Research article

Estimation of genetic divergence, association, direct and indirect effects of yield with other attributes in cotton (*Gossypium hirsutum* L.) using biplot correlation and path coefficient analysis

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Abstract: Genetic variation, Principle component analysis and Path analysis were analysed in sixty cotton (*Gossypium hirsutum* L.) genotypes and Randomized Complete Block Design was followed with three replications. A wide spread variation was observed among all the investigated attributes. Principle component analysis was worked out to identify the diverse genotypes. Bolls per plant, sympodia per plant and boll weight showed noteworthy positively association with seed cotton yields. Path analysis exposed uppermost positive direct consequence of number of bolls per plant on total yield whereas sympodia per plant and boll weight had maximum indirect positive effect through number of bolls on seed yield. The correlation analysis and path coefficient analysis and Principle component analysis together suggested that these attributes and genotypes should be given prime emphasis in effective selection to get better cotton seed yield.
Keywords: Cotton - Path analysis - Principle component analysis - Seed yield.

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) referred as "White gold" is a premier cash and fibre crop. It is major contributor towards financial stability of more than 80 countries with annual production of 20 million tons (Farasat *et al.* 2014). Characterization and conservation of genetic material in form of genotypes, best performing breeding lines, landraces, wild lines is of significance value in evolutionary breeding and genetic process (Haidar *et al*. 2012). Exploitation of genetic diversity through various morphological and agronomic characters have been done for triumphant hybridization program which need perfect selection because environment greatly influence on these traits and selection process (Ahmad *et al*. 2012). Therefore, considerable emphasis should be given to evolve highly productive cotton varieties. Cotton production either in seed yield or lint depends on characters like plant height, direct fruit bearing branches (sympodial) and indirect fruit bearing branches (monopodial), boll weight (BW), bolls per plant, seed index, ginning out tern (Salahuddin *et al.* 2010). Comprehensive understanding about the crop nature, performance level and association of numerous agronomic attributes with yield is necessary for plant researcher to tackle the cotton yield limiting constraints.

Being an important asset to cotton breeders, correlation between yield and yield contributing attributes, is principal endeavour to explore relation among traits and which plant parameters should be selected first to boost up cotton seed and lint yield (Khakwani *et al.* 2012). Path analysis, handy technique, permits plant researchers to select particular attributes that helps in the understanding of contribution of numerous traits in total variation by partitioning the total correlation into direct and indirect effects (Shahriari *et al.* 2014). Multivariate statistical technique mainly principal component analysis (PCA) utilized by breeder to assess genetic variation, which leads to exploration of elite and phenomenal genotypes that could be used as diversified genotype for a future cotton hybridization program (Rehman *et al.* 2015).

Keeping in view the above facts about diversity in cotton, the present investigation was to explore genetic diversity, notify extraordinary genotype and direct and indirect effect of important yield contributing traits on yield.

MATERIALS AND METHODS

The present research study was investigated during 2013 at agricultural experimental area of Bahauddin Zakariya University, Multan. Experimental research material was comprised of sixty Cotton (*Gossypium hirsutum* L.) genotypes and sown in 3 replications following Randomized Complete Block Design (RCBD) with row to row (R×R) and plant to plant (P×P) distance of 2.5 feet and 1 feet respectively. All recommended agricultural implementations like spraying, fertilization; weeding, irrigation and cotton production technology was adopted in every replication. The data were collected from five tagged plants of each replication for plant height (PH), number of monopodial branches, number of sympodial branches, boll weight (BW), number of bolls per plant , seed index (SI), yield per plant (YPP) and ginning out turn (GOT%).

Collected data was subjected to analysis of variance using Statistix 8.1 (Umar *et al.* 2014*).* Principle component analysis (PCA) was performed on the mean data using XLSTAT software (Khodadadi *et al.* 2011) and path analysis was done by following the method of Dewey & Lu (1959) through SPSS Amos v20.0.0.

RESULTS

Analysis of variance (ANOVA) and heritability for various plant attributes

Analysis of variance depicted widespread significant variation (P<0.01) and suggested high level of genetic variability among all yield contributing attributes in studied traits (Table 1). Among all attributes yield per plant presented highest heritability followed by bolls per plant and sympodial branches as shown in table 1.

