



Full Length Article

Genetics and Inheritance of Quantitative Traits using Multiple Segregating Populations in Cotton (*Gossypium hirsutum*)

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Abstract

Segregating populations are necessary for genetic analysis of qualitative and quantitative traits. Inheritance studies may produce reliable results if segregating populations are used. Seven F₂ segregating populations namely F₂(CRIS-134 × FH-Lalazar), F₂(BH-178 × MM-58), F₂(CIM599 × MNH-992), F₂(CRIS-134 × MM-58), F₂(CYTO-177 × CRIS134), F₂(COPPER-210 × MM-58) and F₂(BH-178 × CIM599) were developed through crossing eight varieties in contrasting parental combinations. Yield related data such as seed cotton yield, total counts of bolls, boll weight, plant height, direct fruiting branches counts, inter-nodal distance as well as number of nodes were recorded. Genetics of these traits in seven segregating populations was analyzed by observing correlations, heritability, as well as genetic advances over, mean. The traits showed continuous variation on histogram, indicating the traits are quantitative in nature. Common correlation in seven F₂ populations indicated a positive relationship of seed cotton yield with mediocre plant height, higher boll weight, boll size, number of bolls, counts of fruiting branches and inter-nodal distance. Heritability, as well as genetic advance over mean estimations, were high (>60%) for all the traits. High heritability in the traits depicts that the correlation between the traits was mainly genetic correlation, showing less environmental influence. High genetic advance depicts additive genes controlling for the traits. Higher seed cotton yield may be achieved by selecting mediocre plant height, increased sympodial branches and higher boll size. Segregating populations gives more genetic insight into quantitative traits. © 2020 Friends Science Publishers

Keywords: Cotton; Correlation; Gene linkage; Heritability; Inheritance; Segregation

Introduction

Yield related traits in cotton are quantitative or metric traits in nature (Wang *et al.* 2015; Ayubov *et al.* 2018). Many quantitative traits are correlated with others providing aid to selection aimed at changing the character with which it correlated (Falconer and Mackay 1996a). The genetic studies using non-segregating populations produced variable results, especially for correlation. Although, genetic cause of correlation is pleiotropy, if population developed from cross of two diverse parents, the linkage is a cause of transient correlation (Falconer and Mackay 1996a). Segregant population may be preferred for genetic studies of yield related traits. Being a complex trait, yield is influenced by many morphological traits. It would be fruitful to analyze the extent of transfer of traits related to yield improvement, inheritance and gene action to run breeding program in positive direction (Makhdoom *et al.* 2010). Analyzing the dependency of yield on its traits, correlation analysis is very

important (Iqbal and Rahman 2017; Ribeiro *et al.* 2018) especially in cotton (Salahuddin *et al.* 2010) and provides fruitful way of selection (Reddy *et al.* 2019). In cotton, correlation of fibre quality traits with structural parameters of plant is very important for breeders (Shen *et al.* 2007; Ribeiro *et al.* 2018). As these traits in cotton are quantitative in nature (Ayubov *et al.* 2018), the correlation analysis provides ease of selection and breeding (Arpat *et al.* 2004). Yield in cotton is measured in seed cotton yield per plant and considered as the most important trait. The trait is reported to be correlated with fruiting branches as well as total counts of bolls (Rahman *et al.* 2013; Khalid *et al.* 2018), boll weight (Rao and Gopinath 2013), number of seeds (Ribeiro *et al.* 2018), ginning outturn (Desalegn *et al.* 2009), lint weight (Jahan *et al.* 2019) whereas seed cotton yield had negative correlation with fiber strength (Méndez-Natera *et al.* 2012). Fibre characteristics are of prime importance in selection procedure. Fibre length has been reported to have inverse linkage with fibre fineness (Lin *et*

et al. 2005; Desalegn *et al.* 2009; Khalid *et al.* 2018). Lint weight has positive correlation with the traits related to industry such as length, fineness and strength of fibre (Jahan *et al.* 2019). Many structural features of plant such as height of main stem has an association with seed cotton yield (Rauf *et al.* 2004; Yan *et al.* 2019) whereas Salahuddin *et al.* (2010) observed no association between two traits *i.e.*, plant height and seed cotton yield. Yield in cotton also correlated with physiological traits like stomatal regulation of plants (Mahmood *et al.* 2020), osmotic adjustment and antioxidant activity (Abdel-Kader *et al.* 2015). Positive correlation between traits is of great importance in crop improvements as betterment in one trait indirectly improves other (Khalid *et al.* 2010).

