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Stability analysis for yield-associated traits in desi cotton (*Gossypium arboreum*) genotypes

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ABSTRACT

Cotton, an essential fibrous cash crop, holds significant economic importance globally, especially in India, where it occupies a substantial area of cultivation. Among the four cultivated species, Gossypium arboreum is particularly valued for its resilience, drought tolerance, and resistance to insect pests, making it crucial for low-cost cultivation in marginal conditions. A major challenge in cotton breeding programme is the complexity of GEI, which makes identifying stable, high-yielding genotypes difficult. Therefore, this study investigates genotype-environment interactions (GEI) for yield-related traits in 30 diverse G. arboreum genotypes under two different two locations over two growing seasons. Statistical analysis indicated significant differences among genotypes for various yield-associated traits. High heritability and genetic advance as % mean were observed for seed cotton yield (84.30%, 27.94%), lint yield (82.70%, 27.40%), and bolls per plant (86.40%, 26.41%), indicating strong potential for effective selection. Stability analysis revealed trait-specific and genotype-specific adaptability. For lint yield, regression coefficient ranged from -16.28 to 21.19, with genotype HD 537 showing suitability to favorable environments, while HD 509 demonstrated adaptation to unfavorable conditions. For seed cotton yield, HD 509 exhibited above-average performance with unit regression, indicating broad adaptability, while genotypes HD 514, HD 536, and HD 544 showed high mean values and adaptation to unfavorable environments. These findings highlight the importance of selecting genotypes based on environmental adaptability to enhance yield in G. arboreum.

Keywords: Cotton, genotype-environment interaction, lint yield, textile, variability, regression, , stability, textile, variablity

Introduction

From ancient times, cotton plays an important role as a fibrous cash crop which is also known as white gold. It is grown over an area of 32.95 million hectares in 80 countries across the world. India is at the top with 1st rank by contribution of one-third in total area of the world [1].Cotton is the leading fibre crop of the world which consists of 50 species, out of which 44 are diploid (2n = 2x = 26) and possess A to G and K genomes. The remaining five species are allotetraploids with AD genome (2n = 4x = 52, AADD). There are a total four cultivated species of cotton among these; diploid species (*G. arboreum* L. and *G. herbaceum* L.) are known as old world cotton and tetraploid (*G. hirsutum* L. and *G. barbadense* L.) as new world cotton. In India, all four cultivated species of cotton are being grown commercially. In North India only *G. hirsutum* and *G. arboreum* species are grown. *G. arboreum* is mainly grown under poor crop management conditions and their yield potential is not being realized fully. This species possess special desirable attributes like hardiness, earliness, tolerance to drought and tolerance to insect pests, thereby ensuring low cost of cultivation. Its lint is mainly used for blending purposes and as surgical cotton. Encouragement to cultivation of *G. arboreum* species is more important presently

because more than 95 % area of cotton cultivation is under *Bt* cotton hybrids and farmers are not growing the refugia resulting in breakdown of bollworm resistance in *Bt* hybrids at many places in India, particularly in the states of Gujarat, Maharashtra and Andhra Pradesh *etc*. Cultivation of *G. arboreum* under such situation serves as refugia and may sustain the benefit of *Bt* cotton technology. If proper attention is given to overcoming the weaknesses of this species, it could give higher dividend. The cotton seed contains 18-20% seed oil which is edible after removal of gossypol by hydrogenation [2], and 17- 23% seed protein by weight. Its seed is the second largest source of vegetable oil in the world. After extraction of oil, the cotton seed meal is a protein rich by-product and assumes great importance in feed and fermentation industries. Therefore, cotton seed has an important contribution in helping to feed the world in the future. In addition, the fiber's quality and strength provide durability, making it a sustainable choice for textile manufacturing industries [3]. The annual worldwide cotton seed yield could supply the dietary protein needs of 240 - 350 million people but presence of gossypol is a major deterrent. Ruminant animals could tolerate the gossypol but it is toxic to non-ruminants. Wide range of agro-climatic conditions under which cotton is grown causes considerable influence on yield and quality. The productivity of cotton has not made headway, although high yielding varieties are available but their potential yields are not being harvested by the growers. Evaluation of these varieties under varying environmental conditions and identification of specific environmental conditions for a particular variety to harvest stable potential yield is necessitated.

Yield is a complex and quantitative trait that is highly sensitive to environmental fluctuation as it shows high magnitude of genotype x environment (G x E) interactions. The importance of GEI has long been acknowledged and in the absence of GEI, the best cultivar in any one trial would yield more than all cultivars at all locations every year [4]. The presence of GEI reduces the correlation between phenotype and genotype and makes it difficult to judge the actual genetic potential of a genotype [5]. In the presence of significant GEI, stability parameters are estimated to determine the superiority of individual genotypes across the range of environments. Keeping the above points, the present investigation was carried out to estimate genotype-environment interaction for yield-associated traits in *G. arboretum*.

