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Yield contributing economic traits in upland cotton

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Abstract

The study was conducted to find correlation between different economic traits in cotton using 10 parental genotypes and their 45 F_1 hybrids. The study revealed that plant height had positive correlation with number of sympodial branches per plant (r= 0.359), number of bolls per plant (r= 0.255), fiber length (r= 0.220) and seed cotton yield (r= 0.206) while plant height negatively correlated with fiber fineness (r= -0.299). Monopodial branches per plant had positive correlation with sympodial branches per plant (r= 0.317), number of bolls per plat (r= 0.655) and seed cotton yield (r= 0.418). Sympodial branches per plant had positive correlation with number of bolls per plant (r= 0.397) and seed cotton yield (r= 0.163). Number of bolls per plant showed positive correlation with seed cotton yield (r= 0.596), while number of bolls per plant had negative correlation with fiber length (r= -0.158). Boll weight had positive correlation with number of seeds per boll (r= 0.613) and seed cotton yield (r= 0.527). Number of seeds per boll had positive correlation with fiber length (r= 0.201) and seed cotton yield (r= 0.243). Ginning out turn percentage showed positive correlation with fiber length (r= 0.184) while this trait had negative correlation with fiber fineness (r= -0.194). Fiber length showed positive correlation with fiber strength (r= 0.220) while fiber length and fiber strength negatively correlated (r= -0.548) and (r= -0.188) with fiber fineness, respectively. So, it was concluded that for improvement in yield careful selection should be done for the traits which control yield.

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Introduction

Cotton crop is grown in many countries of the world. It is simultaneously a fiber as well as food crop. In addition to fiber it also provides cotton seed cake which is used for animal feed. It is considered as white gold as it contributes in industrial, economic and agricultural development of a country. Cotton crop contributes 1 % to the GDP and 5.5 % in the value addition of agriculture in Pakistan (Economic Survey of Pakistan, 2017-18). About 1.5 million population of Pakistan earn their livelihood from the cultivation of cotton (Hussain *et al.*, 2010). It is cultivated on 2699 thousand hectares in Pakistan (Economic survey of Pakistan, 2017-18).

There are many factors which influence the seed cotton yield. So for improvement in yield knowledge of correlation of different traits is essential. For the selection criteria of plants it is necessary to know about direct or indirect correlation (Alkudsi *et al.*, 2013). To produce high yielding varieties is the prime objective of plant breeders.

The seed cotton yield depends on many factors such as plant height, monopodial branches plant-1, sympodial branches plant-1, number of bolls plant-1, boll weight, number of seed boll-1 and GOT % etc. So it is necessary for plant breeders to know the extent of association between yield and its components which helps him for selecting the plants with required traits. So for improvement of seed cotton yield, earliness and fiber quality the knowledge about the association is exploited (Iqbal *et al.*, 2003).

So, this study was designed with the objective to find the association among various yield and yield contributing traits of upland cotton.

Material and methods

The research was conducted during 2016-2017 at the University of Agriculture, Faisalabad, Pakistan. Ten genotypes of upland cotton namely CIM-600, CRS-456, MNH-586, PB-38, Gumbo Okra, VH-57, Coker-100/A2, L.A. Fregobract, PB-52-NC-63 and PB-896 were included in this study. During year 2013-14 these parental genotypes were planted in pots in green house in winter season of the year and crossed to produce 45 F1 hybrids. During 22 May 2014 the parental genotypes along with their F1 hybrids were planted under randomized complete block design with three replications at the experimental area of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan.

The plant to plant and row to row spacing were kept 30 and 75 cm, respectively. All the recommended agronomic practices were followed from sowing till harvest. Five guarded plants were randomly selected per genotype from each replication for recording the data on yield and yield related traits including; plant height (cm), number of monopodial branches per plant, number of sympodial branches per plant, number of bolls per plant, boll weight (g), number of seeds per boll, ginning out turn (GOT%), fiber length (mm), fiber strength (g/tex), fiber fineness (µg/inch) and seed cotton yield (g). The collected data was subjected to analysis of variance following the method as by Steel *et al.* (1997) in order to determine significant differences in plant characters among the genotypes/F1 generations under study. The characters showing significant differences were further analyzed for correlation coefficients by the formula as outlined by Dewey and Lu (1959) using Minitab program of computer.

