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Inheritance pattern of yield and lint quality traits in upland cotton (*G. hirsutum* L.)

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Abstract

Present study was conducted during 2013-14 at University of Agricultural, Faisalabad, Pakistan to Fig. out gene action and heritability of lint yield and quality traits in upland cotton. Parental genotypes viz COKER-3113, CRIS-9, BT-122 and CRS-456 were crossed following 4×4 diallelmating design. Genotypes showed significant variations for plant height, monopodia plant^{-1}, sympodia plant^{-1}, bolls sympodia^{-1}, bolls plant^{-1}, seed cotton yield plant^{-1}, fiber length, fiber fineness and fiber strength. On an average, the combinations showed boost over parents for plant height (10.5%), sympodia plant^{-1} (7.04%), bolls sympodia^{-1} (3.73%)and seed cotton yield plant^{-1} (24.07%). Broad sense heritability coupled with higher response to selection was plant height (0.95 and 17.85 cm), monopodia plant-^{1}(0.75 and 0.39), sympodia plant-^{1}(0.82 and 3.46), bolls plant-^{1}(0.89 and 8.95), boll weight (0.93 and 4.43g), yield plant-^{1}(0.72 and 39.00 g), fiber fineness (0.79 and 0.33), fiber length (0.87 and 0.39), fiber uniformity (0.78 and 0.34), fiber strength (0.67and 0.29) and fiber elongation (0.89 and 0.42).Parents CRIS-9 and COKER-3113 performed better in their specific cross combinations and showed significant mean performance. The crosses CRIS-9 × COKER-3113, CRS-456 × CRIS-9 and CRS-456 × CRS-456 showed genetic potential for almost all the traits. Findings suggested that the above three crosses should be used in cotton breeding programmes and selection may be done in late segregating generations for further improvement in lint yield and quality.

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Introduction

Cotton is grown in more than 80 countries of the world and adds about 2.5 % to the world's total cultivated area. Major Cotton producing countries of the world are China, USA, Brazil, India, Uzbekistan and Pakistan. In cotton growing world, Pakistan stands fourth largest producer and third largest consumer of raw cotton (Govt. of Pakistan, 2012-13). Cotton is widely cultivated in arid and semi-arid areas of Punjab and Sindh contributing 80% and 18% area respectively. It contributes 7.0 % in value addition of agriculture and 1.5 % in GDP of Pakistan. More than 1200 ginning factories and 370 textile mills are working in Pakistan that depends upon cotton fiber (Ali *et al.*, 2013).Per acre yield of cotton in Pakistan is below than average production due to biotic and abiotic factors (Panniet *et al.*, 2012). Heritability estimates in seed cotton yield, number of bolls per sympodial branches and number of monopodial were higher that suggested cultivars had better genetic potential for improvement; these could be used for hybrid cotton production (Batool and Khan, 2012).

Imran *et al.* (2012) found non additive type of gene action in the inheritance of bolls per plant, boll size, seed cotton yield, lint percentage, lint per seed, seeds per boll, seed density while additive gene action was involved in the inheritance of seed volume. Khan and Qasim (2012) showed that additive type gene action was present in yield attributes except monopodia per plant that showed over dominance. Iqbal *et al.* (2013) showed lint percentage and average boll weight had additive gene action, while other yield traits showed partial dominance with additive effects. Kumar *et al.* (2013) showed number of sympodial branches, bundle strength and yield of single plant is controlled by non-additive gene action.Ng and Smith (2013) found additive gene action in fiber elongation. To increase the average yield we have to utilize the area that has not already been cultivated as well as per acre yield.

So, it is noteworthy for plant breeders to develop tolerant varieties that perform better in stressed as well as normal environment. Selection in cotton may be useful in F_2 and F_3 generations on the basis of plant height, boll weight, bolls per plant, seed cotton yield and seed index (Soomro *et al.*, 2010) because additive gene action was involved in seed cotton yield, bolls per plant and plant height whereas seed index and boll weight were under the control of non-additive type of gene action. Ali *et al.* (2011) showed over dominance in number of monopodial and sympodial branches, boll weight and number of bolls per plant. Bolek *et al.* (2011) studied heterosis and combining ability in fiber elongation, fiber uniformity, fiber fineness, fiber strength, fiber length, short fiber index and spinning consistency index. Additive type of gene action was found to be present in all characters. Sarwar *et al.* (2011) concluded that number of bolls, boll weight, monopodial branches, plant height, seed cotton yield and lint percentage were controlled by additive gene action with partial dominance whereas over dominance in fiber fineness, staple length, lint index, seed index and seeds per boll. To achieve the objective knowledge about gene action is very necessary for the selection of parents for hybridization (Patil *et al.,* 2011). The information collected from the study will provide better understanding for future breeding programmes.

