

Assessment of Genotype $\times$ Environment Interaction (GEI) by using AMMI Model for Fiber Quality Traits in Inter-Specific Hybrids (*Gossypium hirsutum* L. $\times$ *Gossypium barbadense* L.) of Cotton

B. Balakrishna, V. Chenga Reddy, M. Lal Ahamed

Received 18 April 2016 ; Accepted 23 May 2016 ; Published online 8 June 2016

Abstract The present study was conducted during *kharif* of 2014-15 over three locations to know the stable genotypes for fiber quality traits. AMMI analysis indicated that cotton fiber quality traits showed highly significant differences ($p < 0.01$) affected by environments (E), genotypes (G) and genotype $\times$ environment interaction (GEI). AMMI analysis of variance revealed that ICPA I was significant for all the traits and explained more than 50% of the total $G \times E$ interaction sum of squares. The interaction of seventy two hybrids over three locations was best predicted by ICPA I. The hybrids viz. SCS 793 $\times$ GSB 40 and MCU 5 $\times$ GSB 40 were found to be stable with higher mean than grand mean and IPCA score near zero. These hybrids can be exploited commercially after thorough testing over number of seasons and locations.

Keywords Inter-specific cotton hybrids, AMMI biplot analysis, Fiber quality traits.

Introduction

Cotton (*Gossypium* spp.) is an important cash crop playing a key role in the economic and social affairs of India. Today cotton remains one of the world's

most important economic crop species and a renewable resources providing raw material for textile manufacturing, mulch and cattle feed. It is grown in India under a wide range of climatic conditions. It is a sensitive crop to weather fluctuations, it shows higher magnitude of genotype $\times$ environment interaction [1]. Estimation of phenotypic stability has proven to be a valuable tool in the assessment of varieties adaptability. It is generally agreed that, the more stable genotypes can somehow adjust their phenotypic responses to provide some measures of uniformity in spite of environmental fluctuations. The knowledge about causes of $G \times E$ interaction is needed and would be useful for identifying the areas of optimal cultivar adaptation and stable genotypes over environments. Among the different stability analysis models, AMMI (additive main effects and multiplicative interaction) model is more advanced and provides a graphical representation (biplot) to summarize information on the main effects and interactions of both genotypes and environments simultaneously. The model computes the principal component scores for genotypes and environments that represent the genotype $\times$ interaction. The biplot display of PCA scores plotted against each other provides visual inspection and interpretation of the genotype $\times$ environment interaction components. It permits estimation of interaction effect of a genotype in each location and it helps to identify genotypes best suited for specific locations. According to AMMI model, the genotypes which are characterized by mean greater than the grand mean and the PCA scores nearly zero are con-

B. Balakrishna*, V. C. Reddy, M. L. Ahamed
 Department of Genetics and Plant Breeding, Agricultural College, Bapatla 522101, India
 e-mail: balubreeder@gmail.com

*Correspondence

Table 1. Analysis of variance for stability of performance for six characters in inter-specific hybrids of cotton during *kharif* of 2014-15. *Significant at 5% level. **Significant at 1% level.

Source of variation	df	2.5% span length (mm)		Uniformity ratio		Micronaire value (10 ⁻⁶ g/inch)	
		MSS	% explained	MSS	% explained	MSS	% explained
Trials	215	3.90**		1.24**		0.13**	
Genotypes	71	4.60**	38.99	2.13**	56.38	0.10**	24.59
Environments	2	185.06**	44.15	1.90	1.42	7.91**	57.28
G × E interaction	142	0.99	16.84	0.79	42.19	0.04	18.11
PCA I	72	1.28**	65.34	0.99**	63.10	0.05**	78.65
Residual	70	0.70**		0.59		0.02**	
Error	432	0.39		0.47		0.00	
Total	647	1.55		0.73		0.04	

