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AMMI Biplot Analysis of Genotype × Environment Interactions in Rainfed Grown Green Gram [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Background: Mungbean [*Vigna radiata* (L.) Wilczek] commonly called green gram, holds significant importance as a pulse crop in India and contribute significantly towards the national food security. Pulses present an option for diversifying agricultural systems; however, their low and varying yield under different environmental conditions makes them less competitive compared to cereals, oilseeds and cash crops. Therefore, it is essential to screen and identify stable genotypes those can perform consistently well across various agro climatic conditions.

Methods: The G×E interaction for yield and its component characters in mungbean were analyzed by using the AMMI (additive main effects and multiplicative interaction) model. The data was collected on 40 elite mungbean genotypes which were grown in four rainfed environments.

Result: The study found highly significant effects (P<0.01) of genotype (G), environment (E) and G×E interaction (GEI) for all 10 characters analyzed. Gollob's test showed IPCA I was significant for all traits; IPCA II was significant for all except days to maturity and pod length; IPCA III was significant for plant height, primary branches per plant, number of clusters per plant, number of pods per cluster, total pods per plant, and seed yield per plant. Over 69% of GEI sum of squares were explained by IPCA I. Significant GEI supports AMMI analysis for identifying stable genotypes, with AMMI residual SS non-significant for most traits, indicating model accuracy. Genotypes IPM 02-3 (G9), PM 15-20 (G37) and PM 15-7 (G24) showed low interaction for seed yield per plant. This AMMI model analysis of mungbean yield under rainfed conditions provides valuable insights for breeding drought-tolerant mungbean varieties.

Key words: AMMI model, Breeding, Drought stress, GEI, Mungbean, Yield stability.

Abbreviations: AMMI: Additive main effects and multiplicative interaction, ANOVA: Analysis of variance, IPCA: Interaction principal component axis, RMS: Root mean square, SS: Sum of squares.

INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek.] is also known as moong, greengram, chickasaw or golden gram and belongs to the family *leguminaceae* and subfamily *papilionaceae*. Mungbean is a diploid species with chromosome number 2n=22 (Karpechenko, 1925). According to Vavilov (1926), the centre of origin for the mungbean is the Indian subcontinent and from here it spread to Southeast Asia, Africa, South America, Australia and some other countries. It is the third most important pulse crop in India after chickpea and red gram. It has the potential to fix the biological nitrogen and add this biological nitrogen to the soil. It also adds soil enzymes and biochemicals which create a platform for various beneficial micro-organisms. Mungbean can be used as excellent green manure crop which also improve the soil physical characteristics (Directorate of Pulses Development, 2018). Mungbean is an important source of protein for human consumption as it contains 24-25% of protein, 56-60% carbohydrate, 4.1% fibre, 1.3% fat and 3.5% mineral. It is very rich in different amino acids like leucine, arginine, lysine, valine and tryptophan and can be used to reduce the protein malnutrition (Mekkara and Bukkan, 2021). India accounts for more than 60% of the global production of the mungbean. Majority of the mungbean production (around 70%) in India occurs during the *kharif* season and the remaining production occur during the *rabi* and summer seasons. In India mungbean is grown in about 51.3 lakh hectare area with total production of 35.45 lakh tonnes annually with the productivity about 601 kg/ha and contributes 11% of the total pulses production in India. (Directorate of Economics and Statistics, 2023).

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Stability can be defined as a variety's ability to maintain a constant yield under changing environmental conditions, which can be assessed by numerous stability parameters. The stability of the cultivar is affected by the genotype × environment interactions (G×E interactions). G×E interactions, which can be defined as the variation in genotype response in relation to environmental variation. For one to use full genetic potential, we need to identify the genotypes having high degree of adaptability over various environmental situations. The phenotypic expression of a genotype varies depending on the environment and different genotypes respond to the same environment in different ways, so they will not give the same result. All genotypes must be tested for specific or general adaptability in order to reach the optimum and most consistent output over time and space (Piepho, 1996).

Gauch (1992) proposed the additive main effect and multiplicative interaction (AMMI) model, which is a hybrid analysis model that incorporates both the additive and multiplicative components of a two-way data structure and is considered an effective tool for graphically diagnosing genotype×environment interaction patterns and then used to identify stable and responsive genotypes with magnitude of GEI (Crossa, 1990). It also uniquely separates main and interaction effects (Gauch, 2006). The AMMI model separates the additive variance from the multiplicative variance and then relates principal component analysis (PCA) to the interaction portion to a set of new of coordinate axes that explains the interaction pattern in greater detail, with estimation actually achieved using the least squares principle (Thillainathan and Fernandez, 2001).

MATERIALS AND METHODS

The present experiment was conducted over four seasons *viz*., *kharif* 2020 (E1), spring 2021 (E2), *kharif* 2021 (E3) and spring 2022 (E4) at Norman E. Borlaug Crop Research Center, G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. Forty elite high yielding mungbean genotypes which includes both high yielding cultivars and advanced breeding lines which were developed by different research institutes across country were included in the present investigation and these 40 lines were planted in 3 replications in a randomized block design (RBD). Recommended dose of fertilizers was applied before sowing as basal dose [20 kg/ha N, 35 kg/ha P and 15 kg/ha K] and pesticides applied as per the requirements. In each replication, each genotype was planted in two rows having the length of 4 meters and 30 cm width between the rows. In each row, plant to plant distance was maintained at 10 cm having 40 plants in each row. Observations has been recorded for the 10 characters *viz*., days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, pod length (cm), number of seeds per pod, total pods per plant, 100-seed weight (g) and seed yield per plant (g). Additive main effects and multiplication interaction (AMMI) model was used to analyse the G×E interactions. First, an ANOVA model is used to the data with main effects of genotype and environment (without the interaction) and then, a principal component analysis (PCA) is fitted using the standardized residuals. The main effects and interaction effects significance were estimated using an F-test developed by Gollob (1968). AMMI model equation is as follows:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda n \; y_{in} \; \delta_{jn} + p_{ij} + \varepsilon_{ijr}$$

Y_{ij} = Trait of 'g' genotype in the 'e' environment.
μ = Grand mean of the trait.
g_i = Deviation of genotypes from grand mean and.
e_j = Environment deviation λ_n the eigenvalue of PCA axis n.
y_{in} and δ_{jn} = Genotype and environment PCA scores for PCA axis n respectively.
p_{ij} = Residual of AMMI model.
ε_{ijr} = Random error.

By multiplying the genotype's interaction principal component axis (IPCA) score by the environment's IPCA score, one can estimate the interaction between any genotype and environment.

Postdictive assessments

An effective statistical tool for evaluating the overall goodness of fit is the proportion of the treatment sum of squares (SS) captured by an AMMI biplot. It is calculated by multiplying the treatment SS by the percentage addition of SS (Genotype + Environment + IPCA 1). Additional to this, another statistic that is very useful for model fit is the root mean square (RMS) residual. For each trait, the pertinent portion of the G×E interaction was calculated in order to prevent erroneous interpretation of statistical results. It is crucial to subtract the errors from uncontrolled variation (also known as "noise") from the total G×E interaction SS because the interaction contains the majority of the treatment degrees of freedom and is where most of the noise appears. Calculations were made in accordance with Gauch and Zobel's (1996) instructions to determine "noise" SS, "real structure" SS and target relevant variation percentage. Biplots were used to investigate the relationship between genotype × trait and environment × trait averaged across all environments. These biplots were created to evaluate the genotype or environment based on multiple traits and to visualize the genetic correlation between traits (Lee *et al.,* 2003: Thangavel *et al.,* 2011).

