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Genetic stability analysis in cotton (*Gossypium hirsutum* L.) genotypes

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Abstract
The present study titled "Genetic Stability Analysis in Cotton (*Gossypium hirsutum* L.) Genotypes" was conducted to evaluate the stability and performance of cotton genotypes under varying environmental conditions. The research was carried out at the Agriculture Research Station, Ganganagar (Rajasthan), during the *Kharif* season of 2024, employing three distinct environments created through varying sowing dates. The primary objective was to assess genetic stability and environmental adaptability for key agronomic traits. The analysis of variance (ANOVA) revealed significant differences among genotypes across environments, indicating substantial genotype x environment interactions for most traits. Notably, some traits such as the number of sympodia per plant, number of balls per plant, ball weight, seed index, lint index, and lint yield per plant demonstrated stable behavior, signifying minimal environmental impact. Stability analysis based on the Eberhart and Russell model revealed that all 12 genotypes, comprising parents, crosses and checks exhibited non-significant deviation from regression for panicle length and panicle girth, indicating their stability and predictability for these traits. Notably, genotypes like RCH 776, RCH 773, and Ajeet 155 demonstrated high stability and adaptability under both favorable and unfavorable conditions. Furthermore, several genotypes, including RCH 776, RCH 650 and Ajeet 155, exhibited regression coefficients below unity, highlighting their appropriateness for less favorable conditions. Conversely, genotypes such as RCH 773, Ajeet 177 and Shreeram 321 displayed regression coefficients above unity indicating stable performance in favorable environments. The results of this study emphasize the importance of multi-environment trials for identifying genotypes that not only perform well under specific environmental conditions but also exhibit stable performance across diverse environments. This research contributes to the development of resilient and high-yielding cotton varieties enhancing sustainability and productivity in cotton farming systems.

Keywords: Stability Analysis, Environmental interaction, Deviation, Regression coefficient

Introduction
Cotton is one of the most important commercial crops having profound influence on economics and social affairs of the country. It is a soft, staple fibre that grows around the seeds of cotton plant (*Gossypium* sp.). It is the most important commercial crop contributing nearly 65 per cent of the total raw material needs of the textile industry in our country. The cotton genus, *Gossypium* comprises 50 species, including 45 diploids (2n=2x=26) and 5 tetraploids (2n=4x=52) distributed throughout the arid and semi-arid regions of Africa, Central and South America, the Indian subcontinent, Arabia, the Galapagos and Hawaii. The New World AD-genome species, *G. hirsutum and G. barbadense* are superior as per the lint is concerned (Kavithamani *et al.* 2011) [5]. Cotton seed contains about 15 to 20% oil, which after refining can be used in soap industries. After removing oil, cotton seed cake is obtained which is nutritious feed for livestock and also concentrated organic manure. It contains 6.4% Nitrogen, 2.9% Phosphorus and 2.2% Potassium (Pavasia *et al.* 2002) [10]. Bt cotton is a genetically modified variety of cotton that has been engineered to express a toxin derived from the bacterium *Bacillus thuringiensis* (Bt). The incorporation of this gene into cotton plants provides them with built-in protection against pest attacks, reducing the need for chemical insecticides and leading to higher yields and lower production costs (James, 2013) [4]. Cotton contributes 29.8% of the Indian agricultural gross domestic product in India, cotton is planted in about 11.91 million hectares of land and it occupies first position in production with 31.20 - Million Bales (170 Kg. of each) among all cotton producing countries in the world. Average productivity of India is 445 kg/ha which is low as compared to world average of 764 kg/ha. Rajasthan

occupies acreage of 0.76 million hectares with the production of 2.48 Million Bales. The average productivity of cotton in state (558 kg/ha) is higher than the national average (Agricultural Statistics at a Glance, 2022) [1]. Genotype x Environment (E) interaction is known to interfere with the evaluation of genotypes and reduce the progress of selection in plant breeding programme. The seed cotton yield is quantitatively inherited character and there is considerable interaction between genotypes and environment. The testing of genotypes over environments provides an opportunity to the plant breeders to study the adaptability of a genotype to a particular environment and also the stability of a genotype over different environments.