Table 1. Analysis of variance and heritability values of yield and other quantitative attributes.

S.O.V	DF	PH	MOP	SYP	BPP	BW	SI	GOT	YPP
Reps	2	54.80	0.34	0.82	1.51	0.076	0.44	2.71	5.20
Genotypes	59	3454.2**	0.61**	71.29**	337.9**	0.39**	2.72**	13.16**	1750.46**
Error	118	146.59	0.19	1.31	3.92	0.061	0.24	2.49	17.69
h² (%)		88.26	43.2	94.68	96.59	64.02	77.26	58.82	97.02

Note: DF, Degree of Freedom; PH, Plant height; BPP, Bolls per plant; MOP, Monopodia per plant; YP, Sympodia per plant; BW, Boll weight; SI, Seed Index; GOT, Ginning out turn; YPP, Yield per plant.
**, Highly Significant.

Principal component analysis (PCA)

Mean data of sixty cotton genotypes were calculated and PCA was applied to sum up momentous variation from collected mean data. Out of eight principal components, three principal components (PCs) depicted more than one eigen value so these three components have given due consideration for further explanation (Table 2).

First two principle components PC1 and PC2 explained 47.57% and 16.78% of variation respectively with 63.36% cumulative variance among all attributes. The attributes of worthy importance in PC1 were sympodial branches, number of bolls per plant, boll weight (BW) and yield per plant (YPP) with maximum scores, depicted more contribution towards total variation. The second PC was more associated with plant height and seed index attributes (Table 2).

Relationship among Attributes

Correlation of all recorded data of cotton genotypes presented positive and significant as well as non-significant association among different characters. By keeping the yield as supreme importance we observe the relation of all other traits with yield. Outcome of Biplot graph depicted that sympodial branches per plant, bolls per plant and boll weight (BW) had highly momentous and positive association with cotton yield. Ginning out turn (GOT) and monopodia per plant exhibited positive relationship with cotton yield. In this study bolls per plant have a direct influence and positive correlation with yield. In our study positive and significant correlation was observed between boll weight (BW) and cotton seed yield (Fig. 1).

Genotype by trait analysis

Spread out graph termed as polygon created in PCA showed wide spread variation in cotton genotypes. Genotypes which are present at vertex of polygon in biplot graph has longest distance from the origin, illustrated

maximum variation for quantitative attributes and could be utilized as parental lines in broadening the genetic base of cotton through breeding program. FH-1000, S-120, MG-6, MG-14 RH-1, MNH-147, CIM-20 and CIM-70 present at the vertex of polygon and farthest from origin depicted maximum diversity while CIM-240 followed by CIM-448 and MNH-554 nearest to origin depicted lowest genetic diversity (Fig. 1).

Table 2. Eigen values, proportion of variability and quantitative traits that contributed to the eight principal components.

| Statistical Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigenvalue	3.726	1.343	1.028	0.855	0.664	0.333	0.043	0.008
Variability (%)	46.572	16.784	12.854	10.691	8.302	4.157	0.535	0.105
Cumulative (%)	46.572	63.356	76.210	86.901	95.203	99.360	99.895	100.000
Traits								
PH	0.019	**0.406**	0.323	0.155	0.066	0.033	0.000	0.000
MOP	0.094	0.027	0.535	0.326	0.000	0.017	0.000	0.000
SYM	**0.915**	0.000	0.004	0.000	0.028	0.025	0.027	0.000
NOB	**0.943**	0.009	0.000	0.002	0.021	0.015	0.006	0.004
SI	0.002	**0.696**	0.007	0.023	0.246	0.025	0.000	0.000
BW	**0.639**	0.002	0.003	0.093	0.056	0.207	0.000	0.000
YPP	**0.951**	0.009	0.002	0.001	0.019	0.006	0.010	0.004
GOT	0.162	0.194	0.155	0.256	0.228	0.006	0.000	0.000

