



Research Article

Yield Stability of Upland Cotton Genotypes under Erratic Environments

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Abstract | Genotype by environment interaction (GEI) imposes an influence on the yield stability of a genotype tested under erratic environments. The present experiment was carried out at six sites *viz*; Multan, Faisalabad, Khanpur, Bahawalpur, Vehari and Sahiwal in the Punjab province during Kharif 2020-21. The main objectives of the study were to quantify the GEI component of variation and to assess the yield stability of recently bred upland cotton strains across test environments. Twenty-one cotton strains were sown according to a randomized complete block design (RCBD) with three replications. Additive main effects and multiplicative interaction (AMMI) analysis illustrated that additive effects of genotypes, environments and multiplicative effects (GEI) were significant at ($p < 0.01$). Test sites accounted for the biggest share (74.1%) of the variability, followed by GEI (17.2%) and strains (8.7%), respectively. The first four interaction principal components (IPC) were significant at ($p < 0.01$) wherein the first two IPCs captured (68.4%) of the GEI cumulatively. Strain ST06 (FH-492) won four environs and was declared the overall winner of this trial. The Vehari location was the best location for cotton multi-environment trials (MET) due to the bearing of minimum IPC-1 score. The correlation coefficient between strains in IPC1 was (0.81) and sites in PC1 was (0.76). Strain ST08 (BH-224) bears a yield edge of (84.5%) over general winner strain ST (06) FH-492 at the site of Multan due to micro adaptations. Genotype selection index (GSI: A non-parametric approach to determine yield stability) discriminated ST02 (WEAL-AG-10), ST05 (MNH-1050), ST09 (VH-418) and ST19 (UAM-20) as stable yielder strains bearing the lowest GSI value (11). These strains are important in boosting cotton production hence, their release for general cultivation may be sought from the authorized forum.

Received | March 10, 2022; **Accepted** | June 25, 2022; **Published** | August, 29, 2022

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Citation | Jamil, M., M.H. Babar, A. Hussain, R.A.H. Khan, H. Hussnain and S. Ahmad. 2022. Yield stability of upland cotton genotypes under erratic environments. *Sarhad Journal of Agriculture*, 38(3): 1124-1131.

DOI | <https://dx.doi.org/10.17582/journal.sja/2022/38.3.1124.1131>

Keywords | Cotton strains, Genotype into environment interaction, Genotype selection index, Micro adaptations, Yield stability



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Introduction

Cotton is considered the backbone of the national economy. This crop fetches foreign exchange

through exports of lint, yarn and garments. It adds 0.81% to GDP and bears a 4.12% share of the agriculture sector value addition (GOP, 2020). The global market for cotton and its products reached almost

600 billion dollars annually (Ashraf *et al.*, 2018). The Punjab province remained the hub of cotton production in the past decades, but production is declining in this province each year. Enhanced humidity due to the multi-crop trend is the dominant reason for this decline. Uneven trends in rainfall during the cropping season and hot spells affected the crop growth negatively and resulted in fruit loss. The development of resistance among insect pests against prevailing agrochemicals also added to the crisis.

Breeding of cotton cultivars suitable for the area has remained a key objective of scientists. Many novel varieties of cotton were developed in the past, but only a few survived in the field for more than ten years. Only cultivar NIAB-78 remained in cultivation more than two decades from its release. Performance evaluation of newly bred strains at different locations is a necessary aspect of approval as a variety (Farshadfar *et al.*, 2012). If significant contents of GEI prevail in the study material then the selection of varieties in multi-location experiments on a mean yield basis is misleading and biased (Sharifi *et al.*, 2017).

The AMMI analysis is a biometric tool used to quantify GEI contents of variation in multi-environment trials (Kandus *et al.*, 2010; Verma and Singh, 2020). This tool effectively decomposes the total variation into GEI and the main effects due to genotypes and environments. Further, the PCA method is applied in AMMI analysis to extract interpretable information enfolded in GEI (Bocianowski *et al.*, 2019). For the effective selection of super varieties in multi-environment both stability and mean yield is important with equal weightage (El-Hashash *et al.*, 2019).

