



Genetics of Yield Traits, Seed Cotton Yield and Fibre Quality Traits in Upland Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

Present study was conducted to evaluate the genetics of yield and fibre quality traits in seven upland cotton (*Gossypium hirsutum* L.) cultivars i.e. Narasimha, TCH 1726, TCH 1705, KC2, MCU13, BW4-1 and MCU 3 were crossed in a complete diallel mating design. Genetic analysis revealed that mean degree of dominance was found to be less than one for all characters studied except boll weight. H_1 value was significant and greater than D for all traits studied except boll weight. Narrow sense heritability found to be very high in plant height, 2.5% span length. $H_2/4H_1$ ratio found to less than 0.25 is recorded for all characters studied except for seed index, and boll weight. The character number of bolls per plant, single plant yield, seed index, 2.5 percent span length showed partial dominance nature in the (Vr), (Wr) covariance graph. All other characters exhibited over dominance. The parent TCH 1726 was the dominant parent for plant height and boll weight. The parent Narasimha was the dominant parent for days to first boll bursting in view of its position near the origin in the regression graph. The parent MCU 13 was dominant parent for, micronaire and 2.5% span length. The parent BW4-1 carried recessive genes for plant height.

Keywords: Cotton, diallel analysis, fibre quality traits, gene action, heritability



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INTRODUCTION

Cotton (*Gossypium spp.*) is an important fiber crop and it plays a vital role as a cash crop in many countries. Cotton provides fibre for textile industry, cellulose from its lint, oil and protein rich meal from its seed (Ashokkumar and Ravikesavan, 2011a & b). Cotton, also known as “King of fibres” plays a remarkable role in Indian economy. Development of cotton varieties with high yield and fibre quality is the primary objective of cotton breeders. The first step in a successful breeding program is the selection of appropriate parents. Diallel analysis provides a systematic approach for detection of appropriate parents and crosses in terms of investigated traits and it has been widely used by plant breeders in the selection of parents and crosses in the early generations (Kiani et al., 2007; Karademir and Gencer, 2010; Senthilkumar et al., 2013; Senthilkumar et al., 2015). Numerous studies have been reported on yield and yield attributing traits, but little work has been reported on the genetics of fibre quality traits in cotton breeding. A few recent reports in the literature (Karademir et al., 2011; Bolek et al., 2011; Ashokkumar and Ravikesavan, 2008; Ashokkumar and Ravikesavan, 2010; Ashokkumar et al., 2010; Ashokkumar and Ravikesavan, 2011a; Ashokkumar et al., 2013; Ashokkumar et al., 2014) have determined that cotton genotypes differ in fibre quality traits.

The previous studies reports showed that inheritance of seed cotton yield and its components were controlled with additive and non-additive gene action. Earlier studies of Mukhtar et al. (2000), Iftikhar et al. (2001), and Subhan et al. (2002) revealed additive type of gene action with partial dominance and additive type of gene action with partial dominance for boll weight was observed Shakeel et al. (2001). Though, Ajmal et al. (1998) and Shakeel et al. (2001) reported the presence of genes showing overdominance for yield and yield attributing traits. Additionally, Saravanan et al. (2003) and Soomro et al. (2009) studied diallel set of crosses of some parents of cotton for genetic effects on different traits. The additive type of gene action was noticed for boll weight; however plant height, number of bolls per plant and seed cotton yield per plant revealed effects with over dominance type of gene action. Hence, present study was conducted to obtain the genetic information for yield and fibre quality traits of cotton plant by using diallel analysis method. The information thus generated may help the breeders to launch a successful cotton breeding programme.

MATERIALS AND METHODS

Genetic materials

The field experiment was conducted to evaluate the growth, yield and fibre quality traits performance of seven commercially cultivated varieties of cotton (*Gossypium hirsutum L.*) using seven parents, viz., Narasimha, TCH 1726, TCH 1705, KC2, MCU13, BW4-1 and MCU 3. All the seed materials were obtained from Department of Cotton, Tamil Nadu Agricultural University, Coimbatore, India. The commercial cultivars were cultivated in southern states of India.

