



## Research Article

# Yield Performance of Cotton Genotypes Across Diverse Environments in Punjab, Pakistan

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**Abstract** | An ideal genotype must possess yield constancy under erratic environments to become a popular cultivar. The genotypes contributing least towards genotype by environment interaction (GEI) are considered stable ones. The present experiment was carried out at five locations *viz.*, Multan, Faisalabad, Khanpur, Vehari and Sahiwal in the Punjab province in Pakistan for two years 2020-21 and 2021-22. Ten promising upland cotton genotypes recently bred by different research stations were sown by following a randomized complete block design (RCBD) with three replications. The main objective was to pinpoint cotton genotypes with stable yield performance across the studied environments. Additive main effects and multiplicative interaction (AMMI) analysis results depicted that maximum variability was due to environments (63.9%) followed by GEI (24.1%). The first two interaction principal components (IPCs) were squeezed with 75% of variability due to GEI. The genotype GN01 (SLH-Chandi) produced the maximum seed cotton yield (2181 kg ha<sup>-1</sup>) and was the winner in this trial. The site EN03 (Faisalabad during 2020-21) produced the highest seed cotton yield (2541 kg ha<sup>-1</sup>) with a (-6.82) IPC1 score. Genotype selection index (GSI: A non-parametric approach to determine yield stability) discriminated the genotype UAM-20 (GN08) as yielder cum stable one with the least GSI value of (6) followed by VH-418 (GN03), BH-225 (GN07) and Weal-Ag-11 (GN10) with same GSI value of (8). Approval of these genotypes for general cultivation from an authorized forum may be obtained to boost cotton production in the province.

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**Keywords** | Erratic environments, Genotype selection index, Punjab province, Upland cotton, Yield performance



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## Introduction

Upland cotton (*Gossypium hirsutum* L.) is a real cash crop in Pakistan and is called white gold

in the true sense. It provides lint to the textile sector, the main national export source. Approximately two per cent of our grand domestic product (GDP) is dependent on cotton (Sial *et al.*, 2014). Its economic

impact is approximately six hundred billion U.S dollars worldwide (Ashraf *et al.*, 2018). Cotton seed is also a valuable source of edible oil for the rapidly growing population. The cotton-growing belt consisting of central and south Punjab remained a major production hub in the past, but production is declining each year drastically. The main reason behind this decline is changing climate and uneven performance of cotton cultivars across agro-environments.

Evaluation of elite genotypes under diversified agro-environmental conditions is a prerequisite for assessing yield stability (Farshadfar *et al.*, 2012). Generally, GEI impact is greater on yield, as it is a quantitative character with a low heritability value. Thus, seed cotton yield is dependent on genotypes, environments and GEI. Yield plus stability must be explored together in experiments to exploit the positive effects of GEI for the refined selection of genotypes (El-Hashash *et al.*, 2019). If the GEI is significant, then the selection of genotypes merely on a yield basis is ineffective and misleading (Sharifi *et al.*, 2017).

Different biometrical tools are used by researchers to explore GEI. Additive main effects and multiplicative interaction (AMMI) are prominent among them. The genotype selection index (GSI) was found to be efficient in selection as it combines both mean yield and AMMI stability value (ASV) to single non-parametric criteria, which generates sufficient

information for the selection of stable plant material (Giridhar *et al.*, 2016). It was assumed that stable yielder cotton genotypes can boost production in the province.

The main purpose of this experiment was to quantify the GEI segment of variation. Further, to choose the best environment, and to identify the high-yielding and stable cotton genotypes.

## Materials and Methods

The present experiment was sown at five locations *viz.*, Multan, Faisalabad, Khanpur, Vehari and Sahiwal in the Punjab province in Pakistan for two years 2020-21 and 2021-22. Ten promising upland cotton genotypes recently bred by different research stations were studied (Table 1). Sowing was completed in the first week of May by adopting the protocol of randomized complete block design (RCBD) with three replications. Each plot was comprised of 7.8 m long 4 rows 0.75m apart. Manual thinning maintained a distance of 0.3 m between plants in the rows. The first irrigation was applied within a day after sowing. The remaining irrigations were applied at the interval of 7-21 days till the crop maturity depending upon weather conditions. Fertilizer was applied according to the soil analysis for optimum nutrient supply. Insect pest populations were kept below the economic threshold level (ETL) by spraying recommended agrochemicals.

