purpose after 60-65 days from sowing under irrigated condition provide good quality of fodder and more yield (Oushy, 2012). In India, it covers an area of 7.7 million hectares (Yadav *et al.,* 2010) under major growing states viz., Gujarat, West Bengal, Tamil Nadu, Andhra Pradesh, Kerala and Orissa (Patel *et al.,* 2013).

The livestock sector of India is one of the largest in the world with 11.6% livestock population. In rural areas livestock rearing is the backbone of rural economy and livelihood (GOI, 2014). The widely used ruminants feeds i.e. straw from wheat, rice, barley, sorghum etc. are low in protein content with low energy level due to their lignified cell wall whereas legume feed encompasses high protein which is essential for growth, tissue repair and milk production (Praveena *et al.*, 2019). Our country faced severe fodder shortage during lean period. Thus production of better quality feed at cheap cost is crucial to improves farmer's income (Kumari *et al.*, 2017; Arya *et al.*, 2019).

Interaction of genotype and environment knowledge is extremely beneficial in the improvement of stable verities for diverse environment (Santos *et al.*, 2015). The most widely used method to measure stability was earlier proposed (Finlay and Wilkinson, 1963) and after that improved by (Eberhart and Russell, 1966). In present context, GGE biplot is also became important tool for stability analysis as it elaborate the sources of variation with graphical representation (Susanto *et al.*, 2015). Cowpea being a drought tolerant can thrives best in adverse climatic conditions (Ravish *et al*, 2021). Thus evaluation of genotype and environment interaction in the available fodder cowpea sources is inevitable so that it can contribute to the development of superior fodder cowpea variety to fulfil the fodder demand. This study was undertaken for studying the genotype and environment interaction (G × E) in thirty cowpea genotype for seed yield per plant and days to maturity.

MATERIALS AND METHODS

The field experiment was conducted at Pusa Farm, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, during *Kharif* season of 2019 and 2020 to evaluate fodder cowpea genotypes. Experimental location latitude and longitude were 25.98^{0}N and 85.67^{0}E, respectively. The mean altitude is 52 m above mean sea level and average annual rainfall of 1234 mm. Weather prevailed during experimental period depicted in Fig. 1.

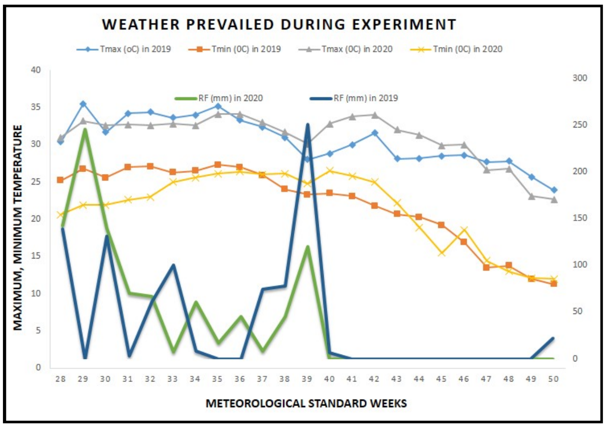

Fig. 1. Weather prevailed during experimental period of kharif season 2019 and 2020.

Treatment details

The study was conducted under six environment with thirty cowpea genotype and three replications in Randomized Block Design (RBD) with a spacing 45 x10 cm. The environment combinations were E_1 (Date of sowing 15 July 2019 in irrigated open field condition), E_2 (Date of sowing 26 July 2019 in irrigated open field condition), E_3 (Date of sowing 15 July 2019 in rain out shelter for drought condition), E_4 (Date of sowing 15 July 2020 in irrigated open field condition), E_5 (Date of sowing 26 July 2020 in irrigated open field condition) and E_6 (Date of sowing 15 July 2020 in rain out shelter for drought condition). For drought condition was created after 15 days of sowing by with holing irrigation. The details of thirty cowpea genotype were obtained from different research station of the country was used for the trial (Table 1). In each replication randomly five plants were selected for recording traits.

Data analysis

Statistical analysis was pursued by using INDOSTAT software. Analysis of variance (ANOVA) was subdivided into variance due to genotypes (G), environments (E) and genotype by environments interaction (G×E). GGE Biplot was utilized to determine the main and genotype-environment interaction effect for days to maturity and seed yield per plant as proposed by Yan *et al*., 2000. The GGE biplot analysis was done using PBTools software version 1.4 (PBTools, 2014).

