Environment and Ecology 36 (2) : 531—534, April—June 2018
Website: environmentandecology.com ISSN 0970-0420

AMMI Bi Plot Analysis for Stability of Grain Yield in Pigeonpea (*Cajanus cajan* L.)

Muniswamy S., S. B. Bellad, G. Girish,
Annaraya Talawar

Received 6 January 2018; Accepted 29 January 2018; Published on 14 February 2018

Abstract Genotype × environment interaction and stability performance were investigated on grain yield with 13 pigeonpea genotypes in four environments. The ANOVA for grain yield revealed highly significant (p<0.01) for genotypes, environments, and their interactions. The significant interaction indicated that the genotypes respond differently across the different environments. The mean grain yield value of genotypes averaged over environments indicated that GRG-152 (G_2) had the highest (24.09 q/ha) where as lowest yield in ICPL-161 (G_{11}) respectively (14.1 q/ha). In AMMI analysis AMMI 1 bi plot showed the genotypes GRG-177 (G_1), GRG-222, (G_3), ICP-14001 (G_8) and GRG-811 (G_{13}) have higher average mean yield with high main (additive) effects coupled with positive IPCA 1 score, the genotypes GRG-152 (G_2) exhibited negative IPCA-1 score though it has highest yield among all genotypes including the interaction effect with the environments. Environments, such as Malnoor (E_3) and Bidar (E_4) could be regarded as more stable site for high yielding pigeonpea genotypes improvement than other locations for grain yield as indicated IPCA scores.

Keywords AMMI analysis, Stability, Pigeonpea, Grain yield.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the major pulse crops of the tropics and sub-tropics. Pigeonpea belongs to agriculturally most important tribe Phaseoleae of the family Fabaceae (Leguminosae). It ranks sixth in global grain legume production and worldwide it is cultivated in about more than 5.5 m ha area. India is the largest producer and consumer of pigeonpea with an area of 5.1 m ha, with annual production of 4.23 m t and productivity of 824 kg/ha (Project Coordinator's report (2016-17) AICRP on Pigeonpea). Pigeonpea (redgram) stands ahead of all the pulses due to its drought tolerance and environment-friendly low cost cultivation.

Performance of genotypes in terms of productivity without stability serves no purpose. It is important that the genotypes must not only productive but also be responsive to increasing fertility status and varied levels of management of the crop. Realizing the significance the Genotype- Environment Interaction (GEI) was studied in the present investigation.

Muniswamy S.*, G. Girish, Annaraya Talawar
Department of Genetics & Plant Breeding

S.B. Bellad
Department of Seed Science and Technology, Agricultural Research Station, Aland Road, Kalaburagi 585101, Karnataka, India
e-mail:muniswamygpb@gmail.com
*Correspondence

Table 1. AMMI, ANOVA for yield in 13 genotypes of pigeonpea. *Significant at $p<0.05$.

Source of variations	df	Sum of squares	Means squares	*F* ratio	Explained SS %
Genotypes	12	448.79	37.40	3.082*	18.3
Environments	3	1116.98	372.33	30.686*	45.8
G*E Interaction	36	436.80	12.13		17.9
PCA I	14	219.26	15.66		8.9
PCA II	12	131.55	10.96		5.4
Pooled residual	10	85.99	8.60		
Total	87	2493.3			
Comparison	S.E.D	CD 5%		Variance	Variance
Genotypes Gi-GJ	1.36	716314.3	PCA I	219.2587	50.20%
Environments	2.46	1291354	PCA II	131.55	30.12
`			Residual	85.99	19.69

Materials and Methods

The experiments were conducted at four locations namely Kalaburagi, Raddewadi, Bidar and Malnoor belong to three Agro Climate Zones (AEZ) of Karnataka. Thirteen genotypes consisting of 11 advanced lines viz., GRG 177, GRG 152, GRG 222, GRG 111, GRG 617, ICPL 15015, GRG 2013, ICPL 14001, PRG 176, ICPL 332 and 2 checks (TS-3R and GRG-811) were used as experimental material. The experiments were carried out in a randomized complete block design (RCBD) with two replications. Each entry was sown in 6 rows with 4 meters length, spacing of 90 cm and 30 cm was followed between the rows and plants respectively. Standard agronomic practices were followed and plant protection measures were taken as and when required following the recommendation of package of practices [1]. The grain yield (q/ha) data were recorded at 10% moisture level. The grain yield data for thirteen (13) genotypes in four locations were subjected to AMMI analysis of variance using statistical analysis package software windostat ver 9.2 (Table 1).

