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RESEARCH ARTICLE

Identification of fodder cowpea (*Vigna unguiculata* L.) genotypes by leveraging GGE Biplot under multi-environment

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Abstract

Cowpea (*Vigna unguiculata* L.) has the immense potential to be used as an important fodder crop under future climate scenarios due to its adaptability. An experiment was carried out with 30 fodder cowpea genotypes (G) including check Bundel Lobia-1 during 2019 and 2020 under diverse environments. The ideal genotypes EC 390268 (G3) with the highest production efficiency (gm/m^2/day) and FD2258 (G29) for the highest green fodder yield (gm/plant) were identified on the basis of GGE biplot analysis, which Won Where GGE biplot results showed the existence of two mega environments, where genotype, EC 390268 (G3) was a winner in both E_3 and E_6 environments for production efficiency. For green fodder yield also, two mega environments were indicated in which the genotypes EC 390268 (G3) were winner in E_6 and FD2258 (G29) in E_4. Environment E_5 was found as best for identifying cowpea genotypes adapted for the region for production efficiency and E_4 was best for green fodder yield.

Keywords: Fodder cowpea, GGE Biplot, green fodder yield and production efficiency.

Introduction

Cowpea (*Vigna unguiculata* L.), generally known as *Lobia* in Hindi, is an underutilized legume fodder cum vegetable crop and a vital part of majority cropping systems for its nitrogen (N_2)-fixing capability, which enhances the soil fertility level. Being a short-duration crop, quickly growing, drought and shade-tolerant crop fix well in any cropping system. In its grain and leaves, approximately 22 to 30% protein is present. (Roy et al. 2016). In a future climate-changing scenario this crop has tremendous potential to be used as fodder crop due to its growing ability in sandy, infertile soils and rainfall deficit areas (Praveena et al. 2019). In Indian farming system, a severe shortage of fodder is seen during the lean-period. So, the availability of better-quality animal feed at a lower cost is crucial for improving the income of farmers (Kumari et al. 2017). Indian livestock division is one of the largest among all other countries and constitutes 11.6% livestock population. There is huge demand for animal products at the world level market. Due to this India has a good opportunity for participation in the world market. The production rate of green fodder yield (GFY) is declining year after year and during the lean period, farmers face a huge fodder shortage for their reared animals.

Also, the feeds of animals sourced from cereal straw encompasses low protein plus low energy, whereas feeds from legume sources comprise a higher amount of protein, which ultimately satisfies animal nutrition and thereby enhances the process of milk production and animal health (Kumari et al. 2017; Praveena et al. 2019). Therefore, there is a greater need for producing better-quality of animal feed at a cheaper rate. The current Intergovernmental Panel on Climate Change (IPCC 2013) evaluation says that at the end of 21st century, annual mean temperatures can increase

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(1.5±4°C). Due to this climate change, plants suffer high temperatures and low soil moisture during the spring and summer seasons. Drought is a status in which a deficiency of water exists due to low precipitation or low soil moisture, which does not support optimal plant growth (Hayatu et al. 2014). Therefore, increasing climate change will result in more extreme weather events including more frequency of drought and flood. The situation when soil moisture and rainfall are not sufficient to support healthy crop growth, thus resulting in extreme water stress and crop wilting, is called agricultural drought (Prasad Rao 2014). Plants are also affected by higher temperatures as it leads to altered responses in physiological, morphological, biochemical and gene expression (Wahid et al. 2007).

The high yielding cultivars development suitable for varied environments is a priority target of any plant breeder. However, it may change due to discrepant genotype performance owing to Genotype (G)x environment (E) interaction (GEI) (Kumar et al. 2021b). This GEI is used it to predict estimated yield along with additional important agronomic characters, although it also estimates yield's stability under both predictable and unpredictable E variation (Kamdi 2001). Therefore, stability analysis of the performance of cowpea genotype across contrasting environments with yield is important for the purpose of selecting high-yielding and stable fodder cowpea genotypes G (Singh et al. 2020).

