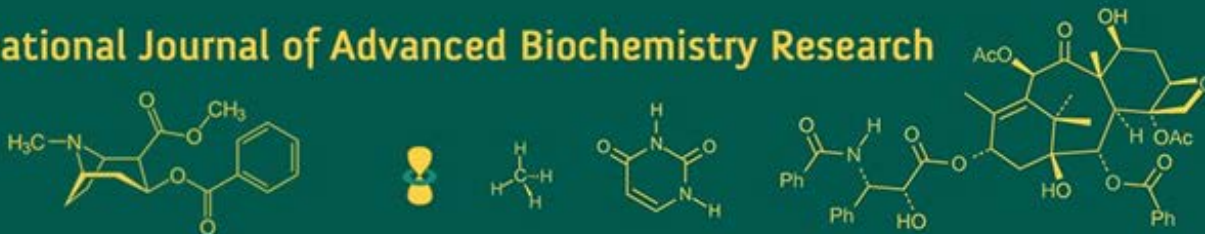


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
 ISSN Online: 2617-4707
 NAAS Rating (2026): 5.29
 IJABR 2026; SP-10(8): 566-571
www.biochemjournal.com
 Received: 18-06-2026
 Accepted: 22-07-2026

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Unravelling genetic architecture and phenotypic diversity for seed cotton yield and associated traits in upland cotton (*Gossypium hirsutum* L.)

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i8Sg.9490>

Abstract

This experiment aimed to extract information regarding genotypic and phenotypic variability, heritability, genetic advance over different locations for various traits in cotton. Experiment was carried out at three different locations of Gujarat, under the jurisdiction of Anand Agricultural University (AAU) during kharif 2023. Three different environments were made available by choosing three different locations of Gujarat i.e., Regional Research Station, AAU, Anand; Agricultural Research Station, AAU, Jabugam and Agriculture Research Station for Irrigated Crops, AAU, Thasra. Analysis of variance revealed significant differences among genotypes for all the traits across the all three environments, indicating sufficient variability existed for various traits under study. There was low variability (<10% GCV and PCV) observed for days to 50 % flowering, days to 50 % boll bursting, ginning outturn, fibre strength and uniformity index among cotton genotypes in all three environments. Whereas, high variability was observed for monopodia per plant. Traits namely, plant height, monopodia per plant, sympodia per plant, bolls per plant, boll weight, seed cotton yield per plant, lint yield per plant, seed index, oil content, span length and fibre fineness exhibited high heritability coupled with high genetic advance as per cent of mean in all three environments.

Keyword: Upland cotton; *Gossypium hirsutum*; Genetic variability; Phenotypic variability; Heritability; Genetic advance; Seed cotton yield; Genotype–environment interaction; Fibre quality; Cotton breeding.

Introduction

Cotton is an immensely important crop for the sustainable economy of India and livelihood of the Indian cotton farming community. Cotton is generating employment for millions of farmers and others engaged in activities relating to cotton, cotton processing, transportation etc. India occupies first place in the world in terms of acreage under cotton cultivation. The cotton genus *Gossypium* of the Malvaceae family occurs naturally throughout the tropics and subtropics and consists of about 50 species that form a monophyletic group. Out of the 50 species, only four species are cultivated and the remaining 46 are wild species (Lee *et al.*, 1984)^[1]. Analysis of variability among the traits and the association of a particular character with other traits contributing to yield of a crop would be of a great importance in planning a successful breeding programme (Mary and Gopalan, 2006)^[2]. Variability present in the population is the prerequisite in response to selection for any crop improvement programme. Selection of superior varieties or populations will be possible only when adequate variability exists in the gene pool. Hence, the insight into the magnitude of variability present in a gene pool of a crop species is of utmost importance to plant breeding programme. It is essential for the plant breeders to measure the variability with the help of parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance. The coefficient of variation expressed in phenotypic and genotypic levels are used to compare the variability observed among different characters. Hence, knowledge about the variability using parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is of paramount importance for an effective breeding programme in crops like cotton. The heritability estimates aid in determining the relative amount of heritable portion in variation and thus helps the plant breeder in selecting the elite genotypes from a diverse population. Therefore, the present study was undertaken for assessing the extent of genetic variability, heritability and genetic advance in cotton genotypes.

