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AMMI Analysis of Some Upland Cotton Genotypes for Yield Stability in Different Milieus

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Abstract: The additive main effects and multiplicative interaction (AMMI) analysis was performed to assess the yield stability of eighteen cotton genotypes across seven different environments during the crop season 2004-05. Lay out of the experiment was Randomized Complete Block Design (RCBD). The AMMI analysis of variance for seed cotton yield indicated that genotypes, environments and G×E interaction were significantly different ($p<0.01$) and it also revealed that the environments, genotypes and G×E accounted for 70.41, 10.70 and 18.89% of the treatment sum of squares, respectively. Consequently, it is clear that the proportion of environmental and G×E interaction variation for seed cotton yield was much larger than that due to genotypes main effects. Two genotypes, NIBGE-2 and PB-899 exhibited negligible interactions with the environments along with above average seed cotton yield and below average cotton leaf curl virus (CLCuV) % age, indicating their broad adaptations and stability across environments plus tolerance to CLCuV and therefore could be recommended for general cultivation in the tested locations. Although MNH-700 was moderately stable, it was not very productive. Within locations/environments, Rahim yar khan, Multan and Vehari which were on the right hand side of the midpoint of the main effect axis, seemed to be favourable environments for seed cotton yield for the genotypes evaluated, Sahiwal and Bahawalpur were moderately favourable while Jhang and Faisalabad were lesser conducive environments for seed cotton yield. It was possible to identify superior cotton genotypes selected with specific or broad adaptation by using the AMMI model.

Key words: AMMI · *Gossypium hirsutum* L. · yield stability · CLCuV

INTRODUCTION

Improvement in seed cotton yield is one of the focal endeavors of cotton (*Gossypium hirsutum* L.) breeding. As cotton is grown in tropical and sub-tropical agroecologies, it is important to assess adaptation and yield stability of promising genotypes across environments. Various methodologies have been explored to study G×E interaction and to predict the phenotypic response to changes in the environment [1]. The success of identifying high yielding genotypes from yield trials depends on the effectiveness of the statistical analysis used to evaluate patterns in the data and estimated yields [2].

The additive main effects and multiplicative interaction (AMMI) model can effectively explain G×E interaction and it has been used because of its easy interpretation, identification of genotypes for specific and wide adaptation and to measure the genetic gain in plant breeding programs [3, 4]. AMMI analysis has the advantage accrued to it over the usual breeders way of apportioning the variance of G×E. Regression analysis assumes linearity in the response of genotypes to the environments but AMMI analysis takes into account the non-linear response of genotypes to environmental variances making it an appropriate tool especially where the characteristic response of the environments are not known.

The AMMI model analyses the additive effects of genotypes [G] and locations [L] by a standard analysis of variance and the multiplicative effects of the G×E interaction by using Principal Component Analysis (PCA). The model computes the principal component scores for genotypes and environments that represent the G×E interaction. The members of the AMMI family are identified according to the number of PCA axes, for example with one PCA axis it is denoted AMMI1, with two PCA axes AMMI2 and so on. The PCA1 genotype and

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environment scores on x-axis and the main effects i.e. genotype and environment means on y-axis can be used to construct a biplot graph showing the main and interaction effects. Genotypes or locations which appear almost on a perpendicular line have similar means; those falling on a horizontal line have similar interaction patterns. Genotypes or environments with large first IPCA scores (either plus or minus) have large interaction while those with values close to zero have small interaction [5, 6] and are considered stable.

This study was conducted with a view to determine the effect of G×E interaction on the yields of new cotton genotypes, to identify most stable and adapted genotypes and CLCuV resistant genotypes.

MATERIALS AND METHODS

The multilocational evaluation trials were carried out during cropping season 2004-05 in National Coordinated Variety Trials (NCVT) conducted at different 7 locations in Punjab, Pakistan that differed with respect to average annual rainfall, temperature and altitude (Table 1). The present plant material consisted of eighteen upland cotton genotypes, sixteen of which were new strains/advanced lines namely; FH-115, FH-2000, CRIS-460, CRIS-461, MJ-7, H-151-F2, TH-41/83, SLH-279, BH-162, MNH-700, PB-899, Neelum-NS-11, NIAB-98, NIAB-884, NIBGE-2, CIM-534 and two standard cultivars; CIM-496 and CIM-499.