GGE biplot analysis exemplifies environment (E), genotype (G) and genotype and environment (G x E) interaction and stability in a graphical representation, which makes an easy evaluation of genotype performance Karimizadeh et al. (2013). This GGE Biplot was proposed by Yan et al. (2000) and the analyses include G plus GE or GEI. It is based on environment-centred PCA. It describes well and is able to denote the most discriminating environment. In the recent past, this model has been applied under diverse crop varieties such as maize (Choudhary et al. 2019) and barley (Yadav et al. 2020). Since cowpea fits well in sole cropping, intercropping, maize-cowpea rotation etc., and thus offers its exploitation in any cropping system. Hence, the present investigation was pursued on this underutilized vegetable-cum-fodder crop for identifying fodder cowpea genotype adapted for the drought-prone region of Bihar based on production efficiency (PE) and green fodder yield (GFY) trait by leveraging GGE-Biplot analyses.

Materials and methods

Materials and experimentation

Thirty diverse genotypes of cowpea, including a check variety Bundel Lobia 1 were taken for the study (Table 1). The experiment was conducted at Pusa-Farm of Dr. RPCAU (Dr. Rajendra Prasad Central Agricultural University), Pusa, Samastipur, Bihar, during two consecutive *kharif* seasons (2019 and 2020) to evaluate the fodder-cowpea genotypes for production efficiency and green fodder yield trait under six diverse environment combination of open field and rain out shelter. Pusa is located at the latitude and longitude of 25.980N and 85.670É, respectively. The mean altitude was 52 meters above mean sea level, with average annual rainfall of 1234 mm.

The material was planted in a randomized block design and was used with three replications and spacing 45 x 10 cm. The environment combinations were E_1 [Date of sowing (DOS) 15th July 2019 in irrigated open field condition], E_2 (DOS- 26th July 2019 in irrigated open field condition), E_3 (DOS- 15th July 2019 in rain out shelter for drought condition), E_4 (DOS- 15th July 2020 in irrigated open field condition), E_5 (DOS- 26th July 2020 in irrigated open field condition) and E_6 (DOS- 15th July 2020 in rain out shelter for drought condition). Thus the total environments were E_1, E_2, E_3, E_4, E_5 and E_6, which were considered for GGE Biplot analysis. Standard agronomic practices were followed to maintain optimum plant growth. Observations on green fodder yield (GFY) g/plant and production efficiency [PE (gm/m^2/day)] were recorded from each plot.

Statistical analysis

The GGÈ Biplot analysis was done by utilizing INDOSTAT software and PBTools software version 1.4 (PBTools 2014). This analysis was used for the determination of GEIfor production efficiency and green fodder yield trait evaluation as projected by Yan et al. (2000). The partitioning of variation was carried out due to genotype (G), environment (E) and G x E interaction (GEI). The pairs of environments were analyzed to identify dissimilarity or similarity.

Results and discussion

To identify widely adaptable and stable fodder cowpea genotypes from this evaluation GGE biplot analysis was attempted. The GFY (gm/plant) of studied genotypes during the *kharif* seasons of 2019 and 2020 ranged from (on pooled basis) 117.38 (G26) to 217.06 (G29) having a general mean of 166.13 (Table 2) and across the six environments, highest GFYof 192.30 gm/plant was obtained in E_4, whereas PE (gm/m^2/day) varied from (on pooled basis) 59.38 (G_{26}) to 130.78 (G3) having general mean 89.96 (Table 2) and across the six environment highest obtained PF was 97.35 at E_4; similar results were recorded in pigeon pea across ten tested environments by Kumar et al. (2021b) and Rao et al. (2020) across 5 environments. The variation observed in the mean GFY and PE was due to different genotypes and environments that were screened in the present study. The adoption of diverse sowing dates were utilized as different environments and similar studies were conducted earlier by Saeidnia et al. (2023), who also employed likewise environment for GGE Biplot analysis. Eleven days interval sowing date under open field conditions have significantly impacted cowpea genotype growth and fodder

