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GENERATION MEAN ANALYSIS IN UPLAND COTTON (*Gossypium hirsutum* L.)

Vishnu K. Ghanghar^{*1}, Kalpesh V. Patel², Saraswathi Indra P. Nadar¹, Mukesh P. Patel³
and Dinesh J. Parmar⁴

¹Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand Agricultural University, Anand-388110 (Gujarat), India

²Medicinal and Aromatic Plant Research Station, Anand Agricultural University, Anand-388110 (Gujarat), India

³Agricultural and Horticulture Research Station, Anand Agricultural University, Khambholaj-388330 (Gujarat), India

⁴Department of Statistics, B. A. College of Agriculture, Anand Agricultural University, Anand-388110 (Gujarat), India

*Corresponding author E-mail: vishnughanghar13@gmail.com

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ABSTRACT

The crop cotton governs by various types of gene action in different traits which was assessed using the generation mean analysis. Six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) each of the four crosses viz., G. Cot 20 $\times$ AHC-37, GSHV-206 $\times$ AHC-36, AHC-33 $\times$ AHC-35 and AHC-29 $\times$ AHC-42 were evaluated. The significance of one or more simple scaling test as well as χ^2 values of joint scaling test indicated presence of non-allelic gene interactions for most of the traits except in seed index for cross AHC-33 $\times$ AHC-35. The value of additive gene action found higher with significant effect in plant height for cross G. Cot 20 $\times$ AHC-37 and seed index in cross AHC-33 $\times$ AHC-35. The magnitude of additive type of gene actions were found to be lower than dominance gene interactions in most of the studied traits. The values of dominance gene action was the highest for seed cotton yield per plant. Epistasis component of gene actions like additive $\times$ additive (i), additive $\times$ dominance (j) and dominance $\times$ dominance (l) were found higher for the inheritance of days to initiation of flowering, plant height, number of monopodia per plant, lint index, lint yield per plant. Duplicate type of epistasis was observed for most of the traits, while complementary epistasis was present for days to initiation of boll bursting in cross G. Cot 20 $\times$ AHC-37 and for lint yield per plant in cross GSHV-206 $\times$ AHC-36.

Key words: Cotton, generation mean, gene action, epistatic and lint index

Introduction

Cotton is one of the major fiber crops as it holds a large share in economy and also serves as a primary source of raw material for textile industry. Cotton, often called as white gold and king of fiber which is economically valuable cash crop as well as fiber crop. Seed cotton yield and its component traits regulated by number of genes in cotton with their expression primarily depending on the types of gene action. Despite the advent of artificial fibers, cotton remains the most widely used textile fiber globally, owing to its natural qualities like durability and versatility. Among all cultivated species *Gossypium hirsutum* covers about 90% in terms of production in the world (Gawande *et al.*, 2016). Plant breeders worldwide have significantly contributed to

enhancing fiber quality traits, which are inherited quantitatively. Understanding the nature and extent of gene action in the breeding material is essential for selecting the appropriate breeding methods to achieve the desired genetic improvements in any crop suggested by Giri *et al.*, (2020).

Generation mean analysis is a quantitative genetic technique used to estimate the components of gene action including additive, dominance and interaction effects for individual traits (Mather and Jinks, 1982). Mather (1949) introduced tests for epistasis using scaling tests which was elaborated by Cavalli (1952). Hayman and Mather (1955) proposed a model to estimate additive, dominance and epistasis effects from six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2). Hayman (1958) detailed how to divide

generation means into six parameters viz., mean (m), additive (d), dominance (h), additive $\times$ additive (i), additive $\times$ dominance (j) and dominance $\times$ dominance (l) effects. Conventional breeders use scaling and joint scaling tests to understand allelic and non-allelic gene actions and nature and magnitude of genetic variance in specific genotypic combinations.

Information on gene effects for different traits is essential for designing an effective breeding program to achieve the desired genetic improvements. Therefore, this investigation was conducted to study gene effects in four crosses of upland cotton for various traits.