TABLE 1

List of thirty cowpea genotypes

S. No.	Genotype	Source	S. No.	Genotype	Source
G1	EC 390216	IIVR, Varanasi	G16	IVTC-1	IGFRI, Jhansi
G2	Kashigauri	IIVR Varanasi	G17	EC 97738	IIVR, Varanasi
G3	EC 390268	IIVR Varanasi	G18	EC 9736	IIVR, Varanasi
G4	Kashikanchan	IIVR Varanasi	G19	PL-2	GBPUA & T, Pant Nagar
G5	RL-1	Local collection	G20	PL-5	GBPUA & T, Pant Nagar
G6	RL-2	Local collection	G21	PL-3	GBPUA & T, Pant Nagar
G7	RL-3	Local collection	G22	FD-2230	TNAU, Coimbatore
G8	RL-4	Local collection	G23	FD-2229	TNAU, Coimbatore
G9	RL-5	Local collection	G24	FD-2233	TNAU, Coimbatore
G10	RL-6	Local collection	G25	FD-2242	TNAU, Coimbatore
G11	PL-4	GBPUA & T, Pant Nagar	G26	FD-2260	TNAU, Coimbatore
G12	EC 97306	IIVR, Varanasi	G27	FD-2262	TNAU, Coimbatore
G13	EC 390252	IIVR, Varanasi	G28	FD-2272	TNAU, Coimbatore
G14	IVTC-8	IGFRI, Jhansi	G29	FD-2258	TNAU, Coimbatore
G15	IVTC-10	IGFRI, Jhansi	G30	Bundel Lobia-1	IGFRI, Jhansi (check)

TABLE 2

Combined analysis of variances for seed yield per plant and days to maturity of thirty cowpea genotypes under six different environment

Sources of variation	Degree of freedom	Mean sum of squares	
		Seed yield/ plant	Days to maturity
Environments	5	458.73527**	8330.36028**
Replication within Environments	12	0.49668	15.51873**
Genotypes (G)	29	154.51233**	98.74708**
G × E	145	3.01459**	10.61432**
Error	348	1.10377	14.21818

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

RESULTS AND DISCUSSION

Stability analysis for seed yield and day to maturity

Thirty cowpea genotypes were analyzed as per Eberhart and Russell model (1966) in which differences among the studied genotypes were highly significant for seed yield per plant and days to maturity and also effect of environments (E) and the interaction of genotype and environment (G×E) were highly significant as shown (Table 2).

The joint regression analysis of variance is represented in (Table 3). The results shows that the magnitude of the G×E (linear) mean squares for seed yield per plant (9.04298) and days to maturity (35.03535) was smaller in comparison to E + (G×E) mean squares value for seed yield per plant (18.20528) and days to maturity (287.93919). The highly significant value of G×E linear suggested that thirty cowpea genotypes were different in their response to tested environments. The highly significant effect of E (linear) is also found for seed yield per plant and days to maturity which indicated the tested trait was highly influenced by the combination of environment. Significant G×E interaction for days to maturity and seed yield was found which showed existence of non-linear response of the genotypes to the changed environment. These results of our study are also appeared to be in harmony with those obtained by other researchers (Adewale *et al.*, 2010, Patel and Jain, 2012 and El-Shaieny *et al.*, 2015).

TABLE 3

The joint regression analysis of variance for seed yield per plant and days to maturity of thirty cowpea genotypes under six different environment

Sources of variation	Degree of freedom	Mean sum of squares	
		Seed yield/ plant	Days to maturity
Genotypes (G)	29	154.51233**	98.74708**
E.+ (G ? E)	150	18.20528**	287.93919**
E (Linear)	1	2293.6763**	41651.80139**
G × E (Linear)	29	9.04298**	35.03535**
Pooled Deviation	120	1.45724*	4.35876
Pooled Error	348	1.10377	14.21818

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

GGE biplot Analysis for Seed yield and days to maturity

The polygon view of GGE biplot indicates the best genotypes for each environment and group of environments (Yan *et al.*, 2002). 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 furthermost genotypes are connected by polygon and perpendicular lines divide the polygon into many sectors. This sectors indicate the mega environments.

