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Correlation and path analysis for genetic divergence of morphological and fiber traits in upland cotton (*Gossypium hirsutum* L.)

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Key words: Correlation, Path coefficient, Heritability, Genetic advance, Principal component analysis. **Abstract**

Seventy five genotypes of cultivated cotton (Gossypium hirsutum L.) were studied for morphological characteristics i-e plant height, monopodial branches, sympodial branches, boll weight, seed volume, seed density, seed index and fiber characters. Data were subjected to analysis of variance and estimates were made for genetic advance, broad sense heritability and coefficient of variance for the traits. ANOVA revealed highly significant variability among genotypes for all the characteristics studied. The estimates for heritability were higher for seed index (0.93) and plant height (0.93). The highest value (6.4) for genetic advance was observed for sympodial branches whereas lowest value was (0.17) for boll weight. Correlation analysis revealed positive and significant for most of the parameters. In path coefficient, the number of sympodial branches, boll weight, lint index and lint weight had maximum direct and positive effect on fiber fineness of seed cotton. Whereas, the number of monopodial branches, plant height, seed index, seed volume, seed density, staple length, fiber strength and ginning out turn (G.O.T%) had direct and negative effects on fiber of seed cotton. The principle component analysis (PCA) revealed significant differences between genotypes and the first four components with Eigen values greater than 1 contributed 66.68% of the variability among the genotypes. The grouping of genotypes possessing excelled traits signifies genetic potential of the germplasm for the improvement of seed and fiber characteristics in cotton crop.

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Introduction

Agriculture is not optional in term of conserving genetic diversity, but essential to maintain natural resources for sustainable agriculture. Evaluation of biodiversity is of prime importance for analysis of genetic medley in genotypes and introgressive hybridization of favorable attributes from sundry germplasm into the accessible genetic base. (Thompson and Nelson, 1998). Cotton has played a key role in the national economy such as in trade, industrial activities, employment, and foreign earning etc. Before initiating any cotton improvement program, the precise knowledge about the nature and genetic potential of existing germplasm, and extent of relationship and association of different morphological and yield contributing traits with the seed cotton yield is of vital importance (Soomro et al., 2005 & 2008).

When affianced with a hefty number of genotypes, multivariate biometrical techniques are generally used to evaluate biodiversity respective of data set. Among these biometrical techniques principal component analysis (PCA), principal coordinate analysis (PCOA), cluster analysis and multi dimensional scaling (MDS) mostly utilized by the plant breeders (Brown- Guedira, *et al.*, 2000).

Correlation coefficient analysis determines the relationship b/w various parameters, so it doesn't determine decisive always results about determination of plant selection criteria mentioned that genetic variances were found almost greater than the environmental variances. Genetic variability and positive correlation were observed for yield traits in G. hirsutum (Iqbal et al., 2003; Wang et al., 2004). The corresponding change and improvement in a particular character can be predetermined at the expense of the proper improvement in different upland cotton cultivars for yield and other economic traits (Ahmad et al., 2008; Rao and Mary, (1996). Path coefficient analysis revealed the relationship among traits and used to develop selection criteria for complex traits in several crop species (Iqbal et al., 2006). Principal component analysis (PCA) improvises pattern of variation existing between the genotypes and each genotype can be allocated to a single group by imitating significance of humongous contributor to the entire variation at every axis of differentiation (Saeed *et al.*, 2014).

Keeping in view the vitality of genetic diversity for cotton breeding, the present investigation was conducted with a high precision level. In this study, a set of seventy five cotton genotypes were evaluated; (i) to assess the extent of variability for twelve parameters (ii) to explore grouping pattern (iii) to notify genetically diverse but agronomically important genotypes.

Material and methods

The present research was conducted in the Department of Plant Breeding and Genetics, University College of Agriculture during 2013-2014. Plant material consists of 75 genotypes of cotton (Table 1).

The experiment was laid out in a randomized complete block design (RCBD) with three replications of each genotype. All agronomic practices were adopted. At maturity, ten plants from each entry were tagged and data were recorded for plant height (cm), no. of monopodial branches, no. of sympodial branches, boll weight (g), seed index (g), lint index (g), seed volume, seed density, Ginning out turn (%), fiber length (mm), fiber strength (g/tex) and fiber fineness (μ g/ inch).

The average plant height (cm) of 10 plants was measured y using meter rod. No. of monopodial branches (indirect fruiting branches) and no. of sympodial branches (direct fruiting branches) were counted at maturity.