Source of variation	df	Bundle strength (g/tex)		Fiber elongation (%)		Lint yield plant ⁻¹ (g)	
		MSS	% explained	MSS	% explained	MSS	% explained
Trials	215	3.16**		0.04**		263.89**	
Genotypes	71	3.12**	32.68	0.10**	39.84	461.01**	57.69
Environments	2	153.38**	45.21	1.71**	37.88	3711.95**	13.08
G × E interaction	142	1.06	22.10	0.01	22.27	116.76	29.22
PCA I	72	1.26**	60.73	0.02**	56.89	137.93**	59.89
Residual	70	0.84**		0.01**		95.00**	
Error	432	0.24		0.01		7.24	
Total	647	1.21		0.02		92.52	

sidered as generally adaptable to all environments. However, the genotypes with high mean performance and with large value of IPCA scores are considered having specific adaptability to the environments [2]. In the present study, the interaction of seventy two inter-specific hybrids over three locations was best predicted by first interaction principal component.

Materials and Methods

The present study was carried out during *kharif* of 2014-15 at three locations viz., Regional Agricultural Research Station (RARS), Lam Farm, Agricultural Research Station (ARS), JM Puram and Agricultural College Farm, Bapatla. The basic material for the present investigation was comprised of 72 inter-specific cotton hybrids produced by crossing 12 *Gossypium hirsutum* L. genotypes with 6 *Gossypium barbadense* L. genotypes in line × tester fashion. Data were recorded on five randomly selected competitive plants of each genotype in every replication for 2.5%

span length (mm), uniformity ratio, micronaire value (10⁻⁶ g / inch), bundle strength fiber elongation and lint yield/plant (g). The experiment was laid out in a randomized complete block design with three replications at each location. The experimental plot comprised of 3 rows of each 6 m length with a spacing of 120 cm × 60 cm. All the recommended package of agronomic practices for inter-specific hybrids of cotton was followed to raise a good crop at all the three locations. Mean values for all the characters were worked out for calculating phenotypic stability as per AMMI model of Gauch [3].

Results and Discussion

2.5% span length (mm)

The genotypes and environments were significant for 2.5% span length. They contributed 38.99% and 44.15% of total variation (Table 1). Genotype × envi-

ronment interaction was explained 16.84% of total variance and IPCA I was significant and exhibited 65.34% of the total $G \times E$ interaction sum of squares. According to AMMI I biplot (Fig. 1) the hybrids, NDLH 1938 $\times$ SUVIN (6), H 1442 $\times$ TCB 37 (11), ADB 542 $\times$ TCB 37 (17), SCS 793 $\times$ GSB 40 (49) and MCU 5 $\times$ GSB 40 (55) were stable with IPCA score zero and above grand

mean (34.91). Similar results are also proposed by Sirisha [4]. NDLH 1938 $\times$ DB 11 (3), NDLH 1938 $\times$ TCB 37 (5), WGCV 48 $\times$ GSB 41 (28), WGCV 48 $\times$ SUVIN (30), SCS 793 $\times$ DB 11 (51), L 1058 $\times$ DB 16 (62), L 762 $\times$ GSB 40 (67) and L 762 $\times$ SUVIN (72) showed low mean with IPCA score nearly zero. J M Puram location had high mean for 2.5% span length but high interaction effects showed the suitability for specially adapted hybrids. Interaction of H 1442 $\times$ SUVIN (12) hybrid with Bapatla location indicate the positive interaction of them. IPCA score of Bapatla was nearly zero with stable performance of all hybrids in this location for 2.5% span length and could be good enough for selection of genotypes with average adaptation.

