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Research Article

AMMI analysis of G × E interaction and identification of fodder cowpea genotypes for phosphorus deficient condition

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Abstract

Phosphorus (P) deficiency affects the productivity of fodder legumes and smallholder farmers do not have the resources to purchase Phosphate fertilizers. An alternative solution to the problem of P deficiency is the development of genotypes with the ability to perform well in P-deficient soils. In the present investigation, genotype × environment interaction (GEI) was assessed in 45 fodder cowpea genotypes for green fodder yield over two seasons under four phosphorus levels to identify stable high-yielding genotypes. Combined analysis of variance revealed that environmental factors (76.20 %) were the primary source of variation, followed by genotype (14.89 %) and G × E effects (8.47 %). The AMMI model for G × E interaction showed that the first two interaction principal components (IPCA1 and IPCA2) were highly significant. IPCA1 and IPCA2 contributed 51.00 % and 15.50 % of total G × E interaction variability. AMMI biplot showed differential interaction of the genotypes in different environmental conditions. Based on these two significant IPCAs, AMMI stability value (ASV) was calculated, that ranged from 0.21 to 7.24. In *rabi* season, genotypes MFC-18-4, MFC-09-1, IFC-9304, UPC-804, MFC-18-8, F-6R-211-184-2 were found to be stable for green fodder yield in phosphorus deficient condition. Genotypes UPC-2001, EC-402154 and UPC-618 were suitable for phosphorus deficient condition during kharif season and recorded stable green fodder yield. Based on ASV parameter, UPC-2001, UPC-805, UPC-804, UPC-4200, FD-739 were identified as the most stable and high-yielding genotypes. Identifying such phosphorus-efficient genotypes can ensure improved yields despite lower phosphorus inputs, reducing the cost for farmers and making agriculture more economically sustainable in resource-limited environments.

Keywords: Fodder cowpea, G × E interaction, Phosphorus deficiency, AMMI, ASV

INTRODUCTION

Fodder cowpea (*Vigna unguiculata* L. Walp.) is a multipurpose leguminous crop widely cultivated for its significant role in animal nutrition, soil fertility enhancement, and sustainable agricultural practices. It is highly valued as high-quality forage, contributing to increased livestock productivity and supporting the overall economy of farmers. Fodder cowpea is rich in protein, energy, and essential nutrients, making it a highly nutritious feed for livestock such as cattle, sheep, and goats. It contains crude protein levels ranging from 14 to 25% and is easily digestible, enhancing livestock growth and milk production. The leaves, stems, and pods are tender and palatable, ensuring high intake by animals. The inclusion of fodder cowpea in livestock diets reduces dependency on expensive commercial feeds and provides a cost-effective alternative for farmers.

Developing new genotypes with high yields and satisfactory stability is a crucial goal in breeding programs. Adaptability and stability of performance are complex genetical traits inherited through the process of evolution (Matsuo, 1975). Evaluating adaptability and stability of performance requires multi-environment testing of genotypes and the traits are assessed on performance criteria in relation to those of the set of genotypes tested. New varieties are typically designed and expected to perform well across diverse environmental conditions, including both natural and agronomic settings. Understanding genotype-by-environment interaction (GEI) patterns in multi-environment testing is vital for plant breeders, as it complicates the selection of promising genotypes by weakening the correlation between genotypic and phenotypic values (Ebdon and Gauch, 2002; Yan and Tinker, 2006). Modelling GEI in multi-environments is essential for assessing the phenotypic stability of genotypes across diverse environments or the adaptability of specific genotypes to varying environmental conditions (Vaezi *et al.,* 2019; Ghazvini *et al.,* 2018). Among the various methods for analyzing genotype stability, biplots derived from additive main effects and multiplicative interaction (AMMI; Gauch, 1988) are widely utilized.