Note: PH, Plant height; BPP, Bolls per plant; MOP, Monopodia per plant; SYP, Sympodia per plant; BW, Boll weight; SI, Seed Index; GOT, Ginning out turn; YPP, Yield per plant.
Bold values of each attribute depicted higher squared cosine value in eight principle components.
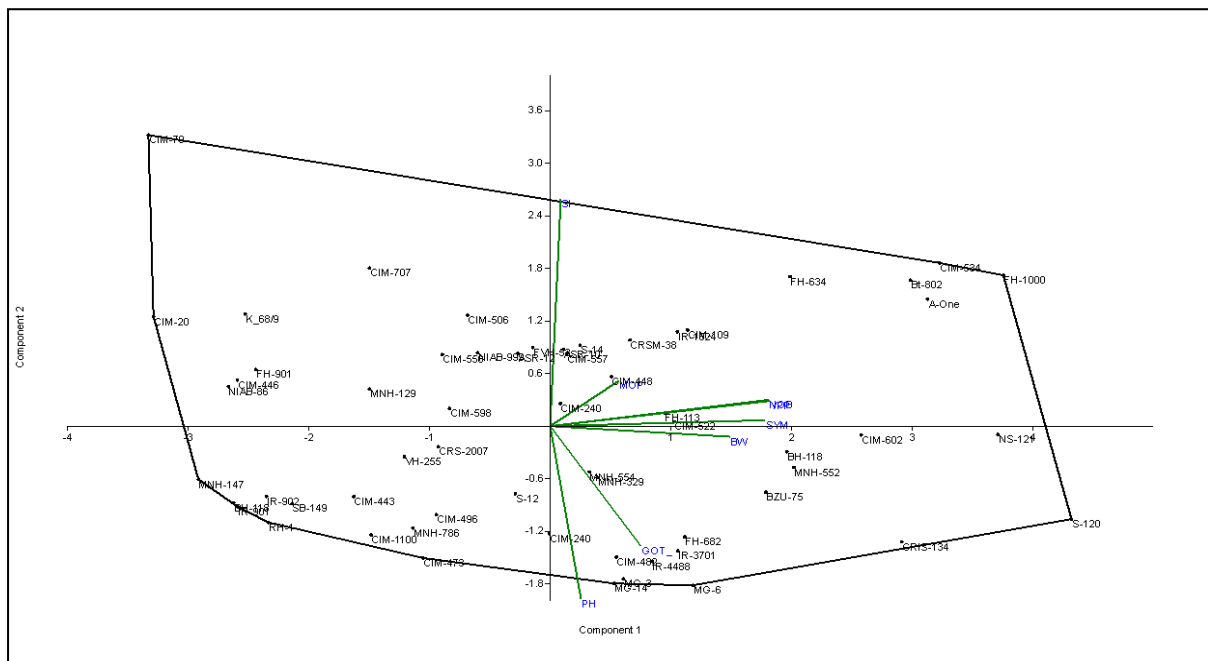
Figure 1. Biplot graph using mean data of sixty cotton genotypes.