Material and methods

The present investigations were carried out in the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad on upland cotton. The climatic data were obtained from Agromet Bullet in Agriculture Meteorology Cell, Department of Crop Physiology, University of Agriculture Faisalabad, Pakistan. Four genotypes of upland cotton namely COKER-3113, CRIS-9, BT-122 and CRS-456 were grown in earthen pots with 30 cm height and 35 cm upper diameter. Nine kg soil was filled in these pots. Soil analyses were done before filling in the pots. The soil pH (8.4), EC (1.2 dS/m), organic matter (1.42%), saturation percentage (31%), phosphorous (28.9 ppm) and potassium (135 ppm) were noted. Seeds were soaked for eight hours before sowing. Four seeds were sown 2 cm deep in each pot and later on at two true leaf stage, the plants were thinned.

The parents were grown under day length of 14 hours, natural light (PAR raged 1400-1600 µmol m^{-2} s^{-1} at noon) and 65-80 % humidity, under optimum temperature throughout the growing period. Water was applied to the earthen pots at the rate of 1400 mL per pot daily during peak flowering period and on alternate days during off-peak flowering period. The period from 50 to 70 days after sowing was considered as peak flowering period.

At peak flowering stage these varieties were crossed in diallel fashion. At maturity, seed cotton of six direct, six indirect hybrids (reciprocal crosses under diallel fashion, keeping male as female under crossing) and four parents were collected. This experiment was terminated after 120 days, and thecrosses were ginned and seeds collected separately.

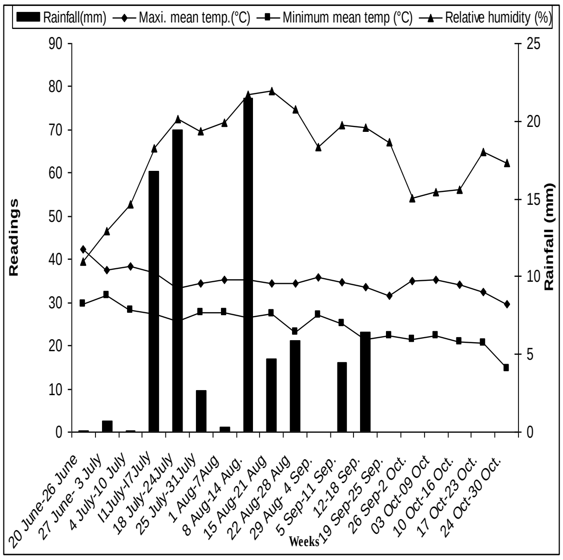

Fig. 1. Climatic conditions during cotton season 2013.

The seeds of 12 F_0crosses and their parents were planted in the field during May 2013-14 in triplicate randomized complete block design.

In each replication, there were 10 plant spaced 30 cm within row and 75 cm between the rows. At the maturity eight middle plants were measured for plant height, number of bolls, boll weight leaf area index, yield per plant and ginning percentage, fiber length, fiber fineness and fiber strength.

Statistical analysis

The data were analyzed by analysis of variance (ANOVA) following Steel *et al.* (1997) to establish the level of significance of differences in plant traits. The characteristics which showed significant genotypic differences were further analyzed genetically following Hayman (1954a, 1954b).

To test suitability of data for additive-dominance model a scaling test i.e. Joint Regression Analysis was carried out. According to Hayman (1954a) the regression co-efficient must deviate significantly from zero but not from unity for the data to be adequate for additive-dominance model. The characters, qualifying for both the tests, were fully adequate for additive-dominance model.

Estimation of Genetic components

Among the genetic components of variation (D, F, H_1, H_2, h^2); the statistic, D was an estimate of additive effects while H_1 and H_2 were variation due to dominance effects of genes. F provided an estimate of relative frequency of dominant to recessive alleles in parental lines and will be positive when the dominant alleles are more frequent than the recessive alleles.