RESULTS AND DISCUSSION

A combined study across contexts was possible because of the homogeneity of variance tests, which revealed homogeneous error variance for each character in the four environments. All of the examined variables showed highly significant ($P<0.01$) variation attributable to genotype, environment and the G×E interaction, according to an ANOVA across environments. In order to quantify G×E interaction for the characters showing significant G×E in the pooled

analysis, AMMI analysis was carried out further. For the traits plant height (46.44%), pod length (40.43%), number of seeds per pod (50.66%) and 100-seed weight (78.16%) major proportion of total sum of squares was contributed by the genotype component. While, for days to maturity (76.31%), number of pods per cluster (48.35%) and total pods per plant (55.14%), major proportion of total sum of squares was contributed by the environment component. GxE interaction component contributed major proportion of total sum of squares for the traits primary branches per plant (50.55%) and number of clusters per plant (37.69%). Major proportion of total sum of squares was explained by the environment for the seed yield per plant (67.96%) which indicates the higher influence of environment on the seed yield per plant (Table 1). Ganta *et al.* (2022) also found similar results. The results of present investigation indicated that main effects (environment and genotype) as well as G×E interaction effects were significant for all the 10 characters studied, which suggested that genotypes performed differentially in different environments under rainfed conditions. Similar results reported by Samyuktha *et al.* (2020); Van Giang *et al.* (2024) and Win *et al.* (2018). As there is an increase in number of axes, there was decreasing contribution of G×E interaction SS *i.e.*, IPCA I was greater than IPCA II and IPCA II was greater than IPCA III for a particular trait. According to the Gollob's test (Gollob, 1968) on IPCA's, IPCA I was significant for all characters; IPCA II was significant for all characters expect for days to maturity and pod length (cm), while third IPCA component (IPCA III) was significant for plant height (cm), primary branches per plant, number of clusters per plant, number of pods per cluster, total pods per plant and seed yield per plant (g) (Table 1) only. For all the characters studied in this investigation, the G×E interaction (GEI) component was found to be significant as shown in Table 2, which allowed for further analysis using AMMI model. Similar results were observed by Singh *et al.* (2018); Vaijayanthi *et al.* (2017); Bhagwat *et al.* (2018); Baraki *et al.* (2020). Major proportion of total sum of squares was explained by the environment (67.96%) for the seed yield per plant which indicated the higher influence of environment in the seed yield per plant. The high influence of environment on seed yield was also reported earlier by Bhagwat *et al.* (2018); Jeberson *et al.* (2019); Abeytilakarathna (2010).

The G×E interaction component was highly significant for all the characters under study and this interaction component was further divided into three principal components axes (IPCA). All three IPCA should be included in the model according to the criteria of postdictive success for AMMI using all three replications and F-tests at the 0.05 probability level. The IPCA I (first principal component) explained about 43.92% (number of pods per cluster) to 99.20% (days to maturity) of G×E interaction SS. IPCA II (second principal component) explained about 0.58% (days to maturity) to 39.92% (number of pods per cluster). IPCA III (third principal component) explained about 0.22% (days

Table 1: Analysis of variance for AMMI model of mungbean for yield and yield component traits under rainfed conditions.

Source of variation	DF	Days to maturity	Plant height (cm)	Primary branches per plant	Number of clusters per plant	Number of pods per cluster	Pod length (cm)	Number of seeds per pod	Total pods per plant	100 seed weight (g)	Seed yield per plant (g)
Treatments	159	423.32**	783.97**	1.75**	58.05**	1.75**	1.76**	8.30**	788.99**	0.92**	39.87**
Genotypes (G)	39	273.46**	1484.20**	1.92**	66.92**	1.36**	2.90**	17.14**	600.65**	2.93**	24.30**
Environments(E)	3	17120.44**	5727.04**	20.88**	1046.86**	44.96**	34.33**	52.22**	23055.97**	4.35**	1436.21**
G*E Interaction	117	45.15**	423.81**	1.20**	29.73**	0.78**	0.55**	4.23**	280.82**	0.16**	9.26**
IPCA I	41	127.80**	641.99**	1.72**	46.44**	0.98**	1.42**	9.80**	475.34**	0.28**	15.99**
IPCA II	39	0.78	395.69**	1.26**	33.62**	0.93**	0.12	2.12**	304.73**	0.18**	10.05**
IPCA III	37	0.32	211.69**	0.57**	7.13**	0.40**	0.03	0.27	40.07**	0.01	0.97**
Error	320	2.86	19.66	0.11	2.70	0.06	0.12	0.61	13.06	0.03	0.56
Total	479	142.93	285.28	0.65	21.07	0.62	0.66	3.16	264.96	0.32	13.61

to maturity) to 16.16% (number of pods per cluster). More than 83% of total G×E interaction SS for all the 10 characters studied was contributed by mean squares of IPCA I and IPCA II components cumulatively. Similar results reported by Thangavel *et al.* (2011); Samyuktha *et al.* (2020) and Win *et al.* (2018). The SS due to noise, relevant variation and pattern variation are given in Table 2. All the characters under the study accounted for noise varied from 4.64% (plant height) to 22.01% (pod length) and real structure (pattern variation) varied from 77.99% (pod length) to 95.36% (plant height). Treatment SS variation explained about real and relevant patterns in the data and capturing more the pattern percentages (real structure) than target percentages (relevant variation) indicating less noise and low irrelevant features in the data. In case of 100-seed weight, the target percentage SS accounted for very close to the real SS, while for the remaining traits target percentage SS was far away from the real SS. The discrepancy between a model's predicted values and the actual observed values is known as the root mean square (RMS) residual. Root mean square residual of AMMI I for seed yield per plant in absolute quantity is 22.34 g per plant, which explains the fitness of the present model. Similar results were reported by Thangavel *et al.* (2011). RMS residuals of the AMMI I and AMMI II models for different characters are given in Table 3. All the characters had residual mean SS except for plant height and total pods per plant with all characters showing non-significant residual mean SS which suggested the greater accuracy of this model. All the genotypes used in the present study were adapted to the conditions present in tropics and sub-tropics and they have maturity period varying from short to long. Fig. 1a, AMMI I biplot (biplot of main effects and IPCA I) of days to maturity clearly distinguishes the genotypes according to their duration of maturity with genotypes having early duration of maturity on the left [PM 15-3 (G20), PM 15-2 (G19), PM 5 (G4), PM 15-14 (G31), SML 1082 (G7), *etc.,*], long duration genotypes at the right side [IPM 02-3 (G9), PM 15-11 (G28), IPM 02-9 (G1), Vamban 2 (G17), PM 15-6 (G23), PM 15-12 (G29), PM 15-15 (G32), *etc.* (g)] and remaining genotypes present in middle were grouped as medium duration. Seed yield/plant is affected by the days to maturity. With increasing maturity, all genotypes produced more total dry matter until they reached physiological maturity. Total dry matter production increased with age in all genotypes until physiological maturity (Mondal *et al.,* 2012). With increased days to maturity, there will be more time to synthesize and accumulate the assimilates which will increase the total dry matter in the plants, but plants with shorter days to maturity tend to avoid or escape the unfavourable growing conditions in the grain development stage (Yoshida, 1981). Hence, if the conditions are favourable then the responsive late maturing genotypes will produce higher yield than shorter duration genotypes and the results of current study also indicates the same. For example, genotypes PM 15-11 (G28), PM 15-15 (G32), PM 15-20 (G37), SML 1815 (G18), LGG 460 (G40) and PM

Table 2: The errors from uncontrolled variation, percent genotype × environment interaction captured by each statistically significant interaction principal component axis (IPCA), IPCA captures percent interaction and root mean squares (RMS) residual of AMMI (in percent).

