EVALUATION OF UPLAND COTTON GENOTYPES FOR STABILITY OVER DIFFERENT LOCATIONS USING AMMI AND GGE BIPLOT ANALYSIS

SAIFULLAH ABRO[1], MUHAMMAD RIZWAN[1*], MUHAMMAD TAHIR RAJPUT[2], MAHBOOB ALI SIAL[1] AND ZAHEER AHMED DEHO[1]

[1]*Nuclear Institute of Agriculture (NIA), Tandojam (70060), Sindh, Pakistan*
[2]*Preston University Karachi, Sindh, Pakistan*
[*]*Corresponding author's email: rzi_rizwan@yahoo.com*

Abstract

Exploration of consistently high performing genotypes of cotton is important for sustainable production in major cotton growing areas of Sindh, Pakistan. In present study fifteen cotton genotypes were evaluated against three check varieties CRIS-342, CIM-496 and CRIS-134 over two years (2016, 2017). These genotypes were evaluated in advance line yield trial at five different locations. Two-way ANOVA was performed to find variation in genotypes and environments. Data were analyzed using AMMI analysis for residual multiplicative interaction. The genotypes stability was estimated by measuring different parameters like IPCA score, AMMI stability value (ASV), yield sustainability index (YSI) and genotype selection index (GSI). Genotypes and multi-locations provided an opportunity to find the best genotypes in the best environment on the basis of yield performance. The genotypes G3 (NIA-83), G13 (NIA-Bt-2) and G15 (Sadori) were found as high yielding with very high stability as compared to check varieties. Hence, recommended across the studied environments. Another genotype G2 (NIA-81) was more stable and can be used as breeding material in cotton breeding program for sustainable cotton production in diverse environments/areas of Sindh province, Pakistan.

Key words: *Gossypium hirsutum* L., Genotypes, Genotype × Environment interaction, Multi-locations, Stability, Seed cotton yield.

Introduction

Seed cotton yield is a complex polygenic trait subjective to changing environmental conditions (Riaz *et al.*, 2013). Cotton genotypes perform differently in different areas especially those with highly variable environmental conditions (Naveed *et al.*, 2006). These conditions reduce their yield stability. Further, it complicates selection procedures for important traits under different environments (Sial *et al.*, 2000). It also leads to unpredictable outcome during genotypes evaluation for yield and related traits at multi-locations over the years due to G × E interface (Deho *et al.*, 2021). The significance of G × E interaction in zonal and national trials has been established in all crop breeding programs (Ahmad *et al.*, 1996; Abro *et al.*, 2020). It is very important to find superior genotypes and their adaptation in diverse agro climatic conditions (Abro *et al.*, 2020). Hence, yield stability appraisal is a good selection parameter that classifies the genotypes as narrow base or wider adaptability.

Cotton is an international agricultural commodity of which quality and quantity are subject to various whims of nature. It occupies an important position in global status of commercial crops with annual impact of > US$50 billion in world's economy (Anon., 2019). The lint quality in general and seed cotton yield in particular is highly sensitive to climatic conditions. It can be seen in case of Pakistan where it was grown on 2.3 million hectares during 2018-19 with average yield of approximately 707 kg ha^{-1} (Anon., 2018-19) compared to 2,320 and 1,765 kg ha^{-1} for Australia and China, respectively (Anon., 2018). The quality of lint produce is also inferior, having short fiber length, coarse fiber fineness, lower uniformity, resulting in higher import of longer fiber and lower price of locally produced cotton lint (Rizwan *et al.*, 2021). It has been observed that cotton is experiencing fluctuations in production due to abrupt climatic changes over the years (Anon., 2014).

The analysis of variance describes main effects only and gives no statistics about separable genotypes and locations which are component of interface (Abbas *et al.*, 2018). This inefficiency of G × E ANOVA, affects genotypes selection for seed cotton yield. Therefore, depending on experimental data, collection accuracy, number and information of environments, different stability models are in use for dealing G × E interaction (Abro *et al.*, 2020).

Among the meta-analysis, AMMI is mostly opted tool to investigate the G × E interaction and determine the genotypes stability over different locations using principal component axis scores, ASV (Adgebeng-Danquah *et al.*, 2017). Genotypes having the least ASV value and IPCA 2 score close to zero are reflected as usually adapted and stable genotypes. The AMMI allows technical interpretation of a large set of data by combining ANOVA and PCA. GGE biplot analysis is another technique which integrates the genotypes and genotypes by environment. Therefore, present study was planned to evaluate suitability and yield stability of a set of newly developed cotton advance lines over multi-environments using AMMI and GGE biplot analysis.