Table 1. List of thirty fodder cowpea genotypes used for test

S. No.	Code/genotype	Source	Sr. No.	Code/genotype	Source
1	G1 (EC 390216)	IIVR, Varanasi	16	G16 (IVTC-1)	IGFRI, Jhansi
2	G2 (Kashigauri)		17	G17 (EC97738)	IIVR, Varanasi
3	G3 (EC 390268) (EC 390268)		18	G18 (EC9736)	
4	G4 (Kashikanchan)		19	G19 (PL2)	GBPUA & T, Pantnagar
5	G5 (RL1)	Local collection (Pusa, Farmer's field)	20	G20 (PL5)	
6	G6 (RL2)		21	G21 (PL3)	
7	G7 (RL3)		22	G22 (FD2230)	TNAU, Coimbatore
8	G8 (RL4)		23	G23 (FD2229)	
9	G9 (RL5)		24	G24 (FD2233)	
10	G10 (RL6)		25	G25 (FD2242)	
11	G11 (PL4)	GBPUA & T, Pantnagar	26	G26 (FD2260)	
12	G12 (EC97306)	IIVR, Varanasi	27	G27 (FD2262)	
13	G13 (EC390252)		28	G28 (FD2272)	
14	G14 (IVTC8)	IGFRI, Jhansi	29	G29 (FD2258) (FD2258)	
15	G15 (IVTC10)		30	G3 (EC 390268)0 (BUNDEL LOBIA-1)	IGFRI, Jhansi (National Check)

development, which are parallel to the work of Liu et al. (2023) where wheat vegetative growth period profoundly reduced to 0.19% per day of delay in wheat sowing date.

Polygon view of the GEE Biplot

The data analysis from the Which-won-where pattern of GGE biplot revealed the polygon view (PV) of GGE Biplot and best G for each E and group of E. Thereby, the polygon is made by joining the G signs that are located farthest away from the biplot origin, such that all other G can be retained in the polygon. Likewise, all the furthermost G are connected by a polygon and perpendicular lines divide the polygon into several sections. This section indicates mega environment. Here, the winner G is located at the vertex in each section.

The GFY polygon view is displayed in Fig. 1(A). The cowpea genotypes *viz*., G3 (EC 390268), G_1, G_{12}, G_{26}, G_{16}, G_{17} and G29 (FD2258) are located at the vertices of the polygon and they were the best genotypes, as their distance is highest from the biplot origin, also these genotypes were considered most G×E interactive with stability. The G,

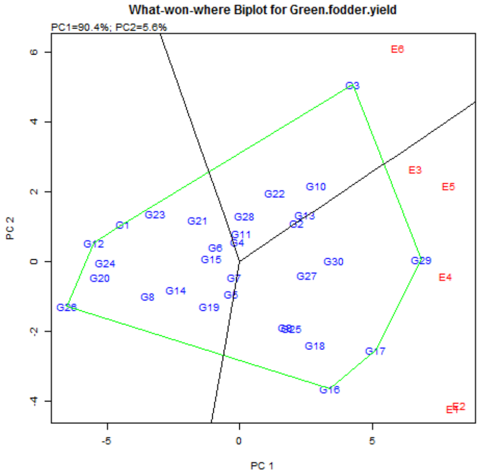

Fig. 1(A). Polygon view (PV) of the GGE biplot based on symmetrical scaling of 30 fodder cowpea 'G' across six environment^6 for GFY

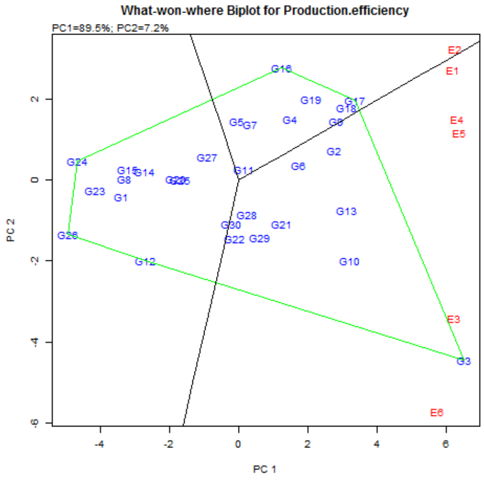

Fig. 1(B). PV of the GGE biplot based on symmetrical scaling of 30 fodder cowpea 'G' across six environment^6 for PE

Table 2. Performance of 30 fodder cowpea genotypes for Green fodder yield (GFY) and production efficiency (PE) under six environments

