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Genetic studies of different agronomic, quality and yield contributing traits in G*ossypium hirsutum L*.

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Abstract

An experiment of 4 × 4 diallel was carried out to study the gene action of different yield and yield contributing traits of four advanced cotton cultivars using Mather and Jinks approach. Significant variation was present for all the characters ($P \leq 0.01$). The data on recorded parameters revealed that most of the traits were fully or partially fit for genetic interpretation. Additive gene action (D) was significant and pre-dominant for all the characters while seeds per locule showed dominance effect of H_1& H_2, and it was confirmed by the value of degree of dominance (H_1/D 0.5). The value of $H_2/4H_1$ and h^2 (measures the direction of dominance) demonstrated asymmetrical division of dominant genes for all traits, except ginning out turn (G.O.T) percentage and fiber length, in parental material. All the studied traits showed high value of narrow sense heritability (h^2_{NS}), however seeds per locule possessed low heritability. The genetic analysis revealed that all the characters could be improved by progeny and pedigree selection, whereas hybrid dynamism could be exploited in the trait like seeds per locule.

Keywords: Components of variation, Ginning out turn%, Fiber, Inheritance pattern, Upland Cotton

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Introduction

Cotton (*Gossypium hirsutum* L.) has prime importance among all natural fiber crops of the world. Pakistan ranks fifth among top cotton producing countries in the world (Anonymous, 2020-2021). Besides equipping local textile industry and provide employment, it fetches a lot of foreign exchange by exports of lint and textile products, and hence has a profound influence on the economy of the country (Sundas & Khan, 2012). However, squeeze of agricultural land, climate change and evolution of new insect pest complex, are the major factors which cause drastic decrease in production and yield of cotton crop (Baloch et al., 2011; Hassan et al., 2015). It is need of time to evolve new cotton genotypes which can mitigate climate change and efficiently utilize the nutrients to produce higher yield than existing cultivars. There are number of genetic factors which determine the fate of cotton cultivars in the field and need to investigate properly. Among them, identification and use of genetically distinct parents with enviable genetic constituent of variance is a basic requirement for the synthesis of physiologically improved and genetically better-quality genotype (Ali & Awan, 2009).

However, low genetic variability and limited knowledge of combining ability are the major restraining factors in the selection of suitable parents for hybridization program (Patil et al., 2011). Therefore, complementary knowledge on gene action and mode of inheritance of economic characters is essential for plant breeders to develop new cotton cultivars with the best combinations of desirable characters (Nadeem & Azhar, 2004).

Information regarding all components of genetic variability for different attributes viz. plant height, branch bearing habit (mono and sympodial branches) and first retention node (showing earliness); yield contributing traits such as number of bolls and boll weight; seed characters including seed weight and number of seeds per locule; ginning out turn (GOT %) and fiber quality traits is essential to investigate for crop improvement exercise (Haidar et al., 2012; Akiscan & Gencer, 2014).

Considering these facts many scientists in past like (Zhang et al., 2106; Arvind et al., 2021) studied the inheritance phenomena of different agronomic and yield related attributes in cotton following diallel crossing design and found that all traits were predominantly controlled by non-additive type of gene action. Similarly, Nabi et al. (2015) used diallel technique to study inheritance pattern of proline accumulation in cotton under saline condition and found additive gene action responsible for salinity tolerance which encouraged the breeders to exploit this potential for improving salinity tolerance in cotton. Many other scientists also used diallel crossing technique in cotton to get the desired results (Murtaza et al., 2005; Ali & Awan, 2009; Khan et al., 2012; Zhang et al., 2017; Giri et al., 2021).

Keeping in view the above facts, four genetically diverse genotypes were crossed following complete diallel set to create the genetic variability, investigate genetic effects and probe the proper genotype and breeding approach associated with suitable plant and quality traits.

Materials and Methods

Current study was conducted at Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan during year 2015-16. F_1 generation in diallel mating design was developed using following accessions i.e. NIAB-112, CIM-616, Cyto-177 and FH-Lalazar, Plant material was evaluated for various plant traits under field trial.