Boll Weight was obtained by dividing the total seed cotton yield of the plant by the total number of effective bolls picked from that particular plant. The average boll weight was recorded for each entry in the three replications. Seed index (g) for each genotype was obtained by weighing 100 seeds in grams. Lint Index (g) is measured from the weight of lint obtained from 100 seeds in grams. However lint index of each genotype was calculated by applying following formula:

Lint index = seed index \times lint % / 100 - lint %

Ginning out turn (%) was estimated by the lint obtained from each sample was weighted and lint percentage was calculated by the following formula; Lint percentage = weight of lint \times 100 / weight of seed cotton

Seed volume was calculated from 100 seeds in a flask as by raising 50 ml water level in flask. Seed density was calculated as by applying the formula:

Seed density = wt. of 100 seed / volume of 100 seed

The fiber characteristics were estimated for fiber length, fiber strength and fiber fineness by using HVI-1000.

Table 1. Names of 75 genotypes of cotton.

Data were subjected to statistical analysis for all morphological, seed and fiber traits in order to determine estimate of variability. Analysis of variance for all the characteristics was carried by following Steel and Torrie (1980).

Correlation analysis was conceded for mean values of each trait.

All recorded traits were analyzed by numerical taxonomic techniques using Principal Component Analysis (PCA) through MINITAB version 13.2.

Results and discussion

Variance analysis

Analysis of variance (Table 3) along with heritability (h²) and genetic advance (GA) for 75 genotypes (Tale 2) indicated significant differences for all the characters. Heritability of characters was greater for all the parameters except for boll weight and staple length which exhibited 0.37 and 0.34 heritability values, respectively.

V. code	Genotype	V. code	Genotype	V. code	Genotype
V1	Khaki 900	V26	CIM-506	V51	M-64
V2	Khaki A	V27	BH-160	V52	ACALA-63-69
V3	Khaki B	V28	Marvi	V53	UA 31-43B
V4	Green	V29	CIM-446	V54	3-508-OP
V5	Khaki ARRI	V30	CRIS-134	V55	Queen of Sindh
V6	B1	V31	CRIS-09	V56	PD-695
V7	B2 Green	V32	GOMAL-93	V57	358
V8	B3	V33	NIAB-846	V58	Cute-98
V9	B4	V34	Shahbaz	V59	PB-899
V10	B5	V35	MNH-786	V60	119-5
V11	B6	V36	CIM-534	V61	D-9
V12	B7	V37	CIM-499	V62	TD-1
V13	B8	V38	CIM-162	V63	RAVI
V14	Arborium yellow diploid	V39	F-280(gl)	V64	SNR
V15	HK-113	V40	Glandles, Rex	V65	C-132
V16	FH-207	V41	LA-566 FG-ne	V66	Goa-18
V17	FH-113	V42	RA-31-55	V67	ANBP
V18	FH-942	V43	ACALA SJ4	V68	FDH-290
V19	FH-941	V44	Stonviolle-697	V69	FDH-170
V20	FH-901	V45	UCD-581	V70	S-2008
V21	NIBGE-2	V46	Coker-310	V71	FDH-313
V22	Hari-Dost	V47	Lambright Gln	V72	FDH-306
V23	CIM-496	V48	WT-ARK-10-8	V73	FDH-228
V24	NIAB-111	V49	PBG-3	V74	FDH-300
V25	CIM-707	V50	RA 31-42-8	V75	FDH-786

The highest estimate of heritability (0.93) was noticed for seed index and plant height. Heritable variation among genotypes which is in close agreement of Khan *et al.* (2010). The highest value of GA (6.4) was recorded for Sympodial branches but for seed density the lowest GA (0.23) was observed. The genotypes

showed a significant (P<0.01) variability for Monopodial branches and for lint index. Similarly, the genotypes showed a marked contrast (P<0.001) for seed index. Greater magnitude of broad sense heritability coupled with higher genetic advance in characters under study provided the evidence that these characters were under the control of additive genetic effects and is also supported by the findings of other workers (Ahmad *et al.*, 2003; Naveed *et al.*, 2004; Muhammad *et al.*, 2012).