Materials and Methods

the experimental material for present investigation was comprised of 42 genotypes (40 genotypes

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and two standard checks) of cotton (*Gossipium hirsutum* L.) procured from Regional Research Station, AAU, Anand. The 42 genotypes and two checks were evaluated in Randomized Complete Block Design (RCBD) with three replications. Each genotype is planted in 2 rows with a spacing of 120 × 45 cm between rows and plants respectively. The experiment was conducted during kharif 2023, at three different locations of Gujarat, under the jurisdiction of Anand Agricultural University (AAU). Three locations were Anand kharif 2023 (: Regional Research Station, AAU, Anand), Jabugam kharif 2023 (: Agricultural Research Station, AAU, Jabugam) and Thasara kharif 2023 (: Agriculture Research Station for Irrigated Crops, AAU, Thasara). Five plants were randomly selected from each experiment unit and those were used for recording the observation for the seed cotton yield, its components and matriculate traits; whereas, the traits days to 50% flowering and days to 50% boll bursting were taken on plot basis. Fibre quality traits such as span length, fibre strength, fibre fineness and uniformity index values were considered for the analysis. Experimental materials used for present study are enlisted in Table 1. ANOVA Analysis of variance suggested by [Snedecor \(1937\)](#) [3] and reviewed by [Panse and Sukhatme \(1978\)](#) [4] was followed to test the significance of difference among the genotypes for all the traits under study. GCV and PCV were categorized as low, moderate and high by following classification given by Shivasubramanian and Menon (1973), where values of 0-10% indicates low variation, 10-20% represents moderate variation and values greater than 20% reflects high variation. Broad-sense heritability was calculated as the percentage ratio of genotypic variance to phenotypic variance. Heritability percentage was categorized as demonstrated by Robinson *et al.*

Table 1: Experimental materials used in the present study.

Sr. No.	Genotypes	Sr. No.	Genotypes
Regional Research Station, AAU, Anand		Regional Cotton Research Station, NAU, Bharuch	
1.	AHC-2	28.	GBHV-256
2.	AHC-4	29.	GBHV-257
3.	AHC-11	Main Cotton Research Station, NAU, Surat	
4.	AHC-16	30.	G.N.Cot.-22
5.	AHC-57	31.	G.Cot.-100
6.	AHC-58	32.	GISV-366
7.	AHC-59	Cotton Research Station, JAU, Junagadh	
8.	AHC-70	33.	GJHV-598
9.	AHC-71	Main Cotton Research Station, NAU, Surat	
10.	AHC-72	34.	GSHV-93/13
11.	AHC-73	Cotton Research Station, SDAU, Talod	
12.	AHC-78	35.	GTHV-13/35
13.	AHC-79	36.	GTHV-15/43
14.	AHC-80	37.	GTHV-18/19
15.	AHC-82	Main Cotton Research Station, NAU, Surat	
16.	AHC-85	38.	Deviraj
17.	AHC-87	39.	JGP-14
18.	AHC-88	40.	Surat Dwarf
19.	AHC-97	Standard Check	
20.	AHC-1904	Cotton Research Station, JAU, Junagadh	
21.	AHC-2001	41.	G.Cot.-38
22.	AHC-2006	Main Cotton Research Station, NAU, Surat	
23.	AHC-2009	42.	G.Cot.-40
24.	AHC-2105		

25.	AHC-2107		
26.	AHC-2108		
27.	AHC-2201		

(1949). Based on the classification by Robinson *et al.*, (1949) [5] heritability was grouped into three categories as low (0-30%), moderate (30-60%) and high (>60%). Similarly, genetic advance was classified into three categories referred as low (0-10%), moderate (10-20%) and high (>20%).