S. No	Genotype (G)	GFY (gm/plant)							PE (gm/m^2/day)						
		E_1	E_2	E_3	E_4	E_5	E_6	Pooled^t	E_1	E_2	E_3	E_4	E_5	E_6	Pooled^t
1	G_1	145.49	138.85	102.14	164.39	145.56	106.72	133.86	69.45	67.21	58.57	80.97	71.84	65.24	68.88
2	G_2	195.44	192.07	145.89	212.99	207.30	139.75	182.24	109.26	108.64	99.50	120.77	114.26	88.98	106.90
3	G3 (EC 390268)	198.51	195.20	169.64	224.53	227.74	181.88	199.58	118.76	117.09	137.25	132.28	136.53	142.81	130.79
4	G_4	184.79	181.80	133.18	182.65	182.63	130.40	165.91	108.16	106.43	80.53	107.91	106.99	84.92	99.16
5	G_5	186.56	178.41	124.55	191.69	187.44	111.47	163.35	97.89	91.89	77.65	101.97	96.66	70.49	89.43
6	G_6	173.30	165.58	119.53	189.71	195.44	111.40	159.16	102.15	103.23	88.02	106.84	114.04	89.90	100.70
7	G_7	182.69	175.36	119.43	200.39	191.75	114.60	164.04	96.10	95.45	75.02	107.74	100.71	76.45	91.91
8	G_8	162.06	156.29	104.94	169.12	149.95	99.16	140.25	73.94	71.00	64.49	77.58	69.38	59.57	69.33
9	G_9	208.86	198.56	134.99	207.19	200.32	118.97	178.15	114.91	112.43	92.98	116.98	117.81	89.25	107.39
10	G_{10}	202.20	198.38	159.87	210.70	203.00	158.58	188.79	109.57	108.17	107.19	115.55	107.53	112.81	110.14
11	G_{11}	181.92	176.63	122.95	191.82	200.02	126.90	166.71	92.74	91.35	75.70	98.95	103.37	83.19	90.88
12	G_{12}	139.53	131.84	93.36	150.54	143.17	93.98	125.40	71.70	68.17	75.63	77.90	72.18	73.80	73.23
13	G_{13}	202.47	191.82	157.31	211.60	201.71	144.71	184.94	111.17	107.57	102.36	121.80	110.07	103.96	109.49
14	G_{14}	174.38	165.37	113.40	171.65	153.14	111.31	148.21	78.96	76.64	63.71	79.78	73.97	64.93	73.00
15	G_{15}	170.95	164.34	114.82	191.77	197.29	105.80	157.49	70.59	67.68	58.91	80.97	81.50	60.08	69.96
16	G_{16}	229.19	223.07	138.88	218.66	209.43	121.33	190.09	108.52	110.27	80.97	105.49	107.14	71.70	97.35
17	G_{17}	234.76	232.05	151.00	238.61	225.06	136.82	203.05	120.89	120.40	94.33	122.10	116.14	90.72	110.76
18	G_{18}	220.05	217.13	140.41	210.16	202.57	129.38	186.62	120.25	117.81	93.36	120.71	112.35	90.48	109.16
19	G_{19}	186.81	179.46	120.64	172.96	170.59	113.83	157.38	114.61	113.68	95.37	108.93	105.69	77.64	102.65
20	G_{20}	146.28	139.92	95.90	149.28	140.46	90.57	127.07	82.64	80.46	76.73	87.94	77.92	66.17	78.64
21	G_{21}	172.72	165.24	113.13	169.29	180.19	128.10	154.78	103.72	97.40	87.83	98.70	100.41	99.21	97.88
22	G_{22}	186.39	183.22	151.24	201.22	198.79	139.12	176.66	88.07	81.83	90.79	97.64	93.49	83.64	89.24
23	G_{23}	154.70	148.09	102.33	160.92	177.87	111.44	142.56	65.13	64.79	52.66	65.48	76.20	60.38	64.11

24	G_{24}	141.20	138.05	92.38	155.81	152.52	89.15	128.18	63.24	64.44	51.22	68.02	67.91	50.72	60.92
25	G_{25}	209.86	208.86	142.05	205.73	186.06	128.28	180.14	86.21	86.02	71.24	82.87	77.19	73.11	79.44
26	G_{26}	138.41	132.72	90.90	142.43	123.56	76.29	117.38	61.97	57.18	49.66	65.11	57.38	64.96	59.38
27	G_{27}	203.79	195.56	138.67	222.19	219.20	127.02	184.41	87.33	86.90	73.97	91.58	93.47	71.58	84.14
28	G_{28}	181.97	175.69	126.57	191.06	198.54	132.35	167.70	93.86	83.72	81.47	94.45	106.83	88.00	91.39
29	G29 (FD2258)	241.75	238.79	172.47	244.27	236.09	168.97	217.06	95.90	94.65	90.85	95.41	92.93	93.73	93.91
30	G3 (EC 390268) (National Check)	214.57	211.75	159.66	215.64	210.82	144.38	192.80	91.16	90.66	89.57	88.11	89.55	83.46	88.75
	Mean	185.72	180.00	128.41	192.30	187.27	123.09	166.13	93.63	91.44	81.25	97.35	95.05	81.06	89.96
	C.V.	5.49	6.48	6.15	6.09	6.22	8.82		6.62	8.82	8.20	8.25	9.00	10.66	
	SE_d	8.32	9.52	6.44	9.57	9.50	8.86		5.06	6.58	5.44	6.56	6.99	7.05	
	CD 5%	16.66	19.05	12.90	19.15	19.03	17.74	10.934	10.13	13.17	10.88	13.12	13.98	14.12	7.568