Materials and Methods

Fifteen advanced lines of cotton along with three check varieties CRIS-342, CIM-496 and CRIS-134 (Table 1) were evaluated for seed cotton yield stability over two years (2016 and 2017) in cotton advance line yield trial at five diverse climatic conditions. The locations included (E1= NIA-Tando Jam, E2= Matiari, E3= Shaheed Benazirabad, E4= Khairpur, E5= Dadu) in Sindh, Pakistan. The multi-environment experiments were conducted in randomized complete block design with four replications.

Plot size was 18 m^2 (6 × 3 m) with rows and plant spacings of 75 cm and 30 cm, respectively. Recommended cultural practices were adopted throughout the growing season at each location. At maturity, seed cotton was picked, and data were recorded on seed cotton yield (kg/plot) at different locations and converted to Kg/ha. Two-way ANOVA, was carried out for each environment (year by location integration) to confirm the differences among genotypes. The AMMI model was used to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of square of the genotype by environment interaction (GEI). The GEI was divided into IPCA. Combined analysis of variance and mean comparisons were performed. The AMMI analysis was carried out using Genstat 12. The genotypes adaptability was determined by ranking genotypes on the basis of IPCA Score, ASV, YSI and GSI. ASV was estimated as per description of Purchase *et al.*, (2000). GSI was calculated following the procedure given by (Farshadfar, 2008). Additionally, AMMI Biplot graph interpretation based on the additive main effects (genotype, environment, genotype and environment mean plotted against IPCA1 and IPCA2) values were used for determination of ideal genotypes.

Results

ANOVA by AMMI model: AMMI analysis of variance for seed cotton yield of 18 cotton genotypes is given in (Table 2). The ANOVA results showed that seed cotton yield was significantly ($p \leq 0.01$) affected by genotype (G), environment (E) and genotype by environment interaction (G ×E). The explained value is highest for E (51.90%) followed by G (26.39%) and G × E (21.69%). G × E sum of square was also significantly ($p \leq 0.01$) affected by five principal components (IPCA1, IPCA2, IPCA3, IPCA4 and IPCA5) with explained values 8.11%, 5.29%, 3.36%, 2.45% and 1.48 %, respectively.

Stability estimation across environments

Components of G × E interaction: Table 3 reveals that the genotypes G15, G16, G13 and G3 had the lowest value of IPCA1 and secured lowest 1st, 2nd, 3rd and 4th positions while the genotypes with lowest IPCA2 values were G2, G15, G3 and G12 with 1st, 2nd, 3rd and 4th positions, respectively. Here the genotype G15 has 0.0107 and -0.6442 values of IPCA1 and IPCA2 and is ranked on 1st and 2nd lowest position for IPCA1 and IPCA2, respectively. Similarly the genotype G3 has -1.2108 and 1.1720 values of IPCA1 and IPCA2 and secured the fourth and third lowest positions, respectively.

AMMI stability value and genotype selection index: The genotypes G15, G2, G3 and G13 have lowest ASV values i.e. 0.6463, 1.6568, 1.9018 and 2.5193 and secured 1st, 2nd, 3rd and 4th position when ASV values were ranked with lowest ASV value as 1st ranked position. Genotype G4 was found with maximum value of ASV i.e., 25.6052 with 18th position (Table 3). The GSI score for all genotypes under evaluation ranged from 6 to 30. G3 genotypes were observed with low score of GSI i.e., 6 followed by G15 (7) and G13 (8). On the other hand, the genotypes G8 and G5 were found with higher GSI score 29 and 30, respectively (Table 3).

Table 1. Genotypes used in this study along with their code.

Genotype	Accession number	Genotype	Accession number
G1	NIA-80	G10	NIA-HM2-1
G2	NIA-81	G11	NIA-HM48
G3	NIA-83	G12	NIA-Bt.1
G4	NIA-84	G13	NIA-Bt.2
G5	NIA-H32	G14	NIA-Okra24
G6	NIA-M30	G15	Sadori
G7	NIA-HM327	G16	CRIS-342
G8	NIA-M31	G17	CIM-496
G9	NIA-Perkh	G18	CRIS-134

Table 2. Additive main effect and multiplicative interaction (AMMI) analysis of variance for seed cotton yield (Kg/ha) of 18 cotton genotypes tested across 10 environments.

Source	df	SS	MS	P Value	Explained Value
Genotypes	17	4993547	293738	0.005	26.39
Environments	9	9817209	1090801	0.005	51.90
G × E	153	4104491	26827	0.005	21.69
IPCA1	25	1533373	61335	0.005	8.11
IPCA2	23	1002189	43573	0.005	5.29
IPCA3	21	636018	30287	0.005	3.36
IPCA4	19	462655	24350	0.005	2.45
IPCA5	17	280477	16499	0.005	1.48
Residual G × E	48	189780	3954	0.005	1.00
Total	**179**	**18915247**			

Table 3. Seed cotton yield mean (Kg/ha), first and second IPCA, ASV and GSI of 18 cotton genotypes over 10 environments.