Experimental design, sampling, and traits measurements

The cotton cultivars were evaluated in randomized block design (RBD) with three replications at Cotton Breeding Station, Tamil Nadu Agricultural University, Coimbatore, and Tamil Nadu in India. The seed of each parental genotype was sown in 20 rows of 6m length in crossing block with a spacing of 90 x 45 cm. Crosses were made between parents in a 7 x 7 full diallel mating design. The crossed bolls were collected and ginned to obtain F₁ seeds. Seven parents and 42 hybrids were raised along with the standard check with three replications. For each genotype and its cross combinations, data were recorded on five randomly selected plants per replication for twelve characters namely, days to boll bursting, number of sympodia per plant, plant height (cm), number of bolls per plant, boll weight (g), lint index, seed index, ginning percent, single plant yield (g), 2.5% span length (mm), elongation percent and fiber fineness. The diallel analysis was performed as model 1 and method 1 suggested by Griffing (1956).





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Genetic and graphical analysis

The graphic and genetic component analysis of the diallel cross was analysed following the methods suggested by Jinks and Hayman (1953) and Aksel and Johnson (1962). The diallel hypothetical assumptions were tested by "t²" test and uniformity of W_r and V_r (Hayman, 1954).

$$t^2 = \frac{n - 2}{4} \times \frac{(\text{Var. } V_r - \text{Var. } W_r)^2}{(\text{Var } V_r \cdot \text{Var. } W_r) - (\text{Cov}^2(V_r \ W_r))}$$

where, n is the number of parents under study.

t² values were compared with statistical tabular values for 4, n-2 degrees of freedom, which is a 'F' test. The t² value when non-significant denotes the uniformity of V_r - W_r and confirms the valuable application of Hayman Postulate (1954). Otherwise, significance of t² values indicates the failure of at least one of the assumptions postulated.

Deviation of Regression co-efficient (b) from zero and unity

The occurrence of non-allelic interactions was further tested and confirmed by calculating the regression co-efficient. The regression of covariance on variance and its standard error were calculated as follows:

$$b_{yx} = \frac{\text{Cov}(W_r, V_r)}{\text{Var}(V_r)}$$

$$\text{Standard Error } (b_{yx}) = \left[\frac{\text{Var } W_r - b \text{ Cov}(W_r, V_r)}{\text{Var } V_r (n - 2)} \right]^{1/2}$$

The significance of b_{yx} from zero and unity was tested as follows:

$$\frac{b - 0}{\text{SE}(b)} \quad \text{and} \quad \frac{1 - b}{\text{SE}(b)}$$

both following 't' distribution

The significance of 'b' from zero and unity was tested against the table value of 't' for n-2 degrees of freedom. A non-significant value justifies the existence of regression of W_r and V_r.

Estimation of genetic components

The theory and method of Hayman (1954) were extended to estimate the genetic components or parameters viz., D, F, H₁, h² and E. Hayman (1954) derived the expectations for the statistics calculated for F₁ diallel table and also the expected values of the parameters of the variation using least square technique as follows:

- (D) = V_{0L0} - E
- (F) = 2 V_{0L0} - 4 W_{0L01} - 2 (n-2) E/n
- (H₁) = V_{0L0} - 4 W_{0L01} + 4 V_{1L1} - (3n-2) E/n
- (H₂) = 4V_{1L1} - 4V_{0L1} - 2E
- (h²) = 4 (M_{L1} - M_{L0})² - 4 (n-1) E/n²
- (E) = 2 (V_{0L0} - W_{0L01} + V_{1L1} - W_r - V_r) - 2 (n-1) E/n

Where,

- D = Component of variation due to additive effects of the genes
- F = The mean of F_r over the arrays. For being the covariance of additive and non-additive effects in the rth array. Additive x dominance variance.
- H₁ = Component of variation due to dominance effects of the genes
- H₂ = H₁ (1-(u-v)²) measures the dominance variance due to positive (u) and negative (v) effects of genes, where, u = proportion of positive alleles while, v = proportion of negative alleles since u + v = 1.