Materials and Methods

This experiment was conducted during *Kharif*-2021, *Kharif*-2022 and *Kharif*-2023 at the Regional Research Station, Anand Agricultural University, Anand in Gujarat, India. In *kharif*-2021, eight parents (AHC-29, AHC-33, AHC-35, AHC-36, AHC-37, AHC-42, G. Cot 20 and GSHV-206) were used to develop four crosses viz., G. Cot 20 $\times$ AHC-37 (cross I), GSHV-206 $\times$ AHC-36 (cross II), AHC-33 $\times$ AHC-35 (cross III) and AHC-29 $\times$ AHC-42 (cross IV). These hybrids were then selfed to obtain F_2 seeds and backcrossed with their respective parents to obtain backcross (BC_1 and BC_2) generations. Parental seeds were obtained by selfing to their respective parents. Thus, six basic generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) were developed for each of the four crosses. In *kharif*-2023, these six generations were evaluated in a compact family block design with three replications to understand the genetic nature of traits through generation mean analysis. The F_2 generation, backcross generations; parents and hybrids were sown in 4:2:1 ratio, respectively.

Observations were recorded on individual plants for various traits viz., days to initiation of flowering, days to initiation of boll bursting, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed index (g), lint index (g), lint yield per plant (g) and seed cotton yield per plant (g). The means were computed for each generation (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) across three replications for each cross. The variance and corresponding standard errors of the means were calculated based on the deviations of individual values from the pooled mean for each generation in each cross. To detect non-allelic interactions, four scaling tests (A, B, C and D) were employed as described by Mather (1949) and Hayman and Mather (1955). The standard errors for A, B, C and D were determined by taking the square root of their respective variances. The t -values were computed by dividing the effects of A, B, C and D

by their standard errors and comparing these with ' t ' table values at 5% and 1% significance levels. The significance of at least one test indicated the presence of epistatic interactions. Mean values over replications were used to estimate gene effects. With six generations in each cross, the six-parameter model proposed by Hayman (1958) comprising the mean (m), additive gene effects (d), dominance gene effects (h) and three types of epistatic gene interactions (additive $\times$ additive (i), additive $\times$ dominance (j) and dominance $\times$ dominance (l)) was employed to estimate gene effects. The additive-dominance model's adequacy was further assessed using Cavalli's (1952) joint scaling test.

Results and Discussion

The analysis of variance for all traits examined in four cotton crosses is presented in Table 1. This analysis showed that the mean square values for the crosses were significant for all traits in all three crosses. Mean data for various traits recorded for all six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) were analysed using scaling and joint scaling tests (Table 2). The significance of these tests indicated that the additive-dominance model was inadequate, revealing the presence of non-allelic gene interactions for all traits in the four crosses, except seed index in cross III (Table 3). The lack of significance for the excepted traits suggests that a simple additive-dominance model was sufficient to estimate the genetic variance components for these traits. Mean value found significant for all crosses in all traits which indicated sufficient variability present for those traits in all crosses.

For days to initiation of flowering, scale A, B and C revealed significant results along with additive $\times$ dominance and dominance $\times$ dominance gene interactions in G. cot 20 $\times$ AHC-37. In GSHV-206 $\times$ AHC-36, only scale B observed significant with additive $\times$ dominance gene interaction. Only scale A found significant in AHC-33 $\times$ AHC-35 with additive and dominance $\times$ dominance gene effects. For AHC-29 $\times$ AHC-42, scale A, B and C found significant and significant effects of dominance $\times$ dominance interaction. All four crosses have epistatic effects which suggest population improvement was more beneficial for improvement of this trait. The similar findings were also reported by Pandiyan *et al.*, (2019), Gnanasekaran and Thiyagu (2021) and Chakholoma *et al.*, (2022) who suggested preponderance of non-additive gene action for inheritance of this trait.

Scaling test A and C observed significant for days to initiation of boll bursting which indicate additive, dominance, additive $\times$ dominance and dominance $\times$ dominance gene effects in G. cot 20 $\times$ AHC-37. Only

Table 1: Analysis of variance of four crosses and their six generations for seed cotton yield and its component traits in cotton.