**Table 1:** Detail of ten cotton genotypes and environments under study.

Code	Genotype	Breeding station	Code	Genotype	Breeding Station
GN01	SLH-Chandni	Cotton Research Station Sahiwal	GN06	SLH-55	Cotton Research Station Sahiwal
GN02	FH-494	Cotton Research Station Faisalabad	GN07	BH-225	Cotton Research Station Bahawalpur
GN03	VH-418	Cotton Research Station Vehari	GN08	UAM-20	MNS University Multan
GN04	FH-414	Cotton Research Station Faisalabad	GN09	FH-498	Cotton Research Station Faisalabad
GN05	RH-King-20	Cotton Research Station Khanpur	GN10	Weal-AG-11	Weal-Ag Seed Corporation Multan
Code	Location year latitude longitude altitude climate soil type average (m) Rainfall (mm)				
EN01	Cotton Research Institute Multan. 2020-21 30° 11' 52" N 71° 28' 11" E 125 Arid Loamy 127				
EN02	2021-22				
EN03	Cotton Research Station Faisalabad. 2020-21 31° 21' 52" N 72° 59' 40" E 184 Semi-Arid - 300				
EN04	2021-22				
EN05	Cotton Research Station Khanpur. 2020-21 28° 25' 12" N 70° 18' 0" E 200 Arid Loamy 104				
EN06	2021-22				
EN07	Cotton Research Station Vehari. 2020-21 29° 23' 44" N 71° 41' 1" E 135 Semi-Arid Loamy 135				
EN08	2021-22				
EN09	Cotton Research Station Sahiwal. 2020-21 30° 39' 52" N 73° 06' 30" E 172 Semi-Arid - 285				
EN10	2021-22				

Other recommended crop husbandry operations were carried out throughout the cropping season in a uniform way to minimize the experimental error. At the end of October, when maximum bolls were opened, picking was done by employing female labour. After cleaning trash seed cotton picked from each plot was weighed with electronic balance and plot yield was converted to kg ha<sup>-1</sup> for comparison and analysis.

*Data analysis*

Yield data from each plot were put for the Analysis of Variance (ANOVA) technique (Steel *et al.*, 1997). This technique can capture main effects due to genotypes and environment but do nothing with multiplicative effects if present. These effects can further be analyzed by using the principal component analysis (PCA) method. In the present study, data were analyzed by additive main effects and multiplicative interaction (AMMI) method as proposed by Gauch (2013). This technique is a novel combination of ANOVA and PCA, developed to handle bottlenecks of both of these as above mentioned. Captured amount of GEI was split into various interaction principal components (IPC) as per the protocol of PCA. A very minute portion of GEI was leftover and treated as residual. AMMISOFT version 1.0 available at (<https://scs.cals.cornell.edu/people/hugh-gauch>) was used for the analysis of data.

AMMI stability value (ASV) was calculated according to the method given by Purchase (1997). Similarly, the genotype selection index (GSI) values were obtained according to Farshadfar (2008). This approach combines both mean yield and ASV to select genotypes in multi-site varietal trials.

**Results and Discussion**

The AMMI analysis depicted that significant ( $p \leq 0.01$ ) differences were present among genotypes, environments and GEI for seed cotton yield (Table 2). This indicated the presence of generous variation among cotton genotypes and test sites. The studied genotypes also illustrated uneven performance concerning seed cotton yield across test sites. Earlier researchers (Workie *et al.*, 2013; Yayas *et al.*, 2014) also reported similar results in field crops. The genotypes, environment and GEI accounted for 6.9, 63.9, and 24.1% of the total variation present in this trial respectively. This shows the largest portion of variation

due to the environments, hence the importance of multi-environmental trials (MET) before variety approval was proved. These findings align with earlier cotton crop research by Riaz *et al.* (2013). A greater sum of squares (SS) value for GEI than genotype effects showed that studied genotypes responded to test environments in an erratic pattern. Zare (2012) also reported GEI > genotype effects in a barley crop. Overall, higher treatment effects (94.9%) compared with error effects (5.1%) proved the accuracy and reliability of the MET experiments.

**Table 2:** AMMI analysis for seed cotton yield in ten cotton genotypes across five locations during 2020-21 and 2021-22.