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- L₂ = Net dominance effects (as the algebraic total over all loci in heterozygous state in all cross combinations)
- E = The expected environmental component of variation derived from error variance divided by number of replications.

V_{OL1} is the variance of mean arrays.

M_{L1} – M_{L0} is the difference between the mean of the parents and the mean of their n² progenies. When F parameter is on positive direction, it explains higher proportion of dominant alleles, while a negative direction reveals more of recessive alleles. All these genetic parameters were tested by 't' test for significance by the use of the respective standard errors of parameters.

These standard errors were estimated from

i) the formula $S^2 = \frac{1}{2} \text{Var} (W_r - V_r)$

ii) the main diagonal or covariance matrix (Hayman, 1954) as corresponding multipliers

$$\text{SE of D} = \left[\frac{(S^2 n^5 + n^4)}{n^5} \right]^{1/2}$$

$$\text{SE of F} = \left[\frac{4S^2 (4n^5 + 20n^4 - 16n^3 + 16n^2)}{n^5} \right]^{1/2}$$

$$\text{SE of H1} = \left[\frac{16S^2 (n^5 - 41n^4 - 12n^3 + 4n^2)}{n^5} \right]^{1/2}$$

$$\text{SE of H2} = \left[16S^2 \frac{(36n^4)}{n^5} \right]^{1/2}$$

$$\text{SE of h}^2 = \left[16S^2 \frac{(16n^4 + 16n^2 - 32n + 16)}{n^5} \right]^{1/2}$$

$$\text{SE of E} = \left[\frac{S^2 n^4}{n^5} \right]^{1/2}$$

Where, n = number of parents

Test for significance of components

The calculated 't' values of every parameter and error was derived by dividing the component value with its standard error and the value was compared with the tabular value of 't' for n-2 d.f.

Proportion of genetic components

The proportionate ratios of different components of variance were compared by the equations given by Crumpacker and Allard (1962), as follows :

1. Mean degree of dominance over all loci
 = (H₁ / D)^{1/2}

- If it is > 1, reveals over dominance
- < 1, partial or incomplete dominance





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- = 0, no dominance
- = 1, complete dominance

2. Proportion of dominant and recessive genes in parents

$$\frac{KD}{KR} = \frac{4(DH_1)^{1/2} + (F)}{4(DH_1)^{1/2} - (F)}$$

If the proportion is equal to 1, it defines the equality of dominant and recessive genes greater than 1, predominance of dominant genes and less than 1, indicates predominance of recessive genes.

3. Proportion of genes with positive and negative effects in the parents

$$= \frac{(H_2)}{4(H_1)}$$

when u and v are symmetrically distributed

(u = v = 0.5) the ratio $H_2 / 4 (H_1) = 0.25$

4. Number of groups of genes controlling the character and exhibiting dominance is derived by (h^2 / H^2)

5. Narrow sense heritability estimates

$$\frac{1/2(D) + 1/2(H_1) - 1/2(H_2) - 1/2(F)}{1/2(D) + 1/2(H_1) - 1/4(H_2) - 1/2(F) + E} \text{ (or)}$$

(Crumpacker and Allard, 1962)

$$\frac{1/4(D)}{1/2(D) + 1/2(H_1) - 1/4(F) + E}$$

6. The correlation between parental order of dominance ($W_r + V_r$) and parental measures (Y_r) was computed. A significant positive correlation indicates that most of the dominant genes had negative effects for those characters, while significant negative value indicates that most of the dominant genes had positive effects (Hayman, 1954).

Graphical Analysis

Wr. Vr. Graph: The essential factors for the graph V_r and W_r were calculated from the diallel table and these values were used in constructing the $W_r. V_r$ Graph for each character.

Where,

V_r is the variance of offspring of the r^{th} parental array

W_r is the covariance of the offspring of the r^{th} array with respect to non-recurrent parent.

Data from F_1 and parents were subjected the analysis proposed by Jinks and Hayman (1953) as illustrated by Aksel and Johnson (1962). In this analysis the following statistical parameters were estimated from the data.