Results and Discussion

Variability analysis

The analysis of variance for 17 traits in individual environment is presented in Table 2. The results revealed that the mean squares due to genotypes were significant for all the traits in individual environment which suggested the presence of a sufficient amount of variability in the genotypes evaluated for seed cotton yield and its component traits. The wide range of diversity allows plant breeders to select superior and desired genotypes for further crop improvement. Genotypic () and phenotypic variance () estimates for each trait were obtained from the analysis of variance. Additional genetic parameters, including the genotypic coefficient of variation (GCV %) and phenotypic coefficient of variation (PCV %), heritability () and genetic advance as per cent of mean (GA % mean) were computed from variance components and mean values (Table 3). Estimates of GCV (32.35%, 32.64% and 31.97%) and PCV (33.45%, 34.02% and 33.44%) were high in , and , indicating a substantial amount of variability within the investigated population for this trait. The close estimates of GCV and PCV values suggested that genetic constitution of trait play important role in the expression of trait in the environment. High GCV and PCV for monopodia per plant were also reported by [Nikhil *et al.* \(2018\)](#) [6], [Premlatha *et al.* \(2020\)](#) [7] and [Patel *et al.* \(2023\)](#) [8]. Moderate GCV and PCV were recorded for several traits, including plant height, GCV (13.87, 13.76 and 13.65 %) and PCV (13.91, 13.95 and 13.71 %) in , and respectively; sympodia per plant, GCV(17.33, 13.67 and 18.24 %) and PCV (18.47, 14.47 and 18.51 %) in and respectively; Bolls per plant, GCV (15.70, 15.98 and 15.89 %) and PCV (16.40, 16.53 and 16.59 %) in , and , respectively. The Moderate GCV values for boll weight in (11.03), (10.79) and (10.88) were very close to the PCV values in (11.19), (11.02) and (11.20), for seed cotton yield GCV was found moderate in (16.84), (16.80) and (16.38), while values of PCV was moderate in (17.64), (17.51) and (17.38), lint yield per plant, GCV in (17.63), (16.87) and (16.66) were moderate, while values of PCV in (18.43), (17.70) and (17.71) found moderate. Moderate estimates of both GCV in (10.63), (10.97) and (11.08) and PCV in (12.75), (12.40) and (12.64) were observed in lint index. For seed index estimates of GCV (11.85, 11.52 and 11.67 %) and PCV (12.04, 11.72 and 11.87 %) were moderate in , and respectively. Oil content, GCV in (16.40), (16.62) and (16.32), while values of PCV in (16.46), (16.65) and (16.36) found moderate. Span length, GCV in (10.46%), (10.21%) and PVC in (10.50%), (10.26%) found moderate. For fibre fineness, GCV in (12.13%), (12.01%) and (13.76%) were moderate, while values of PCV in (12.15%), (12.02%) and (13.78%) were moderate. This moderate values indicated that sufficient genetic variability existed in the studied population under investigation for the trait. Similar findings have been reported by [Nikhil *et al.* \(2018\)](#) [6], [Premlatha *et al.* \(2020\)](#) [7] and [Patel *et al.* \(2023\)](#) [8]. In contrast, for days to 50 % flowering low GCV (3.85, 4.70 and 4.20%) and PCV (4.38, 5.28 and 6.10%) were in , and respectively; days to 50 % boll bursting

GCV (4.33, 4.23 and 4.15%) and PCV (4.53, 4.48 and 4.33%); ginning outturn GCV in (9.02%), (9.75%) and (8.97%) were found low, while values of PCV in (10.42%), (10.54%) found moderate and low in (9.85%); fibre strength, GCV in (9.17%), (8.74%) and (9.40%) were low value while values of PCV in (9.07%), (9.21%) and (8.78%) were lower; Uniformity index GCV in (0.711%), (0.854%) and (0.651%), PCV in (0.717%), (0.931%) and (0.660%) indicating that limited variability existing for all these low GCV and low PCV traits in studied population. These findings are consistent with those of Ujjainkar *et al.* (2024) [9] and Premalatha *et al.* (2020) [7].

Heritability

Higher magnitude of heritability was observed for all traits, days to 50 % flowering (77.57%), (79.16%), days to 50 % boll bursting (91.46), (89.33) and (91.98 %), plant height (99.40), (97.20) and (99.19); monopodia per plant (93.53), (92.05) and (91.43); sympodia per plant (88.05), (89.30) and (97.09); bolls per plant (91.55), (93.49) and (91.72); boll weight (97.06), (94.34) and (95.54), seed cotton yield per plant (91.08), (92.00) and (88.82); ginning outturn (74.93), (85.67) and (82.99); lint yield per plant (91.45), (90.85) and (88.50); lint index (69.57), (78.20) and (76.83); seed index (96.91), (96.65) and (96.72); oil content (99.31), (99.62) and (99.52); span length (99.13), (99.03) and (98.36); fibre strength (99.05%), (99.16%) and (95.03%); fibre fineness (99.65%), (99.64%) and (99.69%) and uniformity index (98.43%), (84.21%) and (97.42%) suggesting that most likely the heritability is due to additive gene effects and selection may be effective. These findings consistent with the Premalatha *et al.* (2020) [7] and Vijay *et al.* (2025) [10].