Materials and Methods
The present investigation was conducted at the research area of cotton section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar and Cotton Research Station, Sirsa, CCS Haryana Agricultural University. The Hisar is situated at the latitude 29°N and longitude 75°46' E and falls in the semi tropical region of the western zone of India. The Sirsa is situated in the semi-arid, sub tropical region of north-western India, in the state of Haryana at 29°25' latitude, 74°40' E longitude and at an altitude of 202 meters above mean sea level.

Experimental materials
The experimental material for the present investigation comprised thirty diverse genotypes, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar Table 1.

Table 1. List of Gossypium arboreum genotypes

S.N	Genotypes	S.N	Genotypes	S.N	Genotypes
1	HD 324	11	HD 535	21	HD 545
2	HD 418	12	HD 536	22	HD 546
3	HD 432	13	HD 537	23	HD 547
4	HD 503	14	HD 538	24	HD 548
5	HD 509	15	HD 539	25	HD 549
6	HD 514	16	HD 540	26	HD 550
7	HD 521	17	HD 541	27	HD 551
8	HD 524	18	HD 542	28	HD 552
9	HD 526	19	HD 543	29	HD 553
10	HD 534	20	HD 544	30	HD 554

Experimental design
Two locations and two seasons were taken to grow the experimental material and these two locations were Hisar and Sirsa. Randomized Block Design was used to raise the crop with three replications. Genotypes were grown in two rows of three-meter length. Row-to-row spacing was kept 67.5cm while plant-to-plant was kept at 30 cm. Agronomical package of practices which are in recommendation were adopted for growing the crop.

Observations
The data was recorded on five randomly selected plants from each replication. Statistical analysis was done using mean data. Days to first flower (DFF) was counted from the date of sowing to the appearance of the first flower on particular plant in every replication and then after it was averaged. Plant height (cm) (PH) was recorded at the time of maturity and the measurement was taken from the cotyledonary node to the apex of the main stem.The number of monopods per plant (NMP) and a number of bolls per plant (NBP) were taken up. Five well-opened bolls were picked separately from each plant, weighed and averaged to get boll weight (BW). The total number of seeds per boll (NSB) is counted manually. One hundred healthy seeds were counted from each of five randomly selected plants. The weight of these hundred seeds were taken and averaged to get seed index (SI). Produce from each plant was taken in a separate bag and weighed. The total seed cotton taken from five randomly selected plants was weighed and averaged to get seed cotton yield per plant (CYP). The proportion of lint to the seed cotton is called as ginning out turn (GOT) and is expressed in percentage.

The lint index (LI) is the weight of the lint produced by 100 seeds and in last lint yield per plant (LYP) was calculated by seed cotton yield per plant and ginning percentage.

Statistical analysis
During the analysis of data following statistical method was applied and average values for each character were taken to analyse the data. To test the significance of differences among the genotypes for each character the analysis of variance was done [6]. For assessing the significance of mean sum of square, the F values were obtained and for comparing the treatment means critical difference (CD) was calculated. Genetic variability parameters were analysed using OPSTAT software. The magnitude of GEI was assessed for each character and each genotype as per the procedure suggested by Eberhart and Russell [7]. A joint consideration of three parameters, the mean performance of the genotype over environments (location), regression coefficient (b_i) and the deviation from linear regression ($S^2 d_i$) were used to define the stability of genotypes.

Results and Discussion
In present study, the statistical analysis of data was done for various genetic variability and stability-based aspects. For all the traits the mean sum of squares has been presented in Table 2. The results revealed that significance for all the traits was shown by mean sum of squares due to genotypes. Experimental materials were appropriate for further statistical analysis which was selected for the present investigation and the materialswere genetically diverse.