- V_r - The variance of offspring of the r^{th} parental array
- W_r - The covariance of offspring of the r^{th} array with respect to non-recurring parent.
- V_{OLO} - The variance of all parental means
- V_{OL1} - The variance of the means of the arrays
- W_{OLO1} - The mean covariance between parents and the arrays
- V_{iL1} - The mean variance of arrays





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$(M_{1L1} - M_{LO})^2$ – The square of difference between the mean of the parents and the mean of their n^2 progeny.

By utilizing the regression values, the W_r , V_r graph was drawn for all the characters studied and the limiting parabola was constructed using the formula

$$W_r^2 = V_r \times V_{OLO}$$

i.e. by plotting V_r . $(V_r \times V_{OLO})^{1/2}$ points starting with $V_r = V_{1L1}$. A few interpolations and extrapolations make it possible to draw the parabola. The hypothesis was tested as indicated earlier.

RESULTS AND DISCUSSION

Genetic analysis

The proper understanding of genetic architecture of the characters of the parents involved in hybridization is essential to genetically improve the crop plants. The genetic analysis of different characters was estimated adopting the method suggested by Hayman (1954) and Griffing (1956). This analysis provides certain additional information such as a) Mean degree of dominance b) proportion of genes with positive effects in parents c) the proportion of dominant and recessive genes in parents d) heritability estimate in narrow sense. In genetic analysis, various genetic parameters D_1 , H_1 , H_2 , F , h^2 and E was estimated and furnished (Table 1). Predominance of dominance effect was observed for plant height, ginning percentage, days to first boll bursting, single plant length, 2.5% staple length, micronaire value, number of sympodial branches, number of bolls per plant, lint index, seed index and bundle strength. The similar results are in confirm with the findings of Sandhu et al., (1992) for plant height, Jagtap, (1994) and Tomer and Singh (1996) for number of bolls per plant, Singh et al. (1988) for lint index, Tomer and Singh (1996) for seed index, Gururajrao et al. (1977) and Bhandari et al., (1981) for 2.5 per cent span length.

The mean degree of dominance was found to be less than one indicating the partial dominance for boll weight. The ratio $H_2/4H_1$ was less than 0.25 for all characters studied except for boll weight and seed index. F value was positive for all characters studied. The heritability in narrow sense was found high for plant height and 2.5 % span length. Heritability in narrow sense is high it indicated that the character is largely governed by additive genes and selection for improvement of such character would be rewarding, Deskmuchet al. (1999) reported similar results for plant height, number of bolls per plant and 2.5% span length. The moderate heritability in narrow sense was recorded in ginning per cent, lint index, days to first boll bursting and micronaire. Similar results are also reported by Gururajrao et al. (1977) for lint index. The characters namely bundle strength, seed index, number of sympodial branches, boll weight, number of bolls per plant, and single plant yield recorded low estimates of heritability. Jagtap and Kolte (1986) also reported low estimates of heritability for seed cotton yield per plant. If narrow sense heritability is found to be moderate/low heritability indicated that preponderance of non-additive gene action and heterosis breeding can be exploited for improvement of such characters.

Graphical Analysis

The graphical analysis was carried out as suggested by Hayman (1954). The validity of assumptions was tested by the t_2 tests for all the traits. T_2 static for $V_r W_r$ regression was significant for all the characters studied. Validity of assumptions was also verified by the regression value of b for $V_r W_r$ graph. Graphical Analysis measures the genetic diversity of the parents involved in diallel cross in terms of the proportion of dominant and recessive genes along with net direction dominance either with favourable effects or unfavorable effects. The values of v_{rand} and w_r for parents are given (Table 2).