Cotton strains studied here were recently bred and never tested earlier. Further stability analysis in cotton by the AMMI method is rarely reported in the literature. It was hypothesized that cotton strains with stable yield performance under varying environs can boost national cotton production and will persist longer period in cultivation. The leading purpose of the present study was to quantify the GEI and to identify cotton strains having stable yield performance across test sites. These identified strains with stable yield performance will help the optimization of cotton production in the province.

Materials and Methods

The present study was carried out at six locations in the Punjab province during Kharif 2020-21. Twenty-one newly bred cotton strains by public and private sector research stations (Table 1) were sown in the first week of May under the arrangement of RCBD with three repeats. Each plot was comprised of six meters long four cotton rows. Three healthy seeds were sown at each hole by hand on 75cm apart raised beds. Pre emergence weedicide s-metachlor @ 2 litres ha⁻¹ was sprayed using a flood jet nozzle within 24 hours after first irrigation. Subsequent irrigations were applied at the interval of 7-21 days till the crop maturity depending upon weather conditions. A distance of 22-25 cm was maintained between the plants by manual thinning at the 4-6 leaved plant stage. Fertilizer was applied according to the soil analysis to ensure optimum nutrients available to plants. Recommended agronomic measures were adopted during the growing season. Insect pest populations were kept below economic injury level by spraying recommended agrochemicals. When maximum bolls were opened picking was done with female labour manually. Further, picking was performed plot-wise and started after drying of moisture due to dew. After cleaning, the plot yield data was converted into kg ha⁻¹ for statistical analysis.

Statistical analysis

Seed cotton yield data were subjected to the analysis of variance (ANOVA) method as suggested by Steel *et al.*, (1997). To quantify the GEI present in this trial concerning the seed cotton yields, data were analyzed with the AMMI technique (Gauch, 2013). This analysis captures interpretable information from GEI by applying the PCA method and yields interaction principal components (IPC). F test is used for determining the significance of IPC sata given degree of freedom (Cornelius *et al.*, 1992).

AMMISOFT version 1.0 software (<https://scs.cals.cornell.edu/people/hugh-gauch>) was used for the analysis of data. Further, the Genotype Selection Index (GSI) a non-parametric approach to determine yield stability given by Farshadfar (2008) was calculated as per the formula given below.

$$GSI = Rank\ of\ ASV + Rank\ of\ Y$$

Where ASV represents AMMI Stability Value and Y denotes to mean yield across test sites.

Table 1: *Detail of test strains and locations.*

Code	Strain	Institute/ Station	Code	Strain	Institute/ station	
ST01	MNH-1086	Cotton Research Institute, Multan	ST12	FH-142	Cotton Research Station, Faisalabad	
ST02	Weal-AG-10	Weal-AG seed corporation, Multan	ST13	FH-414	Cotton Research Station, Faisalabad	
ST03	SLH-Chandni	Cotton Research Station, Sahiwal	ST14	RH-King-20	Cotton Research Station, Khanpur	
ST04	FH-494	Cotton Research Station, Faisalabad	ST15	Weal-AG-201	Weal-AG seed corporation, Multan	
ST05	MNH-1050	Cotton Research Institute, Multan	ST16	FH-Anmol	Cotton Research Station, Faisalabad	
ST06	FH-492	Cotton Research Station, Faisalabad	ST17	SLH-55	Cotton Research Station, Sahiwal	
ST07	Weal-AG-09	Weal-AG seed corporation, Multan	ST18	BH-225	Cotton Research Station, Bahawalpur	
ST08	BH-224	Cotton Research Station, Bahawalpur	ST19	UAM-20	MNS University, Multan	
ST09	VH-418	Cotton Research Station, Vehari	ST20	FH-498	Cotton Research Station, Faisalabad	
ST10	RH-Afnan-II	Cotton Research Station, Khanpur	ST21	Weal-AG-11	Weal-AG seed corporation, Multan	
ST11	Weal-AG-301	Weal-AG seed corporation, Multan				
Code	Location	Latitude	Longitude	Altitude (m)	Climate	Soil type
SIT1	Cotton Research Institute, Multan	30° 11' 52" N	71° 28' 11" E	125	Arid	Loamy
SIT2	Cotton Research Station, Faisalabad	31° 21' 52" N	72° 59' 40" E	184	Semi-Arid	-
SIT3	Cotton Research Station, Khanpur	28° 25' 12" N	70° 18' 0" E	200	Arid	Loamy
SIT4	Cotton Research Station, Bahawalpur	29° 23' 44" N	71° 41' 1" E	116	Arid	Sandy-loam
SIT5	Cotton Research Station, Vehari	29° 23' 44" N	71° 41' 1" E	135	Semi-Arid	Loamy
SIT6	Cotton Research Station, Sahiwal	30° 39' 52" N	73° 6' 30" E	172	Semi-Arid	-