Source	DF	SS	MS	The proportion of the SS %	
				TV	A & IV GEI
Treatments	99	124393847	1256504 <sup>a</sup>	94.9	
Genotypes	9	9082819	1009202 <sup>a</sup>	6.9	
Environments	9	83785024	9309447 <sup>a</sup>	63.9	
G x E	81	31526004	389210 <sup>a</sup>	24.1	100
IPC-1	17	14822599	871918 <sup>a</sup>		47.0
IPC-2	15	8816645	587776 <sup>a</sup>		28.0
IPC-3	13	3003365	231028 <sup>a</sup>		9.6
IPC-4	11	2148214	195292 <sup>a</sup>		6.8
IPC-5	9	1542377	171375 <sup>a</sup>		4.9
IPC-6	7	794849	113550 <sup>ns</sup>		2.5
IPC-7	5	266397	53279 <sup>ns</sup>		0.8
Residual	4	131559	32890 <sup>ns</sup>		0.4
Error	200	6644129	33221	5.1	
Blocks/ Env.	20	1015756	50788 <sup>ns</sup>	0.8	
Pure error	180	5628372	31269	4.3	
Total	299	31037975	438254	100	100

<sup>a</sup>Significant at ( $p \leq 0.01$ ) <sup>b</sup>Significant at ( $p \leq 0.05$ ) <sup>ns</sup> Non-significant. Note: F-test use error as blocks/environments is non-significant. DF= Degree of freedom; SS= Sum of squares; MS=Means sum of squares; TV= Total variance; A and IV=Additive and Interaction variance; GEI= Genotype by environment interaction.

AMMI analysis split GEI variation into 7 IPCs significant at ( $p \leq 0.01$ ) and a minute value of GEI (0.4%) was left as residual. The first two IPCs captured 75% of GEI cumulatively. The SS for the GEI is more than three times greater than the genotype's main effects, hence narrow adaptations are important for this dataset. AMMI model diagnosis is crucial for each data sets for considering biometrical and practical implications. For simplicity AMMI1 model was applied in the current study. Agahi *et al.* (2020)

also used AMMI1 as the default model in the study on spring rape. This (AMMI1) model delineated ten test environments into 3 mega environments (ME) as illustrated (Figure 1). The first ME consists of 5 test environments and is won by the genotype SLH-Chandi (GN01) with a seed cotton yield of 2181 kg ha<sup>-1</sup> (Table 3). This genotype also proved the overall winner of this trial. The second ME was won by genotype VH-418 (GN03) with (2038 kg ha<sup>-1</sup>) yield and consisted of 4 environments. The third ME consisted of only one environment EN07 and was won by the genotype GN06 (Figure 1).

An ideal environment is defined by Zubair *et al.* (2021) in which the performance of studied genotypes is recorded as optimum. The above biplot (Figure 2) revealed that EN08 (Vehari during 2021-22) is the nearest ideal site for cotton MET experiments, while ENT4 and ENT6 are located at the periphery of the biplot due to higher contents of GEI hence not suitable for such trials. Similarly, genotypes located at the centre of the biplot are stable yielders and bear the least GEI contents. The stable genotype was also linked with a lower IPC1 value in a recent study on cotton (Rehman *et al.*, 2022). Similar results were also reported by Sumathi *et al.* (2017).

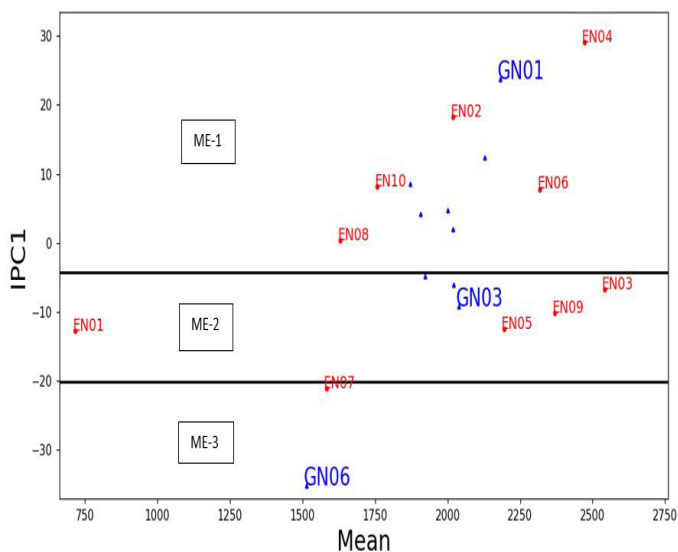


Figure 1: AMMI Biplot showing Seed cotton yield in abscissa and IPC1 scores along ordinate for both environments and genotypes.