		Days to maturity	Plant height (cm)	Primary branches per plant	Number of clusters per plant	Number of pods per cluster	Pod length (cm)	Number of seeds per pod	Total pods per plant	100 Seed weight (g)	Seed yield per plant (g)
Errors from uncontrolled variation	Noise SS	7.99	4.64	9.15	9.08	7.70	22.01	14.43	4.65	18.59	6.05
	Real Structure (pattern)	92.01	95.36	90.85	90.92	92.30	77.99	85.57	95.35	81.41	93.95
	Relevant variation (target)	23.06	48.28	31.57	31.70	21.55	45.46	56.06	19.89	80.55	15.98
Percent G×E interaction	% G×E of IPCA I	99.20	53.08	50.09	54.73	43.92	91.16	81.23	59.32	61.80	60.52
	% G×E of IPCA II	0.58	31.12	35.00	37.69	39.92	7.14	16.75	36.17	37.06	36.18
	% G×E of IPCA III	0.22	15.80	14.91	7.58	16.16	1.70	2.02	4.51	1.14	3.30
IPCA captures percent interaction	% of IPCA I	99.40	78.88	74.67	79.37	85.61	79.23	69.56	84.46	92.02	89.65
	% of IPCA II	99.95	87.62	82.30	85.79	86.45	98.37	93.72	90.52	95.20	93.81
	% of IPCA III	99.98	93.71	92.46	97.14	97.27	99.61	99.24	98.81	99.85	99.43
Root mean squares (RMS) residual of AMMI	RMSAMMI I	63.17	141.64	7.28	38.09	5.48	6.63	17.49	121.87	2.83	22.34
	RMSAMMI II	4.90	111.19	6.24	32.40	5.38	0.94	8.12	97.58	2.24	17.72

7(G6) have exhibited longer duration for maturity and they have high yields. On the other hand, the genotypes Sona Mung 1 (G8), SML 1082 (G7), PM 2 (G10) and PM 15-5 (G22) which had shorter maturity duration yielded comparatively less than the grand mean of genotypes. Ying *et al.* (1998) reported that longer growing period was associated with greater biomass production and therefore higher grain yield which explains the results of this study.

The yield and its component traits were plotted on AMMI I and AMMI II biplots to examine the main effects and interactions across location-year environments. The first IPCA is indicated by the ordinate and the main effects is displayed along the abscissa in case of AMMI I biplot. When a genotype and environment have the same sign on the IPCA axis, their interaction is positive and when they have a different sign, their interaction is negative, according to

Table 3: Mean, IPCA I and IPCA II values of 40 mungbean genotypes for seed yield per plant trait.

Genotype	Code no.	Seed yield per plant (g)		
		Mean	IPCA I	IPCA II
IPM 02-19	1	3.68	-0.21	0.51
IPM 02-13	2	5.28	-0.28	0.12
PM 4	3	7.09	-0.11	-0.21
PM 5	4	8.51	-1.00	-0.17
PM 8	5	5.48	0.17	-0.02
PM 7	6	8.38	-0.11	-0.41
SML 1082	7	4.08	0.42	0.28
Sona Mung 1	8	3.07	-0.15	0.64
IPM 02-3	9	7.48	-0.05	0.15
PM 2	10	5.07	0.04	0.20
PM 3	11	4.83	0.48	0.21
PM 9	12	6.11	-0.21	-0.10
HUM 12	13	7.03	-0.19	-0.50
Pusa vishal	14	6.49	-0.25	0.12
ML 818	15	4.21	-0.56	0.50
IPM 2-14	16	4.74	0.14	0.24
Vamban 2	17	6.10	0.07	-0.15
SML 1815	18	8.40	0.39	-0.60
PM 15-2	19	6.24	0.43	-0.13
PM 15-3	20	7.51	-0.05	-0.56
PM 15-4	21	6.46	0.43	0.04
PM 15-5	22	5.65	0.25	0.37
PM 15-6	23	6.35	-0.08	-0.08
PM 15-7	24	7.34	-0.10	-0.14
PM 15-8	25	7.89	0.51	-0.02
PM 15-9	26	6.50	0.43	0.07
PM 15-10	27	7.15	0.50	0.04
PM 15-11	28	8.54	-0.40	-0.50
PM 15-12	29	6.20	-0.18	0.13
PM 15-13	30	6.54	0.30	0.15
PM 15-14	31	7.79	0.19	-0.40
PM 15-15	32	7.91	0.13	-0.33
PM 15-16	33	6.69	0.10	0.25
PM 15-17	34	7.42	-0.20	0.09
PM 15-18	35	7.26	-0.80	-0.03
PM 15-19	36	7.45	0.17	0.18
PM 15-20	37	8.30	-0.16	-0.09
PM 15-21	38	7.31	-0.27	0.32
SML 1808	39	5.89	0.07	0.21
LGG 460	40	8.83	0.14	-0.39
Mean		6.58		

the interpretation of a biplot assay. This is because negligible interaction effects are indicated by main effects with IPCA scores close to zero. The IPCA I versus IPCA II biplot (*i.e.*, AMMI II biplot), explain the degree of interaction of each genotype and environment. The environments and genotypes that are most responsive when they are farther from their origin fit the least well (less stable). When environments and genotypes are in the same sector, they interact positively if they are in the opposite sector, they interact negatively (Thangavel *et al.*, 2011).

Days to maturity

About 99.93% of the treatment SS was explained by the AMMI I biplot with the main effects plotted against the IPCA I scores. The average days required for maturity for the 40 mungbean genotypes in each environment measured was 91.17 days in E1, 70.63 days in E2, 91.44 days in E3 and 70.60 days in E4. According to the analysis of genotype main effects showed that genotype PM 15-3 (G20) had the lowest mean (72.67) for days to maturity among 40 genotypes in 4 environments. The environment E4 (Spring 2022) had the lowest mean (70.60 days) for days to maturity among all the environments. When considering the nature of responsiveness of genotype, PM 15-17 (G34), PM 15-13 (G30) and PM 5 (G4) exhibited below average mean with low interaction effect (Fig 1a). In location-year environments, as both environment E2 and E4 exhibited the positive IPCA I score displayed similar interactions and their interaction was positive with genotype PM 5 (G4). However, both E1 and E3 showed positive interaction with genotype PM 15-17 (G34) and PM 15-13 (G30) as they both have negative IPCA I score (Fig 1a). The 99.98% of the treatment SS and 99.95% of interaction SS was explained by the AMMI II biplot (Fig 1b). The environments and genotypes that are most responsive when they are farthest from origin fit the worst. When environments and genotypes belong to the same sector, they interact positively; when they do not, they interact negatively. The Genotypes PM 15-17 (G34) and PM 15-13 (G30) were best for both E1 and E3 environment while, PM 5 (G4) was best for environments E2 and E4.