Table 2. Environment-wise analysis of variance of different characters

Traits	Source of variation	df	Mean squares			
			E1	E2	E3	E4
DFF	Replication	2	14.14	10.35	3.43	22.97
	Genotypes	29	35.84*	29.71*	34.41*	31.59*
	Error	58	2.89	3.28	5.26	4.21
PH	Replication	2	277.74	517.91	526.03	1091.24
	Genotypes	29	701.84*	829.76*	1056.15*	1017.67*
	Error	58	366.87	416.34	544.00	485.43
NMP	Replication	2	1.73	1.63	3.01	6.10
	Genotypes	29	2.35*	2.23*	2.96*	2.55*
	Error	58	1.18	1.22	1.52	1.24
NBP	Replication	2	16.03	25.46	7.14	16.68
	Genotypes	29	64.30*	62.22*	53.99*	53.89*
	Error	58	11.24	13.64	7.10	8.34
BW (g)	Replication	2	0.02	0.04	0.03	0.15
	Genotypes	29	0.16*	0.17*	0.08*	0.3*
	Error	58	0.03	0.03	0.02	0.06
NSP	Replication	2	7.43	4.81	11.70	9.48
	Genotypes	29	29.36*	20.10*	25.37*	26.20*
	Error	58	7.57	5.80	5.88	6.34
GOT (%)	Replication	2	2.23	2.60	0.76	27.35
	Genotypes	29	9.86*	7.27*	9.71*	9.01*
	Error	58	1.87	1.48	2.15	1.96
SI (g)	Replication	2	0.03	0.01	0.00	0.09
	Genotypes	29	0.32*	0.40*	0.32*	0.46*
	Error	58	0.07	0.10	0.07	0.12
LI	Replication	2	0.09	0.05	0.01	0.46
	Genotypes	29	0.32*	0.23*	0.28*	0.36*
	Error	58	0.06	0.07	0.06	0.08
LYP (g)	Replication	2	29.39	26.47	4.18	33.53
	Genotypes	29	75.70*	73.01*	51.90*	93.01*
	Error	58	14.20	17.23	11.17	14.39
CYP (g)	Replication	2	116.19	232.58	8.70	52.11
	Genotypes	29	461.73*	462.89*	354.36*	543.95*
	Error	58	83.92	101.28	59.37	87.36

Significant at 5% level, E1, Hisar 2016; E2, Sirsa 2016; E3, GHisar 2017 and E4, Sirsa 2017.

Mean performance

The mean performance of different genotypes for different characters, grand mean, and range are presented in Table 3. Based on pooled data the genotype HD 534 (75.33) took the maximum duration for days to first flower depicting them to be late flowering and ultimately late in maturity while the genotype HD 541 (62.33 days) took minimum time for days to first flower this genotype showed the earliness. On the basis of mean of four environments, the genotype HD 552 (153.41cm) was the lowest in plant height while genotype HD 526 (213.08 cm) was having highest plant height. Genotype HD 553 (1.58) showed the lowest value when averaged over environment while the genotype HD 541 (4.41) showed the highest monopods per plant. On the basis of mean of four environments, HD 550 has the lowest value (21.50). and the genotype HD 544 recorded highest number of bolls per plant (36). Maximum average boll weight was shown by the genotype HD 551 (3.05g) and minimum by the genotype HD 541 (2.20g) among the four environments. Maximum number of seeds was recorded by the genotype HD 509 (21.58) and the minimum by the genotype HD 545 (15.08) over environments. Highest value of ginning out turn was recorded for the genotype HD 548 (43.36%) while the lowest value for the genotype HD 526 (36.75%). Genotype HD 547 (4.75g) revealed the highest seed index and the lowest value was observed for the genotype HD 541 (3.85g) when their average was taken over four environments. On the basis of mean of four environments for this character, genotype HD 548 (3.46g) showed the maximum value, and minimum value was shown by the genotype HD 541 (2.50g). The highest lint yield was observed for the genotype HD 544 (35.73g) and lowest for the genotype HD 541 (18.83g) when the averaged over environments. The maximum value of seed cotton yield per plant was recorded for genotype HD 544 (94.74g) and lowest for the genotype HD 541 (47.75g).

Table 3. Mean performance of 30 cotton genotypes for different yield associated traits over pooled environments

Genotypes	DFF	PH (cm)	NMP	NBP	BW (g)	NSB	GOT (%)	SI	LI	LYP (g)	CYP (g)
HD 324	69.12	186.50	3.33	23.00	2.43	18.16	38.92	4.33	2.76	21.83	56.06
HD 418	64.97	178.16	3.08	24.00	2.35	20.91	39.66	4.57	3.01	22.44	56.51
HD 432	71.25	184.16	2.41	24.58	2.49	19.75	39.51	4.28	2.81	24.34	61.52
HD 503	65.00	185.00	3.08	30.00	2.70	17.91	38.69	4.55	2.86	31.40	81.21
HD 509	64.08	181.08	2.58	28.83	2.73	21.58	40.40	4.30	2.92	31.81	78.69
HD 514	65.16	211.41	2.75	30.66	2.33	17.00	38.24	4.37	2.70	27.23	71.34
HD 521	70.46	178.91	3.83	22.91	2.54	17.83	38.93	4.51	2.87	22.73	58.41
HD 524	72.41	199.58	2.58	29.00	2.41	16.58	39.70	4.72	3.11	27.96	70.30
HD 526	70.41	213.08	2.75	29.25	2.30	20.41	36.75	4.65	2.71	24.70	67.14
HD 534	73.58	194.91	2.50	24.75	2.68	21.08	37.17	4.43	2.63	24.66	66.32
HD 535	72.20	182.58	3.25	30.50	2.88	20.83	38.98	4.65	2.97	34.32	88.24