What-won-where biplot

What-won-where biplot for seed yield per plant is depicted in Fig. 2. The cowpea genotypes

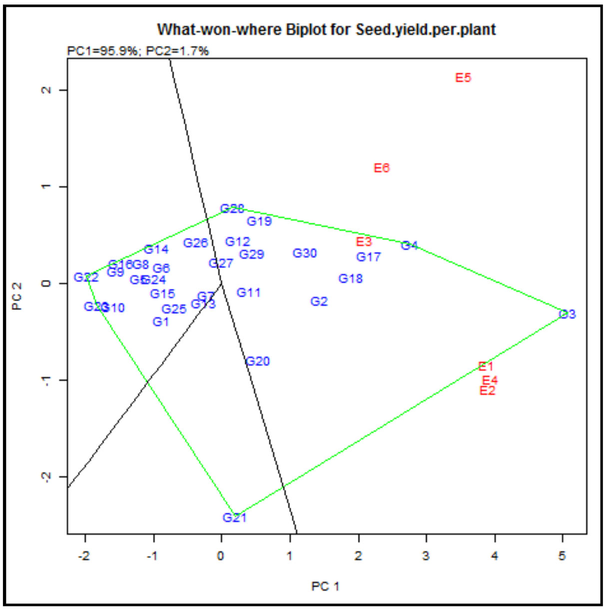

Fig. 2. Polygon view of GGE biplot briefing which genotype performed best seed yield per plant in which environment.

G20, G22, G21, G4, G3 and G23 that are situated at the top of the polygon were the best or the poorest genotype in some or all the environment, as their distance is maximum from the biplot origin. The cowpea genotype G4 can give best yield equally in both E_3 and E_6. The genotype G3 had heighted yield under E_1 followed by E_4 and E_2. The results revealed that there was presence of single mega environment for seed yield per plant. In polygon of 'What-won-where' biplot genotypes positioned as vertex showing longest detachment from the biplot origin was measured as most G×E interactive with stability. In this study the generated biplot based on standard singular value decomposition model of untransformed seed yield per plant data exhibited 97.6% (PC1 = 95.9%, PC2 = 1.7%) of total GGE variation, that strongly explained environment centered data and power of model to ascertain the stability of genotype across environment.

What-won-where biplot for days to maturity are depicted in Fig. 3. The cowpea genotypes *viz*., G14, G9, G23, G10, G29 and G30 are situated at the top of the polygon and they were the best or the poorest genotype in some or all the environments, as their distance is maximum from the biplot origin. The cowpea genotype G29 maturity time was equivalent in both E_4 and E_5 followed by E_1 and E_2. The genotype G14 mature earlier in E3 environment followed by E_6. The results of analyzed data show that there was presence of two mega environments. In polygon of 'What-won-where' biplot genotype positioned at the vertex showing longest detachment from biplot origin; these genotype was measured as most G×E interactive with stability. In this study the generated biplot based on standard singular value decomposition model of untransformed seed yield per plant data exhibited 88.7% (PC 1 = 70.6%, PC 2 = 18.1%) of total GGE variation that strongly explained environment centered data and power of model to ascertain the stability of genotype across environment. The genotypes that located inside the polygon and close to the biplot origin were not sensitive to changing environment. Pagi *et al*., 2017 reported no significant differences among three studied environments (E_1, E_3 and E_4) as they were placed in the same plane on the graph. These results are also found parallel with forage sorghum GGE biplot analysis (Aruna *et al*., 2016).

Stability of genotypes based on GGE biplot for seed yield per plant and days to maturity

Ranking of genotype was done on the basis of comparing all genotypes with the ideal cowpea genotype. The ranking of cowpea genotypes for seed yield per plant is shown in Fig. 4, in which environment and genotype were depicted by E, G and numeric value, respectively. The center of concentric circles indicates ideal cowpea genotype and AEA shows highest mean performance; hence genotype closer to ideal genotypes are more preferred. The results indicated that genotype G3 was an ideal genotype for highest seed yield and also there was presence of total

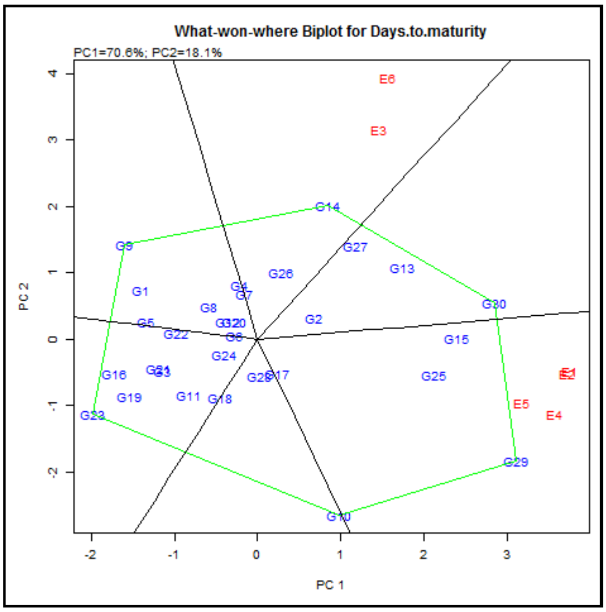

Fig. 3. Polygon view of GGE biplot briefing which genotype performed best days to maturity in which environment.