Micronaire value (10^{-6} g/inch)

AMMI analysis of variance indicated that the genotypes, environment and genotype $\times$ environment interaction accounting for 24.59%, 57.28% and 18.11% of the total variation. Genotypes and environment variances were significant and $G \times E$ interaction presented in one IPCA axis. IPCA I was significant with

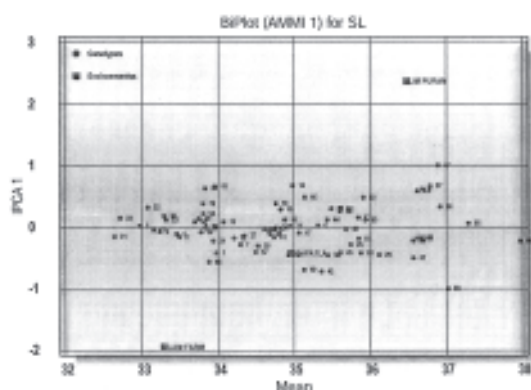


Fig.1. Biplot of interaction principal component analysis 1 against 2.5% span length for three locations.

- | | | |
|------------------------------|------------------------------|-----------------------------|
| 1. NDLH 1938 $\times$ GSB 40 | 25. WGCV 48 $\times$ GSB 40 | 49. SCS 793 $\times$ GSB 40 |
| 2. NDLH 1938 $\times$ DB 16 | 26. WGCV 48 $\times$ DB 16 | 50. SCS 793 $\times$ DB 16 |
| 3. NDLH 1938 $\times$ DB 11 | 27. WGCV 48 $\times$ DB 11 | 51. SCS 793 $\times$ DB 11 |
| 4. NDLH 1938 $\times$ GSB 41 | 28. WGCV 48 $\times$ GSB 4 | 52. SCS 793 $\times$ GSB 41 |
| 5. NDLH 1938 $\times$ TCB 37 | 29. WGCV 48 $\times$ TCB 37 | 53. SCS 793 $\times$ TCB 37 |
| 6. NDLH 1938 $\times$ SUVIN | 30. WGCV 48 $\times$ SUVIN | 54. SCS 793 $\times$ SUVIN |
| 7. H 1442 $\times$ GSB 40 | 31. MR 786 $\times$ GSB 40 | 55. MCU 5 $\times$ GSB 40 |
| 8. H 1442 $\times$ DB 16 | 32. MR 786 $\times$ DB 16 | 56. MCU 5 $\times$ DB 16 |
| 9. H 1442 $\times$ DB 11 | 33. MR 786 $\times$ DB 11 | 57. MCU 5 $\times$ DB 11 |
| 10. H 1442 $\times$ GSB 41 | 34. MR 786 $\times$ GSB 41 | 58. MCU 5 $\times$ GSB 41 |
| 11. H 1442 $\times$ TCB 37 | 35. MR 786 $\times$ TCB 37 | 59. MCU 5 $\times$ TCB 37 |
| 12. H 1442 $\times$ SUVIN | 36. MR 786 $\times$ SUVIN | 60. MCU 5 $\times$ SUVIN |
| 13. ADB 542 $\times$ GSB 40 | 37. TSH 0250 $\times$ GSB 40 | 61. L 1058 $\times$ GSB 40 |
| 14. ADB 542 $\times$ DB 16 | 38. TSH 0250 $\times$ DB 16 | 62. L 1058 $\times$ DB 16 |
| 15. ADB 542 $\times$ DB 11 | 39. TSH 0250 $\times$ DB 11 | 63. L 1058 $\times$ DB 11 |
| 16. ADB 542 $\times$ GSB 41 | 40. TSH 0250 $\times$ GSB 41 | 64. L 1058 $\times$ GSB 41 |
| 17. ADB 542 $\times$ TCB 37 | 41. TSH 0250 $\times$ TCB 37 | 65. L 1058 $\times$ TCB 37 |
| 18. ADB 542 $\times$ SUVIN | 42. TSH 0250 $\times$ SUVIN | 66. L 1058 $\times$ SUVIN |
| 19. ADB 532 $\times$ GSB 40 | 43. BS 37 $\times$ GSB 40 | 67. L 762 $\times$ GSB 40 |
| 20. ADB 532 $\times$ DB 16 | 44. BS 37 $\times$ DB 16 | 68. L 762 $\times$ DB 16 |
| 21. ADB 532 $\times$ DB 11 | 45. BS 37 $\times$ DB 11 | 69. L 762 $\times$ DB 11 |
| 22. ADB 532 $\times$ GSB 41 | 46. BS 37 $\times$ GSB 41 | 70. L 762 $\times$ GSB 41 |
| 23. ADB 532 $\times$ TCB 37 | 47. BS 37 $\times$ TCB 37 | 71. L 762 $\times$ TCB 37 |
| 24. ADB 532 $\times$ SUVIN | 48. BS 37 $\times$ SUVIN | 72. L 762 $\times$ SUVIN |