Table 2: *AMMI analysis for seed cotton yield in 21 cotton strains across 6 locations.*

SOV	DF	SS	MSS	The proportion of variance %		
				TV	A and I V	GEI
Treatments	125	163683617	1309469 ^A	94.8		
Strains	20	14267314	713366 ^A		8.7	
Environments	05	121331758	24266352 ^A		74.1	
Strain x Env.	100	28084545 (Total) 24534220 (Signal) 3550325 (Noise)	280845A ^a		17.2	
IPC1	24	10767168	448632A ^a			38.4
IPC2	22	8420676	382758 ^A			30.0
IPC3	20	4422501	221125 ^A			15.7
IPC4	18	3012592	167366 ^A			10.7
Residual	16	1461608	91350 ^B			5.2
Error	252	8946819	35503	5.2		
Blocks x Env.	12	321934	26828 ^{NS}			
Pure Error	240	8624884	35937			
Total	377	172630435	457906	100	100	100

^A, Significant at ($p < 0.01$); ^B, Significant at ($p < 0.05$); ^{NS}, Non-significant. Note: F-test uses pure error because blocks × environment are non-significant. SOV: Source of variance; DF: Degree of freedom; SS: Sum of squares; MSS: Mean sum of squares; TV: Total variance; A and I V: Additive and Interaction variance; GEI: Genotype × environment interaction.

Results and Discussion

Data of seed cotton yield were subjected to AMMI analysis. Results presented in (Table 2) revealed that treatments contribute (94.8%) towards the total sum of squares (SS), further main effects due to cotton strains and test environments plus GEI multiplicative

effects were significant at ($p < 0.01$). Test environments accounted for the maximum share (74.1%) of total variation due to treatments followed by GEI (17.2%) and strains (8.7%) respectively. GEI was comprised of (87.4%) signal value (Interpretable information) and further split to 4 IPC. IPC1 and IPC2 are enfolded with maximum GEI of 38.4% and 30%, respective-

ly. A minute portion of GEI (5.2%) usually squeezed with noise (the portion not explainable) was placed as residual and hence worthless.

Mega environment delineation and AMMI model diagnosis

Due to the presence of 4 IPCs significant at ($p < 0.01$) AMMI4 model was diagnosed for optimizing predictive accuracy in the current data set. However, for practical implications AMMI1 model was used as the default model. This model divided all six test sites into 3 mega environments (ME). ME-1 was found biggest (Table 3) and consisted of 4 study sites won by ST06 (FH-492) and so this strain was declared as the overall winner of the trial. This winner strain was also top in mean seed cotton yield (2204 kg ha^{-1}) followed by ST09 (VH-418) with (2127 kg ha^{-1}) yield (Figure 1). ST08 (BH-224) was the poorest yielder (1491 kg ha^{-1}) among all tested strains across six locations. ME-2 was comprised of single-site SIT06 (CRS-Sahiwal) and was won by ST09 (VH-418). Similarly, ME-3 was won by ST08 (BH-224) at the SIT1 (CRI-Multan) location. Furthermore, ST08 (BH-224) bears a yield advantage of (84.5%) over general winner strain FH-492 at the CRI-Multan location due to micro adaptations. Similarly, SIT09 (VH-148) holds a 3.97% yield edge at the CRS-Sahiwal site over FH-492.