Plant height (cm)

The AMMI I biplot with the main effects plotted against the IPCA I scores explained 81.34% of the treatment SS. The average plant height for 40 genotypes in each environment measured was 68.95 cm in E1, 62.16 cm in E2, 67.03 cm in E3 and 53.47 cm in E4. Analysis of genotype main effects indicated that genotype HUM 12 (G13) had the highest average for plant height with low IPCA I score near to zero (-0.04) (Fig 2a). Among all the location-year testing environments, environments E1 and E3, displayed similar interaction effect, as they exhibited positive IPCA 1 score with above average plant height. However, environments E2 and E4 also displayed higher positive interaction, as they exhibited negative IPCA 1 score with below average plant height. The IPCA I and IPCA II mean square values were significant and they combinedly explained about 93.71%

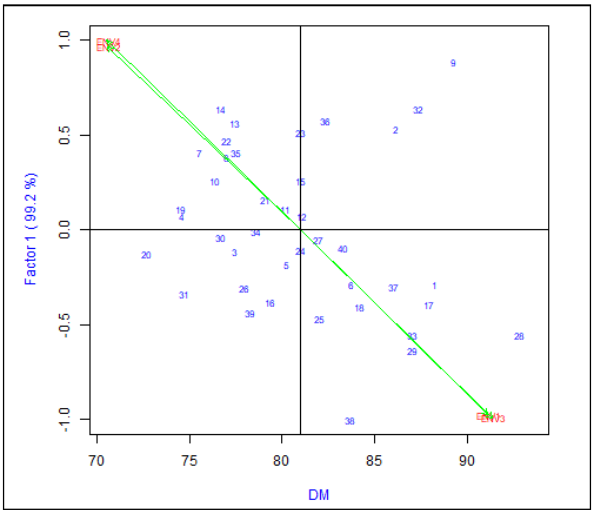


Fig 1a: AMMI I Biplot of days to maturity.

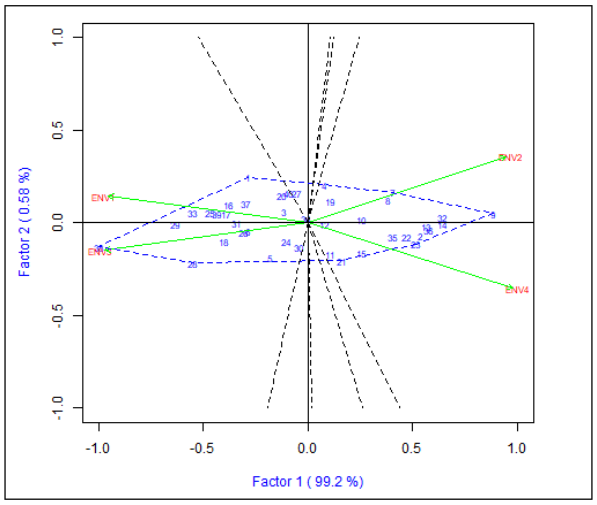


Fig 1b:AMMI II Biplot of days to maturity.

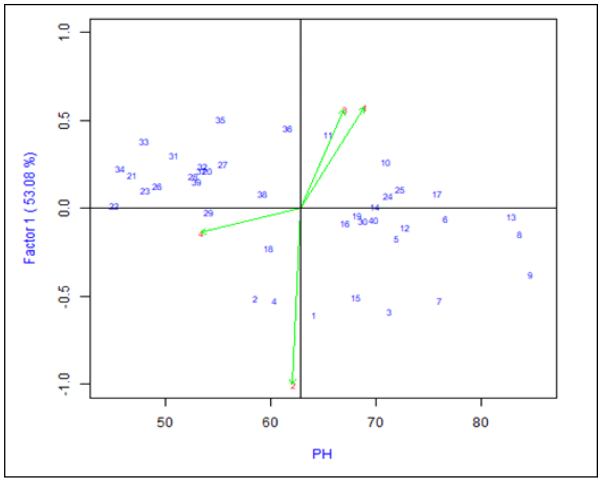


Fig 2a: AMMI I Biplot of plant height.

of treatment SS and 87.62% of interaction SS. For E2 and E4 environments, HUM 12 (G13) was best genotype. Genotypes PM 4 (G3), Sona Mung 1 (G8), PM 2 (G10), Pusa Vishal (G14) and PM 15-18 (G35) are the most responsive genotypes with high interaction effects (Fig 2b). Among all the responsive genotypes, Sona Mung 1 (G8) was highly responsive and particularly stable for E4, PM 2 (G10) for E3, PM 4 (G3) for E2 and Pusa Vishal (G14) for E1. Regarding the test sites, E1 was the most discriminating as indicated by the longest distance between origin and its marker with high IPCA II score.

Primary branches per plant

For primary branches per plant, AMMI I biplot model explains about 74.83% of the total treatment SS of leaving a residual of 7.28 primary branches per plant which can be a useful statistic for assessment of the overall goodness of fit of the model. The average primary branches per plant for 40 genotypes in each environment measured was 2.93 in E1, 2.54 cm in E2, 3.55 in E3 and 3.08 in E4. The environment E2 had IPCA score nearer to zero, having a very little interaction across genotypes and low discrimination among the genotypes. In the location-year environment, both, the environment E1 and E3 displayed similar interaction, as they both exhibited positive IPCA I score but the environment E3 is having the above average mean for primary branches per plant. While, E2 and E4 also displayed similar interaction, as they both exhibited negative IPCA I score but the environment E4 is having the above average mean for primary branches per plant. Genotype PM 15-19 (G36) and genotype SML 1815 (G18) had low IPCA I score as well as above average mean for primary branches per plant (Fig 3a). AMMI II biplot (biplot of IPCA I and IPCA II) captured about 92.53% of treatment SS and 82.30% of the interaction SS. In Fig 3b, sites fell into 4 sectors. The genotypes PM 5 (G4), PM 2 (G10), Pusa Vishal (G14), Vamban 2 (G17) and PM 15-14 (G31) were the most responsive genotypes with high interaction effects (Fig 3b). Genotypes PM 15-14 (G31) was best for the E1, PM 15-17 (G34) for E2,PM 5 (G4) and Pusa Vishal (G14) for E3 and PM 2 (G10) for environment E4.Site E1 was most discriminating location. Site E3 was not discriminating location because it had near zero IPCA 2 score compared to the E1.

Number of clusters per plant

AMMI I biplot (biplot of main effects and IPCA I) explained 82.93% of treatment SS and 79.37% of interaction SS, leaving the RMS residual of 38.09 clusters per plant. The average number of clusters per plant for 40 genotypes was measured as 14.68 for E1, 8.99 for E2, 15.01 for E3 and 10.82 for E4 respectively. According to the analysis of genotype, main effects showed that genotype LGG 460 (G40) had the highest mean (15.60) for number of clusters per plant among 40 genotypes over four environments. Considering the nature of responsiveness of genotype, PM 15-15 (G32), PM 15-19 (G36), PM 15-20 (G37) and

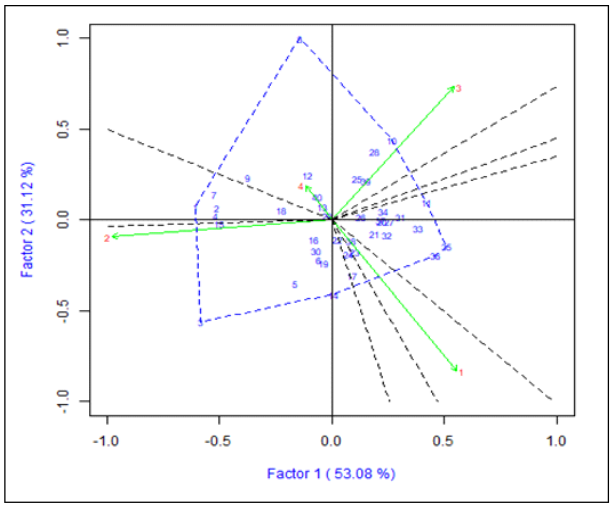


Fig 2b: AMMI II Biplot of plant height.