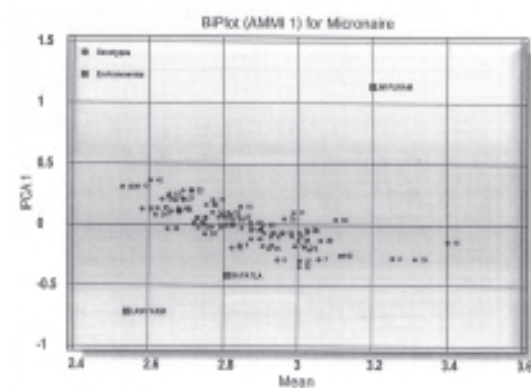


Fig. 2. Biplot of interaction principal component analysis 1 against micronaire value for three locations.

78.65% of total $G \times E$ sum of squares. In AMMI I biplot (Fig. 2) ADB 542 $\times$ GSB 41 (16), ADB 532 $\times$ TCB 37 (23), SCS 793 $\times$ GSB 40 (49) and L 762 $\times$ GSB 41 (70) were stable with IPCA score near to zero and above grand mean (2.85). Sirisha [4] also reported stable hybrids for this character. ADB 542 $\times$ DB 11 (15), SCS 793 $\times$ DB 16 (50), MCU 5 $\times$ TCB 37 (59), L 1058 $\times$ TCB 37 (65) and L 1058 $\times$ SUVIN (66) recorded low mean with IPCA score near to zero. Bapatla location showed favorable conditions with mean performance nearly equal to grand mean for this trait. Whereas, J M Puram location had high mean performance for hybrids but showing high interaction effects indicate the suitability of specially adapted hybrids.

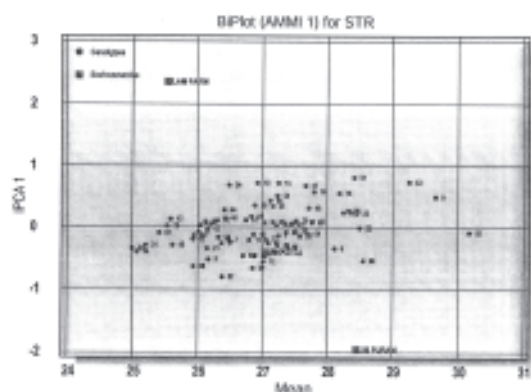


Fig. 3. Biplot of interaction principal component analysis 1 against bundle strength for three locations.

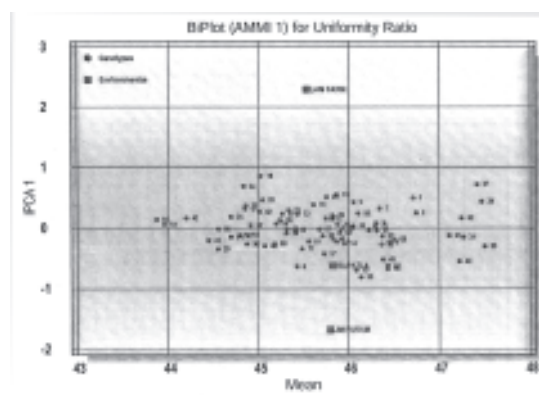


Fig. 4. Biplot of interaction principal component analysis 1 against uniformity ratio for three locations.

