



## Research Article

# Performance Stability Assessment in upland Cotton Strains throughout Cotton-growing Belt in Pakistan

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**Abstract** | Cotton is a real cash crop and contributes to the national economy by enhancing exports. The yield performance of cotton is fluctuating under erratic test conditions due to genotype into environment interaction. The present study was executed at 14 sites throughout Pakistan according to a randomized complete block design replicated 03 times during Kharif (summer season) 2019. The experiment aimed to assess the performance stability of studied strains in terms of seed cotton yield against selected environments. Twenty-five upland cotton strains recently bred by different research stations including the check cultivar (CIM-602) were selected for this study. Additive main effects and multiplicative interaction (AMMI) analysis procedure was followed for the data analysis. The analysis of variance revealed that strains, environments and genotype into environments interaction (GEI) results were significant at ( $p \leq 0.01$ ). Further, the GEI sum of squares (SS) was comprised of (20.5%) out of total variability. Seven interaction Principal Component Axis (IPCA) were found significant at ( $p \leq 0.01$ ). IPCA-1 and IPCA-2 were found enfolded with 37.9% and 22.2% of GEI portion respectively. AMMI-1 was diagnosed as a predictive model which delineated all test sites into 4 mega environments. The strain (NIAB-1011) won seven environments and qualified as the overall winner of the trial by giving the highest 2604 Kg ha<sup>-1</sup> seed cotton yield. Strain GH-U had yielded a maximum of 4070 Kg ha<sup>-1</sup> in the Khuzdar environment. Sahiwal was ranked the top environment with a yield of 3161 Kg ha<sup>-1</sup> followed by Khuzdar (2845 Kg ha<sup>-1</sup>) respectively. The genotype selection index (GSI: A non-parametric approach to determine performance stability) distinguished NIAB-135, BH-224 and FH-Am17 being the most stable strains bearing the least GSI value and may be released for general cultivation to boost national cotton production.

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**Keywords** | Genotype selection index, Mega environments, Pakistan, Performance stability, Upland cotton strains



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## Introduction

Upland cotton (*Gossypium hirsutum*. L) is mainly cultivated for its spinnable fibre worldwide. It is

truly considered a cash crop and the backbone of the country's economy. It accounts for 0.8% accumulation in GDP and 4.2 per cent value addition in the agriculture sector (GoP, 2020). Pakistan is numbered as

the fifth-best cotton producing and consuming state (Nisar *et al.*, 2022). Due to the increasing demand in the textile sector, it became essential to develop the best yielding cotton cultivars bearing quality lint parameters. Breeding of genotypes possessing genetically improved qualitative and polygenic traits is needed to cope with different types of stresses (Bakhtavar *et al.*, 2015).

In routine, conduction of yield trials constituted with newly bred strains along with check at multi-locations is a general practice in the world. The success of crop breeding schemes depends upon the possibility of releasing cultivars bearing definite superior yields across a set of erratic environmental situations (Hasani *et al.*, 2018). Optimum sowing time is a crucial factor for the best yield in a specific environment. Ishaq *et al.* (2022) found mid of the March as the best sowing time for upland cotton in the central zone of the Punjab province. Several statistic tools have been used to isolate stable strains against test locations in cotton crop (Phuke *et al.*, 2017). The additive main effects and multiplicative interaction (AMMI) model is an elegant tool to explore the genotype into environments interaction (GEI) segment of variability in multi-location yield experiments (Verma and Singh, 2020). This model is a hybrid of interaction and additive variability segments. This procedure effectively measures additive effects and multiplicative effects at the same time. The principal component analysis (PCA) module is applied to understand signal information present in the GEI segment (Bocianowski *et al.*, 2019). This analysis is highly effective and catches a major part of the variation present in GEI and splitting additive main effects due to genotypes and environments (Ajay *et al.*, 2019). Stable varieties deviate less from the average yield across test locations. In AMMI analysis results will become biased if the first axis of the interaction principal component is squeezed with less portion of interaction variance (Oyekunle *et al.*, 2017). Researchers can change their priority depending upon the aim of the multi-location experiment for a high yield of a variety instead of increased stability in performance (Verma and Singh, 2021).