Source of variation	d.f.	DIF	DIB	PH	NMP	NSP	NBP	BW	SI	LI	LYP	SCP
Between cross comparison												
Replications	2	0.623	2.239	0.420	0.002	0.034	0.933	0.004	0.088	0.032	7.151	23.099
Crosses	3	4.913*	1.250	282.390**	0.470**	4.210**	19.616**	0.298**	0.520**	0.089*	116.053	571.693**
Error	6	0.537	1.540	8.070	0.003	0.146	0.258	0.011	0.030	0.013	24.606	113.851
Between generation within cross comparison												
Cross-I (G. Cot 20 × AHC-37)												
Replications	2	4.682	16.075	33.120	0.008	0.663	4.567	0.022	0.668	0.180	3.964	43.872
Generations	5	10.791*	39.905*	267.820**	1.570**	10.934**	126.899**	0.542**	2.134*	1.070**	861.371**	9802.001**
Error	10	2.359	8.479	27.590	0.089	1.208	4.644	0.087	0.598	0.174	112.667	621.385
Cross-II (GSHV-206 × AHC-36)												
Replications	2	4.980	6.109	2.020	0.0004	0.429	2.194	0.036	0.052	0.183	152.505**	591.497
Generations	5	16.266**	33.946*	575.120**	2.470**	43.694**	87.821**	0.924**	1.715**	2.450**	603.752**	2558.392**
Error	10	2.851	7.434	40.680	0.124	1.511	5.789	0.053	0.140	0.104	18.955	328.348
Cross-III (AHC-33 × AHC-35)												
Replications	2	2.251	16.708	102.730	0.004	0.463	0.251	0.146	0.014	0.001	101.555	730.593
Generations	5	20.800**	53.490**	350.490**	1.900**	20.201**	26.965**	0.301**	0.479*	0.737**	467.923*	2135.661**
Error	10	3.011	7.541	24.820	0.072	1.189	5.667	0.064	0.134	0.100	101.222	636.052
Cross-IV (AHC-29 × AHC-42)												
Replications	2	1.486	2.254	9.930	0.051	1.280	3.233	0.014	0.336	0.061	227.794*	821.961
Generations	5	17.337*	47.963**	566.080**	1.800**	25.425**	108.362**	1.084**	1.530*	3.060**	524.834**	1252.350*
Error	10	3.201	5.852	35.880	0.088	1.164	5.994	0.091	0.443	0.172	50.929	352.785
DIF: Days to initiation of flowering; DIB: Days to initiation of boll bursting; PH: Plant height; NMP: Number of monopodia per plant; NSP: Number of sympodia per plant; NBP: Number of bolls per plant; BW: Boll weight; SI: Seed index; LI: Lint index; LYP: Lint yield per plant; SCP: Seed cotton yield per plant												

scale B found significant with dominance and additive × dominance gene interaction in GSHV-206 × AHC-36. Scaling test A and C observed significant and dominance and additive × dominance gene effects significant in AHC-33 × AHC-35. All type of scaling test observed significant with all type of epistatic found significant in cross AHC-29 × AHC-42. Dominance gene effects found prominent in GSHV-206 × AHC-36 and AHC-33 × AHC-35, so hybridization more useful while in G. cot 20 × AHC-37 and AHC-29 × AHC-42 epistatic effects observed more prominent which suggest population improvement approach like biparental mating or recurrent selection would be more suitable. Pandiyan *et al.*, (2019) and Kanasagra *et al.*, (2022) also found predominance of non-additive gene action for inheritance of this trait.

For plant height, × showed significant results for scale A and C, indicating additive and additive × dominance epistatic effects, suggesting direct selection for this trait. GSHV-206 × AHC-36 has significant results for scales B, C and D indicate additive, dominance, additive × additive and additive × dominance interactions. AHC-33 × AHC-35 has significant results for scales A, C and D showing all types of gene action. AHC-29 × AHC-42 revealed significant results for scales C and D indicate additive, dominance, additive × additive and dominance

× dominance gene effects. Duplicate type of gene interaction observed in AHC-33 × AHC-35 and AHC-29 × AHC-42. The cross G. cot 20 × AHC-37 suggests direct selection due to its higher additive gene action, while the other crosses indicate the need for hybridization followed by selection due to higher dominance gene effects. The present findings were in line with the results of Giri *et al.*, (2020) who reported additive and non-additive gene action responsible for plant height. The predominant role of additive gene effect was reported by Pandiyan *et al.*, (2019), Gohil *et al.*, (2020) and Chakholoma *et al.*, (2022).

In the scaling test for G. cot 20 × AHC-37, A and C showed significant results indicating significance of additive, dominance, additive × dominance and dominance × dominance gene effects for the number of monopodia per plant. Scale A, B and C observed significant for cross GSHV-206 × AHC-36 with epistatic effects of additive × dominance and dominance × dominance. The cross AHC-33 × AHC-35 showed significant scale of B and C with only dominant gene effects while AHC-29 × AHC-42 revealed significance of A scale with significant effects of additive, dominance, additive × dominance and dominance × dominance. Higher magnitude of dominance effect in AHC-33 × AHC-35 and dominance and dominance × dominance in G. cot 20 × AHC-37 suggested

Table 2: Mean value of seed cotton yield and its component traits in cotton.

