

AMMI analysis to comprehend genotype-by-environment ($G \times E$) interactions in rainfed grown mungbean (*Vigna radiata* L.)

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Abstract

The additive main effects and multiplicative interaction (AMMI) model was used to analyse the yield and yield component traits data of 58 mungbean genotypes grown in six moisture stress location-year environments. Main effects due to environments (E), genotypes (G) and $G \times E$ interaction were found significant for plant height, number of branches per plant, number of clusters per plant, number of pods per plant, 100 seed weight and grain yield per plant ($P < 0.01$). Gollob's test declared two components, Interaction Principal Component Axis 1 (IPCA 1) and IPCA 2, statistically significant ($P < 0.01$) for all the traits studied. The IPCA 1 of traits studied were accounted more than 62% of the $G \times E$ sum of squares. This study revealed that expression of mungbean genotypes varies between locations under drought condition, and brings out the suitability of specific genotype to rainfed condition through the biplot. Furthermore, biplot reflects maturity groups for the genotypes, with short duration mungbean at the bottom, medium duration genotypes in the middle and long duration genotypes at the top. AMMI provided such insight into $G \times E$ interactions. Trait by environment biplot clustered the location into four distinct groups. Site E4 was characterized by strong positive associations of yield, number of seeds per pod and 100 seed weight. Correlation between environmental scores and environmental variables gives a useful insight about the interaction effects. In the present study, statistical analysis of yield trials of mungbean under moisture stress with the AMMI model has revealed practical implications for plant breeding research towards drought tolerance in mungbean.

Keywords: Biplot; breeding; drought; Genotype \times Environment interaction; yield; *Vigna radiata*.

Abbreviations: AMMI: Additive Main effects and Multiplicative Interaction; IPCA: Interaction Principal Component Axis; RMS: Root mean square; PCA: Principal Component Analysis.

Introduction

Mungbean (*Vigna radiata* L.) is an important short season summer grown grain legume, well suited to smallholder production under adverse climatic conditions and commonly used in Indian cuisine (Vijayalakshmi et al., 2003). Like other legumes, mungbeans are high in protein, having around 25% of the seed dry weight and its amino acid profile is complementary to cereal grains. Mungbean is produced in tropical and sub-tropical rainfed environments with little or no impounding of water, and it is prone to drought when soil moisture or rainfall is inadequate to meet plant requirements. It is an important pulse crop in developing countries of Asia, Africa and Latin America where it is consumed as dry seeds, fresh green pods (Karuppanapandian et al., 2006). The regions that have grown traditionally mungbean are becoming limited due to water scarcity. Tolerance at emergence followed by seedling survival and establishment are important in the maintenance of optimal crop stand in the field and ultimately the economic yield (Bayuelo-Jimenez et al., 2002). Mungbean lacks osmotic adjustment, developmental plasticity and water extraction capacity during the vegetative period (Chiang and Hubbell, 1978). Rainfall distribution pattern varies across region and year. Hence, characteristics of drought events vary across regions. Low and variable rainfall during the early stage of crop development contribute to terminal drought stress. Drought at vegetative stage reduces biomass and at reproductive stage, it

can delay or prevent flowering. Therefore, target of rainfed mungbean program is to develop cultivars with stable grain yield under drought. Direct selection for yield under drought integrates whole-plant response to water stress, but it is complicated by the potentially large interaction of grain yield with environment (Lafitte and Courtois, 2002). Breeders have targeted the development of high-yielding, drought tolerant mungbean cultivars. High yielding was positively correlated to the relative water content and number of pods per plant (Kumar and Sharma, 2009). Among the yield components number of clusters per plant, number of pods per cluster and pod length are important for grain yield under stress (Biradar et al., 2007). Kang et al. (1985; 1986) selected drought tolerant genotypes in a wide range of mungbean germplasm lines. Tolerant lines possessed various traits, such as continued leaf lamina expansion, stem elongation, root dry weight, specific leaf weight and leaf area duration. Alternatively, research efforts have concentrated on targeting specific traits that can contribute to drought response (Lafitte, 1999). Traits such as, leaf water potential, photosynthesis, pod density and total biomass may contribute to higher yields under drought stress (Pannu and Singh, 1987). However, morphological and physiological traits have been shown and identified as marker for selecting drought tolerant genotypes, breeding for high yield potential in drought prone environments which remain unidentifiable, because of the

complexity in the nature of drought stress. Therefore to identify genotypes with stable grain yield under drought and to evaluate genotype \times environment ($G \times E$) interaction requires more sophisticated statistical tool. Additive main effects and multiplicative interaction (AMMI) compared to other models, was however espoused by Gauch (2006) thus affirming its importance in environment based selection for genotype breeding and selection for optimum performance. In addition, it was observed that AMMI uniquely separates G , E , and GE as required for most agricultural research purposes, and also separates structural variation from noise as well as any other method for the purpose of gaining accuracy (Anandan et al., 2009). The objective of this research are i) to determine the basis of adaptive response for yield and yield component traits in range of environments using the AMMI statistical model, and ii) to find association between genotype and trait and trait and environment using biplot technique. The water scarcity has multifarious effects on plant growth and productivity. Therefore present investigation provide insight into the selection strategies required for identifying superior genotypes for target growing environments.