Yield stability studies in upland cotton strains using AMMI analysis tested at 14 locations including newly emerging cotton pockets of Balochistan and Khyber Pakhtunkhwa provinces are missing in the literature. Further, strains tested in this study are newly bred

bearing diversified genetic bases never tested earlier. It was postulated that cotton strains with stable yield performance can boost national cotton production. The main purpose of this study was to identify the environment most suitable for the highest cotton yield. Further to quantify stability in yield performance of cotton strains tested over erratic environments and to get approval from concerned authorities for their release.

## Materials and Methods

The present experiment was executed at fourteen prominent locations across Pakistan in the National coordinated varietal trial (NCVT) during Kharif (summer season) 2019. The trial was sown at all locations in the first week of May. An experiment was comprised of twenty-five cotton strains (Table 4) bred by different research stations including one check variety CIM-602. The layout of the experiment was a randomized complete block design (RCBD) repeated thrice. The experimental unit was comprised of 5 m long four rows 0.75 m apart from each other. A distance of 0.3 m was maintained between plants after thinning. Irrigation was applied according to the needs of the plant and weather conditions. 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. At crop maturity, data of seed cotton yield was collected from all sites repeat wise and converted into kg ha<sup>-1</sup>.

### Data Analysis

Repeat wise data of seed cotton yield in kg ha<sup>-1</sup> collected from all sites was analyzed with the analysis of variance (ANOVA) tool (Steel *et al.*, 1997). To measure the segment of GEI for seed cotton yield, data were analyzed to the AMMI procedure described by Gauch (2013). This procedure applies ANOVA to split variability into additive main effects due to genotype, environment and GEI portion. Variability captured by the GEI portion is further analyzed by employing the PCA technique. F-test is used to test the significance of the interaction principal component axis (IPCA) at a given degree of freedom. AMMIS-OFT version 1.0 available at (<https://scs.cals.cornell.edu/people/hugh-gauch>) was used for data analysis in the present study. The AMMI equation is as below.

**Table 1:** Description of 14 test sites along with 25 studied cotton strain.

14-Environments					
S.N	Code	Description	Soil Type	Climate	
1	EN01	Central Cotton Research Institute, Multan	Loam type	Semi-Arid	
2	EN02	4B farm Multan	Loam type	Semi-Arid	
3	EN03	Cotton Research Station, Bahawalpur	Sandy loam	Arid	
4	EN04	Cotton Research Station, Sahiwal	Loam type	Semi-Arid	
5	EN05	Cotton Research Station, Khanpur (Rahim Yar Khan)	Clay loam	Arid	
6	EN06	Cotton Research Station, Vehari	Sandy loam	Semi-Arid	
7	EN07	Central Cotton Research Institute, Sakrand	-	Arid	
8	EN08	Cotton Research Station, Ghotki	Loamy	Arid	
9	EN09	Cotton Research Station, Mir Pur Khas	-	Arid	
10	EN10	Nuclear Institute for Agriculture, Tando Jam	-	Arid	
11	EN11	Cotton Research Station, Lasbella	Loamy	-	
12	EN12	Cotton Research Station, Sibbi		-	
13	EN13	Agriculture Research Institute, Khuzdar		-	
14	EN14	Cotton Research Station, Dera Ismail khan	Clay	Temperate	
25-Strains along with a standard variety					
S.N	Code	Description	S.N	Code	Description
1	GN01	NIAB-512	15	GN15	RH-670
2	GN02	NIAB-973	16	GN16	Himalaya
3	GN03	NIAB-819	17	GN17	GH-sultan
4	GN04	NIAB-135	18	GN18	GH-Uhad
5	GN05	NIAB-1011	19	GN19	FH-Anmol
6	GN06	NIA-89	20	GN20	FH-492
7	GN07	IUB-73	21	GN21	FH-155
8	GN08	VH-383	22	GN22	FH-Super 2017
9	GN09	VH-189	23	GN23	FH-Am 17
10	Std	CIM-602 (check)	24	GN24	BH-224
11	GN11	VH-402	25	GN25	BH-223
12	GN12	SLH-33			
13	GN13	RH-Kashish			
14	GN14	RH-Afnan-2			