Genotype	Mean seed cotton yield	Rank seed cotton yield	IPCA1	Rank IPCA1	IPCA2	Rank IPCA2	ASV	Rank ASV	GSI
G1	3369	2	1.4291	6	5.3377	11	5.6228	7	9
G2	3197	8	1.3207	5	-0.2759	1	1.6568	2	10
G3	3323	3	-1.2108	4	1.1720	3	1.9018	3	6
G4	3040	14	7.0325	10	-12.1393	17	14.9342	13	27
G5	3075	12	20.3890	18	4.4249	8	25.6052	18	30
G6	3509	1	-7.9418	13	-2.9793	6	10.2654	10	11
G7	3160	9	-13.429	17	11.2091	16	20.0400	17	26
G8	3002	17	-10.067	15	-6.7346	13	14.1578	12	29
G9	3259	7	5.6036	9	17.4750	18	18.7994	16	23
G10	3305	5	-9.6240	14	-10.1386	14	15.6366	14	19
G11	3075	13	7.2271	12	-3.8428	7	9.7305	9	22
G12	3150	10	-12.963	16	1.6609	4	16.1214	15	25
G13	3319	4	-1.0509	3	2.1580	5	2.5193	4	8
G14	2786	18	4.6927	8	-6.3613	12	8.6116	8	26
G15	3286	6	0.0107	1	-0.6442	2	0.6463	1	7
G16	3123	11	-0.7405	2	5.2775	10	5.3564	5	16
G17	3008	16	2.25213	7	4.60231	9	5.3797	6	22
G18	3030	15	7.0721	11	-10.2015	15	13.4385	11	26
Grand Mean	3168								

Table 4. Mean, Maximum, Minimum, standard deviation of seed cotton yield (Kg/ha) and Yield Sustainability Index (YSI %) of 18 cotton genotypes over 10 environments.

Genotype	Mean	Maximum	Minimum	SD	YSI %	Stability
G1	3369	3856	2960	277.84	80.17	High
G2	3197	3610	2726	256.91	81.44	Very high
G3	3323	3698	2956	220.11	83.91	Very high
G4	3040	3589	2354	375.28	74.25	High
G5	3075	3752	2498	365.15	72.22	High
G6	3509	3965	3159	233.64	79.68	High
G7	3160	3789	340	564.29	68.51	Moderate
G8	3002	3526	2545	288.62	76.95	High
G9	3259	3696	2856	268.04	80.92	Very high
G10	3305	3800	2864	250.27	80.38	High
G11	3075	3550	2468	342.30	76.98	High
G12	3150	3700	350	538.63	70.58	Moderate
G13	3319	3765	2996	233.29	81.96	Very high
G14	2786	3362	2321	297.50	74.02	High
G15	3286	3612	2956	210.21	85.15	Very high
G16	3123	3500	2596	254.57	81.76	Very high
G17	3008	3421	2456	237.55	79.90	High
G18	3030	3652	2598	291.81	74.98	High

Stability as per YSI% = Very low (up to 30%), low (31-50%), moderate (51-70%), high (71- 80%) and very high (>80 %)

Yield sustainability index: YSI value of each genotype is given in Table 4. Stability as per YSI % is categorized into Very low (up to 20%), low (21-40%), moderate (41-60%), high (61- 80%) and very high (>80%). YSI % for studied genotypes ranged from 68.51% to 85.15%. This categorization of genotypic stability shows that the genotypes G15, G3 and G13 are in very high range of stability with YSI values of 85.15%, 83.91% and 81.96%, respectively. Ten genotypes were placed in high range stability whereas only two genotypes (G7 and G12) were categorized in a group with moderate stability. Genotype

G7 was observed with lowest YSI % value (68.51) among all the genotypes under evaluation.

Estimation of genotypes adaptability: The position of a high performing generally adapted genotype would be on the right hand side of the grand mean value and near to the line showing IPCA value equal to zero showing very little genotype by environment interaction. In present study, the genotypes G15, G3 and G13 had low IPCA values with mean yield more than the overall mean yield of all the genotypes. But G6 was best

performing genotype among all the genotypes with maximum average yield of 3509 kg/ha across all the environments (Table 3).

AMMIbiplot of genotype IPCA1 score versus means: Figure 1 showed that the Genotypes G6 was farthest and genotype G14 was closest on x-axis from its origin. The genotypes G16, G12 and G7 occupy almost same location along x-axis while genotypes G5 and G11 are at a position slightly left along the x-axis of (Fig. 1). Comparison of genotypes along Y- axis showed that the genotypes G3, G15, G16 and G2 were on the right hand side and very close to the zero.