Selected parental lines were grown in pots of dimension 30 × 30 cm under glass house. Each pot contained field soil supplemented 5% farm yard manure. Moreover fertility of soil was raised by adding 0.25 g of Urea (46% N). Two seeds were sown in single pot which were thinned to single seedling upon germination. Temperature was maintained closed to 30°C through natural sunlight and electric heater. A photoperiod of 16 hours length was maintained through filament bulb as narrated by Murtaza et al. (2005). All pots were irrigated close to field capacity on regular basis to avoid water stress (Ali et al., 2008). Each parental line was represented by 20 pots. Flower bud was tagged as it borne on leaf node and covered with butter bag before opening. Anthers were removed manually with the help of forcep. Crosses were attempted among the parental lines in all possible combinations under diallel fashion. Seed cotton was harvested and ginned to get F_1 cotton seed.

All F_1 seeds of hybrids, reciprocals and their parents were planted under randomized complete block design (RCBD) with three replications during cropping season 2015-16. Two seeds were dibbled on beds with Px P distance of 30 cm while beds were 75 cm apart. Crop was raised by the production package suggested by the Agriculture department, Punjab, Pakistan. Field was irrigated with canal water while plants were protected through recommended insecticides before their damaged reached threshold level. 10 plants within each row were selected for evaluation of traits related to yield and its components. All mature bolls were harvested, dried and put in paper bags to estimate seed cotton yield (g). Seed cotton was ginned through lab grade ginning machine. Lint yield was estimated by measuring the lint mass on digital balance. Moreover, measuring rod was used to determine plant height. Monopodial, sympodial branches and number of nodes and number of bolls plant^{-1} were counted manually. Number of nodes was used to estimate internodal distance. Seed cotton yield plant^{-1} was divided by number of bolls plant$^{-1.}$ Stem thickness/diameter was measured by Vernier caliper. 1st retention node; yield contributing characters including boll numbers and boll weight; seed character like seeds/locule were collected in the field while 100 seed weight was recorded after ginning. The lint characters like fibre fineness, fibre strength and fibre length were recorded through HVI-900 fibrograph.

Data was subjected to the analyses of variance on computer based software as per originally described by Steel *et al*. (1997) to determine statistical differences among the evaluated genotype. Gene action associated with traits of interest was determined through method outlined by Hayman (1954) and Jinks (1954), modified by Mather and Jinks (1982) and Singh and Chaudhry (1985).

Results and Discussions

A combined analyses of variance for plant material was done which showed significant variability ($P \leq 0.01$) due to parental accessions and their developed crosses (Table 1).

Table 1. Mean sum square estimates of various traits in cotton breeding material

Trait	Mean sum of square		
	Replication	**Genotype**	**Error**
Degree of freedom	2	15	30
Plant height	1.05	179.39**	18.39
Monopodial	0.174	7.79**	0.307
Sympodial	0.493	4.043**	0.591
Inter. distance	0.393	0.327**	0.556
Stem thickness	0.033	0.143**	0.027
1st node	0.138	0.348**	0.064
Boll no.	30.66	504.70**	41.77
Boll wt.	0.106	0.755**	0.74
Seed /locule	0.028	0.161**	0.446
Seed wt.	0.289	2.231**	0.12
GOT	0.258	6.466**	1.981
Fiber fineness	0.173	46.915**	0.897
Fiber Strength	0.073	0.231**	0.044
Fiber Length	1.176	10.125**	1.023

Where; ** = Significant at $P \leq 0.01$ levels, respectively.

Data assessment for additive-dominance (AD) model: The data were assessed for AD model by applying both regression co-efficient (b) and the mean squares of Wr + Vr & Wr–Vr arrays tests given in Table 2-4. Mather and Jinks (1982) reported that data could only be interpreted for genetic analysis, if value of regression coefficient (b) exhibits significant deviation from zero but not from unity. In this study, the value of ‘b’ showed significant divergence from zero but not from unity for all the traits except for seeds per locule as shown in the Table 2. Epistatic effects were found absent in the phenotypic expression of all studied traits as confirmed by the non-significant mean square values of arrays (Wr-Vr) over replication. From the graph Fig. 1, the regression line meet the Wr-axis positively showed the additive nature of gene action for all the traits except seed per locule in which regression line meets the Wr-axis on negative side below the origin which suggested the over dominance nature of gene action. For the distribution of dominance and recessive genes, the genotype got the maximum dominant genes closest from the origin, whilst the genotypes farthest from the origin got the maximum recessive genes. The significant values of mean square (Wr + Vr) arrays suggested full validity of these traits while non-significant values rendered the partial validity of traits for further genetic interpretation. This is consistent with the results of Khan et al. (2009), Ali & Awan (2009) and Sundas & Khan (2012) in diallel crosses of different genotypes of *G. hirsutum* L. It is concluded that due to regression and variance of arrays analysis, model was partially adequate for the characters like plant height (PH), sympodial numbers, internodal distance, stem thickness, 1st retention node, boll number, seeds per locule, fiber fineness (FF), fiber strength (FS) and fiber length (FL) while model was fully adequate, by regression and variance of arrays analysis, for the characters like number of monopodial, boll weight, seed weight and gin turn out percentage (Table 4).