HD 536	66.57	158.33	3.16	32.50	2.22	20.58	40.54	4.39	3.00	29.35	72.41
HD 537	70.08	197.33	3.08	33.65	2.31	19.25	38.92	4.33	2.76	30.19	77.58
HD 538	66.00	171.91	2.75	23.41	2.35	18.16	38.37	4.25	2.65	21.41	55.97
HD 539	71.83	163.75	3.50	25.66	2.47	16.16	42.20	4.37	3.20	26.71	63.29
HD 540	71.66	173.75	3.33	26.00	2.31	15.50	39.19	4.53	2.93	23.52	60.11
HD 541	63.08	189.25	4.41	21.75	2.20	19.08	39.42	3.85	2.50	18.83	47.75
HD 542	67.59	160.75	3.66	32.58	2.66	17.58	39.14	4.13	2.66	33.99	86.84
HD 543	64.41	193.75	2.33	34.00	2.28	19.58	38.59	4.40	2.76	29.92	77.53
HD 544	64.91	176.83	2.75	36.00	2.62	18.75	37.73	4.36	2.65	35.73	94.74
HD 545	67.91	164.25	2.83	25.83	2.50	15.08	41.20	4.68	3.28	26.71	64.90
HD 546	72.34	165.75	3.08	30.33	2.35	15.50	38.38	4.24	2.65	27.34	71.39
HD 547	69.41	198.58	3.00	32.16	2.41	15.58	39.75	4.75	3.14	30.85	77.51
HD 548	65.69	181.91	4.41	23.83	2.86	20.91	43.36	4.52	3.46	29.57	68.19
HD 549	70.24	190.16	2.50	32.25	2.58	15.91	40.76	4.33	2.98	33.92	83.13
HD 550	66.60	192.91	2.25	21.50	2.75	15.41	38.05	4.43	2.72	22.34	58.70
HD 551	71.66	199.58	2.00	25.41	3.05	19.50	40.80	4.05	2.81	31.67	77.52
HD 552	73.20	153.41	1.83	23.50	2.70	21.16	40.65	4.33	2.97	26.03	63.80
HD 553	71.64	203.33	1.58	22.58	2.32	16.75	39.24	4.35	2.81	20.52	52.23
HD 554	67.20	204.16	3.91	32.41	2.41	19.91	39.80	4.57	3.04	31.29	78.44
Mean	68.69	184.51	2.95	27.76	2.51	18.41	39.43	4.41	2.88	27.44	69.59

Genetic variability parameters

The results representing the genetic variability, heritability, and genetic advance as percent of mean are presented in Table 4. Moderate estimate of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for NBP (14.83% and 13.79%), NSB (12.00% and 10.40%), LYP (16.07% and 14.62%) and CYP (16.08% and 14.77%). Similarly moderate PCV and low GCV was observed for LI (10.12% and 9.06%). DFF, PH, NMP, BW andGOT exhibited low PCV and GCV of 6.2% and 5.59%, 6.00% and 4.16%, 7.41% and 5.00%, 8.40% and 7.62%, 3.38% and 2.89%, 7.24% and 6.34%, PCV and GCV respectively.The estimates of high heritability was observed in traits like NBP (86.40%), CYP (84.30%), LYP (82.70%), BW (82.10%), LI (80.20%), SI (76.70%) NSB (75.10%), GOT (73.10%) and PH (48%), and NMP (45.50%) showed moderate heritability. Recording of high estimates of genetic advance percent of mean was done for CYP (27.94%), LYP (27.40%) and NBP (26.40%) whereas, NSB (18.58%), LI (16.72%), BW (14.22%), SI (11.45%) and DFF (10.41%) were recorded moderate values. In contrast, for NMP (6.94%), PH (5.93%) and GOT (5.09%), the genetic advance percent of mean values were recorded low. High heritability coupled with high genetic advance was observed for NBP, CYP and LYP indicating that most likely additive gene effect is the main reason of heritability and selection will be effective for these characters. Similarly high heritability coupled with low genetic advance was shown for GOT indicating that non additive gene action and selection for these characters may be rewarding.