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

Where;

$Y_{ge}$ : Yield of genotype g (Kg per ha.) in environment e  
 $\mu$ : Grand mean  
 $\alpha_g$ : Mean Deviation for particular genotype g  
 $\beta_e$ : Mean Deviation from environment means  
 $\lambda_n$ : Singular Value for IPC (Interaction Principal Component) Axis n  
 $\gamma_{gn}$ : represents to Genotype g eigenvector value to IPC axis n  
 $\delta_{en}$ : the value of eigenvector of environment for IPC axis n  
 $\rho_{ge}$ : denotes to residual.  
 Further, AMMI stability value (ASV) was derived to rank cotton strains according to stability parameter by employing the formula given by Purchase (1997) as under:

$$ASV = \sqrt{[(SS \text{ of IPCA} - 1 / SS \text{ of IPCA} - 2) (IPCA - 1 \text{ score})]^2 + [IPCA - 2 \text{ score}]^2}$$

Where;

SS: Sum of Squares. IPCA-1: Interaction Principal Component Axis 1, IPCA-2: Interaction Principal Component Axis 2. As per protocol, lower (ASV) indicates stable genotypes and vice versa.

The genotype selection index (GSI) given by (Farshadfar *et al.*, 2008) was calculated by the following formula.  $YSI = RASV + RY$  where RASV: Rank of AMMI Stability Value; RY: Rank of the mean yield across environments.

**Table 2:** Analysis of variance for seed cotton yield in 25 strains across 14 locations during 2019–20.

SOV	DF	SS	MSS	The proportion of variance %		
				TV	A&I V	GEI
Treatments	349	557257931	1596728 <sup>A</sup>	98.3		
Strains	24	60161677	2506737 <sup>A</sup>		10.6	
Environments	13	380925564	29301966 <sup>A</sup>		67.2	
S x E	312	116170690 (Total) 112060101 (Signal) 4110588 (Noise)	372342 <sup>A</sup>		20.5	
IPCA-1	36	43981556	1221710 <sup>A</sup>			37.9
IPCA-2	34	25784853	758378 <sup>A</sup>			22.2
IPCA-3	32	11965735	373929 <sup>A</sup>			10.3
IPCA-4	30	9103409	303447 <sup>A</sup>			7.8
IPCA-5	28	5795883	206996 <sup>A</sup>			5.0
IPCA-6	26	5248821	201878 <sup>A</sup>			4.5
IPCA-7	24	4076585	169858 <sup>A</sup>			3.5
IPCA-Residual	102	10213848	100136			8.8
Error	700	9647297	13782	1.7		
Blocks x Env.	28	793723	28347 <sup>B</sup>		0.1	
Pure Error	672	8853575	13175		1.6	
Total	1049	566905228	540424	100	100	100

<sup>A</sup> Significant at ( $p \leq 0.01$ ) <sup>B</sup> Significant at ( $p \leq 0.05$ )

**Note:** F-test uses pure error because blocks x environments are significant at ( $p \leq 0.05$ )

**SOV:** Source of variance **DF:** Degree of freedom **SS:** Sum of squares **MSS:** Mean sum of squares **TV:** Total variance **A&IV:** Additive and Interaction variance **GEI:** Genotype x Environment interaction **IPCA:** Interaction Principal Component Axis.

