

Phenotypic Stability Analysis in Soybean [*Glycine max* (L.) Merrill] Using Eberhart and Russell and AMMI Models

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ABSTRACT

Twelve genotypes of soybean were studied under three environments to assess the stability for thirteen characters using Eberhart and Russell (1966) model. The genotypes showed significant differences for all characters studied except for number of pods per plant, 100 seed weight, protein content and harvest index when tested against both pooled error and pooled deviation. The $G \times E$ (linear) was significant for characters like days to 50% flowering, days to maturity and plant height while the non-linear component of interaction was predominant for all characters except for number of branches per plant, pod length, number of seeds per pod, 100 seed weight, protein content and harvest index. The magnitude of non-linear component of interaction was higher than linear component for most of the traits under study. AMMI model explained 100% of total genotype environment interaction component for number of pods per plant, harvest index and seed yield per plant and 99.99% for biological yield per plant. Based on both AMMI and Eberhart and Russell (1966) models, genotypes RKS 18 and JS 93-05 for number of pods per plant, JSS 335 for biological yield per plant and JS95-60 for seed yield per plant were identified as stable genotypes.

Key words : AMMI, Soybean, Stability

Soybean [*Glycine max* (L.) Merrill] is a major oil seed crop in the world and is called as a golden bean, because of its versatile nutritional qualities having 20% oil and 38 to 43% protein. Genotype (G) X Environment (E) interaction not only underlies 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 model combine to constitute the additive main effects and multiplicative interactive (AMMI) model (Zobel *et al.*, 1988).

MATERIAL AND METHODS

Present experiment was conducted at Regional Agricultural Research Station, Lam, Guntur in Andhra Pradesh to assess the stability of twelve genotypes of soybean over three environments i.e., *kharif*, *rabi* and late *rabi*, 2006-07. The dates of sowing of three environments were 30-07-2006, 17-11-2006 and 2-12-2006. Each genotype was replicated three times in all the three environments

with inter-and intra-row spacing of 30 X 7.5 cm. Recommended package of practices and plant protection measures were followed to raise a good crop. Data were recorded on ten randomly selected plants from each genotype in each replication on plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, biological yield per plant (g) and seed yield per plant (g). Days to 50% flowering, days to maturity, 100 seed weight (g), harvest index (%), protein content (%) and oil content (%) were recorded on plot basis. 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 (1966) a 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 GXE, 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 GXE interaction for specific genotypes and environments

since the GXE interaction effect is determined by the product of the correct PCA scores, cultivars or environments with a small GXE interaction will have small scores and be close to the center of the axis i.e., they are stable across environments (Bahman Shafii *et al.*, 1992).

RESULTS AND DISCUSSION

The pooled analysis of variance (Table 1) revealed that mean sum of squares due to genotype was significant for all characters except for number of pods per plant, 100 seed weight, protein content when tested against both pooled error and pooled deviation indicating presence of variability among the genotypes. Environment (Genotype x environment interaction) showed significance for all the characters studied, except for number of seeds per pod, 100 seed weight, protein content, oil content and harvest index when tested against both pooled error and pooled deviation. The genotype x environment was non-significant for all the characters except for plant height (when tested against both pooled error and pooled deviation) indicating non-differential response of the genotypes in different environments. Reddy and Sriramulu (1984) reported non-significant genotype x environment (linear) component of interaction. Genotype x environment (linear) interaction was non-significant for all character except days to 50% flowering, days to maturity and plant height when tested against both pooled error and pooled deviation, indicating linear response of genotypes to environmental changes. The pooled deviation was significant for all the characters except number of braches per plant, pod length (cm), number of seeds per pod and 100 seed weight (g). When tested against pooled error, indicating that non linear component of genotype x environment interaction was also predominant for all the characters studied except for number of branches per plant, pod length, number of seeds per pod, 100 seed weight, protein content and harvest index.

The stability parameters mean (X), regression coefficient (b_i) and deviation from regression ($S^2 d_i$) of each genotype were calculated and presented (Table 2). The linear regression was regarded as measure of responsiveness and $S^2 d_i$ as measure of stability. A genotype with unit b_i and non-significant $S^2 d_i$ values is considered as stable genotype.

In case of seed yield per plant eight genotypes (LSb₁, JS 335, LSb 13, LSb 21, JS 95-60, RKS 18, LSb 23 and JS 93-05) revealed lesser influence of environment as indicated by their unit

b_i and non-significant $S^2 d_i$. Therefore, prediction of performance was perfect in case of these genotypes. Out of these genotypes LSb 21 had highest mean value. Ramana and Satyanarayana (2005) also reported similar results.