Crosses	Generations						S.Em. (±)	C.D. (0.05)	C.V. (%)
	P ₁	P ₂	F ₁	F ₂	B ₁	B ₂			
Days to initiation of flowering									
I	58.00	54.00	53.67	57.00	57.67	57.33	0.89	2.79	2.74
II	60.67	56.33	53.67	56.33	56.00	56.67	0.98	3.07	2.98
III	56.67	61.33	53.00	56.66	56.33	58.00	1.00	3.16	3.05
IV	55.00	56.67	49.67	54.00	54.67	54.67	1.03	3.26	3.31
Days to initiation of boll bursting									
I	103.67	107.00	96.67	103.67	105.67	101.67	1.68	5.30	2.82
II	108.00	103.33	97.67	102.33	102.67	102.33	1.57	4.96	2.66
III	102.33	109.67	96.67	103.00	101.33	102.00	1.58	5.00	2.68
IV	105.67	101.00	97.33	105.00	106.67	108.00	1.40	4.40	2.33
Plant height (cm)									
I	164.67	158.00	179.00	179.35	181.67	171.17	3.03	9.56	3.05
II	160.67	169.67	201.07	177.00	185.67	179.17	3.68	11.60	3.57
III	160.33	141.67	155.00	171.08	162.17	146.33	2.88	9.06	3.19
IV	187.67	151.13	157.67	171.25	172.50	155.33	3.46	10.90	3.61
Number of monopodia per plant									
I	5.00	3.73	3.93	3.50	2.83	3.40	0.17	0.54	7.99
II	4.33	2.67	1.87	3.80	3.77	3.67	0.20	0.64	10.54
III	4.47	5.53	3.73	3.37	3.60	3.87	0.16	0.49	6.56
IV	3.53	2.13	4.33	3.32	2.57	3.43	0.17	0.54	9.21
Number of sympodia per plant									
I	22.33	24.60	27.33	25.35	25.87	27.47	0.64	2.00	4.31
II	18.47	24.73	30.40	25.30	25.90	25.10	0.71	2.24	4.92
III	18.13	22.53	24.53	24.78	24.17	24.73	0.63	1.98	4.71
IV	21.47	28.07	29.20	24.47	24.17	27.37	0.62	1.96	4.18
Number of bolls per plant									
I	43.80	39.40	57.60	50.25	45.67	52.17	1.24	3.92	4.48
II	44.33	55.27	60.27	52.57	56.17	56.33	1.39	4.38	4.44
III	51.13	46.33	55.27	49.32	50.83	52.47	1.37	4.33	4.68
IV	54.20	60.40	57.27	48.97	50.27	43.83	1.41	4.45	4.66
Boll weight (g)									
I	4.94	5.36	5.95	4.84	5.16	5.64	0.17	0.54	5.56
II	5.26	4.55	6.26	5.13	5.42	5.16	0.13	0.42	4.34
III	5.36	5.54	5.95	5.06	5.61	5.22	0.15	0.46	4.65
IV	4.61	3.79	5.35	5.44	4.72	4.56	0.17	0.55	6.35
Seed index (g)									
I	9.07	10.00	10.53	8.25	9.50	8.70	0.45	1.41	8.27
II	8.40	9.67	10.27	8.75	9.27	8.37	0.22	0.68	4.10
III	9.07	8.47	9.67	9.15	9.33	8.70	0.20	0.62	3.79
IV	8.00	8.80	9.53	8.50	7.67	7.77	0.38	1.21	7.94
Lint index (g)									
I	5.61	6.10	5.08	4.89	5.21	4.37	0.24	0.76	8.01
II	5.12	6.24	6.66	5.13	4.58	4.42	0.19	0.59	6.01
III	5.81	4.63	5.91	5.27	4.93	5.21	0.18	0.57	5.96
IV	5.18	5.59	6.37	5.01	3.97	3.67	0.24	0.75	8.35
Lint yield per plant (g)									
I	100.27	59.53	104.13	98.80	93.20	103.27	6.13	19.31	11.39
II	98.00	108.47	134.27	99.88	98.47	99.37	2.51	7.92	4.09
III	113.33	86.00	121.40	97.03	103.57	108.87	5.81	18.30	9.58
IV	92.60	104.07	117.27	104.27	87.53	81.00	4.12	12.98	7.30
Seed cotton yield per plant (g)									
I	262.27	157.13	318.33	265.67	263.03	308.40	14.39	45.35	9.50
II	258.33	276.27	341.47	271.03	298.27	289.17	10.46	32.96	6.27
III	290.53	243.40	319.87	266.17	297.37	293.67	14.56	45.87	8.84
IV	235.60	267.80	292.13	281.20	256.63	252.80	10.84	34.17	7.10

hybridization followed by selection for this trait while in GSHV-206 × AHC-36 and AHC-29 × AHC-42 had preponderance of epistatic effects which indicated population improvement approaches would be more suitable. Preponderance of non-additive gene effect for this trait was also observed by Uday and Patil (2020), Gnanasekaran and Thiyagu (2021), Kanasagra *et al.* (2022) and Vadodariya *et al.*, (2022), while role of additive and non-additive gene actions reported by Komal *et al.*, (2014) and Chakholoma *et al.*, (2022).