Result

Homogeneity of variance tests indicated homogenous error variance for each trait in the six environments and allowed for a combined analysis across environments. ANOVA across environment indicated variances due to genotypes, environments and $G \times E$ interaction are highly significant ($P < 0.01$) for all the traits observed except number of seeds per pod (data not shown). AMMI analysis was continued further to estimate $G \times E$ for the traits exhibited significant $G \times E$ in pooled analysis. The AMMI ANOVA (Table 2) shows that genotype, environment, and the $G \times E$ interaction were significant ($P < 0.01$). The $G \times E$ interaction accounted for a high percentage of SS for number of branches per plant (52%) and genotypes accounted for a large percentage of SS remaining for all traits and ranged from 41 to 61% of the treatment variation. The $G \times E$ was highly significant and was further partitioned into four interaction PCA (IPCA) axes. The criterion of postdictive success for AMMI using all three replications and F -tests at the 0.05 probability level recommended including the first two IPCA in the model. The first IPCA components explained 44.27% (number of branches) to 61.67% (plant height). The second IPCA components explained between 21.49% (number of branches) and 29.42% (seed yield). The mean squares for the IPCA 1 and IPCA 2 cumulatively contributed more than 75% of the total $G \times E$ interaction for all the traits except number of branches per plant (66%), where 66% was not sufficient to consider a completely reliable interpretation of the behaviour of $G \times E$ interaction. The noise SS, pattern and relevant variation are presented in Table 3. Among all the traits studied, number of branches per plant and number of pods per plant accounted for 77% noise with less than 23% real structure. Treatment SS variation explained real and relevant patterns in the data and capturing more than the target percentages (relevant variation) would be noise and irrelevant features in the data. Except the traits number of branches per plant and number of pods per plant, remaining traits accounted for very close to the target percentage SS (Table 3). The first IPCA component of seed yield per plant explained 75% of the treatment SS, which was close to the target percentage SS explained (71%). Root mean square (RMS) residual is the difference between a model's expected values and the actual observed values. RMS residual of

AMMI 1 for seed yield per plant in absolute quantity is 15.4 g per plant, explaining the fitness of the model. The RMS residual of the AMMI 1 and 2 models for other traits are presented in Table 3.

To investigate the main effects and interactions across location - year environments, AMMI 1 and AMMI 2 biplots were constructed for yield and yield component traits (Fig 1a - 1j). AMMI 1 biplot of main effects are shown along the abscissa and the ordinate represents the first IPCA. The interpretation of a biplot assay is that if main effects have IPCA score close to zero, it indicates negligible interaction effects and when a genotype and an environment have the same sign on the IPCA axis, their interaction is positive; if different, their interaction is negative. The IPCA 1 versus IPCA 2 biplot (i.e. AMMI 2 biplot), explain the magnitude of interaction of each genotype and environment. The genotypes and environments that are farthest from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact positively; negatively if they fall into opposite sectors (Anandan et al., 2009).

Plant height

The AMMI 1 biplot with the main effects plotted against the IPCA 1 scores explained 88% of the treatment SS. The average plant height for the 58 genotypes in each environment measured was 41.36 cm in E1, 35.81 cm in E2, 41.37 cm in E3, 40.00 cm in E4, 35.15 cm in E5 and 43.89 cm in E6. Analysis of the genotype main effects showed that G12 had the tallest plant (68.67 cm). All other genotypes secured 28 cm or more except G30 (26.99 cm). Among the environments, E2 and E5 had the shortest averaged plant height (35 cm). In location-year environments, E1, E3, E4 and E6 displayed similar interaction effect, as they exhibited negative IPCA with above average plant height. However, environments E2 and E5, the same environment in two different years, displayed higher positive interaction than others with below average plant height (Fig 1a). AMMI2 biplot accounted for 95.6% of treatment SS and 86.1% of interaction SS (Fig 1b). The genotypes and environments that are farthest from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact positively; negatively if they fall into opposite sectors. The best genotype with respect to sites E2 and E5 was G5; genotypes 40 and 21 were best for sites E3 and E6; and for E1 and E4 the best genotypes were G38 and G13.

Number of branches per plant

The AMMI 1 biplot model for the number of branches per plant captured 71.26% of the treatment SS, leaving a RMS residual of 7.6 branches per plant (Fig 1c). The average number of branches per plant for 58 genotypes in each environment measured was 1.78 in E1, 1.47 in E2, 1.58 in E3, 1.59 in E4, 1.55 in E5 and 1.57 in E6. Among all the location - year testing environments, environments E3 and E6 displayed similar interaction effect, as they exhibited positive IPCA with above average number of branches per plant. However, E1 and E4 the same environment in two different years, displayed higher positive and negative interaction respectively. Analysis of the genotype main effects showed that G34 and the maximum number of branches per plant showed minimum responsiveness. The mean squares for the IPCA 1 and IPCA 2 were significant and they cumulatively

Table 1. Temperature, status of rainfall, relative humidity, soil properties, latitude, altitude and code for each environment is given