High heritability combined with high genetic advance as a percentage of the mean was witnessed for plant height (28.48, 27.94 and 28.00 %); monopodia per plant (64.45 , 64.51 and 62.98 %); sympodia per plant (33.50, 26.82 and 37.03 %); bolls per plant (30.94, 31.84 and 31.35 %); boll weight (22.38, 21.77 and 21.77 %); seed cotton yield per plant (33.10, 33.19 and 31.80); lint yield per plant (34.73, 33.13 and 32.28 %); seed index (33.67, 34.17 and 33.53 %); oil content (33.67, 34.17 and 33.53); span length (18.80, 17.93 and 18.87 %); fibre fineness

(24.94, 24.69 and 28.30 %) in and respectively. These results suggest that heritability is predominantly due to additive gene effects, making selection effective for improvement through the utilization of fixable genes. Similar findings reported by Premalatha *et al.* (2020) [7], Meena *et al.* (2022) [11] and Patel *et al.* (2023a) [8]. High heritability with moderate genetic advance as a percentage of the mean was recorded for ginning outturn (16.08, 18.60 and 16.84 %); lint index (18.27, 19.99 and 20.01 %) and fibre strength (18.80, 17.93 and 18.87 %) in and respectively. These results suggest the influence of both additive and non-additive gene actions, indicating that desired outcomes may not be achieved through simple selection alone. Similar results have been noted by Nikhil *et al.* (2018) [6], Premalatha *et al.* (2020) [7] and Vijay *et al.* (2025) [10]. High heritability combined with low genetic advance as a percentage of the mean was noticed for days to 50 % flowering (6.99, 8.61 and 5.95 %); days to 50 % boll bursting (8.53, 8.24 and 8.20 %) and uniformity index (1.45, 1.61 and 1.32 %) in and respectively; indicating the predominance of non-additive gene action, which offers limited potential for improvement through selection. Estimates of GCV and PCV were moderate to high for all the characters except days to 50% flowering, days to 50% boll bursting, fibre strength and uniformity index offering better scope for selection due to less influence of environment and suggesting potential variability available in germplasm for these traits. High heritability coupled with high genetic advance as per cent mean were noticed for all the characters except viz., days to 50% flowering, days to 50% boll bursting, ginning outturn, lint index, fibre strength and uniformity index which suggested additive gene action and hence, these traits may be improved through selection. Ginning outturn on the other hand, exhibited high heritability and moderate genetic advance which suggest that character could be improved by hybridization followed by selection. Whereas uniformity index had high heritability coupled with low genetic advance, suggesting preponderance of non-additive gene action for this trait.

Table 2: Analysis of variance (mean squares) for various characters under individual environments

Sr. No.	Source of variation	d.f.	Days to 50% flowering			Days to 50% boll bursting			Plant height		
1.	Replications	2	17.01* *	6.60	17.17	31.29**	4.41	10.02**	3.88	25.47	8.67
2.	Genotypes	41	21.27* *	31.76**	32.17**	68.15**	66.16**	63.06**	1198.43**	1167.84**	1162.10**
3.	Error	82	1.87	2.56	8.69	2.06	2.53	1.78	2.42	11.09	3.16
Sr. No.	Source of variation	d.f.	Monopodia per plant			Sympodia per plant			Bolls per plant		
1.	Replications	2	0.13	0.30*	0.04	8.77**	1.39	0.86	7.31	34.01*	27..81*
2.	Genotypes	41	2.19**	2.23**	2.14**	35.96**	20.32**	37.87**	216.68**	222.17**	222.54**
3.	Error	82	0.05	0.06	0.06	1.56	0.78	0.37	6.47	5.04	6.50
Sr. No.	Source of variation	d.f.	Boll weight			Seed cotton yield per plant			Ginning outturn		
1.	Replications	2	0.04**	0.004**	0.01	548.4*	467.5*	600.1*	11.00*	2.05	
2.	Genotypes	41	0.66**	0.64**	0.66**	4437.3**	4418.0**	4304.7**	23.83**	26.72**	
3.	Error	82	0.01	0.01	0.01	140.3	124.5	173.4	2.39	1.41	
Sr. No.	Source of variation	d.f.	Lint yield per plant			Lint index			Seed index		
1.	Replications	2	53.25*	18.68	104.80**	0.44*	0.15	0.20	0.06	0.02	0.09
2.	Genotypes	41	414.03**	400.68**	397.06**	1.00**	1.03**	1.09**	6.21**	5.90**	6.15**
3.	Error	82	12.51	13.01	16.48	0.13	0.09	0.10	0.06	0.07	0.07