Phosphorus is an essential macronutrient for legume crops, playing a critical role in their growth, development, and nitrogen-fixation processes. Phosphorus is a vital component of adenosine triphosphate (ATP), which is the energy currency of cells. It facilitates energy transfer for various physiological processes like photosynthesis, nutrient uptake, and respiration in legumes. Phosphorus promotes the development of a robust root system, which is essential for legumes to access water and nutrients efficiently from the soil. Plants have evolved various strategies to adapt to phosphorus (P) availability, including modifications to their root architecture. Developing crop varieties with enhanced root traits capable of accessing and utilizing bound soil P resources could significantly improve the efficiency of applied fertilizers (Abelson, 1999). Studies have documented genotypic variations in cowpea with respect to the influence of P on yield (Sanginga *et al*., 2000). Ensuring adequate phosphorus availability significantly boosts legume productivity and soil health through improved biological nitrogen fixation. Phosphorus (P) deficiency affects the productivity of fodder legumes and smallholder farmers do not have the resources to purchase P fertilizers. An alternative solution to the problem of P deficiency is the development of cowpea genotypes with the ability to perform well in P-deficient soils as well as respond to P fertilization. In the present investigation an attempt has been made to assess genotype by environment interactions in green fodder yield of cowpea under different phosphorus regimes to identify high yielding stable genotypes.

MATERIALS AND METHODS

The experimental materials of the present investigation consisted of 45 fodder cowpea genotypes collected from different parts of India (**Table 1**). These genotypes were evaluated using a randomised block design with three replications across eight environments. The environments were created by combining four levels of phosphorus (0, 20, 40 & 60 kg P_2O_5/ha) with two growing seasons (*rabi*, 2022-23 and *kharif* 2023). The eight environments were designated as E1 (RP_0), E2 (RP_{20}), E3 (RP_{40}), E4 (RP_{60}), E5 (KhP_0), E6 (KhP_{20}), E7 (KhP_{40}) and E8 (KhP_{60}). The experiments were conducted at AICRP on Forage Crops & Utilisation, OUAT, Bhubaneswar, Odisha. The soil of the experimental site was sandy loam with p^H of 4.78; Available soil phosphorus content was 33.52 kg/ha as per Brays method. Single super phosphate was applied @ 0, 125, 250 & 375 kg /ha to obtain 0 kg P_2O_5/ha, 20 kg P_2O_5/ha, 40 kg P_2O_5/ha & 60 kg P_2O_5/ha respectively. The plot size was 7.2 m^2 and 0 g SSP, 90 g SSP, 180 g SSP & 270 g SSP was applied per plot. The recommended dose of fertiliser for fodder cowpea was 20:40:40 kg N: P_2O_5: K_2O/ha. At the time of planting, 20 kg of N/ha (urea) and 40 kg of K_2O/ha (muriate of potash) were applied as basal along with 0, 20, 40 & 60 kg of P_2O_5/ha (SSP) as per the treatment schedule. Farmyard manure was applied @ 10 tonnes/ ha at the time of last ploughing. Seeds were sown in 6 rows of 4 m length with row to row spacing of 30 cm and plant to plant spacing of 10 cm. Observation was recorded on green fodder yield per plot (kg) at the time of 50 % flowering and converted to tonnes/ha. Mean data of eight environments were used to assess G × E interaction following R-Studio software (2020). The G × E interaction was analysed in Additive Main and Multiplicative Interaction (AMMI) model (Zobel *et al.,* 1988 and Gauch,1992) with a view to identify fodder cowpea genotypes better adapted to varying phosphorus levels. The mathematical function of the AMMI model is:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{k=1}^{n} \lambda_k \gamma_k \delta_k + \theta_j$$

where

Y_{ij} = mean yield of i^{th} genotype (i=1, 2, ...,45) in j^{th} environment (j= 1,2,...,8), m is the grand mean, a_i = mean deviation/effect of i^{th} genotype, b_j = mean deviation/effect of j^{th} environment, l_k = eigen value of k^{th} IPCA axis, g_{ik} = genotypic score of i^{th} genotype on k^{th} IPCA, d_{jk} = environment score of j^{th} environment on k^{th} IPCA, q_{ij} = residual of G × E interaction effect in Y_{ij}, n = number of IPC axes retained in the model.