located inside the polygon and very close to the biplot's origin was not sensitive to the changing environment. In present study, which-won-where biplot standard singular value decomposition model of untransformed GFY data unveiled 96.0% (PC_1=90.4%, PC_2=5.6%) of total GGE variation that strongly explained environment-centered data. The result shows that there was the presence of two mega environments as E_1, E_2, E_3, E_4 and E_5, which are situated in same sector and E_6 on another sector. The fodder cowpea genotype G3 (EC 390268) was at the apexes of the E_6 sector and G29 (FD2258) in E_4 sector, indicating that this genotype was the best performer in that location. These results are in accord with Kumar et al. (2021b), who have identified widely adaptable pigeon pea genotypes.

The PE Polygon view is displayed in Fig. 1(B). The cowpea genotypes viz., G_{16}, G_{24}, G_{26}, G_{12}, G3 (EC 390268) and G_{17} are situated at the top of the polygon and they were the best genotypes, as their distance was maximum from the biplot origin. Also, this genotype was measured as most G×E interactive along with stability. Genotype G_{11} was positioned close to origin, which signifies its in-sensitivity to changing environment. Here, PC 1 = 89.5% and PC 2 = 7.2% of total GGE variation have existed, which strongly explained environment-cantered data. Two mega environments were present in which E_2 in one and the rest of the environment fell into a single mega environment. The cowpea genotype G3 (EC 390268)was highly responsive both in E_3 and E_6. The ray line in which – won - where the figure was perpendicular to the sides of the polygon has spliced it into several sectors, which were in agreement with Bhartiya et al. (2017).

Test environment relationship

In Fig. 2(A), the relationship among the test environments is depicted for GFY. The first principal component (PC1) clarified 90.4% and the second principal component (PC2) clarified 5.6 %. Here, E_1 and E_2 environments had the longest vector from the origin and were the most discriminating among the tested environments with the shortest vector E_3 and E_6 was considered as least discriminable environment due to its capacity to provide little information on genotype differences. With angle $<90^0$, all the E were positively correlated which indicated test environments were closely associated with each other.

Among test environments relationship as depicted in Fig. 2(B) for PE, where PC1 clarified 89.5% and PC2 clarified 7.2%. For PE, E_5 and E_3 had longest vector from the origin, thus identifying them as most discriminating among all while E_1 and E_6 were found to be least discriminating. On the contrary, approximately less than 90^0 angle existed among all the 'E', signifies a positive correlation. So, the environmental variation occurred in the same direction and similar fodder cowpea genotypes can be nominated for growing in both open field and drought conditions. Therefore, the current GGE Biplot study analysed well to

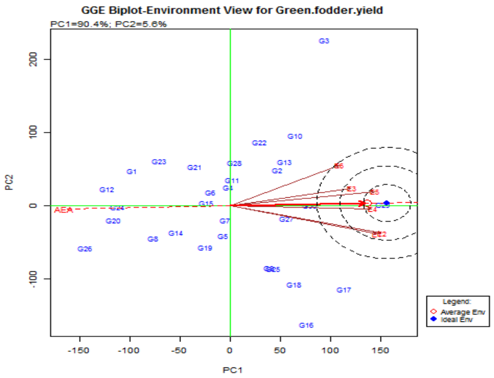

Fig. 3(A). 'GGE biplot' graph based on 'E' focused scaling for comparison of 6 tested 'E' with the ideal environment for 30 fodder cowpea 'G' for GFY