Site	E1	E2	E3	E4	E5	E6
Environmental factors	(Illavampatti)	(Mettupallayam)	(Chinnapanikkanur)	(Illavampatti)	(Mettupallayam)	(Chinnapanikkanur)
Temp. (Max)	37.5	38.2	38	38.5	39.3	39.5
Temp. (Mini)	25.2	27	27.1	26.1	27.5	27.2
RH (%)	69	75	68	68	69	68
Rainfall (mm)	71	34.5	30	81	50.5	21
Soil texture	Red sandy soil	Black cotton soil	Red sandy soil	Red sandy soil	Black cotton soil	Red sandy soil
Soil pH	7.1	8.0	7.2	7.4	8.1	7.4
Latitude	11° 39'N	11° 38'N	11° 39'N	11° 39'N	11° 38'N	11° 39'N
Longitude	77° 56' E	77° 56' E	77° 56' E	77° 56' E	77° 56' E	77° 56' E
Altitude (ft)	771	788	773	771	788	773

Table 2. Analysis of variance for AMMI model of mung bean for yield and yield component traits under drought

Source of variation	df	Plant height (cm)	No. of branches plant ⁻¹	No. of clusters plant ⁻¹	No. of pods plant ⁻¹	100 seed wt. (g)	Grain yield plant ⁻¹ (g)
Treatments	347	314.8**	0.947**	10.3**	97.6**	0.62**	10.45**
Genotypes (G)	57	1137.7**	2.626**	32.8**	362.4**	1.55**	38.57**
Environments (E)	5	2053.3**	1.878**	85.0**	335.4**	9.75**	72.73**
G*E Interaction	285	119.7**	0.595**	4.4**	40.5**	0.28**	6.54**
IPCA I	61	345.0**	1.229**	11.5**	108.5**	0.75**	8.42**
IPCA II	59	141.8**	0.616*	5.2**	55.2**	0.32**	6.31**
IPCA III	57	50.2	0.492	2.1	14.1	0.12	2.01
IPCA IV	55	25.3	0.367	1.5	9.1	0.08	1.51
Residual	53	8.7	0.188	1.0	6.9	0.05	0.74
Error	684	42.4	0.458	2.5	34.1	0.10	4.13
Total	1043	134.1	0.618	5.1	56.0	0.27	6.33

*P < 0.05 and **P < 0.01

contributed to 82.34% of the treatment SS, leaving a RMS residual of only 5.5 branches per plant. In AMMI 2 biplot, genotypes 15, 21, 23, 26 and 5 in the vertex were more responsive than other genotypes (Fig 1d). Among all the genotypes, G15 was responsive and particularly stable for E1, E3 and E6. Regarding the test sites, E5 was most discriminating as indicated by the longest distance between its marker and the origin. However, due to its large IPCA 1 and IPCA 2 score, genotypic differences observed at E₅ may not exactly reflect the genotypes in average number of branches per plant.

Number of clusters per plant

The percentage of the treatment SS captured by an AMMI biplot is a useful statistic for assessing the overall goodness of fit. The AMMI 1 model captures 84.26% of the treatment SS, leaving a RMS residual of 15.9 clusters per plant. The environment E4 scores near zero had a little interaction across genotypes and low discrimination among genotypes (Fig 1e). In location – year environment, E1, E2, E3, E5 and E6 had negative values for IPCA 1 with low main effect except in E₁. Genotypes with maximum number of clusters per plant with low IPCA score are G34 and G12. The biplot of two IPCA axes, together accounted for 92.8% of treatment SS and 80% of interaction SS. This AMMI 2 model leaves an RMS residual of 11.6 clusters per plant. In figure 1f, the sites fell into four sectors: the best genotype with respect to site E4 was G26. Genotype 5 was best for sites E2 and E5; genotype 15 was best for sites E3 and E6; and for E1 the best genotype was G21. Among all the environments, E4 was most discriminating site as indicated by the longest vector with the largest IPCA 2 score.

Number of pods per plant

The biplot of AMMI 1 (Fig1g) captured 85.46% of the treatment SS, leaving a RMS residual of 40.9 pods per plant. Analysis of the genotype main effects showed that G34 had the highest pod numbers per plant (33). All other genotypes produced 9 numbers of pods or more except G4 (8 pods per plant). Among the environments, E1 had the lowest number of pods and E5 had the highest number of pods per plant. When considering the nature of responsiveness of genotype, G34, G12 and G22 exhibited high main effect with low interaction effect. Among all the location-year testing environments, E3 and E4 displayed differences in interaction effect but not in main effect with above average number of pods per plant. IPCA 1 and IPCA 2 cumulatively contributed to 95% of the treatment SS, leaving a RMS residual of 29.4 pods per plant. Genotypes G5, G57, G14, G13, G1 and G12 were the most responsive genotypes, while E2 was most discriminating location (Fig 1h). Site E5 was not the most discriminating, but genotypic differences at E5 should be highly consistent with those averaged over sites, because it had near-zero IPCA 2 scores compared to the other except that the IPCA 2 score for E1 was smaller than that of E5.