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The regression line of Vr-Wr graph passes exactly the origin indicating the presence of complete dominance for days to first boll bursting. The parents Narasimha, MCU 3 and TCH 1705 were located near to the origin showing the presence of dominant genes in these lines (Fig. 1A). However, In Vr-Wr graph, the regression lines passes below the origin indicating the presence of over dominance in Number of sympodial branches per palnt, plant height and Number of bolls per plant (Fig. 1B – 1D).In Vr-Wr graph the regression lines passes above the origin indicating the presence of partial dominance for boll weight. The parents TCH 1726, MCU 13, TCH 1705 and Narasimha are located near to the origin indicating the presence of more dominant genes (Fig. 1E). However, additive type of gene action was noticed for boll weight, Shakeel et al. (2001). For lint index trait, the regression line passes below the origin indicating the presence of over dominance. The parents KC 2 and MCU 3 are located very far from origin and indicated that it contains more recessive genes for this trait (Fig. 2A). However, the regression line of the VrWr graph passes above the origin indicating the presence of partial dominance for seed index. The parent Narasimha and MCU 3 were located very far from origin and it contains more recessive genes (Fig 2B). For ginning percentage trait, regression line of the VrWr graph passes below the origin indicating the presence of over dominance. The parent BW 4-1 and MCU 13 are located near to the origin indicating the presence of more dominant genes. The parent TCH 1726 was located far from origin indicating that it contained more of recessive alleles (Fig 2C).The regression line passes below the origin showing the presence of over dominance in single plant yield. The parent BW4-1 and TCH 1726 was located far from origin indicating that it contained more of recessive alleles (Fig. 2D). It was supported by previous studies of Ajmal et al. (1998) and Shakeel et al. (2001) reported that the presence of genes shows overdominance for seed cotton yield and yield attributing traits.

For 2.5% Span length trait, the regression line passes above the origin, showing the presence of partial dominance. The parent MCU 13 and TCH 1726 was located far from the origin indicating found to contain more of recessive alleles (Fig. 3A). However, regression line passes below the origin showing the presence of over dominance for bundle strength trait. The parent KC 2, TCH 1726, TCH 1705 and BW- 4 -1 were located far from origin indicating that it contained more of recessive alleles (Fig. 3B). Furthermore, for micronaire trait, regression line passes below the origin showing the presence of over dominance. The parent MCU 13 was located near to the origin indicating the presence of more dominant genes. The parent TCH 1726 was located far from origin indicating that it contained more of recessive alleles (Fig 3C). Similar results also reported by Shimna (2004) that T2 statistic for Vr-Wr regression was significant for all the characters studied except boll weight, single plant yield and bundle strength. Similar also confirm with the findings of saravananet al. (2003) reported that parent MCU 12 had most of dominant genes for plant height and number of bolls per plant. Parent Suvin had most dominant genes for boll weight, number of seeds per boll and 2.5 per cent span length.

CONCLUSION

The present study conclude that predominance of dominance effect was observed for plant height, ginning percentage, days to first boll bursting, single plant yield, number of sympodial branches, number of bolls per plant, lint index, seed index ,2.5% span length and bundle strength and micronaire. The mean degree of dominance was found to be less than one indicating partial dominance for boll weight. The ratio $H_2/4H_1$ was less than 0.25 for all characters studied except for boll weight and seed index. The heritability in narrow sense was found high for plant height and 2.5 % span length. For single plant yield and bundle strength the parent Bw4-1 had located far from origin indicating that it contained more of recessive alleles as against ginning percentage where dominant gene was noticed by that parent. Parent Narasimha had recorded both dominant and recessive alleles for boll weight and number of bolls, respectively. The distribution of array points along the regression line for different plant traits indicated the existence of genetic variation in plant material. Thus variation could be exploited through appropriate breeding programme.





