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Phenotypic Stability Analysis in Greengram [*Vigna radiata* (L.) Wilczek] Using Eberhart and Russell and AMMI Models

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ABSTRACT

Twelve genotypes of greengram [*Vigna radiata* (L.) Wilczek] were studied under six environments for nine characters to assess the stability, using Eberhart and Russell (1966) and AMMI methods. Based on pooled ANOVA genotypes showed significant differences for all characters under study except thousand seed weight when tested against both pooled error and pooled deviation. The GXE (linear) was significant for characters *viz.,* plant height, number of pods per plant, seed yield per plant and protein content. While the non-linear component of interaction was predominant for all characters except for days to maturity and plant height. The magnitude of non-linear component of interaction was higher than linear component for most of the traits under study. AMMI model explained 98.43% of the total genotype environment interaction component for number of clusters per plant, 95.48% of total genotype- environment interaction component for number of pods per plant, 93.73% of the total genotype- environment interaction component for 1000 seed weight, 98.65% of total genotype environment interaction component for seed yield per plant and 99.04% of the total genotype- environment interaction component for protein content. Based on both AMMI and Eberhart and Russell (1966) model genotypes LGG 407 and LGG 450 for seed yield per plant; MGG 295 and MGG 351 for number of clusters per plant and number of pods per plant; genotype MGG 341 for 1000 seed weight and genotypes MGG 341and ML 267 for protein content were identified as stable genotypes.

Key words : AMMI, Greengram, Mungbean, Stability

Mungbean is an important pulse crop cultivated round the year in diverse climatic conditions of India. GenotypeX Environment interaction not only under lies the very success of stability of genotypes but also the post-breeding adaptive evaluation of improved strains. However, the ordinary analysis of variance (ANOVA) is useful for identifying and testing sources of variability, it provides no insight into the particular pattern of the underlying interaction. The ordinary ANOVA model is additive and effectively describes the main (additive) effects, while the interaction (residual from the additive model) is non-additive and requires other techniques, such as Principal Component Analysis (PCA) to identify interaction patterns. Thus ANOVA and PCA models combined to constitute the Additive Main effects and Multiplicative Interaction (AMMI) model (Zobel *et al.*, 1988).

MATERIAL AND METHODS

The present experiment was conducted during *rabi,* 2006-07 at Agricultural Research Station (ARS) Madhira, Khammam district in Andhra Pradesh to assess the stability of twelve genotypes of greengram over six environments. The six environments were three dates of sowing i.e., 15-09-2006, 30-09-2006 and 15-10-2006; two fertility levels [i.e., 20Kg N: 50Kg P ha^{-1} (only basal) and 20Kg N: 50Kg P ha^{-1} (basal) + 20Kg N ha^{-1} (top dressing at 30 DAS)] in each date of sowing. Each genotype was replicated three times in all the six environments with spacing of 30´10 cm. Recommended package of practices were followed to raise a good crop. Data was recorded on ten randomly selected plants or plot wise from each genotype in each replication for nine characters *viz.,* days to 50% flowering, days to maturity, plant height, number of clusters per plant, number of pods per plant, number of seeds per pod, 1000 seed weight, seed yield per plant and protein content. The data were subjected to stability analysis as per the procedure outlined by Eberhart and Russell (1966) and AMMI model (Gauch, 1988). According to Eberhart and Russell the genotype with high mean, unit regression coefficient and non-significant deviation from regression was considered to be stable over environments. According to AMMI model, when one interaction PCA axis accounts for most of G ´ E, a feature of AMMI model is the biplot procedure in which genotypes and environments taking mean values on abscissa and IPCA1 scores on ordinate are plotted on the same diagram, facilitating inference about specific interactions as indicated by the sign and magnitude of IPCA1 values of individual genotypes and environments (Sharma *et al.*,1998).The biplot of the first two IPCA axis

demonstrates the relative magnitude of the GE interaction for specific genotypes and environments. Since the GE interaction effect is determined by the product of the correct PCA scores, cultivars or environments with a small GE interaction will have small scores and be close to the center of the axis *i.e*., they are stable across environments (Bahman Shafi *et al*., 1992).

RESULTS AND DISCUSSION

The pooled analysis of variance (Table 1) revealed that mean sum of squares due to genotype was highly significant for all characters except for 1000 seed weight (it showed significance when tested against pooled error only) when tested against both pooled error and pooled deviation, indicating presence of variability among the genotypes. The genotype X environment interaction component was non- significant for all the characters except for number of pods per plant (when tested against both pooled error and pooled deviation) and 1000 seed weight showed significance when tested against pooled error only indicating non-differential response of the genotypes in different environments. Reddy and Sriramulu (1984) reported a non-significant first order interaction of GxE interactions. While genotype X environment (linear) component of interaction was significant for all characters except for days to 50% flowering, days to maturity, number of clusters per plant, number of seeds per pod and 1000 seed weight when tested against both pooled error and pooled deviation, indicating linear response of genotypes to environmental changes. The pooled deviation was highly significant for all the characters except for days to maturity and plant height when tested against both pooled error and pooled deviation, indicating that non-linear component of genotype X environment interaction was also predominant for all the characters studied except days to maturity and plant height.

The stability parameters, mean (X) regression coefficient (bi) and deviation from regression (S^2 di) of each genotype were calculated and presented in Table 2 and 3. The linear regression was regarded as measure of responsiveness and S^2di as measure of stability. A genotype with non-significant bi and S^2di values will be considered as stable genotype.