The IPCA scores of genotypes and environments were estimated by appropriate analytical procedure. AMMI analysis of variance was carried out and the contributions of different IPCA's to G × E interaction were analysed and their statistical significance tested by F-test.

Table 1. List of fodder cowpea genotypes evaluated in different phosphorus regimes during rabi and kharif season

Code	Genotype	Source	Code	Genotype	Source
G1	MFC-08-14	Mandya	G24	CO-(FC)-8	Coimbatore
G2	MFC-09-3	Mandya	G25	Vijayar	Hyderabad
G3	MFC -18-2	Mandya	G26	TSFC-20-06	Hyderabad
G4	MFC-18-8	Mandya	G27	F-6R-211-184-2	Mandya
G5	MFC-18-10	Mandya	G28	Sweta	Hyderabad
G6	MFC-20-3	Mandya	G29	UPC 625	Pantanagar
G7	EC-107120	Mandya	G30	TNFC 926	Coimbatore
G8	MFC-09-1	Mandya	G31	KBC-2	Mandya
G9	NBC-40	Mandya	G32	MFC-18-4	Mandya
G10	IC-219489	Mandya	G33	MFC-20-7	Mandya
G11	NBC-43	Mandya	G34	EC-402154	Mandya
G12	UPC-4200	Pantanagar	G35	IC-402096	Mandya
G13	UPC-5287	Pantanagar	G36	EC-458418	Mandya
G14	UPC-9202	Pantanagar	G37	UPC-618	Pantanagar
G15	UPC-801	Pantanagar	G38	UPC-628	Pantanagar
G16	UPC-802	Pantanagar	G39	UPC-5286	Pantanagar
G17	UPC-804	Pantanagar	G40	UPC-803	Pantanagar
G18	UPC-805	Pantanagar	G41	FD-739	Coimbatore
G19	UPC-2001	Pantanagar	G42	FD-1052	Coimbatore
G20	UPC-2002	Pantanagar	G43	FD-1259	Coimbatore
G21	N-311	Coimbatore	G44	C0-9	Coimbatore
G22	IFC-9304	Coimbatore	G45	IFC-24094	Coimbatore
G23	FD-1161	Coimbatore			

RESULTS AND DISCUSSION

Phosphorus plays a vital role in the growth and development of legume crops by supporting energy transfer, root development, and nitrogen fixation. It is a key component of ATP, driving metabolic processes like photosynthesis and nutrient uptake. High cost of P-fertiliser creates great problems for farmers. Developing P-efficient genotypes is an alternative solution to handle this problem. In the present investigation fodder cowpea genotypes were evaluated at different phosphorus regimes. Singh *et al.* (2015) evaluated groundnut genotypes at different phosphorus levels.