AMMIbiplot of genotype & environment IPCA2 score versus means: Figure 2 showed that the genotypes G7 and G9 were not within the IPCA scale range and G4, G10 and G18 were far from the origin of IPCA score, so these genotypes had strong G×E interaction and least stable ones. However, the genotypes G2, G3, G12, G13 and G15 are very close to zero value along y-axis and proved to be more stable.

GGE biplot symmetric scaling/scatter plot: The scatter plot visualizes G × E interaction (Fig. 3). The origin of the biplot represented the mean phenotypic performance of all genotypes across different environments. The genotypes G2, G3, G13 and G15 were very close to the origin. The genotypes G8 and G5 were located away from origin. Here the environment factors were represented as vectors. The length of the vector represented the interactive force of that environment. We see that the environments E3 and E4, clustering very close to the origin with small vector length elicit only weak interactive forces. Similarly, the environment E1 with comparatively longer vector elicits a little strong interactive force. The graph showed that the environment E2, E5, E6, E7, E8, E9 and E10 were much far from the origin so these environments have strong interactive forces (Fig. 3).

Identification of mega environments and "which won where": There were total three mega environments (Fig. 4). The two mega environments constitutionsare E2 and E7. However, the third mega environment has broad spectrum encompassing eight environments in it. The scatter biplot has been divided into four sectors by drawing lines from its origin. The genotypes G1, G2, G3, G10, G15 and G16 are located in the largest sector consisting of environments E1, E3, E4, E5, E6, E8, E9 and E10. The polygon shows that the genotypes G1, G5, G8, G9, G10, G12 and G14 form the extremes of the polygon, contrary to this the genotypes G2, G3, G4, G6, G7, G11, G13, G15, G16, G17 and G18 are enclosed by this polygon.

GGEbiplot average environment coordination (AEC) scaling to rankgenotypes: The AEC ordinate separates genotypes with below-average means from those with above-average means (Fig. 5). Therefore, genotypes with above-average means were G6 (highest) to G12, whereas those with below-average means were G5 to G14 with G14 scoring the lowest. Stability of genotypes is more imperative in addition to good mean yield. Therefore, genotypes G3, G13 and G15 are more stable with better average seed cotton yield other than the check (G16, G17 and G18). Conversely, genotypes G9 and G12 are more variable.
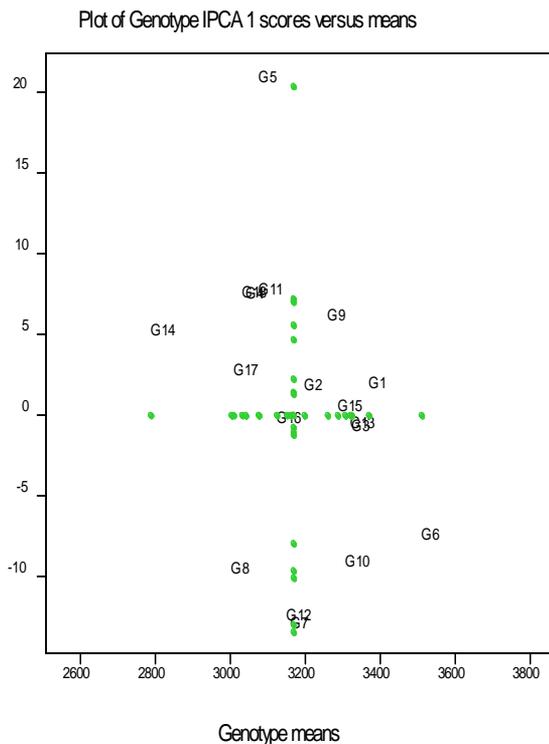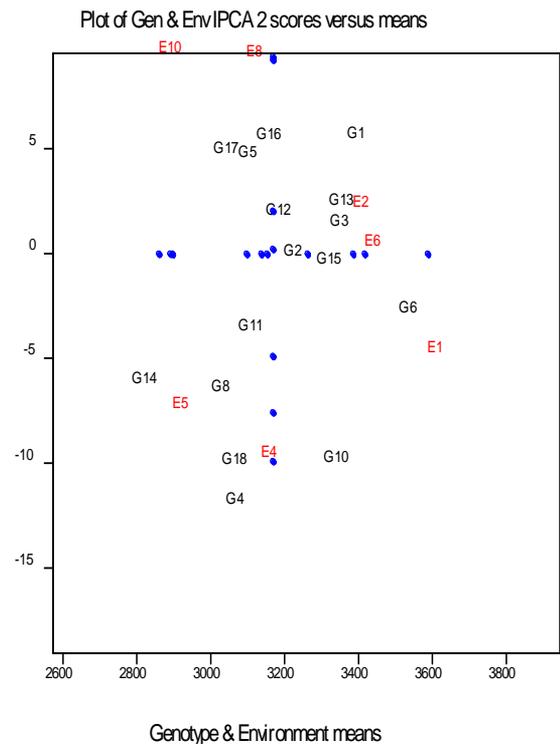

