RESEARCH PAPER

Genetic variability, association analysis and path analysis in advance breeding material of *Gossypium hirsutum* L.

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Abstract

Pakistan is known as an agricultural land around the world and cotton (*Gossypium hirsutum* L.) is an economically substantial rich harvesting crop in Pakistan having a good share in GDP. This experiment was planted to observe the associated relationship of different agronomic traits with the foremost seed cotton yield (SCY). Fifteen F_4 lines and a cotton standard variety (S12) were under investigation. The recorded data was processed through analysis of variance which depicted the significant genetic variation among the germplasm. The genotypic correlation coefficient analysis revealed that number of bolls (NB), boll weight (BW) and staple length have significant positive interrelations with the seed cotton yield (SCY) but plant height (PH), sympodial branches (SB) and monopodial branches (MB) have positive and non-significant interrelations with seed cotton yield (SCY). The path coefficient analysis showed(0.6987)ginning out turn (GOT), number of bolls (NB) (0.4136) and boll weight (BW) (0.4295) have direct impact on the seed cotton yield (SCY). Consequently, our study revealed that ginning out turn (GOT), number of bolls (NB) and boll weight (BW) should be considered substantial while selecting the genotypes for the breeding purpose.

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Introduction

Cotton (*Gossypium hirsutum* L.) is one of the substantial rich harvesting crops of many agricultural areas. It is cultivated in tropical and subtropical areas as an annual crop. Cotton seeds comprises of 18% oil (Stewart and Russi, 2010), so cotton not only fulfill the fiber requirements but also take part in food availability in the form of edible oil (Sahito *et al.*, 2016). Cotton plays a substantial role in Pakistan economy as export commodity. The cotton fiber is mostly composed of cellulose and botanical purpose of fiber is to disperse seeds for next generation. Seed cotton yield (SCY) is supported by its other interrelated yield components. This relation may be because of phenotypic or genetic factors (Wahid *et al.*, 2014). These agronomic characters show up in a systematized way and produce the main returns seed cotton yield (SCY). It is obvious that these yield components are interlinked with seed cotton yield (SCY) in one way or the other (Abdullah *et al.*, 2016). Interrelation study is a substantial tool for the cotton breeders. It is because, most of the traits are associated with other characters, and such relationship may be due to pleiotropic effect of a gene or presence of 2 genes on the single chromosome or because of environmental effect (Salahuddin *et al.*, 2010). It also occurs that due to yield components interrelations, improvement of the one character may have some influence on the other traits. The improvement in the yield of seed cotton may result in the reduction of fiber length and vice versa (Azeem and Azhar, 2006).Path coefficient analysis is division of correlation into unidirectional or alternate pathways which permit the breeders to identify the appropriate characters which have influence on the yield in this way it is helpful in the effective selection in cotton breeding (Reddy *et al.*, 2015). Present experiment of interrelation coefficient and path coefficient analysis involves fifteen F_4 lines with standard variety (S12) of cotton to study the relationship between seed cotton yield (SCY) and other yield elements and to separate the observed genotypic interrelation into their indirect and direct effects by other yield components which could be used as assortment criterion in the breeding process.

Many physiological and morphological characters affect the yield, for breeders it is important to know more about direct and indirect correlation among the different traits while selecting plants for breeding. Path coefficient analysis also provides aid in selection because simple correlation coefficient analysis is not enough. As path coefficient analysis portioned the correlation into direct and indirect components. So it's important to know more about the traits which contribute to the yield and their direct and indirect association to successfully design an effective breeding program. It is helpful in the procedure of selection and empowers the breeders to select a genotype on the basis of two or more traits simultaneously (Salahuddin *et al.*, 2010).

Methodology

Material and sowing method

The field trial was carried on in the department of plant breeding and genetics farm of the University of Agriculture Faisalabad during the normal period of cotton. The genotypes of fifteen F_4 lines from the following crosses 149F x H499, NF 801-2 x CIM446, BUO1724 x NF801-2, FH1000 x NF801-2, BUO1724x149F, FH1000 x H499, DPL 26 x H499, CIM 446 x 149F, H499 x B557, CIM 506 x NIAB 111, CIM 506 x MNH516, MNH 516 x NIAB 111, CIM 506 x CRIS 191, CRIS 191 x NIAB 111, MNH 516 x FH 901 along with a standard variety S12.