Based on stability parameters LSb₁, LSb 3, JS 95-60, RKS 18, LSb 23 and JS 93-05 were found to be stable for biological yield per plant with lower mean values. All the twelve genotypes except MRSB 345, LSb 36 and PK 1029 were identified as stable genotypes for harvest index. Among twelve genotypes studied LSb 1, JS 335, LSb 13, LSb 21, JS 95-60 and JS 93-05 were found to be stable for number of pods per plant.

As per AMMI analysis (Table 3) all the four characters showed significant differences among genotypes (except 100 seed weight) as well as environments (except number of seeds per pod, 100 seed weight and oil content) when tested against genotype-environment interaction component. Three interaction principal component axis (IPCA's) were explained for all the characters studied and were significant. Only IPCA1 has explained majority of the genotype-environment interaction component. AMMI model explained 100% of total genotype-environment interaction component for seed yield per plant, 100% for number of pods per plant 99.99% for biological yield per plant, 100% for harvest index.

For number of pods per plant, the genotypes 5 (LSb 21), 7 (JS 95-60), 9 (RKS 18) and 12 (JS 93-05) were stable genotypes. However, genotypes 9 (RKS 18) and (JS 93-05) have higher mean values. Genotypes, 4 (MRSB 345), 6 (LSb 3), 8 (LSb 36), 10 (LSb 23) and 11 (PK 1029) were suitable to specific environments as indicated by higher mean of IPCA 1 values from zero. Genotype 4 (MRSB 345) was suited to environment 2. According to AMMI 1 biplot (Fig. 1) as indicated by same signs of IPCA 1 scores for genotype as well as environment.

However, according to interaction (AMMI 2) biplot, the stable genotypes were 3 (LSb 13), 5 (LSb 21), 7 (JS 95-60), 8 (LSb 36), 9 (RKS 18) and 12 (JS 93-05) and the rest of the genotypes have specific adaptation for number of pods per plants. The environments 2 and 3 were identified as most discriminating ones as indicated by the longest distance between their marker and the origin. Among the environments, environment 2 is most suitable location as indicated by high mean value of IPCA 1 and low values of IPCA 2 (Fig. 2).

For biological yield per plant, according to AMMI 1 biplot genotypes 2 (JS 335) 4 (MRSB 345), 10 (LSb 23) and 12 (JS 93-05) were stable genotypes. However, genotypes 2 (JS 335) and 10

Table 1 Pooled analysis of variance (Eberhart and Russell, 1966) for 12 soybean genotypes over three environments

Source	Df	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100 seed weight (g)	Protein content (%)	Oil content (%)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Varieties	11	13.6 ⁺⁺	141.07 ⁺⁺⁺	33.83 ⁺⁺⁺	0.37 ⁺	50.00 ⁺⁺	0.18 ⁺⁺⁺	0.108 ⁺⁺⁺	3.81 ⁺⁺	9.51 ⁺⁺	4.06 ⁺⁺	27.02 ⁺⁺	36.73 [*]	6.09 ⁺⁺
Environment + (variety x environment)	24	6.9 ⁺⁺⁺	36.76 ⁺⁺⁺	39.22 ⁺⁺⁺	0.39 ⁺⁺	108.68 ⁺⁺⁺	0.06 ⁺⁺⁺	0.01	0.30	2.78	0.82	27.97 ⁺⁺	27.93	5.89 ⁺⁺
Environments	2	52.77 ⁺⁺⁺	262.86 ⁺⁺⁺	383.33 ⁺⁺⁺	2.52 ⁺⁺⁺	1099.89 ⁺⁺⁺	0.50 ⁺⁺⁺	0.01	0.15	19.09 ⁺⁺⁺	0.27	236.13 ⁺⁺⁺	189.57 ⁺⁺⁺	51.49 ⁺⁺⁺
Variety x environment	22	2.81	16.21	7.94 ⁺⁺	0.20	18.57	0.02	0.01	0.32	1.30	0.87	9.05	13.24	1.75
Environments (Linear)	1	105.55 ⁺⁺⁺	525.73 ⁺⁺⁺	766.67 ⁺⁺⁺	5.05 ⁺⁺⁺	2199.79 ⁺⁺⁺	1.01 ⁺⁺⁺	0.00	0.31	38.18 ⁺⁺⁺	0.53	472.26 ⁺⁺⁺	379.14 ⁺⁺⁺	102.99 ⁺⁺⁺
Variety x environment (linear)	11	4.33 ⁺⁺	24.49 ⁺⁺	13.01 ⁺⁺⁺	0.26	10.11	0.03	0.00	0.33	1.17	0.40	9.88	11.80	1.20
Pooled deviation	12	1.18 ⁺⁺	7.26 ⁺⁺	2.63 [*]	0.12	24.78 ⁺⁺	0.01	0.01	0.28	1.31	1.23 ⁺⁺	7.54 ⁺⁺	13.45	2.09 ⁺⁺
Pooled error	66	0.41	0.78	1.27	0.06	6.52	0.01	0.01	0.18	1.79	0.28	1.23	5.25	0.44
Total	35	9.07	69.54	37.53	0.39	90.24	0.09	0.04	1.41	4.90	1.84	27.68	30.70	5.95