The genotypes showed significant differences in their green fodder yield in eight environments (**Table 2**). The maximum genotypic variance was observed in E2 (14.43) and the minimum genotypic variance was recorded in E5 (3.54) (**Table 2**). The yield data of 45 genotypes in eight environments is presented in box plots (**Fig.1**). The rectangular box plot in the figure explained distribution of middle 50 % data and the line inside the box was the median (second quartile Q2). The bottom end of the box is the lower quartile (Q1), and the upper end of the box represents upper quartile (Q3). The two lines outside the box are the whiskers (T- shaped structure) explaining the highest and the lowest observations in green fodder yield (range in green fodder yield). Unusual observations in the data set are called outliers. In **Fig.1**, green fodder yield of G19 (UPC-2001) in E6 was 38.71 t/ha and it was considered as an outlier (**Table 2**). The median value of green fodder yield was 14.22, 20.50, 24.45, 27.49, 21.61, 27.81, 34.33 & 37.16 t/ha in E1, E2, E3, E4, E5, E6, E7 and E8, respectively. The lowest median green fodder yield was observed in E1 (14.22 t/ha) and the highest median green fodder yield was recorded in E8 (37.16 t/ha). In E1 (RP$_0$) the minimum green fodder yield was 8.02 t/ha (lower whisker) and the maximum green fodder yield was 20.07 t/ha (upper whisker) with a median value of 14.22 t/ha. At P$_0$ level (control condition) the median yield was the highest in kharif season (E5 - 21.61 t/ha) than rabi season (E1 – 14.22 t/ha). The same trend was observed at P$_{20}$ (*rabi*: 20.50 t/ha & *kharif*: 27.51 t/ha); P$_{40}$ (*rabi*: 24.54 t/ha & *kharif*: 33.97 t/ha) and P$_{60}$ (*rabi*: 27.08 t/ha & *kharif*: 36.12 t/ha) levels. This result indicated that the green fodder yield was low in rabi season as compared to kharif season. The maximum and minimum green fodder yield of cowpea genotypes in different environment are presented in **Table 3**. The genotype N-311 was found to score the highest yield in E2, E3 & E4 while UPC-2001 recorded the highest yield in E7 & E8 (**Table 3**; **Fig. 1**).

Table 2. ANOVA for green fodder yield in eight individual test environments

Environment	Mean Sum of Squares			Genotypic variance
	Replication (df:2)	Genotype (df: 44)	Error (df:88)	
E1(RP$_0$)	2.30	39.8**	3.33	12.15
E2(RP$_{20}$)	6.79	50.2**	6.89	14.43
E3(RP$_{40}$)	21.11	36.3**	11.30	8.33
E4(RP$_{60}$)	13.15	44.2**	13.41	10.26
E5(KhP$_0$)	19.21	20.7**	10.08	3.54
E6(KhP$_{20}$)	24.77	46.8**	13.77	11.01
E7(KhP$_{40}$)	30.54	55.6**	17.78	12.61
E8(KhP$_{60}$)	24.50	52.2**	21.98	10.07

** Significant at 1% level of probability

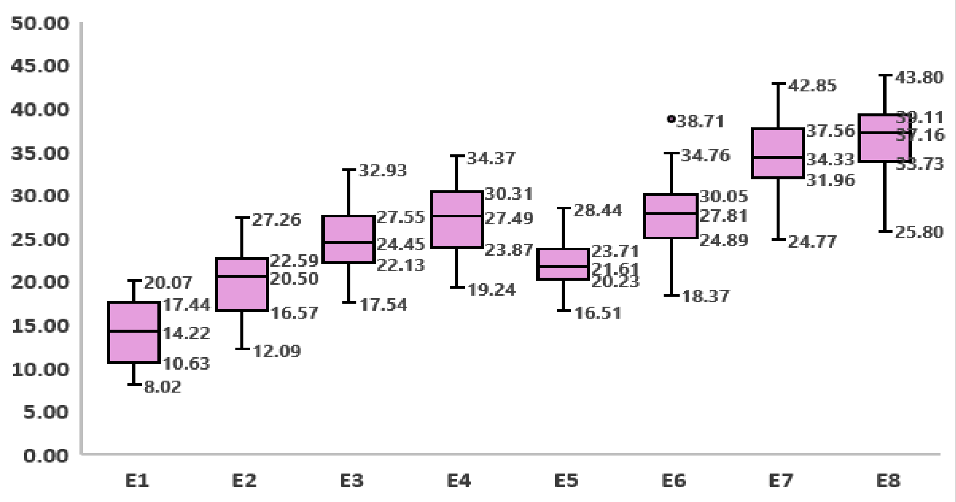

Fig. 1. Box plots showing green fodder yield (tonnes/ha) of cowpea genotypes across eight environments

Table 3. Environment wise green fodder yield of cowpea genotypes at lower whisker and upper whisker