The statistic h^2 provided direction of dominance i.e. positive sign shows dominance of genes with increasing effect at most of loci and negative sign shows dominance of genes with decreasing effect.

These components were used to compute further information as (H_1/D) 0.5, mean degree of dominance; $H_2/4H_1$, proportion of genes with positive and negative effects in parents and equation in brackets $[(4DH_1)\ 0.5+ F]/[(4DH_1)0.5\text{-}F]$ provides the proportion of dominant and recessive genes in parents. Narrow sense heritability (h^2n.s.) and broad sense heritability (h^2b.s.) were also based on these parameters that reflected the amount of additive and total genetic variation in parents.

Table 1. Simple additive-dominance model *The data fit for genetic analysis b. value deviate significantly from zero but not from unity.

Character	Regression Coefficient*	Adequacy of data
Plant height	b = 0.89± 0.24	Fit for simple additive-dominance model
Monopodia plant^{-1}	b = 0.85± 0.13	Fit for simple additive-dominance model
Sympodia plant^{-1}	b = 0.98± 0.11	Fit for simple additive-dominance model
Bolls plant^{-1}	b = 0.86± 0.16	Fit for simple additive-dominance model
Seed cotton yield	b = 0.99± 0.22	Fit for simple additive-dominance model
Boll weight	b= 0.98 ± 0.12	Fit for simple additive-dominance model
Fiber uniformity	b = 0.94± 0.11	Fit for simple additive-dominance model
Fiber length	b = 0.98± 0.16	Fit for simple additive-dominance model
Fiber elongation	b = 0.88± 0.19	Fit for simple additive-dominance model
Fiber fineness	b = 0.97± 0.12	Fit for simple additive-dominance model
Fiber strength	b = 0.85± 0.25	Fit for simple additive-dominance model

Results and discussion

Results of the joint regression analysis suggested that the data for all characters were found to be adequate for simple additive-dominance model.

Estimation of components of variation for all components are presented in the table 2. The results showed that D was positive ($P \le 0.05$) for all seed cotton yield components and lint quality traits. The greater value of D than those of H_1 and H_2 suggested that additive gene affect was predominant in plant height, boll weight, yield per plant, fiber length, fiber fineness, fiber uniformity and fiber elongation.

The degree of dominance $\sqrt{H_1/D}$ was less than unity, thus showing partial dominance of genes.

The genes were unequally distributed for number of bolls, plant height, boll weight and yield per plant as the magnitude of $H_1$was not equal to H_2. The positive value of F supported by high ratio of $[\sqrt{4DH_1}+F] / [\sqrt{4DH_1}-F]$ forall the characters showed that the dominant genes were more than recessive in the parents.

Mean square values presented in table 3 showed significant genotypic differences for almost all the characters except boll weight and fiber fineness. According to analysis of variance (Table 4), the mean values of F_1diallel hybrids and their six parents showed significant differences for plant height, monopodia per plant, sympodia per plant, bolls per plant, seed cotton yield per plant and fiber characteristics. Plant height varied from 74.79 to 109.8 cm among the parents, while 79.60 to 139.80 cm in their F_1s.

The cross COKER-3113 × COKER-3113 showed highest plant height (139.80 cm) however, it was found statistically at par with 10 other F_1 hybrids ranged from 106.00 to 137.79 cm. CRIS-9 revealed minimum plant height (69.84 cm) and was found at par also with three parents and 6 F_1 hybrids ranged from 79.65 to 98.71 cm.

Table 2. Components of Variation

Components	Plant Height	Monopodia plant^{-1}	Sympodia plant^{-1}	Bolls plant^{-1}	Boll Weight	Yield plant^{-1}	Fiber Length	Fiber Fineness	Fiber Uniformity	Fiber Elongation
D	11.216	0.181	1.83	3.03	8.80	10.14	1.75	0.15	0.24	0.62
H_1	-124.07	0.132	0.06	2.65	-1.71	-2.81	-0.64	-0.01	-0.66	-0.19
H_2	-18.953	0.019	6.34	0.10	-1.56	-2.14	-0.51	-5.92	-0.51	-0.15
F	-6.729	-4.007	0.18	7.66	9.09	-0.36	0.23	-2.61	-0.31	-0.16
$\sqrt{H_1/D}$	0.987	0.342	0.19	0.11	0.44	0.53	0.60	0.29	0.65	0.55
$H_2/4H_1$	0.197	0.225	0.24	0.11	0.23	0.19	0.20	0.11	0.19	0.20
$[\sqrt{4DH_1} + F] / [\sqrt{4DH_1}-F$	0.66	0.512	1.69	1.26	1.26	0.93	1.25	0.55	0.44	0.62