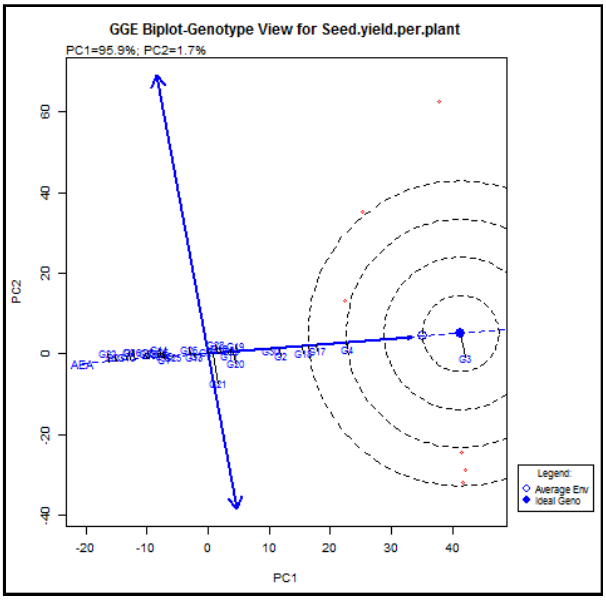

Fig. 4. Comparison of cowpea genotypes with the ideal cowpea genotype for seed yield per plant.

four cowpea genotypes that laid in the concentric area i.e., G3, G4, G17 and G18 and these genotype stability was in following order G3>G4>G17>G18 followed by other genotypes. Susanto *et al*., 2015 reported the BP9474C-1-1-B as highest yielding genotypes but with less adaptability and stability across the studied environments and A691 as most stable as the vector of genotype was most nearest to the origin point.

The ranking of cowpea genotypes for day to maturity is shown in Fig. 5, in which environment and genotype were depicted by E, G and numeric value, respectively. The center of concentric circles indicates ideal cowpea genotype. The results indicated that genotype G30 was an ideal genotype and had highest maturity days, and total seven cowpea genotypes lay in the concentric area. The stability for days to maturity are in following order G30 > G29 > G15 > G25 > G13 > G27 > G14 where followed by other genotypes.

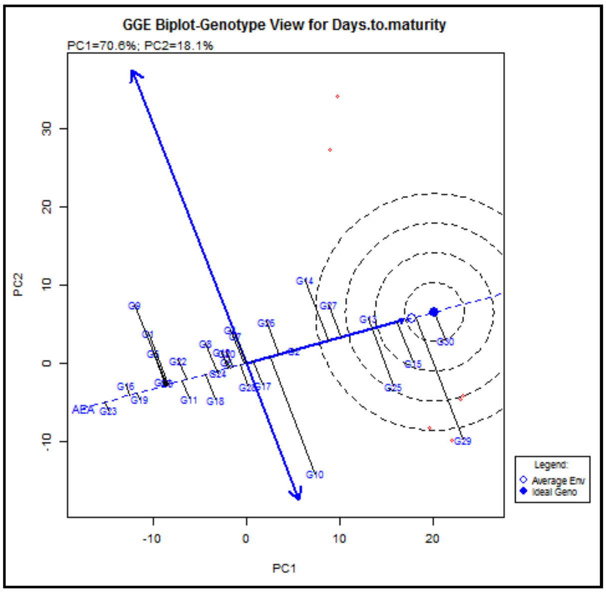

Fig. 5. Comparison of cowpea genotypes with the ideal cowpea genotype for days to maturity.

Evaluation of environment based on biplots for seed yield per plant and days to maturity

Identification of ideal test environment which is more informative and representative is important for selection of generally adapted genotype. Evaluation of environment for seed yield per plant is depicted in Figure 6. It elaborate an ideal test environment which is the center of the concentric circles and it is a point on the Average Environment coordination Axis (AEA) in the positive direction with a distance to the GGE biplot origin equal to the longest vector of all environments. Here, the studied results revealed that E_1 was nearest to concentric point; therefore considered best, followed by E_2 and E_4 for selecting cowpea genotype adapted for the region. In Fig. 6, the angle between any two environments is less than 90^0 which indicate negative correlation and moderately smaller interaction of genotype and environment (G×E). Therefore, these environments tend to discriminate among genotypes in a similar fashion. As per Pagi *et al*., 2017 strong relationship is present between any two environment is exist if there is minimum angle between the vectors of them; also environment which had shortest projection onto average environment Y- axis (AEA) denoted most discriminating. These results are in close association with Zhang *et al*., 2016.