Bundle strength (g/tex)

For bundle strength, genotypes and environments were significant and exhibited 32.68% and 45.21% of the total variation. Genotype $\times$ environment interaction explained 22.10% of total variance and presented in one IPCA axis which was significant and contributed 60.73% of $G \times E$ interaction sum of squares. In AMMI I biplot presentation (Fig. 3) the hybrids, NDLH 1938 $\times$ GSB 41 (4), ADB 542 $\times$ SUVIN (18), ADB 532 $\times$ GSB 41 (22), ADB 532 $\times$ SUVIN (24), WGCV 48 $\times$ GSB 40 (25), WGCV 48 $\times$ DB 16 (26), WGCV 48 $\times$ TCB 37 (29), BS 37 $\times$ TCB 37 (47), SCS 793 $\times$ GSB 40

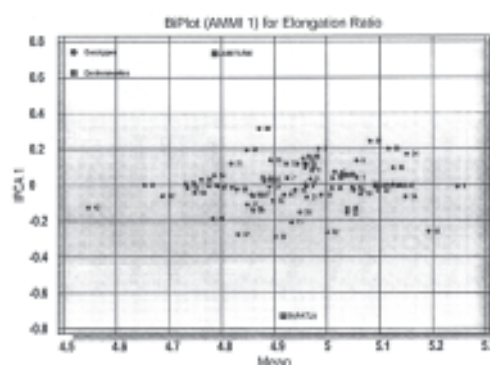


Fig. 5. Biplot of interaction principal component analysis 1 against fiber elongation % for three locations.

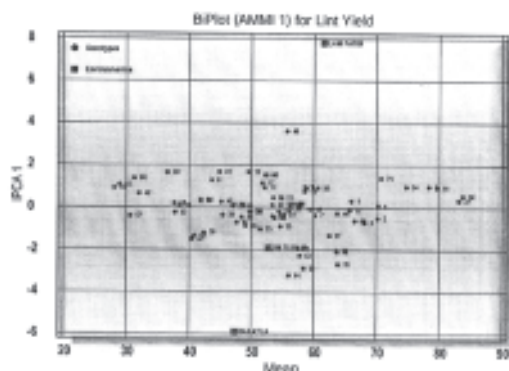


Fig. 6. Biplot of interaction principal component analysis 1 against lint yield plant⁻¹ for three locations.

(49), MCU 5×GSB 40 (55), L 1058×DB 11 (63) and L 1058×GSB 41 (64) were found to be stable as they have above grand mean (27.02 g/tex) with IPCA score near zero. Low mean with IPCA score near zero exhibited by L 1058×DB 16 (62), L 762×GSB 41 (70) and L 762 × TCB 37 (71). J M Puram location suitable for specially adapted hybrids as it had high mean with negative interaction effects. Bapatla location had stable performance of hybrids for bundle strength as its IPCA score was near to zero. These findings are in accordance with findings of Sirisha [4].

Uniformity ratio

AMMI analysis for uniformity ratio showed that genotypes and environments were significant for this character. The genotype, environment and genotype × environment interaction exhibited 56.38%, 1.42% and 42.19% of the total variation. IPCA I was significant and contributed 63.10% of the total G×E interaction sum of squares. The hybrids, NDLH 1938×DB 11 (3), ADB 542×DB 11 (15), ADB 542×GSB 41 (16), ADB 532×GSB 40 (19) and ADB 532×DB 11 (21) were identified as stable genotypes with zero IPCA I score and higher mean than grand mean (45.72) (Fig. 4). Sirisha [4] also reported stable hybrids for this trait. IPCA score near to zero and low mean performance was showed by H 1442×SUVIN (12), MCU 5×DB 11 (57), MCU 5×TCB 37 (59), L 1058×DB 16 (62), L 1058×TCB 37 (65) and L 1058×SUVIN (66). Hybrids overall mean performance was same in all the three locations i.e.

Bapatla, JM Puram and Lam Farm.