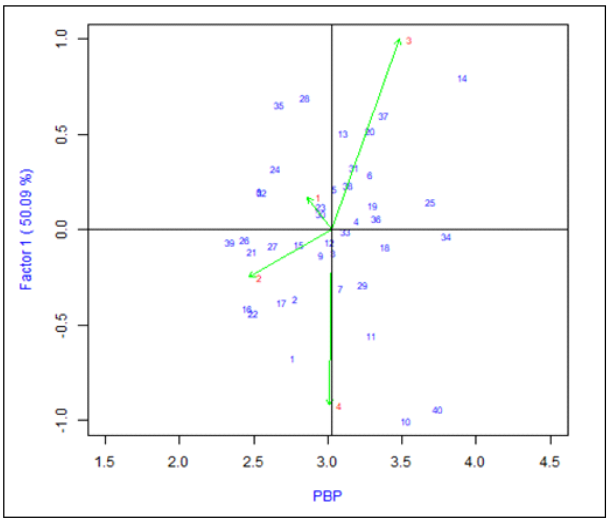


Fig 3a: AMMI I Biplot of primary branches per plant.

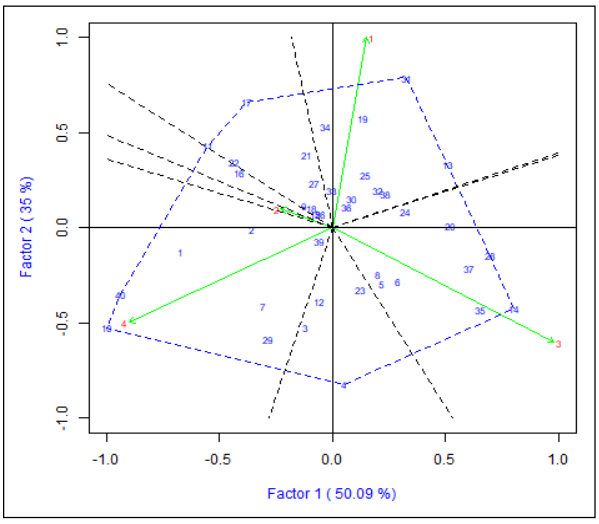


Fig 3b: AMMI II Biplot of primary branches per plant.

PM 15-16 (G30) exhibited above average mean for number of clusters per plant with low interaction effect (Fig 4a). Environments E2, E3 and E4 displayed similar interaction had negative IPCA I score, while E1 had positive IPCA I score. The environment E3 had highest mean for number of clusters per plants while E2 had lowest mean. AMMI II biplot (biplot of IPCA I and IPCA II) explained about the 97.13% of treatment SS and 85.79 % of the interaction SS, leaving the RMS residual about 32.40 clusters per plant. Genotypes PM 5 (G4), SML 1815 (G18), PM 15-2 (G19), PM 15-14 (G31) and LGG 460 (G40), were the genotypes with most responsiveness but with worst fit (Fig 4b). In Fig 4b, sites fell into 3 sectors. Genotypes PM 15-2 (G19) was best for the E1, PM 5 (G4) for E2 and E4, LGG 460 (G40) for E3. Site E3 was most discriminating location. Site E1 was not discriminating location because it had near zero IPCA 2 score compared to the E3.

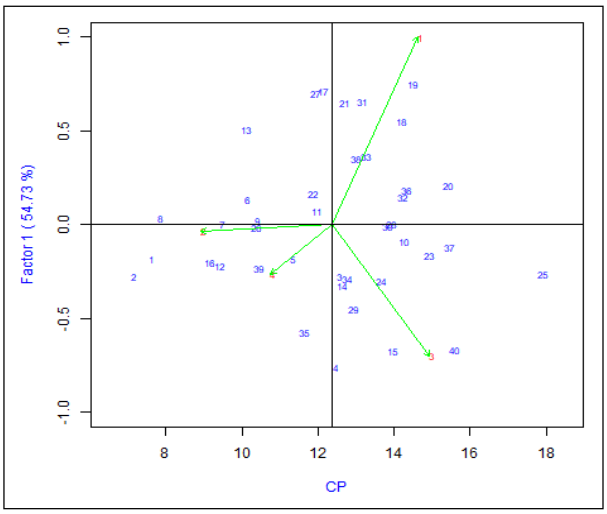


Fig 4a: AMMI I Biplot of number of clusters per plant.

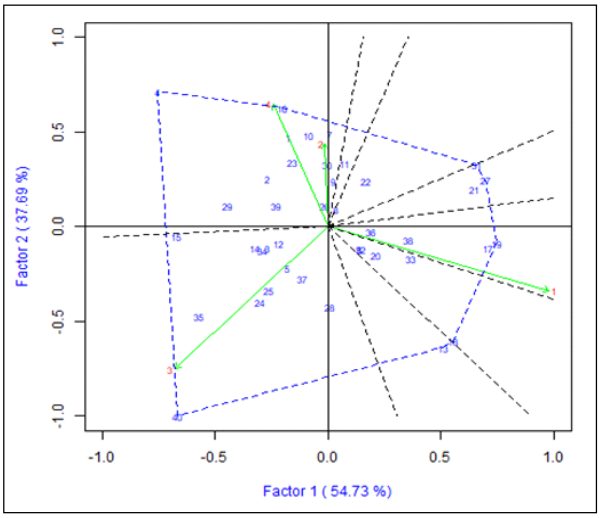


Fig 4b: AMMI II Biplot of number of clusters per plant.

Number of pods per cluster

The AMMI I biplot explains about 83.33% of treatment SS and 85.61% of interaction SS, leaving the RMS residual about 5.48 pods per cluster. The average number of pods per cluster for 40 genotypes was measured as 3.46 in E1, 2.69 in E2, 3.92 in E3 and 2.67 in E4 respectively. According to the analysis of genotype main effects showed that genotype PM 4 (G3) had the highest mean (4.19) for number of pods per cluster among 40 genotypes in 4 environments. When considering the nature of responsiveness of genotype, PM 15-15 (G32), PM 15-18 (G35) and PM 7 (G7) exhibited above average mean for number of pods per cluster with low interaction effect (Fig 5a). Among all the location-year environments, only E1 had negative IPCA I score while E2, E3 and E4 had positive IPCA I scores with E3 having the highest average for number of pods per cluster. Both IPCA I and IPCA II mean squares were significant and they cumulatively captured the 96.41% of the treatment SS and 86.45% of interaction SS. In AMMI II biplot, genotypes IPM 02-13 (G2), PM 4 (G3), PM 5 (G4), PM 2 (G10), HUM 12 (G13) and Pusa Vishal (G14) in the vertex were more responsive than other genotypes (Fig 5b). The genotypes PM 5 (G4) was best suited for E1, Pusa Vishal (G14) for E2 and E4. Site E3 was the most discriminating. Site E1 was not discriminating location because it had near zero IPCA 2 score compared to the E3.

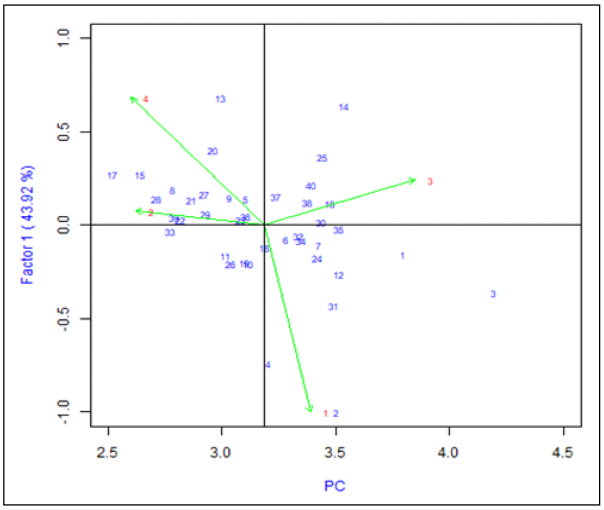


Fig 5a: AMMI I Biplot of number of pods per cluster.