Results and Discussion

The AMMI analysis of variance for grain yield (q/h) of 13 genotypes tested in four environment showed that the main effect of G and E accounted for 18.3% and 45.79% variation respectively. The analysis revealed that variances due to genotypes and environments are significant ($p<0.01$). The large sum of squares for genotypes indicated that the genotypes were diverse with large differences among genotypic means causing most of the variation in grain yield, which is in harmony with the findings earlier [2, 3]. The presence of genotypes environment interaction (GEI) was clearly demonstrated by the AMMI model when the interaction was partitioned among two interaction principal component axis (IPCA). The principal component axis 1 (PCA 1) explained 8.9% of the interactions sum of square in 14% of the interaction degrees of freedom (DF). Similarly, the second principal component axis (IPCA 2) explained a further 5.39% of GEI sum of squares. This implied that the interaction of the pigeonpea genotypes with four environments was predicted by the first two components of genotypes and environments. In general, factors like type of crop, diversity of the germplasm and range of environment conditions will affect the degree of complexity of the best predictive model.

Stability analysis by AMMI model

Biplot analysis is possibly the most powerful interpretive tool for AMMI models. There are two basic AMMI biplots, the AMMI 1 biplot where the main effects (genotypes mean and environment mean) and IPCA 1 scores for both genotypes and environments are plotted against each other. On the other hand, the second biplot is AMMI 2 biplot where scores for IPCA 1and IPCA 2 are plotted (Table 2). The mean grain yield value of genotypes averaged over environments indicated that the genotypes GRG-152 (G_2) and GRG-177 (G_1) had the highest (22.09 q/ha) and the lowest (22.92 q/ha) yield respectively. Different genotypes

Table 2. Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield (t/ha) of 13 genotypes across 4 environments. GM=Grand mean, Var=Variety, Env=Environment.

Genotypes/Envt	Gulbarga (E_1)	Raddewadi (E_2)	Malnoor (E_3)	Bidar (E_4)	Var mean	Var index	PCA I	PCA II	G*E Res SS
GRG-177 (G_1)	17.9	21.05	26.65	26.1	22.92	2.57	0.05	-1.09	0.25
GRG-151(G_2)	17.2	28.25	25.75	25.15	24.09	3.73	-1.36	-1.56	12.75
GRG-222 (G_3)	13.9	21.75	24.85	30.7	22.8	2.45	0.04	0.5	8.38
GRG-111 (G_4)	14.4	13.75	23	29.5	20.16	-0.19	1.01	0.86	4.87
GRG-617 (G_5)	18.75	20.25	23.75	25.6	22.09	1.73	-0.04	-0.83	5.51
GRG-15015 (G_6)	12.1	20.5	16.95	24.75	183.58	-1.78	-1.35	0.26	2.22
GRG-2013 (G_7)	12.65	19.85	13.05	28.55	18.52	-1.83	-1.79	1.74	0.01
GRG-14001 (G_8)	18.8	16.8	24.75	23.45	20.95	0.6	0.28	-1.31	16.35
GRG-176 (G_9)	3.15	9.5	25	23.3	15.24	-5.12	2.42	-0.06	24.47
GRG-332 (G_{10})	14.4	14.85	21.9	30.25	20.35	0.0	0.66	1.14	3.48
ICP-161 (G_{11})	9.5	9.0	16.9	20.65	14.04	-6.34	0.58	0.03	6.78
TS-3R (G_{12})	16.1	21.75	24.35	29.75	22.99	2.63	-0.21	0.2	0.88
GRG-811 (G_{13})	15.8	19.45	23.9	28.5	21.91	1.56	0.06	0.1	0.04
Env Mean	14.2	18.21	22.37	26.63					
Env Index	-6.15	-2.14	2.01	6.28					
PCA I	-0.8	-2.57	2.66	0.71	GM=20.3				
PCA II	-0.7	-0.6	-1.56	2.86					
G*E Res SS	57.28	23.4	5.08	0.23	85.99				

showed inconsistent performance across all environments. The environments mean grain yield ranged from (11.20 q/ha) for E_1, to 26.63 q/ha for E_4 and average grain yield over environments and genotypes is 20.30 q/ha. On the basis of positive E_1 and E_2 are poor and E_3 and E_4 are rich environments. With in genotypes GRG-177 (G_1) GRG-152 (G_2) and GRG-222 (G_3) have higher average yields and these genotypes adapted to favorable environments, while ICP-15015 (G_6), GRG-2013 (G_7), PRG-176 (G_9) and ICP-161 (G_{11}) are poor yielders as indicated by the varieties index and average yield across locations.

AMMI 1 biplot display

Biplots are graphs where aspects of both genotypes and environments are plotted on the same axes so that inter relationships can be visualized. In the AMMI biplot, the usual interpretation of biplot is that the displacements along the abscissa indicate difference in main (additive) effects, where as displacements along the ordinate indicate difference in interaction effects. Genotypes that group together have similar adaption while environments which group together influence the genotypes in the same way. The best adapted genotypes can plot far from the environments.

If a genotypes or an environments has a IPCA 1 score of nearly zero, it has small interaction effects and considered as stable. When a genotype and environment have the same sign on the PCA axis, their interaction is positive and if different, their is negative. The AMMI 1 biplot expected yield clearly indicated for any genotype and environment combination can be calculated from Figure 1.