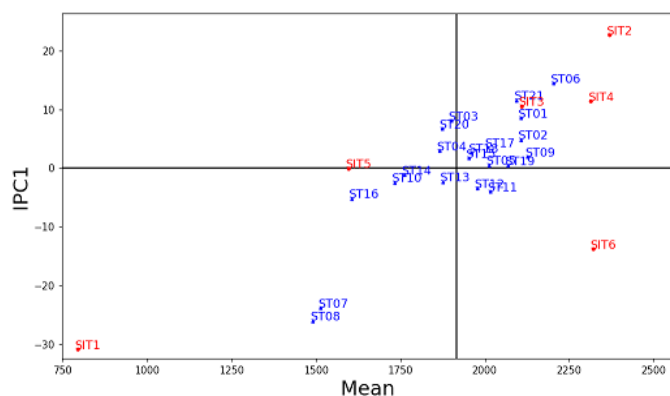


Figure 1: Values of IPC-1 plotted against the mean yield for cotton strains and test locations.

SIT2 (CRS- Faisalabad) location gave the highest seed cotton yield (2369 kg ha^{-1}) followed by SIT6 (CRS-Sahiwal) with (2320 kg ha^{-1}) mean seed cotton yield (Figure 1). SIT1 (CRI-Multan) location gave the poorest mean yield (794 kg ha^{-1}) among tested sites. SIT5 (CRS-Vehari) was found best location for cotton MET due to the bearing of minimum IPC1 score (Figure 1). A high correlation coefficient value between strains mean yield and IPC1 score was (0.81) similarly, correlation value for test location mean yield

performance and IPC1 score was (0.76).

Selection of stable strains across tested locations

The GSI discriminated ST02 (WeaL-AG-10), ST05 (MNH-1050), ST09 (VH-418) and ST19 (UAM-20) as stable in yield performance strains bearing the lowest (11) GSI value (Table 4) followed by ST18 (BH-225) with (15) GSI ranks value, respectively. Contrary to this ST08 (BH-224) and ST07 (WeaL-AG-9) was found unstable and poor performer bearing the highest GSI ranks (> 40) hence likely to be rejected.

The presence of significant variation concerning seed cotton yield at ($p < 0.01$) among strains, environments and GEI components depicted uneven performance of cotton strains across test environs. Earlier researchers (Workie *et al.*, 2013) also reported similar results in the MET study. Occurrence of highly significant ($p < 0.01$) contents of GEI in studied upland cotton strains provided sufficient grounds for AMMI analysis. This component also poses a hindrance in determining strains inbuilt genetic potential. A successful variety must perform well throughout the proposed area for its cultivation. It was a proven fact that yield was diverged by environment additive effects and GEI components (Ntawuruhunga *et al.*, 2016). Results presented in (Table 2) revealed that treatment SS (94.8%) indicated the perfection of the present experiment. Results also depicted that the biggest share of SS was due to environments (74.1%) hence effectiveness of MET trials in cotton was proved. These results are in accordance with earlier findings on the cotton crop (Riaz *et al.*, 2013; Naveed *et al.*, 2017). GEI multiplicative effects were found to be more than double the additive effects by strains (Table 2) indicating that strains responded to test environments unevenly. Earlier researchers (Zare, 2012; Naveed *et al.*, 2017) also reported similar findings in the cotton crop. GEI was splitted to 4 IPCs significant at ($p < 0.01$) while a small portion (5.2% of GEI) was placed as leftover. Usually, earlier IPC captures signal (interpretable) information, while later IPC and residual are squeezed with noise (unexplainable information). Removal of noise in the form of residual increases the accuracy of results and the simplified conclusion. The first two IPC are important because they are enfolded with (1.34) times greater variability than additive main effects by cotton strains. This indicated that GEI played a greater role in the yield performance of tested strains.