Table 2. Joint regression of adequacy of additive dominance model in selected germplasm accessions

Sr. No.	Characters	Regression Coefficient (b)	t test for b=0	t test for b=1
1	Plant Height (cm)	1.01± 0.07	12.787**	-0.160^{NS}
2	Monopodial Branches	0.99± 0.18	5.44**	0.034 ^{NS}
3	Sympodial Branches	0.95±0.06	14.75**	0.73 ^{NS}
4	Internodal Distance(cm)	1.01 ± 0.13	7.31**	-0.15 ^{NS}
5	Stem Thickness(mm)	0.99 ± 0.16	5.85**	0.04 ^{NS}
6	1st Retention Node	0.96 ± 0.00	8.81**	0.34 ^{NS}
7	Boll Number	0.99±0.09	10.45**	0.38 ^{NS}
8	Boll Weight (g)	0.94 ±0.17	5.39*	0.32 ^{NS}
9	Seed/Locule	0.87 ±0.12	7.27**	1.05*
10	100Seed Weight (g)	0.95 ±0.20	3.86*	0.17 ^{NS}
11	Gin Turn Out (G.O.T %)	0.87±0.24	3.64*	0.51 ^{NS}
12	Fiber Fineness (ug/inch)	0.98±0.03	26.54**	0.48 ^{NS}
13	Fiber Strength (g/tax)	0.87±0.24	3.56*	0.51 ^{NS}
14	Fiber Length (mm)	0.91±0.14	6.37**	0.57 ^{NS}

Table 3. Analysis of variance of arrays for adequacy of additive-dominance (AD) model in cotton

Traits	Mean sum of square (Adequacy test)	
	Wr+Vr (Between arrays)	**Wr-Vr (Between arrays)**
Plant height	2484.622 (NS)	87.00 (NS)
Monopodial branches	14.43**	0.26 (NS)
Sympodial branches	1.71 (NS)	1.30 (NS)
Internodal distance	0.004 (NS	0.0002 (NS)

Stem thickness	0.002 (NS)	0.0001 (NS)
Boll weight	0.02 (NS)	0.0007 (NS)
Seed Locule^{-1}	39566.14 (NS)	196.86 (NS)
Seed mass	1.25**	0.002 (NS)
Ginning Out Turn	8.94*	0.0004 (NS)
Fiber Fineness	33.46 (NS)	0.04 (NS)
Fiber strength	0.03 (NS)	0.25 (NS)
Fiber Length	8.56 (NS)	0.10 (NS)

Table 4. Joint regression of adequacy of additive dominance model in selected germplasm accessions

Characters	**Joint regression analysis**	**Analysis of variance of array**	**Final conclusion**
Plant Height (cm)	The data were fit for additive dominance model	Not fit for A-D Model	Partial
Monopodial Branches	The data were fit for additive dominance model	Fit for A-D Model	Full
Sympodial Branches	The data were fit for additive dominance model	Not fit for A-D Model	Partial
Internodal Distance(cm)	The data were fit for additive dominance model	Not fit for A-D Model	Partial
Stem Thickness(mm)	The data were fit for additive dominance model	Not fit for A-D Model	Partial
1st Retention Node	The data were fit for additive dominance model	Not fit for A-D Model	Partial
Boll Number	The data were fit for additive dominance model	Not fit for A-D Model	Partial
Boll Weight (g)	The data were fit for additive dominance model	Fit for A-D Model	Full
Seed Locule^{-1}	The data were not fit for additive dominance model	Fit for A-D Model	Partial
100Seed Weight (g)	The data were fit for additive dominance model	Fit for A-D Model	Full
Gin Turn Out (G.O.T %)	The data were fit for additive dominance model	Fit for A-D Model	Full
Fiber Fineness (ug inch^{-1})	The data were fit for additive dominance model	Not fit for A-D Model	Partial
Fiber Strength (g tax^{-1})	The data were fit for additive dominance model	Not fit for A-D Model	Partial
Fiber Length (mm)	The data were fit for additive dominance model	Not fit for A-D Model	Partial

