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Effect of Heritability, Genetic Advance and Correlation on Yield Contributing Traits in Upland Cotton

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ABSTRACT

This research was planned to study the heritability (broad sense), correlation, genetic advance and behavior of different characters in segregating population of upland cotton. The material consists of segregating population of fourteen crosses along with their seven parents. Parental varieties and segregating population show significant difference for all traits under the study. Plant height, ginning out turn (GOT), bolls per plant and yield per plant showed heritability ranging from 78.9 to 27.3. Significant genotypic correlation of yield with plant height was 0.698, bolls per plant was 0.930, GOT was 0.692, fiber strength was 0.548 and with fiber fineness was 0.435. Phenotypic correlation of yield per plant with plant height was 0.520, boll per plant was 0.894 and GOT was 0.476. It can be suggested that plant height, GOT and bolls per plant are important yield contributing traits as they are positively correlated with seed cotton yield per plant. High value for bolls per plant, GOT and yield per plant was recorded in BH-167 × V4 and CIM-534 × V4, which can be utilized in future breeding program.

Keywords: Ginning out turn, Broad sense, Gene action, *Gossypium hirsutum*, Segregating population

1. Introduction

Cotton is mainly cultivated for its fiber and seed oil (Masood et al. 2019). Worldwide, there are eighty countries which are cotton producers. Among them top six are China, India, USA, Pakistan, Brazil and Australia (Shuli et al. 2018). Cotton production plays a significant role in Pakistan's economy as its share in GDP is approximately 0.8% and value addition in agriculture is approximately 4.8%. In 2017-18, cotton production was 11.95 million bales and in 2018-19 production was 9.861 million bales, which was about 17.5% lower than the previous year (Pakistan Economic survey 2018-19). Major problems in yield reduction were mainly due to climatic change along with low genetic variability of cotton varieties, biotic and abiotic stresses (Panni et al. 2012). Developing a cultivar of upland cotton, having high yield, required genetic knowledge of yield contributing characters of cotton, which can be useful for breeder in the improvement of genetic structure of plant (Abbas et al. 2008). In yield improving program of cultivar through hybridization, success is based on heritable variability, selection and use of parental cultivars (Gul et al. 2014).

The study of genetic advance (GA) and broad sense heritability (H^2) will be helpful in identifying superior lines in segregating population. Those characters which have moderate to high value of GA and H^2 can be utilized in improvement of yield (Abbas et al. 2013). High to moderate value of H^2 was observed in number of seed per boll, boll weight and plant height (Raza et al. 2016), yield and boll per plant (Abbas et al. 2013).

In cotton, yield is influenced by different traits like boll weight, bolls number per plant and GOT (Ahmad et al. 2008). So, the indirect selection procedure for yield improvement was always preferred. Correlation study will be useful to understand the behavior of yield contributing characters (Alkuddsi et al. 2013). It can be helpful to understand the inter-relationships between different traits and in evolving selection principles (Kloth 1998). Different characters are either positively or negatively correlated with one another, so in case of positive correlation improvement in one trait may lead to an increase in the quality of other traits or vice versa (Desalegn et al. 2009). Yield was positively correlated with plant height (Salahuddin et al. 2010), boll weight, boll number per plant (Iqbal et al. 2006; Rasheed et al. 2009; Salahuddin et al. 2010) and monopodial branches (Iqbal et al. 2006). Thus, selection for these can be helpful in improving yield. For the improvement in yield, the behavior of yield contributing traits will be helpful in selection. For this reason, current experiment was designed to understand the behavior of yield contributing traits and also to access that the variation present in population was either due to genetic or environment. Purpose of this research was to assess H^2, GA and correlation in fourteen crosses and that information will be helpful in selection of subsequent generations and in development of genotypes, which have enhanced yield.