As revealed from Table 3, incase of seed yield per plant nine genotypes (MGG 295, MGG 341, MGG 347, MGG 348, LGG 407, LGG 450, LGG 460 and TM 96-2) did not interact with environments as indicated by both bi and S^2 di, being non-significant. Therefore, prediction of performance was perfect in case of these genotypes. Out of these genotypes LGG 460 had highest mean value. ML 267 genotype possessed higher mean value than population mean and exhibited significant higher 'bi' value leading to the inference that it is suitable for high yielding environments. This was in accordance with the earlier reports of Manivannan (2003) and Appalaswamy and Reddy (2004)

Based on stability parameters MGG 295 and MGG 353 found to be stable for days to 50% flowering and days to maturity with lower mean values. All the twelve genotypes except MGG 351, MGG 353 and LGG 407 were identified as stable genotypes for plant height. Among twelve genotypes studied, MGG 295, MGG 347, MGG 348, MGG 351, LGG 407, LGG 450, ML 267 and PDM 54 were found to be stable for seeds per pod. While, MGG 341 and LGG 407 were found to be stable for 1000 seed weight. Genotypes MGG 341 and ML 267 were stable for protein content.

LGG 460 had higher number of pods per plant and clusters per plant along with regression coefficient (bi) approaching unity and non-significant deviation from regression (S^2 di), thus turned out stable for these traits. Stable genotypes for number of clusters per plant and number of pods per plant was earlier reported by Appalaswamy and Reddy (2004) and Raje and Rao (2004). This indicated that the stability of various components traits might be responsible for observed stability of seed yield per plant. Patil and Narkhede (1995) also arrived at similar conclusion regarding stability of seed yield.

Based on ANOVA of AMMI analysis (Table 4) all the five characters showed significant differences among genotypes as well as environments (except number of seeds per pod) and genotype environment interaction (except number of clusters per plant, seed yield per plant and protein content). Four Interaction Principal Component Axis (IPCAs) were explained for all the five characters studied. Only IPCA1 has explained majority of the genotype environment interaction component and were significant. AMMI model explained 98.65% of total genotype environment interaction component for seed yield per plant, 98.43% of the total genotype-environment interaction component for number of clusters per plant, 95.48% of the total genotype-environment interaction component for number pods per plant, 93.73% of the total genotype- environment interaction component for 1000 seed weight and 99.04% of the total genotype- environment interaction component for protein content.

According to AMMI1 (biplot) genotypes 1 (MGG 295), 2 (MGG 341), 3 (MGG 347), 4 (MGG 348), 7 (LGG 407), 8 (LGG 450) and 11 (PDM 54) were identified as stable genotypes for seed yield per plant. However, genotype 7 (LGG 407) had

Table 1. Analysis of variance as per Eberhart and Russell (1966) of 12 greengram genotypes for ten characters in six different environments.

Source	df	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of clusters per plant	No. of pods per plant	Seeds per pod	Yield per plant	1000 seed weight	Protein content
Varieties	11	50.1333*++	48.692	104.363**++	2.146**++	26.710**++	1.307**++	2.531**++	8.555*	9.570**++
Environment + (Variety* Environment)	60	0.948**++	1.275	103.09**++	0.597**++	9.112**++	0.320*	1.433**++	6.473*	2.139
Environment	5	0.331	1.058	43.033**++	3.680**++	50.243**++	0.343*	11.087**++	19.887**++	4.629*+
Variety * Environment	55	1.005	1.295	7.334	0.317	5.373*+	0.318*	0.556	5.254*	1.914
Environment (Linear)	1	1.656	5.290*+	215.166**++	18.401**++	251.216**++	1.715*+	55.433**++	99.436**++	23.143**++
Variety* Environment (Linear)	11	0.916	1.025	15.457**++	0.319	13.014**++	0.291	0.988*+	3.682	3.008*+
Pooled deviation	48	0.941*+	1.249	4.862	0.290**++	3.174**++	0.297**++	0.410**++	5.176**++	1.50**++
Pooled error	132	0.646	1.137	5.439	0.100	1.526	0.131	0.226	1.264	0.755
Total	71	8.569	8.621	24.881	0.837	11.838	0.473	1.603	6.796	3.290

* significant 5% probability level against pooled error + significant 5% probability level against pooled deviation
** significant 1% probability level against pooled error ++ significant 1% probability level against pooled deviation

Table 2 . Estimates of stability parameters for days to 50% flowerig, days to maturity, plant height, number of clusters per plant and number of pods per plant in greengram.