Environment	Green fodder yield (tonnes/ha) of genotype at lower whisker		Green fodder yield (tonnes/ha) of genotype at upper whisker		Green fodder yield (tonnes/ha) of outlier	
	Genotype	Yield	Genotype	Yield	Genotype	Yield
E1	UPC 625	8.02	IFC-9304	20.07		-
E2	UPC-9202	12.09	N-311	27.26		-
E3	UPC 625	17.54	N-311	32.93		-
E4	MFC-20-3	19.24	N-311	34.37		-
E5	MFC-18-4	16.51	FD-739	28.44		-
E6	UPC-5286	18.37	EC-107120	34.76	UPC-2001	38.71
E7	Vijayar	24.77	UPC-2001	42.85		-
E8	MFC-18-4	25.80	UPC-2001	43.80		-

The green fodder yield data of eight environments were subjected to combined analysis of variance after confirming the homogeneity of error variance through Bartlett's chi-square test ($p > 0.05$). Combined ANOVA results indicated the presence of significant variation in environments, genotypes, and G × E interaction at 1%

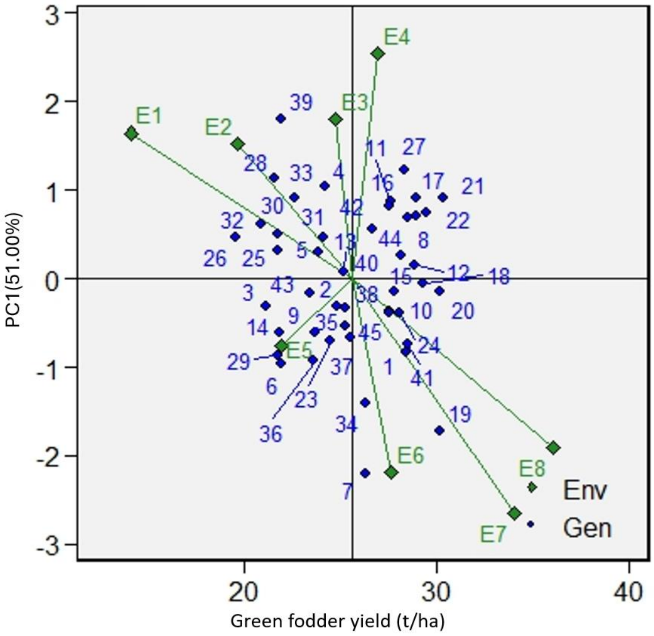

Fig. 2. AMMI 1 biplot of main effects and G × E interaction of 45 fodder cowpea genotypes

probability level (**Table 4**). Presence of significant G × E interaction leads to stability analysis and stability analysis was done following AMMI model. The AMMI analysis revealed significant variation ($p < 0.01$) among the studied genotypes, environments, and genotype by environment interactions. Environments contributed a large portion of total variation (76.20 %), whereas the genotype and G × E interaction component contributed about 14.89 and 8.47 % of total variation, respectively (**Table 4**). Again, the analysis revealed that genotype by environment interaction was significantly explained by the first two IPCAs. The first PCA contributed 51.00 % toward the total G × E variation while second, PC contributed 15.50%. PC1 and PC2 together contributed 66.50 % of total variability of G × E component.

AMMI is one of the essential models for assessing the impact of genotype × environment interactions on economically important traits like grain yield and its related traits across several environments. Understanding the interplay between genotypes and the relevant environments is made possible by the AMMI model. AMMI 1 is primarily used to discover high potential yield and stability, according to Olivoto *et al.* (2019). While analyzing AMMI 1, Kilic (2014) reported that the genotype and environment mean when positioned parallel to the ordinate indicates nearly equal performance.