2. Material and Methods

2.1. Experimental material

The current research was designed to study H^2, GA and correlation to assess the performance of fourteen crosses along with parentage in segregating population of upland cotton. The germplasm of seven parents and their fourteen crosses (Table 1) were provided by the department of Plant Breeding and Genetics, Faculty of Agricultural Sciences and Technology (FAST), Bahauddin Zakariya University (BZU), Multan. Theses crosses were developed during 2013-2014 (Munir et al. 2016). The selection of parents for hybridization process was based on different morphological, yield characters and fiber traits. The experiment was conducted in a RCBD (randomized complete block design) with three replications and each replication consisted of 30 plants of each cross along with parental lines, during 2015, at the experimental area of the department of Plant Breeding and Genetics, FAST, BZU, Multan (30° 15' 33.0" N, 71° 30' 57.5" E) on loamy soil. The climate of Multan is arid to semi-arid with annual rainfall of up to 175 mm and average temperature during the growing season ranged from 28 °C to 37 °C. Row to row distance was 75 cm and distance between plants was maintained at 30 cm. Agricultural practices were applied consistently from seedling stage to harvesting. Data was recorded at maturity for characters such as plant height, number of bolls per plant (B/P), node of first fruiting branch (NFB), monopodial branches, number of seeds per boll (S/B), boll weight, ginning out turn (GOT), fiber fineness (FF), staple length (SL), fiber strength (FS) and yield/plant.

Table 1- List of parents and F_2 population

Breeding material	*Genotypes*
Parents	BT CIM-599, CIM-573, MNH-786, CIM-554, BH-167, MNH-886, V4
Crosses	BT CIM-599 × MNH-886, CIM-573 × MNH-886, MNH-786 × MNH-886, CIM-554 × MNH-886, BH-167 × MNH-886, BT CIM-599 × V4, CIM-573 × V4, MNH-786 × V4, CIM-554 × V4, BH-167 × V4, BT CIM-599 × BH-167, CIM-573 × BH-167, MNH-786 × BH-167, CIM-554 × BH-167

2.2. Statistical analysis

Data of all above mentioned traits was subjected to analysis of variance (Thomas & Maurice 2008) to evaluate variation among genotypes. Genetic parameters, genotypic, environmental and phenotypic variance equations were given below (Equations 1, 2 and 3, respectively), H^2 and GA equations were also given (Equations 4 and 5, respectively) were determined through method of variance component (Breese 1972; Larik et al. 1980 & 1987).

$$Genetic\ Variance = Genotype\ MS - Error\ MS \quad (1)$$

$$Enviromental\ Variance = Error\ MS \quad (2)$$

$$Phenotypic\ Variance = Genotype\ variance + Error\ variance \quad (3)$$

$$Broad\ Sense\ Heritability\ (H^2) = \frac{Genotype\ variance}{Phenotypic\ variance} \quad (4)$$

$$Gentic\ advance\ (GA) = \sqrt{Phenotypic}variance \times H^2\ \times k \quad (5)$$

K is constant = 2.06 at 5% selection intensity.

H^2 was categorized in three groups: High value was > 60%, moderate value was 30-60% and low value was 0-30% (Robinson et al. 1966). Johnson et al. (1955) also classified GA into different categories: High value (> 20), moderate value (10-20), and low value (0-10). The correlation between yield and yield contributing traits was identified through phenotypic and genotypic correlation analysis. Correlation study was carried out using statistical method given by Kwon & Torrie (1964) and formulae for calculation of genotypic and phenotypic correlation are given below (Equations 6 and 7). The analysis was performed using R STAT software for analysis of ANOVA, H^2 and correlation.

$$rp = {}^{Mij}\!\Big/\!_{\sqrt{[Mii).(Mjj)]}} \quad (6)$$

$$rg = {}^{\text{Covgij}}\Big/\sqrt{[\text{Var gi}).(\text{Var gj})]} \tag{7}$$

3. Results and Discussion

According to ANOVA, highly significant variation was found for plant height, NFB, monopodial branches, B/P, S/B, boll weight, GOT, SL, FS, FF and yield/plant (Table 2). Mean performance of crosses and their genotypic, phenotypic and environmental variations is given in Table S1 and S2, respectively.