S.No	Genotypes	Days to 50% flowering			Days to maturity			Plant height			No. of clusters / plant			No. of pods / plant		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	MGG 295	33.167	5.33	0.64	60.778	2.48	-0.07	33.583	1.32	1.90	4.167	1.08	-0.09	13.194	0.97	0.63
2	MGG341	35.000	-2.55*	-0.42	65.056	-0.76	-0.47	31.170	1.15	-4.85	4.161	1.21	0.05	14.000	0.51	4.66**
3	MGG347	36.222	1.19	-010	69.000	3.16	1.42	31.800	0.38	1.10	3.978	0.60	0.19*	14.111	1.60	0.73
4	MGG348	33.722	1.49	-0.31	64.333	0.79	-0.72	28.789	0.53	-2.80	5.111	1.80	0.44**	16.168	0.11	0.72
5	MGG351	37.833	-2.78*	-0.43	68.889	0.50	2.91**	34.644	1.82*	-4.70	4.339	1.24	-0.03	15.122	0.88	0.71
6	MGG353	32.944	1.53	-0.37	64.444	0.15	-0.23	37.578	-0.98*	-2.63	4.594	1.24	1.06**	12.622	-0.74*	2.25*
7	LGG407	39.611	3.95	2.90**	72.778	1.82	-0.59	36.172	1.53*	4.65	5.128	0.42*	-0.06	18.144	0.77	2.32*
8	LGG450	39.556	2.39	-0.19	68.833	-2.18	0.31	36.060	0.04	0.63	4.678	1.05	-0.07	17.017	0.99	2.28*
9	LGG460	41.556	-1.83	2.72**	66.333	2.74	0.36	45.961	1.92	1.34	4.806	0.99	0.06	19.233	1.83	0.44
10	ML 267	34.444	-0.31	0.06	66.333	1.87	-0.20	34.989	1.58	5.04	5.617	0.44	0.56**	17.039	2.06	2.98*
11	PDM54	39.222	3.40	-0.56	69.611	0.88	-0.55	35.517	2.23	4.92	4.994	0.39	0.12	15.428	1.36	0.16
12	TM96-2	37.333	0.20	-0.37	68.667	0.64	-0.37	34.117	0.48	-0.15	5.928	1.55	0.07	18.028	1.65	2.02
	Population mean	36.718			67.255			35.086			4.792			15.844		

Table 3. Estimtes of stability parameters for number of seeds per pod, 1000 seed weight, seed yield per plant and protein content in greengram.

S.No.	Genotypes	No. of seeds per pod			1000 seed weight (g)			Seed yield per plant (g)			Protein content (%)		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	MGG 295	9.706	1.52	-0.07	33.893	1.14	5.31**	3.886	0.84	-0.10	26.885	1.07	1.56*
2	MGG341	9.877	0.53	0.50**	31.914	0.86	0.45	4.371	0.82	0.07	25.922	1.69	-0.57
3	MGG347	9.987	0.68	-010	33.409	1.54	2.34*	3.785	0.99	0.03	26.444	0.15	-0.20
4	MGG348	10.242	1.18	-0.10	31.317	0.56	8.68**	4.926	0.56	0.14	22.687	2.90	3.60**
5	MGG351	9.164	1.35	-0.09	33.103	0.51	4.79**	4.297	0.50	0.24	24.341	2.03	-0.32
6	MGG353	9.945	-2.19	1.51**	36.014	0.19	1.84**	4.366	0.16	0.99**	25.713	2.74	1.06*
7	LGG407	10.001	1.57	-0.09	32.432	1.22	0.60	5.173	1.41	-0.09	26.213	-0.15	-0.01
8	LGG450	10.282	1.58	0.00	32.593	2.15	11.28**	4.949	1.03	0.01	24.249	-0.39	1.49*
9	LGG460	10.850	4.09	-0.02	32.275	0.11	5.88**	6.095	1.55	0.07	23.474	0.57*	-0.572
10	ML 267	9.563	0.83	0.07	32.492	2.08*	-1.00	4.876	1.70*	-0.05	25.201	1.09	-0.22
11	PDM54	9.219	1.00	-0.05	32.625	1.00	2.28*	4.086	1.00	0.95**	25.838	1.46	2.21**
12	TM96-2	10.139	-0.14	0.44**	31.818	0.64	4.06**	5.010	1.44	0.00	24.716	-1.15	1.33
	Population mean	9.915			32.849			4.652			25.133		

* significant 5% probability level ** significant 1% probability level bi = regression coefficient S^2di = Deviation form regression coeffiicient

Table 4. ANOVA of AMMI for number of clusters per plant, number of pods per plant, 1000 seed weight, seed yield per plant and protein content in greengram.

Source	No. of clusters per plant			No. of pods per plant			1000 seed weight			Seed yield per plant			Protein content		
	df	MSS	per cent ex-plained	df	MSS	per cent ex-plained	df	MSS	per cent ex-plained	df	MSS	per cent ex-plained	df	MSS	per cent ex-plained
Trials	71	0.837**		71	11.850**		71	6.72		71	1.603**		71	3.290*	
Genotypes	11	2.147**	39.73	11	26.710**	35.01	11	8.79*	20.26	11	2.531**	24.45	11	9.570**	45.05
Environment	5	3.680**	30.96	5	50.243**	30.07	5	19.91**	20.88	5	11.087**	48.70	5	4.628*	9.90
G x E															
Interaction	55	0.317	29.38	55	5.373*	34.92	55	5.11*	58.87	55	0.556	26.85	55	1.912	45.01
IPCA 1	15	0.648**	55.84	15	10.979*	56.06	15	10.45**	55.82	15	1.036*	50.84	15	4.528**	64.59
IPCA 2	13	0.331	24.70	13	4.825	21.35	13	3.44	15.95	13	0.835	33.51	13	1.581	19.54
IPCA 3	11	0.147	9.28	11	2.709	10.14	11	2.64	13.50	11	0.200	7.19	11	1.106	11.57
IPCA 4	9	0.167	8.61	9	2.592	7.94	9	2.51	8.47	9	0.174	5.11	9	0.390	3.34
Residual	7	0.039	1.57	7	1.896	4.52	7	2.94	6.27	7	0.059		7	0.144	0.96
Pooled residual	40	0.192		55	5.342		40	6.72		55	0.556		40	0.931	