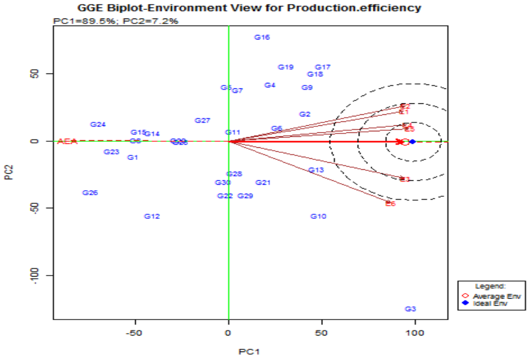

Fig. 3(B). 'GGE biplot' graph based on 'E' focused scaling for comparison of 6 tested 'E' with the ideal environment for 30 fodder cowpea 'G' for PE

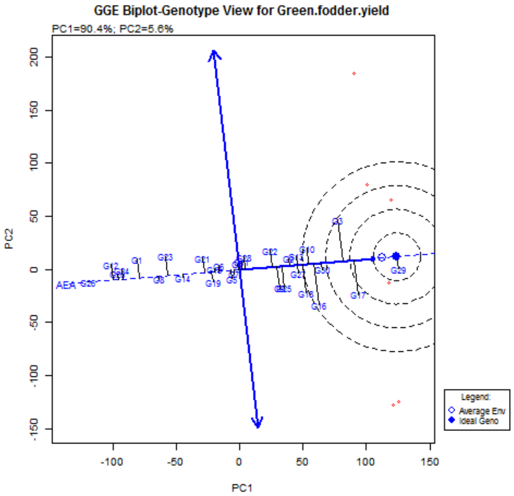

Fig. 4(A). The AECV to rank 'G' relative to an ideal genotype for GFY trait

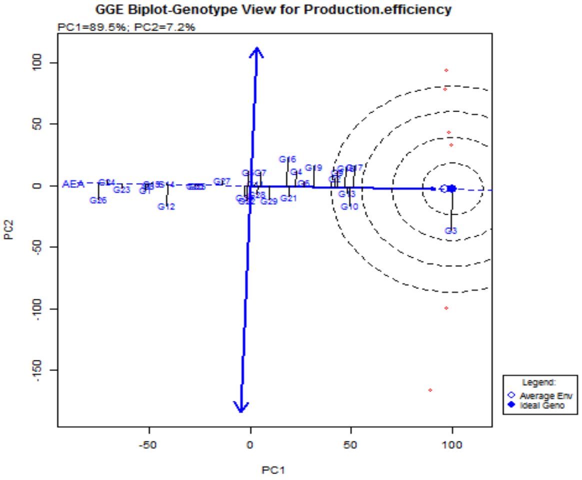

Fig. 4(B). The AECV to rank 'G' relative to an ideal genotype for PE trait

identify stable fodder cowpea genotypes, whereas many researchers reported similar findings in other crops like pigeonpea (Kumar et al. 2021b), soybean (Kumar et al. 2014a), rice (Susanto et al.), groundnut (Lal et al. 2019) and in urdbean by Kumar et al. (2020d).

Genotypes and environment evaluation

The ideal test environment is one which is present inside of concentric circles on graph. Here, the results for both the characters are depicted in Fig. 3(A) and 3(B). Fig. 3(A) explains the E_4 and E_5 as the ideal environments for GFY trait and G29 (FD2258) was the best-tested genotype as it was in close proximity to a concentric circle. It suggests genotype's suitability and potential under this evaluation. The numbers of ideal environments (E_4 and E_5) were alike for PE trait (Fig. 3B). Therefore, this environment tends to discriminate among genotypes in a similar fashion.

Stability of genotypes

The ranking of cowpea genotypes for green fodder yield (gm/plant) has been shown in Fig. 4(A) in which environment and genotype were depicted by E, G and numeric values, respectively. The center of concentric circles indicates the ideal fodder cowpea genotype. Here, the average environment coordination view (AECV) is utilized to rank G relative to an ideal genotype. The results indicated that genotype G29 (FD2258) was an ideal genotype and had the highest green fodder yield (gm/plant) and total of seven cowpea genotypes laid in the concentric area. The stability for green fodder yield (gm/plant) are in the following order G29 (FD2258)> G_{17} >G3 (EC 390268)>G3 (EC 390268)$_0$> G_{16}> G_{10}> G_{16} were followed by other genotypes. In the case of production efficiency (gm/m^2/day), fodder cowpea genotypes ranking is presented in Fig. 4(B). The ideal genotype was G3 (EC 390268), which exhibited the highest PE value. The stability order of genotypes was laid as follows G3 (EC 390268)> G_{17}> G_{10}> G_{13}. These results are supported by reports published earlier (Susanto et al. 2015; Yan et al. 2000; Kumar et al. 2021b).