Table 2- Mean squares of parents and F_2 population in cotton genotypes

Trait	*DF*	*MS*
PH	20	264.766**
NFB	20	9.072**
B/P	20	118.044**
MB	20	0.296*
S/B	20	39.925**
BW	20	0.463**
GOT	20	27.191**
SL	20	8.725*
FS	20	13.789*
FF	20	1.39*
YP	20	2051.27**

*; Significant at 5%, **; Significant at 1%; PH, Plant height; NFB, Node of first fruiting branch, B/P; Number of bolls per plant, MB; Monopodial branches per plant, S/B; Number of seeds per boll, BW; boll weight, GOT; Ginning out turn, SL; Staple Length, FS; Fiber Strength, FF; Fiber Fineness, YP; Yield per plant

High value (>60) of H^2 was found for B/P (81.9), yield/plant (78.9), plant height (78.5), GOT (78.1) and boll weight (60.5). While, moderate H^2 (30-60) were observed for NSPB (58.0), SL (54.1) and low value (0-30) of H^2 was observed for FF (27.3). GA showed high value for yield/plant (45.84), plant height (16.42), B/P (11.28), GOT (5.24) and SL (2.28). Boll weight and FF showed low value of GA that was 0.57 and 0.09, respectively (Figure 1).

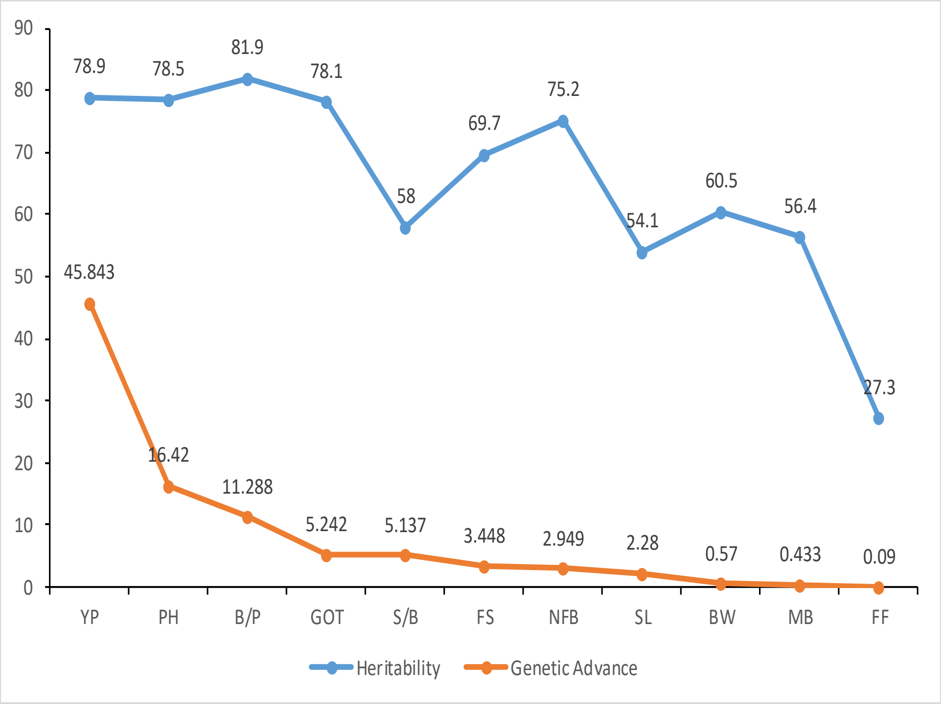

Figure 1- Estimation of heritability and genetic advance for seed cotton yield and its components (parents and F_2 population)

Genotypic relationship of yield/plant was found positive and statistically significant with plant height (0.689), B/P (0.93), GOT (0.692), FS (0.548), FF (0.435) and SL (0.43). Non-significant but favorable relationship was found among yield/plant and boll weight (0.311). B/P correlation with GOT (0.655) and FS (0.579) was positive and significant. Whereas, GOT was negatively correlated with FF (-0.248). In order to improve yield/plant selection is supposed to be based on B/P and GOT (Table 3). Phenotypic association between yield and B/P (0.894) was highly significant and favorable in selection. Favorable and significant correlation was also found between yield and plant height (0.52) as shown in Table 3.

