Phenotypic Stability Analysis in Italian Millet Utilizing Regression and AMMI Models for Root Characters

G Usha Kiran, C Panduranga Rao, J S V Samba Murthy, V Srinivasa Rao and M Lal Ahamed

Department of Genetics and Plant Breeding, Agricultural College, Bapatla 522101, A P

ABSTRACT

Twenty italian millet genotypes were evaluated for root characters over 16 environments (8 sowing dates with 2 fertility levels).The analysis of variance of Eberhart and Russell indicated that G´E interaction was significant for 2 characters under study and that genotypes differed significantly. Among the AMMI components first four IPCA axis were explained most of the portion of G X E interaction than other IPCA axis. The ANOVA (Eberhart and Russell,1966) indicated non-significant G X E (linear) interaction for VRM, when tested against pooled deviation. As per AMMI analys, is the IPCA significantly contributed to WRM and VRM while IPCA contributed significantly to G X E interaction for WRM and VRM. This brings out clearly the advantage of AMMI ANOVA in bringing out G ´ E interaction through IPCA which gets combined with error in the other two ANOVA and points out the utility of AMMI models in studying the significant G X E interaction and identifying stable genotypes for characters which so undetected in the earlier analysis. According to AMMI analyses, the genotypes GS 467, GS 486 and GS 489 (for weight of the root at main field); GS 445, GS 450 and GS 465 (for volume of the root at main field) are more stable as IPCA score was near zero *i.e,* interaction with environments was less. According to Eberhart and Russell the genotypes, GS 444, GS 479 and GS 487 (for weight of the root at main field); GS 486 and GS 487 (for volume of the root at main field); showed desirable performance.

Key words : AMMI, Italian millet, Stability

Italian millet [*Setaria italica* L. Beauv] is the most important small millet in India next to Finger millet. It is commonly known as korra, in Andhra Pradesh. It is grown extensively in diverse agro-climatic regions. It is grown for grain and fodder. The ordinary analysis of variance (ANOVA) is useful for identifying and testing sources of variability, but 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 (Gauch and Zobel, 1988).

MATERIAL AND METHODS

Twenty genotypes namely GS 440(1), GS 444 (2), GS 445 (3), GS 450 (4), GS 462 (5), GS 463 (6), GS 465 (7), GS 467 (8), GS 477 (9), GS 479 (10), GS 480 (11), GS 482(12), GS 486(13), GS 487(14), GS 488 (15), GS 489(16), Krishnadevaraya (17), Narasimharaya (18) and Srilakshmi (19) and Prasad (20) were sown during *kharif* 2009 (four sowing dates) and *rabi* 2009-10 (four sowing dates) with two fertility levels (high fertility N: 80 kg ha^{-1}, P_2O_5 20 kg ha^{-1}, K_2O 20 kg ha^{-1} and normal fertility N: 40 kg ha^{-1}, P_2O_5 20 kg ha^{-1}, K_2O 20 kg ha^{-1}), thus providing 16 environments at Agricultural College Farm, Bapatla. Material was grown in randomized block design with three replications with 3m long plots of 4 rows per genotype per replication. An inter and intra row spacing of 25 cm and 10 cm was practiced. The observations were recorded on two characters in (Table 1). 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 ´ E, a feature of AMMI model is the biplot procedure in which genotypes and environments taking mean values on abscissa and IPCA scores on ordinate are plotted on the same diagram,

facilitating inference about specific interactions as indicated by the sign and magnitude of IPCA values of individual genotypes and environments (Śharma *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 analysis of variance (Table1) indicated significant genotypic differences for all the characters. The environments also varied widely as evidenced from significant differences for environments and the environment (linear) component for all the characters. The genotype-environment interaction component also showed high significance for all the characters. This indicated valid differences exist among genotypes for regression over environmental means. This requires careful interpretation of results based on non-significance of S^2d values (a parameter to measure stability) of genotypes for a particular character than the fluctuating linear component for regression coefficient (a parameter which measures responsiveness) with expected desirable performance. The genotypes GS 467, GS 486 and GS 489 (for weight of the root at main field); GS 445, GS 450 and GS 465 (for volume of the root at main field) one the stage genotypes(Table 2).