Table 4. Genetic variability components for different traits in 30 cotton genotypes

Traits	DFF	PH (cm)	NMP	NBP	BW (g)	NSB	GOT(%)	SI	LI	LYP (g)	CYP (g)
PCV (%)	6.20	6.01	7.41	14.84	8.41	12.00	3.38	7.24	10.12	16.08	16.09
GCV (%)	5.60	4.16	5.00	13.79	7.62	10.41	2.89	6.34	9.06	14.62	14.77
h^2_{bs}	81.50	48.00	45.50	86.40	82.10	75.10	73.10	76.70	80.20	82.70	84.30
GA	6.93	10.99	0.21	7.16	0.36	3.55	2.01	0.50	0.48	7.41	19.14
GAM (%)	10.41	5.93	6.95	26.41	14.23	18.58	5.09	11.45	16.72	27.40	27.94

GCV- Genotypic coefficient of variation, **PCV**- Phenotypic coefficient of variation, **h^2_{bs}**– heritability.(broad sense), **GA**- Genetic Advance, **GAM**- Genetic Advance expressed as a percentage of mean.

Stability analysis

A narrow range of phenotype producing ability of a genotype under variable environments called as stability and the genotype is said to be stable. In the absence of the environmental influences as well as GEI genotypes will be stable. Eberhart and Russell (1966) model, which is commonly used for stability analysis was used for the assessment of genotype x environmental interaction and environmental influence on genotypes for each character. Partitioning of total sum of squares due to genotype × environment interactions was done into *predictable* and *unpredictable* source of variations when the genotype × environment interaction were significant for the characters found by using the procedure given by Eberhart and Russell (1966). Pooled analysis of variance for yield contributing traits and seed cotton yield across four environments are given in Table 5. following Eberhart and Russell (1966) model. Significant differences were revealed by the results among the genotypes tested at both the 5 and 1 percent level of significance for all the characters which were studied. The environment also differed significantly in which recording of all the observations was done (both at 5 and 1% probability) to influence significant variation in all the recorded characters. Against pooled error, the mean squares due to genotypes were highly significant as well as pooled deviation for various characters under study showing presence of sufficient genetic variability among the genotypes. High significance was also observed for Environmental mean squares except days to first flower against pooled error and pooled deviation which indicated that environments chosen in the study were highly variable. Significance of E+ (G x E) interaction means square for most of the characters against pooled error and for all the characters against pooled deviation indicated presence of genotype × environment interaction. Significance was recorded for mean square due to genotype × interaction (linear) tested against pooled error for six characters *viz.* NMP, NBP, BE, SI, GOT and CYP. But high significance was recorded for all the characters when tested against pooled deviation. This indicates the presence of substantial genetic variability among the genotypes, which is essential for effective selection. Moreover, the environmental factors also contributed significantly to trait variation, underscoring the importance of environmental conditions in determining yield outcomes.

The significance of genotype × environment interactions for most traits, as tested against pooled error and deviation, further supports the role of GEI in cotton yield performance [8-13]. Prediction is possible due to the higher preponderance of linear component of genotype × environment interaction than non linear component.

Table 5. Analysis of variance for stability parameters of various traits

Source	df	DFF	PH (cm)	NMP	NBP	BW (g)	NSB	GOT (%)	SI	LI	LYP (g)	CYP (g)
Rep within Env.	8	1.72**	201.08**	0.54*	5.44**	0.020*	2.79**	0.87	0.011*	0.022*	7.80**	34.13**
Varieties	29	40.27**	1001.11**	1.84**	73.33**	0.186**	17.32**	7.86**	0.159*	0.189**	83.95***	531.70**
Env.+ (Var.* Env.)	90	1.17	112.30**	0.59*	1.59**	0.018**	5.83**	1.32**	0.116*	0.068*	4.51*	24.54**
Environments	3	0.57	1429.09**	2.99**	1.21**	0.013**	16.85**	0.03*	0.173**	0.060*	0.52**	2.04**
Var.* Env.	371	2.78**	154.1**	0.71**	5.71**	0.018**	5.45**	1.37**	0.114*	0.068*	7.6*	43.12*
Environments (Lin.)	1	1.72	4287.26**	8.98**	3.64**	0.038**	50.55**	0.09**	0.519*	0.181*	1.56**	6.12**
Var.* Env.(Lin.)	29	0.85	93.08**	0.54**	1.00**	0.034**	2.50**	1.08*	0.176**	0.091*	8.02**	41.59**
Pooled Deviation	60	1.32**	52.02**	0.48**	1.84**	0.010*	6.70**	1.46**	0.08**	0.054**	2.85**	16.60**
Pooled Error	232	1.39	101.05	0.45	3.36	0.012	2.13	0.69	0.030	0.023	4.75	27.66