Table 3- Genotypic (upper diagonal) and phenotypic correlation (lower diagonal) in parents and F_2 population for yield and its components

Traits	*PH*	*NFB*	*B/P*	*MB*	*S/B*	*BW*	*GOT*	*SL*	*FS*	*FF*	*YP*
PH	1	0.404	0.592*	0.031	0.521*	0.238	0.298	0.301	0.255	-0.634*	0.689*
NFB	0.286	1	0.196	0.309	0.338	-0.29	0.007	-0.287	-0.087	-0.457*	0.1
NBP	0.423	0.151	1	0.14	0.223	-0.054	0.655*	0.206	0.579*	-0.433*	0.930**
MB	0.026	0.249	0.088	1	0.343	-0.187	0.027	-0.345	-0.201	-0.506*	0.069
NSPB	0.316	0.236	0.149	0.176	1	0.391	-0.203	0.208	-0.472*	-0.054	0.361
BW	0.224	-0.215	-0.093	-0.15	0.195	1	0.162	0.626	-0.093	0.068	0.311
GOT	0.24	0.051	0.462	0.082	-0.195	0.115	1	0.029	0.536	-0.248	0.692**
SL	0.289	-0.19	0.193	-0.248	0	0.366	-0.035	1	0.102	-0.353	0.430*
FS	0.157	-0.076	0.406	-0.164	-0.24	-0.101	0.396	0.04	1	-0.289	0.548*
FF	-0.297	-0.218	-0.28	-0.169	-0.061	0.119	-0.113	-0.201	-0.16	1	0.435*
YP	0.520*	0.063	0.894**	0.013	0.235	0.352	0.476*	0.34	0.359	0.22	1

*; Significant at 5%, **; Significant at 1%, PH, Plant height; NFB, Node of first fruiting branch, B/P; Number of bolls per plant, MB; Monopodial branches per plant, S/B; Number of seeds per boll, BW; boll weight, GOT; Ginning out turn, SL; Staple Length, FS; Fiber Strength, FF; Fiber Fineness, YP; Yield per plant

H^2 provide an idea of variation present in a population either due to the environment (non-heritable) or genetics (heritable variation). But GA provides information of genetic variation that is either fixable (additive) or non-fixable variation (dominance or epistasis). H^2 estimation along with GA provide reliable tool for selecting segregating population (Alkudsi et al. 2013). Yield/plant is a complex trait and controlled by several polygenic characters, such as B/P, boll weight, GOT, NSPB and plant height. In current experiment, high value of H^2 was found for B/P, boll weight, GOT and plant height except NSPB. GA value for B/P and plant height was moderate, while other traits showed low value. Results showed that those traits which have moderate value of GA along with high value of H^2 can be improved by simple selection procedure, because of the presence of additive type of gene action. In Pakistan, cotton is usually grown in wheat-cotton crop rotation, where early maturing cotton varieties are preferred. Various characters contributed in earliness of cotton plant (Shappley et al. 1998). Earliness in genotypes can be predicted based on NFB trait in cotton. High H^2 value and low value of GA exhibited that this trait was under the influence of dominant gene action. Due to presence of non-fixable gene action, selection should be made in later generations (F_5 generation) in order to develop earliness in cotton. Additionally, monopodial branches were less desirable to breeder because of high infestation rate of pest. Usually, lower number of monopodial branches is preferred due to this reason (Munir et al. 2018). High value of H^2 was detected but GA value was low, which meant that non-dominant type of gene action was present. Muhammad et al. (2016) also found high H^2 value and low GA value and recommended that selection should be delayed up to later generation because of existence of non-additive type of gene action. In addition, monopodial branches were influenced by dominant gene action due to non-fixable variation therefore, selection should be delayed (Abro 2003). In the weaving industry, fiber traits have considerable importance. So, FS, SL and FF are significant fiber characters. Good spinning required better SL that is mandatory because of upgrading of spinning methodology (Tabasum et al. 2012). In fiber traits FS, FF and SL exhibited high to low H^2 value with low GA value. Therefore, for the improvement of such traits, selection should be delayed to later generations (F_4 or F_5 generation). Yield/plant has considerable importance in breeding program. GA along with H^2 showed high valuefor yield/plant which showed the presence of additive gene action. Khan et al. (2010) also described high value of H^2 and GA for yield/plant and recommended that selection can be performed in early population because of the presence of additive type of gene action. High H^2 and GA values were observed for yield/plant, B/P and plant height (Soomro et al. 2010). However, high H^2 value and low value of GA was also detected for boll weight (Rasheed et al. 2009), GOT (Shahzad et al. 2015) and S/B (Soomro et al. 2010). High H^2 value and moderate GA value was observed for B/P (Rasheed et al. 2009) and plant height (Khan et al. 2010; Raza et al. 2016). Moderate to high value of H^2 was reported for SL, FF and FS with low value of GA (Shahzad et al. 2015). The results exhibited the presence of non-heritable variations and suggesting the selection of these traits in later generations (Desalegn et al. 2009; Shahzad et al. 2015).