* significant at 0.05 level ** significant at 0.01 level

Fig 1. AMMI 1 biplot-IPCA1 scores of twelve genotypes and six environments plotted against seed yield per plant in greengram [*Vigna radiata* (L.) Wilczek]

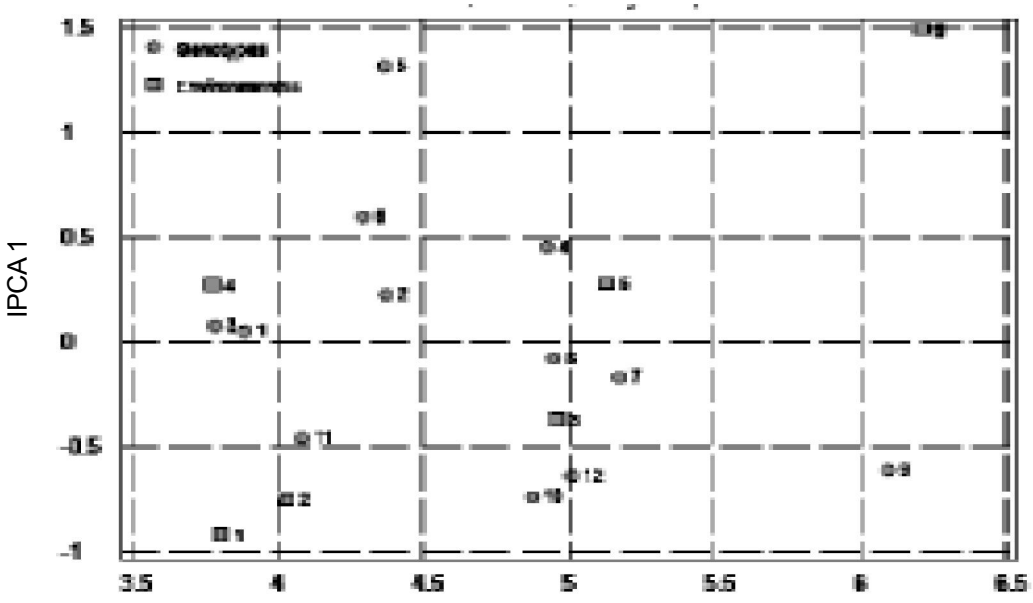
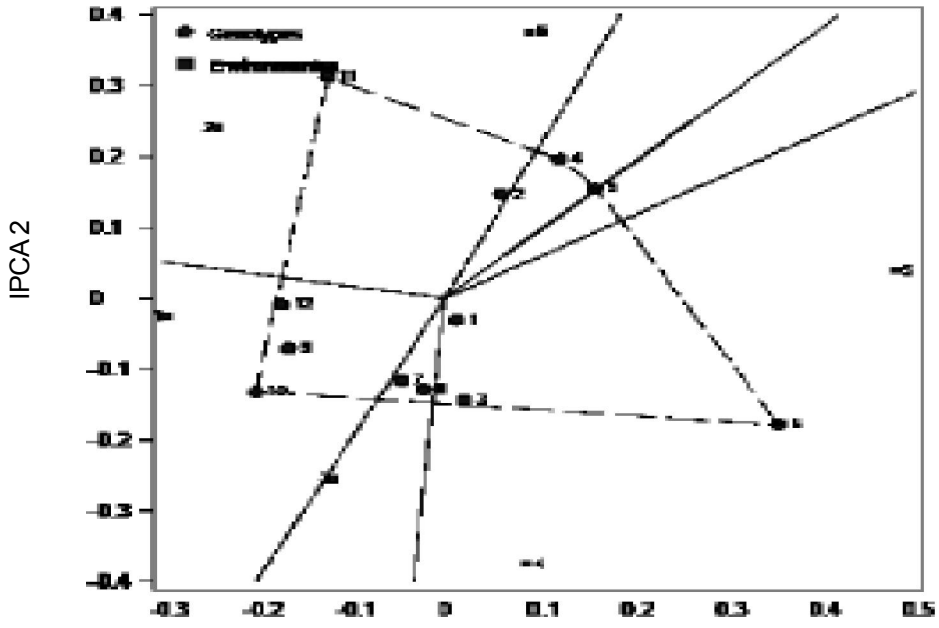


Fig 2. AMMI2 biplot- IPCA1 and IPCA2 scores of twelve genotypes and six environments for seed yield per plant in greengram [*Vigna radiata* (L.) Wilczek]



Genotypes of greengram

1= MGG 295	3= MGG 347	5= MGG 351	7= LGG 407	9= LGG 460	11= PDM 54
2= MGG 341	4= MGG 348	6= MGG 353	8= LGG 450	10= ML 267	12= TM 96-2

Fig 3. AMMI 1 biplot-IPCA1 scores for twelve genotypes and six environments plotted against number of clusters per plant in greengram [*Vigna radiata* (L.) Wilczek]