100 seed weight

The AMMI 1 model captures on SS of 182.33, which is 84.7% of the treatment SS and 58.03% of interaction SS, leaving a RMS residual of 3.73 g for 100 seeds. Environments E2 and E5 showed more variability for interaction effects. On the other hand, environment E1 and E4, the same environment in two different years, were clustered together and they exhibited positive IPCA 1 score

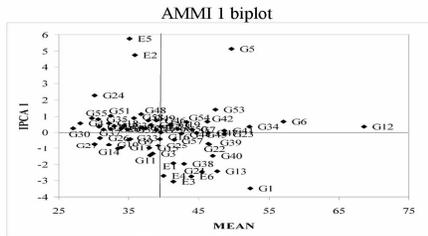


Figure 1a. Plant height

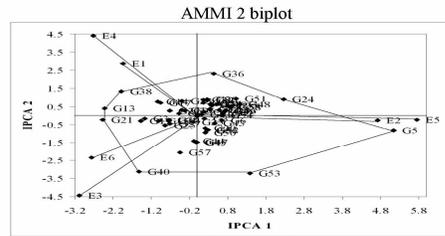


Figure 1b. Plant height

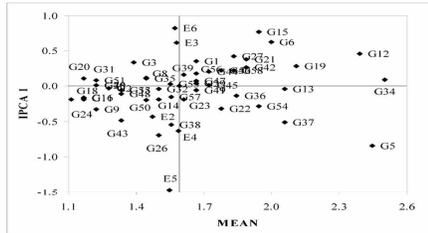


Figure 1c. No. of branches plant⁻¹

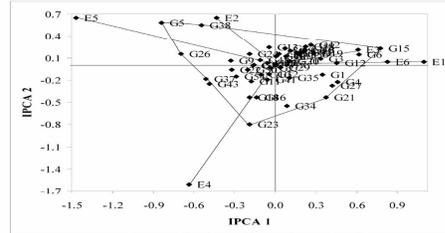


Figure 1d. No. of branches plant⁻¹

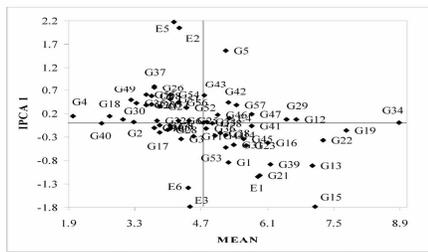


Figure 1e. No. of clusters plant⁻¹

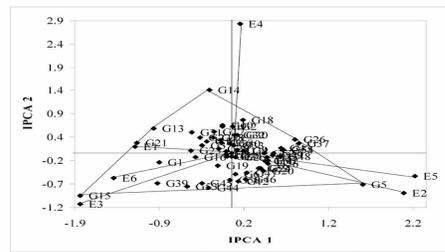


Figure 1f. No. of clusters plant⁻¹

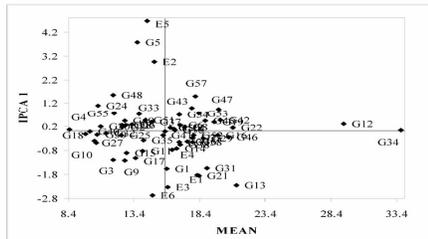


Figure 1g. No. of pods plant⁻¹

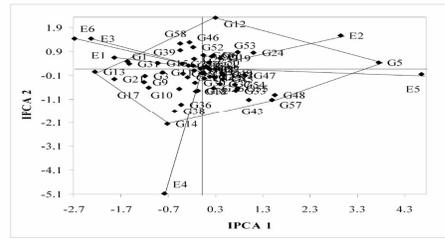


Figure 1h. No. of pods plant⁻¹

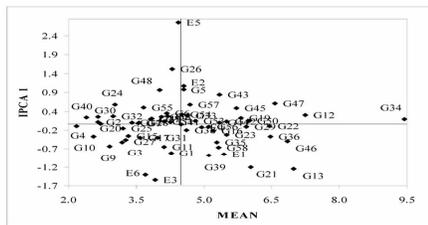


Figure 1i. Grain yield plant⁻¹

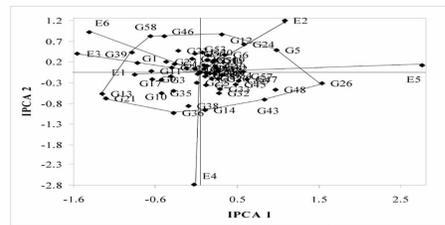


Figure 1j. Grain yield plant⁻¹

Figures 1(a-j). AMMI 1 and 2 models for the mung bean data of yield and yield component traits under drought. G - genotype; E - environment; G suffix with number represents genotype from 1 to 58; E suffix with number represents environment number from 1 to 6.

with above average 100 seed weight. Genotypes G40, G50, G45, G22, G57, G55 and G37 differ in their main effect considerably with low interaction effect. The AMMI 2 biplot captured 84.7% of treatment SS, leaving a RMS residual of 2.63 g for 100 seeds. Among the six environments, E1 alone exhibited interaction considerably lower than others. However, the three locations E1, E2 and E3 were cluster with their corresponding locations E4, E5 and E6 respectively in the same sector. Among all the genotypes, G35, G38, G48, G16, G22, G27, G39, G23 and G36 were more responsive and the remaining genotypes were positioned around the plot origin with low interaction effect.