In results, positive association was found between yield/plant and plant height, B/P, GOT, FF and SL. It showed that strong correlation was present between these traits. Selection criteria based on these characters will lead to enhancement in yield/plant. Plant height and B/P showed high H^2 value and moderate GA value indicating that selection based on traits like plant height and B/P will be helpful in improvement of yield. However, selection based on GOT, FF and SL will not be productive due to presence of non-fixable gene action. Those traits which show high H^2 and GA values are easily improved through selection process and for those that have a low H^2 value, selection must be delayed to later generation. B/P was positively associated with GOT and FS. Thus, by selecting plants which have high number of B/P will lead to improvement in GOT and SL. Selection based on plant height will ultimately result in the increase in B/P because the presence of positive linkage between these traits. Positive correlation was found between plant height and GOT and B/P, ultimately leading to enhancement in yield/plant (Joshi et al. 2006). GOT had positive association with B/P, plant height and NFB and with yield/plant (Mustafa et al. 2007). For improvement in yield/plant, selection criteria depend on B/P and plant height because by improving yield/plant the following traits will also improve like GOT, FS and FF due to positive association of these traits with plant height and B/P. Significant and positive association was found between yield/plant and B/P (Iqbal et al. 2006; Rasheed et al. 2009) and plant height (Shahzad et al. 2015). Based on results and finding of other scientists, it can be suggested that for the improvement in yield/plant selection should be based on B/P.

4. Conclusions

A significant difference was shown by parental varieties and segregating population. Plant height, B/P, GOT and yield/plant show high H^2 value, but plant height and B/P showed moderate value of GA indicating that these traits were under the influence of additive type of gene action. It can be predicted that the traits which have a low H^2 value and also low GA value have non-fixable variation. Therefore, selection for such traits must be delayed to later generation. Plant height, B/P and GOT are important yield/plant contributing traits and are found to be positively correlated with yield/plant. Selection criteria based on plant height and B/P will lead to improvement in yield/plant. High number for B/P, GOT and yield/plant was recorded in BH-167 × V4 and CIM-534 × V4. This cross can be utilized in future breeding program and for yield improvement in cotton.

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This experiment is a part of MSc. (Hons.) thesis of the first author.

Abbreviations and Symbols	
H^2	Broad sense Heritability
GA	Genetic advance
PH	Plant height
MB	Monopodial branches
BW	Boll weight
YP	Yield per plant
NFB	Node of first fruiting branch
B/P	No. of bolls per plant
S/B	No. of seeds per boll
GOT	Ginning out turn
FF	Fiber fineness
FS	Fiber Strength
SL	Staple length

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Supplementary data Table 1- Mean performance of parents and F_2 population