Materials and Methods

The current investigation was conducted at the Agriculture Research Farm within the Department of Genetics and Plant Breeding at SGVU, Jaipur, Rajasthan, during the *Kharif* season of 2024. The experiment employed a Randomized Block Design and featured 12 different Genotypes, each replicated three times. These genotypes were randomly distributed across 36 plots and was experimented in 3 different environments. For data collection, five competitive plants were tagged within each replication, and observations were made at various stages of crop growth. Ten different characteristics were recorded, including parameters such as days to 50 percent flowering stage, plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, Boll weight (g), Seed index (g), Lint index (%), Lint yield per plant (g), Seed cotton yield per plant (g). Mean values were computed, and the data underwent analysis of variance following the method recommended by (Panse and Sukhatme 1978) [8]. Stability analysis were estimated in accordance with the guidelines outlined by (Eberhart and Russell 1966) [3]. The regression coefficient estimates were derived using the formula proposed by (Eberhart and Russell 1978).

Results and Discussions

Analysis of variance revealed significant variations among the genotypes across all the traits. This analysis encompassed various yield-related parameters within each environment as well as collectively across all environments. The results indicated highly significant differences among genotypes for all the characters across the three environments except number of monopodia per plant in E3. The observed significant variations among genotypes particularly in morpho-physiological traits, underscore the presence of substantial genetic diversity. The perusal of the Table [1] showed pooled analysis of variance, implying that the mean sums of squares due to genotypes were found significant for all the traits. The variance due to environments was found highly significant for all the traits suggesting role of different environmental conditions on expression of the traits. The interactions between genotype x environment were found significant for days to 50% flowering (0.66), plant height (3.43), number of monopodia (0.01) and seed yield per plant (0.64) on pooled basis whereas, number of sympodia per plant (1.01), number of bolls per plant (3.73), boll weight (0.07), seed index (0.09), lint index (0.01) and lint yield per plant (0.16) these exceptions indicated that genotypes for these traits were found uninstructive with different environmental conditions. These findings align with previous research by (Sirisha *et al.* (2019) [14], and Kumbhalkar *et al.* (2021) [6].

per se performance of the genotypes

The per se performance of the genotypes Table [2] across three environments (E1, E2, E3) revealed significant variability in key traits, influenced by both genetic factors and environmental conditions.

- **Days to 50% Flowering:** RCH 776 flowered the earliest across all environments (15.578 days), making it suitable for short-duration cropping systems, while RCH 926 took the longest to flower (57.00 days), ideal for longer growing seasons.
- **Plant Height:** RCH 776 was the shortest (20.333 cm), fitting high-density planting systems, whereas Ajeet 155 was the tallest (29.444 cm), better for biomass production.
- **Number of Monopodia & Sympodia:** RCH 776 had the fewest monopodia (1.267) and sympodia (10.111), suitable for compact plant structures. Ajeet 155 and RCH 926 had higher monopodia and sympodia, making them ideal for maximizing yield.
- **Boll Weight & Lint Index:** RCH 776 had the lowest boll weight (3.944 g) and lint index (3.944), suggesting it may be better for systems with lower boll production. Ajeet 155 had the highest boll weight (4.978 g) and lint index (4.978), making it a prime candidate for high yield environments.
- **Seed Yield & Lint Yield:** RCH 776 Consistently recorded lower seed yield (38.511 g) and lint yield (15.578 g), making it suitable for systems prioritizing other traits. Ajeet 155 exhibited the highest seed yield (48.400 g) and lint yield (24.667 g), ideal for maximizing production. The variability in performance highlights the potential for selecting genotypes based on specific environmental needs. These results align with previous studies conducted by (Kavithamani *et al.* 2011, Chapepa *et al.* 2022, Tuteja *et al.* 2006 and Patil *et al.* 2007 [5, 2, 13, 9].