* = Significant at 5% probability level against pooled error

** = Significant at 1% probability level against pooled error

+ = Significant at 5% probability level against pooled deviation

++ = Significant at 1% probability level against pooled deviation

Table 2 Stability parameters for number of pods plant⁻¹, biological yield plant⁻¹ (g), harvest index (%) and seed yield plant⁻¹ (g) in soybean [*Glycine max* (L.) Merrill]

Genotype	Number of pods plant ⁻¹			Biological yield plant ⁻¹ (g)			Harvest index (%)			Seed yield plant ⁻¹ (g)		
	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
LSb 1	21.84	0.38	2.59	14.32	0.44	-0.53	31.43	1.38	6.51	4.69	0.43	0.18
JS 335	33.48	1.19	5.29	21.74	0.91	5.43*	38.32	1.55	-3.23	8.50	1.38	0.62
LSb 13	22.68	0.77	2.22	18.55	0.22	8.16**	26.30	0.84	2.73	4.89	0.46	0.16
MRSB 345	25.54	0.88	78.47**	18.26	0.86	19.18**	29.92	1.22	33.65**	5.59	0.69	5.60**
LSb 21	25.00	1.15	-0.76	18.60	0.77	16.61**	29.15	1.20	-4.68	5.41	0.73	0.20
LSb 3	30.06	1.20	56.43**	21.27	2.13	0.58	37.00	-0.18	-4.63	7.88	1.57	3.41**
JS 95-60	21.97	1.00	-6.50	18.29	1.34	0.22	29.97	0.91	-5.26	5.60	1.13	-0.42
LSb 36	26.84	1.03	20.56*	20.08	1.36	6.68*	29.19	1.48	43.31**	6.00	0.99	3.42**
RKS 18	27.20	1.16*	-6.53	19.18	1.37	-1.10	34.06	-0.03	2.70	6.65	1.08	1.29
LSb 23	34.41	1.17	36.76*	27.15	0.79	0.96	33.29	1.86	-2.30	9.20	1.49	0.73
PK 1029	27.02	0.97	34.93*	19.52	0.75	20.03**	34.45	0.71	26.42**	6.83	0.89	4.95**
JS 93-05	26.24	1.05	-4.76	20.79	1.00	-1.25	31.30	1.04	0.73	6.66	1.12	-0.35
Population mean	26.86			19.81			32.03			6.49		

* = Significant at 5% probability level,

** = Significant at 1% probability level

b_i = Regression coefficient

S²d_i = Deviation from regression coefficient

Table 3 ANOVA of AMMI for number of pods per plant, biological yield per plant (g), harvest index (%) and seed yield per plant (g) in soybean
[*Glycine max* (L.) Merrill]

Source	Number of pods per plant			Biological yield per plant (g)			Harvest index (%)			Seed yield per plant (g)		
	Df	MSS	% explained	Df	MSS	% explained	Df	MSS	% explained	Df	MSS	% explained
Trials	35	90.240**	-	35	27.679**	-	35	30.669*	-	35	5.956**	-
Genotypes	11	50.003*	17.414	11	27.029*	30.689	11	36.729*	37.601	11	6.091**	32.132
Environments	2	1099.896**	69.648	2	236.131**	48.774	2	189.271**	35.285	2	51.496**	49.399
G × E interaction	22	18.572	12.936	22	9.055	20.562	22	13.242	27.113	22	1.749	18.462
PCA 1	12	24.975	73.350	12	9.835	59.250	12	16.938	69.770	12	2.125	66.270
PCA II	10	10.890	26.653	10	8.117	40.746	10	8.807	30.233	10	1.298	33.738
PCA III	8	0.000	0.000	8	0.001	0.007	8	0.000	0.000	8	0.000	0.000
Residual	-8	0.001	0.000	-8	0.000	0.000	-8	0.001	0.000	-8	0.000	0.000
Pooled residual	10	10.889		10	8.118		10	8.807		10	1.298	

* = Significant at 0.05 level

** = Significant at 0.01 level

Fig 1 AMMI 1 biplot-IPCA 1 scores of twelve genotypes and three environments plotted against number of pods per plant in soybean [*Glycine max* (L.) Merrill]