## Results and Discussion

ANOVA results related to 25 cotton strains tested at 14 locations in the country for seed cotton yield are presented in Table 2. The main effects due to strains, environments and GEI were found significant ( $p \leq 0.01$ ). This significant GEI segment of variation provided sufficient grounds for AMMI analysis. Environmental main effects were found biggest portion (67.2%) of total variability followed by the GEI segment, which was (20.5%) of total variation present in the studied cotton strains. The main effects of strains were found (10.6%), which is approximately half than GEI effects. These findings are in line with the results given by Riaz *et al.* (2013), this researcher also found a similar proportion of variability in cotton. The occurrence of significant GEI effects is challenging for breeders in breeding superior cultivars. A successful variety must perform well throughout the areas for which, released for cultivation. The high GEI variation component creates complexity in the assessment of genotype inbuilt genetic potential. It was established fact that yield was deviated by environment main effects and GEI segment (Ntawuruhunga *et al.*,

2001). GEI portion was further analyzed and found that it was composed of more than 96% of signal information. Seven interaction principal components axis (IPCA) were found significant at ( $p \leq 0.01$ ). The first two IPCA captured more than (60%) of the GEI portion of variability. The residual portion of IPCA was (8.8%) of GEI. These results are confirmatory to the findings of Krishnamurthy *et al.* (2021). All seven calculated IPCA captured 91.2% of variability present in the GEI portion.

### AMMI Model diagnosis and winner genotypes

AMMI consists of model family members such as AMMI-0, AMMI-1, and AMMI-2 so on possessing 0, 1 and 2 IPCA respectively. Predictive based accuracy, biometrical significance and results interpretability are the top criteria basis for model identification. AMMI-0 represents a simple linear model without any interaction segment of variability. GEI portion left behind capturing by last IPCA was treated as residual. Early IPCA usually picks the signal information portion (a portion of data from which we can draw some conclusion) while the last few IPCA and residual capture mostly noise. In the present study



(96.5%) GEI was measured as a signal portion and leftover 3.5% as noise. AMMI-F denoted a full model consisting of all GEI segments and no residual portion. AMMI-F was considered near to raw data and lacks any practical utilization.

As argued by [Gauch \(2013\)](#), in a well-known published article relevant to AMMI analysis, the model diagnosis was not executed. Instead, AMMI-1 was chosen as the default model because appropriate bi-dimensional graphs are possible to plot in such models. For simplicity during mega environment delineation AMMI-1 model was also selected by [Agahi et al. \(2020\)](#). A however simpler model like AMMI-1 would be more suitable due to practical simplicity that involves a few mega-environments, which is justified when the most emphasis was put on the usage of wider adaptation. Genotype NIAB-1011 was found winner of the yield trial and won all AMMI model family ([Table 3](#)). According to the AMMI-1 default model, NIAB-1011 won a maximum of seven environments followed by GH-U and NIAB-135 with the winner of three environments each. VH-189 also won one environment in the AMMI-1 model.

**Table 3:** *Winners of AMMI model family across 14 locations during 2019–20.*

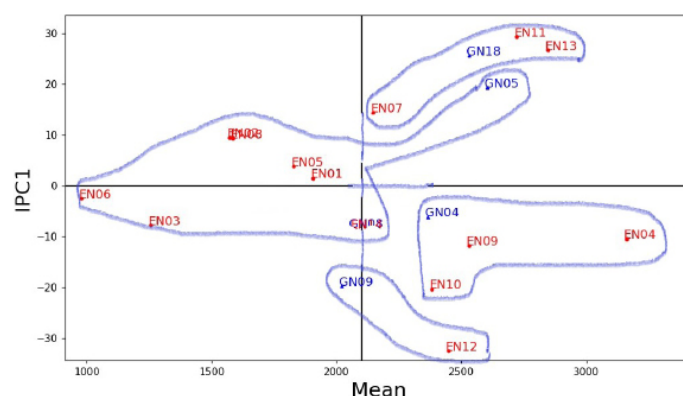
Strains	AMMI model family									
	0	1	2	3	4	5	6	7	F	
GH-Uhad		3	2	3	3	2	3	3	3	
NIAB-1011	14	7	8	5	5	6	5	5	3	
GH-Himaliya						1	1	1	2	
FH-Super 2017							1	1	1	
GH-Sultan					1				1	
RH-670				1	1	1	1	1	1	
NIAB-135		3	2	1	2	2	2	1	1	
NIA-89			1	2	1			1	1	
VH-189		1	1	2	2	1	1	1	1	
Mega environments	1	4	5	6	6	7	7	8	9	