Fig. 1. Genotype main effect against IPCA1.
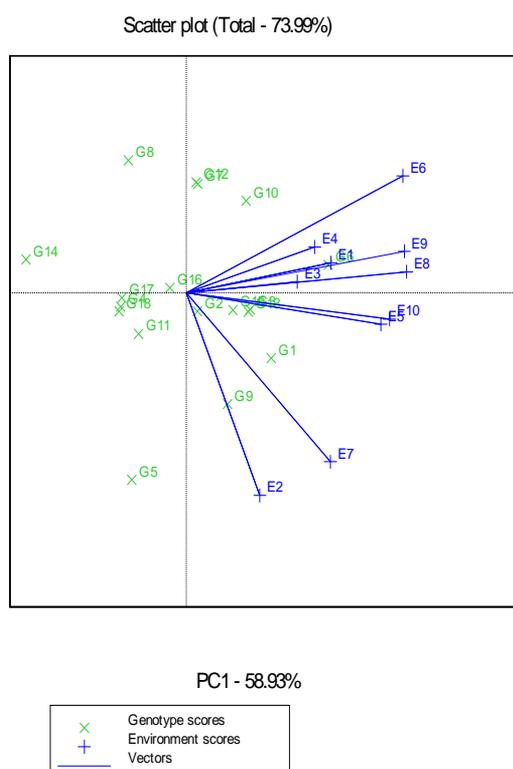

Fig. 2. Genotype and environment main effect vsIPCA2.

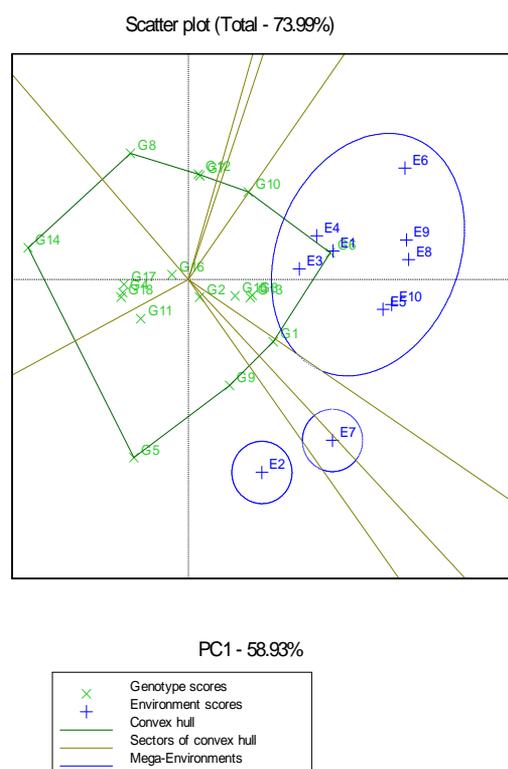Fig. 3. GGEbiplot symmetric scaling.

Fig. 4. "Which won where" view of the GGEbiplot of 18 cotton genotypes across 10 testing environments.
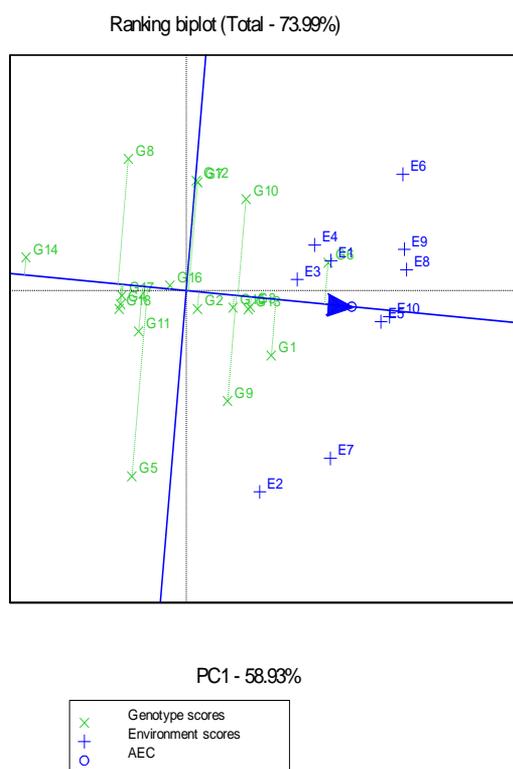

Fig. 5. Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the means performance and stability of genotypes.