Layout of all the experiments was Randomized Complete Block Design (RCBD) with four replications. For each entry, plot size measured 4.572 m×6.096 m, comprising six rows set 75 cm apart. Distance between plants within rows was 30 cm. Agronomic and cultural practices i.e., weeding, hoeing, irrigation and fertilizer application were adopted as and when required. However, none of plants were sprayed against sucking insects especially white fly. Data was collected on cotton leaf curl virus (CLCuV) occurrence by following Siddiq's [7] method of scaling of symptoms of CLCuV (Table 2). Any plant showing any symptom mentioned in Table 2 was considered susceptible. Then %age of CLCuV occurrence on each genotype was worked out by using the following formula;

$$\text{CLCuV \%age} = \frac{\text{\# of infected plants}}{\text{Total \# of plants}} \times 100$$

Seed cotton was picked when the crop was mature and recorded as kg plot^{-1} and extrapolated in kg/hectare.

Statistical analysis: Data of 18 cotton genotypes yields were subjected to analysis of variance (ANOVA) using the Mstatc package (Russell, D. Freed, Michigan State University, USA). Where the "F" statistics indicated significance, the means were separated using Fisher's protected Least Significance Difference test (LSD) at p = 0.05. To determine the effects of genotype×environment interaction on yields, the data were subjected to Additive Main effects and Multiplicative Interaction (AMMI) analysis using IRRISTAT [8] Version 4.4 computer package and the biplot drawn by placing both genotype and environment means on the x-axis or abscissa and the respective eigenvectors or scores (IPCA 1) on the y-axis or ordinate [9].

The AMMI model is:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + C_{ger}$$

Wheren Y_{ger} = yield of genotype g in environment e for replicate r; μ = grand mean; α_g = mean deviation of the genotype g [genotype mean minus grand mean] and β_e = mean deviation of environmental mean; λ_n = the singular value for IPCA axis n; γ_{gn} = the genotype g eigenvector value for IPCA axis n; δ_{en} = the environment e eigenvector value for IPCA axis n; ρ_{ge} = the residual and C_{ger} = the error.

Table1: Sites where yield performance of 18 cotton genotypes tested in Punjab, Pakistan during 2004-05

Sr.	Sites	Locations	Average rainfall (mm)	Temperature range (°C)	Altitude a.m.s.l.
1	Cotton Research Institute (CRI), Faisalabad.	Central Punjab	400	4.0-48.0	185.6
2	Cotton Research Station (CRS), Sahiwal.	Southern Punjab	97	2.0-47.0	165.0
3	Cotton Research Sub-Station (CRSS), Jhang.	Central Punjab	130	1.0-48.4	148.1
4	Cotton Research Station (CRS), Multan.	Southern Punjab	127	1.0-49.0	121.9
5	Cotton Research Station (CRS), Vehari.	Southern Punjab	127	1.0-48.7	135.0
6	Cotton Research Institute (CRI), Rahim yar khan.	Southern Punjab	165	6.8-49.7	82.93
7	Cotton Research Station (CRS), Bahawalpur.	Southern Punjab	200	1.5-50.0	110.0

Source: Pakistan Meteorological Department

RESULTS AND DISCUSSION

The AMMI analysis of variance for seed cotton yield (Table 3) indicated that genotypes, environments and G×E interaction were significantly different ($p<0.01$). The AMMI model supplied an adequate fit to the data as first Interaction Principle Component Axis (IPCA) was significant ($p<0.01$). The sum of squares for genotypes, environments and IPCA1 provided 91.03% of treatment sum of squares indicating that AMMI1 model effectively partitioned treatment sum of squares [7]. Hence treatment sum of squares contain 91% pattern related to treatment design and only 9% noise related to experimental design.

The AMMI analysis for seed cotton yield (Table 3) also revealed that the locations, genotypes and G×E accounted for 70.41, 10.70 and 18.89% of the treatment sum of squares, respectively. This result indicated that the proportion of environmental and G×E interaction variation for seed cotton yield was much larger than that due to genotypes main effects. These results concurred with the findings of many G×E studies [10, 11], which have shown that the proportion of sum of squares due to difference among sites ranged from 40-90% and G×E was usually larger than genotypes main effects. It also implied that yield was affected by both the environment and G×E interaction effects [12].

Yield performance of the genotypes: Performance of genotypes at various sites is presented in Table 4. The highest yields were recorded at Rahim yar khan (3358.68 kg ha^{-1}), Multan (3228.31 kg ha^{-1}) and Vehari (2999.92 kg ha^{-1}) where yield was more than grand mean yield (2537.28 kg ha^{-1}). So, these sites were conducive/favourable for higher yield. Lowest yields were obtained at Jhang, Faisalabad, Bahawalpur and Sahiwal where yield averaged only 1527.78, 1689.97, 2426.64 and 2537.28 kg ha^{-1}, respectively depicting that these sites were less conducive/unfavourable for higher yield. Mean yield of genotypes over environmental index ranged 874.72 kg ha^{-1} at Faisalabad to 4303 kg ha^{-1} at Multan.