Genetic Analysis of Plant Agronomic, Boll, Seed and Quality Traits: Inheritance patterns of all parameters under study were examined by the computation of genetic constituent of variation *i.e.* D, H_1, H_2, F and h^2. The traits viz. number of sympodial branches, internodal distance, 1st retention node, seeds/locule and gin turn out showed significant dominant components (H_1 & H_2) of variation while other traits showed non-significant participation of dominance. Higher extent of D component over H_1& H_2 for number of sympodial branches, internodal distance, 1st retention node, seed per locule and gin turn out exposed additive nature of gene action in these traits (Table 5). In term of seeds per locule trait the variability was accounted by dominant gene action. These findings confirm the earlier studies in cotton by Subhan et al. (2001), Mahmoud et al. (2004) and, Ali & Awan (2009). Presence of additive nature of genes for all the traits suggested that it could be enriched through selection procedure right from F_2 population following pedigree method. Whereas, for seeds per locule, prominent genes having dominant effects were noticed at most of the loci, thus parents may be useful for heterosis breeding for this specific attribute (Singh et al., 1990; Chandio et al., 2003; Murtaza et al., 2005).

Degree of dominance ($H_1/D^{0.5}$) is an expression of dominance additive ratio. The value of this component greater than unity indicates over dominance, near unity refers complete dominance and lesser than unity indicates partial dominance type of gene nature (Falconer, 1989). Degree of dominance for all the traits except seeds/locule showed additive gene action. The character like seeds per locule displayed value of ($H_1/D^{0.5}$) higher than unity indicating the presence of over dominance effect. Similar findings for seed per locule were also reported by Nadeem & Azhar (2004) and Basal & Turgut (2005).

The parameter h^2 measures the direction of dominance (Ali & Awan, 2009). Significance value of h^2 showed unidirectional dominance (from parents to offspring). Value of $H_2/4H_1$ lies between 0.2 to 0.25 for most of the characters, confirming the irregular distribution of dominant and recessive genes. These findings coincided with the earlier studies by Basal and Turgut (2005), Murtaza et al. (2005) and Ali & Awan (2009).

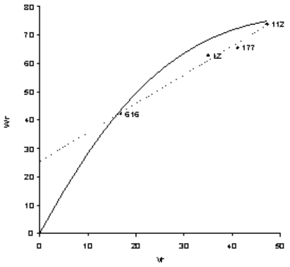
Estimates of the virtual occurrence of recessive and dominant alleles in the parental genotypes (F) was negative for sympodial branches, 1st retention node, stem thickness, boll no., gin turn out, inter nodal distance and fiber length. This exhibited that excessive number of recessive alleles are present in the material under study. This claim was confirmed by the values of $(4DH_1)^{0.5} + F / (4DH_1)^{0.5} - F$ which were lower than unity. However, the positive values for number of monopodial branches, boll weight, seeds per locule and seed weight revealed the prevalence of most dominant genes in the parental material. The significant blocking component (E) for most of the traits like number of sympodial branches, stem thickness, boll number, seed weight, seeds per locule, ginning out turn and fiber quality parameters pointed that these traits were mainly influenced by the environment.

Narrow sense heritability (h^2_{NS}) is to assess the extent of genetic variance in the studied material which is the main contributor in delta of genetic configuration through selection procedure (Falconer, 1989). Estimates of this component showed high values for most of the studied characters except seed per locule which was only 23%. High values of heritability indicated the involvement of additive genes which further indicates that selection procedure could be responsive for these characters. Improvement in these characters could be possible by following an appropriate selection procedure. However, lower heritability estimates for seeds per locule demonstrated the involvement of dominance effects in its inheritance. Naeem & Azhar (2008) and Ali & Awan (2009) also claimed high heritability values for most of the traits in cotton plant, whilst Murtaza, (2005) found low values ranges from (0.23) to high (0.75) for the studied cotton traits.