Segregating populations provide a wide range of selection material for breeders. Important quantitative traits may be determined through the correlation analysis in segregating population thus providing basis for the selection (Sahito *et al.* 2016). Plant breeding necessitates correlation as well as heritability studies among different traits for the purpose of selection. Heritability of quantitative characters is the most important property, useful for its predictive role, expressing the importance of values which serves as guide to the breeding value. When heritability is high in correlated traits it shows that the correlation is mainly genetic correlation (Falconer and Mackay 1996b). Heritability estimates in segregating populations along with genetic advance estimation are also very useful in the selection process (Baloch *et al.* 2015). The correlations over the environments among the yield enhancing traits in a particular plant population help breeder in selection of desirable traits and combinations (Alkuddsi *et al.* 2013).

The F_2 population possesses maximum genetic variation because it is derived from selfing of heterozygous germplasm and is useful for breeder to select plants with the best possible trait combination leading to a better crop variety (Ahmad and Azhar 2000). The F_2 population is also very useful to study inheritance and gene linkage of different traits. Many researchers have worked on correlation analysis using the F_2 segregating population (Salahuddin *et al.* 2010; Ahmad *et al.* 2016; Jawahar 2017). Heritability (broad sense) studies were carried out by many researches in F_2 population (Baloch *et al.* 2015; Jawahar and Patil 2017; Kumar and Katageri 2017; Joshi and Patil 2018). Yield is an important trait and many other characters influence it and many researches have been conducted so far for accessing the linkage of the yield related trait in cotton (Tariq *et al.* 1992; Muthu *et al.* 2004; Alishah *et al.* 2008; Deguine *et al.* 2008; Bibi *et al.* 2011).

Most of the studies describing the results for heritability and association are based on true to type genotypes or cultivars which could not be representative of segregating generations. In this study we used seven diversified segregating F_2 populations to analyze inheritance pattern of quantitative traits.

Materials and Methods

Population development

A total number of eight cotton varieties were selected on the basis of diverse origins (Table 1). The seed was sown for germination in pots filled with sandy-loam soil following triplicated Complete Randomized Design in the glasshouse. An optimum temperature was maintained for seed germination at 24°C and for plant growth at 30°C. When flowering started, crossing was done in seven parental combinations (Table 1) to develop F_1 seed. Standard protocol for emasculation and crossing was followed (Poehlman and Sleper 1995). The F_1 plants were grown in the field next season to produce F_2 seeds. F_1 seed of each cross was sown on a single row. All field related practices were performed for the normal growth of the plants. When flowering started, plants were tagged and covered with butter paper bags to avoid contamination. Mature bolls were collected from field; seed was separated carefully through ginning.

Field evaluation

A total of seven F_2 populations (Table 1) were sown in the field following RCBD layout in three replications. Distance between rows was kept 60 cm and distance between plants was kept 45 cm. All field requirements such as irrigation and fertilizer were given as per cotton crop requirements.

Morphological data

Data were recorded from all plants of all three replications at maturity. Morphological data included vegetative traits. Plant height (cm) from the ground level to the topmost bud of main stem was calculated and noted by using wooden ruler. Total number of monopodial and sympodial branches was counted from each plant. Number of nodes was counted from zero node to the most upper node. Distance from the zero node to first node and distance between nodes on each plant was measured in centimeter. Yield related important traits such as total counts of bolls from all entries was observed. Size of cotton boll was observed from each plant. Boll size was observed from equally developed bolls as date of boll development was recorded. For statistical analysis small boll was recorded as 1, medium boll was recorded as 2 and large boll was recorded as 3. Boll weight (g) was recorded for each boll of each plant followed by dividing total bolls weight per plant by number bolls per plant to have average boll weight per plant. Number of locules per boll was counted from all entries. Seed cotton yield (g) is the total weight of seed and fibre before ginning were recorded at the mature stage.