The present study highlights the considerable genetic variability present among the cotton genotypes for all evaluated traits. Genotypes such as Ajeet 155 consistently outperformed others in most traits, making it ideal for maximizing yield and quality. In contrast, RCH 776 with its compact growth habit and early flowering could be valuable in systems requiring shorter more resilient plants. The results demonstrate the need for multienvironment trials to identify stable genotypes that perform well under diverse agronomic conditions. These insights will assist breeders in selecting promising genotypes to enhance cotton productivity and sustainability.

Stability analysis Stability analysis plays a crucial role in identifying genotypes that perform consistently across diverse environments, thereby ensuring reliable yield and performance under varying conditions. In the present study, stability analysis was carried out using the Eberhart and Russell model (1966) [3], which is widely recognized for its robust approach to assessing genotype stability. Table [3] showed pooled analysis of variance implying that the mean sums of squares due to genotypes and the variance due to environments was found highly significant for all the traits. However, the significance of deviations from regression (S2di) determines the predictability of a genotype's behaviour in diverse environments that showed in Table [4]. The results demonstrated that most genotypes displayed non-significant deviations from regression for days to 50% flowering suggesting a stable performance for this trait. Notably, genotypes RCH 951 and Shreeram 331 exhibited bi values below unity, indicating their stability under unfavorable conditions. Conversely, genotypes RCH 776 and RCH 773 demonstrated bi values greater than unity, suggesting adaptation to favorable conditions. These findings are consistent with those reported by Sirisha *et al*. 2019 [14] in cotton genotypes. In terms of plant height, six genotypes showed non-significant deviations from regression, indicating stability for this trait. Among them, RCH 776, Ajeet 946 and Shreeram 331 demonstrated bi values greater than unity, reflecting their adaptability to favorable environments despite comparatively lower mean values than the parental average. This pattern aligns with earlier studies emphasizing genotype adaptation to specific environmental conditions. Stability analysis for the number of monopodia per plant revealed that most genotypes exhibited non-significant deviations from regression, indicating stable performance. Genotypes Ajeet 177, Shreeram 331 and Shreeram 321 with bi values below unity and higher mean values than the average demonstrated stability under unfavorable conditions. On the other hand, RCH 650, which exhibited a bi value greater than unity, indicated superior performance in favorable conditions, aligning with findings reported by Sirisha *et al*. (2019) [14]. Similarly, stability analysis for the number of sympodia per plant revealed nonsignificant S2di values for all genotypes. RCH 650, Shreeram 331 and Shreeram 321 which had bi values below unity, performed well under unfavorable conditions while RCH 951, RCH 926 and Ajeet 177 showed bi values greater than unity, indicating their suitability for favorable environments. Regarding the number of bolls per plant, stability was observed across all genotypes with non-significant S2di values. Genotypes RCH 926, RCH 650, RCH 653, Shreeram 331 and Shreeram 321 displayed bi values below unity indicating adaptability to adverse environments, while Ajeet 177 and Ajeet 155, with bi values greater than unity, exhibited superior performance in favorable conditions. These findings are consistent with reports by Kavithamani *et al*. (2011) [5] and Chapepa *et al*. (2022) [2]. For boll weight, all genotypes exhibited non-significant deviations from regression, confirming stability for this trait. RCH 926 and Ajeet 155, with bi values below unity, remained stable under adverse conditions, while RCH 951 and Ajeet 177, which had bi values exceeding unity, demonstrated adaptability to favorable environments. These results align with previous studies by Tuteja *et al*. (2006) [13], Patil *et al*. (2007) [9] and Kavithamani *et al*. (2011) [5]. Analysis of the seed index revealed that all genotypes demonstrated non-significant deviations from regression indicating stable performance. Genotypes RCH 650, Shreeram 331 and Shreeram 321, which exhibited bi values below unity, maintained stable performance under unfavorable conditions. Meanwhile, RCH 951, RCH 926 and Ajeet 177 with bi values greater than unity showed better performance in favorable environments. Stability analysis of the lint index also indicated non-significant values across all genotypes. Genotypes RCH 926, RCH 650, RCH 653, Ajeet 177 and Shreeram 321 with bi values below unity remained stable under adverse conditions, whereas Ajeet 155 and Shreeram 331 with bi values exceeding unity adapted well to favorable environments. For lint yield per plant, stability was observed as all genotypes exhibited non-significant deviations from regression. Genotypes RCH 926 and RCH 650 with bi values less than unity, remained stable under unfavorable conditions, while Ajeet 177, Ajeet 155, Shreeram 331 and Shreeram 321 with bi values greater than unity showed better adaptation to favorable environments. These observations align with the findings of Satish *et al*. (2009) [11] and Kavithamani *et al*. (2011) [5]. Additionally, most genotypes exhibited non-significant deviations from regression for seed yield per plant, indicating stable performance. Genotypes RCH 650, RCH 653, Shreeram 331 and Shreeram 321 which had bi values below unity consistently performed well under unfavorable conditions. In contrast, RCH 926 with a bi value greater than unity demonstrated good adaptability to favorable conditions. These results corroborate the findings of Shinde *et al*. (2009) [12] and Maleia and Filho (2010) [7].