**AMMI:** *Additive Main effects and Multiplicative Interaction.*

### Delineation of mega environments

A ranking of the five best yielding cotton strains through 14 testing environments in AMMI-1 and AMMI-F model results are presented in [Table 4](#). Test environments are arranged in the table according to IPCA-1 scores so that upper and bottom-placed sites bear opposite GEI interaction behavior. Test sites and genotypes are enlisted in [Table 1](#) along with codes used in biplots. In the AMMI-1 model 14 environ-

ments were delineated into 4 mega environments (ME). A mega environment is a combination of test sites with statistically non-significant effects on yield. ME-1 was the largest and won by GN05 (NIAB-1011) consisting of 7 environments DI Khan, Ghotki and all Punjab locations except Sahiwal. ME-2 won by strain GN18 (GH-Uhad) across locations of Sakrand, Lasbella and Khuzdar ([Figure 1](#)). ME-3 consists of three sites Viz: Sahiwal, Mir Pur Khas & Tando Jam in Sindh province and won by GN04 coded for strain NIAB-135. ME-4 was the smallest and won by GN09 (VH-189) against a single site of Sibbi, Balochistan. Signal information in the AMMI-F model is complicated, complex and difficult to interpret. The ratio mentioned in ([Table 4](#)) is obtained as a ratio of winner genotype in a particular environment divided by the yield of the overall winner, which is GN05 (NIAB-1011) in the present case ([Gauch, 2008](#)). So the strain GN18 (GH-Uhad) bears a yield advantage of 29.4% across site EN11 (Lasbella) and EN13 (Khuzdar) 24.5% in enhanced yield than the overall winner genotype. This edge was due to minor adaptations acquired by respective strains at specific sites due to GEI interaction. Similarly, GN04 (NIAB-135) possessed a yield advantage of (8.4–11.3%) across sites Sahiwal, Mir Pur Khas & Tando Jam respectively ([Table 4](#)).



**Figure 1:** *AMMI biplot indicating a mean yield of cotton strains (Kg per ha) in abscissa and IPCA-1 scores on the ordinate axis. Four mega environments are encircled along with winner genotypes.*

### Identification of stable cum yielder cotton strains

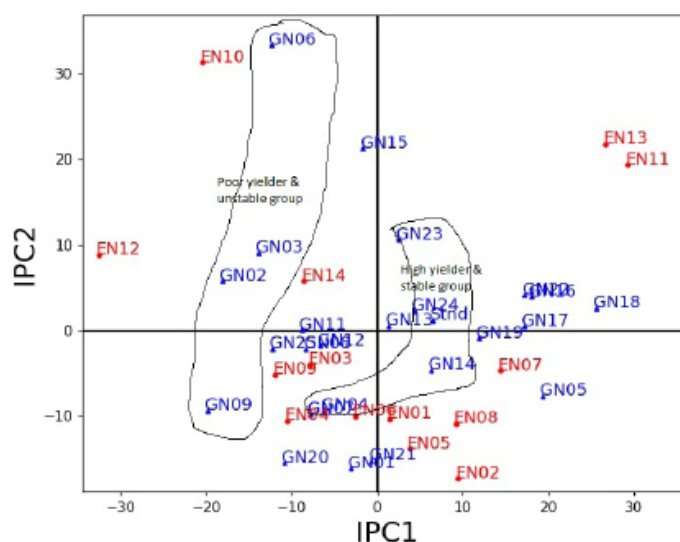
A lot of cotton varieties were released in the country in the past but most of them were not survived in the field except NIAB-78 and MNH-93 after 5 years of their release due to unstable yield across changing environments. [Riaz et al. \(2013\)](#) also found uneven behavior of cotton genotypes for stability regarding the seed cotton yield. Breeding for adaptable varieties