For weight of root at main field, AMMI analysis showed that genotypes and environments were significant. The genotype, environment and genotype x environment interaction accounting for 73.48%, 5.17% and 21.32% of the total variation, respectively. The ANOVA indicated that the IPCA 1 axis explained 36.97% of the total G x E interaction sum of squares with 33 degrees of freedom. The IPCA 2, IPCA 3 and IPCA 4 were explained 23.41%, 18.43% and 10.06% of the total G x E interaction sum of squares with 31, 29 and 27 df, respectively. According to AMMI1, genotypes like 8, 13 and 16 are more stable because their IPCA scores are near to zero. By AMMI2 interaction biplot the genotypes like 1, 12 and 14 were identified as most stable ones because they are situated close to the center of IPCA axis. Environment XVI is the most suited as it is indicated with high mean value of IPCA1 and low mean value of IPCA 2.

For volume of root at main field AMMI analysis for volume of root at main field showed that genotypes and environments were significant. The genotype, environment and genotype x environment interaction accounting for 86.45%, 0.17% and 13.37% of the total variation, respectively. The ANOVA indicated that the IPCA 1 explained 47.91% of the total G x E interaction sum of squares with 33 degrees of freedom. The IPCA 2, IPCA 3 and IPCA 4 were explained 23.92% ,15.37% and 7.56% of the total G x E interaction sum of squares with 31, 29 and 27 df, respectively. According to AMMI1, genotypes like 1 and 13 are generally adaptable to all environments and more stable. Genotypes like 3, 4, 7 and 16 are more stable because their IPCA scores are near to zero. By AMMI2 interaction biplot the genotypes like 13, 16 and 14 were identified as most stable ones because they are situated close to the center of IPCA axis. Environment XIV is most suited as it is indicated with high mean value of IPCA1 and low mean value of IPCA 2.

As per AMMI analysis the IPCA $_1$ significantly contributed to both characters while IPCA$_2$ contributed significantly to G X E interaction weight of root at main field and volume of root at main field. This brings out clearly the advantage of AMMI ANOVA in bringing out G X E interaction through IPCA which gets combined with error in the other two ANOVA and points out the utility of AMMI models in studying the significant G X E interaction and identifying stable genotypes for characters which so undetected in the earlier analysis.

The results discussed here confirm that AMMI analysis with its biplot is a very useful tool in analyzing data. It explains comprehensively both the effects due to genotypes and environments and also their interaction patterns. ANOVA could explain only the genotypes and environments but not their interaction. 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).