No uniform stability and response pattern for various traits was exhibited by the genotypes included in this investigation. The value of environment indices for this trait ranged from -0.11 to 0.19. Table 6. reveals the stability parameters for lint yield per plant. Among the environment, the average value for LYP was 27.44. The maximum value was recorded by the genotypes HD 544 (35.73g) while the minimum value was recorded by the genotype HD 541 (18.83g).for this trait the estimates of regression coefficient (bi) ranged from -16.28 (HD 538) to 21.19 (HD 554) (Table 6). Two genotypes showed no GEI and revealed their nonsignificant bi and S^2d_i values (Table 7). Simultaneous significance was not observed by any genotype for bi and S^2d_i values. Due to the significance of bi value the existence of a linear component of GEI was noticed for twenty six genotypes. The non significant S^2d_i value was recorded for all the genotypes. A high mean value was recorded by the genotype HD 537 with above average response (bi>1) indicated its suitability to favourable environments. Above mean value along with bi < 1 was recorded by the genotype HD 509 and this indicated its specific adaptation to unfavorable environments. The range of environment indices for the seed cotton yield per plant was from -0.22 to 0.33 indicating wider variation from one environment to the other. The mean value for CYP across four environments was 69.59 g. The highest and lowest mean values were recorded by the genotypes HD 544 (94.74 g) and HD 541 (47.75 g), respectively.The estimates of regression coefficient for CYP ranged from -20.25 (HD 503) to 47.86 (HD 552) and that of deviation from regression (S^2d_i) ranged from -27.20 (HD 553) to 59.46 (HD 538). No GEI was found in four genotypes owing to their insignificant bi and S^2d_i values (Table 7). These results suggest that no genotype exhibited both significant bi and S^2di values simultaneously, a finding consistent with studies by Nanjundan *et al.* [9] and Yadav *et al.* [11]. The existence of a linear component of GEI due to significant bi value was noticed for twenty six genotypes (Table 6). Among four stable genotypes, HD 509 possessed above average mean value with regression coefficient bi=1 indicating their adaptability to different environments. The genotypes HD 514, HD 536 and HD 544 recorded high mean values with below average response (bi < 1) indicated that specific adaptation to unfavorable environments.

Table 6. Regression coefficient for all characters in 30 cotton genotypes

Genotypes	DFF	PH (cm)	NMP	NBP	BW (g)	NSB	GOT (%)	SI	LI	LYP (g)	CYP (g)
HD 324	-0.96	1.94	0.8	-2.88*	-3.47*	2.58*	9.50*	0.78*	-0.54*	3.06*	4.43*
HD 418	1.87*	0.16*	0.71	2.37*	-1.31*	1.25	-1.58	-0.43*	-0.42*	-4.42*	-3.57*
HD 432	0.11	0.54*	-0.33	-1.80*	-0.32*	1.4	-17.60*	1.72*	2.87*	-3.05*	-4.00*
HD 503	-4.36*	0.01	-0.83	1.14	-4.87*	0.53*	18.38*	5.18*	3.61*	-13.85*	-20.25*
HD 509	7.37*	1.49	2.82*	1.55	5.59*	0.35*	-8.02*	4.13*	4.48*	0.84	1.62
HD 514	-3.72*	2.08	3.64*	-0.21*	1.80*	0.7	41.66*	1.90*	0.22*	4.73*	-1.3
HD 521	1.11	1.66	0.8	0.18*	-1.37*	2.18*	17.01*	2.42*	-0.96	5.64*	3.30*
HD 524	-1.97*	2.27	1.1	7.51*	0.00*	2.66*	13.44*	6.94*	7.20*	-12.09*	-18.29*
HD 526	3.38*	1.7	1.4	3.32*	0.13*	1.99*	-34.70*	2.37*	5.12*	-10.43*	-7.63*
HD 534	-1.88*	0.09	0.61	6.62*	4.05*	0.52*	1.18	0.65*	1.46*	3.05*	6.99*
HD 535	14.87*	0.49	2.20*	-2.94*	8.52*	1.80*	-7.57*	-2.95*	-3.13*	19.51*	27.51*
HD 536	3.19*	0.61	0.45*	0.23*	-1.97*	-0.04*	-18.61*	1.82*	5.33*	-6.55*	0.55
HD 537	4.20*	1.72	-1.15	-2.29*	0.49*	1.49*	-1.76*	0.83*	2.24*	1.92	3.21*
HD 538	1.5	0.42**	2.90*	5.09*	-14.40*	0.73	28.26*	-1.23*	-0.35*	-16.28*	-16.15*
HD 539	-2.63*	0.81	-0.44*	3.92*	-0.03*	-0.67	0.56	1	0.53*	2.81*	2.74*
HD 540	1.99*	1.89	1.18	4.80*	3.07*	1.75*	-25.02*	4.57*	4.47*	-1.03	1.81*
HD 541	3.11*	0.53**	1.09	-2.35*	0.95*	0.83	-22.19*	5.22*	5.90*	6.85*	12.98*
HD 542	4.78*	0.27	-0.05*	1.28	-0.94*	0.75	-7.53*	1.90*	1.52*	-6.79*	-4.19*
HD 543	-3.47*	-0.45	0.21*	-1	1.64*	-0.48*	-9.21*	-0.34*	0.54*	4.56*	10.10*
HD 544	-0.52	1.46	0.7	0.85	-2.38*	-2.78*	16.15*	0.8	-1.42*	-4.81*	-1.92
HD 545	-1.34	1.17	-1.29	-1.80*	0.01*	2.37*	-0.45	-4.97*	-5.51*	-14.29*	-19.88*
HD 546	1.64	1.58	4.16*	2.55*	1.04	1.16	-1.71*	1.87*	2.09*	-0.34	2.75*
HD 547	2.88*	1.7	-0.15*	3.23*	-0.02*	0.6	-23.68*	6.64*	9.29*	-8.62*	-6.12*