The AMMI 1 biplot gave clear picture about G and E interaction. Genotypes and environment on the same parallel line, relative or ordinate have similar yields and a genotype or environment on the right

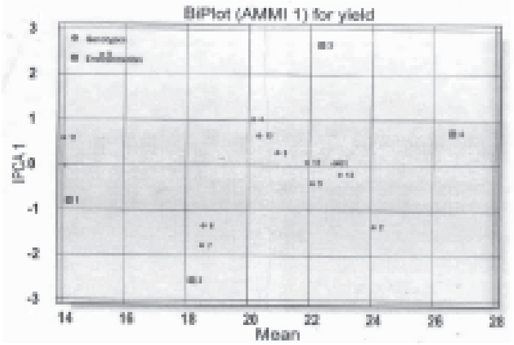

Fig. 1. AMMI 1 biplot for grain yield (q/ha) of 13 pigeonpea genotypes (G) and four environments using genotypic and environmental scores.

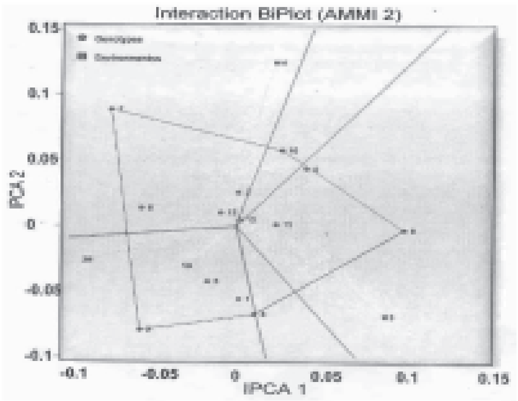

Fig. 2. AMMI 2 biplot for grain yield (q/ha) showing the interaction of IPCA2 againest IPCA 1 scores of 13 pigeonpea genotypes (G) in four environments.

side of the mid point of this has higher yields than those of left hand side. Consequently, the genotypes GRG-177 (G_1), GRG-222 (G_3), GRG-811 (G_{13}) and ICP-14001 (G_8) were exhibited high yield with high main (additive) effects showing positive IPCA 1 score. The genotype GRG-152 (G_2) though having highest yield, but recorded negative IPCA 1 score indicating it's environment sensitivity. The environment Malnoor (E_3) and Bidar (E_4) had positive IPCA 1 score and all the genotypes performed well in these locations and are considered as most favorable environments [4, 5]. On the other hand the genotypes GRG-2013 (G_7), ICP-15015 (G_6) had less yield negative IPA 1 score.

AMMI 2 biplot display

In AMMI 2 biplot (Fig. 2) the environment scores are joined to the origin by side lines. Sites with short spokes do not exert strong interaction. The Gulbarga (E_1) and Raddewadi (E_2) had short spokes and they do not exert strong interactive forces.

The genotypes GRG-2013 (G_7) GRG-152 (G_2), ICP-14001 (G_8), PRG-176 (G_9) and ICP-332 (G_{10}) are aways from the origin and are narrow interactive to environment. Among the environment Gulbarga (E_1) and Raddewadi (E_2) were near to the origin and they do not exert strong interactive forces compared to Malnoor (E_3) and Bidar (E_4).

Conclusion

Crop yield is a complex trait that is influenced by number of component characters along with the environment directly or indirectly. AMMI statistical model could be a great tool to select the most suitable and stable high yielding hybrids for specific as well as for diverse environment. In the present study, AMMI model has shown that the largest proportion of the total variation in grain yield was attributed to environment. Here most of the genotypes showed environment specificity. The mean grain yield value of genotypes averaged over environment indicated that GRG-152 (G_2) had highest 24.0 q/ha and the lowest yield ICPL-161 (G_{11}) (14.01 q/ha) respectively. The genotypes GRG-177 (G_1), GRG-222 (G_3), GRG-811 (G_{13}) and ICP-14001 (G_8) were hardly affected by the GXE interaction and this would perform well across a wide range of environments.

References

1. Anonymous (2014) Improved agronomic practices, UAS Dharwad and UAS Raichur, pp 94—104.
2. Fentie M, Assefa A, Belete K (2013) AMMI analysis of yield performance and stability of finger millet genotypes across different environments. World J Agric Sci 9 : 231—237.
3. Misra RC, Das S, Patnaik MC (2009) AMMI model analysis of stability and adaptability of late duration finger millet *(Eleusine coracana)* genotypes. World Appl Sci J 6 : 1650—1654.
4. Adugna A (2007) Assessment of yield stability in Sorghum. Afr Crop Sci J 15 : 83—92.
5. Anandan A, Eswaran R, Sabesan T, Prakash M (2009) Additive main effects and multiplicative interactions analysis of yield performances in rice genotypes under coastal saline environments. Adv Biol Res 3 : 43—48.