Table 1: Pooled analysis of variance for different characters in cotton

S.No.	Characters	Genotype	Env	G*E	Pooled error
	d.f	[11]	[2]	[22]	[66]
1.	Days to 50% flowering	6.24**	77.69**	0.60**	0.06
2.	Plant height (cm)	95.51**	428.26**	3.43**	0.41
3.	Number of monopodia per plant	0.04**	0.39**	0.01**	0.00
4.	Number of sympodia per plant	13.23**	202.50**	1.01	4.96
5.	Number of bolls per plant	23.51**	320.47**	3.73	6.80
6.	Boll weight (g)	0.30**	2.60**	0.07	0.11
7.	Seed index	1.13**	9.50**	0.09	0.12
8.	Lint index	0.41**	2.93**	0.01	0.03
9.	Lint yield per plant (g)	22.09**	199.34**	0.16	0.22
10.	Seed yield per plant	24.81**	348.69**	0.64**	0.21

(d.f - Degree of freedom, Env - Environment, G*E- Genotype × Environment interaction, [**] highly significant)

Table 2: Pooled mean values of per se performance in cotton for all the 10 characters

Pooled mean values of per se performance											
S.No	**Genotypes**	**D.F. 50%**	**P.H.**	**NMPP**	**NSPP**	**NBPP**	**B.W.**	**S.I.**	**L.I.**	**LYPP**	**SYPP**
1.	RCH 951	55.67	27.22	1.37	14.56	24.22	4.52	10.38	4.62	18.67	43.48
2.	RCH 846	57.11	25.56	1.31	13.67	22.56	4.28	10.19	4.48	17.47	41.52
3.	RCH 926	58.89	31.33	1.43	17.44	28.33	4.54	10.94	5.09	21.33	45.92
4.	RCH 776	54.44	23.33	1.27	10.11	20.33	3.94	9.47	4.23	15.58	38.51

5.	RCH 650	56.00	30.11	1.59	15.89	27.11	4.40	11.06	5.08	20.42	44.78
6.	RCH 653	58.11	28.45	1.38	14.33	25.45	4.43	10.22	4.92	19.41	44.23
7.	RCH 773	54.33	26.11	1.36	12.33	23.11	4.02	9.73	4.50	16.17	39.76
8.	Ajeet 177	56.67	30.89	1.52	16.00	27.89	4.80	11.02	5.28	22.82	45.92
9.	Ajeet 155	57.56	32.44	1.69	17.44	29.44	4.98	11.54	5.50	24.67	48.40
10.	Ajeet 946	54.67	25.44	1.37	13.11	22.44	4.07	10.17	4.68	17.54	41.79
11.	Shreeram 331	56.33	32.11	1.49	13.89	25.78	4.59	10.88	4.91	19.71	43.99
12.	Shreeram 321	56.67	30.11	1.48	14.67	27.11	4.69	10.93	5.09	21.50	46.26