For number of sympodia per plant, scaling test B and D observed significant with all type of gene action except additive × dominance in G. cot 20 × AHC-37 with duplicate type of gene action. Scale A and B found significant with higher magnitude of dominance gene effects for GSHV-206 × AHC-36. Cross AHC-33 × AHC-35 had significant effects of A, B and C with significant epistatic effects additive × dominance and dominance × dominance. All type of scales, A, B, C and D observed significant with additive, dominance and additive × additive gene effects with greater magnitude of dominance gene effects. Biparental mating or recurrent selection would be more suitable for G. cot 20 × AHC-37 and AHC-33 × AHC-35 while hybridization suggested in cross GSHV-206 × AHC-36 and AHC-29 × AHC-42 for this trait improvement. Gohil *et al.*, (2020), Uday and Patil (2020) and Kanasagra *et al.*, (2022) also noted a predominance of non-additive gene effects for this trait, while Govanakoppa and Khadi (2023) and Shubhashini *et al.*, (2023) reported the involvement of both additive and non-additive gene effects.

For number of bolls per plant, A and B scale observed significant and major gene effects additive and dominance with epistatic effects of additive × dominance in G. cot 20 × AHC-37. In GSHV-206 × AHC-36, scale A, C and D found significant with dominance and all type of epistatic effects with preponderance of dominance gene effects. Duplicate type of gene action observed in cross GSHV-206 × AHC-36 due to opposite sign of dominance and dominance × dominance interaction. In scaling test, scale A, C and D with dominance, additive × additive and additive × dominance found significant in cross AHC-33 × AHC-35. In cross AHC-29 × AHC-42, all scale observed significant except D with significant effects of additive, additive × dominance and dominance × dominance. Higher value of dominance gene effects found in G. cot 20 × AHC-37, GSHV-206 × AHC-36 and AHC-33 × AHC-35 while in cross AHC-29 × AHC-42 had significant value of additive and epistatic effects which suggest population improvement for accumulating desirable genes or breaking undesirable linkage for number of bolls per plant. Larger magnitude of non-

Table 3: Estimation of simple scaling test and gene effects for various characters in cotton.

Days to initiation of flowering				
	Cross I	Cross II	Cross III	Cross IV
A	3.13**	-2.07	2.73**	4.67**
B	7.20**	3.60**	1.67	3.33*
C	8.20**	0.13	2.00	5.4*
D	-1.07	-0.70	-1.20	-1.30
χ^2	27.74**	15.42**	21.56**	45.92**
<i>m</i>	56.97**	56.13**	56.50**	54.05**
<i>d</i>	0.01	-0.63	-1.80**	-0.07
<i>h</i>	-0.1	-3.6	-3.33	-3.73
<i>i</i>	2.13	1.4	2.4	2.6
<i>j</i>	-2.03**	-2.83**	0.53	0.67
<i>l</i>	-12.47**	-2.93	-6.80*	-10.60**
Days to initiation of boll bursting				
A	11.00**	-0.40	4.47**	10.20**
B	-0.33	4.20*	-2.00	17.73**
C	10.33**	3.07	7.47*	18.40**
D	-0.17	-0.37	2.50	-4.77**
χ^2	43.67**	16.54**	24.67**	68.84**
<i>m</i>	103.62**	102.33**	103.08**	104.97**
<i>d</i>	4.00**	0.23	-0.47	-1.5
<i>h</i>	-8.40*	-7.33**	-14.50**	3.47
<i>i</i>	0.33	0.73	-5	9.53**
<i>j</i>	5.67**	-2.30*	3.23**	-3.77**
<i>l</i>	-11.00*	-4.53	2.53	-37.47**
Plant height				
A	19.67**	9.60	9.00*	-0.33
B	5.33	-12.40**	-4.00	1.87
C	36.73**	-24.47**	72.33**	30.87**
D	5.87	-10.83**	33.67**	14.67**
χ^2	48.88**	24.62**	86.63**	14.23**
<i>m</i>	179.35**	177.00**	171.08**	171.25**
<i>d</i>	10.50**	6.50*	15.83**	17.17**
<i>h</i>	5.93	57.57**	-63.33**	-41.07**
<i>i</i>	-11.73	21.67**	-67.33**	-29.33**
<i>j</i>	7.17**	11**	6.50**	-1.1
<i>l</i>	-13.27	-18.87	62.33**	27.80*
Number of monopodia per plant				
A	-3.27**	1.33*	-1.00	-2.73**
B	-0.87	2.80**	-1.53**	0.40
C	-2.60**	4.47**	-4.00**	-1.07
D	0.77	0.17	-0.73	0.63
χ^2	63.36**	47.96**	23.12**	44.37**
<i>m</i>	3.50**	3.80**	3.37**	3.32**
<i>d</i>	-0.57*	0.1	-0.27	-0.87**
<i>h</i>	-1.97*	-1.97	0.20*	0.23
<i>i</i>	-1.53	-0.33	1.47	-1.27
<i>j</i>	-1.20**	-0.73*	0.27	-1.57**
<i>l</i>	5.67**	-3.80*	1.07	3.60*

