Phenotypic Stability Analysis in Sesamum (*Sesamum indicum* L.) utilizing Regression and AMMI models

P Sumalatha, P V Rama Kumar, C Panduranga Rao and R Srinivasulu
Department of Genetics and Plant Breeding , Agricultural College, Bapatla 522 101, Andhra Pradesh

ABSTRACT

Genotype-environment interaction was studied for seed yield in 10 genotypes of sesame during *kharif* 2006 and *rabi* 2006-07. Significant genotype and environment interaction was observed for all the characters except harvest index and oil content. Both linear and non-linear components of GXE interaction were found to be significant for all the characters. None of the genotypes exhibited stable performance for all the traits, however, genotypes Nellore Brown Local and Madhavi were stable for both seed yield per plant and seed yield per plot. The analysis of variance exhibited that all the three sources *i.e.,* genotype main effect, environmental additive effect, GXE (non-additive effects) and IPCA 1 have significant effects for days to 50% flowering, 1000-seed weight, seed yield per plot and harvest index. In AMMI 1 biplot, the genotypes BPT Local and Nellore BrownLocal for days to 50% flowering,YLM-11 and EC 358022 for 1000-seed weight, Madhavi and Nellore Brown Local for seed yield per plot and harvest index were stable. In AMMI 2 biplot, genotype Vinayak for days to 50% flowering, EC 358022 and Vinayak for 1000-seed weight, Nellore Brown Local for seed yield per plot and harvest index were nearer to the IPCA origin hence, these genotypes were stable over environments.

Key words : AMMI,Sesamum, Stability.

Sesame (*Sesamum indicum* L.) is an important ancient oilseed crop of semiarid and arid areas. Its productivity is very low and fluctuating mainly due to non-availability of suitable high yielding stable genotypes. Genotype x environment interactions were known to interfere with the evaluation of genotype and reduces the progress of selection in plant breeding programmes as the genotype expression is masked and as such, these interactions are of considerable importance in developing improved varieties. To achieve the best and maximum expression of genotypes Andrew (1993) suggested to grow the material at sufficient test locations. 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 combine to constitute the Additive Main effects and Multiplicative Interaction (AMMI) model (Gauch and Zobel, 1988).In the present study, an attempt was made to study the stability of genotypes by using both regression and AMMI models.

MATERIAL AND METHODS

The experimental material comprising 10 sesamum genotypes were grown in randomized block design with three replications during *kharif* 2006 (3 sowing dates *i.e.,* 3.8.2006, 19.08.2006 and 3.9.2006) and *rabi* 2006-07 (3 sowing dates *i.e.,* 17.1.2007, 2.2.2007 and 18.02.2007), at Agricultural College Farm, Bapatla. Each plot consisted of 3 rows, each 2 m long with a crop geometry of 30x10 cm. Ten genotypes of sesamum were sown on 6 sowing dates . Data were recorded on 12 characters *viz.,* number of primaries, number of secondaries, plant height, days to 50% flowering, number of capsules per plant, days to maturity, number of seeds per capsule, 1000 seed weight, harvest index, oil content, seed yield per plant and seed yield per plot. Stability parameters were analysed using regression model (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 X E, a feature of AMMI model is the biplot procedure in which genotypes and environments taking mean values on abscissa and

$IPCA_1$ scores on ordinate are plotted on the same diagram, facilitating inference about specific interactions as indicated by the sign and magnitude of $IPCA_1$ 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

Pooled analysis of variance (Table 1) indicated highly significant differences among the genotypes for all the traits and the environments also varied widely as evidenced from significant differences for environment and the environment (linear) component for all the characters. Most of variances were attributed due to environments with profound influence of environment on seed yield as reported by Thiyagarajan and Ramanathan (1996).

Significant mean squares due to genotypex environment interaction indicated the differential behaviour of genotypes across the environments (Verma and Mahto, 1994). A major portion of genotype environment interaction was also attributed to linear component suggesting that variation in the performance of genotypes is due to the genotypes on environments and as such, performance is predictable in nature. Environmental linear (Table 2) for days to 50% flowering, number of capsules per plant, number of seeds per capsule, 1000 seed weight, harvest index, oil content, seed yield per plant and seed yield per plot indicated the suitability of genotypes to these characters in 6 different environments. The three parameters X, bi and S2d together gave the idea of suitability of genotypes across environment, (Eberhart and Russell, 19966.) The genotypes were classified into three groups based on the stability parameters for all the traits at a time (Table 3).