Sr.#	PLANT CHARACTERS	C.V (%)	G.A	Heritability (%)
1	Seed index	7.74	5.6	0.93
2	Boll weight	16.58	0.17	0.37
3	Lint index	26.48	0.90	0.68
4	Plant height	15.17	5.4	0.93
5	Monopodial branches	44.26	2.5	0.79
6	Sympodial branches	17.94	6.4	0.85
7	Seed volume	13.79	3.1	0.90
8	Seed density	18.00	4.2	0.84
9	GOT %	13.23	4.7	0.72
10	Staple length	12.18	0.69	0.34
11	Fiber strength	14.21	2.48	0.57
12	Fiber fineness	12.44	3.9	0.79

Table 2. Coefficient of Variation, Genetic Advance and Heritability.

h²= heritability, GA= genetic advance and CV =coefficient of variance.

Table 3. Estimation of means squares of all 12 characters from analysis of variance (ANOVA) in 75 cotton genotypes.

SOV	D.f	Seed	Boll	Lint	Plant	Monopodial	Sympodial	Seed	Seed	GOT	Fiber	Fiber	Fiber fineness
		index	weight(g)	index	Height(cm)	branches	branches	volume	density	(%)	length	strength	(µg/inch)
											(mm)	(g/tex)	
Replication	2	0.55	0.33	0.26	500.5**	7.96**	14.57**	2.77**	0.017	6.63**	2.7**	2.0**	0.814
Genotypes	74	4.53**	0.31	12.64**	5380.6**	16.35**	86.51**	18.81**	0.119	64.2**	12.5**	2.08*	1.98*
Error	148	0.30	0.19	0.832	351.0	3.34	12.19	1.86	0.019	17.6	17.6	12.4	0.409

Correlation analysis

Genotypic and phenotypic correlation coefficients between attributes were calculated and their significance was determined.

Table 4 represents a positive and significant correlation of seed index with lint index, seed volume, seed density, GOT, staple length and fiber strength where as phenotypically negative but highly significant coefficient of correlation (P<0.05) was determined in case of boll weight, plant height, sympodial branches and fiber fineness.

Parameter, boll weight possesses negative and highly significant correlation with lint index, GOT and staple

length phenotypically and positive and significant correlation with plant height and fiber strength. It was observed that lint index had negative and significant phenotypic correlation with plant height, sympodial branches and fiber fineness but positive and significant correlation was found with seed density and GOT (%) both phenotypically and genotypically.

Plant height showed negative and highly significant correlation with seed volume, seed density, staple length and fiber strength phenotypically but positive and significant correlation with monopodial and sympodial branches and fiber fineness.

		Seed index	Boll weight (g)	Lint index	Plant height (cm)	Monopodial branches	Sympodial branches	Seed volume (ml)	Seed density (g/ml)	G.O.T (%)	Staple length (mm)	Fiber strength (g/tex)	Fiber Fineness (µg/inch)
Seed index	G	1.00	-0.31	0.77*	-0.69	-0.14	-0.24	0.28*	0.49*	0.14*	0.59*	0.38*	-0.43
	Р	1.00	-0.18**	0.64**	-0.64**	-0.13*	-0.21**	0.25**	0.46	0.12	0.36**	0.27**	-0.38**
Boll weight	G		1.00	-0.66	0.42*	0.12	0.11	0.19	-0.12	-0.58	-0.43	0.44*	0.39
(g)	Р		1.00	-0.38**	0.23**	0.06	0.06	0.12	-0.05	-0.32**	-0.20**	0.16*	0.21**
Lint index	G			1.00	-0.47	0.03	-0.19	0.06	0.55*	0.82*	0.15	-0.22	-0.26
	Р			1.00	-0.38**	0.04	-0.15*	0.06	0.42**	0.78**	0.16*	-0.09	-0.19**
Plant height					1.00	0.38*	0.38*	-0.36	-0.24	0.02	-0.36	-0.20	0.69*
(cm)	Р				1.00	0.32**	0.33**	-0.34**	-0.20**	-0.01	-0.21**	-0.16*	0.60**
Monopodial	G					1.00	0.19*	-0.07	-0.07	0.13*	-0.35	-0.26	0.27*
Branches	Р					1.00	0.17**	-0.07	-0.05	0.11	-0.12	-0.15*	0.22**
Sympodial	G						1.00	-0.05	-0.13	0.05*	0.09*	-0.01	0.15*
Branches	Р						1.00	-0.05	-0.09	0.02	-0.02	-0.01	0.12
Seed volume								1.00	-0.60	-0.13	-0.17	0.11*	-0.38
(ml)	Р							1.00	-0.61**	-0.11	-0.06	0.08	-0.33**
Seed density	G								1.00	0.25*	0.58*	0.15	0.04
	Р								1.00	0.19**	0.30**	0.09	0.03
G.O.T	G									1.00	-0.23	-0.54	0.08
(%)	Р									1.00	-0.02	-0.32**	0.05
Staple	G										1.00	0.06	-0.14
length	Р										1.00	0.12	-0.02
(mm)													
Fiber	G											1.00	-0.13
strength (g/tex)	Р											1.00	-0.11
Fiber	G												1.00
Fineness (µg/inch)	Р												1.00