Grain yield per plant

Analysis of the genotype main effects showed that G34 had the highest yield (9.45 g/plant). All other genotypes yielded 2.4 g or more except G4 (2.18 g/plant). Among the environments, E1 had the highest mean yield (5.44 g/plant). The AMMI 1 model for the grain yield captures 84.8% of the treatment SS, leaving a RMS residual of 15.4 g per plant. Among all the location-year testing environments, environments E2, E3, E4 and E5 displayed similar main effects, but they differed in their interactions effects (Fig 1i). The IPCA 1 score of genotypes G34, G12, G19, G22, G29,

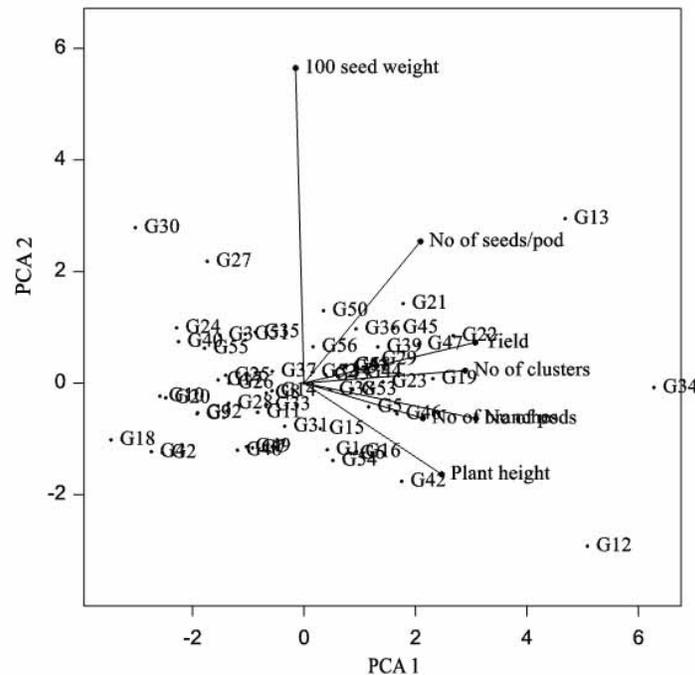


Figure 2. A genotype by trait biplot representing 58 mung bean genotypes measured for seven traits under drought (data were averaged across locations). G – genotype; G suffix with number represents genotype from 1 to 58; Biplot was constructed to visualize the genetic correlation among traits, and evaluation of the genotype on the basis of multiple traits

G50, G53 and G56 are similar but they show a different mean yield response (above the grand mean). The biplot of two IPCA axes, together accounted for 93.4% treatment SS and 77.63% of interaction SS. AMMI 2 model leaves an RMS residual of 11.05 g per plant. In the figure 1j, the sites fell into three sectors. The best genotypes with respect to sites E2 and E5 were G12 and G5; genotypes G36, G21 and G13 were best for sites E1 and E4; and for E3 and E6 the best genotypes were G39, G58 and G46. Regarding the test sites, E4 was most discriminating, due to its large IPCA 2 score, genotypic differences observed at E4 and this may not exactly reflect the genotypes in average yield over all sites. Site E5 was not the most discriminating, but genotypic differences at E5 should be highly consistent with those averaged over sites, because it had near-zero IPCA 2 scores compared to the others except that the IPCA 2 score for E1 was smaller than that of E5.

Correlation between IPCA axes and external factors

Correlation between environmental IPCA scores and environmental factors varied in relationship from moderate to high (Table 4) Axis 1 of plant height positively correlated with minimum temperature, relative humidity, soil pH and altitude and negatively correlated with latitude. On the other hand, Axis 2 of plant height positively correlated with rainfall and negatively correlated with minimum temperature. Axis 1 of branches per plant exhibited significantly negative association with maximum and minimum temperature, soil pH, and altitude, while axis 2 exhibited positive association with minimum temperature, relative humidity, soil pH and altitude. The r^2 between axis 1 of pods per plant and soil pH was found to be 0.944**, while axis 2 had an r^2 of -0.779** with rainfall. Axis 1 and 2 of grain yield per plant was

positively correlated with temperature, relative humidity, soil pH and altitude. A significant negative correlation was observed between environmental factor rainfall and PCA 2 score of grain yield.

Discussion

Understanding of $G \times E$ interaction in plant species is important because it has implications for economic yield. In view of influence of environmental factors on crop growth, it is necessary to explore this variation among genotypes and select materials with desirable traits. The mungbean genotypes in this study revealed significant difference for yield and yield component traits under drought in diverse environments. The selected study material comprised of diverse genotypes of improved varieties, advanced breeding lines and land races. Inclusion of land races is an imperative in any research investigation, since they are adaptable to local environment and source of valuable genetic resources (Anandan et al., 2011). Plant drought tolerance is modulated by the genetic potential and prevailing environmental conditions. Plant grown in water stress condition often depict reduced morphological (plant growth, leaf lamina expansion and root dry weight) (Kang et al., 1985) and physiological (leaf water potential, evapotranspiration, transpirational cooling, photosynthetic rate) (Pannu and Singh, 1987) expression. The AMMI analysis of variances indicated highly significant variation for genotypes, environments and $G \times E$ interaction for all the traits, except number of seeds per pod. Suggesting, genotypes exhibited differential expression under soil moisture stress condition. There is a decreasing contribution of the $G \times E$ SS with an increasing number of IPCA axes. For example, IPCA 1 is two times larger than IPCA 2. The Gollob's test (Gollob, 1968) on the IPCAs

Table 3. The errors from uncontrolled variation, percent genotype × environment interaction explained by each statistically significant interaction principal component axis (IPCA), IPCA captures percent interaction and root mean square (RMS) residual of AMMI (in percent).