The germplasm was sown in bed sowing method using randomized complete block design. Plants were sown in 30cm and 75cm PxP and RxR distance respectively in three replications. All recommended treatments were carried out equally throughout the whole experiment and data was collected from five well protected plants from all replications.

Phenotypic data collection

Data of the following characters was recorded, monopodial branches (MB), sympodial branches (SB), plant height (PH), number of bolls (NB), boll weight (BW), seed cotton yield (SCY), fiber fineness (FF), fiber strength (FS), staple length (SL) and lint percentage.

Statistical analysis

Data was processed through biometrical techniques of analysis of variance; phenotypic correlation and genotypic correlation among the agronomic traits under research were followed as recommended by Kwon and Torrie, (1964).

Path coefficient analysis was implemented using genotypic interrelation according to Dewey and Lu, (1959) in yield concerning characters keeping seed cotton yield (SCY) per plant as consequential variable.

Results and discussion

The analysis of variance of the traits exhibited that highly significant variations were found among all the characters under investigation. These results showed that research material used for the experiment were genetically different, so the breeding material can be used for the improvement of these traits.

Table 1. Genotypic correlation coefficient.

	SB	MB	NB	BW	PH	GOT	SL	FF	FS	SCY
						Genotypic Interrelation Matrix				
SB	1.000	0.4051*	0.1650	-0.0614	0.0072	0.1268	0.0256	0.2575	-0.0180	0.0632
MB		1.000	0.2372	0.0562	-0.0575	-0.0957	-0.0778	-0.3965	0.2751	0.1870
NB			1.000	0.4659*	-0.1765	0.3477	0.0167	0.1583	0.3840	0.6089**
BW				1.000	0.2241	0.4584*	0.7092**	-0.2375	-0.5077*	0.9580**
PH					1.000	-0.4531*	0.1559	-0.1280	-0.1083	0.1035
GOT						1.000	-0.4567*	0.4284	0.0692	-0.2466
SL							1.000	-0.3281	-0.1475	0.6264*
FF								1.000	0.0685	-0.1695
FS									1.000	-0.5185*
SCY										1.000

Genotypic and Phenotypic Correlation

Table 1 showed genotypic correlation matrix and table 2 exhibited phenotypic correlation matrix, correlation amongseed cotton yield (SCY) with characters which has impact on seed cotton yield (SCY). Plant height (PH), sympodial branches (SB), monopodial branches (MB) had positive but nonsignificant interrelation with seed cotton yield (SCY) at genotypic level. While number of bolls (NB), boll weight (BW) and staple length (SL) had highly significant interrelation with seed cotton yield (SCY).

Table 2. Phenotypic correlation coefficient.

Phenotypic Interrelation Matrix										
	SB	MB	NB	BW	PH	GOT	SL	FF	FS	SCY
SB	1.000	0.4286*	0.2285	-0.089	0.0370	0.0676	0.1377	0.1368	-0.0183	0.1431
MB		1.000	0.0690	-0.0281	2.6658	0.0253	0.0461	-0.2651	0.1631	0.0135
NB			1.000	0.3240	-0.1482	0.2574	0.0676	0.1579	0.3277	0.6189**
BW				1.000	0.1874	0.3578	0.2179	0.2175	-0.4284	0.8189**
PH					1.000	-0.2685	0.2878	-0.0470	-0.0868	0.0762
GOT						1.000	-0.1675	0.3689	0.0853	-0.2147
SL							1.000	-0.1555	-0.3362	0.1853
FF								1.000	0.06476	1.1688
FS									1.000	-0.3578
SCY										1.000

Ginning out turn (GOT), fiber fineness, and fiber strength had negative interrelation with seed cotton yield (SCY). Boll weight (BW) had +ive and significant interrelation with ginning out turn (GOT) and staple length but negative interrelation with fiber fineness (FF) and fiber strength (FS). Plant height (PH) had negative interrelation with ginning out turn (GOT), fiber fineness (FF) and fiber strength (FS). On the other hand sympodial branches (SB) had positive and significant interrelation with monopodial branches (MB). Similar findings were observed in previous studies of Rasheed *et al.*, (2009), Salahuddin *et al.*, (2010), Reddy *et al.*, (2015), Sahito *et al.*, (2016) and Abdullah *et al.*, (2016). Contrasting results were also observed by Preetha and Raveendran, (2007) and Erande *et al.*, (2014).