Additive Main Effects and Multiplicative Interaction 1 biplot
AMMI 1 biplot for green fodder yield of 45 genotypes at eight environments (4 phosphorus regimes & 2 growing seasons) is presented in **Fig. 2**. The main effects (G & E) accounted for 91.09 % of total variation. G × E interaction accounted for 8.47 % and IPCA 1 accounted for 51.00 % of G × E variation (**Table 4**). In AMMI 1, the genotype and environment means were taken on X-axis and IPCA1 was taken on Y-axis. The genotypes were scattered in four different quadrants indicating four adaptive groups of genotypes (**Fig. 2**). The eight environments were also scattered in four quadrants indicating that the environments were different. From **Fig. 1**, it was noted that E6, E7 & E8 were similar in their interaction effect but different from E1, E2 & E3 which were similar in their interaction to each other. The environments E7 and E8 were farthest from biplot origin, with long vectors indicating strong interaction forces, whereas E3 and E5 were nearer to origin and have short vectors representing weak interaction forces. Genotypes G19 (UPC-2001), G20 (UPC-2002) and G21 (N-311) exhibited higher green fodder yield. Genotype G12 (UPC-4200) and G40 (UPC-803) had higher yield with low positive interaction effect. G7 (EC-107120**)** and G9 (NBC-40) had high mean yield with high negative interaction. G39 (UPC-5286**)** had low mean but accompanied high positive interaction.

Additive Main Effects and Multiplicative Interaction 2 biplot
AMMI 2 biplot was constructed taking IPCA1 (PC1) on X-axis and IPCA2 (PC2) on Y-axis and it is illustrated in **Fig. 2**. AMMI 2 explains the genotype × environment interaction to understand the response of genotypes in each test environment. Genotypes G2 (MFC-09-3), G3 (MFC-09-3), G15 (UPC-801), G18 (UPC-805), G20 (UPC-2002), G40 (UPC-803), G43 (FD-1259) scattered in different quadrants were very close to the origin, indicating that these genotypes had negligible interaction effect, and they were considered as stable in their performance.

Table 4. AMMI ANOVA of cowpea genotypes for green fodder yield

Source	Df	Mean Sum of Squares	% of G – E Sum of Squares	F -Calculated	% contribution of G × E Interaction SS
Replications in environment	16	17.81	0.43	1.44	-
Genotype	44	220.44**	14.89	17.89	-
Environment	7	7089.47**	76.20	398.16	-
Genotype x Environment	308	17.90**	8.47	1.45	-
IPCA1	50	56.24**	4.32	4.56	51.00
IPCA2	48	17.78**	1.31	1.44	15.50
IPCA3	46	14.33	1.02	1.16	12.00
IPCA4	44	9.71	0.68	0.79	7.70
IPCA5	42	7.79	0.51	0.63	5.90
IPCA6	40	5.96	0.36	0.48	4.30
IPCA7	38	5.17	0.31	0.42	3.60
Residuals	704	12.32	-	-	-