Continue 3

Number of sympodia per plant				
A	2.07	2.93*	5.67**	-2.33*
B	3.00**	-4.93**	2.40*	-2.53*
C	-0.2	-2.8	9.40**	-10.07**
D	-2.63**	-0.4	0.67	-2.60**
χ^2	17.44**	28.44**	43.83**	46.38**
<i>m</i>	25.35**	25.30**	24.78**	24.47**
<i>d</i>	-1.60**	0.8	-0.57	-3.20**
<i>h</i>	9.13**	9.60**	2.87	9.63**
<i>i</i>	5.27**	0.8	-1.33	5.20**
<i>j</i>	-0.47	3.93**	1.63*	0.1
<i>l</i>	-10.33**	1.2	-6.73*	-0.33
Number of bolls per plant				
A	-10.07**	7.73**	-4.73*	-10.93**
B	7.33**	-2.87	3.33	-30.00**
C	2.6	-9.87**	-10.73**	-33.27**
D	2.67	-7.37**	-4.67*	3.83
χ^2	75.53**	25.60**	19.60**	352.87**
<i>m</i>	50.25**	52.57**	49.32**	48.97**
<i>d</i>	-6.50**	-0.17	-1.63	6.43**
<i>h</i>	10.67**	25.20**	15.87**	-7.7
<i>i</i>	-5.33	14.73**	9.33*	-7.67
<i>j</i>	-8.70**	5.30**	-4.03**	9.53**
<i>l</i>	8.07	-19.60**	-7.93	48.60**
Boll weight				
A	-0.56*	-0.68**	-0.09	-0.52*
B	-0.02	-0.48*	-1.05**	-0.03
C	-2.84**	-1.78**	-2.58**	2.64**
D	-1.13**	-0.31	-0.72**	1.60**
χ^2	59.68**	26.87**	51.33**	66.40**
<i>m</i>	4.84**	5.13**	5.06**	5.44**
<i>d</i>	-0.48**	0.25	0.39**	0.16
<i>h</i>	3.06**	1.98**	1.94**	-2.04**
<i>i</i>	2.26**	0.62	1.43**	-3.2**
<i>j</i>	-0.27	-0.1	0.48**	-0.25
<i>l</i>	-1.68*	0.53	-0.29	3.75**
Seed index				
A	-0.6	-0.13	-0.07	-2.20**
B	-3.13**	-3.20**	-0.73	-2.80**
C	-7.13**	-3.60**	-0.27	-1.87
D	-1.70**	-0.13	0.27	1.57**
χ^2	50.20**	37.35**	0.95	34.85**
<i>m</i>	8.25**	8.75**	8.69**	8.50**
<i>d</i>	0.80*	0.90*	0.32*	-0.1
<i>h</i>	4.40**	1.5	0.89	-2
<i>i</i>	3.40**	0.27	-	-3.13**
<i>j</i>	1.27**	1.53**	-	0.3
<i>l</i>	0.33	3.07	-	8.13**