Table 3. Path coefficient analysis.

Path Analysis									
	SB	MB	NB	BW	PH	GOT	SL	FF	FS
SB	-0.0087	0.4610	0.2902	0.0064	0.0001	-0.1625	0.0009	-0.2956	0.0033
MB	1.1296	-0.0067	0.4367	-0.0051	-0.0047	0.1275	-0.0037	0.4589	0.3872
NB	-0.2664	1.8759	0.4136	-0.3345	-0.1853	-0.5719	0.2529	0.2931	0.6820
BW	-0.0071	0.8230	0.0864	0.4295	0.2134	-0.5719	0.2529	0.2931	0.6820
PH	0.0777	-0.3534	-0.1717	0.5590	-0.4399	0.5853	0.0003	0.1461	0.1483
GOT	0.1159	0.6615	-0.3571	-0.4496	0.2146	0.6987	-0.1635	0.4703	0.0091
SL	0.0093	0.0031	-0.5439	0.1477	-0.1389	0.4249	-0.5021	0.3891	0.1980
FF	0.4524	0.2960	0.1983	-0.1230	0.3444	0.4091	-1.1459	0.3427	0.0090
FS	-0.3277	0.7533	0.3921	-0.9915	0.0039	0.0059	-0.0087	-1.3397	0.2272

While at the phenotypic interrelation of seed cotton yield (SCY) with other characters under study were seed cotton yield (SCY) had positive interrelation with sympodial branches (SB), monopodial branches (MB), plant height (PH), staple length (SL) and fiber fineness (FF). Number of bolls (NB) and boll weight (BW) had positive and highly significant interrelation with seed cotton yield (SCY). Ginning ou turn and fiber strength had negative interrelation with the constant factor. Sympodial branches (SB) had positive and significant interrelation with monopodial branches (MB). Boll weight (BW) had negative interrelation with number of sympodial and monopodial branches (MB).

Path coefficient analysis
Path coefficient analysis is used to observe indirect and direct correlations which have impact on the traits of interest. Genotypic interrelation was used for path coefficient analysis because genotypic level is more substantial in breeder's point of view. Results of path coeffient analysis are in table 3. As path coefficient analysis results revealed that sympodial branches (SB), monopodial branches (MB), plant height (PH), and staple length (SL) had indirect correlation with the seed cotton yield (SCY). A critical over view of table 3 exhibited that number of bolls (NB) (0.4136), boll weight (BW) (0.4295) and 0.6987ginning out turn (GOT) were the characters which had direct and utmost contribution to the seed cotton yield (SCY). With this respect these characters can be used for assortment of good germplasm. Abdullah *et al.*, (2016), also revealed similar findings that boll weight (BW) and number of bolls (NB) had direct effect on seed cotton yield (SCY). Rasheed *et al.*, (2009), Reddy *et al.*, (2015) and Sahito *et al.*, (2016) also had alike results, while Salahuddin *et al.*, (2010) narrated that sympodial branches (SB) also had small effect on seed cotton yield (SCY).

Conclusion
From the findings of this research we would be able to know that among ten characters related to yield studied, that ginning out turn (GOT) (0.698) had major effect on seed cotton yield (SCY) followed by number of bolls (NB) (0.4136) and boll weight (BW) (0.4295). Number of bolls (NB) and boll weight (BW) also had extremely significant positive interrelation

with the seed cotton yield (SCY) along with staple length. These results are concerning with genotypic interrelation. While from phenotypic interrelation results showed just number of bolls (NB) and boll weight (BW) along with significant correlation among number of sympodial with number of monopodial. However it was clear through the correlation and path coefficient analysis that ginning out turn (GOT), number of bolls (NB) and boll weight (BW) had extreme effect on the seed cotton yield (SCY). It is concluded from instant experiment that selection of high yielding genotypes during any research, these yield components ginning out turn (GOT), number of bolls and boll weight (BW) should be considered as major characters.

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