Genotype selection index

When significant GEI was present then the selection of genotypes on a mean yield basis leads to biased results. AMMI analysis captures GEI efficiently but is unable to find stable genotypes. GSI was found reliable parameter for genotype selection in MET experiments. It is based on the ranks of mean yield and AMMI stability value. GSI values are presented in (Table 4). GN08 (UAM-20) was found most stable cum yielder genotype with the least GSI value of (6) followed by GN03 (VH-418), GN07 (BH-225) and GN10 (Veal AG-11) respectively. Contrary to this GN06 (SLH-55) was found most unstable plus poor yielders with the highest GSI value of 20.

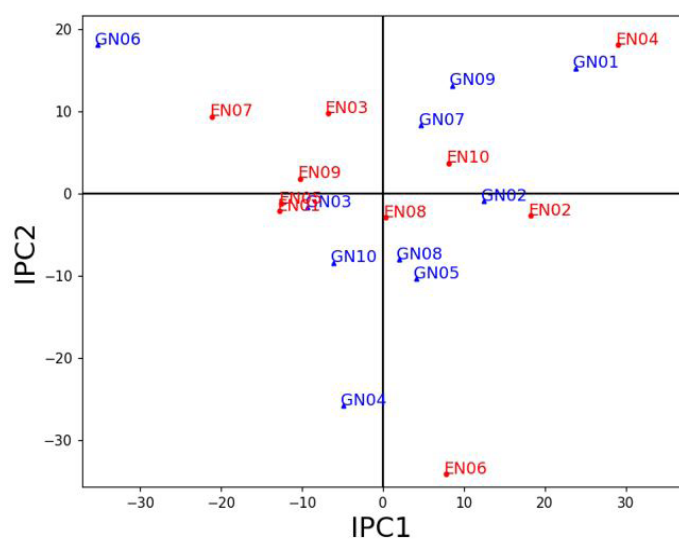
Table 3: Mean performance (kg/ha) of 10 cotton genotypes in 10 environments (5 locations in 2 years) for seed cotton yield.