Fiber elongation (%)

Variation due to genotypes and environments was significant showed 39.84% and 37.88% of the total variation, whereas, genotype × environment interaction was exhibited 22.27% of the total variation. IPCA I was significant and explained 56.89% of the total G×E interaction sum of squares. According to AMMI I biplot (Fig. 5) NDLH 1938 × DB 16 (2), NDLH 1938 × GSB 41 (4), WGCV 48 × DB 11 (27), BS 37 × GSB 41 (46) and L 1058 × DB 11 (63) hybrids were stable with near zero IPCA score and higher mean than grand mean (4.93%). These results are in accordance with the findings of Sirisha [4]. The hybrids, NDLH 1938 × TCB 37 (5), H 1442 × TCB 37 (11), ADB 532 × TCB 37 (23), MR 786 × SUVIN (36), TSH 0250 × TCB 37 (41), MCU 5 × DB 11 (57) and L 1058 × GSB 41 (64) possessed low mean with IPCA score near to zero. IPCA score of J M Puram location was nearly zero with high mean indicate stable performance of genotypes.

Lint yield plant⁻¹ (g)

Genotypes, environments variances were significant and accounted for 57.69% and 13.08% of the total variance. The genotype × environment interaction contributed 29.22% of total variance. IPCA I was significant and exhibited 59.89% of the total G×E interaction sum of squares. In AMMI I biplot presentation (Fig. 6) the hybrids, NDLH 1938 × GSB 41 (4), ADB 542 × GSB 41 (16), WGCV 48 × DB 16 (26), MR 786 × DB 16 (32), BS 37 × GSB 41 (46), SCS 793 × DB 11 (51) and L 762 × DB 11 (69) were found close to IPCA score zero and high mean than grand mean (53.90) indicating stable performance of these hybrids over locations. ADB 542 × SUVIN (18), ADB 532 × SUVIN (24), WGCV 48 × TCB 37 (29), TSH 0250 × GSB 41 (40) and L 762 × GSB 40 (67) were recorded low mean with IPCA score near to zero. Lam Farm location had good potential for lint yield plant⁻¹ but exhibiting high interaction effects showed the suitability for specially adapted hybrids. The results are in accordance with the results of earlier workers [5–8].

References

1. Campbell BT, Jones MA (2005) Assessment of genotype $\times$ environment interactions for yield and fiber quality in cotton performance traits. *Euphytica* 144 : 69—79.
2. Sharma PK, Gupta PK, Govila OP (1998) AMMI analysis of a pearl millet yield trial. *Ind J Genet and Pl Breed* 58 : 183—192.
3. Gauch MG (1988) Model selection and validation for yield traits with interaction. *Biometrics* 44 : 705—715.
4. Sirisha ABM (2015) Genetic analysis of yield and quality traits in upland cotton (*Gossypium hirsutum* L.). PhD thesis. Acharya NG Ranga Agric Univ, Hyderabad.
5. Nidagundi JM, Patil SS, Salimath PM, Kajjdoni PM, Patil BC, Hegde MG (2012) Heterobeltosis in multiple environments for seed cotton yield and yield attributes in cotton (*Gossypium hirsutum* L.). *Karnataka J Agric Sci* 25 : 301—304.
6. Riaz M, Naveed M, Farooq J, Farooq A, Mahmood A, Rafiq Ch M, Nadeem M, Sadiq A (2013) AMMI analysis for stability, adaptability and GE interaction studies in cotton (*Gossypium hirsutum* L.). *J Appl Sci* 22 : 865—871.
7. Shaarawy SA, Abdel B, AMR, Hamoud HM, Yehia WMB (2013) Use of high efficient AMMI method to evaluate new Egyptian cotton genotypes. https://www.icac.org/meetings/wcrc/wcrc4/presentations/Paper_1704.pdf
8. Reddy RY, Sarma ASR (2014) Stability analysis of diploid cotton (*Gossypium arboreum* L.). *Pl Arch* 14 : 593—596.