Table 3: Winner strains in three mega environments.

Mega Env.	Env. Code	Ratio	AMMI-1 Ranks					AMMI-F Ranks				
			1	2	3	4	5	1	2	3	4	5
ME-1	SIT2	1	ST06	ST21	ST01	ST02	ST09	ST06	ST04	ST21	ST20	ST01
	SIT4	1	ST06	ST21	ST01	ST02	ST09	ST02	ST06	ST01	ST19	ST21
	SIT3	1	ST06	ST21	ST01	ST02	ST09	ST09	ST11	ST05	ST02	ST12
	SIT5	1	ST06	ST09	ST02	ST01	ST21	ST11	ST17	ST06	ST15	ST09
ME-2	SIT6	1.0397	ST09	ST11	ST019	ST02	ST12	ST16	ST20	ST18	ST19	ST04
ME-3	SIT1	1.8450	ST08	ST07	ST11	ST12	ST09	ST08	ST07	ST05	ST19	ST09

Table 4: Classification of cotton strains for mean seed cotton yield ($Kg ha^{-1}$), AMMI stability value (ASV) and genotype selection index (GSI).

Strains	Codes	Mean yield	Rank	IPC-1 score	IPC-2 score	ASV	Rank	GSI
MNH-1086	ST01	2106	4	8.549	2.484	11.21	12	16
WeaL-AG-10	ST02	2107	3	4.862	6.764	9.19	8	11
SLH-Chandni	ST03	1900	13	8.093	1.862	10.51	10	23
FH-494	ST04	1866	16	2.980	-17.375	17.79	17	33
MNH-1050	ST05	2012	8	0.531	4.114	4.17	3	11
FH-492	ST06	2204	1	14.493	0.968	18.56	18	19
WeaL-AG-9	ST07	1514	20	-23.764	7.195	31.23	20	40
BH-224	ST08	1491	21	-26.002	-6.977	33.97	21	42
VH-418	ST09	2127	2	1.934	9.529	9.84	9	11
RH-Afnan-II	ST10	1733	18	-2.407	-11.351	11.76	13	31
WeaL-AG-301	ST11	2017	7	-3.982	18.519	19.21	19	26
FH-142	ST12	1978	10	-3.375	4.400	6.16	6	16
FH-414	ST13	1875	14	-2.320	0.597	3.03	2	16
RH-King-20	ST14	1761	17	-1.115	-2.119	2.55	1	18
WeaL-AG-201-II	ST15	1953	12	1.741	10.468	10.70	11	23
FH-Anmol	ST16	1606	19	-5.174	-14.971	16.37	15	34
SLH-55	ST17	2008	9	3.541	4.940	6.70	7	16
BH-225	ST18	1960	11	2.636	3.419	4.80	4	15
UAM-20	ST19	2068	6	0.472	-6.015	6.05	5	11
FH-498	ST20	1873	15	6.727	-14.210	16.61	16	31
WeaL-AG-11	ST21	2094	5	11.578	-2.242	14.97	14	19

AMMI comprises a family of models depending upon significant IPC count. The simplest model is AMMI0 composed of only additive effects without any GEI value. The last model is AMMIF consist of all GEI information in the form of several IPC, hence no residual. AMMIF represents raw data (Averages/rep) and bears no practical value. AMMI model diagnosis is crucial for accuracy and practical implications in each data set. Higher AMMI models enhance complexity and create many mega environments (ME) with limited practical value. Simpler models gave ME workable limits but with limited accuracy in results and prediction. [Gauch \(2013\)](#) in