D = additive Variance
H_1 = dominance Variance
H_2 = proportion of positive and negative genes in the parents
F = relative frequency of dominant and recessive alleles in the parents
$\sqrt{H_1/D}$ = degree of dominance
$H_2/4H_1$ = proportion of genes with positive and negative effects in parents
$[\sqrt{4DH_1} + F] / [\sqrt{4DH_1}-F]$ = proportion of dominant and recessive genes in the parents

Table 3. Mean squares of different characters in 4×4 diallel.

Parameters	Genotypes	Error
Plant height	95.18 **	32.13
Monopodia plant^{-1}	0.33**	0.03
dia plant^{-1}	2.31**	0.08
Bolls plant^{-1}	5.42**	0.99
Boll weight	0.13^{NS}	0.04
Seed cotton yield plant^{-1}	17.99**	5.3
Fiber fineness	0.29^{NS}	0.04
Fiber length	2.46**	0.85
Fiber uniformity	1.98**	0.78
Fiber elongation	1.56**	0.33

** Significant at $p \leq 0.01$

Table 4. Mean values of parental genotypes and their crosses

Genotypes	Monopodia plant^{-1}	Sympodia plant^{-1}	Boll weight	Bolls plant^{-1}	SCY
Coker-3113	0.62	10.99	4.47	11.56	49.65
Coker-3113 × Coker-3113	0.69	11.09	4.71	13.12	49.62
Coker-3113 × CRIS-9	0.46	15.34	5.39	13.91	51.07
Coker-3113 × BT-122	0.47	16.9	4.65	13.89	49.97
Coker-3113 × CRS-456	1.18	18.22	5.97	14.28	54.09
CRIS-9	0.29	16.13	4.71	12.67	50.22
CRIS-9 × Coker-3113	1.49	21.09	4.69	15.05	58.80
CRIS-9 × CRIS-9	1.42	19.07	5.33	13.99	51.86
CRIS-9 × BT-122	0.56	12.87	5.16	14.78	59.12
CRIS-9 × CRS-456	0.19	18.91	5.56	15.01	68.32
BT-122	0.47	15.19	5.43	11.05	49.87
BT-122 × Coker-3113	0.82	17.98	4.96	13.73	50.09
BT-122 × CRIS-9	0.31	14.69	4.42	14.51	60.05
BT-122 × BT-122	0.47	15.79	4.25	14.87	61.89
BT-122 × CRS-456	1.29	22.99	4.92	14.53	61.02
CRS-456	0.99	17.61	5.02	19.82	78.16
CRS-456 × CRS-456	0.87	23.56	4.87	25.21	97.08
CRS-456 × Coker-3113	0.67	15.71	5.97	19.78	79.07
CRS-456 × CRIS-9	0.32	22.09	4.83	14.21	52.66
CRS-456 × BT-122	1.19	16.92	5.47	14.07	63.51

Parental genotype CRS-456 showed highest seed cotton yield that was nearly equal to a cross CRS-456× COKER- 3113 (79.07) and was higher than all the parents and crosses except a cross (CRS-456×CRS-456) that showed best performance (97.08) over all the material tested, presented in table 4. Broad sense heritability (bs) and response to selection for said traits were 0.95 and 18.05 cm, respectively (Table 5). The heritability with high response to selection indicated the role of genetic variance in the inheritance of plant height. The results are in line with Khan *et al*., (2009). Monopodial branches ranged from 0.41 to 0.99 among the parental genotypes while 0.21 to 1.49 in their F_{1s}. Less number of monopodia was observed in CRIS-9 × CRS-456 (0.19), that was equal with two parental genotypes and 8 F_1s ranged from 0.29 to 0.56. The cross CRIS-9 × COKER-3113 depicted highest monopodia (1.49) and was at par with seven other F_1 genotypes ranged from 1.18 to 1.49. High genetic diversity with enviable decrease in monopodia was also shown in F_1diallel hybrids compared with parents (Khan *et al.*, 1991, 2000; Ahmad *et al.*, 2008). Similarly sympodial branches ranged from 10.99 to 17.61 among the genotypes, while 11.09 to 23.56 in crosses.