It is observed that no genotype was suitable for all the characters. However, genotypes Nellore Brown Local and Madhavi showed stable performance for yield and some of the component traits under average environmental conditions.

The combined analysis of variance (ANOVA) of 10 genotypes in 6 environments pertaining to AMMI model is shown in Table 4.The IPCA scores of a genotype in the analysis are an indication of the stability of a genotype over environments.

AMMI analysis for days to 50% flowering showed that genotypes and environments were significant. The genotype, environment and genotype x environment interaction accounted for 30.02%, 56.58% and 13.44% of the total variation, respectively indicating the G x E proportion is low in total sum of squares. The ANOVA indicated that G x E interaction was partitioned into four interaction principal component axes (IPCAs). Only the IPCA 1 axis was significant and explained 76.14% of the total G x E interaction sum of squares percentage. The IPCA 2, IPCA 3 and IPCA 4 explained 17.32% ,5.76% and 0.47% of the total G x E interaction sum of squares percentage and were non-significant. According to AMMI 1 biplot (Fig.1), genotypes 1 (BPT Local) and 3 (Nellore Brown Local) were identified as stable genotypes. The genotype 3 (Nellore Brown Local) and environment 2 (II) have the same sign on IPCA axis, their interaction is positive *i.e.,* specifically adapted to that environment. In AMMI 2 biplot (Fig.2), the genotypes 7 (Vinayak) and 2 (Tanuku Brown) were nearer to IPCA origin, hence these genotypes were stable over environments.

AMMI analysis for 1000- seed weight showed that genotypes and environments were significant. The genotype, environment and genotype x environment interaction accounted for 68.64%, 20.12% and 9.53% of the total variation, respectively. The ANOVA indicated that only the IPCA 1 axis was significant and explained 81.25% of the total G x E interaction sum of squares percentage. The IPCA 2, IPCA 3 and IPCA 4 explained 10.40% ,5.89% and 1.76% of the total G x E interaction sum of squares percentage and were non-significant. According to AMMI 1 biplot (Fig.3), genotypes 8 (EC 358022) and 10 (YLM-11) were identified as stable genotypes. In AMMI 2 biplot (Fig.4), the genotypes 8 (EC 358022) and 7 (Vinayak) were nearer to IPCA origin, hence these genotypes were stable over environments. Among the environments, environment I is most suitable as indicated by high mean value of IPCA 1 and low value of IPCA 2.

For seed yield per plot, the analysis of variance exhibited that all the three sources *i.e.,* genotype main effect, environmental additive effect and G X E (non-additive) effects have significant effects and accounted for 43.60, 47.49 and 8.90% of the total variance, respectively, indicating differential response of genotypes with the change of locations. The G X E interaction was significant and was further partitioned into AMMI components IPCA 1, IPCA 2, IPCA 3 and IPCA 4 with the contribution of 53.08, 21.03, 16.53 and 6.51% , respectively to the total G XE interaction variance. The first three AMMI

Table 1. Analysis of variance (as per Eberhant and Russell, 1966) for stability performance of characters in sesamumSesamum (Sesamum indicum L.) .

Source	d.f.	Days to 50% flowering	No.of capsules plant⁻¹	No.of seeds capsule⁻¹	1000 seed weight	Harvest index	Oil content	Seed yield plant⁻¹	Seed yield plot⁻¹
Mean squares									
Genotype	9	12.400**++	192.042**++	160.891**++	0.361**++	8.380**++	15.654**++	18.035**++	45907.916**++
Environments	5	42.062**++	306.564**++	454.078**++	0.188**	17.242**++	2.015**	29.025**++	90014.947**++
Genotype X environment	45	1.112**+	18.086*++	19.732**	0.012**	0.431**+	0.439**	0.714**+	1874.150**++
Environment (linear)	1	210.309**++	1532.821**++	2270.388**++	0.942**	86.211**++	10.077**++	145.126**++	450074.739**++
Genotype X environment (linear)	9	3.818**++	28.975*+	6.963++	0.040**	0.774*	0.209	1.529**	4163.601**+
Pooled deviation	40	0.392**	13.828**	20.632**	0.004	0.311	0.447**	0.459	1171.609
Pooled error	108	0.087	3.519	2.636	0.004	0.243	0.047	0.326	838.436

* Significant at 0.05 level   When tested against pooled error
** Significant at 0.01 level
++ Significant at 0.01 level when tested against pooled deviation

Table 2. Environment index values (I_j) for different characters (Eberhant and Russell, 1966) in sesamum(Sesamum indicum L.) .