		Plant height (cm)	No. of branches plant ⁻¹	No. of clusters plant ⁻¹	No. of pods plant ⁻¹	100 seed wt. (g)	Grain yield plant ⁻¹ (g)
Errors from uncontrolled variation	Noise SS	35.41	77.05	56.37	84.19	36.38	40.63
	Real structure (pattern)	64.59	22.95	43.63	15.81	63.62	59.37
	Relevant variation (target)	79.54	57.40	68.02	66.36	64.11	70.53
Percent genotype × environment interaction	% G × E of IPCA 1	61.67	44.27	55.70	57.33	58.03	48.21
	% G × E of IPCA 2	24.52	21.49	24.29	28.21	24.14	29.42
IPCA captures percent interaction	% of IPCA 1	78.63	68.40	72.31	80.51	62.07	74.79
	% of IPCA 2	86.29	79.48	80.94	90.12	70.86	83.43
Root mean square (RMS) residual of AMMI	RMS AMMI I	68.71	7.63	15.91	40.89	3.73	15.40
	RMS AMMI II	43.07	5.49	11.62	29.42	2.63	11.05

Table 4. Correlation between IPCA axes and environmental factors for the AMMI analysis of yield and yield component traits of mung bean under drought

Characters	IPCA axes	Temp. (Max)	Temp. (Mini)	RH (%)	Rainfall (mm)	Soil pH	Latitude	Altitude (ft)
Plant height (cm)	PCA 1	0.247	0.449**	0.659**	-0.11	0.943**	-0.993**	0.980**
	PCA 2	-0.247	-0.721**	0.018	0.919**	-0.043	0.058	-0.162
No. of branches plant ⁻¹	PCA 1	-0.419**	-0.441**	-0.248	-0.225	-0.831**	0.736**	-0.708**
	PCA 2	0.07	0.477**	0.457**	-0.644**	0.453**	-0.604**	0.653**
No. of clusters plant ⁻¹	PCA 1	0.262	0.342**	0.639**	0.117	0.942**	-0.933**	0.898**
	PCA 2	-0.046	-0.522**	-0.320*	0.816**	-0.225	0.360**	-0.435**
No. of pods plant ⁻¹	PCA 1	0.267*	0.419**	0.560**	0.049	0.944**	-0.962**	0.938**
	PCA 2	-0.044	0.342**	0.331*	-0.779**	0.081	-0.232	0.299*
100 seed wt. (g)	PCA 1	-0.022	0.054	0.618**	0.340*	0.792**	-0.861**	0.802**
	PCA 2	0.310*	0.670**	0.271*	-0.852**	0.375**	-0.447**	0.526**
Grain yield plant ⁻¹ (g)	PCA 1	0.328*	0.348**	0.410**	0.184	0.901**	-0.893**	0.858**
	PCA 2	0.099	0.466**	0.451**	-0.831**	0.263*	-0.380**	0.449**

* $P < 0.05$ and ** $P < 0.01$

declared two components significant, while a third IPCA is non significant. This is in line with Yan et al. (2002) that most of the interaction occurs in the first few axes. Conversely, Sivapalan et al. (2000) recommended an AMMI model with the first four IPCAs. The residual SS of AMMI for all the traits were non significant with minimum residual mean SS and demonstrates a greater accuracy of the model. The genotypes utilized in the present investigation are adapted to tropics and subtropics and they have short to long maturity period. The AMMI I biplot of yield (Fig 1i) clearly groups the genotype related to maturity period, with early duration genotype at the bottom (G1, G11, G35, G58, G39, G21 and G13), long duration genotype at the top (G43, G5, G48 and G26) and remaining genotypes grouped in the middle are medium duration mungbeans. Drought or moisture stress did not effect days to flower initiation significantly (Kumar and Sharma, 2009). However, days to flowering effects grain yield. Longer days to flowering, directly influences source availability and accumulation of assimilate, which are later remobilized for grain production. A shorter day to flowering helps to avoid unfavourable growing conditions (Yoshida, 1981). In the present experiment, the mungbean cultivars exhibited differences in growth and grain yield when subjected to drought conditions during the growing season. This is in line with Thomas et al. (2004). The presence of significant G × E interaction renders overall means, less reliable and often confounds attempts at identifying high yielding genotypes for specific site as well as for wide adaptability. To gain insight into the interaction, AMMI biplot has a clear agricultural interpretation (Zobel et al., 1988). Among the tested genotypes G34, G12, G47, G22, G45, G23, G53, G6, G41, G44 and G29 (medium duration);