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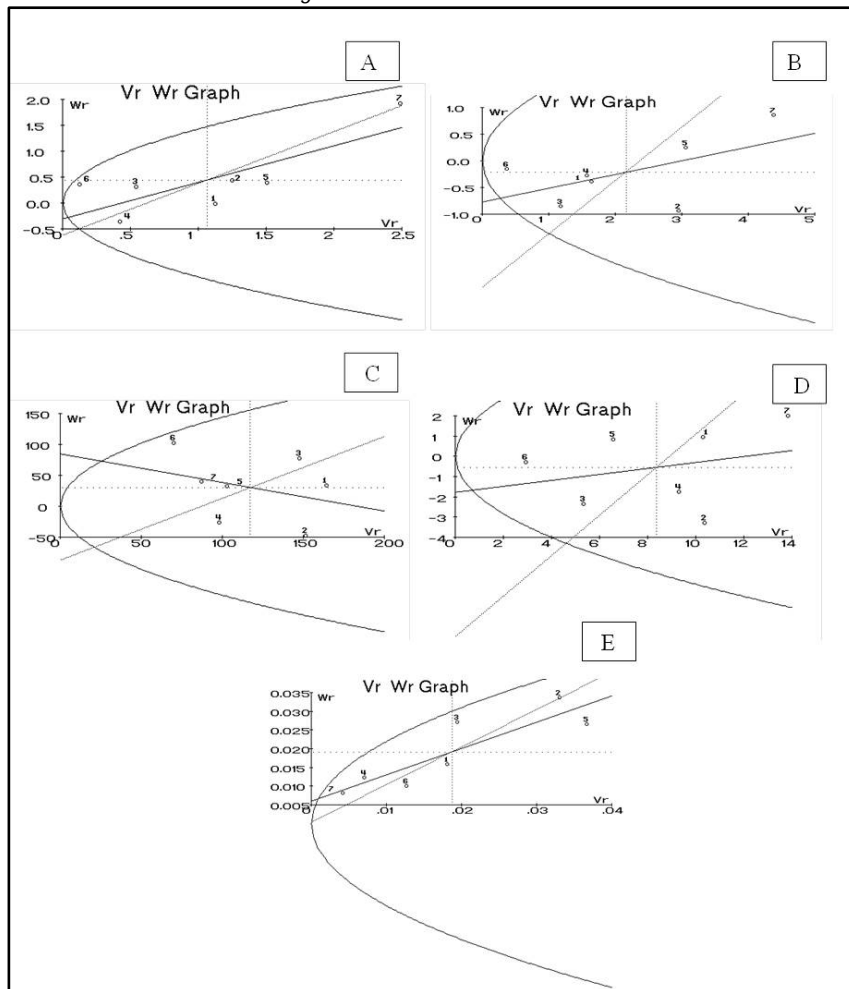


Fig. 1. Vr-Wr graph analysis for metric traits. A), Days to first boll bursting; B), Number of symbodial branch per plant; C), Plant height, D), Number of bolls per plant; and E), Boll weight.

Note: (1).Narasimha, (2). KC 2, (3). MCU 3, (4). TCH 1705, (5). BW4-1, (6). MCU 13 and (7). TCH 1726.