Character	Environment indices					
	E I	E II	E III	E IV	E V	E VI
1. Days to 50% flowering	-2.133	0.200	-1.667	1.600	3.133	-1.133
2. No. of capsules plant⁻¹	-9.304	-2.964	1.503	5.056	0.226	5.483
3. No. of seeds capsule⁻¹	-8.821	-8.024	2.709	7.402	3.252	3.482
4. 1000 seed weight	-0.203	-0.124	0.072	0.151	0.008	0.098
5. Harvest index	-2.020	-1.025	0.169	1.492	0.319	1.065
6. Oil content	-0.293	-0.267	-0.610	0.383	0.497	0.290
7. Seed yield plant⁻¹	-2.490	-1.458	-0.005	1.980	0.584	1.388
8. Seed yield plot⁻¹	-134.972	-82.267	-10.766	109.831	38.339	79.834

Table 3. Sesamum (*Sesamum indicum* L.) genotypes classified into different groups of environmental conditions as per Eberhant and Russell, 1966.

Character	Group I	Group II	Group III
Days to 50% flowering	BPT Local	Gowri	Tanuku Brown, EC 358039
Number of capsules per plant	-	YLM-11	Madhavi
Number of seeds per capsule	NRD 1110, Madhavi	YLM-11	-
1000 seed weight	-	Gowri,Madhavi YLM-11	BPT local, Nellore Brown Local
Harvest index	Nellore Brown Local	YLM – 11	Madhavi, EC 358039
Oil content	-	Gowri	NRD 1110, Vinayak
Seed yield per plant	Nellore Brown Local, Madhavi	YLM-11	BPT Local
Seed yield per plot	Nellore Brown Local, Madhavi	YLM-11	BPT Local

Group I   : Stable genotypes for average environmental conditions. Genotypes with high mean, regression coefficient near to unity and least deviation from regression

Group II   : Stable genotypes for favourable conditions. Genotypes with high mean, regression coefficient significant and higher than unity and least deviation from regression

Group III.   : Stable genotypes for poor environmental conditions. Genotypes with high mean, less than unity regression and least deviation from regression

Table 4. Analysis of variance of the AMMI model in sesamum (*Sesamum indicum* L.)

Source	Days to 50% flowering			1000 seed weight			Seed yield per plot			Harvest index		
	df	MS	% explained	df	MS	% explained	df	MS	% explained	df	MS	% explained
Trials	59	6.30**		59	0.08**		59	16060.7**		59	3.07**	
Genotypes	9	12.40**	30.02	9	0.36**	68.64	9	45907.8**	43.60	9	8.38**	41.66
Environments	5	42.06**	56.58	5	0.19**	20.12	5	90014.8**	47.49	5	17.24**	47.66
G × E Interaction	45	1.11	13.44	45	0.01	9.53	45	1874.1	8.90	45	0.43	1.07
PCA I	13	2.93**	76.14	13	0.13**	81.25	13	3443. 6*	53.08	13	0.68*	45.83
PCA II	11	0.79	17.32	11	0.005	10.40	11	1612.5	21.03	11	0.57	32.79
PCA III	9	0.32	5.76	9	0.003	5.89	9	1549.3	16.53	9	0.24	11.02
PCA IV	7	0.03	0.47	7	0.001	1.76	7	784.3	6.51	7	0.23	8.14
Residual	5	0.03	0.32	5	0.001	0.69	5	479.5	2.84	5	0.09	2.22
Pooled residual	45	1.11		45	0.011		5	479.5		32	0.33	

  *Significant at 0.05 level   MS = Mean Squares
  ** Significant at 0.01 level   df = Degrees of freedom

Fig. 1 : Biplot (AMMI 1) for days to 50% flowering
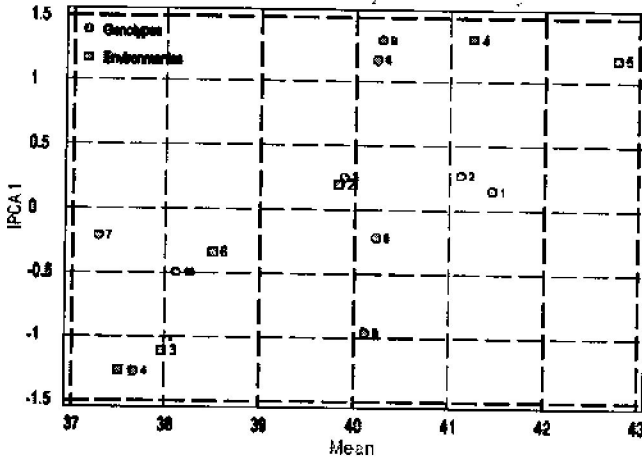