Table 4. Genotypic and phenotypic correlation among Gossypium hirsutum L. genotypes.

*= Significant, **= Highly Significant.

Table 5. Direct (diagona	l) and indirect	(off-diagonal)) effects of	different	parameters of cotton.
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	Seed	Boll weight	Lint	Plant height	Monopodial	Sympodial	Seed	Seed	G.O.T	Staple	Fiber	Fiber
	index	(g)	index	(cm)	branches	branches	volume	density	(%)	length	strength	Fineness
							(ml)	(g/ml)		(mm)	(g/tex)	(µg/inch)
Seed index	-0.536	-0.03	0.235	0.127	-0.452	0.017	0.007	0.079	0.255	-0.065	-0.016	-0.057
Boll weight (g)	0.166	0.102	-0.201	-0.011	0.278	-0.014	-0.003	-0.054	-0.067	0.260	0.011	-0.006
Lint index	-0.415	-0.067	0.303	0.256	-0.312	-0.004	0.006	0.018	0.284	-0.368	-0.004	0.034
Plant height (cm)	-0.189	-0.003	0.216	0.360	0.027	-0.033	0.001	-0.018	0.151	-0.316	-0.004	0.002
Monopodial Branches	0.372	0.043	-0.145	0.015	0.651	-0.045	-0.012	-0.1.1	-0.124	-0.001	0.009	0.031
Sympodial Branches	0.080	0.12	0.011	0.104	0.253	-0.11	-0.006	-0.021	-0.037	-0.059	0.009	0.039
Seed volume (ml)	-	0.012	-0.059	-0.015	0.252	-0.022	-0.031	-0.015	-	-	-0.002	0.001
Seed density	-0.152	-0.020	0.020	-0.023	-0.23	0.009	0.001	0.277	-0.311	0.059	0.008	-0.017
G.O.T %	-0.265	-0.013	0.167	0.105	-0.157	0.008	0.004	-0.167	0.515	-	-0.015	-0.023
Staple length (mm)	-0.07	-0.059	0.250	0.255	0.001	-0.015	-0.001	-0.036	0.133	-0.446	0.006	0.081
Fiber strength (g/tex)	-0.32	-0.044	0.047	0.054	-0.235	0.041	-0.003	-0.048	0.300	0.105	-0.027	-0.010

Monopodial branches showed negative and significant association with fiber strength phenotypically where as positive and significant correlation was observed for sympodial branches and fiber fineness both phenotypically and genotypically. Sympodial branches possessed positive and signicant association with GOT and fiber fineness Liaqat et al.

genotypically. Thus the results were in close conformity to the finding of Naveed *et al.* (2004), Rauf *et al.* (2004), Salahuddin *et al.* (2010) and Khan *et al.* (2010). Seed volume had negative and highly significant correlation with seed density and fiber fineness where as positive and significant correlation for fiber strength was observed. Seed density had positive and significant correlation for GOT (%) and staple length at genotypic level while phenotypically highly significant for these characters. GOT (%) represented negative and highly significant correlation for fiber strength. These results are in accordance with Ibo *et al.* (2003), Abuja *et al.* (2006), Hussain *et al.* (2009).