Genotype environment interaction has the incredible potential to utilize for interpretating phenotypic stability of a genotype. The present study optimally utilized GGE biplot for identifying ideal genotypes according to environment specificity and GEI along with their stability. The fodder cowpea G29 (FD2258) was an ideal genotype, whereas E_4 was most discriminating for green fodder yield (gm/plant) and for production efficiency (gm/m^2/day) G3 (EC 390268) was ideal and E_5 was the most discriminating environment for selecting fodder cowpea genotype adapted for the region. The findings are expected to promote the suitable fodder genotype of cowpea for appropriate environments.

Authors' contribution

Conceptualization of research (N, MB); Designing of the experiments (N, MB, RK, VKS); Contribution of experimental materials (N); Execution of field/lab experiments and data collection (N, MB); Analysis of data and interpretation (N, MB, RK, VKS); Preparation of the manuscript (N, MB, AKM, RK,VKS).

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References

Bavandpori F., Ahmad J. and Hossaini S. 2018. Stability analysis of bread wheat landraces and lines using biometrical genetic models. Genetika, **50**: 449-464.

Bhartiya A., Aditya J.P., Singh K., Pushpendra, Purwar J.P. and Agarwal A. 2017. AMMI and GGE biplot analysis of multi environment yield trial of soybean in North Western Himalayan state Uttarakhand of India. Legume Res., **40**(2): 306-312.

Choudhary M., Kumar B., Kumar P., Guleria S.K., Singh N.K., Khulbe R., Kamboj M.C., Vyas M., Srivastava R.K., Puttaramanaik, Swain D., Mahajan V. and Rakshit S. 2019. GGE biplot analysis of genotype × environment interaction and identification of megaenvironment for baby corn hybrids evaluation in India. Indian J. Genet. Plant Breed., **79**(4): 658-669.

Dwivedi A., Basandrai D. and Sarial A. K. 2020. AMMI biplot analysis for grain yield of basmati lines (*Oryza sativa* L.) in North Western Himalayan Hill regions. Indian J. Genet. Plant Breed, **80**(2): 140-146. doi: 10.31742/ IJGPB.80.2.3

Eberhart S.A. and Russell W.L.1966. Stability parameters for comparing varieties. Crop Sci., **6**:36-40. doi:10.2135/cropsci1966.0011183X000600010011

Gaur A.K., Verma S. K., Panwar R. K. and Sharma R. K. 2020. Estimation of G x E interaction by AMMI model in some elite pigeonpea [Cajanus cajan (L.) Millspaugh] genotypes. Indian J. Genet. Pant Breed., **80**(2): 173-178. doi: 10.31742/IJGPB.80.2.7.

Hayatu M., Muhammad S.Y. and Abdu H.U. 2014. Effect of water stress on the leaf relative water content and yield of some cowpea [*Vigna unguiculata* (L) Walp.] genotypes. Inter. J. Sci. Tech. Res., **3**: 148-152.

Kanouni H. 2018. Stability of Chickpea (*Cicer arietinum* L.) landraces in National Plant Gene Bank of Iran for Drylands. J. Agril. Sci. Technol., **20**: 387-400.

Karimizadeh R., Mohammadi M., Sabaghni N., Mahmoodi A.A., Roustami B., Seyyedi F. and Akbari F. 2013. GGE biplot analysis of yield stability in multi environment trials of lentil genotypes under rainfed condition. Not. Sci. Biol., **5** (2): 256-262.

Kumar M.V. Nagesh, Ramya V., Kumar C.V.S., Raju T., Kumar N.M.S., Seshu G., Sathish G., Bhadru D. and Ramana M.V. 2021b. Identification of pigeonpea genotypes with wider adaptability to rainfed environments through AMMI and GGE biplot analyses. Indian J. Genet. Plant Breed., **81**(1): 63-73. DOI: 10.31742/IJGPB.81.1.7.