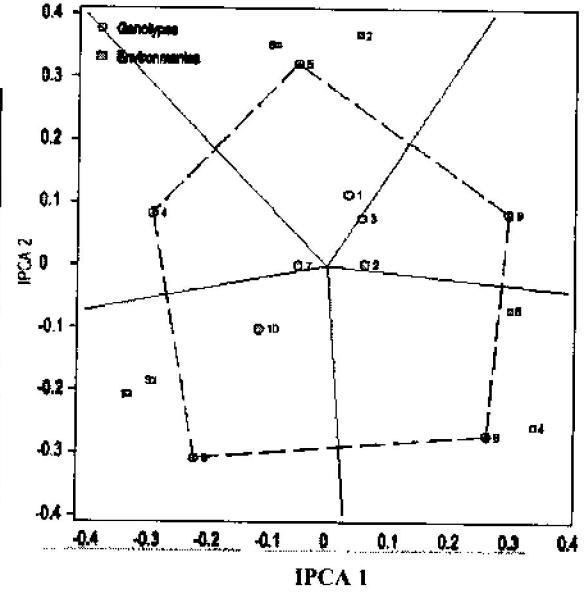**Fig.2 : Interaction Biplot (AMMI 2) for days to 50% flowering**
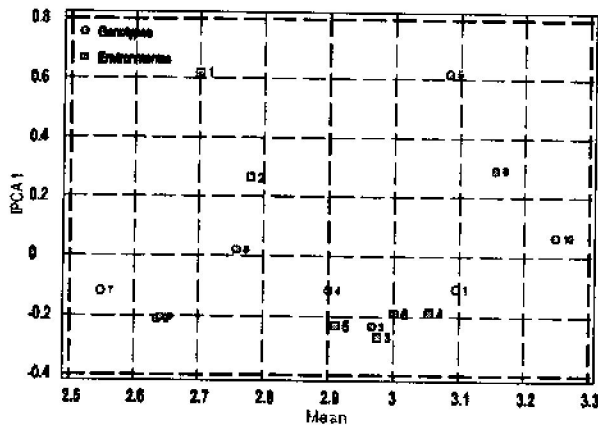

Fig.3 : Biplot (AMMI 1) for 1000 seed weight

Fig.4: Interaction Biplot (AMMI 2) for 1000 seed weight
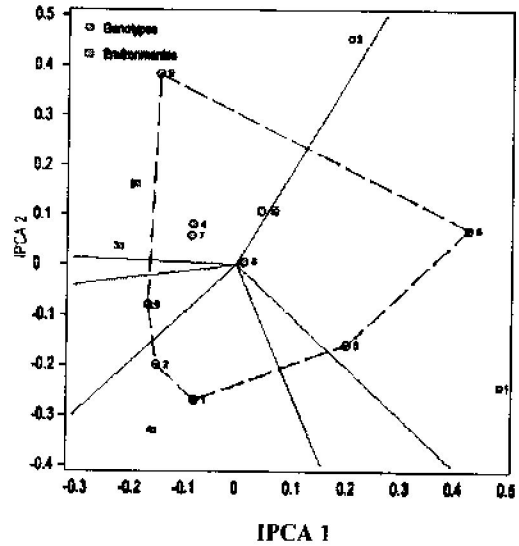
GENOTYPES

1.	BPT local	2. Tanuku Brown	3. Nellore Brown Local	4. NRD 1110	5. Gowri
6.	Madhavi	7. Vinayak	8. EC 358022	9. EC 358039	10. YLM-11

ENVIROMENTS

Kharif	1. 03.08.2006	2. 19.08.2006	3. 03.09.2006
Rabi	4.17.01.2007	5. 02.02.2007	6. 18.02.2007