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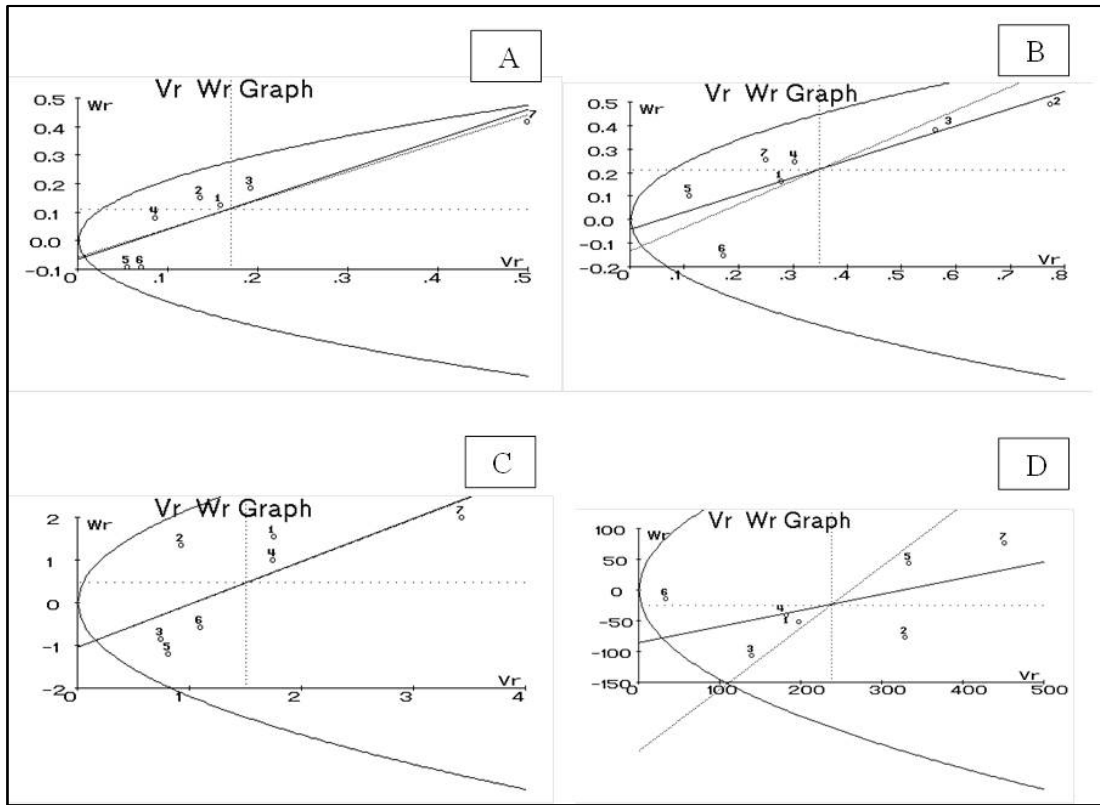


Fig. 2. Vr-Wr graph analysis for seed traits and single plant yield. A), Lint index; B), Seed index; C), Ginning percentage, and D), Single plant yield.

Note: (1).Narasimha, (2). KC 2, (3). MCU 3, (4). TCH 1705, (5). BW4-1, (6). MCU 13 and (7). TCH 1726.





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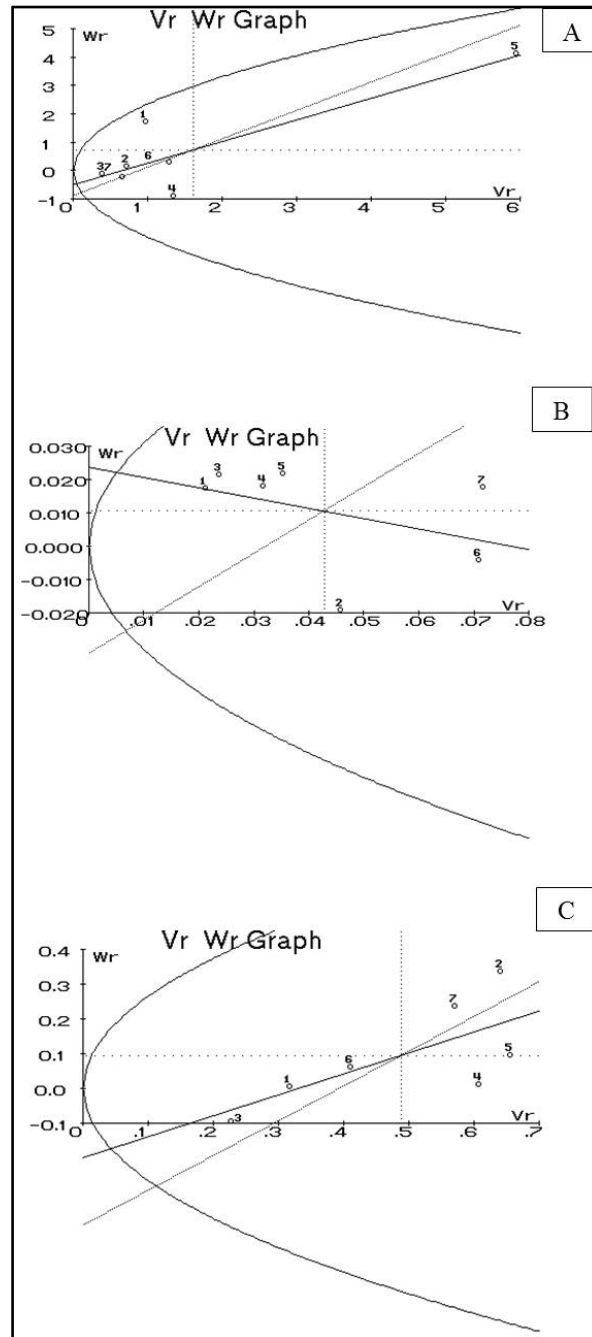