Table 5. Components of variation for different agronomic, boll, seed and lint traits in cotton for F1 generation

Traits	**Source of variation**									
	D	**H_1**	**H_2**	**F**	**h^2**	**E**	**$(H_1/D)^{0.5}$**	**$H_2/4H_1$**	**$(4.._1)^{0.5}$ + $F/(4..)^{0.5}$-F**	**$h^2_{n.s.}$**
P.H.	112.03 ± 1.17 *	-2.08 ±3.40	0.54 ± 3.14	-12.66 ± 3.05*	20.19 ± 2.13*	7.10 ± 0.52*	0.14	-0.064	0.41	0.9
Mono	6.31 ± 0.22*	1.14 ±0.63	0.87 ± 0.53	1.24 ± 0.56*	0.04 ± 0.39	0.12 ± 0.09	0.42	0.2	1.6	0.89
Symp.	2.03 ± 0.02*	-0.37 ±0.0*	- 0.29 ± 0.057*	-0.41 ± 0.05*	-0.18 ± 0.039*	0.24 ± 0.009*	0.43	0.21	0.62	0.88
Inter. di	0.21 ± 0.002*	-0.04 ± 0.00*	-0.005 ± 0.006*	-0.04 ± 0.006	-0.01 ± 0.004*	0.02 ± 0.001*	0.46	0.2	0.95	0.88
Stem thi	7.97 ± 0.002*	-0.01 ± 0.00^{NS}	-0.006 ± 0.005*	-0.01 ± 0.005*	0.0054 ± 0.004	0.01 ± 0.0009*	0.37	0.15	0.53	0.83
1st node	0.18 ± 0.005*	-0.03 ± 0.01*	-0.03 ± 0.01*	-0.05 ± 0.01*	-0.002 ± 0.009	0.03 ± 0.002*	0.46	0.2	0.5	0.84
Boll no.	219.28 ± 5.82*	18.10 ± 16.93	12.57 ± 15.63	-83.70 ± 14.97*	27.08 ± 10.60*	16.85 ± 2.60*	0.29	0.17	0.2	0.88
Boll wt.	0.54 ± 0.03*	0.12 ± 0.10	0.11 ± 0.09	0.12 ± 0.09	0.12 ± 0.06	0.03 ± 0.0	0.47	0.22	1.63	0.79
Seed/loc	0.04 ± 0.007*	0.08 ± 0.02*	0.08 ± 0.02*	0.02 ± 0.02	0.17 ± 0.01*	0.02 ± 0.003*	1.45	0.24	1.38	0.23
Seed wt.	1.45 ± 0.09 *	0.31 ± 0.25	0.27 ± 0.23	0.12 ± 0.22	0.11 ± 0.16	0.05 ± 0.04$_{NS}$	0.46	0.22	1.19	0.85
GOT %	2.15 ± 0.28*	-0.24 ± 0.80	-0.05 ± 0.74*	-1.50 ± 0.71*	-0.14 ± 0.50	0.77 ± 0.12*	0.33	0.06	-0.02	0.7
F.F.	17.84 ± 0.08 *	0.04 ± 0.24*	3.93 ± 0.22	-3.80 ± 0.21*	0.29 ± 0.15	0.35 ± 0.03*	0.05	0.23	-0.37	0.97

F.S.	0.12 ± 0.01*	0.03 ± 0.04	0.03 ± 0.03	0.02 ± 0.03	-.006 ± 0.03	0.02 ± 0.006*	0.48	0.24	1.42	0.66
F.L.	6.68 ± 0.15*	-0.02 ± 0.45	0.08 ± 0.42	-0.65 ± 0.40	-0.28 ±0.28	0.42 ± 0.07*	0.05	-1.14	0.02	0.89



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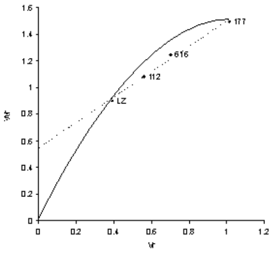

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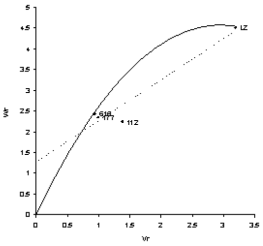

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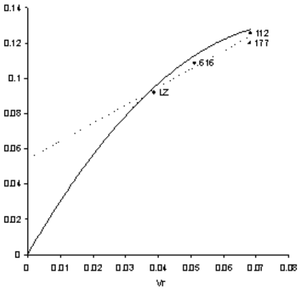

