Short Communication

AMMI approach for seed yield and stability of french bean (*Phaseolus vulgaris* L.)

C. A. Nimbalkar, A. P. Baviskar and V. H. Bajaj

National Agricultural Research Project (Plain Zone), R.F.R.S., Ganeshkhind, Pune 411 007

Eleven french bean (*Phaseolus vulgaris* L.) genotypes including four checks (Table 1) maturing in 68 to 75 days were grown in 1.8 × 4.5 m² plot with 30 and 10 cm spacing between and within rows, respectively in a randomized block design with three replications during *kharif* 2002 at five different agro-climatic locations in the french bean growing region of plain zone in University multilocation trial. Recommended dose of fertilizers 60 kg N and 80 kg P_2O_5/ha was applied. The data generated on seed yield of french bean were analysed as per Zobel et al., [1] and Gauch and Zobel [2], using IRRISTAT software developed by International Rice Research Institute, Phillippines. Hierarchial cluster analysis was also performed on the residuals from the additive model in order to cluster varieties and environments with respect to interaction effects.

The analysis of variance exhibited that all the three sources i.e. genotype main effect, environmental additive effect and G × E (non-additive effects have significant effects accounted 7.62, 81.37 and 10.98 %

of the total variance, respectively, indicating thereby a differential response of genotypes with the change of locations and influencing genotypes. The G × E interaction was significant and was further partitioned into AMMI components with contribution of 49.35, 31.98, 16.27 and 2.39 % to the total G × E interaction variance. The first three AMMI components representing interaction pattern were significant and jointly contributed 97.5 % of the interaction component with 82.5 % of the degrees of freedom for G × E interaction, and thus satisfying the goals of an efficient statistical model. There was a drop in G × E contribution between second and third Inteaction Principal Component Axes (IPCA's) but one fifth of the variation contained in G × E term could still be explained by IPCA3 and IPCA4.

The seed yields of eleven french bean genotypes ranged from 227 to 2428 kg/ha (Table 1). The average yield per gertotype across the location was more than grand mean except for HPR-35, Vaghya and HUR-137. The AMMI estimates of means are also presented

Table 1. Seed yield (kg/ha) and AMMI scores for GE interaction of different french bean genotypes

Genotypes	Ganesh khind	Pune	Karad	Borgaon	Kolhapur	Mean	Rank	AMMI I	Rank	AMMI II
GRB-9810	2428(2432)	1238(1230)	1358(1344)	1679(1675)	340(363)	1409	1	−15.16	11	−13.14
Varun (C)	1996(1990)	1420(1437)	1275(1304)	1627(1635)	516(469)	1367	2	−1.34	7	−8.09
GRB-9811	1914(1906)	1284(1303)	1346(1377)	1647(1656)	531(479)	1344	3	1.36	5	−6.32
GRB-9701	2201(2203)	1077(1073)	1633(1628)	1362(1360)	446(455)	1344	4	−11.80	10	4.82
GRB-9710	1935(1946)	1389(1359)	1609(1559)	1279(1265)	453(536)	1333	5	−4.36	8	9.08
GRB-9801	2016(2014)	1379(1383)	1527(1534)	1205(1211)	522(511)	1331	6	−7.40	9	9.21
GRB-9702	1707(1706)	1194(1198)	1300(1306)	1525(1527)	415(404)	1228	7	4.18	4	−3.75
GRB-9812	1626(1617)	1000(1023)	1432(1471)	1127(1138)	451(386)	1127	8	0.94	6	11.11
HPR-35 (C)	1420(1428)	1035(1013)	1201(1165)	1580(1570)	240(299)	1095	9	11.12	2	−7.40
Vaghya (C)	1194(1198)	991(982)	1185(1169)	1278(1273)	243(270)	978	10	13.20	1	2.34
HUR-137(C)	1305(1303)	701(707)	1243(1253)	1284(1287)	227(210)	952	11	9.27	3	2.14
Mean	**1795**	**1155**	**1374**	**1418**	**398**	**1228**				
Rank	1	4	3	2	5					
AMMI I	-24.92	2.23	2.37	12.43	7.89					
Rank	5	4	3	1	2					
AMMI II	-5.34	0.77	13.72	-18.47	7.31					