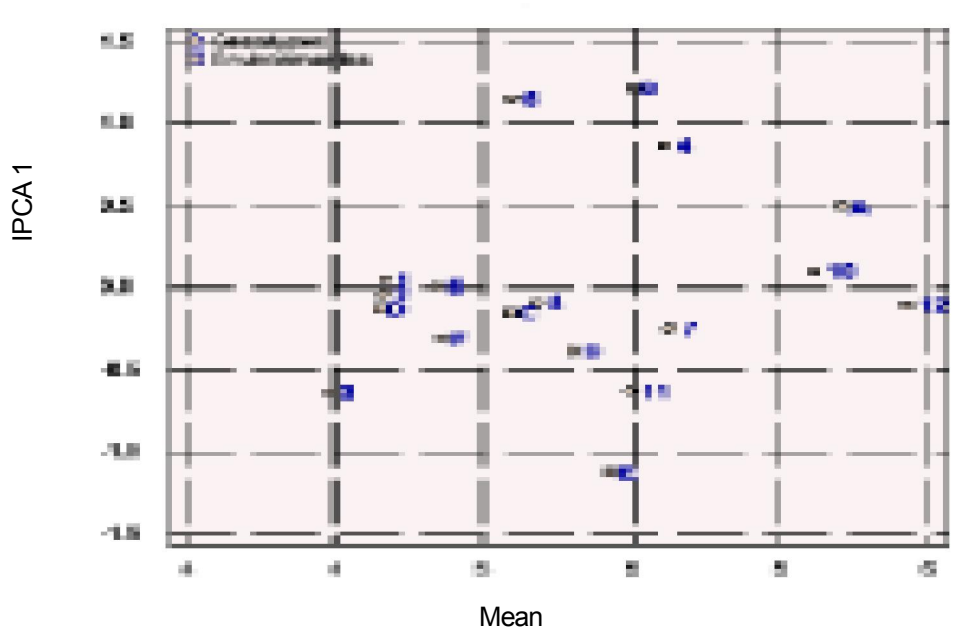
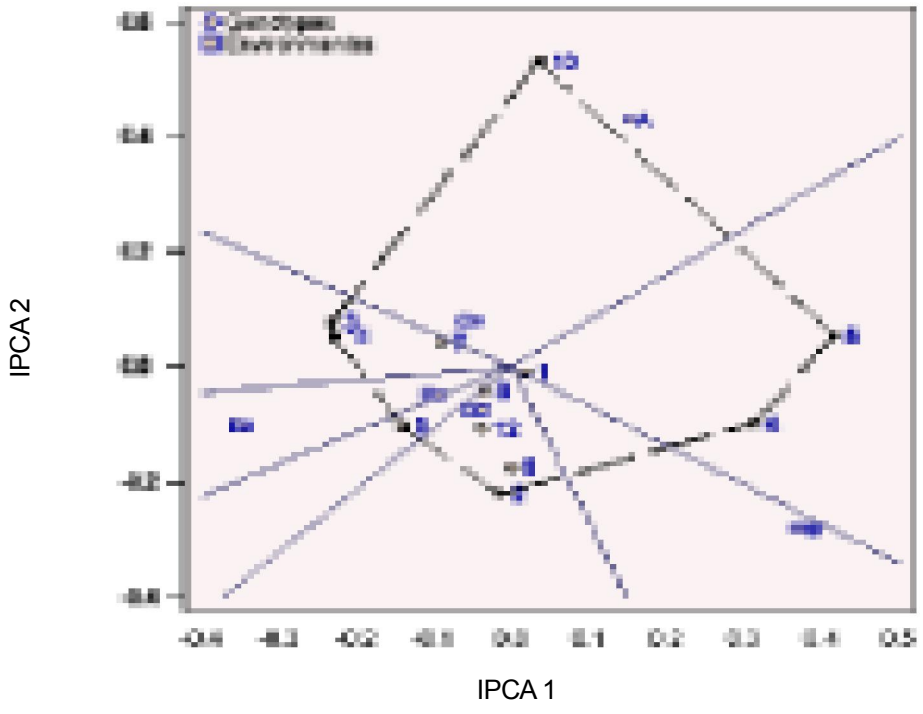


Fig 4. AMMI2 biplot- IPCA1 and IPCA2 scores of twelve genotypes and six environments for number of clusters per plant in greengram [*Vigna radiata* (L.) Wilczek]



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2= MGG 341	4= MGG 348	6= MGG 353	8= LGG 450	10= ML 267	12= TM 96-2

Fig 5. AMMI 1 biplot-IPCA1 scores of twelve genotypes and six environments plotted against number of pods per plant in greengram [*Vigna radiata* (L.) Wilczek]