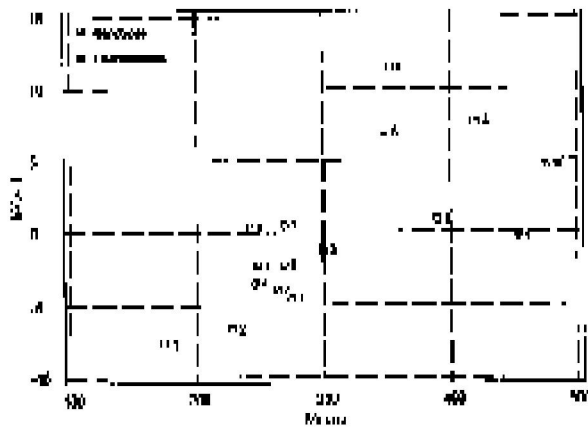Fig.5 : Biplot (AMMI 1) for seed yield per plot

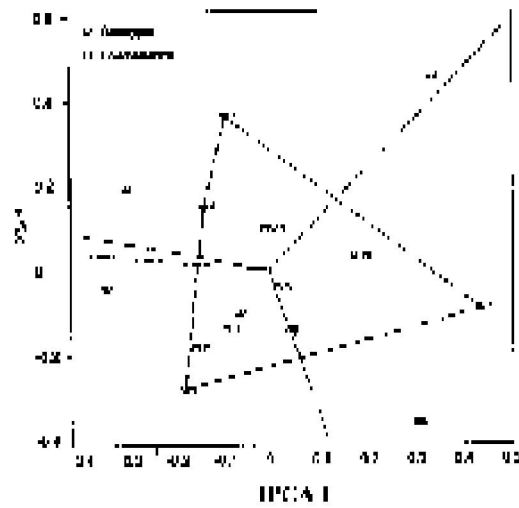Fig.6 : Interaction Biplot (AMMI 2) for seed yield per plot
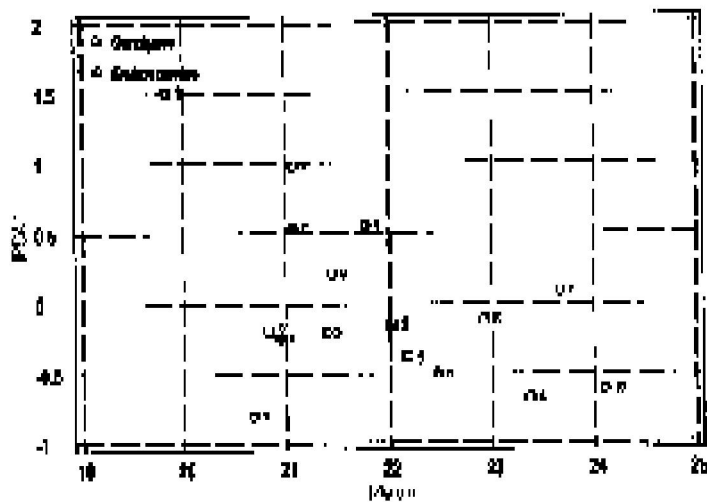

Fig. 7 : Biplot (AMMI 1) for harvest index

Fig.8 : Interaction Biplot (AMMI 2) for harvest index
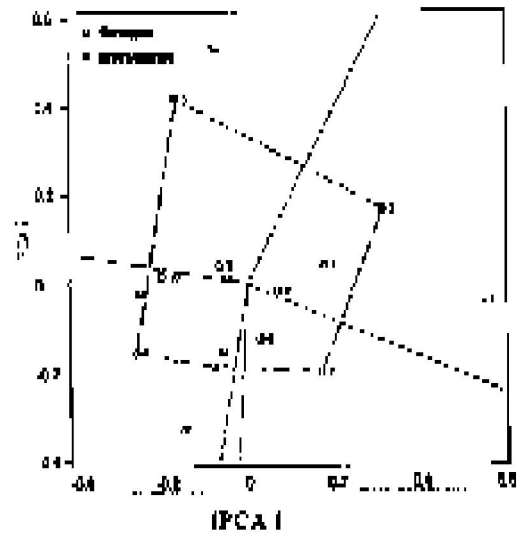
GENOTYPES
1. RPT local   2. Lunoka Brown   7. Kellare Brown Local   4. NB13 1110   5. Gowri
6. Madhavi   7. Vanngali   8. IC0058022   9. IC0758030   10. YLM 11

ENVIRONMENTS

Kharif   1. 05.08.2006   2. 19.08.2006   3. 03.09.2006

Rabi   4. 17.01.2007   5. 02.02.2007   6. 18.02.2007

components representing interaction pattern were significant and jointly contributed 90.64% of the interaction component with 73.33% of the degrees of freedom for G X E interaction.