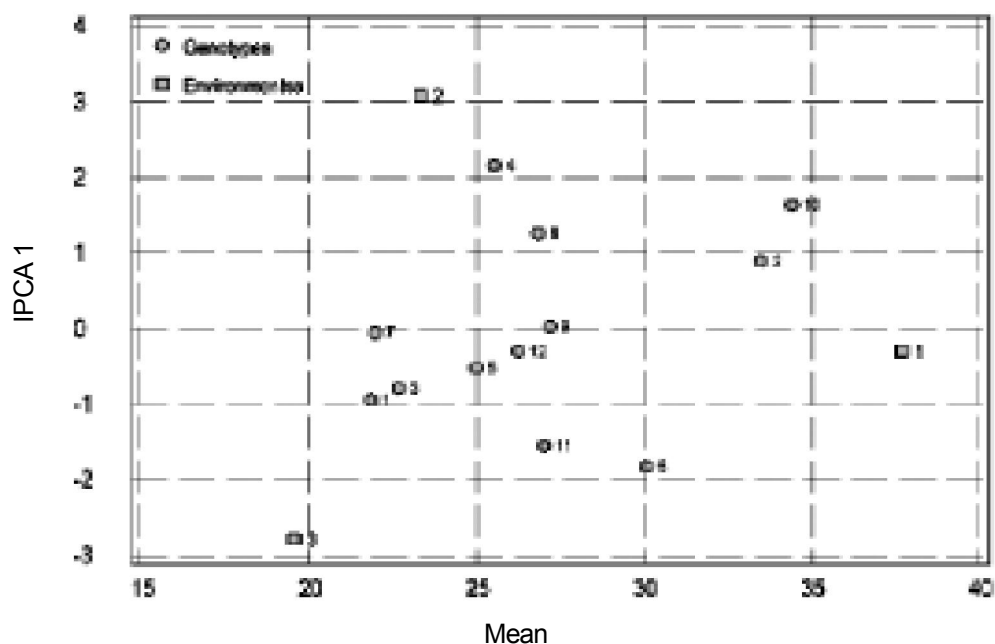
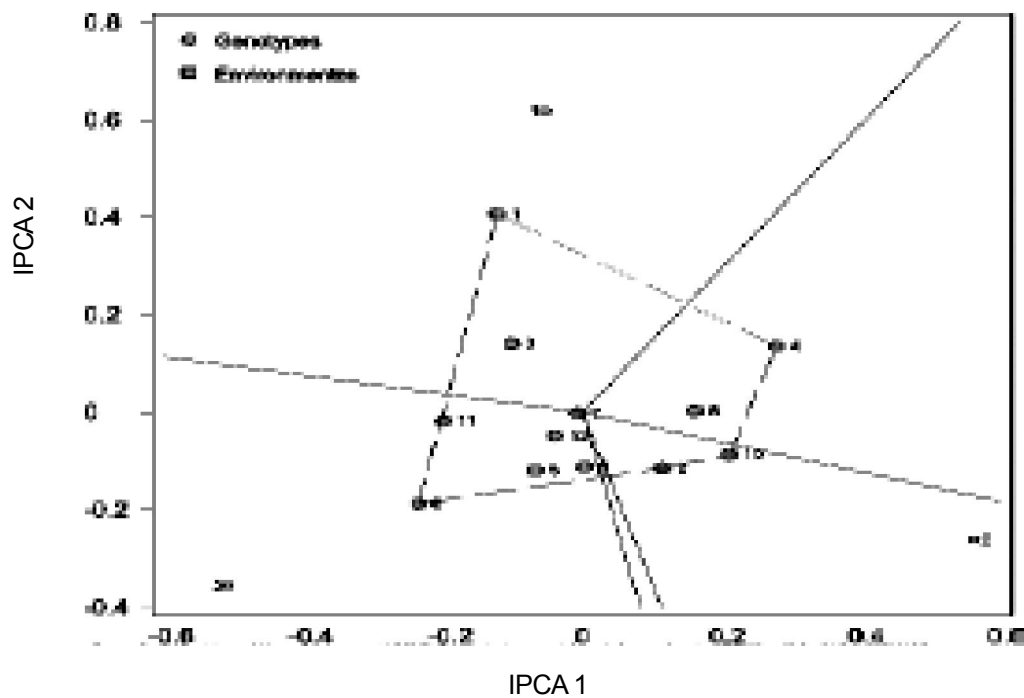


Fig 2 AMMI 2 biplot-IPCA 1 and IPCA 2 scores of twelve genotypes and three environments plotted against number of pods per plant in soybean [*Glycine max* (L.) Merrill]



Genotypes of soybean

- | | | | |
|------------|--------------|--------------|---------------|
| 1 = LSb 1 | 4 = MRSB 345 | 7 = JS 95-60 | 10 = LSb 23 |
| 2 = JS 335 | 5 = LSb 21 | 8 = LSb 36 | 11 = PK 1029 |
| 3 = LSb 13 | 6 = LSb 3 | 9 = RKS 18 | 12 = JS 93-05 |

Fig. 3 AMMI 1 biplot-IPCA 1 scores of twelve genotypes and three environments plotted against biological yield per plant (g) in soybean [*Glycine max* (L.) Merrill]