Pod length (cm)

For pod length, the AMMI I biplot model contributed about 98.02% of the treatment SS and 79.23% of the interaction SS, leaving RMS residual of 6.63 cm pod length. The average pod length for 40 genotypes was measured as 7.77 cm in E1, 6.78 cm in E2, 7.69 cm in E3 and 6.83 cm in E4 respectively. According to the analysis of genotype main effects, genotype PM 15-16 (G33) had the highest mean (8.29 cm) for pod length among 40 genotypes over 4 environments. When considering the nature of responsiveness of genotype, the genotypes PM 15-18 (G35), PM 15-14 (G31), PM 15-21 (G38), PM 15-8 (G25) and PM

15-12 (G29) exhibited above average mean for pod length with low interaction effect (Fig 6a). In case of environments, E2 and E4 had negative IPCA I scores with below average pod length while E1 and E3 had positive IPCA I scores with above average pod length. The genotypes *viz.* HUM 12 (G13), ML 818 (G15), IPM 2-14 (G16), PM 15-3 (G20), PM 15-5 (G22), PM 15-8 (G25), PM 15-11 (G28) and PM 15-19 (G36) were responsive with high interaction effect (Fig 6b). IPCA I and IPCA II cumulatively contributed about 99.64% of the treatment SS and 98.37% of the interaction SS. The genotype PM 15-16 (G33) was best suited for E1, IPM 2-14 (G16) for E2 and E4, PM 15-3 (G20) and PM 15-11 (G28) for E3.

Number of seeds per pod

For number of seeds per pod, the AMMI I biplot model contributed about 92.96% of the treatment SS and 69.56% of the interaction SS, leaving RMS residual of 617.49 seeds per pod. According to the analysis of genotype main effects showed that genotype PM 9 (G12) had the highest mean (13.09) for number of seeds per pod among 40 genotypes over 4 environments. When considering the nature of responsiveness of genotype, the genotypes *viz.* SML 1815 (G18), PM 15-21 (G38), PM 2 (G10), PM 15-11(G28) and IPM 02-19 (G1) exhibited above average mean for number of seeds per pod with low interaction effect (Fig 7a). The average number of seeds per pod for 40 genotypes were measured as 11.89 in E1, 10.43 in E2, 11.17 in E3 and 10.60 in E4 respectively. In case of environments, E2 and E4 had negative IPCA I scores with below average mean while E1 and E3 had positive IPCA I scores with above average mean for number of seeds per pod. The most responsive genotypes were PM 4 (G3), PM 8 (G5), PM 2 (G10) ML 818 (G15), Vamban 2 (G17), PM 15-13 (G30) and PM 15-19 (G36) with above average mean but they fit least (Fig 7b). The AMMI II biplot accounted for 99.24% of treatment SS and 93.72% of interaction SS, leaving RMS

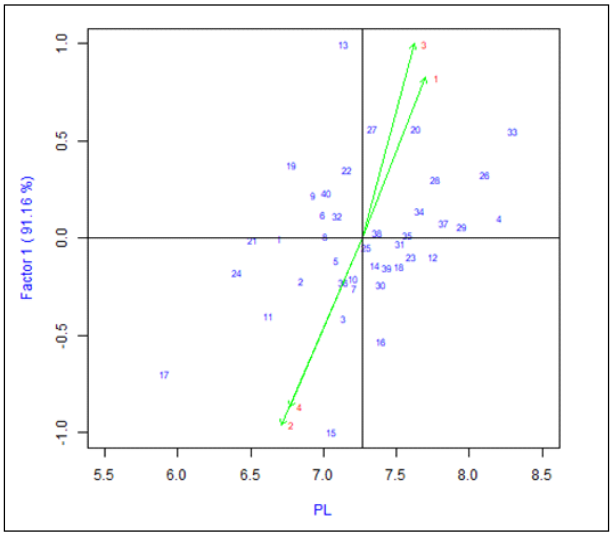


Fig 6a: AMMI I Biplot of pod length.

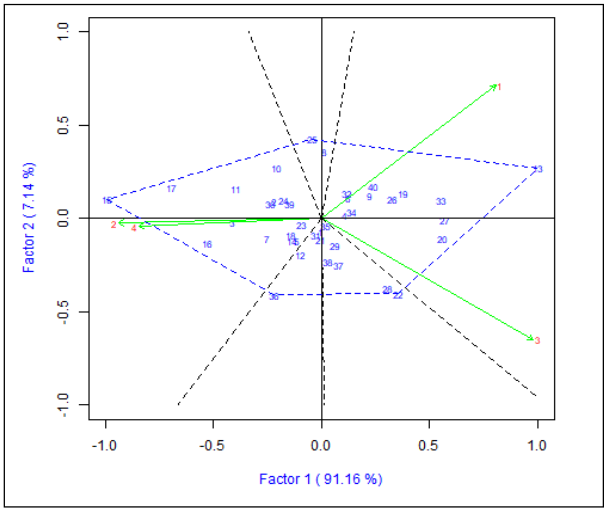


Fig 6b: AMMI II Biplot of pod length.

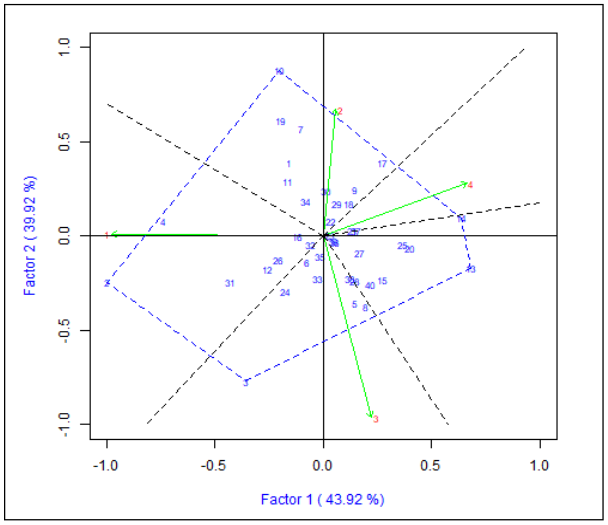


Fig 5b: AMMI II Biplot of number of pods per cluster.

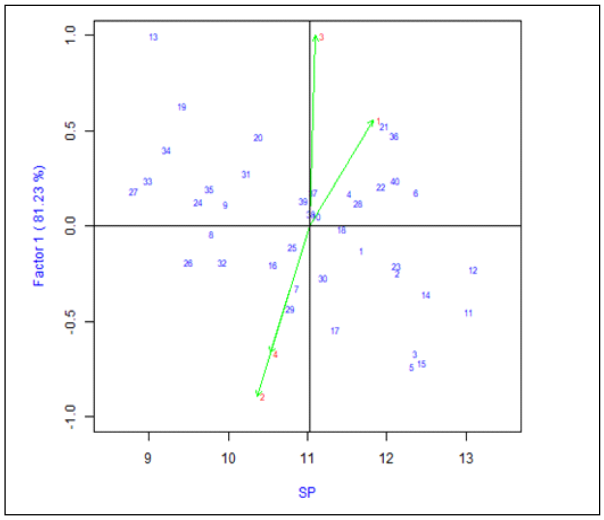


Fig 7a: AMMI I Biplot of number of seeds per pod.

residual of 8.12 seeds per pod. The genotype PM 15-19 (G36) was best for E1 environment, PM 4 (G3), PM 8 (G5) and ML 818 (G15) were best suited for E2 and E4, PM 2 (G10) for E3. The environment E1 was the most discriminating environment.