Statistical analysis

Correlation analysis was done by following the method of Dewey and Lu (1959). Heritability was estimated by following the method of Wright (1968). Genetic advance for all the traits in all seven F₂ populations was estimated by formula according to Falconer and Mackay (1996b). Stacked frequency distribution graphs were computed using Origin Lab 8.5.1. Software, which helped to show in a single 2-D graph, segregation of a trait in seven F₂ populations. Heritability results were considered as high (>60%), moderate (30–60%) and low (0–30%) as described by Robinson (1966). Genetic advance per mean criteria was considered by following as proposed by Johnson *et al.* (1955), >10 (low), 10–30 moderate and high is more than 30% high.

a) The phenotypic correlations (r_p) between two traits x and y were calculated by using following formula:

$$r_p = PCOV(X, Y) / (PV_x \cdot PV_y)^{1/2}$$

Where;

PCOV (x, y) is the mean phenotypic covariance of x and y traits.

PV_x and PV_y are the phenotypic variance of the same traits respectively.

b) Following function of Wright (1968) is used for heritability estimates;

$$h^2B = \left[VF_2 - \frac{(VP_1 + VP_2 + 2VF_1)}{4} \right] / VF_2$$

Where;

VP₁ = Variance of P₁ populations

VP₂ = Variance of P₂ Populations

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c) Genetics advance in the next generation can be computed following formula by Falconer and Mackay (1996b).

$$\text{Genetic advance (GA)} = K \cdot \delta p \cdot h^2$$

Where;

K = selection differential, being 2.06 and 1.75 at 10% selection intensity, respectively.

δp = standard deviation of the phenotypic variance of the population under selection.

h^2 = heritability estimate in fraction of the traits under study

Results

The traits under study showed continuous variation as more or less smooth curves appeared showing the traits are quantitative in nature (Fig. 1 and 2). For plant height, the F₂ population of the cross (Copper-210×MM-58) exhibited the highest values (Table 2). The sympodial branches, internodal distance, zero node and seed cotton yield, with the population F₂ (CIM-599×MNH-992) showed upper values

Table 1: Parents their sources and Seven F₂ populations

Variety	Source	Segregant Populations	No. of plants
1: CRIS-134	CRI, Sakrand	1: (CRIS-134 × FH- Lalazar)F ₂	113
2: FH- Lalazar	ARI, Faisalabad	2: (BH-178 × MM-58)F ₂	142
3: BH-178	CRS, Bahawalpur	3: (CIM599 × MNH-992)F ₂	151
4: MNH-992	CRS, Multan	4: (CRIS-134 × MM-58)F ₂	89
5: CIM599		5: (CYTO-177 × CRIS-134)F ₂	131
6: CYTO-177		6: (COPPER-210 × MM-58)F ₂	127
7: COPPER-210	CCRI, Multan	7: (BH-178 × CIM599)F ₂	172
8: MM-58			

of mean. Highest mean for total bolls weight was from the population F₂ (BH-178×MM-58) and population F₂ (CRIS-134×Lalazar). The population F₂ (BH-178×CIM-599) showed maximum mean for the total number of nodes (Table 2). Correlations have been analyzed for all traits in each seven population and common correlations in all populations are selected (Table 2). Common correlation results depict that the genes for major yield trait seed cotton yield had were linked with the genes of boll weight, number of nodes and zero node. However, negative correlation also appeared between plant height and total counts of bolls. The trait size of boll had a strong gene linkage with the total locules, total counts of bolls, boll weight, number of fruiting branches, plant height and seed cotton yield. Locules numbers appeared in positive linkage with seed cotton yield, height of plant, fruiting branches and total counts of bolls. Number of locks appeared in variation from 3–5 locks per boll, increased number locks showed association with the yield. Number of fruiting branches, the most important trait for yield, had positive association with the total number of bolls and zero node. Inter-nodal distance showed correlation with all the traits under study except three traits boll weight, boll size and total number of nodes. Higher seed cotton yield, the main goal of a breeder, showed a strong correlation with higher sympodial branches as well as total counts of bolls.