his famous paper suggested the AMMI1 model as the default, for simplicity and practical implementations. [Agahi et al. \(2020\)](#) in a study also used the default AMMI1 model. In the present study AMMI1 divided test sites into three ME ([Table 3](#)) and one winner strain for each ME. ME1 was the largest containing 4 locations bearing IPC1 score values in the plus form ([Figure 2](#)) and won by ST06. This strain was also the overall winner of this trial because this had won maximum locations along with the highest ($2240 kg ha^{-1}$) mean yield. ME2 and ME3 possessing negative values of IPC1 score are small containing one location each and won by ST09 and ST08 strains,

respectively. Strains responses are a linear function of IPC1 scores similar to Finlay Wilkinson's regression. The nominal yield is strains mean yield plus AMMI estimated interaction value effects. ST08 (BH-224) winner of ME3 gave the highest nominal yield at SIT1 (CRI-Multan) nearly 2300kg ha⁻¹ (Figure 2). This increase at SIT1 was due to micro adaptation by ST08 than the overall winner strain in this trial. These findings are in line with the results presented by Krishnamurthy (2021). The results derived in the present study indicated that IPC1 discriminated sites and strains on both +/- sides. Large correlation coefficient values of sites and strains with IPC1 indicated a strong discriminating effect of the first interaction axis.

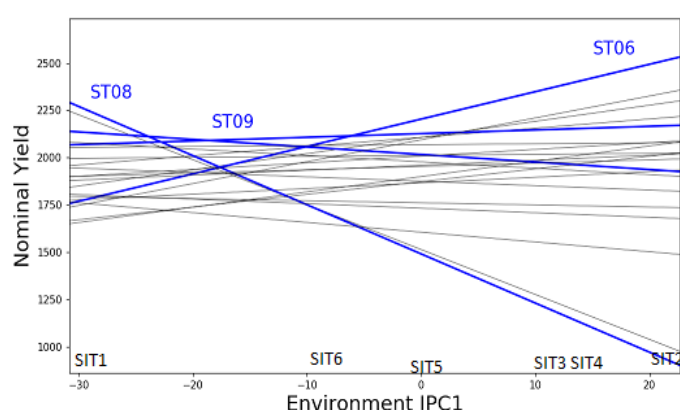


Figure 2: AMMI linear model showing test sites IPC1 score along the abscissa and nominal yield of winner strains on the ordinate axis.

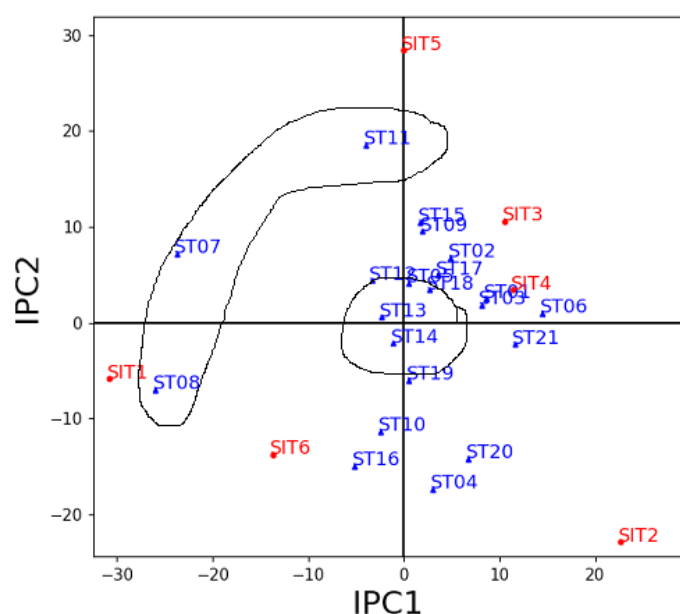


Figure 3: AMMI biplot drawn between the first two IPC scores.