Kumar S., Sharma J.P., Kumar A., Choudhary H. K., Singh A. P., Sandghu R., Gupta R., Singh M. and Singh A. K. 2020d. Genotype x environments interactions for grain yield and its components in urdbean (*Vigna mungo* L Wilczek) under rainfed conditions of Jammu region. Indian J. Genet. Plant Breed., **80**(2): 194-203. doi: 10.31742/IJGPB.80.2.10.

Kumar V., Verma R.P.S., Kumar D., Kharub A.S. and Singh G. P. 2018e. Assessment of barley genotypes for malting quality: Genotype x environment interactions. Indian J. Genet. Plant Breed., **78**(4): 523-526. doi: 10.31742/IJGPB.78.4.16.

Kumari V.V., Gopinath K.A., Venkatesh G., Chandran M.S. and Srinivasa C.R. 2017. Fodder Constraints in Rainfed areas of India: Constraints and Strategies. Forage Res. **43**(2): 81-88.

Lal C., Ajay B. C., Chikani B. M. and Gor H. K. 2019. AMMI and GGE biplot analysis to evaluate the phenotypic stability of recombinant inbred lines (RILs) of peanut under mid-season water stress conditions. Indian J. Genet. Plant Breed., **79**(2): 420-426. doi: 10.31742/IJGPB.79.2.5.

Liu J., He Q., Zhou G., Song Y., Guan Y., Xiao X., Sun W., Shi Y., Zhou K., Zhou S., et al. 2023. Effect of sowing date variation on winter wheat yield: conclusions for suitable sowind dates for high and stable yield. Agron. J., **13**: 991.

Manu B., Kumara P.S., Biradar S., Chauhan D., Phuke R., Ambati D., Sai Prasad S. V., Mishra P.C., Mishra K.K., Harikrishna Jain N., Singh P.K., Singh G.P. and Prabhu K.V. 2020. Genetic gain and morphophysiological characterization of BILs (Backcross Inbred Lines) under different moisture regimes in wheat (*Triticum aestivum* L). Indian J. Genet. Plant Breed., **80**(1): 84-93. doi: 10.31742/IJGPB.80.1.11.

Praveena V.S., Abraham M. and kumar V. 2019. Genetic divergence studies in fodder cowpea (*Vigna unguiculata*) using D2 statistics. Forage Res., **44**(4): 230-236.

Roy A.K., Malaviya D.R. and Kaushal P. 2016. Genetic improvement of fodder legumes especially dual-purpose pulses. Indian J. Genet. Plant Breed., **76**: 608-625.

Saeidnia F., Taherian M. and Nazeri S. M. 2023. Graphical analysis of multi-environmental trials for wheat grain yield based on GGE-biplot analysis under diverse sowing dates. BMC Plant Biol., **23**:198**.**

Singh J., Kumar A., Fiyaz R.A. and Singh M.K. 2018. Stability analysis of pigeonpea genotypes by deployment of AMMI model under rainfed environment. Legume Res., **41**(2): 182-188.

Singh O.V., Shekhawat N. and Singh K. 2020. Stability analysis for yield and some of yield component traits in cowpea [*Vigna unguiculata* (L.) Walp] germplasm in hot arid climate. Legume Res., **43**(5): 623-62.

Susanto S., Wage R., Rohaeni, Sarah B. and Johnson, A.J. 2015. GGE biplot analysis for genotype x environment interaction on yield trait of high Fe content rice genotypes in Indonesian irrigated environments. Agrivita, **37**: 0126-0537.

Wahid A., Gelani S., Ashraf M.Y. and Foolad M.R. 2007. Review Heat tolerance in plants: An overview. Environ. Exp. Bot., **61**: 199–223.

Yadav O.P., Razdan A.K., Kumar B., Singh P. and Singh A.K. 2020. Using AMMI approach to delineate genotype by environment interaction and stability of barley (*Hordeum vulgare* L.) genotypes under northern Indian Shivalik hill conditions. Indian J. Genet. Plant Breed., **80**(3): 339-342. doi: 10.31742/IJGPB.80.3.15.

Yan W., Hunt L.A., Sheng Q. and Szlavnics Z. 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci., **40**(3): 597-605.

Yan W.K. 2002. Singular-value partitioning in biplot analysis of multi-environment trial data. Agron. J., **94**: 990- 996.