By comparing these two models for both characters, weight of root at main field and volume of root at main field, the results shown that according to AMMI analyses the genotypes 8, 13 and 16 (for weight of root at main field); 3, 4 and 7 (for volume of root at main field) are more stable because they are having IPCA score near zero that is they show less interaction with environments. According to Eberhart and Russell in table 3, the genotypes 2, 10 and 14 (for weight of root at main field); 13 and 14 (for volume of root at main field); showed desirable performance.
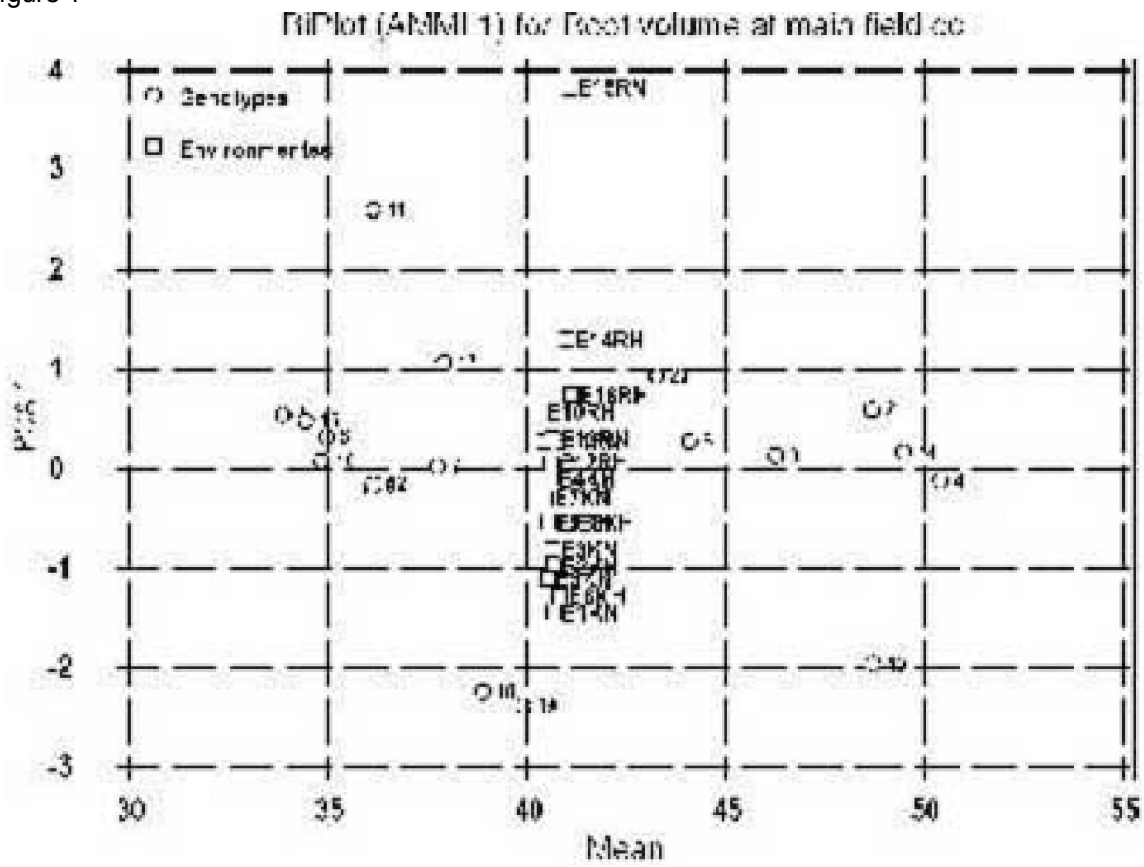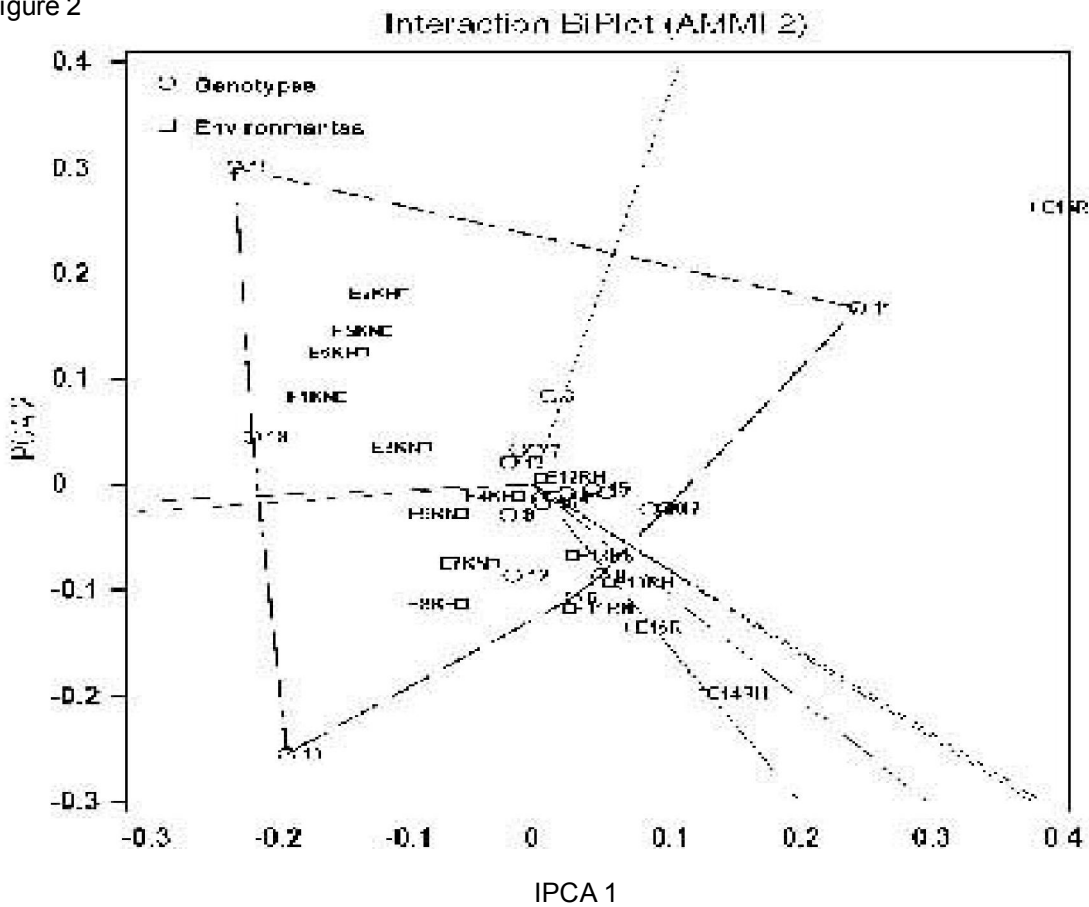
Figure 1