Values in parentheses are AMMI estimates of means
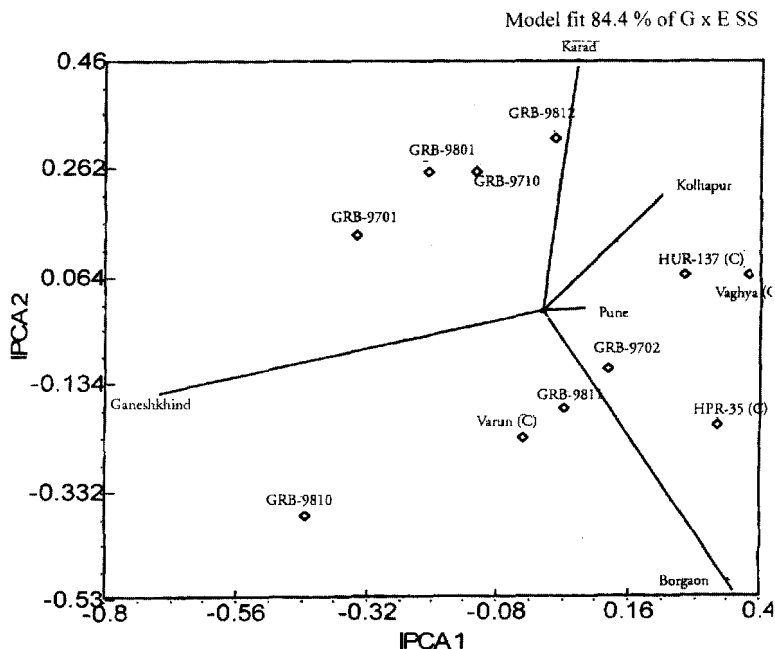
Model fit 84.4 % of G x E SS

Fig. 1. Interaction biplot for AMMI model

which ranged from 210 to 2432 kg/ha. It is in consonance with the results of Nimbalkar *et al.*, [3]. The check HUR 137 exhibited maximum (71 %) squared correlation between residuals from the main effects model and the location indices followed by genotypes Vaghya (C) (54 %), GRB-9810 (46 %) and HPR-35 (C) (31 %) indicating their adaptability over the locations in different agro-climatic zones. GRB-9810 has maximum contribution to interaction followed by GRB-9701 and Vaghya (C). Similarly, GRB-9810 exhibited maximum deviation from regression component of interaction, indicating its best performance in a favourable environment.

The highest yielding genotypes and locations were having negative Principal Component Axis (PCA) score, whereas low yielder genotypes and locations were having maximum positive PCA score (Table 1). Therefore, AMMI model for these genotypes will predict the yield that is close to those of AMMI in location Karad larger than AMMI in Borgaon, Kolhapur and Pune and smaller than simple additive model in Ganeshkhind. GRB-9702 has the smallest interaction for giving a consistent yield under different environments.

The interaction biplot with location and genotypes superimposed (Model fit is 84.4 % of G × E) can be used to determine the stability of genotypes and their adoption to a given set of locations (Fig. 1). GRB-9702 and GRB-9811 situated close to the centre can be regarded as stable across a gradient of soil fertility and weather parameters because of their consistent yield performance across locations. On the other hand,

the genotypes far from centre can be regarded as sensitive to environmental factors differing over locations, because their performance varies across locations. This is the case for GRB-9810, GRB-9701, GRB-9801 and GRB-9812. The dendrogram structured by interaction pattern shows some degree of agreement with biplots. The first split is towards checks HPR-35, Vagya and HUR-137 from other genotypes. GRB-9810, GRB-9702, GRB-9811 and Varun (C) are pooled together in second split, which are high yielding genotypes. The cluster dendrogram for genotypes appears to be well related with the clustering based on isozymic groups. Cluster dendrogram for environment also appears to be good formation of groups of locations.

Crossa *et al.*, [4] and Vijaykumar *et al.*, [5] in maize and hybrid rice, respectively, found that AMMI analysis significantly improved the probability of selection of genotypes and that the analysis picked different winners than that by cell mean model. In the present investigation also the overall ranking of genotypes based on mean and AMMI have great discrepancies and therefore the selection based on mean estimation will not be precise. The present analysis, therefore, indicates that, before 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 × E interaction.

References

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

2. **Gauch H. G. and Zobel R. W.** 1989. Accuracy and selection success in yield trial analysis. Theoretical Applied Genetics, **77**: 473-481.

3. **Nimbalkar C. A., Baviskar A. P. and Navale P. A.** 2004. Genotye × environment interaction effect on seed yield of french bean (*Phaseolus uulgaris* L.). Indian J. agri. Sci., **74**: 367-370.

4. **Crossa J., Gauch H. G. (Jr.) and Zobel R. W.** 1990. Additive main effect and multiplicative interaction analysis of two international maize cultivar trials. Crop Science, **30**: 493-500.

5. **Vijaykumar C. H. M., Ilyas Ahmed M., Viraktamath B. C., Balkrishnan R. and Ramesha M. S.** 2001. Genotype × Environment interaction effects on yield of rice hybrids in India. Indian Journal of Genetics and Plant Breeding, **61**: 101-106.