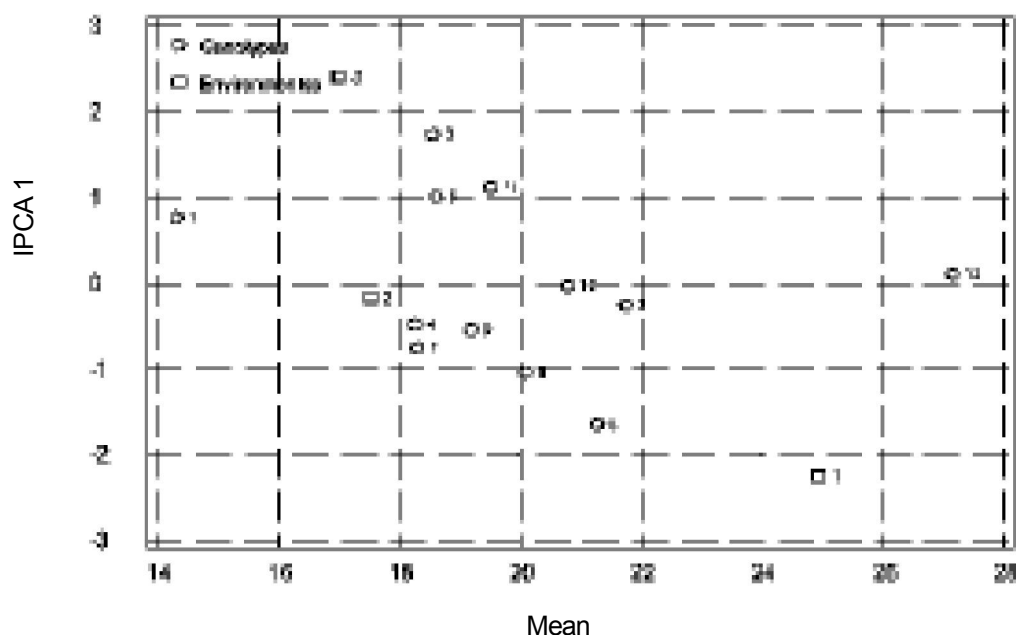
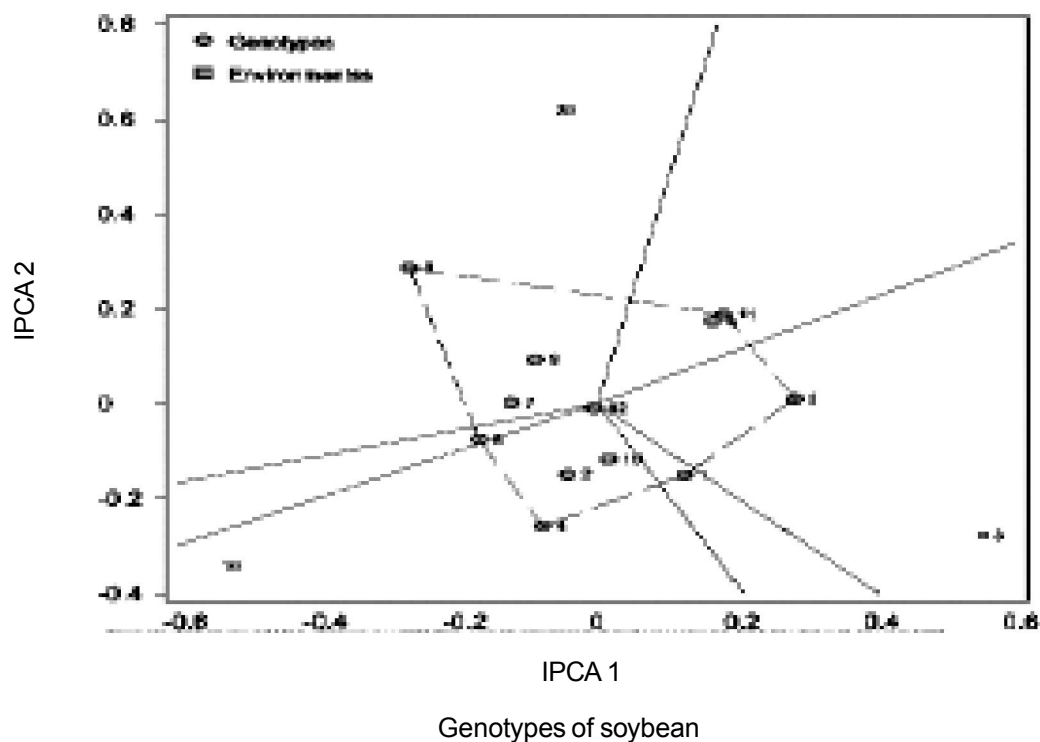