BiPlot (AMMI 1) for Root volume at main field co

Figure 2

Interaction BiPlot (AMMI 2)
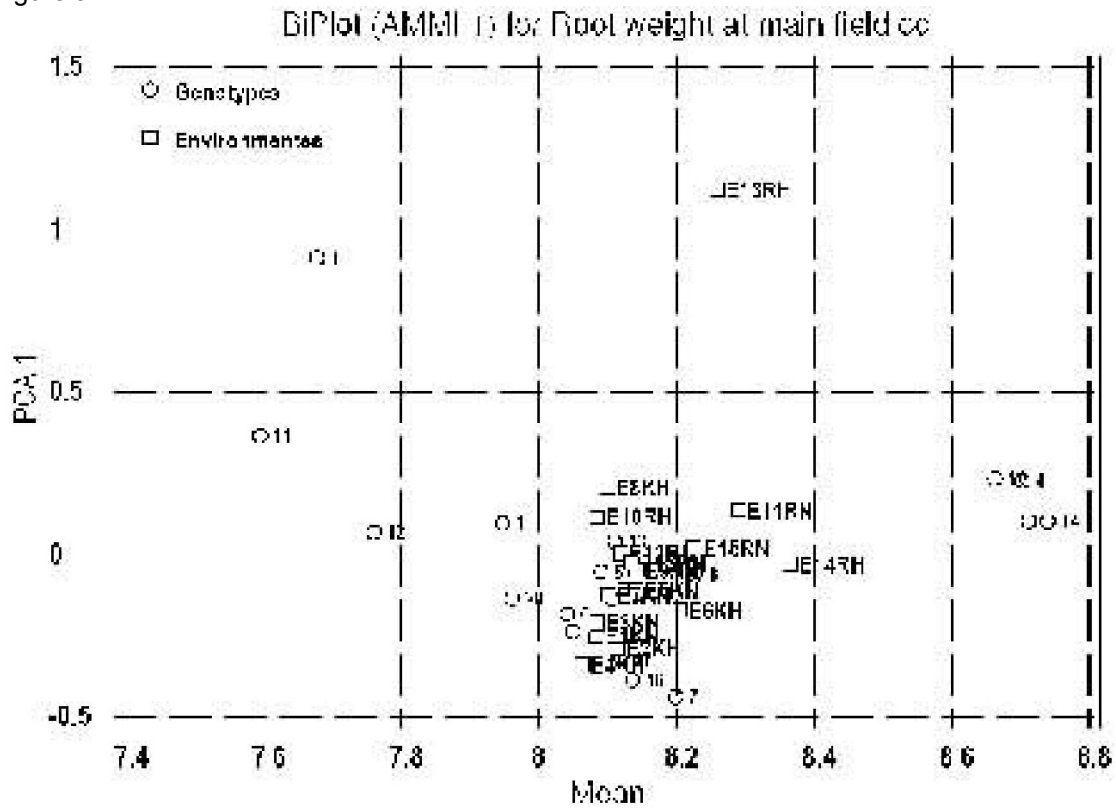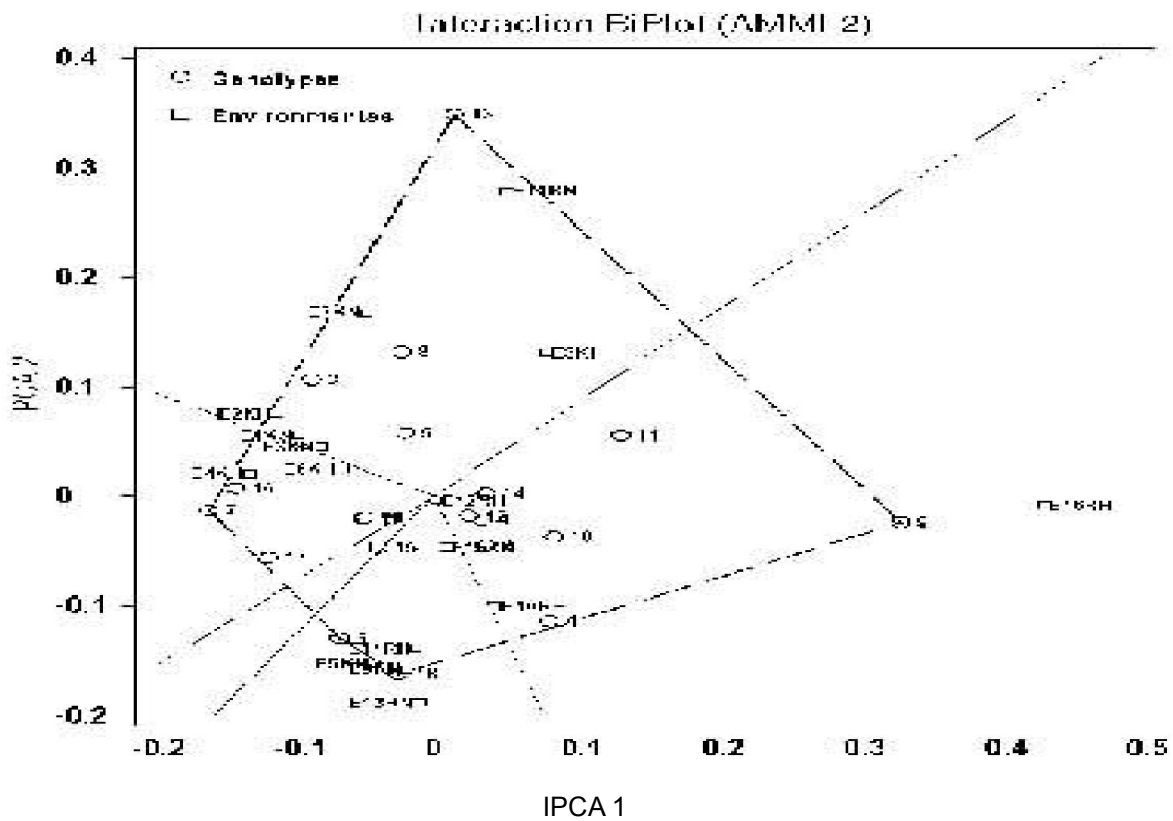
Figure 3