Statistical Variables	PC1	PC2	PC3	PC4
Eigen values	3.3616	2.4111	1.6799	1.2192
Proportion of variance	25.858	18.547	12.922	9.378
Cumulative variance (%)	25.85	44.40	57.32	66.70
	Att	ributes		
Seed index	0.0960	0.7905	0.0779	0.3147
Boll weight (g)	0.4404	0.3464	0.3336	0.6348
Lint index	0.1961	-0.4574	0.7343	0.1963
Plant height(cm)	-0.9386	0.1989	0.0115	-0.4059
MonopodialBranches	-0.8425	0.2239	0.0241	0.3015
Sympodial Branches	0.7170	-0.4201	-0.4106	0.3109
Seed volume (ml)	-0.5030	-0.3897	0.1956	0.2167
Seed density (g/ml)	-0.8341	-0.4251	-0.2651	0.3547
G.O.T (%)	-0.7548	0.0493	0.2445	-0.2415
Staple length(mm)	-0.3800	-0.4452	-0.5403	-0.4831
Fiber strength(g/tex)	0.0213	-0.2234	0.4314	0.5612
Fiber Fineness(µg/inch)	0.1352	0.2581	-0.3154	-0.0013

Path coefficient analysis

Table_5 exhibited that direct contribution of seed index to fiber fineness was negative. While indirect effects via seed volume, seed density, ginning out turn, sympodial branches, plant height, and lint index was found positive. Direct and positive effect of boll weight towards fiber fineness was observed as indicated in Table-5. While indirect effects via seed volume, seed density, ginning out turn, sympodial branches, plant height, and lint index are negative. Positive direct effect of lint index towards fiber fineness was observed as while indirect effects via monopodial branches, seed index, staple length, fiber strength sympodial branches, and boll weight was found negative. The results are in accordance with Khan et al. ((2010), Tariq et al (2002). A study of Table_5 revealed the positive direct effect of plant height on fiber fineness. While negative indirect effect was observed via seed index, boll weight, seed density, staple length, fiber strength, sympodial branches. Direct effect of monopodial branches to was observed via seed volume, seed density, ginning out turn, staple length, sympodial branches, and lint index was negative. An examination of Table-5 revealed negative direct effect of Sympodial branches on fiber fineness while indirect effect were observed via seed index, monopodial branches, boll weight, fiber strength, plant height, and lint index was observed positive. Azhar et al (2009), Iqbal et al (2003), Abuja et al (2006) also reported the same investigations. The negative direct effect of seed volume on fiber fineness. While indirect positive effects were observed via seed index, monopodial branches, boll weight and ginning out turn. An examination of the Table-5 revealed the positive direct effect of seed density to fiber fineness while indirect negative effects were observed via seed index, plant height, boll weight, monopodial branches and ginning out turn. Direct effect of ginning out turn was found positive with fiber fineness (Amudha et al., 1996) .Negative direct effect of staple length to fiber

fiber fineness was positive where as indirect effect

fineness was observed while indirect positive effects were observed via plant height monopodial branches, ginning out turn, fiber strength, and lint index. A study of Table-5 revealed the negative direct effect of fiber strength on fiber fineness (Kaushik *et al.* 2003).

Principal component analysis

Mean data matrix of 12*75 was subjected to principal component analysis to find out genetic diversity. Out of twelve principal components (PC's) four exhibited more than 01 eigen value contributing 66.68% of total variation among genotypes (Table 6). The remaining o8 PC's showed less than 01 eigen values and were less significant therefore could not be considered for additional validation. The first PC and second PC possessed 25.85 % and 18.54% respectively of the total variation. PC 1 was more related to boll weight and sympodial branches while attributes seed index and boll weight also contributed maximum variation in PC 2.

Spread out plot

A principal component spread out plot group genotypes together with greater genetic similarity and variability based on the genotypes and twelve variables studied (Fig.1).

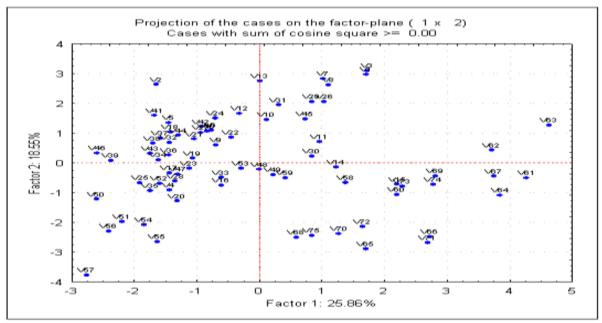


Fig. 1. Scattered diagram of two principal components based on mean values of 75 genotypes of cotton.

Greater the distance between genotypes and base of spread out plot represents more genetic divergent nature of genotypes. It is evident from the Figure 1, that the genotypes V2, V57, and V63 exhibited higher variability thus are spatially evaluated from other genotypes. Thus desirable genotypes may be selected from a particular group for future breeding programmes (Murtaza *et al.*, 2004; Shoaib *et al.*, 2015; Rana *et al.*, 2015).

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