(D.F.50% - Days to 50% flowering stage, P.H. - Plant height, NMPP - Number of monopodia per plant, NSPP - Number of sympodia per plant, B.W. - Ball weight, S.I. - Seed index, L.I. - Lint index, LYPP - Lint yield per plant, SYPP - Seed yield per plant)

Table 3: Analysis of variance Eberhart and Russel (1966) [3]

S.N.	Characters	Genotype	E+(G x E)	E (L)	G x E (L)	Pool dev.	Pool Error
1.	Days to 50% flowering	6.24	7.02	155.38	0.89	0.29	0.06
2.	Plant height (cm)	95.51	38.83	856.52	2.71	3.80	0.06
3.	Number of monopodia per plant	0.04	0.04	0.77	0.01	0.01	0.00
4.	Number of sympodia per plant	13.23	17.80	405.01	0.58	1.31	4.96
5.	Number of bolls per plant	23.51	30.12	640.93	5.49	1.80	6.80
6.	Boll weight (g)	0.30	0.28	5.19	0.07	0.06	0.11
7.	Seed index	1.13	0.87	19.00	0.03	0.14	0.12
8.	Lint index	0.41	0.26	5.85	0.02	0.01	0.03
9.	Lint yield per plant (g)	22.09	16.76	398.69	0.19	0.12	0.22
10.	Seed yield per plant	24.81	29.64	697.37	0.86	0.38	0.21

Table 4: Regression coefficient of stability parameters

Deviation for Regression coefficient of Stability parameters (S2di)											
S.No.	Genotypes	D.F.	P.H.	NMPP	NSPP	NBPP	B.W.	S.I.	L.I.	LYPP	SYPP
1.	RCH 951	-0.30	-2.34	-0.01	-1.22	-6.58	-0.11	0.00	-0.01	0.00	-0.16
2.	RCH 846	-0.43	3.12**	-0.02	-4.77	-3.62	0.14	-0.10	-0.02	0.12	-0.19
3.	RCH 926	-0.39	-0.73	-0.02	-3.47	-6.49	-0.07	-0.11	-0.02	0.05	0.07
4.	RCH 776	-0.40	-2.82	-0.02	-2.79	-5.01	-0.11	0.01	-0.02	-0.15	1.04*
5.	RCH 650	-0.00**	-0.15**	-0.02	-4.94	-0.52	0.16	0.21	-0.03	-0.22	0.05
6.	RCH 653	-0.42	7.73**	0.00*	-3.75	-5.24	-0.11	0.17	-0.02	-0.18	-0.21
7.	RCH 773	-0.30	6.24**	-0.02	-4.88	-6.78	-0.10	-0.13	-0.01	-0.19	0.76*
8.	Ajeet 177	-0.41	-1.78	-0.02	-4.41	-6.76	-0.11	-0.06	-0.01	-0.18	0.00
9.	Ajeet 155	0.25**	-2.67	0.01**	-3.09	-6.19	-0.09	-0.12	-0.03	-0.12	0.98*
10.	Ajeet 946	1.32**	-1.66	-0.02	-4.91	-6.72	-0.07	0.21	-0.02	-0.13	-0.21
11.	Shreeram 331	-0.24	-2.13	-0.02	-0.94	-6.68	-0.11	-0.13	-0.01	0.01	-0.18
12.	Shreeram 321	-0.43	4.50**	-0.02	-4.61	0.60	-0.02	0.12	-0.02	-0.20	0.13