Table 5. Heritability and response to selection estimates yield and lint quality traits.

Parameters	Heritability (bs)	RE
Plant height	0.95 **	17.85
Monopodia plant^{-1}	0.75**	0.39
Sympodia plant^{-1}	0.82**	3.46
Bolls plant^{-1}	0.89**	8.95
Boll weight	0.93**	4.43
Yield plant^{-1}	0.72**	39.0
Fiber fineness	0.79**	0.33
Fiber length	0.87**	0.39
Fiber uniformity	0.78**	0.34
Fiber elongation	0.67**	0.29
Fiber strength	0. 89**	0.42

Additive with partial dominance gene action was involved in plant height because regression line intercepts the Wr-axis above the point of origin. (Fig.2). Most of the genes in this trait were additive.

Genotype CRIS-9 contained maximum dominant genes being nearest to the point of origin and BT-122 contained maximum recessive genes being farthest from origin. Same results were observed by Keerio *et al.* (1995), Ahmad *at al.* (2000) and Channa *et al.* (2008). Fig 3 depicts additive with partial dominance type of gene action monopodial branches as the regression line intercepts the Wr-axis above the point of origin. Genotype COKER-3113 contains maximum dominant genes and genotype CRS-456 being away from origin has maximum recessive genes. Similar results were found by Ali and Khan (2007), Abbas *et al.* (2008), Sarwar *et al.* (2011) and Khan *et al.* (2012). Additive with partial dominance type of gene action was involved in the inheritance of sympodia plant^{-1} as the regression line intercepts the Wr-axis above the point of origin. Genotype CRS-456 has maximum dominant genes because it is near the point of origin whereas the genotype COKER-3113 being farthest from point of origin contained maximum recessive genes (Fig. 4). Same results were observed by Keerio *et al.* (1995), Ahmad *et al.* (2000), Kiani *et al.* (2008), Ali *et al.* (2011), Batool and Khan (2012).