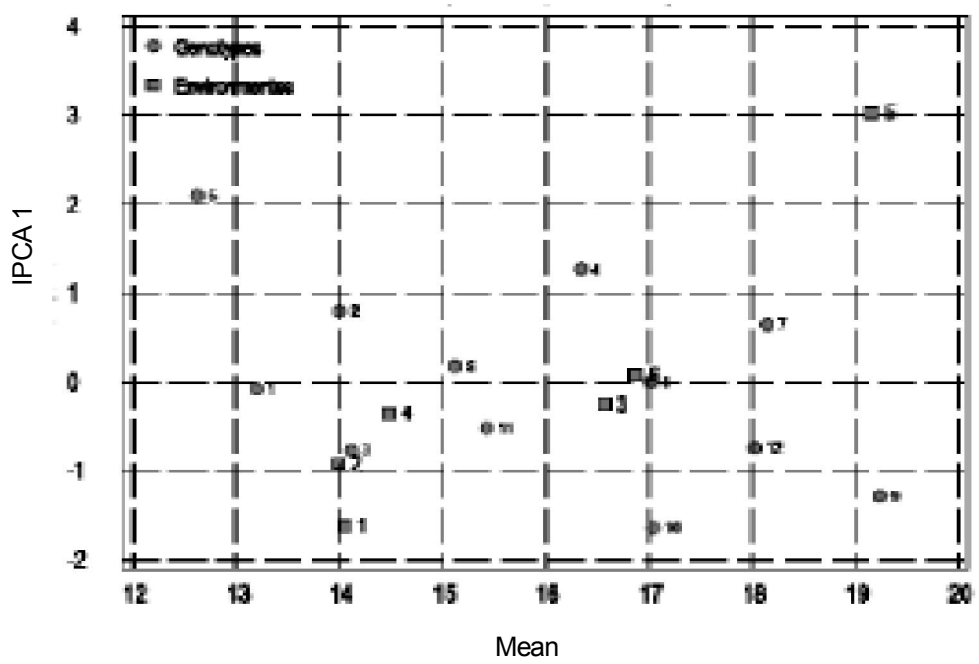
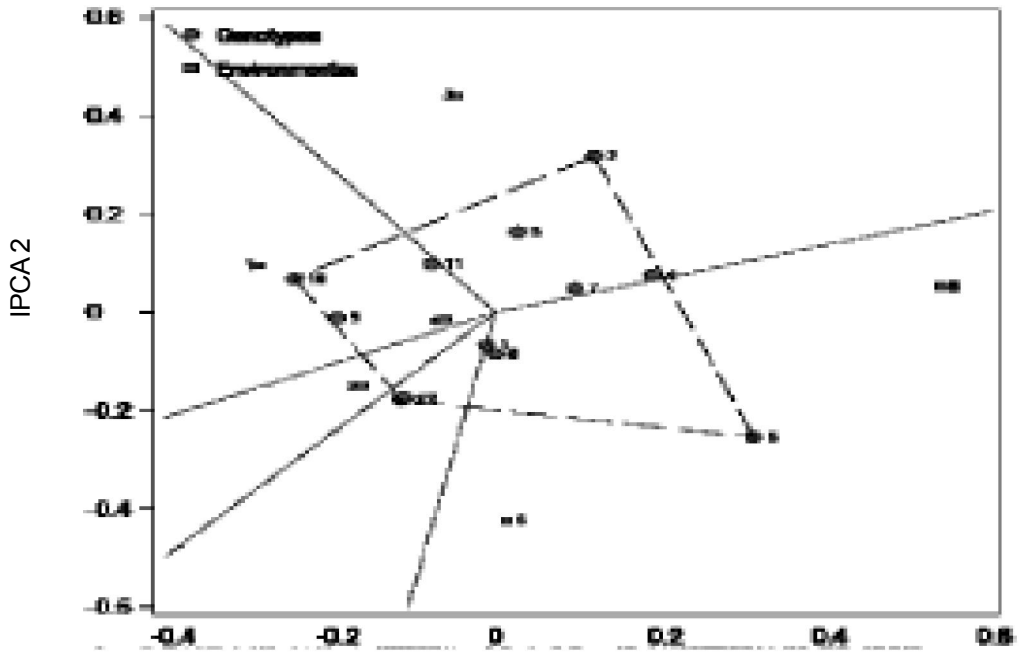


Fig 6. AMMI2 biplot- IPCA1 and IPCA2 scores of twelve genotypes and six environments for number of pods per plant in greengram [*Vigna radiata* (L.) Wilczek]



Genotypes of greengram

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2= MGG 341	4= MGG 348	6= MGG 353	8= LGG 450	10= ML 267	12= TM 96-2

Fig 7. AMMI 1 biplot-IPCA 1 scores of twelve genotypes and six environments plotted against 1000 seed weight in greengram [*Vigna radiata* (L.) Wilczek]