Results exhibited high heritability for plant height, fruiting branches, boll weight, inter-nodal distance, seed cotton yield and total counts of bolls/plants in all studied F₂ populations (Table 4). Genetic advance estimates per mean were high for all populations except population F₂ (CIM-599×MNH-992) which showed moderate value. High values of genetic advance were detected in traits such as number of sympodial branches, total counts of bolls, zero node, counts of nodes, internodal distance, boll weight as well as in seed cotton yield in all F₂ populations.

Discussion

Genetic segregation shows continuous variation mainly because of two reasons; one is simultaneous segregation of many genes controlling the trait and another reason is superimposition of truly continuous variation produced because of non-genetic causes (Falconer and Mackay 1996c). The range values of traits in populations show

Table 2: Mean Table of seven F₂ populations for morphological and yield traits

Crosses	PH	SYM	TB	BW	SCY	NN	DBN	ZN	BS
F ₂ (CRIS-134×LALAZAR)	76.3	15.1	14.9	3.4	61.2	9.2	2	5.1	M
F ₂ (BH-178×MM-58)	93	17.1	14.7	2.8	48.8	9.2	2.5	4	S
F ₂ (CIM-599×MNH-992)	105.8	20.8	16	3	63.8	11	5.2	9.3	M
F ₂ (CRIS-134×MM-58)	108.9	10.3	11.1	2.4	50.9	5.4	3.8	4.3	S
F ₂ (CYTO-177×CRIS-134)	91.9	18.6	16.6	2.2	38.2	6.6	1.9	4	M
F ₂ (COPPER-210×MM-58)	111.8	21.4	20.5	2.7	55.3	8.9	3.4	5	S
F ₂ (BH-178×CIM-599)	75.4	12.6	8.9	3.1	27.1	11.1	2	5.1	S

Plant height (PH, cm), Sympodial branches (SYM), Total boll (TB), Boll weight (BW, g), Seed cotton yield (SCY, g), No. of nodes (NN), Distance between nodes (DBN, cm), Zero node (ZN, cm), Boll size (BS)

Table 3: Common correlations for important traits in seven F₂ populations (CRIS-134 × FH- Lalazar) F₂, (BH-178 × MM-58)F₂, (CIM599×MNH-992)F₂, (CRIS-134 × MM-58)F₂, (CYTO-177 × CRIS-134)F₂, (COPPER-210 × MM-58)F₂ and (BH-178×CIM599)F₂

Parameters	BS	BW	DBN	LOC	NN	PH	SCY	SYM
BW	0.69*							
DBN	0.11	-0.01						
Loc	0.16**	-0.01	0.14**					
NN	-0.062	0.26**	0.09	-0.04				
PH	0.18**	-0.24**	0.36**	0.26**	-0.18**			
SCY	0.31**	0.36**	0.20**	0.12**	-0.06	0.32**		
SYM	0.24**	0.009	0.30**	0.16**	0.06	0.47**	0.58**	
TB	0.25**	-0.15**	0.24**	0.13*	-0.22**	0.49**	0.83**	0.60**

Boll weight (BW), Boll size (BS), Distance b/w nodes (DBN), Number of locules (LOC), Number of nodes (NN), Plant height (PH), Seed cotton yield (SCY), Sympodial branches (SYM), Total boll (TB)

Table 4: Heritability and Genetic advance estimations of seven F₂ populations Plant height (PH), Sympodial branches (SYM), Total bolls (TB), Number of nodes (NN), Distance b/w nodes (DBN), Zero nodes (ZN), Boll weight (BW), Seed cotton yield (SCY)