GGEbiplot comparison of environment and genotypes: E and G comparison biplots revealed the 73.99% (PC1: 58.93% and PC2: 15.07%) of total

variablity for seed cotton yield in cotton genotypes across different environments (Fig. 6). Arrow at the center of concentric circles presented the position of ideal environments for evaluating the cotton genotypes regarding consistent performance. Among studied environments, E10 was closer to the arrow i.e. best environment followed by E5 and E6. E2, E7 and E6 were poor environments. Genotype, G6, G1, G13, G15, G9, G10, G2, G12, G16 were high yielding whereas genotypes G14, G8, G18, G17, G5 and G11 were low yielding with reference to the ideal genotype.

Discussion

Results show that environment is the most contributing factor with explained value (51.90%) followed by G (26.39 %) and then by G × E (21.69%). Formerly, significant G × E interaction in different cash crops has been conveyed by different researchers (Sayar *et al.*, 2016; Mortazavian *et al.*, 2014; Kendal & Sayar, 2016). The results reported by Sayar (2017) match our findings that the environment was the most dominant factor in yield performance of genotypes. Sabaghnia *et al.*, (2013) also concluded the same results and found environment as the major factor to control variation explaining 96.43% of total variability in durum wheat followed by G × E interaction and G explained values 3.14% and 0.43%, respectively. Largest proportion of E in total sum of square implies that environment is the main cause of variation for seed cotton yield at different cotton production areas of Sindh. The greater magnitude of G ×E interaction implies greater differences in genetic systems controlling physiological process contributing

to yield stability in different environments. In our study, the explained values of first two components IPCA1 and IPCA2 i.e., 8.11% and 5.29% significantly contributed in variation caused by G × E interaction.This is the simplest method for selection of stable genotypes (Purchase *et al.*, 2000; Kilic, 2014; Sayar *et al.*, 2016). As per IPCA1 and IPCA2 values and ranks, the genotypes G3, G13 and G15 are to be stable genotypes as their IPCA1 and IPCA2 values are close to zero. Our results were in close agreement with other researchers who also found that the genotypes with IPCA1 and IPCA2 score values closer to zero were going towards stability across different environments (Kendal *et al.*, 2016; Farshadfar *et al.*, 2011).

ASV is a useful parameter for the estimation of genotypic stability. The genotypes, G15, G2, G3 and G13 with minimum ASV value with 1st, 2nd, 3rd and 4th positions, respectively are stable genotypes. Purchase *et al.*, (2000) is also of the same view that lowers the ASV value, greater will be genotype stability and vice versa. It was observed that the genotypes with ASV ranked value 1, 2, 3 and 4 are although the stable genotypes but not highest yielder too. The genotype G15 has lowest ASV value but ranked at 6th position regarding mean seed cotton yield. It shows that the genotypes with high stability are not necessarily high in yield performance and vice versa. Abro *et al.*, (2020) also reported similar results and found some genotypes as most stable genotypes but

with yield compromise of 7.6% - 18% when compared with the first rank genotype. It implies that the selection of genotypes on the basis of stability alone for variety release would be misleading because some stable genotypes might be lower yielder across different environments (Singh & Agarwal, 2003) and selecting such genotypes without considering yield will result in development of non-competent variety. GSI is another parameter for estimation of stability. This parameter is more reliable and informative than ASV because it involves both the values of ASV rank and seed cotton yield mean rank. Many researchers used the parameter YSI in order to select stable genotypes on the basis of yield (Tuteja, 2006; Bose *et al.*, 2014). In present study, the genotypes G3, G13 and G15 are the most stable genotypes for their yield performance across different locations. According to YSI%, these genotypes showed very high stability (>80%). The most interesting thing is that the results of ASV and GSI are similar to the YSI parameter and make our results more valid.