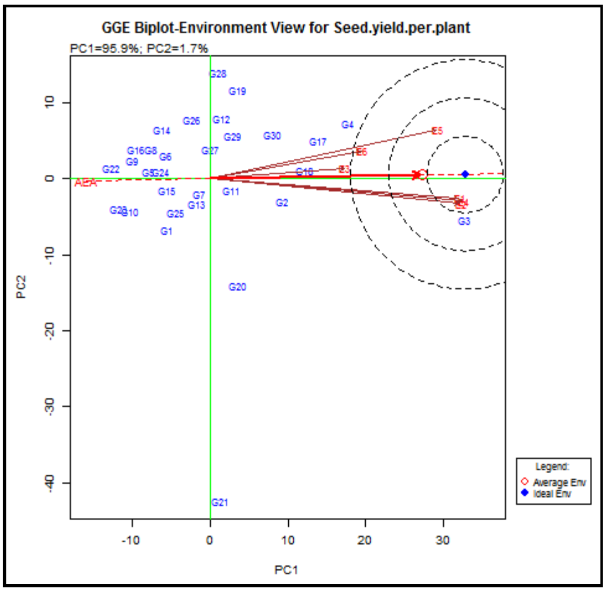

Fig. 6. Comparison of all the environments with ideal environment for seed yield per plant.

Identification of ideal test environments for days to maturity which is more informative and representative for selection of generally adapted genotype is depicted in Fig. 7. It elaborates an ideal test environment which is the center of the concentric circles. For days to maturity, E_1 was found nearest to concentric point; therefore considered best, followed by E_2 and E_4 for selecting cowpea genotype adapted for the region.

Analysis of GGE biplot is very beneficial as it illustrate the environment (E), genotype (G) stability and genotype and environment (G×E) interaction with graphical picture for easy evaluation of genotype performance (Karimizadeh *et al*., 2013). The present study results were also in agreement with Susanto *et al*., 2015.

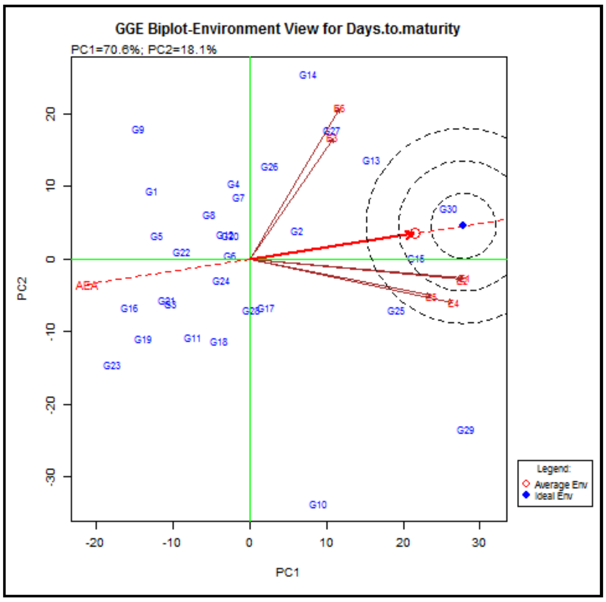

Fig. 7. Comparison of all the environments with an ideal environment for days to maturity.

CONCLUSIONS

Thirty cowpea genotypes interacted significantly with the studied environment. Genotype, environment and genotype and environment component was highly significant which suggest stability of the cowpea for predictable and unpredictable environment. GGE-biplot analysis clearly indicates positive correlation between tested environments. The studied cowpea genotypes although located in separate sections but did not form different mega environment for seed yield per plant trait but two mega environments was formed in case of days to maturity. G4 (Kashikanchan) genotype was winner equally in E_3 and E_6 environment i.e. performed similarly. Genotype G3 (EC 390268) was ideal high seed yielder under E_1; for days to maturity genotype G29 was winner in both E_4 and E_5. Genotype G30 (Bundel Lobia-1) was an ideal genotype for days to maturity. E_1 was found as best environment followed by E_2 and E_4 for selecting fodder cowpea genotype adapted for the region. In future, fodder crop improvement program these of stable genotype can be utilize in development of stable variety.

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