**Table 4:** Ranking of top 5 cotton strains according to AMMI-1 and AMMI-F model families for 25 cotton strains in 4 mega environments.

Mega Env.	Env. code	Ratio	AMMI-1 ranks					AMMI-F ranks				
			1	2	3	4	5	1	2	3	4	5
ME-2	EN11	1.0294	GN18	GN05	GN16	GN17	GN22	GN18	GN05	GN16	GN17	GN22
	EN13	1.0245	GN18	GN05	GN16	GN17	GN22	GN18	GN05	GN16	GN22	GN17
	EN07	1.0059	GN18	GN05	GN16	GN17	GN22	GN05	GN16	GN22	GN18	GN17
ME-1	EN02	1	GN05	GN18	GN16	GN17	GN22	GN05	GN18	GN04	GN17	GN19
	EN08	1	GN05	GN18	GN16	GN17	GN22	GN17	GN05	GN21	GN18	GN22
	EN05	1	GN05	GN18	GN16	GN17	GN22	GN05	GN04	GN25	GN18	GN01
	EN01	1	GN05	GN18	GN16	GN17	GN04	GN18	GN04	GN16	GN05	GN17
	EN06	1	GN05	GN18	GN16	GN04	GN17	GN16	GN04	GN01	GN18	GN22
	EN03	1	GN05	GN04	GN18	GN16	GN17	GN22	GN13	GN11	GN04	GN01
	EN14	1	GN05	GN04	GN18	GN16	GN17	GN16	GN17	GN18	GN11	GN09
ME-3	EN04	1.0084	GN04	GN05	GN18	GN16	GN09	GN09	GN01	GN08	GN15	GN18
	EN09	1.0226	GN04	GN05	GN09	GN25	GN18	GN04	GN21	GN05	GN25	GN17
	EN10	1.1130	GN04	GN09	GN25	GN01	GN15	GN15	GN06	GN03	GN04	GN16
ME-4	EN12	1.2969	GN09	GN04	GN25	GN02	GN03	GN06	GN08	GN04	GN25	GN02

**AMMI:** Additive Main effects and Multiplicative Interaction.

across a wide range of target locations is the real challenge to the breeders (Bose *et al.*, 2014). AMMI stability value (ASV) was calculated for cotton strains studied based on IPCA-1 and IPCA-2 scores (Table 5). Bigger the absolute value of ASV, the better the adaptability of a particular genotype for a certain location. On the contrary, smaller ASV values highlight genotype general stability across tested environments. Stability itself is not a reliable selection indicator as stable cultivars were mostly found to be poor yielders (Mohammadi *et al.*, 2017), so the use of yield plus stability as a single non-parametric index is generally required (Farshadfar *et al.*, 2008). Genotype selection index (GSI) was obtained by adding ranks of ASV and yield of the respective strain at that particular site. This index depicted GN04 (NIAB-135) and GN24 (BH-224) followed by GN23 (FH-Am 17) and GN14 (RH-Afnan-2) as stable strains bearing minimum GSI values respectively. (Table 5). GN04 (NIAB-135) bears little edge of high yield, while GN24 (BH-224) was more stable than the former strain. On the other hand, GN06 (NIA-89) followed by GN02 (NIAB-973) were proved as poor yielders and unstable in performance across test sites respectively. AMMI-2 biplot indicated strains plotted near origin represent stable types while strains on the periphery were unstable entries in this trial (Figure 2). Similarly, stable and high yielder group was encircled separately from poor yielder and unstable cotton strains.