Path analysis

Path analysis partitioned the observed correlation into undeviating and deviating effect of cotton variables presented in figure 2. Path analysis depicted that bolls per plant exhibited highest positive and undeviating effect on cotton yield. While other attributes depicted low direct effects on yield. Negative direct effect was observed for plant height and seed index on yield (Table 3). Whereas, sympodia per plant and boll weight (BW) depicted maximum indirect positive effect on seed yield via number of bolls per plant. In our study monopodial branches put undeviating and highly positive effect on yield via number of bolls per plant. In our investigation ginning out turn illustrated good positive indirect effect on yield via bolls per plant.
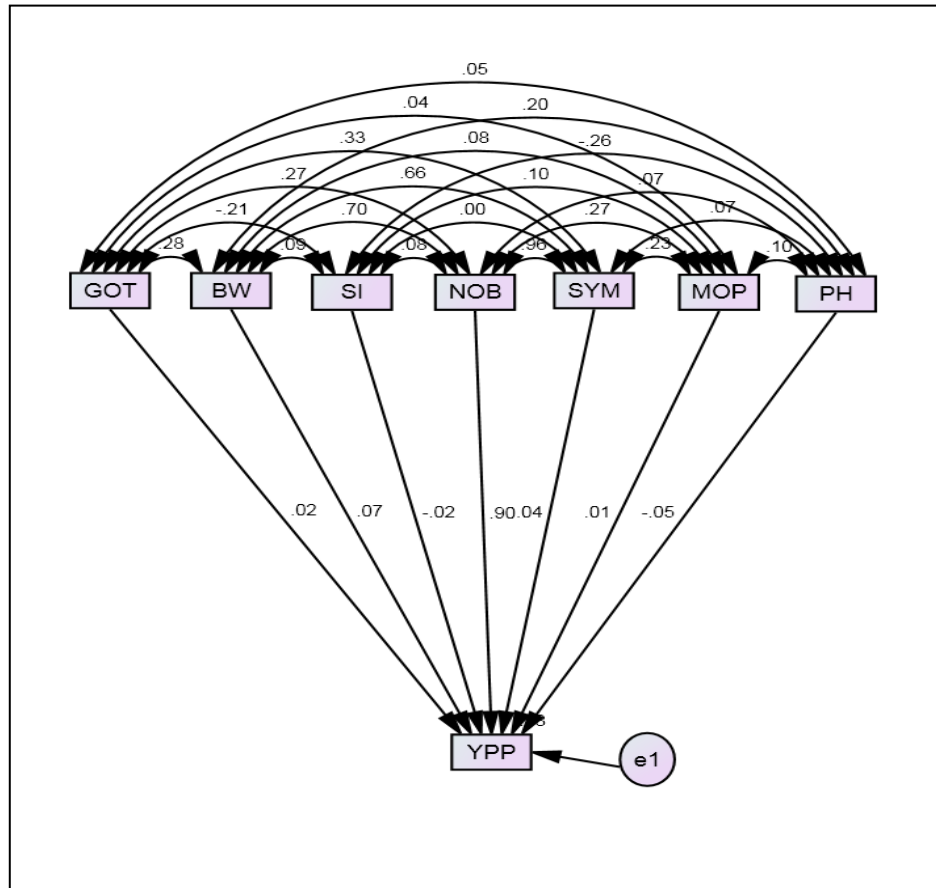
Figure 2. Diagrammatic illustration of undeviating (direct) and deviating (indirect) consequences of independent attributes on dependent attributes. (PH, Plant height; BPP, Bolls per plant; MOP, Monopodia per plant; SYP, Sympodia per plant; BW, Boll weight; SI, Seed Index; GOT, Ginning out turn; YPP,Yield per plant)

Table 3. Path analysis of numerous attributes in (*Gossypium hirsutum* L.).

Traits	PH	MOP	SYM	NOB	SI	BW	GOT
PH	**-0.0611**	0.00456	0.00218	0.05701	0.00954	0.02015	0.00089
MOP	-0.0096	**0.02892**	0.00989	0.28861	-0.0058	0.01289	0.00094
SYM	-0.0038	0.0081	**0.0353**	0.84836	0.0001	0.06647	0.00547
NOB	-0.004	0.0095	0.03409	**0.87857**	-0.0027	0.07004	0.00442
SI	0.01722	0.00495	-0.0001	0.07074	**-0.0338**	0.0087	-0.003
BW	-0.0133	0.00401	0.02527	0.66274	-0.0032	**0.09285**	0.0052
GOT	-0.0038	0.00189	0.01337	0.26886	0.00713	0.03343	**0.01444**

Note: Bold values representing direct effects.

DISCUSSION

It is evident from the Table 1 that all the genotypes in present study depicted considerable variation for all investigated traits. This variation has ample scope for plant breeder and high magnitude of variability is pre requisite for successful breeding programs to improve numerous traits (Ahsan *et al*. 2015). Judgment of heritability ($h^2_{B.S}$) values of various characters is of worth significance because higher heritability (h^2) makes selection process easier which lead to greater response of selection (Khan *et al*. 2010). Above 80% heritability (high heritability) permits plant breeder to select traits in earlier generations and less than 60% heritability considered as low heritability illustrated selection of traits lead to unfruitful results (Rehman *et al*. 2015). In this study mostly traits showed higher heritability, hence these attributes are heritable and favourable for selection of superior genotypes for genetic improvement of cotton yield (Kaydan & Yagmur 2008). Similar results of study were in complete conformity with (Khan *et al*. 2015).