In AMMI 1 biplot (Fig. 5) the genotypes 6, 3 and 8 (Madhavi, Nellore Brown Local and EC 358022 respectively) are stable because IPCA scores are near to zero with high mean. The genotypes 5, 10 and 3 (Gowri, YLM-11 and Nellore Brown Local) and environments 5 and 4 (V and IV), respectively have the same sign on IPCA axis, their interaction is positive *i.e.,* they are specifically adapted to these environments. In AMMI 2 biplot (Fig.6), genotypes 3, 6 and 8 (Nellore Brown Local, Madhavi and EC 358022) are nearer to the IPCA origin. Hence, they are stable over environments for this trait. These results are in conformity with Manivannan and Ganesan (2001).

AMMI analysis for harvest index showed that genotypes and environments were significant. The genotype, environment and genotype x environment interaction accounted for 41.66%, 47.62% and 1.07% of the total variation respectively. The ANOVA table indicated that only the IPCA 1 axis was significant and explained 45.83% of the total G X E interaction sum of squares percentage. The IPCA 2, IPCA 3 and IPCA 4 explained 32.79% ,11.02% and 8.14% of the total G x E interaction sum of squares percentage and were non-significant. According to AMMI 1 biplot (Fig.7), genotypes 6 (Madhavi) and 3 (Nellore Brown Local) were identified as stable genotypes. In AMMI 2 biplot (Fig.8), the genotypes 9 (EC 358039) and 3 (Nellore Brown Local) were nearer to IPCA origin, hence these, genotypes were stable over environments. Among the environments, environment I is most suitable as indicated by high mean value of IPCA 1 and low value of IPCA 2.

The present analysis, therefore, indicates that making recommendation for identification of a genotype which is at present done on the basis of mean yield, it is important to analyse and patternise G X E interaction. The results discussed here confirm that AMMI analysis with its biplot is a very useful tool in analyzing data. AMMI partition the non-linear interaction component of genotype with environment interaction and also helps in having deeper insight into study of environmental contribution to G X E interaction as also pointed out by Zobel *et al.* (1988).

The genotypes 6 and 3 (Madhavi and Nellore Brown Local) respectively showed desirable performance for seed yield per plot using both regression and AMMI models.

The G X E was non-significant for 1000 seed weight when tested aginst pooled deviation, while G X E (I) non-significant for 1000-seed weight, harvest index and seed yield plot^{-1} when tested against pooled deviation as per Eberhart and Russell (1966).

However, days to 50% flowerings, 1000-seed weight, seed yield plot-1 and harvest index expressed significant IPCAI Score in AMMI analysis which points out the superiority of AMMI analysis in interpreting stable genotypes compared to Eberhart and Russell (1966) model.

LITERATURE CITED

Andrew D J 1993. In: Advances in small millets (Eds.Riley *et al.*) Oxford and IBH. New Delhi, 417.

Bahman Shafii, Karen A Mahler, Willian J P and Dick L Auld 1992. Genotypex environment interaction effects on winter rape seed and oil content.Crop science, 32:922-927.

Eberhart S A and Russell W A 1966. Stability parameters for comparing crop varieties. Crop Science, 6 : 36- 40.

Gauch H G 1988. Model selection and validation for yield trials with interaction. Biometircs, 34:705-715.

Gauch H G and Zobel R W 1988. Predictive and postdictive success of statistical analysis of yield trials. Theoritical and Applied Genetics, 76:1-10.

Manivannan N and Ganesan J 2001. Stability of sesame (*Sesamum indicum* L). hybrids in multilocation trails. Journal of Oilseeds Research, 18(1):10-16.

Sharma P K, Gupta P K and Govila O P 1998. AMMI analysis of a pearl millet yield trial. Indian Journal of Genetics and Plant Breeding, 58(2): 183-192.

Thiyagarajan K and Ramanathan T 1996. Character association and path coefficient analysis of components of seed yield in sesamum. Madras Agricultural Journal, 83 : 683 – 687.

Verma A K and Jay Lal Mahto 1994. Stability for yield and yield attributing characters in sesame under rainfed conditions. Journal of Oilseeds Research, 11 (2): 170-173.

Zobel R W, Wright M J and Gauch H G 1988. Statistical analysis of a yield trial. Agronomy Journal, 80: 388-393.