Parameters	H2 % (b.S)							Genetic Advance							Genetic Advance per Mean						
	PP1	PP2	PP3	PP4	PP5	PP6	PP7	PP1	PP2	PP3	PP4	PP5	PP6	PP7	PP1	PP2	PP3	PP4	PP5	PP6	PP7
PH	90	92	89	90	93	88	91	29.1	33.8	28.6	41.4	37.6	41.0	39.3	38.1	36.4	26	37.9	40.8	36.6	52.1
SYM	58	88	81	69	37	87	74	5.0	7.5	5.5	5.1	2.1	8.5	4.4	54.0	81.6	43.6	60.8	27.7	68.0	76.9
TB	93	91	90	96	94	95	90	18.1	19.3	11.3	16.9	15.4	16.5	8.1	80.3	92.4	54.3	79.8	92.7	80.6	90.9
NN	85	80	88	94	90	65	86	8.2	5.1	6.6	2.6	8.1	3.5	4.7	88.8	55.1	59.7	47.8	48.3	38.6	41.8
DBN	98	74	92	98	86	75	87	1.5	1.1	3.43	1.4	1.7	1.1	0.0	70.1	45.3	62.7	37.9	84.6	33.2	0.4
ZN	87	86	84	87	86	86	63	4.0	2.5	4.5	2.9	3.5	3.4	2.5	77.1	62.7	54.7	65.6	85.8	66.5	49.6
BW	87	88	82	89	84	86	86	1.4	1.0	1.21	1.9	0.4	0.8	1.1	41.2	34.6	39.5	74.9	16.1	28.9	34.6
SCY	88	87	84	86	88	87	84	54.9	43.0	46.3	41.1	36.1	47.0	25.7	68.8	78.5	72	73.8	89.8	84.8	94.7

Pop1=F₂ (Cris-134×Lalazar) Pop2=F₂ (BH-178×MM-58) Pop3=F₂ (CIM-599×MNH-992) Pop4=F₂ (CRIS-134×MM-58)
 Pop5=F₂ (CYTO-177×CRIS-134) Pop6=F₂ (COPPER-210×MM-58) Pop7=F₂ (BH-178×CIM-599)

extent of variation in segregant population. Yield in cotton and number of bolls are inter-related (Alishah *et al.* 2008; Makhdoom *et al.* 2010). Negative correlation was observed in this study between total counts of bolls per plant and boll weight, showing improvement in boll number counts would reduce boll weight. This correlation is in common observation in fields, the variety with high number of bolls produces low weighted bolls and vice versa. Boll size is an important trait in high yield selection, it appears in this study that the traits is positively affected by both vegetative and reproductive growth.

The plant height has positive correlation with seed cotton yield (Suinaga *et al.* 2006; Karademir *et al.* 2010; Khalid *et al.* 2018), whereas some reported no association between two traits (Salahuddin *et al.* 2010; Masood *et al.* 2019). The positive correlation observed between plant height and seed cotton yield in present study (Table 3) and may depend whether the plants are tall or extra tall. Plant height in cotton with the range of 58.6–163.2 cm had negative gene linkage with yield whereas plant height with

range of 80–120 cm, which is required for mechanical harvesting had correlation positive with the yield (Yan *et al.* 2019). Mean values for plant height in this research were between 75–118 cm, as commercial varieties were used, which indicated positive correlation with yield. Plant height in cotton showed positive correlation with number of fruiting branches, total counts of bolls and zero node (Hussain *et al.* 2000; Naveed *et al.* 2004; Jawahar and Patil 2017).

Boll numbers and sympodial branches appeared in positive linkage, this is a natural correlation as sympodial branches are fruit bearing branches (Rauf *et al.* 2004; Rahman *et al.* 2013). The yield enhancing traits also showed association with the growth parameter first node. The trait is considered as an indicator of yield (Hussain *et al.* 2000; Iqbal *et al.* 2006; Taohua and Haipeng 2006; Leela *et al.* 2007; Khan *et al.* 2009; Karademir *et al.* 2010).

High heritability of different traits simplifies the selection process as it increases the reliability of selection (Baloch 2004) and it also indicates that the correlation was