Figure 4

IPCA 1

Table 1. Analysis of variance for stability performance of characters in Italian millet [*Setaria italica* (L.) Beauv]

Source	d.f.	WRM (g)	VRM (g)
Genotype	19	1.713**++	492.247**++
Environments	15	0.153**++	1.236++
Genotype × environment	285	0.033++	5.075**++
Environment (linear)	1	2.294**++	18.537**++
Genotype × environment (linear)	19	0.431++	7.296**++
Pooled devia-tion	280	0.031++	4.671++
Pooled error	608	0.022	1.804

+ = Significant at 0.05 level   + + = Significant at 0.01 level

Table 2. Stability parameters for different characters as per regression model of Eberhart & Russell (1966) in Italian millet [*Setaria italica* (L.) Beauv]

Genotypes	VRM			WRM		
	$\overline{X}$	B	S^2d	X	B	S^2d
GS440	40.69	1.13	-1.52	7.94	0.68	-0.01
GS444	48.67	1.45	2.34**	8.71	1.08*	0.00
GS445	46.27	-1.41*	0.29	8.05	0.96	0.00
GS450	50.40	0.70	1.12	8.70	1.29	0.01*
GS462	44.08	1.76	-1.11	8.09	0.56	0.00
GS463	34.95	0.50	1.87*	8.04	0.91	0.01
GS465	37.75	0.19	1.12	8.19	0.18	0.02*
GS467	36.09	1.42	-0.86	8.22	0.47	-0.00
GS477	33.86	3.45	1.41*	7.67	2.86	0.07***
GS479	48.71	-4.60	9.60***	8.66	0.93	-0.01
GS480	36.14	7.77	10.26***	7.59	1.45	0.01
GS482	36.14	0.49	-0.02	7.76	1.04	-0.01
GS486	41.26	0.52	-0.85	8.11	1.20	0.06***
GS487	49.48	0.74	-0.67	8.74	1.28	-0.01
GS488	34.45	3.91	0.21	8.12	0.18*	-0.01
GS489	34.84	-0.17	-0.24	8.13	0.27	0.01
KDR	37.91	1.50	4.91***	8.11	0.48	0.00
NSR	38.89	0.32	13.96***	8.18	1.50	0.01
SRL	39.92	-4.63	17.16***	8.10	1.38	-0.01
PRD	43.26	4.98*	0.00	7.96	1.32	0.03***
General mean	40.69			8.15		
S.Em ±	0.55	2.24		0.04	0.51	

VRM = Volume of the root at main field WRM = Weight of the root at main field

LITERATURE CITED

Bahman Shafii, Karen A Mahler, Willian J P and Dick L Auld. 1992. Genotype X 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 post dictive success of statistical analysis of yield trials. Theoritical and Applied Genetics 76:1-10.

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

Zaval - Garcia F, Bramel - Cox P J and Eastin J D. 1992. Potential gain from selection for yield stability in grain sorghum populations. Theoritical and Applied Genetics 85: 112-119.

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