(D.F.50% - Days to 50% flowering stage, P.H. - Plant height, NMPP - Number of monopodia per plant, NSPP - Number of sympodia per plant, B.W. - Ball weight, S.I. - Seed index, L.I. - Lint index, LYPP - Lint yield per plant, SYPP - Seed yield per plant)

Conclusion

The study emphasizes the potential of using genetic stability analysis as a tool for selecting cotton genotypes that can thrive under varying climatic and agronomic conditions. This research contributes valuable insights into the development of cotton varieties with stable performance, thereby, enhancing productivity and sustainability in cotton farming systems. Stability analysis revealed that certain genotypes, including RCH 776, RCH 773 and Ajeet 155, were highly stable and suitable for diverse environmental conditions, making them ideal candidates for cotton breeding programs aimed at improving stability and yield.

References

1. Government of India. Agricultural Statistics at a Glance 2023. New Delhi: Ministry of Agriculture & Farmers Welfare, Department of Agriculture & Farmers Welfare, Economics & Statistics Division; 2023.
2. Chapepa B, Mare M, Mubvekeri W, Kutywayo D. Implications of genotype by environment interactions on heritability estimate and variance components of cotton (*Gossypium hirsutum* L.). Cogent Food Agric. 2022;8(1):2121204.
3. Eberhart SA, Russell WA. Stability parameters for comparing varieties. Crop Sci. 1966;6(1):357-361.
4. James C. Global status of commercialized biotech/GM crops: 2019. ISAAA Brief No. 55. Ithaca (NY): International Service for the Acquisition of Agri-biotech Applications; 2019.
5. Kavithamani D, Balu AP, Rajarathinam S. Stability analysis of seed cotton yield and its components in *Gossypium barbadense* genotypes. Madras Agric J. 2011;98(10-12):321-326.
6. Kumbhalkar HB, Gawande VL, Deshmukh SB, Gotmare VP, Waghmare VN. Stabilized heterosis studies for seed cotton yield and component traits in upland cotton (*Gossypium hirsutum* L.). Int J Curr Microbiol Appl Sci. 2021;10(7):99-113.
7. Maleia MP, Vidigal Filho PS. Stability and adaptability of commercial cotton cultivar (*Gossypium hirsutum* L. race *latifolium* H.) in Mozambique. Afr J Agric Res. 2010;5(7):539-550.
8. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. New Delhi: Indian Council of

Agricultural Research; 1967. p. 145.

9. Patil BC, Vijay K, Ratna Kumari S. Stability of *Gossypium hirsutum* genotypes for performance across Indian rainfed ecosystems. In: Proceedings of the World Cotton Research Conference-4; 2007 Sep 10-14; Lubbock, TX, USA. p. 1-6.
10. Pavasia MJ, Shukla PT, Patel UG. Stability of seed cotton yield and quality characters in intra-*Gossypium hirsutum* hybrids. Indian Soc Cotton Improv. 2000;25(2):97-99.
11. Satish Y, Jain PP, Chhabra BS. Stability analysis for yield and its component traits in American cotton (*Gossypium hirsutum* L.). J Cotton Res Dev. 2009;23(2):175-182.
12. Shinde GC, Mehetre SS, Jagtap PK. Stability analysis of CGMS-based hybrids and their parents for seed cotton yield in cotton (*Gossypium hirsutum* L.). J Cotton Res Dev. 2009;23(2):188-192.
13. Tuteja OP, Mahendar S, Singh DP. Stability analysis for seed cotton yield and its component traits in intra-specific hybrids of *Gossypium hirsutum*. J Cotton Res Dev. 2006;20(2):174-177.
14. Sirisha P, Anuradha T. Detection of permission driven malware in android using deep learning techniques. In2019 3rd International conference on electronics, communication and aerospace technology (ICECA) 2019 Jun 12 (pp. 941-945).