G13, G21, G35, G58 and G39 (early duration) and G43 and G5 (late maturing) exhibited high yield irrespective of their responsiveness (Fig 2). High yielding low responsive genotypes exhibited higher plant height than above average with low interaction effect. Similarly, poor yielding low responsive genotypes exhibited shorter plant height. For example, less responsive genotypes 12 and 34 produced significantly higher grain yield, which also showed higher values for plant height. On the other hand, the least responsive genotypes G2, G30, G4 and G40 exhibited lesser yield, which also showed lower values for plant height. The plant may be stunted due to the threshold turgor for stem cell elongation is not attained under moisture stress. Kang et al. (1985) reported significant reduction in plant height of mungbean cultivars grown without water when compared to the same grown with water. Thus, G × E interaction biplot of plant height provides additional information regarding drought response. The increased plant height by adaptive genotypes, certainly harvest more sunlight to prepare more photosynthates. Sangakkaran et al. (2000) reported that drought tolerant mungbean diverted more carbon to roots under moisture stress. When mungbean is grown under rainfed condition, greater rooting depth should help to acquire stored water from various depths to improve stability in grain yield. Droughted plants diverted significantly higher dry matter to roots and stems, while well watered plants diverted to pods and grains (Kumar and Sharma, 2009). The grain yield of nine low responsive genotypes (G12, G19, G22, G29, G34, G42, G44, G50 and G53) pooled over environments was not significantly reduced than average yield with a reduction in soil moisture. The genotypes which showed an enhanced yield over environments has higher

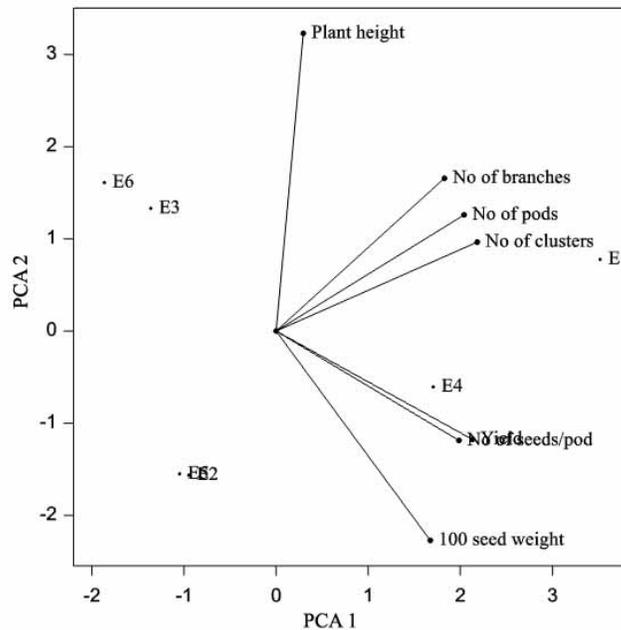


Figure 3. A trait association by environment biplot, based on the six location-year environment data on mung bean under drought. E - environment; E suffix with number represents environment number from 1 to 6; Biplot was constructed to evaluate environment on the basis of multiple traits.

plant height, number of branches, number of clusters, number of pods, 100 seed weight and number of seeds per pod (Fig 3) than population mean with less responsiveness (Fig 1a-1j). The increase in yield among the genotypes might have been due to continuous leaf expansion and root even under conditions of reduced soil moisture (Kang et al., 1986). Wahid and Rasul (2004) reported that green pods contributes upto 20% of carbon from its own photosynthesis. Many reports document the changes in seed yield as reliable yardsticks to appraise drought tolerance. Drought tolerance at the reproductive stage is the most important in terms of economic yield. The development of reproductive organs, which is under the control of photoassimilate production and partitioning by the source tissues, is at this stage the most critical (Taiz and Zeiger, 2002; Wahid and Rasul, 2004). Therefore, increased drought at this stage, has a pronounced effect on fruit development and yield. This study revealed the $G \times E$ interaction pattern on grain yield, plant height number of branches, pod number, cluster number and 100 seed weight in mungbean in response to moisture stress. The environments show much variability in both main effects and interactions. Trait association by environment biplot, clustered environments into four distinct groups: Group 1 includes E1, group 2 consists of E4, group 3 includes E2 and E5 and Group 4 consists of E6 and E3. Among all the location-year testing environments, environment E1 interacts with genotypes in much of the same way as E4. These two sites displayed low interaction effect with above average main effect. Therefore, E1 and E4 were classified as low responsive environments and suitable site to study the response of drought tolerant mechanism in mungbean. Trait association by environment biplot (Fig 3) separated E1 and E4, the same environment in two different years. The sites E2 and E3 clustered with their corresponding environments (years) E5 and E6 respectively. The clustering of corresponding sites can be explained by similar weather

condition and rainfall pattern in both years. Soil texture, distribution, and amount of rainfall received differentiated the environment E2 and E5 from the other four environments. Rainfall received during germination and late reproductive stage and nature of Black Cotton Soil has differentiated E2 and E5 from the rest of the environments. Black cotton soil has good water holding capacity with sufficient phosphorous and other minerals required for the growth of legumes. Separation between E1 and E4 might have been due to differences in total rainfall received during the crop growth. In location-year testing environments, environments E1 and E4 received higher rainfall (Table 2) than other environments. Similarly, there was sufficient rainfall during germination, vegetative and reproductive stage. However, environment E1 has received rainfall during initial reproductive stage, while E4 received rainfall during two intervals of its reproductive stage. Therefore, E4 has been plotted near grain yield in trait association by environment biplot (Fig 3). Among all the locations, E5 has been categorized as highly interactive environment, because it exhibited high positive interaction (IPCA score) effect with above average main effect for most of the traits studied. The high interaction effect of E5 might probably be due to higher amount of rainfall received than its corresponding E2 environment. Furthermore, the environments E3 and E6 displayed lower main effects and higher negative interactions than other environments, which can be explained by differences in available soil moisture, soil texture, rainfall and nutrient status of the soil. Correlations between environmental factors and the environment IPCA scores can lead to useful biological interpretation of the interaction effects. All traits of environmental IPCA axes were correlated with environmental factors with moderate to high interaction effect in positive or negative direction. IPCA axes 1 of plant height, number of clusters, number of pods per plant and grain yield was favoured by environmental factors