Dozens of high yielding varieties of cotton were evolved in the past decades but most of them vanished from cultivation within five years of approval due to uneven yield in changing climatic conditions

(Bose *et al.*, 2014). A successful variety must be able to perform better in a different ecological zones. Performance stability is also required along with a high mean yield. AMMI analysis itself was unable to determine stability values, for this concept of AMMI Stability Value (ASV) was given by Purchase (1997). The ASV is the derivative product of the first 2 IPC values and the sum of squares obtained from the ANOVA table. Biplot generated by the software discriminated strains and sites with relative positions at which they occur respectively (Figure 3). Strains like ST13 and ST14 situated near the center of the biplot are bearing the least values for GEI and are considered stable genotypes (Figure 3). Similarly, strains located at the periphery of biplot like ST07, ST08 and ST11 are unstable in yield performance. As it is evident (Figures 1 and 3) mostly stable genotypes are not the best yielders. The Gr is a non-parametric tool which combines both mean yield and stability values in a single parameter (Farshadfar, 2008). The genotypes with lower GSI ranks values are stable in yield performance among all strains tested in this trial.

Conclusions and Recommendations

The cotton strains MNH-1050, UAM-20, WeaL-AG-10, and VH-418 were found stable in yield performance as in the given order with same GSI score (11) over-tested locations in this study. Their release for general cultivation from an authorized forum is needed at the earliest in the public interest.

Novelty Statement

Cotton strains studied in this trial are recently bred and never tested earlier for yield stability analysis. Furthermore, the AMMI technique is rarely reported for stability analysis in cotton.

Author's Contribution

Muhammad Jamil: Conducted the trial at the Vehari site and wrote the manuscript.

Muhammad Hussain Babar: Reviewed the literature.

Aamir Hussain: Analyzed the data.

Rana Abdul Hameed Khan: Prepared figures and tables.

Hammad Hussain: Compiled trial results from all sites.

Saghir Ahmad: Supervised the study and proofread

the manuscript.

Conflict of interest

The authors have declared no conflict of interests.