Genotypes	Multan		Faisalabad		Khanpur		Vehari		Sahiwal		Mean yield Kg/ha
	2020-21 EN01	2021-22 EN02	2020-21 EN03	2021-22 EN04	2020-21 EN05	2021-22 EN06	2020-21 EN07	2021-22 EN08	2020-21 EN09	2021-22 EN10	
GN01 SLH-Chandni	506 <sup>d</sup>	2416 <sup>ab</sup>	2572 <sup>bc</sup>	3820 <sup>a</sup>	2186 <sup>b</sup>	2336 <sup>de</sup>	1722 <sup>abc</sup>	1752 <sup>ab</sup>	2178 <sup>a</sup>	2320 <sup>a</sup>	2181
GN02 FH-494	822 <sup>b</sup>	2559 <sup>a</sup>	2965 <sup>a</sup>	2835 <sup>b</sup>	2197 <sup>b</sup>	2477 <sup>cd</sup>	1130 <sup>d</sup>	2061 <sup>a</sup>	2387 <sup>a</sup>	1840 <sup>c</sup>	2127
GN03 VH-418	980 <sup>a</sup>	2057 <sup>de</sup>	2387 <sup>cde</sup>	2374 <sup>c</sup>	2868 <sup>a</sup>	2314 <sup>de</sup>	1902 <sup>ab</sup>	1704 <sup>bc</sup>	2276 <sup>a</sup>	1520 <sup>d</sup>	2038
GN04 FH-414	777 <sup>b</sup>	2033 <sup>de</sup>	2183 <sup>e</sup>	1814 <sup>e</sup>	2239 <sup>b</sup>	3104 <sup>a</sup>	1471 <sup>bcd</sup>	1651 <sup>bc</sup>	2378 <sup>a</sup>	1580 <sup>d</sup>	1923
GN05 RH-King-20	578 <sup>cd</sup>	2105 <sup>cd</sup>	2179 <sup>e</sup>	2178 <sup>cd</sup>	2008 <sup>bc</sup>	2568 <sup>bcd</sup>	1363 <sup>bcd</sup>	1600 <sup>bc</sup>	2367 <sup>a</sup>	2120 <sup>ab</sup>	1907
GN06 SLH-55	699 <sup>bc</sup>	813 <sup>g</sup>	2546 <sup>bcd</sup>	1320 <sup>f</sup>	2083 <sup>b</sup>	992 <sup>g</sup>	2027 <sup>a</sup>	1154 <sup>d</sup>	2344 <sup>a</sup>	1160 <sup>e</sup>	1514
GN07 BH-225	603 <sup>cd</sup>	2225 <sup>bcd</sup>	2329 <sup>de</sup>	2779 <sup>b</sup>	2174 <sup>b</sup>	2060 <sup>ef</sup>	1758 <sup>ab</sup>	1686 <sup>bc</sup>	2465 <sup>a</sup>	1920 <sup>bc</sup>	2000
GN08 UAM-20	1034 <sup>a</sup>	1818 <sup>f</sup>	2559 <sup>bcd</sup>	2753 <sup>b</sup>	2221 <sup>b</sup>	2804 <sup>b</sup>	1417 <sup>bcd</sup>	1614 <sup>bc</sup>	2456 <sup>a</sup>	1520 <sup>d</sup>	2020
GN09 FH-498	555 <sup>d</sup>	2272 <sup>bc</sup>	2777 <sup>ab</sup>	2703 <sup>b</sup>	1824 <sup>c</sup>	1767 <sup>f</sup>	1202 <sup>cd</sup>	1404 <sup>cd</sup>	2467 <sup>a</sup>	1740 <sup>cd</sup>	1871
GN10 Weal-AG-11	609 <sup>cd</sup>	1890 <sup>ef</sup>	2912 <sup>a</sup>	2139 <sup>d</sup>	2147 <sup>b</sup>	2763 <sup>bc</sup>	1830 <sup>ab</sup>	1674 <sup>bc</sup>	2376 <sup>a</sup>	1860 <sup>c</sup>	2020
Environment mean	716	2019	2541	2472	2195	2319	1582	1630	2369	1758	
CV%	11.1	5.8	5.4	4.9	6.3	7.5	19.9	11.9	9.7	8.2	
LSD 5%	136.6	202	236	208	236	297	539	333	392	248	

Note: Figures labelled with the same alphabets are statistically non-significant at (p≤0.05) and vice versa.

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

Genotypes	Code	Mean yield	Rank	IPC 1 score	IPC 2 score	ASV	Rank	GSI
SLH-Chandni	GN01	2181	1	23.730	15.319	42.7	9	10
FH-494	GN02	2127	2	12.399	-0.861	20.9	7	9
VH-418	GN03	2038	3	-9.293	-1.667	15.7	5	8
FH-414	GN04	1923	7	-4.861	-25.772	27.0	8	15
RH-King-20	GN05	1907	8	4.119	-10.332	12.4	3	11
SLH-55	GN06	1514	10	-35.246	18.112	62.0	10	20
BH-225	GN07	2000	6	4.720	8.345	11.5	2	8
UAM-20	GN08	2019	5	1.988	-7.985	8.7	1	6
FH-498	GN09	1871	9	8.552	13.192	19.5	6	15
Weal-AG-11	GN10	2020	4	-6.110	-8.350	13.2	4	8



**Figure 2:** Biplot showing IPC1 and IPC2 score values plotted on opposite axes.

### Conclusion and Recommendations

The cotton genotypes UAM-20, Weal-AG-11, BH-225 and VH-418 were found stable in yield performance in this study. Their release for general cultivation is needed to boost cotton production.

### Novelty Statement

The AMMI analysis in cotton based on two-year data for yield stability is rarely reported in the literature. Further, the studied cotton genotypes are newly bred and have never been tested before.

### Author’s Contribution

**Muhammad Jamil:** Conducted the trial and wrote the initial draft.

**Hira Saher and Ayesha Bibi:** Assisted in the write-up.

**Khezir Hayat and Abdul Sattar:** Reviewed recent literature.

**Umair Faheem:** Analyzed the data.

**Rana Abdul Hameed Khan:** Prepared figures and tables.

**Saeed Ahmad:** Compiled trial results.

**Rao Sohail Ahmad Khan:** Proofread the manuscript and added expert input.

### Conflict of interest

The authors have declared no conflict of interests.

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