like minimum temperature, high relative humidity, increased soil pH and reduced photoperiod. IPCA axis 2 of plant height and clusters per plant was highly favoured by rainfall. Correlating the external environmental factors with the environmental IPCA scores will help to identify the particular factor responsible for the interaction effects.

Materials and methods

Plant material and experimental details

The experiment was conducted during the summer season at Salem district North West zone of Tamil Nadu, India during 2009-2010 in three locations over two years. The test environments were chosen to represent environments typically rainfed, which receives less than 80 mm rainfall during single mungbean cropping period. The location details, planting dates, soil types, rainfall distribution pattern were presented in Table 1. The Mungbean genotypes used in this study comprised two genetically distinct approved varieties (Co 6 and Co 7), 39 promising advanced lines and 17 local cultivars were evaluated in six environments. At each location the experiment was a randomized complete block design with three replications. Essential plant nutrients, 25 kg ha⁻¹ N (urea), 17.4 kg ha⁻¹ P₂O₅ (Single super phosphate), 20 kg ha⁻¹ K₂O (muriate of potash) were supplied as basal dose before sowing. Two rows, 4m in length were planted with a spacing of 30 cm between rows. Each row contains 40 plants spaced at 10 cm apart. Plots were managed conventionally following the established normal practices. Plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod and grain yield per plant (g) was observed in 10 plants selected at random in each replication. A sample of 100 seeds were collected at random for each genotype to estimate 100 seed weight and presented in grams.

To analyze the G × E interaction, the AMMI model was used (Gauch, 1988). The AMMI statistical model is a combination of customary analysis of variance (ANOVA) and principal component analysis (PCA). The equation of this model is:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \epsilon_{ger}$$

with Y_{ge} is the trait of genotype g in environment e ; μ is the grand mean, α_g is the genotypes deviation from grand mean and the environment deviation β_e , λ_n is the eigenvalue of PCA axis n ; γ_{gn} and δ_{en} are the genotype and environment PCA scores for PCA axis n ; ρ_{ge} is the residual of AMMI model and ϵ_{ger} is the random error. AMMI uses ordinary ANOVA to analyze main effects and principal component to analyze the non-additive residual (interaction) left over by the ANOVA model. PCA decomposes the interaction into PCA axes 1 to N and a residual remains if all axes are not used. If most of the $G \times E$ interaction sum of squares (SS) can be captured in the first N PCA axes, a reduced AMMI model, incorporating only the first N axes, can be used. The interaction between any genotype and environment can be estimated by multiplying the score of the interaction principal component axis (IPCA) of genotype by an environment IPCA score.

Postdictive assessments

The percentage of the treatment sum of squares (SS) captured by an AMMI biplot is a useful statistic for assessing the overall goodness of fit. It is calculated by percentage addition of SS (Genotype + Environment + IPCA 1) divide treatment

SS. In addition, root mean square (RMS) residual is a useful summary statistic regarding model fit. To avoid spurious interpretation of statistical result, the relevant portion of $G \times E$ interaction was calculated for each trait. Factoring the errors from uncontrolled variation ("noise") out of the total $G \times E$ interaction SS is important because most of the noise appears in the interaction, since the interaction contains majority of the treatment degrees of freedom. "Noise" SS, "real structure" SS and target relevant variation percentage were calculated as described by Gauch and Zobel (1997). For a full description of AMMI models and interpretations see Gauch and Zobel (1996; 1997). Genotype × trait and environment × trait averaged across all environments were investigated using biplots. These biplots were constructed to visualization of the genetic correlation among traits, and evaluation of the genotype or environment on the basis of multiple traits (Lee et al., 2003). Correlation with external factors helps to study the measurable changes in the environments or genotypes, which are related to the interaction in the data (McLaren and Chaudhary, 1998; Anandan et al., 2009). Correlation between environment IPCA scores of a trait and some factors represents the particular environmental factors influence on the trait.

Conclusion

Increased drought tolerance should contribute to yield stability across the environments. Therefore, our analyzes have shown the insight into the nature of $G \times E$ interaction in the mungbean raised under rainfed and emphasises importance of varietal development for moisture stress condition. Further, this study brings out that, drought tolerance in mungbean is related to better vegetative growth for more efficient photoassimilates partitioned to root growth to acquire higher yield under drought condition. Correlation studies revealed that minimum temperature, relative humidity, soil pH and rainfall had highly interacted and influenced the yield and component traits of mungbean. Biplots generated by AMMI model gives more valuable and hidden useful information from the data, which gives an overall picture of genotype behaviour under moisture stress condition.

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