The values of environment and genotype mean closer to zero point of y-coordinate means little contribution of these values in interaction and away from zero point either in upward or downward direction means more contribution of genotype by environment interaction and reduced adaptability accordingly (Pouresmael *et al.*, 2016).
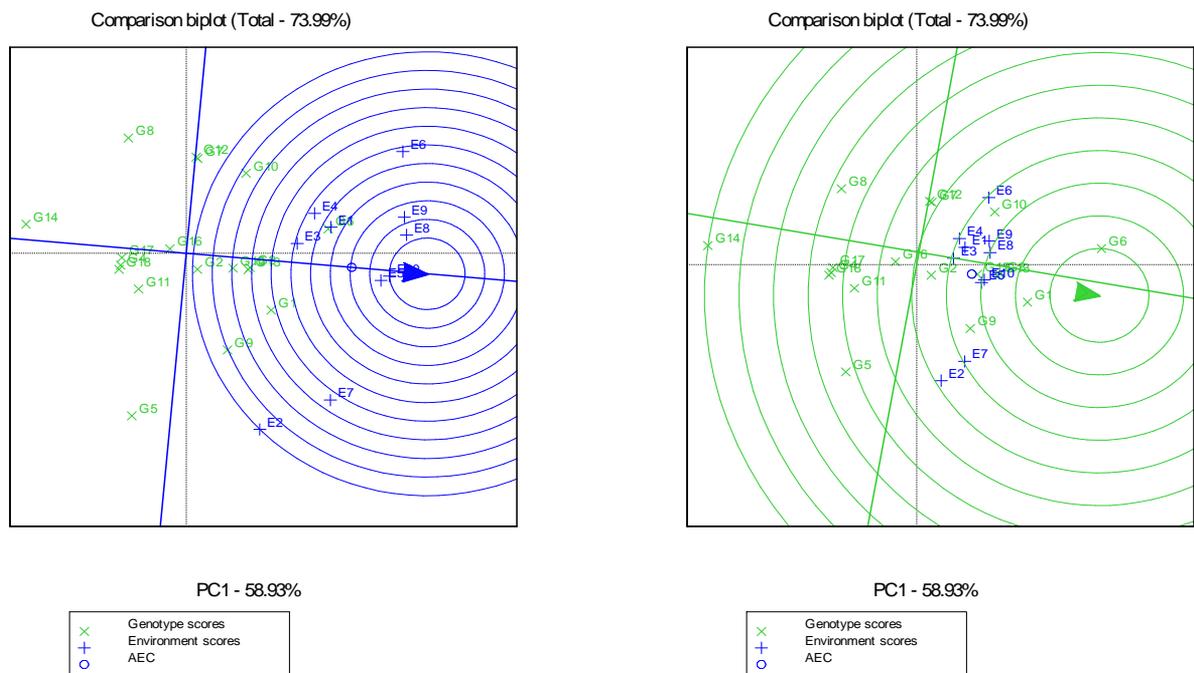

Fig. 6. Comparison biplot of environments and genotypes.

Conclusion

The divergent locations caused variation in seed cotton yield. AMMI and GGE biplot indicated the genotypes G15 (Sadori), G3 (NIA-83) and G13 (NIA-Bt-2) as most stable and high yielding with average yield greater than check varieties (CRIS-342, CIM-496 and CRIS-134), hence recommended across the environments.

Genotype G6 (NIA-M30) was observed as highest yielding genotype in comparison with check varieties and stability range almost touching to very high stability group. It was also indicated that E5 and E10 (Dadu 2016; 2017) were the environments with the greatest effect of G × E interaction. Hence, the information generated is useful and can be utilized for cotton genotype selection and variety development.

References

Abbas, G., M.J. Asghar, M. Rizwan, M. Akram, J. Hussain and F. Ahmad. 2018. Genetic analysis of yield and yield components for the improvement of mungbean germplasm. *Pak. J. Agric. Res.,* 31(2): 158-165.

Abro, S., M.T. Rajput, M.A. Sial, Z.A. Deho and M. Rizwan. 2020. Stability analysis for seed cotton yield of newly developed upland cotton genotypes. *Pak. J. Agric. Agric. Eng. Vet. Sci.*, 36(1): 97-100.

Adgebeng-Danquah, J., J. Manu-Aduening, V.E. Gracen, I.K. Asante and S.K. Offei. 2017. AMMI stability analysis and estimation of genetic parameters for growth and yield components in Cassava in the forest and Guinea Savannah ecologies of Ghana. *Intern. J. Agron.*, DOI: org/10.1155/2017/8075846.

Ahmad, J., M.H. Chaudhry, S. Salah-ud-Din and M.A. Ali. 1996. Stability for grain yield in wheat. *Pak. J. Bot.*, 28: 61-65.

Anonymous. 2018-19. Economic survey of Pakistan. Ministry of Finance, Govt. of Pakistan, Islamabad.

Anonymous. 2018. 'Cotton: Review of the World Situation': The 2018/19 Season Featured Rollercoaster Prices, with Decreasing Production, Area and Yields.https://icac.org/News/ NewsDetails?NewsId=2314&YearId=2019.

Anonymous. 2019. "OECD-FAO Agricultural Outlook", OECD Agriculture statistics (database). http://dx.doi.org/ 10.1787/agr-outl-data-en.

Anonymous. 2014. Summary Progress report of National Coordinated Varietal Trials, 2013-14. PCCC, Karachi, Ministry of Textile Industry, Govt. of Pakistan.