Genotypes H-151-F$_2$, SLH-279, PB-899, NIBGE-2, NIAB-98, CIM-496, FH-115, BH-162, CRIS-460, CRIS-461, NIAB-884 and Neelum-NS-11 in general performed better than the other genotypes across all the seven locations/environments. Mean yield over locations identified H-151-F$_2$ (3025.16 kg ha^{-1}) as the best yielding genotype and TH-41/83 (1982.25 kg ha^{-1}) as poorest genotype.

The results of this study satisfied one of the breeder's goals for selecting such varieties with acceptable yield. Mean yield performance of H-151-F$_2$, SLH-279, PB-899, NIBGE-2 and NIAB-98 over all the locations was better than both the standard cultivars i.e. CIM-496 and CIM-499. Mean seed cotton yield of FH-115, BH-162, CRIS-460, CRIS-461, NIAB-884 and Neelum-NS-11 was more than CIM-499 but less than CIM-496 over all the locations. CIM-499 performed poorly over all the locations except at Rahim yar khan.

Table 2: Scale of symptoms of cotton leaf curl virus (CLCuV)

Scale	Description
0	Complete absence of symptoms
1	Few small scattered vein thickening
2	Small scattered vein thickening
3	Vein thickening involving small group of vein
4	Large group of vein involved
5	All vein involved
6	All vein involved and severe curling
E	Enations

Table 3: AMMI 2 ANOVA of seed cotton yield for 18 cotton genotypes at seven locations in Punjab, Pakistan during 2004-05

SOV	DF	SS	MS	Probability
Total	503	370994339.81	737563.30	
Treatments	125	318581772.20	2548654.18	**
Genotypes	17	34074679.06	2004392.89	**
Locations	6	224321373.71	37386895.62	**
G×E	102	60185719.44	590056.07	**
IPCA 1^{a}	22	31619600.00	1437254.54	**
Residual	80	28566119.40	1506640.40	**
Error	378	52412567.60	138657.59	

a = Interactive principle component axis 1

Stability and adaptation of the genotypes: The AMMI analysis provides a graphical representation or biplot (Fig. 1) to summarize information on the main effects and the first principal component scores of the interactions (IPCA1) of both genotypes and environments simultaneously [13]. Displacement along the abscissa reflected differences in main effects, whereas displacement along the ordinate exhibited differences in interaction effects. Genotypes and environments on the same parallel line, relative to the ordinate, have similar yields and a genotype or location on the right side of the midpoint of this axis has higher yields than those on the left hand side. Consequently, the genotypes H-151-F$_2$, SLH-279, PB-899, NIBGE-2, NIAB-98, CIM-496, FH-115, BH-162, CRIS-460, CRIS-461, NIAB-884 and Neelum-NS-11 produced higher yields with H-151-F$_2$ being the overall best. In contrast, CIM-534, MNH-700, MJ-7, FH-2000, CIM-499 produced below average and