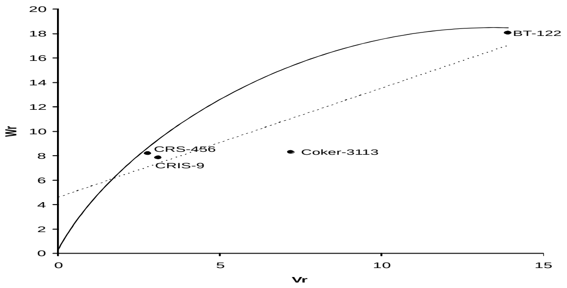

Fig. 2. Wr./Vr. graph for plant height

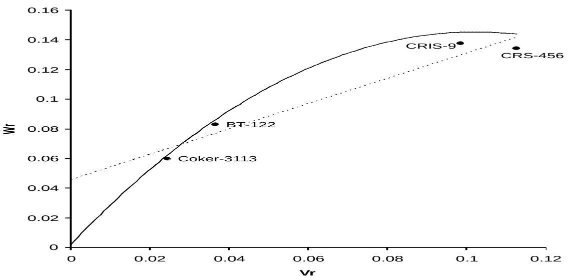

Fig.3. Wr./Vr. graph monopodia plant^{-1}

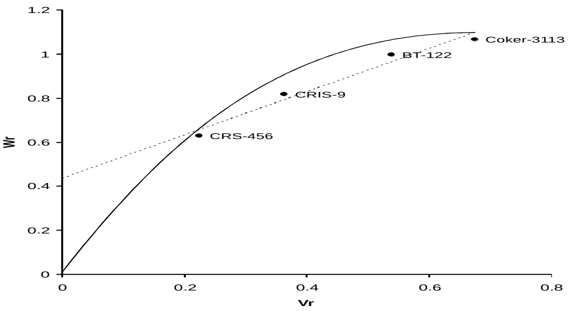

Fig. 4. Wr./Vr. graph for sympodia plant^{-1}

Partial dominance type of gene action was involved in boll per plant because regression line intercepts the Wr-axis above the point of origin. Genotype CRIS-9 contains dominant genes and the genotype BT-122 has recessive genes as it is farther from origin (Fig. 5). Similar type of gene action was observed by Khan *et al.* (1991), Khan *et al.* (1999), Mukhtar *et al.* (2000), Ahmad *et al.* (2001), Iqbal *et al.* (2003), Sarwar *et al.* (2011) and Khan *et al.* (2012). Fig. 6 shows that partial dominance type of gene action was involved in the inheritance of boll weight because regression line intercepts the Wr-axis above the point of origin. CRS-456 has more dominant genes and the genotype COKER-3113 being farther from point of origin carries more recessive genes. Similar type of gene action was observed by Khan *et al.* (1999), Mukhtar *et al.* (2000), Ahmad *et al.* (2001), Iqbal *et al.* (2003), Azhar and Khan (2005), Sarwar *et al.* (2011) and Khan *et al.* (2012). Presence of partial dominance type of gene action was involved in seed cotton yield because regression line intercepts the Wr-axis above the point of origin. (Fig. 7). Most of the genes in this trait were additive. Similar results were observed by Mushtaque *et al.* (2003), Mehetro *et al.* (2003), Nistor *et al.* (2005), Rauf *et al.* (2006), Campbell *et al.* (2007), Batool and Khan (2012) and Imran *et al.* (2012). Partial dominance was involved in the inheritance of fiber fineness because regression line intercepts the Wr-axis above the point of origin (Fig.8). Most of the genes in this trait were additive. The genotype CRIS-9 had maximum dominant genes because it is placed near the point of origin while genotype BT-122 contained maximum recessive genes because it placed farther from point of origin. Ahmad *et al.* (2003), Mehetre *et al.* (2003), Ali *et al.* (2008) and Sarwar *et al.* (2011) observed similar results.

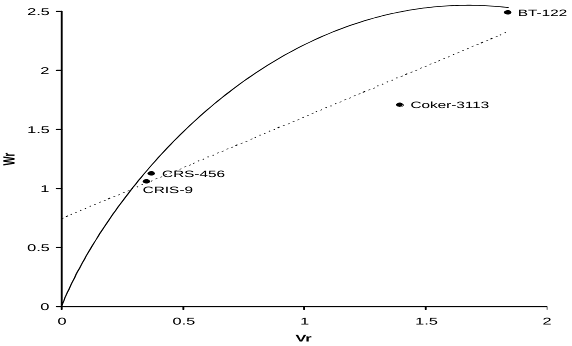

Fig. 5. Wr./Vr. graph for bolls plant^{-1}.

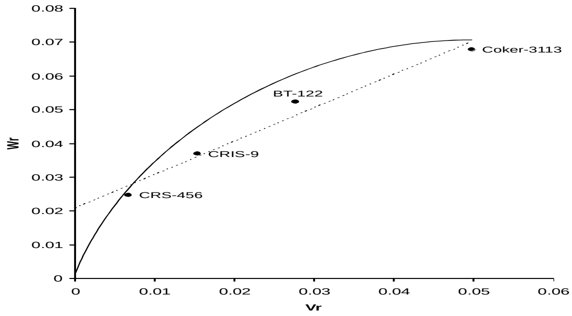

Fig.6. Wr./Vr. graph for boll weight.

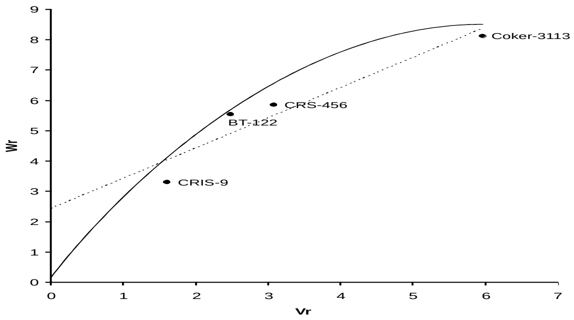

Fig. 7. Wr./Vr. graphseed cotton yield plant^{-1}.

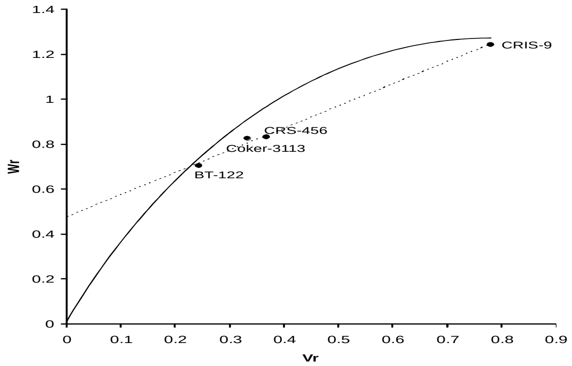

Fig. 8. Wr/Vr graph for fiber length.