Fig. 4 AMMI 2 biplot-IPCA 1 and IPCA 2 scores of twelve genotypes and three environments plotted against biological yield per plant (g) in soybean [*Glycine max* (L.) Merrill]



1 = LSb 1

4 = MRSB 345

7 = JS 95-60

10 = LSb 23

2 = JS 335

5 = LSb 21

8 = LSb 36

11 = PK 1029

3 = LSb 13

6 = LSb 3

9 = RKS 18

12 = JS 93-05

Fig. 5: AMMI 1 biplot-IPCA 1 scores of twelve genotypes and three environments plotted against seed yield per plant (g) in soybean [*Glycine max* (L.) Merrill]

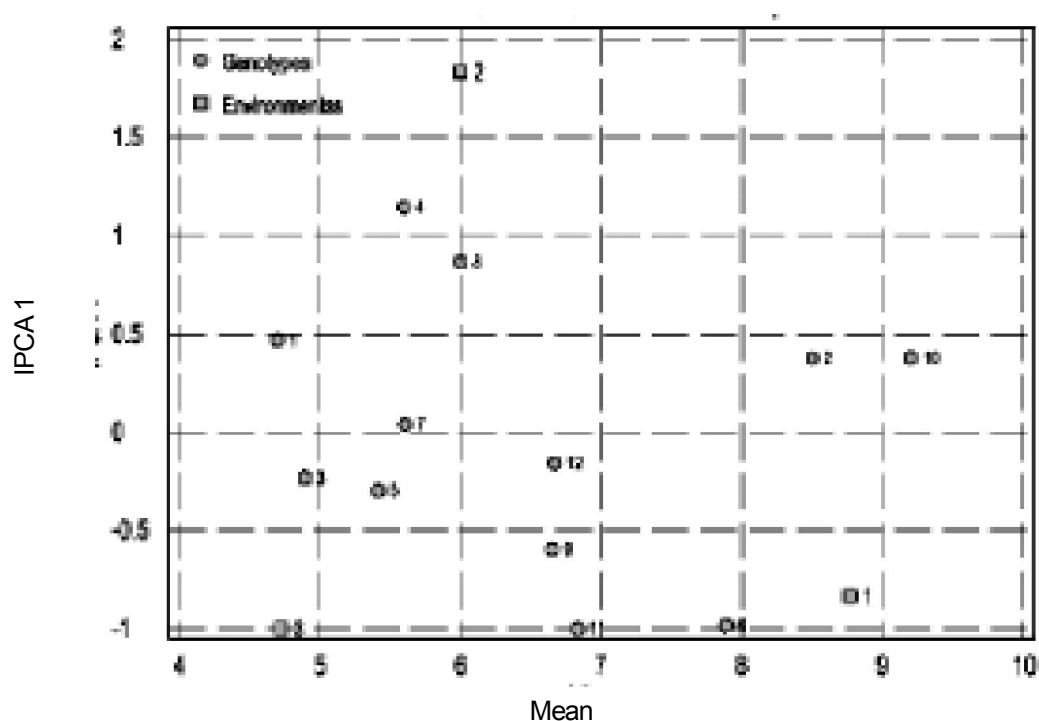
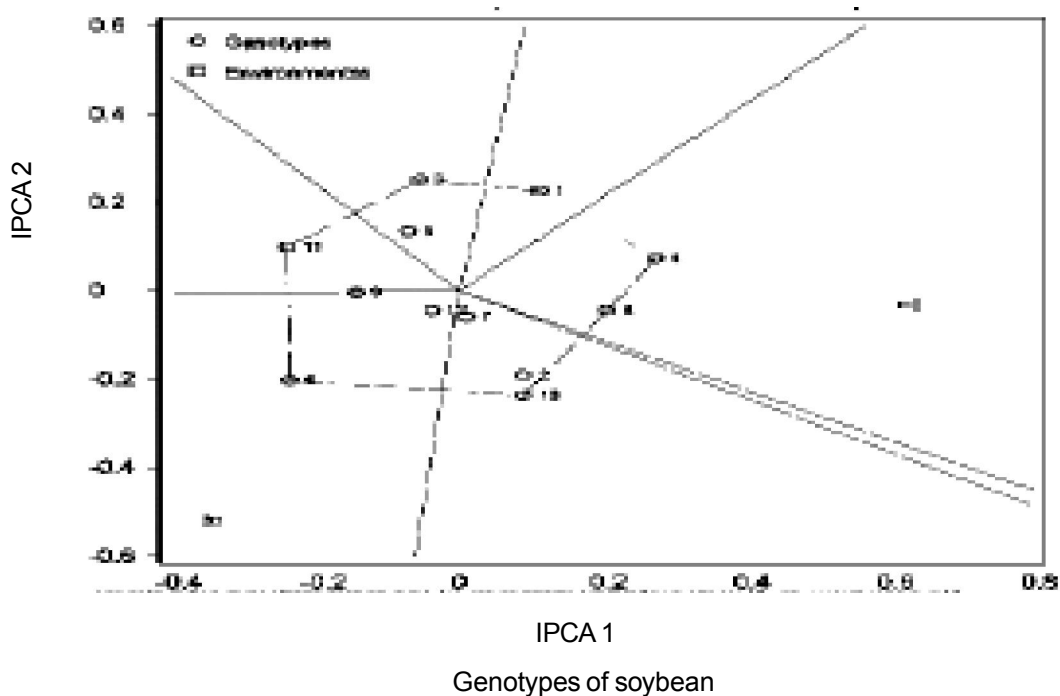