Total pods per plant

The AMMI I biplot explains about 89.34% of treatment SS and 84.86% of interaction SS. The average total pods per plant for 40 genotypes were measured as 46.40 in E1, 23.82 in E2, 48.78 in E3 and 23.47 in E4 respectively. According to the analysis of genotype main effects showed that genotype PM 15-8 (G25) had the highest mean (51.38) for total pods per plant among 40 genotypes over 4 environments. When considering the nature of responsiveness of genotype, PM 15-21 (G38), PM 15-15 (G32), PM 15-3 (G20) and PM 15-20 (G37) exhibited above average mean for total pods per plant with low interaction effect (Fig 8a). In case of environments, only E3 had negative IPCA I scores with highest average mean for total pods per plant while E1, E2 and E4 had positive IPCA I scores. The IPCA I and IPCA II combinedly contributed about 98.82% of the treatment SS and 90.52% of the interaction SS. The genotypes *viz.* PM 4 (G3), SML 1815 (G18), PM 15-2 (G19), PM 15-13 (G30) and LGG 460 (G40) were highly responsive with above average mean but they fit least (Fig 8b). The genotypes SML 1815 (G18) and PM 15-2 (G19) was best suited for environment E1 and for E2 and E4 sites, genotype PM 15-13 (G30) was best, while genotype LGG 460 (G40) was best for E3 site. Among all the environments, E1 was the most discriminating environment.Site E3 was not discriminating location, because it had near zero IPCA 2 score compared to the site E1.

100-seed weight

The AMMI I biplot (biplot of main effects and IPCA I) of 100-seed weight accounted about 95.05% of treatment SS and

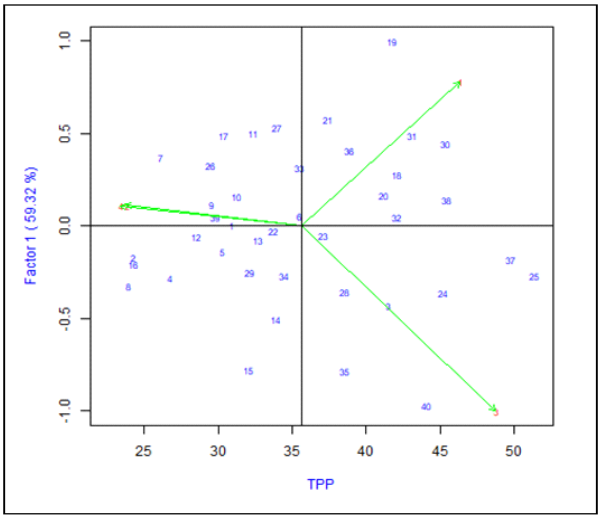


Fig 8a: AMMI I Biplot of total pods per plant.

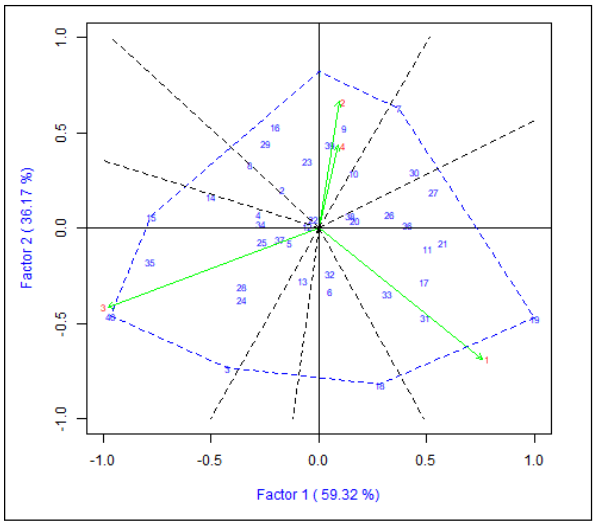


Fig 8b: AMMI II Biplot of total pods per plant.

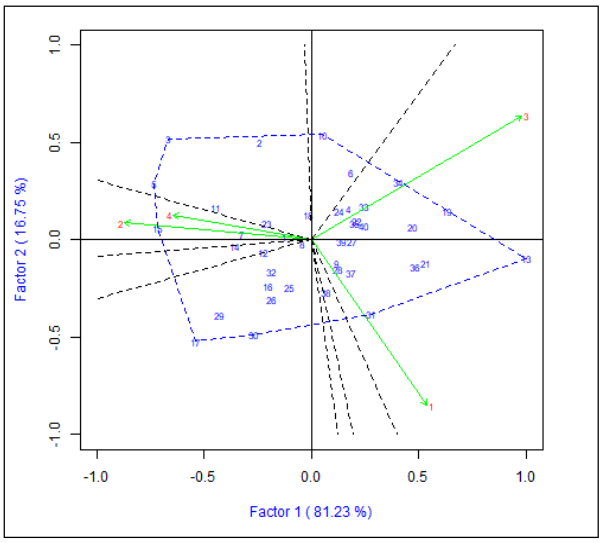


Fig 7b: AMMI II Biplot of number of seeds per pod.

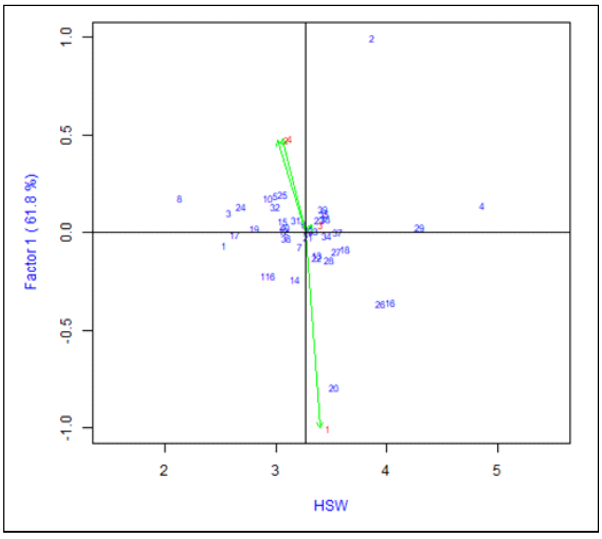


Fig 9a: AMMI I Biplot of 100-seed weight.

92.02% of the interaction SS, leaving the RMS residual of 2.83 g of 100-seed weight. The average 100-seed weight for 40 genotypes was measured as 3.47 g in E1, 3.09 g in E2, 3.40 g in E3 and 3.13 g in E4, respectively. According to the analysis of genotype main effects, the genotype PM 5 (G4) had the highest mean (4.86 g) for 100-seed weight among 40 genotypes over 4 environments. When considering the nature of responsiveness of genotype, PM 15-17 (G34), PM 15-4 (G21) and PM 15-12 (G29) exhibited above average mean for 100-seed weight with low interaction effect (Fig 9a). In case of environments, only E1 had negative IPCA I scores with highest average mean for 100-seed weight while E2, E3 and E4 had positive IPCA I scores and exhibited similar interaction effects. The AMMI II biplot (biplot of IPCA I and IPCA II) explained about 99.85% of the treatment SS and 95.20% of the interaction SS, leaving the RMS residual of 2.24 g of 100-seed weight. The genotypes IPM 02-13 (G2), IPM 2-14 (G16), PM 15-3 (G20), PM 15-10 (G27) and PM 15-21 (G38) had above average mean and hence, they are very responsive but they fit least (Fig 9b). Genotype IPM 2-14 (G16) was the best for E1 site, IPM 02-13 (G2) for E3 and PM 15-21 (G38) for E2 and E4 sites.