Continue 3

Lint index				
A	-0.28	-2.63**	-1.86**	-3.61**
B	-2.44**	-4.07**	-0.13	-4.63**
C	-2.34**	-4.18**	-1.19	-3.47**
D	0.19	1.26**	0.4	2.39**
χ^2	66.16**	149.00**	32.61**	300.38**
<i>m</i>	4.89**	5.13**	5.27**	5.01**
<i>d</i>	0.83**	0.16	-0.28	0.31
<i>h</i>	-1.16	-1.54*	-0.11	-3.78**
<i>i</i>	-0.39	-2.52**	-0.8	-4.77**
<i>j</i>	1.08**	0.72**	-0.87**	0.51**
<i>l</i>	3.11**	9.21**	2.79**	13.02**
Lint yield per plant				
A	-18.00**	-35.33**	-27.60**	-34.80**
B	42.87**	-44.00**	10.33**	-59.33**
C	27.13**	-75.47**	-54.00**	-14.13
D	1.13	1.93	-18.37**	40.00**
χ^2	119.22**	270.08**	75.30**	216.04**
<i>m</i>	98.8**	99.88**	97.03**	104.27**
<i>d</i>	-10.07**	-0.9	-5.3**	6.53**
<i>h</i>	21.97*	27.17**	58.47**	-61.07**
<i>i</i>	-2.27	-3.87	36.73**	-80.00**
<i>j</i>	-30.43**	4.33	-18.97**	12.27**
<i>l</i>	-22.6	83.20**	-19.47	174.13**
Seed cotton yield per plant				
A	-54.53**	-3.27	-15.67	-14.47
B	141.33**	-39.4**	24.07**	-54.33**
C	6.6	-133.4**	-109.00**	37.13
D	-40.10**	-45.37**	-58.70**	52.97**
χ^2	139.86**	54.41**	56.59**	39.89**
<i>m</i>	265.67**	271.03**	266.17**	281.20**
<i>d</i>	-45.37**	9.1	3.7	3.83
<i>h</i>	188.83**	164.90**	170.30**	-65.50**
<i>i</i>	80.20**	90.73**	117.40**	-105.93**
<i>j</i>	-97.93**	18.07*	-19.87*	19.93**
<i>l</i>	-167.00**	-48.07	-125.80**	174.73**
* and ** indicate significance at 5 % and 1% levels of significance, respectively				

additive gene effects also found in Komal *et al.*, (2014), Uday and Patil (2020), Gnanasekaran and Thiyagu (2021), vaid *et al.*, (2022), Chakholoma *et al.*, (2022), Kansagra *et al.*, (2022) which were accordance to the findings.

For boll weight, scale A, C and D along with all type of gene action observed significant with duplicate gene interaction for G. cot 20 × AHC-37. In cross GSHV-206 × AHC-36, scale A, B and C found significant with only dominance gene effects which suggest presence of other higher order interaction. Scaling test B, C and D observed significant with all type of gene interaction for cross AHC-33 × AHC-35 which indicated higher magnitude of dominance gene effects with epistatic effects. In AHC-29 × AHC-42, scale A, C and D observed significant

with dominance, additive $\times$ additive and dominance $\times$ dominance gene effects with duplicate type of gene interaction. For improvement of this trait, hybridization followed by selection found more convenient in G. cot 20 $\times$ AHC-37, GSHV-206 $\times$ AHC-36 and AHC-33 $\times$ AHC-35. Epistatic effects also observed significant which suggested biparental mating or reciprocal selection for accumulation of desirable genes. These results align with the findings of Komal *et al.*, (2014), Govanakoppa and Khadi (2023) and Shubhashini *et al.*, (2023) who reported the involvement of both additive and non-additive gene effects in the expression of this trait. Whereas, Gohil *et al.*, (2020), Vaid *et al.*, (2022) and Chakholoma *et al.*, (2022) identified non-additive gene action as the key factor in the inheritance of this trait.

Scaling test B, C and D along with all gene action except dominance $\times$ dominance observed significant for seed index in cross G. cot 20 $\times$ AHC-37 with higher value of dominance gene effect. Scaling test B and C with additive and additive $\times$ dominance interaction found in GSHV-206 $\times$ AHC-36 with higher magnitude of epistatic effects. In cross AHC-33 $\times$ AHC-35, all scale found non-significant along with non-significance of $\div^2$ which indicate absence of non-allelic interactions so only three parameter model was fit in which higher magnitude of additive gene action. All scale except C found significance along with additive $\times$ additive and dominance $\times$ dominance gene interaction in cross AHC-29 $\times$ AHC-42. Direct selection would be beneficial in cross AHC-33 $\times$ AHC-35 while population improvement for gathering desirable genes and break down linkage in remaining three crosses. The findings of the present study align with those of Giri *et al.*, (2020) who identified the influence of both additive and non-additive gene actions on the expression of this trait. Additionally, the predominance of additive gene effects for this trait was also noted by Rajamani *et al.*, (2015), Vadodariya *et al.*, (2022) and Govanakoppa and Khadi (2023).