, Significant at $P = 0.05$ and $P = 0.01$ levels, respectively.

Table 2: Contd...

Sr.No.	Source of variation	d.f.	Oil content			Span length			Fibre strength		
1.	Replications	2	0.41*	0.33**	0.15	0.05	0.13	0.21	0.01	0.01	0.17
2.	Genotypes	41	46.14**	46.47**	43.54**	24.01**	22.62**	17.93**	20.47**	18.75**	21.88**
3.	Error	82	0.11	0.06	0.07	0.07	0.07	0.10	0.06	0.05	0.37
Sr.No.	Source of variation	d.f.	Fibre fineness			Uniformity Index					
1.	Replications	2	0.001	0.0003	0.001	0.01	0.05	0.0004			
2.	Genotypes	41	0.78**	0.75**	0.98**	1.08**	1.64**	0.91**			
3.	Error	82	0.001	0.001	0.001	0.01	0.10	0.01			

, Significant at $P = 0.05$ and $P = 0.01$ levels, respectively.

Table 3: Genetic parameters of variation for seed cotton yield and its component traits in cotton (*Gossypium hirsutum* L) genotypes.

Characters	Environment	Mean	Range				GCV (%)	PCV (%)	(%)	GA% Mean
			Min	Max						
Days to 50 % flowering		65.97	58.33	73.17	6.47	8.34	3.85	4.38	77.57	6.99
		66.40	56.67	74.17	9.73	12.30	4.70	5.28	79.16	8.61
		66.64	58.83	75.50	7.83	16.52	4.20	6.10	47.37	5.95
Days to 50 % ball bursting		108.40	99.67	119.50	22.03	24.09	4.33	4.53	91.46	8.53
		108.75	99.33	118.17	21.21	23.74	4.23	4.48	89.33	8.24
		108.90	99.67	117.50	20.43	22.21	4.15	4.33	91.98	8.20
Plant Height		143.98	95.40	192.93	398.67	401.09	13.87	13.91	99.40	28.48
		142.74	90.27	187.07	385.58	396.67	13.76	13.95	97.20	27.94
		143.99	94.47	190.07	386.31	389.47	13.65	13.71	99.19	28.00
Monopodia per Plant		2.61	1.27	4.27	0.71	0.76	32.35	33.45	93.53	64.45
		2.60	1.40	4.53	0.72	0.78	32.64	34.02	92.05	64.51
		2.60	1.13	4.27	0.69	0.76	31.97	33.44	91.43	62.98
Sympodia per Plant		19.54	11.53	25.80	11.47	13.02	17.33	18.47	88.05	33.50
		18.66	14.00	23.20	6.51	7.29	13.67	14.47	89.30	26.62
		19.38	12.34	26.27	12.50	12.87	18.24	18.51	97.09	37.03
Bolls per Plant		53.33	32.87	70.53	70.07	76.54	15.70	16.40	91.55	30.94
		53.22	34.60	68.93	72.38	77.42	15.98	16.53	93.49	31.84
		53.41	35.27	70.40	72.01	78.51	15.89	16.59	91.72	31.35
Boll Weight		4.23	3.47	5.09	0.218	0.224	11.03	11.19	97.06	22.38
		4.25	3.45	5.08	0.210	0.219	10.79	11.02	95.94	21.77
		4.26	3.43	5.11	0.215	0.228	10.88	11.20	94.34	21.77
Seed Cotton Yield per Plant		224.77	141.23	280.68	1432.35	1572.63	16.84	17.64	91.08	33.10
		225.19	140.61	295.80	1431.15	1555.66	16.80	17.51	92.00	33.19
		225.50	141.43	297.25	1377.09	1550.49	16.38	17.38	88.82	31.80
Ginning Outturn		29.64	25.46	35.59	7.15	9.54	9.02	10.42	74.93	16.08
		29.77	25.12	35.95	8.43	9.85	9.75	10.54	85.67	18.60
		29.95	25.39	35.20	7.22	8.70	8.97	9.85	82.99	16.84
Lint Yield per Plant		65.62	41.52	88.47	133.84	146.35	17.63	18.43	91.45	34.73
		67.37	38.69	85.91	129.22	142.23	16.87	17.70	90.85	33.13
		67.61	39.80	84.05	126.86	143.34	16.66	17.71	88.50	32.28
Lint Index		5.07	4.03	6.31	0.29	0.42	10.63	12.75	69.57	18.27
		5.11	4.16	6.74	0.31	0.40	10.97	12.40	78.20	19.99
		5.20	4.27	6.79	0.33	0.43	11.08	12.64	76.83	20.01
Seed index		12.07	9.33	14.41	2.05	2.11	11.85	12.04	96.91	24.04
		12.10	9.41	14.49	1.94	2.01	11.52	11.72	96.65	23.33
		12.19	9.56	14.71	2.03	2.09	11.67	11.87	96.72	23.65
Oil Content		23.89	14.80	30.38	15.35	15.45	16.40	16.46	99.31	33.67
		23.66	14.68	30.39	15.47	15.53	16.62	16.65	99.62	34.17
		23.59	15.37	30.33	14.82	14.89	16.32	16.36	99.52	33.53
Span Length		27.02	22.09	32.60	7.98	8.05	10.46	10.50	99.13	21.45