**Figure 2:** AMMI-2 biplot indicating IPCA-1 (Interaction Principal Component Axis-1) scores in abscissa and IPCA-2 scores on the ordinate axis. Two groups (high yielder & stable) and (Poor yielder & unstable) are encircled separately.

## Conclusions and Recommendations

The present experiment highlighted that cotton strains behaved differently to test environments. Strain NIAB-1011 was found optimum yielder and suitable for DI Khan, Ghotki and all Punjab locations except the Sahiwal site. GH-U was suitable for the new emerging sites of Balochistan and bears a 24-30% yield advantage due to minor adaptations. Three

**Table 5:** Ranking of 25 strains of cotton for mean yield ( $Kgha^{-1}$ ), AMMI stability value (ASV) & genotype selection index.

Strains	Code	Mean yield	Rank	IPCA-1 score	IPCA-2 score	ASV	Rank	GSI
NIAB-512	GN01	2184	8	-3.059	-16.211	17.0	12	20
NIAB-973	GN02	1856	22	-18.080	5.767	31.4	21	43
NIAB-819	GN03	1898	20	-13.822	8.892	25.2	17	37
NIAB-135	GN04	2365	5	-6.183	-9.412	14.1	7	12
NIAB-1011	GN05	2604	1	19.293	-7.915	33.8	22	23
NIA-89	GN06	1882	21	-12.379	33.240	39.4	24	45
IUB-73	GN07	1672	25	-7.814	-9.848	16.6	11	36
VH-383	GN08	2062	15	-8.312	-2.292	14.4	8	23
VH-189	GN09	2022	16	-19.796	-9.531	35.1	23	39
CIM-602(check)	Stnd	1954	18	6.491	1.163	11.1	3	21
VH-402	GN11	1843	23	-8.781	0.050	15.0	9	32
SLH-33	GN12	1920	19	-6.668	-1.830	11.5	5	24
RH-Kashish	GN13	1691	24	1.324	0.273	2.3	1	25
RH-Afnan-2	GN14	2084	13	6.331	-4.898	11.9	6	19
RH-670	GN15	2201	7	-1.634	21.173	21.4	15	22
GH-Himalaya	GN16	2434	3	18.022	3.890	31.0	20	23
GH-sultan	GN17	2408	4	17.216	0.381	29.4	18	22
GH-Uhad	GN18	2531	2	25.602	2.428	43.7	25	27
FH-Anmol	GN19	2071	14	11.937	-1.020	20.4	13	27
FH-492	GN20	1995	17	-10.835	-15.564	24.2	16	33
FH-155	GN21	2108	11	-0.657	-15.227	15.3	10	21
FH-Super 2017	GN22	2327	6	17.226	4.096	29.7	19	25
FH-Am 17	GN23	2174	9	2.481	10.508	11.3	4	13
BH-224	GN24	2164	10	4.311	2.104	7.6	2	12
BH-223	GN25	2098	12	-12.216	2.207	21.0	14	26

cotton strains NIAB-135, BH-224 and FH-Am 17 were found to yield cum stable types. Their release from respective seed councils for general cultivation may be perused to boost cotton production in the country.

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## Novelty Statement

Genotype into environment interaction (GEI) study in cotton by AMMI method at 14 diversified locations including new emerging cotton sites of Khyber Pakhtunkhwa and Balochistan is rarely explored in Pakistan.

## Author's Contribution

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

**Ghulam Sarwar:** Critically read the manuscript and added input.

**Imran Akhtar:** Prepared figures and tables.

**Ghayour Ahmad:** Analyzed the data with software.

**Saeed Ahmad:** Reviewed recent literature.

## Conflict of interest

The authors had declared no conflict of interests regarding this article.

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