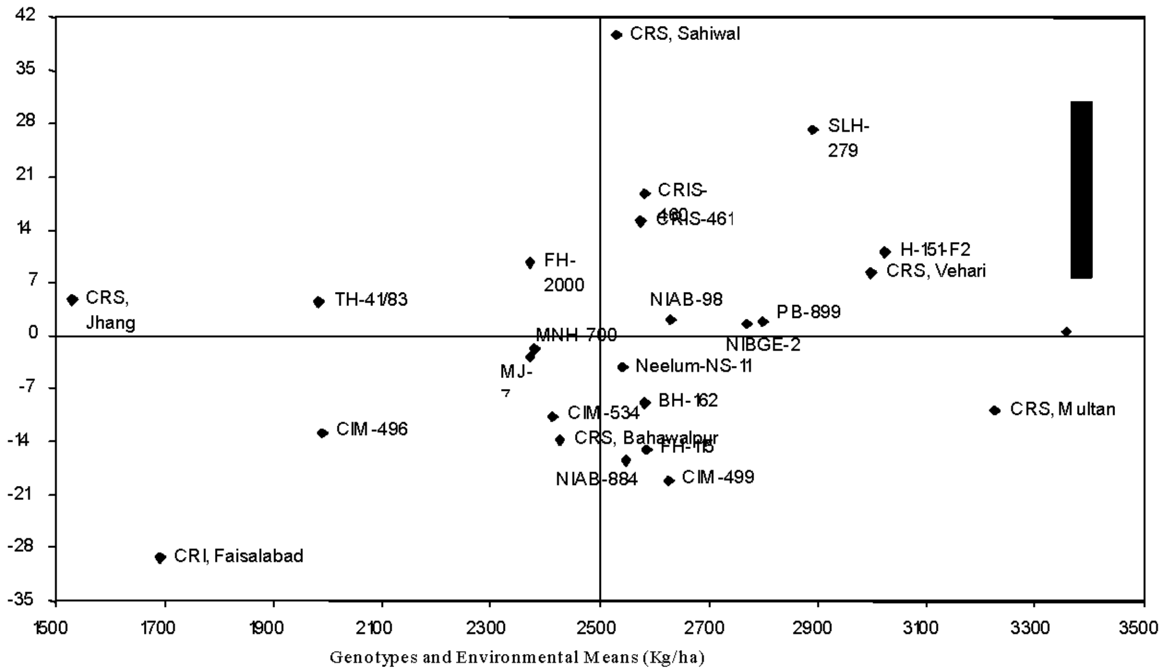

Fig. 1: AMMI biplot of 18 cotton genotypes evaluated for seed cotton yield at seven locations of Punjab, Pakistan during 2004-05

Table 4: Mean yields (kg h^{-1}) of 18 cotton genotypes at seven locations in Punjab, Pakistan during 2004-05

	Locations							
Genotype	CRI, Faisalabad	CRS, Sahiwal	CRSS, Jhang	CRS, Multan	CRS, Vehari	CRS, Rahim Yar Khan	CRS, Bahawalpur	Genotype mean
FH-115	2023.00	1831.25	1325.00	3577.00	3357.00	3327.75	2661.25	2586.04
FH-2000	1284.68	2765.00	1287.50	2922.50	2980.50	3229.00	2123.00	2370.31
CRIS-460	1216.91	3124.00	1712.50	2743.00	3260.75	4117.25	1895.75	2581.45
CRIS-461	1420.66	3270.00	1712.50	3254.25	2855.50	3498.50	2033.00	2577.77
MJ-7	1953.00	2514.00	1675.00	3075.00	2380.00	2834.50	2176.75	2372.61
H-151-F2	1493.37	3380.00	1893.75	4303.00	3695.25	3588.25	2822.50	3025.16
TH-41/83	874.72	2082.50	1343.75	2653.50	2287.00	2780.50	1853.75	1982.25
SLH-279	1417.19	4022.25	1806.25	2859.75	3900.00	3570.25	2661.00	2890.96
BH-162	2004.75	2299.50	1387.50	3326.00	3026.75	3220.25	2810.50	2582.18
CIM-534	1862.17	1939.25	1462.50	3478.50	2642.50	3399.75	2111.25	2413.70
MNH-700	1247.00	2082.00	1468.75	3191.50	2704.00	3649.00	2308.50	2378.68
PB-899	1555.34	2754.75	1812.50	3380.00	3094.50	3956.00	3049.75	2800.41
Neelum-NS-11	1661.25	2298.75	1581.25	3828.00	3027.00	3157.50	2248.25	2543.14
NIAB-98	1901.75	2803.00	1831.25	3218.25	3100.75	3094.50	2481.50	2633.00
NIAB-884	2276.00	1831.50	1243.75	3056.75	3378.25	3247.25	2800.50	2547.71
NIBGE-2	2095.38	3088.75	1500.00	3523.00	3324.25	3049.50	2810.50	2770.20
CIM-496	2270.90	2154.25	1550.00	3397.75	3094.50	3274.00	2649.25	2627.24
CIM-499	1861.41	1293.00	906.25	2321.75	1890.00	3462.50	2182.50	1988.20
Location mean	1689.97	2529.65	1527.78	3228.31	2999.92	3358.68	2426.64	2537.28
CV (%)	25.42	5.58	15.12	14.22	11.11	12.47	10.09	15.14
LSD (p = 0.05)	609.75	199.21	327.88	654.30	475.40	592.20	347.65	538.7

Table 5: Mean CLCuV % age of 18 cotton genotypes at seven locations in Punjab, Pakistan during 2004-05