Seed yield per plant

AMMI I biplot (biplot of main effects and IPCA I) of seed yield per plant accounted for 93.25% treatment SS and 89.65% of the interaction SS, leaving the RMS residual of the 22.34 g seed yield per plant. The genotype LGG 460 (G40) had the highest yield of 8.83 g per plant according to the analysis of genotype main effects and except genotype Sona Mung 1 (G8) and IPM 02-19 (G1) all other genotypes have mean above 4 g per plant (Fig 10a). When considering the nature of responsiveness of genotype, IPM 02-9 (G9), PM 15-7 (G24), PM 15-20 (G37), PM 4 (G3) and PM 15-17 (G34) exhibited above average mean for seed yield per plant with low interaction effect (Fig 10a). The average seed yield per plant for 40 genotypes was measured as 10.77 g in E1, 3.81 g in E2, 8.08 g in E3 and 3.67 g in E4 respectively. Among the location-year environments, only environment E3 had negative IPCA I score while environment E1, E2 and E4 had positive IPCA I score with E1 having highest average mean for 100-seed weight. The genotypes, PM 5 (G4), ML 818 (G15), SML 1815 (G18), PM 15-3 (G20), PM 15-8 (G25), PM 15-10 (G27) and PM 15-11 (G28), had above average mean, hence they are very responsive but they fit least (Fig 10b). The AMMI II biplot (biplot of IPCA I and IPCA II) accounted for 99.44% of the treatment SS and 93.81% of the interaction SS, leaving the RMS residual of 17.72 g of seed yield per plant. In the Fig 10b, the sites fell into 3 sectors. For E1 site, best genotype was SML 1815 (G18) and PM 15-8 (G25); for E2 and E4 sites, genotype PM 15-10 (G27) was best suited, while for E3 site, genotypes PM 5 (G4), PM 15-3 (G20) and PM 15-11 (G28) were best suited.

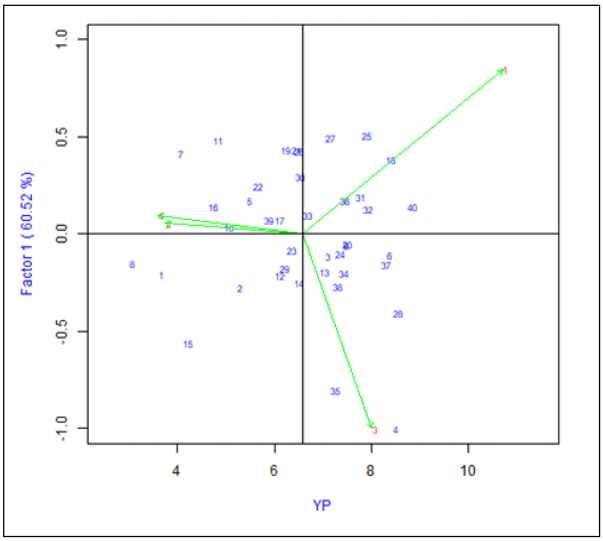


Fig 10a: AMMI I Biplot of seed yield per plant.

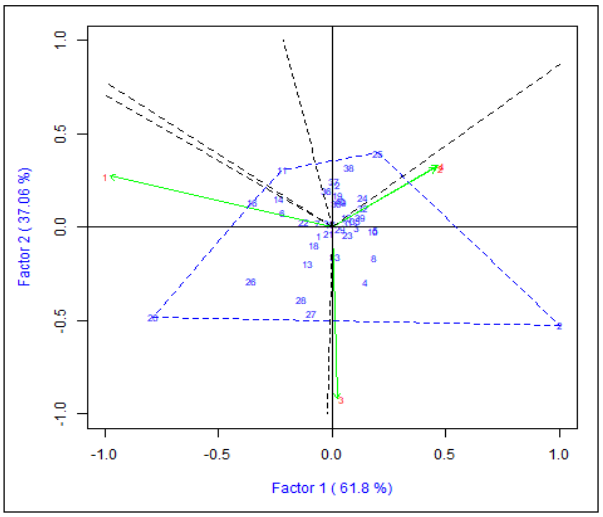


Fig 9b: AMMI II Biplot of 100-seed weight.

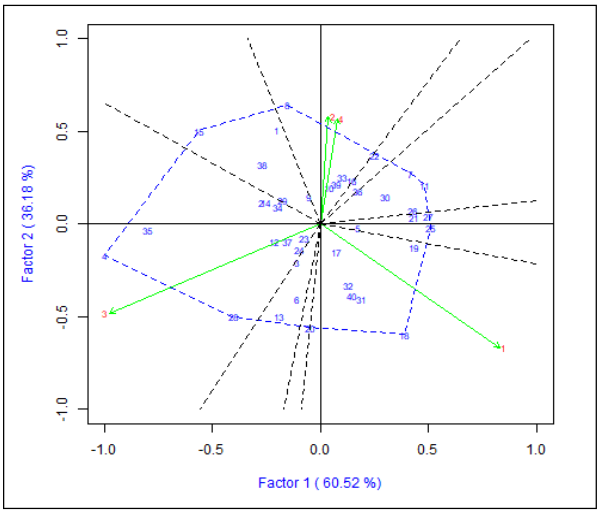


Fig 10b: AMMI II Biplot of seed yield per plant.

Site E1 was the most discriminating environment. Site E3 was not discriminating location because it had near zero IPCA 2 score compared to the site E1. Mean, IPCA I and IPCA II values of 40 mungbean genotypes for the trait seed yield per plant were given in Table 3.

There were observable differences found in growth, development and seed yield among the genotypes as they were subjected to drought conditions during their growth. Islam *et al.* (1994) reported that seed yield of the mungbean plants was significantly affected by water stress. Greater rooting depth in rainfed mungbean should assist to collect stored water from deeper depths, improving the plant's ability to give stable yield. Drought-stricken plants moved much more dry matter (assimilates) to their roots and stems, whereas well-watered plants redirected it to their pods and seeds (Kumar and Sharma, 2009). The presence of significant G×E interaction makes the overall means less reliable and often confounds efforts to identify high-yielding genotypes for a specific location and for broader adaptability. Pod number is also an important character affecting the seed yield (Board and Tan, 1995). High yielding low responsive genotypes have produced a higher pods per plant when compared to the grand mean. For example, genotypes PM 15-8 (G25), PM 15-20 (G37), LGG 460 (G40), SML 1815 (G18), PM 15-14 (G31) and PM 15-15 (G32) exhibited higher mean pods per plant and high yield. While, genotypes Sona Mung 1 (G8), IPM 2-14 (G16), SML 1082 (G7), IPM 02-13 (G2), IPM 02-19 (G1) and PM 2 (G10) had lower mean for pods per plant and have below average yields.

Flinn *et al.* (1977) reported that 69% of photosynthates produced by green pods were converted into dry matter of seeds. During drought conditions, if the green pod produces more photosynthates then it will be helpful in increasing the seed yield. So, plants with longer pods tend to produce denser seeds therefore increasing the 100-seed weight. For example, in the present investigation, the genotypes PM 5 (G4), PM 15-9 (G26) and PM 15-12 (G29) had highest pod length among the genotypes and they had high 100-seed weight which was higher than population mean.

CONCLUSION

G×E interaction in plant species is crucial to comprehend because it affects economic yield. It is important to investigate genotypic variation and choose genotypes with desirable traits because environmental factors have an impact on crop growth and development which will results in varied yields. Under rainfed conditions in various environments, the 40 mungbean genotypes in this study showed significant differences for yield and yield component traits. Based on mean performance over environments, genotypes PM 15-8 (G25), PM 15-20 (G37), LGG 460 (G40), SML 1815 (G18), PM 15-14 (G31) and PM 15-15 (G32) exhibited higher mean pods per plant and high yield. Therefore, the potential of these genotypes should be investigated for incorporation into mungbean improvement programs and their suitability for commercial cultivation.

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Conflict of interest

All authors declare that there is no conflict of any interest what so ever among them.

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