To get better knowledge about associations among all genotypes multivariate analytical techniques *i.e.* principal component analysis (PCA) was executed to discover diverse genotypes for successful hybridization program (Tarighaleslami *et al.* 2012). In this study PCA abridged the total variation into eight principle components. Out of which three principle components depicted more than one eigen values and these outcomes were supported by the findings of Ahmad *et al.* (2015). Biplot analysis based on first two principle components revealed genetically diverse genotypes via pattern of scattering (Fig. 1). The division of all genotypes in biplot exposed the presence of considerable genetic variation (Mafakheri *et al.* 2010). In biplot graph the distance between base of graph to traits presented the diverse nature of studied genotypes. Greater distance revealed greater diversity among genotypes and provided significant information about the genotypic performance (Rana *et al.* 2013). Genetic variation not only depends on geographical distribution of genotypes but this may be due to other components like genetic flow, environmental variability, natural and non-natural selection and interchange of hereditary materials. Thus for cotton breeding hybridization parental lines should be based on genetics rather than geographical distribution (Bates *et al.* 1973).

The straight line connecting marked point of any attribute and base point of a biplot graph is mentioned as ''traits vector'' and the cosine angle between parameters illustrated relationship among all the attributes. Attributes having $< 90^{o}$ presented positive correlation while attributes with $>90^{o}$ showed negative correlation and attributes at right angle (90°) presented independent behavior. Correlation through biplot graph depicted momentous and positive association between sympodial branches per plant, bolls per plant and boll weight (BW) and yield because these characters showed $< 90^{o}$ with cotton yield. Haidar *et al.*(2014) outlined similar positive association for sympodial branches per plant, bolls per plant and boll weight (BW) with total yield. Boll weight (BW) is considered as major contributor followed by bolls per plant in improvement of cotton seed yield because it is supposed that greater the boll weight higher will be the cotton yield (Baloch *et al*. 2014). Our findings are in confirmatory with (Ahmad *et al*. 2008) who also assumed direct effect of boll weight (BW) on cotton seed yield but observed its significant convincing effect by means of number of bolls per plant. Our results showed direct influence of number of bolls on yield. Therefore it is suggested that increasing number of bolls and sympodia per plant lead to enhancing cotton seed yield. Similar results of authors were also supported by the findings of Qayyum *et al.* (2012).

A straightforward association does not provide ideal picture of the contribution of numerous traits in total yield. Therefore, Path coefficient analysis a practical biometrical tool utilized to partitioned the correlation into direct and indirect effects on yield using genotypic correlation values (Dinakaran *et al.* 2012). In this present study, bolls per plant exact direct effect on yield, similar findings were shown by Rao & Gopinath (2013) who also reported direct effect of bolls per plant on yield. Therefore it is suggested that selection based on bolls per plant will help plant breeder in the improvement of cotton yield. Salahuddin *et al.* (2010) reported alike outcomes of indirect effect of sympodia per plant and boll weight (BW) on cotton yield as driven in our study. Karademir *et al.* (2009) reported positive indirect effect of ginning out turn on high yield via bolls per plant. However Haidar *et al.* (2014) reported contradictory results regarding indirect effect of ginning out turn (GOT) on yield by mean of bolls per plant. This might be due to utilization of different genotypes in investigation.

CONCLUSION

Analysis of variance (ANOVA) indicated the extensive amount of divergence of all the studied traits. The outcome of principle component analysis confirmed that genotypes A-One, S-120, FH-1000, CRIS-134, MNH-147, CIM-20 and NS-121 depicted humungous genetic variability in germplasm. Parallel outcomes of correlation through biplot and path analysis showed that bolls per plant, boll weight (BW) and sympodial branches per plant has positive significant correlation and direct effect on cotton yield. Therefore these positive and significant association and divergent parental genotypes notify through principle component analysis (PCA) would be more effective to get breakthrough in successful cotton breeding program.

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