Fig. 3. Vr-Wr graph analysis for fibre quality traits. A), 2.5% span length; B), Bundle strength, and C), Micronaire value.

Note: (1).Narasimha, (2). KC 2, (3). MCU 3, (4). TCH 1705, (5). BW4-1, (6). MCU 13 and (7). TCH 1726.





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Table 1. Expression of genetic parameters for yield and fibre quality characters.

Character	$(H_1/D)^{1/2}$	$H_2/4 H_1$	$\frac{4DH_1^{1/2} + F}{4DH_1^{1/2} - F}$	h^2/H_2	Heritability in narrow sense (%)
Days to first boll bursting	1.46	0.203	2.17	0.522	58.8
Number of sympodial branches	2.74	0.172	3.18	0.202	33.4
Plant height	1.69	0.165	2.51	0.168	89.1
Number of bolls per plant	3.99	0.171	2.54	1.199	15.8
Boll weight	0.17	0.880	0.40	-2.434	30.9
Lint index	1.16	0.187	2.36	2.119	60.6
Seed index	1.25	0.254	1.04	4.699	29.7
Ginning percentage	1.34	0.14 1	4.05	0.204	75.3
Single plant yield	2.65	0.169	3.22	0.171	37.6
2.5% Span length	1.24	0.144	3.81	1.701	98.7
Bundle strength	2.02	0.130	2.18	1.521	31.7
Micronaire	1.51	0.148	3.17	-0.053	70.5

Table 2. Graphical analysis of genetic diversity of parents through expression of Vr and Wr

Character	Narasimha		KC 2		MCU 3		TCH 1705		BW 4-1		MCU 13	
	Vr	Wr	Vr	Wr	Vr	Wr	Vr	Wr	Vr	Wr	Vr	Wr
Days to first boll bursting	1.12	-0.008	1.24	0.42	-0.36	1.50	0.39	0.12	0.35	0.43	0.54	0.32
Number of sympodial branches	1.64	-0.39	2.95	1.57	1.64	3.06	2.95	0.36	0.14	-0.93	1.18	-0.84
Plant height	60.2	34.2	151.5	164.4	34.2	151.5	-48.0	147.5	77.2	-48.0	147.5	77.2
Number of bolls per plant	10.29	0.95	10.37	9.29	-1.75	6.55	0.82	2.93	-0.28	-3.27	5.32	-2.36
Boll weight	0.018	0.016	0.033	0.007	0.012	0.037	0.027	0.013	0.010	0.034	0.019	0.027
Lint index	0.15	0.12	0.13	0.086	0.081	0.055	-0.091	0.070	-0.091	0.15	0.19	0.18
Seed index	0.27	0.16	0.77	0.30	0.24	0.10	0.10	0.17	-0.15	0.49	0.56	0.38
Ginning percentage	-2.77	0.002	5.44	1.74	0.99	0.81	-1.20	1.09	-0.58	0.07	0.57	0.032
Single plant yield	198.0	-52.1	328.3	181.5	39.9	322.8	43.8	32.9	-14.2	-76.9	138.7	-106.8
2.5% span length	0.97	1.74	0.71	1.34	-0.89	5.94	4.15	1.28	0.32	0.15	0.38	-0.11
Tenacity	0.31	0.007	0.64	0.607	0.011	0.65	0.097	0.41	0.063	0.33	0.22	-0.093
Micronaire	0.021	0.017	0.04	0.032	0.018	0.035	0.022	0.071	-0.004	-0.019	0.024	0.021