Presence of partial dominance gene action is depicted as regression line intercepts the Wr-axis above the point of origin. (Fig. 9). Most of the genes in fiber length were additive.

The genotype BT-122 had maximum dominant genes because it falls near the point of origin while genotype CRIS-9 contains maximum recessive genes due to distance from point of origin. Same results were obtained by Mehetre *et al.* (2003). The opposite results were found by Ali *et al.* (2008), Basal *et al.* (2009) and Bolek *et al.* (2011). Additive with partial dominant genes were found to be involved in the inheritance of fiber uniformity because regression line intercepts the Wr-axis above the point of origin (Fig. 10).

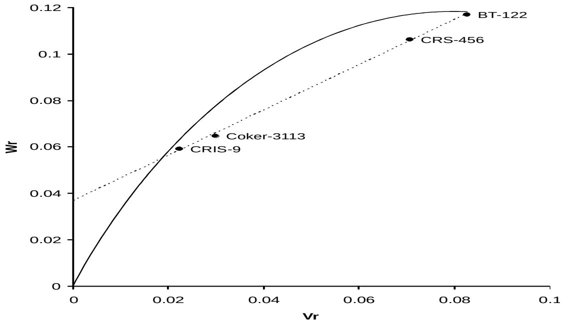

Fig. 9. Wr/Vr graph for fiber fineness.

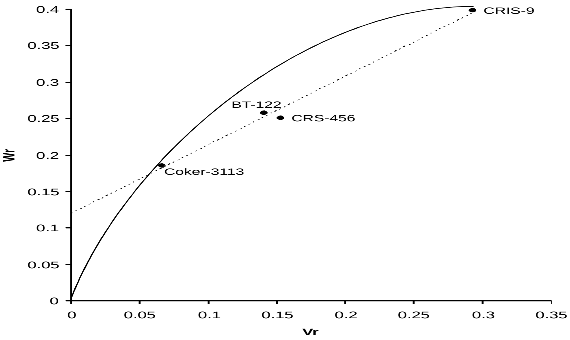

Fig. 10. Wr/Vr graph for fiber uniformity.

Most of the genes in this trait were additive. COKER-3113 has maximum number of dominant genes because it is near the point of origin while genotype CRIS-9 contains maximum recessive genes because it is placed far away from point of origin. Similar results were reported by Mehetre *et al.* (2003), Ali *et al.* (2008) and Singh *et al.* (2010). The contrasting results were reported by Aguiar *et al.* (2007) and Bolek *et al.* (2010). Involvement of partial dominance is depicted in the inheritance of fiber elongation because regression line intercepts the Wr-axis above the point of origin. (Fig.11). Most of the genes in this trait are additive.

The genotype CRS-456 has more dominant genes because it is placed near the point of origin while genotype BT-122 contains maximum recessive genes because it is placed farther from point of origin. Pareetha and Raveendran (2008), Batool and Khan (2012) reported similar findings.

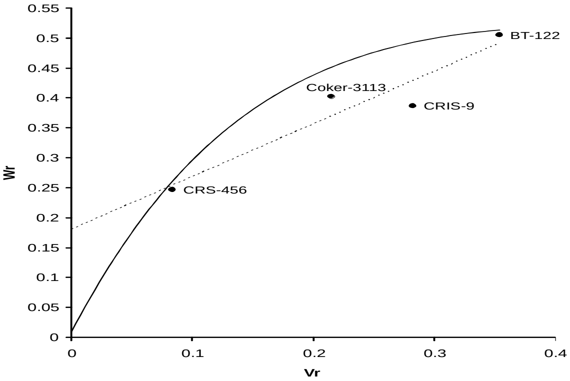

Fig. 11. Wr/Vr graph for fiber elongation.

CONCLUSION

These F_1hybrids CRS-456 × CRS-456, CRIS-9 × COKER-3113 and CRS-456 × CRIS-9 presented best genetic potential and highest genetic variability for majority of the traits which can be used in hybrid breeding program and selection in late segregating generations for further improvement.

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