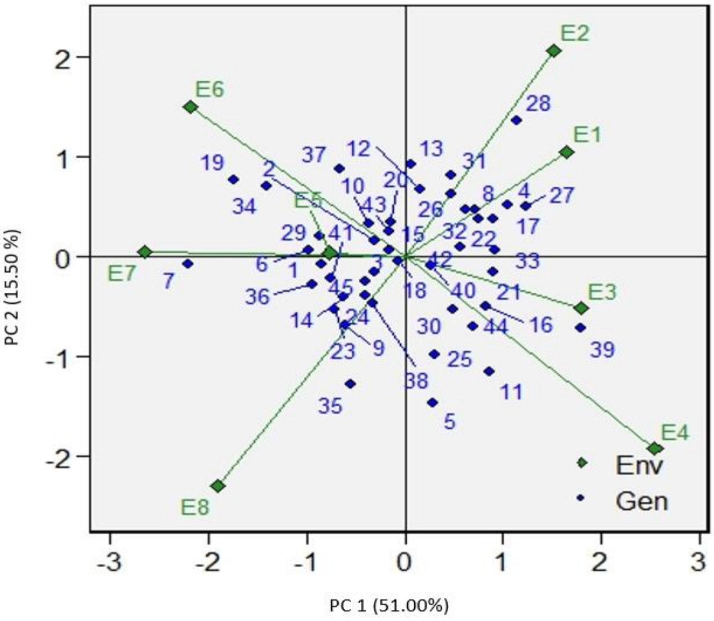

Fig. 3. AMMI 2 biplot of G × E interaction of 45 fodder cowpea genotypes

G5 (MFC-18-10), G11 (NBC-43), G39 (UPC-5286), G28 (SWETA), G19 (UPC-2001), G7 (EC-107120), G35 (IC-402096) were far away from the origin, indicating their high degree of sensitivity to environmental interactive forces. The interactive forces of the environments were decided by the length of the environment spoke. Higher spoke length indicated high degree of interactive force. From AMMI 2 biplot it was noted that E8 environment had the highest interactive force followed by E4, E2, E7 & E6. E5 had the smallest interactive forces followed by E1 and E3. Interaction of genotypes with specific environmental conditions was judged by the projection of genotype points onto environment spokes (**Fig. 3**). Genotypes G16 (UPC-802), G21 (N-311), G30 (TNFC 926), & G44 (C0-9) were specifically adapted to E3 and E4. Genotypes G32 (MFC-18-4), G8 (MFC 09-1), G22 (IFC-9304), G17 (UPC-804), G4 (MFC-18-8), G27 (F-6R-211-184-2) were suitable for E1 whereas G26 (TNFC-20-06), G31 (KBC-2), G28 (SWETA) were adapted to E2. Genotype G19 (UPC-2001), G34 (EC-402154) and G37 (UPC-618) were suitable for E6 (KhP$_{20}$). Genotype G9 (NBC-40), G38 (UPC-628), G24 (CO-(FC)-8) had specific adaptation to E8.

Table 5. Stable genotypes based on AMMI stability value (ASV)

Genotype code	Genotype	Mean green fodder yield (tonnes/ha)	Green fodder yield Rank	ASV	ASV rank	Remarks
G21	N-311	30.36	(1)	4.00	(40)	-
G19	UPC-2001	30.23	(2)	1.65	(15)	Stable
G20	UPC-2002	30.22	(3)	4.08	(41)	-
G22	IFC-9304	29.48	(4)	2.87	(32)	-
G18	UPC-805	29.30	(5)	1.41	(14)	Stable
G8	MFC-09-1	28.99	(6)	2.76	(30)	-
G17	UPC-804	28.93	(7)	1.36	(13)	Stable
G12	UPC-4200	28.90	(8)	1.03	(8)	Stable
G44	C0-9	28.52	(9)	2.38	(26)	-
G41	FD-739	28.50	(10)	1.75	(18)	Stable
G1	MFC-08-14	28.40	(11)	2.76	(31)	-
G27	F-6R-211-184-2	28.34	(12)	3.01	(35)	-
G40	UPC-803	28.14	(13)	1.31	(12)	Stable
G24	CO-(FC)-8	28.11	(14)	1.72	(16)	Stable
G15	UPC-801	27.82	(15)	2.48	(29)	-
G11	NBC-43	27.61	(16)	5.76	(43)	-
G16	UPC-802	27.60	(17)	2.40	(27)	-
G10	IC-219489	27.54	(18)	0.21	(1)	Stable
G45	IFC-24094	27.53	(19)	2.13	(22)	Stable
G42	FD-1052	26.66	(20)	3.18	(38)	-
G7	EC-107120	26.29	(21)	0.52	(2)	Stable
G34	EC-402154	26.29	(22)	3.48	(39)	-

Genotype showing high G × E interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific environment and is therefore best suited to that environment. AMMI analysis permits estimation of interaction effect of a genotype in each environment, and it helps to identify genotypes best suited for specific environmental conditions. Analysis of G x E interaction of multilocation yield data in AMMI model have been reported by Gumede *et al.* (2022) and Mekonnen *et al.* (2022) in cowpea, Fentie *et al.* (2013) and Islam *et al.* (2014) in rice; Hariprasanna *et al*. (2008) in groundnut; Balapure *et al.* (2016) in chickpea. All these workers found significant G × E interaction for grain yield.