		26.85	21.27	32.35	7.52	7.59	10.21	10.26	99.03	20.93
		27.10	21.81	31.93	5.94	6.04	9.00	9.07	98.36	18.38
Fibre Strength		28.44	23.36	33.96	6.80	6.86	9.17	9.21	99.05	18.80
		28.56	23.54	33.71	6.23	6.28	8.74	8.78	99.16	17.93
		28.49	23.16	33.39	7.17	7.54	9.40	9.64	95.03	18.87
Characters	Environment	Mean	Min	Max			GCV (%)	PCV (%)	(%)	GA% Mean
Fibre Fineness		4.19	3.22	5.09	0.258	0.259	12.13	12.15	99.65	24.94
		4.16	3.18	5.04	0.249	0.251	12.01	12.02	99.64	24.69
		4.15	3.14	4.99	0.326	0.327	13.76	13.78	99.69	28.30
Uniformity Index		84.17	83.03	85.01	0.358	0.364	0.711	0.717	98.43	1.45
		84.10	82.47	85.51	0.516	0.612	0.854	0.931	84.21	1.61
		84.37	83.44	85.29	0.302	0.310	0.651	0.660	97.42	1.32

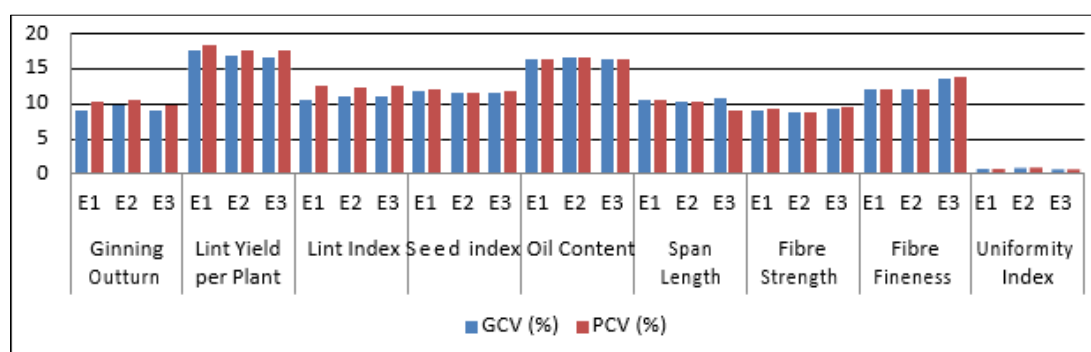
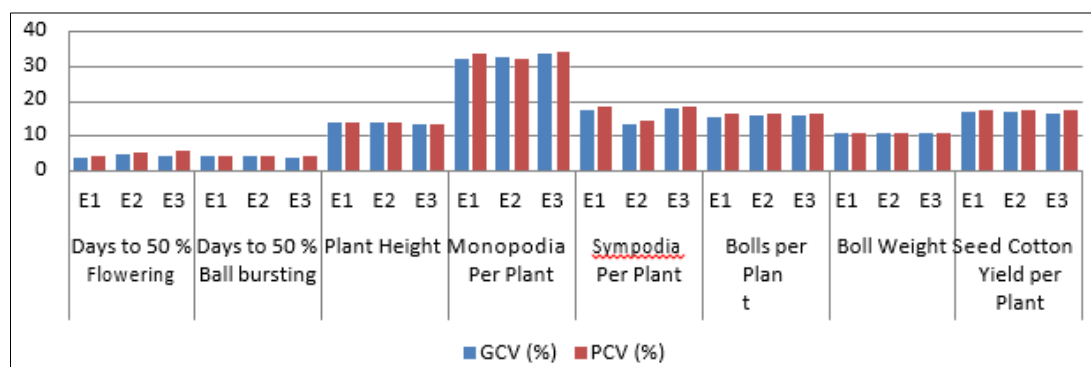
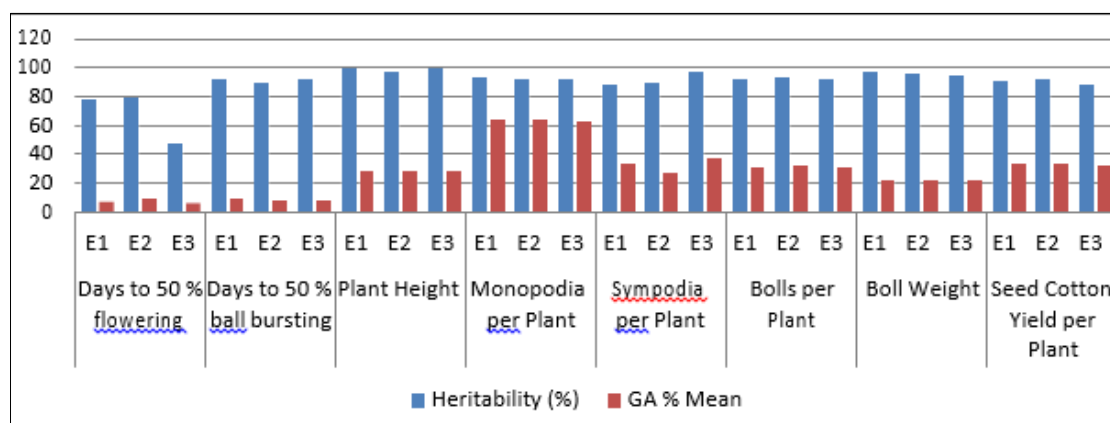


Fig 1: Graphical representation of GCV and PCV for cotton (: Anand, Jabugam, Thasra)



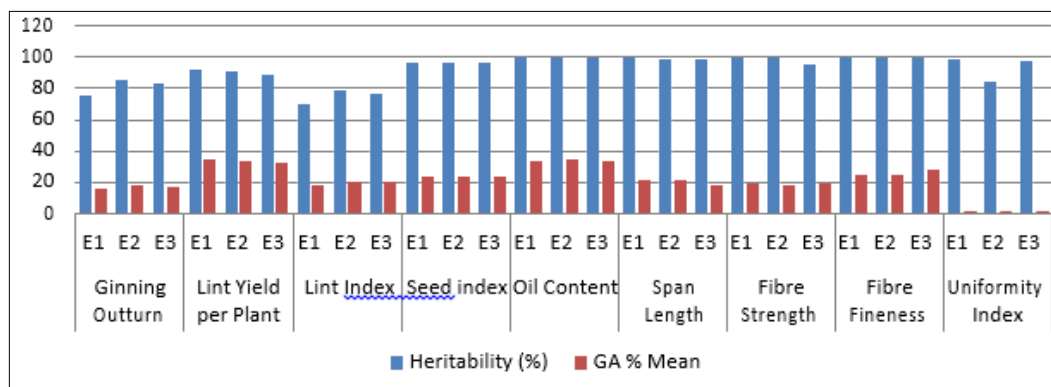


Fig 2: Graphical representation of broad sense heritability and genetic advance as percent of mean for cotton (: Anand, : Jabugam, : Thasra)

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