For lint index, B and C scale found significance with additive, additive $\times$ dominance and dominance $\times$ dominance gene effects in G. cot 20 $\times$ AHC-37. All type of scaling test with gene effects of dominance, additive $\times$ additive, additive $\times$ dominance and dominance $\times$ dominance in GSHV-206 $\times$ AHC-36 as well as AHC-29 $\times$ AHC-42 with duplicate type interaction due to opposite sign of dominance and dominance $\times$ dominance. In AHC-33 $\times$ AHC-35, only A scale observed significance with additive $\times$ dominance and dominance $\times$ dominance gene interaction. Epistatic interaction was high in all crosses for this character which suggest population improvement strategy for improvement of lint index. The results of the present study align closely with those of Chakholoma *et*

al., (2022) and Govanakoppa and Khadi (2023), who all observed both additive and non-additive gene effects influencing this trait.

In cross G. cot 20 $\times$ AHC-37, scale A, B and C observed significant with additive, dominance and additive $\times$ dominance gene effects for lint yield per plant whereas in GSHV-206 $\times$ AHC-36 also exhibited significance of A, B and C scale with dominance and dominance $\times$ dominance gene interaction with similar sign which indicate complementary gene action. All scales observed significant with all type of gene action except dominance $\times$ dominance in cross AHC-33 $\times$ AHC-35 while scaling test A, B and D found significant with significant effects of all type of gene action in cross AHC-29 $\times$ AHC-42. Duplicate type of gene action observed in that cross AHC-29 $\times$ AHC-42 which indicate decrease variability in the segregating generations and hinder the pace of progress through selection. High magnitude of dominance and dominance $\times$ dominance with significant effects suggests selection in later generation in cross GSHV-206 $\times$ AHC-36 while in other crosses additive and dominance gene effects observed significant with higher magnitude of epistatic effects which suggest population improvement for breakdown undesirable linkage. Govanakoppa and Khadi (2023) also reported same result as both additive and non-additive gene effect affecting the trait.

For seed cotton yield per plant, scale A, B and D observed significant along with all type of gene interaction for G. cot 20 $\times$ AHC-37. In cross GSHV-206 $\times$ AHC-36, scale B, C and D exhibited significance effects with dominance, additive $\times$ additive and additive $\times$ dominance gene effects. In AHC-33 $\times$ AHC-35 also scale B, C and D found significant with dominance, additive $\times$ additive, additive $\times$ dominance and dominance $\times$ dominance gene effects. In AHC-29 $\times$ AHC-42, scale B and D found significant with all gene actions except additive type. Duplicate type of gene action observed in G. cot 20 $\times$ AHC-37, AHC-33 $\times$ AHC-35 and AHC-29 $\times$ AHC-42 which indicate suppress variability in F_2 and subsequent generations for this trait. All crosses expressed significance effects of dominance gene effects with epistatic effects with higher magnitude of dominance which suggested hybridization would be beneficial for improvement of seed cotton yield per plant. The results align with Shubhashini *et al.*, (2023), who identified both additive and non-additive gene effects in this trait, whereas Komal *et al.*, (2014), Srinivas and Bhadraru (2015), Pandiyan *et al.*, (2019), Gnanasekaran and Thiyagu (2021), Vaid *et al.*, (2022), Chakholoma *et al.*, (2022), Kanasagra *et al.*, (2022), Govanakoppa and Khadi (2023) and Madugula *et al.*, (2023) observed non-additive gene effects.

Conclusion

For seed cotton yield per plant, most of the scaling tests were significant, indicating presence of epistasis and the insufficiency of the additive-dominance model as well as the role of non-allelic gene interactions. Both additive and non-additive gene interactions were found to be significant for most of the study traits. This investigation suggested that non-allelic gene interactions along with additive and dominant gene actions played a significant role in the inheritance of various traits in cotton. When both additive and non-additive gene effects are involved in trait inheritance, it is recommended to use parental mating followed by population improvement breeding methods, including conventional selection methods for desirable recombinants. Inter-mating can develop elite homozygous recombinants with desirable quality and high yielding ability. Most traits exhibited duplicate type epistasis, making it difficult to stabilize genotypes because the effect of one parameter would be nullified by the negative effect of another. In such cases, selection in later generations would be beneficial.

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