	Locations							
Genotype	CRI, Faisalabad	CRS, Sahiwal	CRSS, Jhang	CRS, Multan	CRS, Vehari	CRS, Rahim Yar Khan	CRS, Bahawalpur	Genotype mean
FH-115	1.30	93.80	0.00	7.00	12.03	0.00	4.64	16.97
FH-2000	0.00	66.30	0.00	11.70	22.47	0.00	8.74	15.60
CRIS-460	2.90	71.30	0.00	3.00	23.78	0.00	17.81	16.97
CRIS-461	3.90	72.50	3.32	7.20	18.72	0.00	2.87	15.50
MJ-7	0.00	72.50	0.00	3.70	12.74	0.00	4.53	13.35
H-151-F2	0.00	73.70	0.00	5.40	15.91	0.00	3.33	14.05
TH-41/83	1.75	52.50	36.42	7.40	16.70	5.00	42.42	23.17
SLH-279	2.10	62.50	0.00	3.30	12.81	0.00	1.37	11.73
BH-162	1.65	92.50	0.00	7.00	14.86	0.00	5.84	17.41
CIM-534	0.00	58.80	34.26	5.80	10.36	0.00	3.04	16.04
MNH-700	2.40	95.70	35.36	24.40	16.18	0.00	7.36	25.91
PB-899	0.80	82.50	0.00	4.70	12.12	0.00	3.70	14.83
Neelum-NS-11	0.00	57.50	0.00	3.20	11.07	0.00	1.50	10.47
NIAB-98	0.00	72.50	0.00	5.80	11.90	0.00	5.97	13.74
NIAB-884	1.40	80.00	0.00	9.20	15.29	0.00	5.85	15.96
NIBGE-2	1.40	42.00	0.00	6.10	8.62	0.00	2.34	8.64
CIM-496	0.90	78.70	0.00	5.40	18.09	0.00	2.42	15.07
CIM-499	1.90	98.70	0.00	19.30	17.40	0.00	17.85	22.16
Location Mean	1.24	73.56	6.08	7.76	15.06	0.28	7.87	15.98
C.V (%)	12.80	5.27	15.17	16.43	19.48	8.49	16.21	13.41
LSD(p = 0.05)	0.26	6.43	1.53	2.12	4.87	0.04	2.12	2.48

TH-41/83 being the overall fewer yielder. Locations such as Rahim yar khan, Multan and Vehari which were on the right hand side of the midpoint of the main effect axis, seemed to be favourable environments for seed cotton yield among the genotypes evaluated, Sahiwal and Bahawalpur were moderately favourable while Jhang and Faisalabad were less favourable environments.

Genotypes with IPCA1 scores near zero (either positive or negative) had little interaction across environments and, *vice versa* for environments [14]. Genotype and environment mean combinations with IPCA1 scores of the same sign produced positive specific interaction effects, whereas combinations of opposite sign had negative specific interactions. Four groupings were evident from the biplot (Fig. 1): FH-2000, MJ-7, TH-41/83, CIM-534 and CIM-499 low yielding and unstable; MNH-700 was low yielding and moderately stable across environments; NIBGE-2 and PB-899 were high yielding and stable. Genotypes NIAB-98, Neelum-NS-11, BH-162, H-151-F_2, CIM-496, CRIS-461, FH-115, NIAB-884, CRIS-460 and SLH-279 were high yielding but unstable across environments.

Genotypes NIBGE-2 and PB-899 had negligible interactions with the environments, indicating their broad adaptations and stability across environments as Queme *et al.* [15] pointed out that genotypes exhibiting small interaction with the environments can be considered more stable and adapted to the testing environments. Although, MNH-700 was moderately stable, it was not very productive. Genotypes, SLH-279, CIM-499 and CRIS-460 were highly unstable and generally poorly adapted across all the environments.

Stability in performance of genotypes in field is prone to prevailing biotic and abiotic trauma [16]. Resistance to biotic stresses in addition to tolerance of common abiotic factors in the environments would ensure good varietal performance. In this study, the most stable genotypes (IBGE-2 and PB-899) generally had below average CLCuV%age (Table 5). On the other hand, TH-41/83 and CIM-499 (the lowest seed cotton yielder) had the highest %age for CLCuV disease. Environments that exhibited stable genotype yields especially Rahim yar khan, generally had lowest CLCuV disease pressure compared with locations that exhibited unstable yields such as Sahiwal with relatively lower temperature and low average rainfall.

CONCLUSIONS

The study indicated that the genotypes were closely related but responded differently to the differences in environments as the proportion of locations/ environments variance and the G×E interaction were greater than genotypic variance. It is apparent that one could rely more on suitability of the environment and crop management to attain high yields. The best performing genotypes should be tested along with the standard cultivars on farm under farmers own practices in order to assess their yield performance and stability.

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