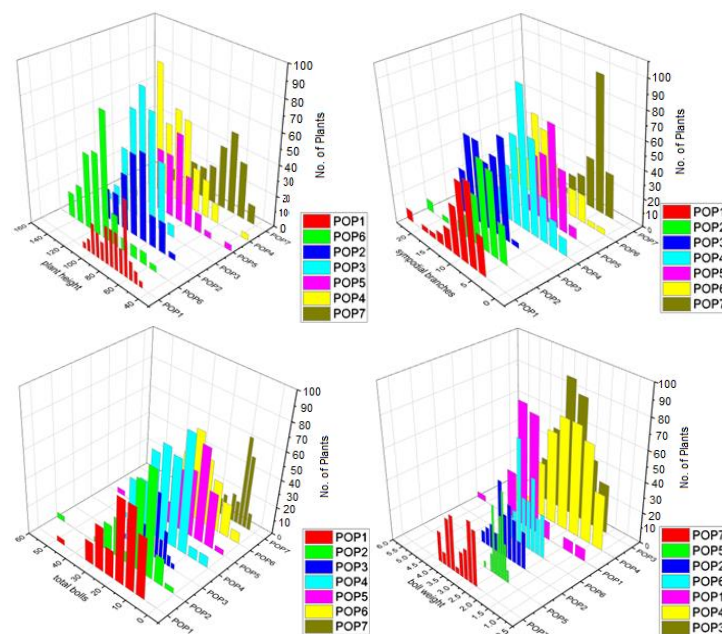


Fig. 1: Frequency distribution stacked graphs of seven F_2 populations for plant height, sympodial branches, total number of bolls and boll weight

Pop1= F_2 (Cris-134×Lalazar) Pop2= F_2 (BH-178×MM-58) Pop3= F_2 (CIM-599×MNH-992) Pop4= F_2 (CRIS-134×MM-58)
Pop5= F_2 (CYTO-177×CRIS-134) Pop6= F_2 (COPPER-210×MM-58) Pop7= F_2 (BH-178×CIM-599)

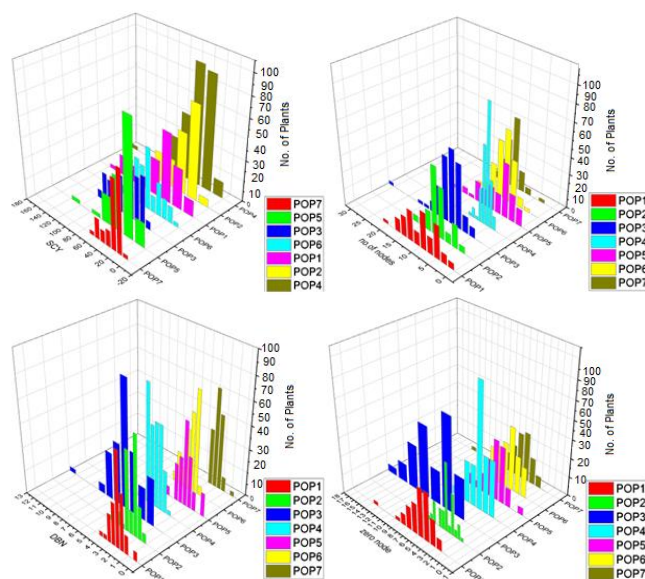


Fig. 2: Frequency distribution stacked graphs of seven F_2 populations for seed cotton yield (SCY), No. of nodes, distance b/w nodes (DBN) and zero node

Pop1= F_2 (Cris-134×Lalazar) Pop2= F_2 (BH-178×MM-58) Pop3= F_2 (CIM-599×MNH-992) Pop4= F_2 (CRIS-134×MM-58)
Pop5= F_2 (CYTO-177×CRIS-134) Pop6= F_2 (COPPER-210×MM-58) Pop7= F_2 (BH-178×CIM-599)

genetic rather than environmental (Falconer and Mackay 1996c). The high heritability observed for the traits indicates low environmental influences in the inheritance. For yield traits in cotton high heritability estimates (Dhamayanathi *et al.* 2010) and high genetic advance per mean (Jawahar and Patil 2017) are reported.

Conclusion

Seed cotton yield is quantitative trait in nature. Genes for high yield are associated with the genes of boll size, boll weight, number of locules, plant height, sympodial branches, distance between nodes and number of nodes.

Selecting these traits would enhance seed cotton yield in cotton. Traits correlated positively may be selected together, but care must be taken in selecting desirable traits that are negatively correlated with the yield. This information may be very helpful for the cotton breeders for selection of economic traits in segregating generations.

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Author Contributions

Muhammad Asif Saleem has planned and supervised the research. Arfa Zaheer, Muhammad Kashif, and Muhammad Ismael conducted field experiments. Muhammad Waqas Amjid conducted statistical analysis. Hammad Afzal and Muhammad Farjad Ateeq helped in write-up of the manuscript.

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