References

- Agahi, K., J. Ahmadi, H.A. Oghan, M.H. Fotokian and S.F. Orang. 2020. Analysis of genotype x environment interaction for seed yield in spring oilseed rape using the AMMI model. *Crop Br. Appl. Biotechnol.*, 20(1): e26502012. <https://doi.org/10.1590/1984-70332020v20n1a2>
- Ashraf, J., D. Zuo, Q. Wang, W. Malik, Y. Zhang, M.A. Abid and G. Song. 2018. Recent insights into cotton functional genomics, progress and future perspectives. *Plant Biotechnol.*, 16(3): 699-713. <https://doi.org/10.1111/pbi.12856>
- Bocianowski, J., J. Niemann and K. Nowosad. 2019. Genotype-by environment interaction for seed quality traits in interspecific cross-derived Brassica lines using additive main effects and multiplicative interaction model. *Euphytica*, 215(7): 1-13. <https://doi.org/10.1007/s10681-018-2328-7>
- Bose, L.K., N.N. Jambhulkar, K. Pande and O.N. Singh. 2014. Use of AMMI and other stability statistics in the simultaneous selection of rice genotypes for yield and stability under direct-seeded conditions. *Chillian J. Agric. Res.*, 7(1): 1-9.
- Cornelius, P.L., M.S. Seyed and J. Crossa. 1992. Using the shifted multiplicative model to search for "reparability" in crop cultivar trials. *Theor. Appl. Genet.*, 84: 161-172. <https://doi.org/10.1007/BF00223996>
- El-Hashash, E.F., S.M. Tarek, A.A. Rehab and M.A. Tharwat. 2019. Comparison of non-parametric stability statistics for selecting stable and adapted soybean genotypes under different environments. *Asian J. Res. Crop Sci.*, 4(4): 1-16. <https://doi.org/10.9734/ajrcs/2019/v4i430080>
- 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. <https://doi.org/10.3923/pjbs.2008.1791.1796>
- Farshadfar, E., R. Mohammadi, M. Aghaei and Z. Vaisi. 2012. GGE biplot analysis of genotype into environment interaction in wheat-barley disomic addition lines. *Aust. J Crop Sci.*, 6(6): 1074-1079.
- Gauch, H.G., 2013. A simple protocol for AMMI analysis of yield trials. *Crop Sci.*, 53: 1860-1869. <https://doi.org/10.2135/cropsci2013.04.0241>
- GOP, 2020. Agricultural statistics year book 2019-20. Economic survey, finance division, economic advisor's wing, Govt. of Pakistan, Islamabad.
- Kandus, M., D. Almorza, B. Ronceros and J.C. Salerno. 2010. Statistical models for evaluating the genotype-environment interaction in maize (*Zea mays L.*). *Phyton-Rev. Int. Bot. Exp.*, 79(26): 39-46. <https://doi.org/10.32604/phyton.2010.79.039>
- Krishnamurthy, S.L., P.C. Sharma, D.K. Sharma, Y.P. Singh, V.K. Mishra, D. Burman, B. Maji, S. Mandal, S.K. Sarangi, R.K. Gautam, P.K. Singh, K.K. Manohara, B.C. Marandi, K. Chattopadhyay, G. Padmavathi, P.B. Vanve, K.D. Patil, S. Thirumeni, O.P. Verma, A.H. Khan, S. Tiwari, S. Geetha, R. Gill, V.K. Yadav, B. Roy, M. Prakash, A. Anandan, J. Bonifacio, A.M. Ismail and R.K. Singh. 2021. Additive main effects and multiplicative interaction analyses of yield performance in rice genotypes for general and specific adaptation to salt stress in India. *Euphytica*, 217(20): 1-15. <https://doi.org/10.1007/s10681-020-02730-7>
- Naveed, M., M. Nadeem and N.I. Khan. 2017. AMMI Analysis of some upland cotton genotypes for yield stability in different milieus. *World. J. Agric. Sci.*, 3(1): 39-44.
- Ntawuruhunga, P.H., P.R. Rubaihayo, J.B.A. Whyte, A.G.O. Dixon and D.S.O. Osiru. 2016. Additive main effects and multiplicative interaction analysis for storage root yield of cassava genotypes evaluation in Uganda. *Afr. Crop. Sci. J.*, 9: 591-598. <https://doi.org/10.4314/acsj.v9i4.27581>
- Purchase, J.L., 1997. Parametric analysis to describe G x E interaction and yield stability in winter wheat. Ph. D thesis. Dep. Agron. Fac. Agric., Univ. Orange Free State, Bloemfontein, South Africa.
- Riaz, M., M. Naveed, J. Farooq, A. Farooq, A. Mahmood, C. Rafiq, M. Nadeem and A. Sadiq. 2013. AMMI analysis for stability, adaptability and GE interaction studies in cotton (*Gossypium hirsutum L.*). *J. Anim. Plant Sci.*, 23(3): 865-871.
- Sharifi, P., A. Hashem, E. Rahman, M. Ali and A. Abouzar. 2017. Evaluation of genotype x en-

- vironment interaction in rice based on AMMI model in Iran. *Rice Sci.*, 24: 173-180. <https://doi.org/10.1016/j.rsci.2017.02.001>
- Steel, R.G.D., J.H. Torrie and D.A. Dickey. 1997. Principles and procedure of statistics: A biometrical approach 3rd ed. McGraw-Hill Book Co., New York.
- Verma, A., and G.P. Singh. 2020. G x E interaction Analysis of wheat genotypes evaluated under restricted irrigated timely sown conditions of north eastern plains zone using AMMI and yield stability measures. *Int. J. Curr. Microbiol. App. Sci.*, 9(11): 957-970. <https://doi.org/10.20546/ijcmas.2020.911.114>
- Workie, A., H. Zeleke and Y. Dessalegn. 2013. Genotype into environment interaction of maize (*Zea mays* L.) across north western Ethiopia. *J. Plant Breed. Crop Sci.*, 5(9): 171-181. <https://doi.org/10.5897/JPBCS2013.0406>
- Zare, M., 2012. Evaluation of drought tolerance indices for the selection of Iranian barley (*Hordeum vulgare*) Cultivars. *Afr. J. Biotechnol.*, 11(4): 975-981. <https://doi.org/10.5897/AJB12.2127>