Fig. 6: AMMI 2 biplot-IPCA 1 and IPCA 2 scores of twelve genotypes and three environments plotted against seed yield per plant (g) in soybean [*Glycine max* (L.) Merrill]



1 = LSb 1	4 = MRSB 345	7 = JS 95-60	10 = LSb 23
2 = JS 335	5 = LSb 21	8 = LSb 36	11 = PK 1029
3 = LSb 13	6 = LSb 3	9 = RKS 18	12 = JS 93-05

Fig. 7 AMMI 1 biplot-IPCA 1 scores of twelve genotypes and three environments plotted against harvest index (%) in soybean [*Glycine max* (L.) Merrill]

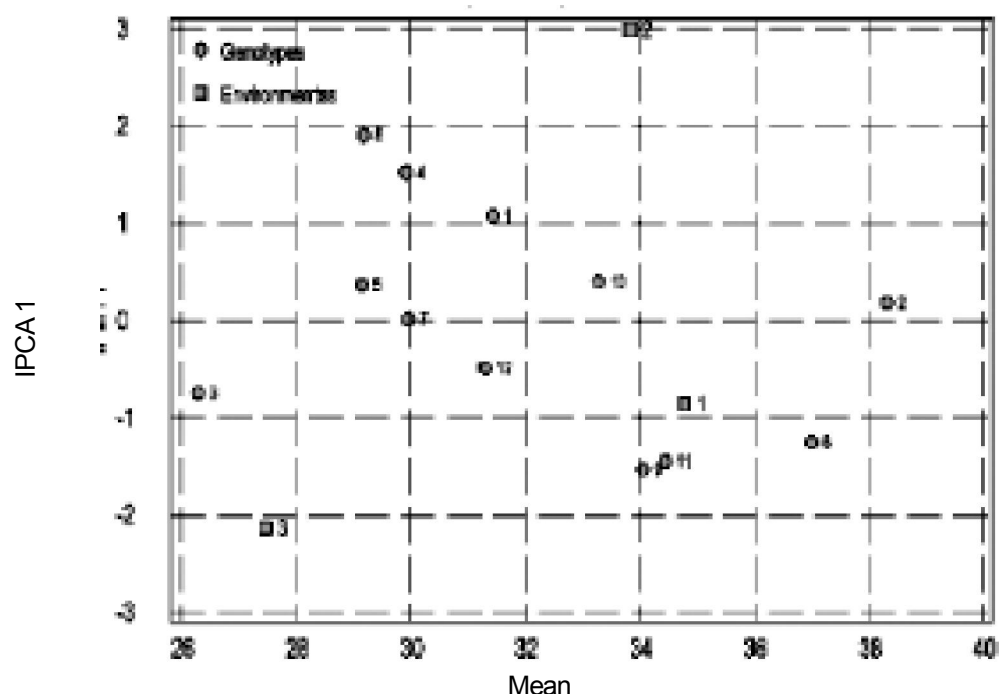
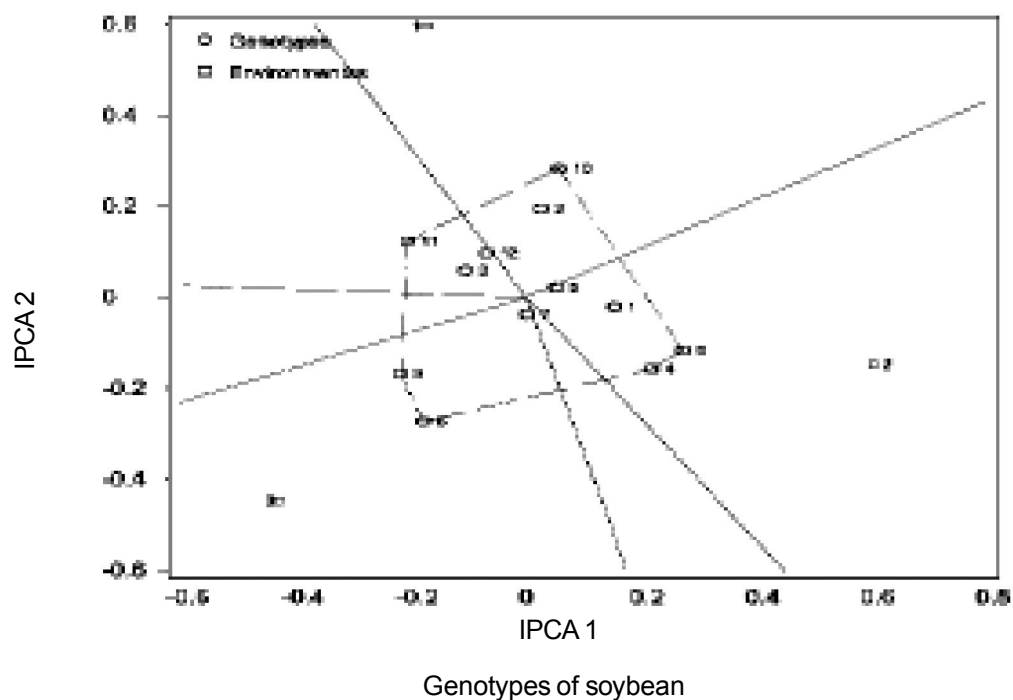