Bose, L.K., N.N. Jambhulkar, K. Pande and O.N. Singh. 2014. Use of AMMI and other stability statics in the simultaneous of rice genotype for yield and stability under direct seeded condition. *Chillian J. Agric. Res.*, 74(1): 3-9.

Deho, Z.A., S. Abro, S.A. Abro, M. Rizwan and F. Kharo. 2021. Impact of early and normal sowing dates on seed cotton yield and fibre traits of elite cotton lines (*Gossypium hirsutum* L.). *Pak. J. Bot.*, 53(4): 1-4.

Farshadfar, E. 2008. Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. *Pak. J. Biol. Sci.*, 11: 1791-1796.

Kendal, E. and M.S. Sayar. 2016. The stability of some spring triticale genotypes using biplot analysis. *J. Ani. Pl. Sci.*, 26(3): 754-765.

Kendal, E., M.S. Sayar, S. Tekdal, H. Aktaş and M. Karaman. 2016. Assessment of the impact of ecological factors on yield and quality parameters in triticale testing GGE Biplot and AMMI analysis. *Pak. J. Bot.*, 48: 1903-1913.

Kilic, H. 2014. Additive main effect and multiplicative interactions (AMMI) analysis of grain yield in barley genotypes across environments. *Tarım Bilimleri Dergisi- J. Agric. Sci.*, 20: 337-344.

Mortazavian, S.M.M., H.R. Nikkhah, F.A. Hassani, M. Sharif-Al-Hosseini, M. Taheri and M. Mahlooji. 2014. GGE biplot and AMMI analysis of yield performance of barley genotypes across different environments in Iran. *J. Agric. Sci. Tech.*, 16: 609-622.

Naveed, M., N. Mukhtar, J. Farooq, M. Ilyas and N. Islam. 2006. Evaluation of some new strains of *Gossypium hirsutum* L. for yield stability across environments. *J. Agric. Soc. Sci.*, 1813-2235/2006/02-1-17-19.

Pouresmael, M., H. Kanouni, M. Hajihasani, H. Astraki, A. Mirakhorli, M. Nasrollahi, M.S. Sayar and Y. Han. 2016. Forage yield performance of forage pea (*Pisum sativum* spp. *Ravense* L.) Genotypes and assessments using GGE Biplot analysis. *J. Agric. Sci. Tech.*, 18: 1621-1634.

Purchase, J.L., H. Hatting and C.S. Van Deventer. 2000. Genotype × environment interaction of winter wheat in South Africa: II. stability analysis of yield performance. *Afri. J. Pl. Soil*, 17: 101-107.

Riaz, M., M. Naveed, J. Farooq, A. Farooq, A. Mahmood, C.M. Rafiq, M. Nadeem and A. Sadiq. 2013. AMMI analysis for stability, adaptability and GE interaction studies in cotton (*Gossypium hirsutum* L.). *J. Ani. Pl. Sci.*, 23: 865-871.

Rizwan, M., S. Abro, M.U. Asif, A. Hameed, W. Mahboob, Z.A. Deho and M.A. Sial. 2021. Evaluation of cotton germplasm for morphological and biochemical host plant resistance traits against sucking insect pests complex. *J. Cott. Res.*, 4(1): 1-8.

Sabaghnia, N., M. Mohammadi and R. Karimizadeh. 2013. Parameters of AMMI model for yield stability analysis in durum wheat. *ACS*, 78(2): 119-124.

Sayar, M.S. 2017. Additive main effects and multiplicative interactions (AMMI) analysis for fresh forage yield in common vetch (*Vicia sativa* L.) genotypes. *Agric. Forest.*, 63: 119-127.

Sayar, M.S., A.E. Anlarsal and M. Başbag. 2016. Additive main effects and multiplicative interactions (AMMI) analysis for biological yield in Hungarian Vetch (*Vicia pannonica* CRANTZ.) genotypes. *J. Fiel. Crop. Cent. Res. Inst.*, 25: 235-240.

Sial, M.A., M.A. Arain and M. Ahmad. 2000. Genotype × environment interaction on bread wheat grown over multiple sites and years in Pakistan. *Pak. J. Bot.*, 32: 85-91.

Singh, P. and D.K. Agarwal. 2003. Sustainability index as an aid for determining the genotypic stability in diploid cotton (*Gossypium arboreum*). *J. Cotton Res.*, 17: 90-92.

Tuteja, O.P. 2006. Comparative studies on stability parameters and sustainability index for selecting stable genotypes in upland cotton (*Gossypium hirsutum* L.) *Ind. J. Genet. Plant Breed.*, 66: 221-224.

(Received for publication 15 January 2021)