Genotypes	*PH (cm)*	*NFB*	*B/P*	*S/B*	*MB*	*BW (g)*	*GOT (%)*	*SL (mm)*	*FS (g/tex)*	*FF (μg/inch)*	*YP (g)*
BT CIM-599 x MNH-886	123.93	10.10	23.30	27.92	1.38	4.28	32.14	28.32	27.21	4.23	99.88
CIM-573 x MNH-886	108.92	9.83	15.95	26.16	2.00	4.27	33.18	22.89	25.20	4.32	68.09
MNH-786 x MNH-886	123.56	13.56	18.47	28.14	1.82	3.27	35.30	21.93	28.21	4.19	60.09
CIM-554 x MNH-886	110.91	9.81	21.70	26.19	2.00	3.50	29.61	24.91	30.32	4.16	75.22
BH-167 x MNH-886	101.99	9.80	29.65	22.03	2.00	3.08	37.48	23.46	29.18	4.13	91.19
BT CIM-599 x V4	124.55	11.54	29.47	27.48	1.60	3.36	35.43	24.47	26.90	4.28	99.10
CIM-573 x V4	137.38	10.20	33.03	28.74	1.36	4.39	37.84	26.13	30.43	4.08	145.15
MNH-786 x V4	116.91	11.22	31.71	22.60	1.76	3.63	38.44	24.47	29.37	4.26	114.84
CIM-554 x V4	122.13	12.32	24.27	30.67	1.75	4.43	38.05	25.33	27.98	4.22	107.85
BH-167 x V4	134.64	12.76	36.23	26.24	2.15	4.03	39.44	28.03	32.17	4.05	147.23
BT CIM-599 x BH-167	127.86	12.93	25.89	23.00	1.60	3.55	37.46	24.47	28.10	4.17	89.63
CIM-573 x BH-167	128.55	11.45	30.33	29.61	2.30	3.84	37.37	23.17	28.25	4.36	116.52
MNH-786 x BH-167	124.12	10.45	20.68	19.49	1.36	3.63	34.08	26.23	29.67	4.13	75.05
CIM-554 x BH-167	124.31	12.85	28.03	31.82	1.61	3.40	28.77	25.67	26.00	4.26	94.30
BT CIM-599	111.14	13.67	25.69	22.31	1.64	3.40	36.46	24.59	29.37	4.20	87.25
CIM-573	126.40	9.71	26.53	20.94	1.93	3.60	37.45	25.17	30.00	4.06	95.37
MNH-786	134.66	12.57	40.70	31.61	1.95	3.86	39.44	26.67	29.33	3.96	157.03
CIM-544	114.42	10.82	29.65	21.83	1.45	3.90	37.78	24.83	29.53	4.33	115.71
BH-167	123.25	13.95	21.20	29.15	2.47	3.81	32.74	25.78	22.43	3.98	80.87
MNH-886	112.85	11.95	18.70	24.31	1.49	4.15	34.23	26.05	28.05	4.24	77.46
V4	110.83	6.86	16.95	25.84	1.50	4.16	36.57	28.32	26.00	4.34	70.51

PH; Plant height, NFB; Node of first fruiting branch, B/P; Number of bolls per plant, MB; Monopodial branches per plant, S/B; Number of seeds per boll, BW; boll weight, GOT; Ginning out turn, SL; Staple Length, FS; Fiber Strength, FF; Fiber Fineness, YP; Yield per plant

Supplementary data Table 2- Estimation of genotypic, phenotypic and environmental variance of parents and F_2 population

Traits	*GV*	*PV*	*EV*	*Mean*
YP	627.76	795.75	167.98	98.49
PH	80.89	102.99	22.10	121.11
B/P	36.65	44.74	8.08	26.10
S/B	10.72	18.48	7.76	26.00
GOT	8.29	10.61	2.32	35.68
FS	4.02	5.76	1.74	28.27
NFB	2.73	3.62	0.89	11.35
SL	2.27	4.19	1.92	25.28
BW	0.13	0.21	0.08	3.79
MB	0.08	0.14	0.06	1.77
FF	0.01	0.03	0.01	4.19

GV; Genotypic Variation, PV; phenotypic Variation, EV; Environmental Variation, PH; Plant height, NFB; Node of first fruiting branch, B/P; Number of bolls per plant, MB; Monopodial branches per plant, S/B; Number of seeds per boll, BW; boll weight, GOT; Ginning out turn, SL; Staple Length, FS; Fiber Strength, FF; Fiber Fineness, YP; Yield per plant