Fig. 8 AMMI 2 biplot-IPCA 1 and IPCA 2 scores of twelve genotypes and three environments plotted against harvest index (%) in soybean [*Glycine max* (L.) Merrill]



1 = LSb 1

4 = MRSB 345

7 = JS 95-60

10 = LSb 23

2 = JS 335

5 = LSb 21

8 = LSb 36

11 = PK 1029

3 = LSb 13

6 = LSb 3

9 = RKS 18

12 = JS 93-05

(LSb 23) had higher mean value. Genotypes 3 (LSb 13), 4 (MRSB 345) and 6 (LSb 3) were suited to some environments only, according to AMMI biplot (Fig. 3).

According to interaction (AMMI 2) biplot the stable genotypes were 2 (JS 335), 7 (JS 95-60), 9 (RKS 18), 10 (LSb 23) and 12 (JS 93-05) and the rest of the genotypes have specific adaptation for biological yield per plant. The environments 1 and 3 were identified as most discriminating ones as indicated by the longest distance between their marker and the origin. Among environments, environment 3 is most suitable environment as indicated by high mean value of IPCA 1 and low values of IPCA 2 (Fig. 4).

In case of harvest index, the genotypes 2 (JS 335), 5 (LSb 21), 7 (JS 95-60), 10 (LSb 23) and 12 (JS 93-05) were identified as stable genotypes. Among five, genotypes 2 (JS 335) and 10 (LSb 23) had high mean values, which are most desirable. Genotypes 3 (LSb 13), 6 (LSb 3), 9 (RKS 18) and 11 (PK 1029) were specific to different environments. Genotypes 6 (LSb 3), 9 (RKS 18) and 11 (PK 1029) were suited to environment 1 according to AMMI 1 biplot (Fig. 7).

According to interaction (AMMI 2), biplot the genotypes 1 (LSb 1), 2 (JS 335), 3 (LSb 13), 5 (LSb 21), 7 (JS 95-60) and 12 (JS 93-05) were identified as most stable genotypes which were present within the polygon. The environments 2 and 3 were identified as most discriminating ones as indicated by the longest distance between their marker and the origin. The environment 2 was identified as most suitable environment for harvest index as indicated by high IPCA 1 value and low IPCA 2 values (Fig 8).

For seed yield per plant the genotypes 3 (LSb 13), 7 (JS 95-60) and 12 (JS 93-05) were identified as stable genotypes and among three, genotype 12 (JS 93-05) had high mean value which is most desirable. Genotypes 4 (MRSB 345), 6 (LSb 3), 8 (LSb 36), 9 (RKS 18) and 11 (PK 1029) were specific to different environments. Genotypes 4 (MRSB 345) and 6 (LSb 3) were suited to environment 2 and 1, respectively according to AMMI 1 biplot (Fig 5).

However, according to interaction (AMMI 2) biplot the stable genotypes were 2 (JS 335), 5 (LSb

21), 7 (JS 95-60), 9 (RKS 18) and 12 (JS 93-05) were identified as most stable genotypes and presented within the polygon for seed yield per plant. The environments 2 and 3 were identified as most discriminating ones as indicated by the longest distance between their marker and the origin. Among the environments, environment 2 is most suitable environment as indicated by high mean value of IPCA 1 and low values of IPCA 2 (Fig 6).

While in AMMI model, IPCA1 component significantly explained the genotype environment interactions, in case of number of pods per plant (73.35%), biological yield per plant (59.25%), harvest index (69.77%) and seed yield per plant (66.27%) 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.

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