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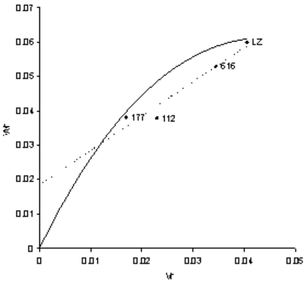

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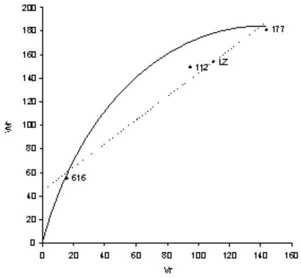

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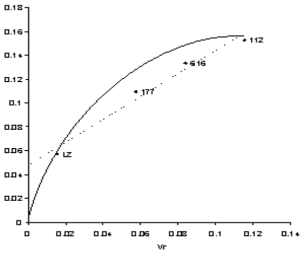

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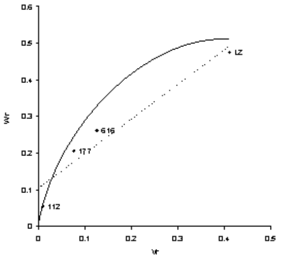

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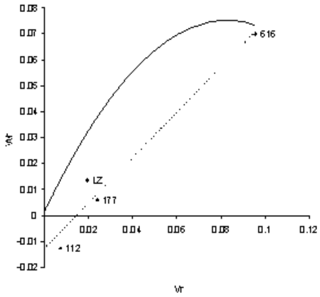

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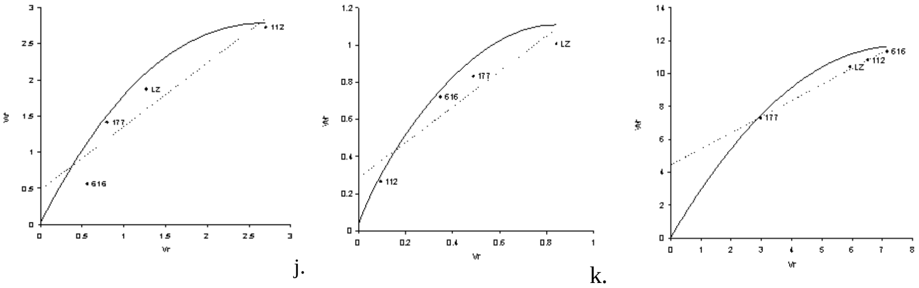
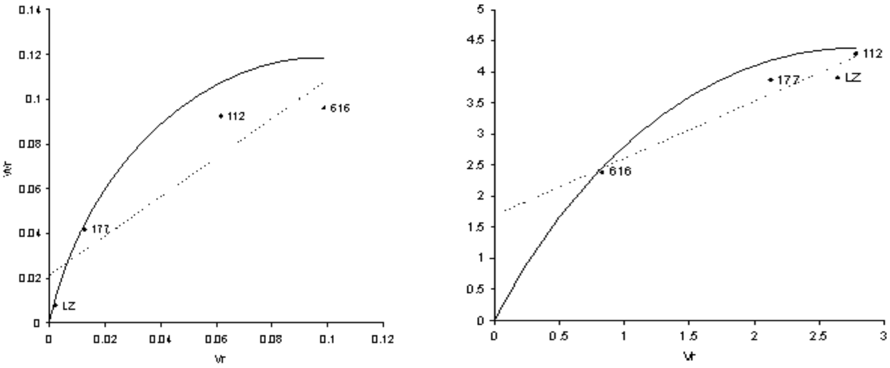


j. k. l.

Figure 1. Vr Wr graphs of (a). plant height (b). Sympodial branches (c). Monopodial branches (d). Internodal distance (e). Stem thickness (f). number of bolls (g). Ist retention boll (h). Boll weight (i). Seed locule (j). G.O.T% (k). Seed weight (l). Fiber finess



m. n.

Figure 1. Vr Wr graphs of (m). Fiber strength (n). Fiber length

Conclusion

Current study indicates significant genetic variation in the data depicting the effectiveness of genetic analysis. Although the pattern of inheritance of variation for most of the quantitative characters is appeared to be complex, however presence of additive gene action linked with high narrow sense heritability encourages the breeders to make improvement in all the characters following appropriate selection procedures. Presence of dominant gene effect in seeds per locule might be fruitful for hybrid vigor.

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