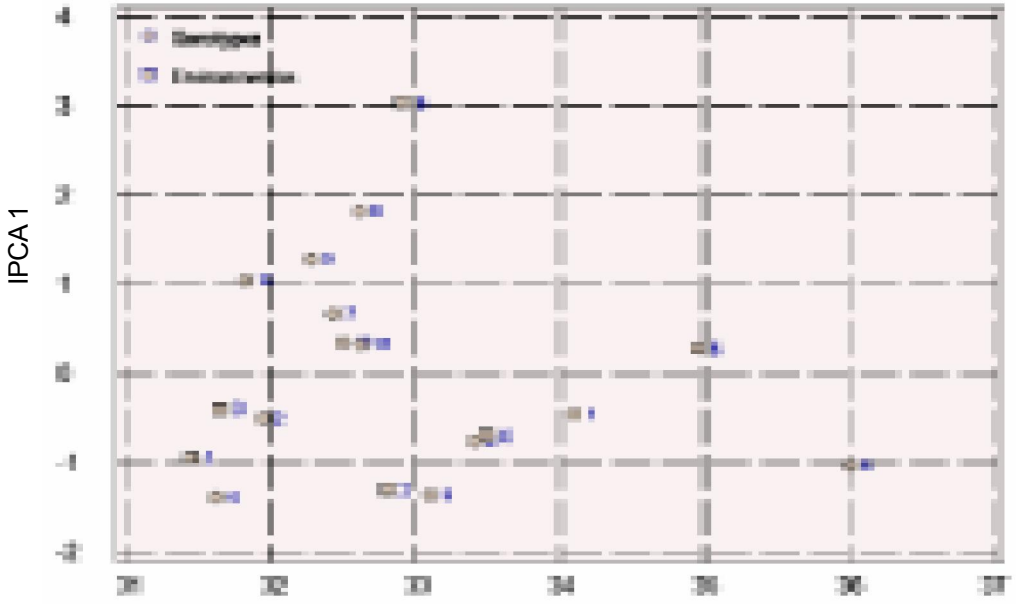
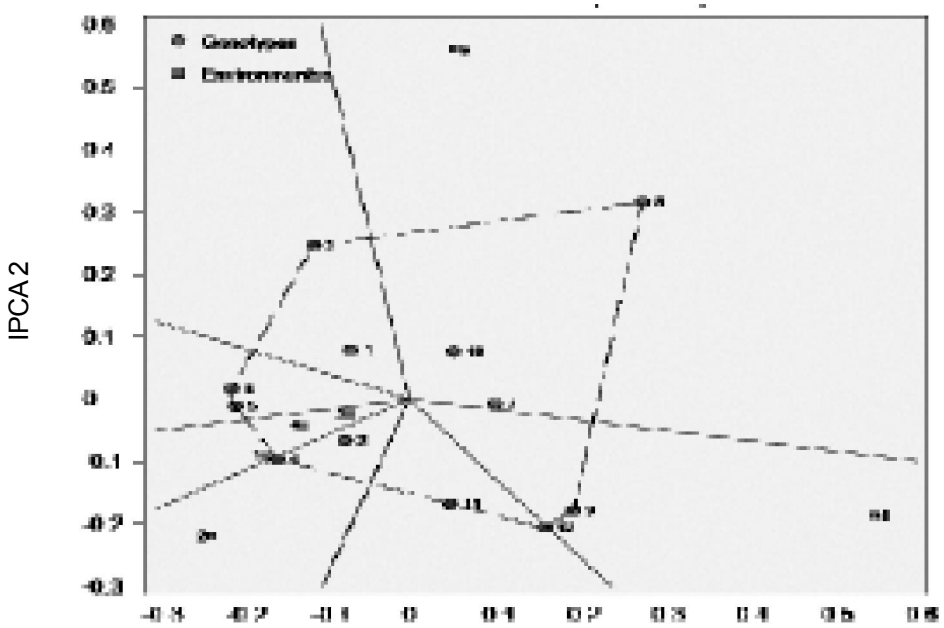


Fig 8. AMMI 2 biplot- IPCA 1 and IPCA 2 scores of twelve genotypes and six environments for 1000 seed weight in greengram [*Vigna radiata* (L.) Wilczek]



Genotypes of greengram

1= MGG 295 3= MGG 347 5= MGG 351 7= LGG 407 9= LGG 460 11= PDM 54
2= MGG 341 4= MGG 348 6= MGG 353 8= LGG 450 10= ML 267 12= TM 96-2

Fig 9. IPCA1 AMMI 1 biplot-IPCA1 scores for twelve genotypes and six environments plotted against protein content in greengram [*Vigna radiata* (L.) Wilczek]

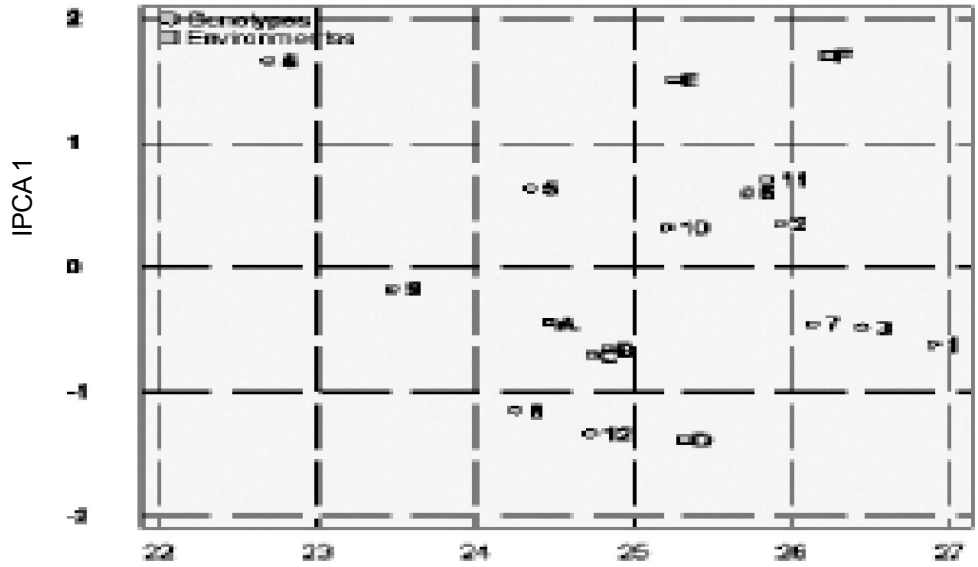
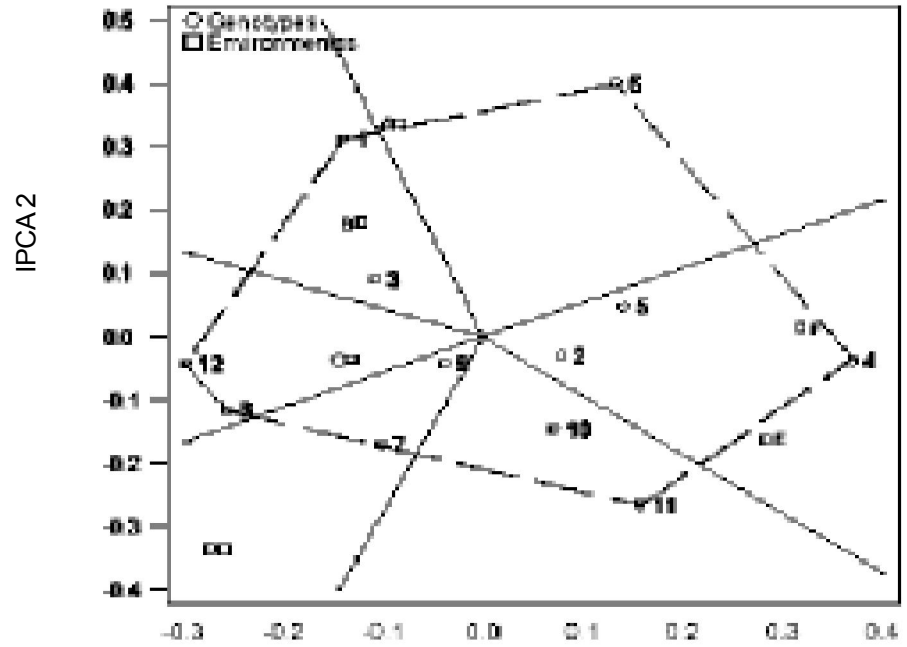