Results and discussion

Analysis of variance

The mean squares from the analysis of variance (Table 1) showed significant differences for all the traits i.e. plant height(PH), number of monopodial branches per plant(MB), number of sympodial branches per plant(SB/P), number of bolls per plant(BN), boll weight(BW), number of seeds per boll (SPB), ginning out turnpercentage (GOT%), fiber length(FL), fiber strength(FS), fiber fineness (FF) and seed cotton yield(SCY). Similar significant differences have been reported in cotton genotypes for PH, BN, BW, FLand FS(Farooq *et al.,* 2014). Dinakaran *et al.* (2012) also reported significant differences for BN, BW, GOTand SCY.

Table 1. Mean squares from ANOVA for various morphological plant traits used to characterize the upland cotton varieties and F_1 hybrids.

SOV	DOF	PH	MB	SB	BN	BW	SPB	GOT%	FL	FS	FF	SCY
Replications	2	9.55	0.95	44.71**	138.56*	0.004	0.086	32.05*	0.487*	8.73**	0.52	2.91
Varieties	54	508.90**	0.79**	5.77**	91.38**	0.39**	23.54**	204.53**	4.07**	2.91**	26.49**	1365.17**
Error	108	10.76	0.33	2.64	36.83	0.012	0.159	10.24	0.153	1.64	0.79	1.69

** = Significant at 0.05 and 0.01 probability levels, respectively

ns = Non-significant

Source of variation (SOV), Degree of freedom (DOF).

Correlation

A perusal of the data depicted that the magnitude of various correlation coefficients among genotypes were relatively higher than that among crosses. Yield is an ultimate objective of any plant-breeding program. It is a complex character particularly when it is considered in interaction with different yield contributing traits.PH had significant positive correlation with SB (0.359), BN/P(0.255), FL (0.220) and SCY(0.206) (Table 2).

Table 2. Correlation matrix among different cotton traits.

	PH	MB	SB	BN	BW	SPB	GOT%	FL	FS	FF
MB	0.074									
SB	0.359**	0.317**								
BN	0.255**	0.655**	0.397**							
BW	0.013	0.088	-0.004	0.133						
SPB	0.151	-0.063	0.102	-0.005	0.613**					
GOT	0.124	0.028	0.071	-0.101	0.021	0.075				
FL	0.220**	-0.141	-0.054	-0.158*	0.151	0.201**	0.184*			
FS	-0.057	-0.085	0.007	-0.093	-0.146	-0.074	-0.029	0.220**		
FF	-0.299**	-0.076	-0.012	-0.028	0.078	-0.049	-0.194*	-0.548**	-0.188*	
SCY	0.206**	0.418**	0.163*	0.596**	0.527**	0.243**	0.073	-0.110	-0.117	-0.010

*= $p<0.05$

**= p<0.0.

These results were also confirmed by Rahman *et al.* (2013) who reported that SCY had positive correlation with SB and BN. Khokhar *et al.* (2017) also reported PH had positive significant genotypic correlation (0.241) with SB. Erande *et al.*(2014) found positive significant correlation between PH with BN (0.783) and SCY (0.48). Positive association of MB with SB (0.317), BN (0.655) and SCY (0.418) was observed as earlier same finding was reported by Farooq *et al.* (2013) for MB with SB and BN. Alishah *et al.* (2008) noted that MB had highly significant genotypic association with BN (0.693). On the other hand, SB showed positive correlation with BN (0.397) and SCY (0.163). BN were positively correlated with SCY (0.596). These results were in confirmatory with Kamrul *et al.*, 2013. BW with SPB (0.613) and SCY (0.527) were positively linked. It was also confirmed by Rao and Gopinath (2013) that BW positively influenced the SCY. Salahuddin *et al.* (2010) found SCY had positive and strong correlation with SB (0.567), BN (0.959) and BW (0.597). Khokhar *et al.* (2017) reported BW had high positive significant genotypic correlation (0.531) with SCY. Alishah *et al.* (2008) also observed that BW had positive genetic correlation (0.428) with SCY. SPB positively associate with FL (0.201) and SCY (0.243). Chattha *et al.*, 2013 observed the same finding. Positive link of GOT % with FL (0.184) was found. GOT% showed positive association with lint index (Erande *et al.*, 2014). A positive correlation recorded between FL with FS (0.220). El-Yazied *et al.* (2014) reported the same finding for these traits.

Conclusion

From this study, it is concluded that PH, MB, BN, BW, and SPB had highly significant positive correlation with SCY. Similarly, SB exhibited significant association with SCY. So, more attention should be given to these traits for the improvement of SCY during breeding program and may be focused on the selection priority to these traits for development of high yielding varieties.

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