HD 548	-3.46*	1.91	0.35*	-1.62	0.97*	2.43*	18.82*	-2.50*	-6.07*	3.38*	-1.82*
HD 549	0.69	1.69	1.27	-0.82	4.56*	2.53*	6.11*	1.06	1.90*	9.17*	6.77*
HD 550	1.87*	0.58	3.10*	3.96*	-1.59*	-0.84	24.37*	-6.16*	-6.79*	-6.31*	-10.73*
HD 551	1.59	0.91	1.24	1.19	6.36*	1.26	-24.86*	-0.30*	2.26*	2.43*	-0.11*
HD 552	-1.19	-0.06	1.68*	-2.40*	17.80*	0.89	39.58*	3.01*	1.43*	47.19*	47.86*
HD 553	1.74*	0.43	0.49*	-1.03	-0.03*	-0.04*	-5.60*	-2.55*	-4.03*	2.46*	4.98*
HD 554	-2.39*	1.49	1.35	1.35	5.71*	2.03*	5.05*	-3.49*	-3.27*	21.19*	22.69*

Table 7. Deviation from regression coefficient for all characters in 30 cotton genotypes

Genotypes	DFF	PH (cm)	NMP	NBP	BW (g)	NSB	GOT (%)	SI	LI	LYP (g)	CYP (g)
HD 324	0.78	-52.03	0.01	0.17	-0.01	5.14*	-0.30	0.00	-0.01	-1.12	-11.71
HD 418	0.70	-150.63	0.18	-2.55	0.00	-1.54	-0.41	0.01	-0.01	-4.16	-25.17
HD 432	-0.92	-150.18	-0.20	-1.25	-0.01	-1.89	-0.68	-0.02	-0.02	-1.75	-10.05
HD 503	1.50	-77.72	-0.40	-2.06	0.00	0.53	-0.30	0.14	0.04	-3.19	-15.31
HD 509	-0.81	-93.41	0.29	-2.40	-0.01	-1.99	0.08	-0.01	0.00	-4.31	-16.05
HD 514	2.03	-130.82	0.16	-0.43	-0.01	-0.46	-0.56	0.01	-0.01	-3.10	-4.22
HD 521	-0.83	-108.13	-0.27	-2.61	-0.01	2.34	2.01	0.00	0.00	-3.23	-25.60
HD 524	-1.14	-17.09	0.41	0.81	-0.01	28.68**	0.04	0.06	0.04	-4.71	-19.27
HD 526	0.42	-130.53	-0.37	-2.27	-0.01	1.20	0.48	-0.02	-0.01	-3.93	-21.62
HD 534	1.32	-120.42	0.10	-0.38	0.00	-1.78	0.96	0.09	0.09	0.49	-12.04
HD 535	-1.00	-33.91	-0.35	-1.45	0.00	7.37*	0.30	0.21	0.08	-3.68	1.32
HD 536	1.87	-143.28	1.02	-3.37	0.00	-1.67	0.74	0.14	0.06	-2.12	-4.28
HD 537	-0.31	-87.43	0.17	-1.52	0.00	32.00**	1.01	0.01	-0.01	-1.85	-10.68
HD 538	0.42	-152.55	0.11	-1.51	0.03*	4.77*	2.94	0.00	0.00	5.81	59.46
HD 539	-0.66	-106.25	-0.42	0.41	-0.01	0.74	-0.59	0.03	0.02	-1.66	-6.54
HD 540	-0.41	-25.16	0.34	-2.49	0.00	-0.12	2.90	0.03	0.12	-3.87	-24.37
HD 541	-0.53	-152.52	0.08	-2.28	0.00	-1.59	-0.07	-0.02	-0.01	-3.47	-26.71
HD 542	-0.21	-130.55	-0.01	-2.82	-0.01	1.63	1.70	0.00	-0.01	-1.79	-25.80
HD 543	-1.26	-138.89	0.21	-1.71	0.00	3.68	1.15	0.01	-0.02	-2.99	-24.20
HD 544	1.41	-115.33	-0.04	-1.47	0.00	8.91*	0.93	-0.01	-0.02	-3.28	-12.31
HD 545	-1.30	-85.41	-0.42	2.20	-0.01	10.91**	-0.63	-0.02	-0.02	-0.28	-12.33
HD 546	-1.37	9.86	-0.11	-1.04	0.00	1.42	-0.62	0.21	0.05	-2.66	-9.68
HD 547	-0.71	-64.61	0.32	-2.89	0.00	3.02	-0.61	0.02	0.02	-3.22	-20.49
HD 548	-0.23	-128.44	0.68	-3.31	0.00	4.00	-0.10	0.07	0.03	-3.93	-17.96
HD 549	0.36	-122.15	-0.41	-2.98	0.00	-1.40	0.37	0.21	0.08	-0.19	-12.29
HD 550	0.42	-147.75	0.48	-2.43	0.00	10.73**	-0.06	0.00	0.00	-3.81	-24.61
HD 551	-0.25	-124.84	-0.12	-0.91	0.00	8.11**	5.76	0.05	0.19	11.79	16.40
HD 552	-1.15	-144.91	0.07	0.49	0.04*	-0.55	-0.32	0.15	0.05	-2.79	31.73
HD 553	-1.18	-101.98	-0.33	-3.23	0.00	11.33**	3.07	0.12	0.02	-3.81	-27.20
HD 554	0.64	5.97	-0.35	-2.27	0.00	2.86	3.73	0.03	0.16	-3.00	-26.63