Fig 10. AMMI2 biplot- IPCA1 and IPCA2 scores of twelve genotypes and six environments for seed protein t in greengram [*Vigna radiata* (L.) Wilczek]



Genotypes of greengram

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highest mean value. Genotypes 9 (LGG 460) was specifically suited to environment 1, 2 and 3 as indicated by same signs of IPCA 1 (Fig 1).

According to interaction biplot (AMMI2), genotypes 1 (MGG 295), 2 (MGG 341), 3 (MGG 347), 7 (LGG 407), 8 (LGG 450), 9 (LGG 460) and 12 (TM 96-2) were identified as most stable genotypes for seed yield per plant, which were close to origin of polygon. All the environments were most discriminating ones as indicated by the longest distance between their marker and the origin. Among the environments, environment 5 is suitable for seed yield per plant as indicated by high IPCA1 score and low IPCA2 score. (Fig 2).

According to AMMI1 biplot (Fig. 3), genotypes 1 (MGG 295), 2 (MGG 341), 5(MGG 351), 8 (LGG 450), 10 (ML 267) and 12 (TM 96-2) and according to interaction biplot (AMMI2) (Fig 4) genotypes 1 (MGG 295), 8 (LGG 450), 7 (LGG 407), 12 (TM 96-2) and 5 (MGG 351) were identified as stable for number of clusters per plant. Based on AMMI1 biplot (Fig 5), genotypes 4 (MGG 348), 6 (MGG 353), 9 (LGG 460) and 10 (ML 267) and based on AMMI2 biplot (Fig 6) genotypes 1 (MGG 295), 4 (MGG 348), 5 (MGG 351), 7 (LGG 407), 8 (LGG 450), 9 (LGG 460) and 11 (PDM 54) identified as stable for number of pods per plant. According to AMMI1 biplot (Fig 7), genotypes 1 (MGG 295), 10 (ML 267), 2 (MGG 341) and 11 (PDM 54) and according to AMMI2 biplot (Fig 8) genotypes 2 (MGG 341), 7 (LGG 407), 1 (MGG 295) and 10 (PDM 54) were identified as stable for 1000 seed weight. According to AMMI1 biplot (Fig 9), genotypes 9 (LGG 460), 10 (ML 267), 7 (LGG 407), 3 (MGG 347) and 2 (MGG 341) and according to AMMI2 biplot (Fig 10) genotype 9 (LGG 460), 2 (MGG 341) 3 (MGG 347), 5 (MGG 351) and 10 (ML 267) were identified as stable genotypes for protein content.

In the pooled Analysis of variance the genotype- environment interaction component was non-significant for number of clusters per plant, seed yield per plant and protein content. Where as genotype-environment interaction (linear) component as per Eberhart and Russell (1966) was non-significant for number of clusters per plant and 1000 seed weight. But significant only for number of pods per plant, seed yield per plant and protein content.

While in AMMI model IPCA1 component significantly explained the genotype-environment interactions, incase of number of clusters per plant (55.84%), number of pods per plant (56.08%), 1000 seed weight (55.82%), seed yield per plant (50.84%) and protein content (64.59%) bringing out the specific use of AMMI in assisting the breeder to pinpoint the stable genotypes for the above characters, which is not possible in case of linear regression model.

Based on both AMMI and Eberhart and Russell models genotypes LGG 407 and LGG 450 for seed yield per plant; MGG 295 and MGG 351 for number of clusters per plant and number of pods per plant; genotype MGG 341 for 1000 seed weight and genotype MGG 341and ML 267 for protein content were identified as stable genotypes.

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