In the present investigation it was noticed that environments explained the maximum contribution towards total variability indicating that different phosphorus levels and growing seasons are sufficient to study genotype by environment interactions in fodder cowpea. Tolessa *et al*. (2013) in wheat, and Singamsetti *et al.* (2021) in maize also observed a large proportion of total variation by the environment component but Anuradha *et al.* (2022) in their study in finger millet reported that genotypes contributed a large proportion of total variation followed by environment. In the present study, it was observed that IPCA1 and IPCA2 were significant, and they together contributed 66.5 % of total G × E interaction variability. Sheelamary and Karthigeyan (2021) found similar result in their study on stability of sugarcane clones across the environments where the first two principal components together contributed to 63.6 % of the genotype by environment interaction. Atakora *et al.* (2023) found that environmental factors accounted for 63.1% of the variation for grain output in cowpea. Bomma *et al.* (2024) also reported that IPCA1 and IPCA2 were significant, and they together contributed 64.5 % of total G × E interaction variability in pigeonpea. Zhou *et al*. (2016) evaluated soybean genotypes under P- deficient and P sufficient condition for selection of P-efficient genotypes.

AMMI stability value (ASV) and selection of high yielding and stable fodder cowpea genotypes: AMMI biplots are highly effective for simultaneously visualizing the mean green fodder yield and genotype stability. However, they do not provide the precise numerical value required for comparison. Therefore, the AMMI stability value (ASV) was calculated in the current study using the scores of the first two interactive principal components (IPCA1 and IPCA2), which significantly contributed to the total genotype × environment interaction variance for green fodder yield (**Table 5**). Lower ASV indicated greater

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stability. Among the tested genotypes, ASV ranged from 0.21 for G10 (IC-219489) to 7.25 for G43 (FD-1259). Genotypes ranked 1 to 22 for green fodder yield (green fodder yield) were considered high yielding, while those ranked 1 to 22 for ASV were identified as having low ASV, signifying higher stability. Based on both high green fodder yield and low ASV, the following genotypes were identified as high-yielding and stable: G19 (UPC-2001), G18 (UPC-805), G17 (UPC-804), G12 (UPC-4200), G41 (FD-739), G40 (UPC-803), G24 (CO-(FC)-8), G10 (IC-219489), G45 (IFC-24094), and G7 (EC-107120). Danakumar *et al.* (2023) in their study on chickpea found that genotypes having low ASV scores were found to be most stable. Mbeyagala *et al.* (2021) also found similar results in his study for grain yield in cowpea genotypes. Sujitha *et al.* (2024) in their comparative analysis of various models for identification of stability in pearl millet reported similar result where genotypes with higher mean yield and lower estimates of ASV were found to be most stable.

Based on AMMI stability value genotypes, G19 (UPC-2001), G18 (UPC-805), G17 (UPC-804), G12 (UPC-4200), G41 (FD-739), G40 (UPC-803), G24 (CO-(FC)-8), G10 (IC-219489), G45 (IFC-24094), and G7 (EC-107120) were found to be stable and high yielding. Genotype G9 (NBC-40), G38 (UPC-628), G24 (CO-(FC)-8) had specific adaptation to P- sufficient condition during kharif. Genotypes G32 (MFC-18-4), G8 (MFC-09-1), G22 (IFC-9304), G17 (UPC-804), G4 (MFC-18-8), G27 (F-6R-211-184-2) were identified as suitable for P- deficient condition during rabi season. Phosphorus-efficient genotypes with high stability can perform well in soils with varying phosphorus content. On the other hand, stability ensures that the yield of these phosphorus-efficient varieties will be least affected by fluctuations in phosphorus availability hence they can continue to show efficient phosphorus uptake and utilization, whether the soil is rich or deficient in phosphorus.

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