The stability and response levels appeared to be specific for individual characters within an individual genotype and are not common for all the characters of that genotype. A similar pattern in stability for various characters has been reported by Anandan *et al.* [8]. Identification of a better genotype was done by considering stability parameters namely mean, regression coefficient and deviation from regression. The genotype which exhibited above average mean, above unity responsiveness and high stability. The estimation of the environmental additive effect (I_j) revealed that environment 2 was the best for NMP, NBP and NSP. Environment 3 was found to be favorable for DFF, PH and NBP. Environment 4 was best for PH, NSB, LYP and CYP (Table 8). This environmental variation further emphasizes the importance of choosing the right genotypes for specific environmental conditions, as supported by earlier findings from Murthy *et al.* [10] and Verma *et al.* [13].

Table 8. Environmental indices for different characters in upland cotton in different environment expressed as deviation from the grand mean

Traits	DFF	PH (cm)	NMP	NBP	BW (g)	NSB	GOT (%)	SI	LI	LYP (g)	CYP (g)
E_1	-0.08	-9.12	-0.42	-0.13	0.01	-0.68	-0.04	0.05	0.03	-0.11	-0.22
E_2	-0.06	-0.98	0.35	0.12	-0.02	0.44	0.00	0.08	0.05	-0.06	-0.17
E_3	0.21	7.03	0.02	0.21	-0.02	-0.58	0.00	-0.05	-0.03	-0.02	0.05
E_4	-0.07	3.07	0.05	-0.21	0.03	0.83	0.04	-0.08	-0.04	0.19	0.35
Mean	68.69	184.51	2.95	27.76	2.51	18.42	39.44	4.41	2.88	27.45	69.60

Along with the variation among environment different genotypes also vary and the stability is a property of genotype. The stability and response levels appeared to be specific for individual character within genotype and common for all the characters of that genotype. This study conducted by earlier researchers Nanjundan *et al*. [9]; Murthy *et al*. [10]; Yadav *et al*. [11]; Tuteja *et al.* [12] and Verma *et al*. [13] on stability and GEI in cotton confirm the factors reported in this study. Overall this study highlights the complexity of GEI and the importance of stability analysis in *desi* cotton breeding programs. By identifying genotypes with consistent performance across diverse environments, breeders can select more resilient varieties suited to both favorable and unfavorable growing conditions.

Conclusions

This study highlights the complex nature of G × E interaction in *Gossypiumarboreum* genotypes and their impact on yield-associated traits. Significant genetic variability and stability were observed among the genotypes across diverse environments. Genotypes such as HD 544 and HD 541 exhibited remarkable yield potential and stability, making them suitable for specific and favorable environments. The findings suggest that focusing on genotype selection based on environmental adaptation can significantly enhance yield in *G. arboreum* cultivation, thus contributing to sustainable cotton production. Further research should aim at enhancing these genotypes' performance under varied agronomic practices.

Data availability

The authors confirm that the data supporting the findings of this study are available within the article and its supplementary materials.

Conflict of interest

No potential competing interest was reported by the authors.

Authors contribution

Kuldeep Jangid: Conceptualization (lead), writing- original draft. Sagar and Sanjay K Sanadya: Software, formal analysis, review, and editing. Omender Sangwan: writing original manuscript.

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