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Correlation, path coefficient and D^2 analysis study of seed cotton yield and fibre quality traits in American cotton (*Gossypium hirsutum* L.)

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Abstract
The present Investigation was carried out to study the correlation, path coefficient and D^2 analysis in American cotton. The material was evaluated in a Randomized Block Design (RBD) with three replications during kharif 2019. In this experiment association analysis revealed significant positive correlation for seed cotton yield per plant with number of bolls per plant. The path analysis revealed that the days to boll opening, number of bolls per plant, boll weight, ginning percentage, and 2.5% span length and fibre fineness exhibited high direct effect on seed cotton yield per plant. D^2 analysis indicated wider genetic diversity among fifty genotypes of cotton which were grouped into twelve clusters. Maximum genetic divergence was observed between cluster XI and cluster XII followed by cluster VI and cluster XII.

Keywords: correlation, path coefficient, D^2 analysis and genetic divergence

Introduction
Cotton (*Gossypium hirsutum* L.) (2n=52), is one of the most important fiber and cash crop of India and plays a dominant role in the industrial and agricultural economy of the country. It provides the basic raw material (cotton fibre) to cotton textile industry. Cotton in India provides direct livelihood to 6 million farmers and about 40-50 million people are employed in cotton trade and its processing. It is an important fibre and oilseed crop of nearly 80 countries with India, China, United States, Pakistan and Brazil being five of the largest producers of cotton.
Cotton, a semi-xerophyte, is grown in tropical and sub-tropical conditions. A minimum temperature of 1 5℃ is required for better germination at field conditions. The optimum temperature for vegetative growth is 21-27 ℃ and it can tolerate temperature to the extent of 43 ℃ but temperature below 21 ℃ is detrimental to the crop. Warm days of cool nights with large diurnal variations during the period of fruiting are conducive to good boll and fibre development. Cotton is grown on a variety of soils ranging from well drained deep alluvial soils in the north to black clayey soils of varying depth in central region and in black and mixed black and red soils in south zone. Cotton is semi-tolerant to salinity and sensitive to water logging and thus prefers well drained soils.
There are four cultivated species of cotton *viz.*, *Gossypium arboreum*, *G. herbaceum*, *G. hirsutum* and *G. barbadense*. The first two species are diploid (2n=26) and are native to old world. They are also known as Asiatic cottons because they are grown in Asia. The last two species are tetraploid (2n=52) and are also known as New world cottons. *G. hirsutum* is also known as American cotton or upland cotton and *G. barbadense* as Egyptian cotton or Sea Island cotton or Peruvian cotton or Tanguish cotton or Quality cotton.

Materials and Methods
Plant material
The present investigation carried out at Cotton Research Station, Junagadh Agricultural University, Junagadh during *kharif* 2019. The experimental material consisted of fifty diverse genotype of cotton (*Gossypium hirsutum* L.). The pure seeds of these genotypes were obtained from the Cotton Research Station, Junagadh Agricultural University, Junagadh.

Field trial
Fifty genotypes of cotton were sown on 26th June, 2019 in a Randomized Block Design (RBD) with three replications at Cotton Research Station, Junagadh Agricultural University, Junagadh. Each line was sown in a single row plot of 6.3 × 1.2 m length with each row spaced 120 cm apart and plant to plant distance within row was 45 cm. The genotypes were randomly allotted to the plots in each replication.

Fertilizers at recommended doses were applied and other cultural practices were carried out at regular intervals during the course of experimentation. Application of N was split into two equal instalments i.e., basal and top dressing. All the recommended agronomical practices along with necessary plant protection measures were followed timely for the successful raising of the crop. The observations were recorded on five randomly selected plants from each genotype in each replication for days to flowering, days to boll opening, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant (g), ginning percentage (%), seed index (g), lint index (g), oil content (%), 2.5% span length (mm), fibre strength (g/tex) and fibre fineness (mv).

Results and Discussion

Correlation Analysis

The phenotypic correlation of seed cotton yield with various component traits in this population are presented in Table-1.

In the present investigation, seed cotton yield per plant had highly significant and positive correlation with number of bolls per plant at both the genotypic and phenotypic levels indicating that these attributes were more influencing the seed cotton yield and therefore, these were important characters for bringing genetic improvement in seed cotton yield. On the other hand, seed cotton yield per plant had non significant and positive correlation with days to flowering, days to boll opening, plant height, number of sympodia per plant, boll weight, ginning percentage, seed index, lint index, oil content, 2.5% span length and fibre fineness at both genotypic and phenotypic levels, while number of monopodia per plant and fibre strength had negative and non significant association at both genotypic and phenotypic levels.

Among all the component traits, days to flowering exhibited positive and highly significant correlation with days to boll opening and number of sympodia per plant at both genotypic and phenotypic levels and it is an important component in identifying and deciding the duration of the cotton crop. Similar relationship has been reported by Sambamurthy *et al.*, 2006 [19]; Leela Pratap *et al.*, 2006 [10]; Ashokkumar and Ravikesavan, 2010 [3] and Padmavathi *et al.*, 2015 [15]. The days to boll opening exhibited positive and highly significant correlation with number of sympodia per plant at both genotypic and phenotypic levels and significantly positive correlation with oil content at genotypic and phenotypic levels Plant height exhibited highly significant and positive correlation with number of sympodia per plant at both genotypic and phenotypic levels. Similar findings were reported by Tuleja *et al.*, 2006 [21]; Katageri *et al.*, 2015 [6]; Padmavathi *et al.*, 2015 [15] and Shabana *et al.*, 2016 [20]. Number of monopodia per plant showed positive and non significant correlation with number of bolls per plant, ginning percentage, oil content, 2.5% span length, fibre strength and fibre fineness. Number of sympodia per plant showed positive and non significant correlation with number of bolls per plant, ginning percentage, lint index, oil content and fibre fineness. Similar finding were reported by Pradeep *et al.*, 2014 [16] and Nawaz *et al.*, 2019 [13]. Number of bolls per plant recorded negative and highly significant correlation with boll weight at both genotypic and phenotypic levels. Similar results were obtained by Latif *et al.*, 2015 [9]; Nikhil *et al.*, 2018 [14] and Nawaz *et al.*, 2019 [13]. Boll weight recorded positive and non significant association with seed index and fibre fineness at both genotypic and phenotypic levels. Ginning percentage exhibited positive and highly significant correlation at both genotypic and phenotypic levels with lint index. Similar finding were reported by Muthu *et al.*, 2004 [12]; Leela Pratap *et al.*, 2006 [10]; Padmavathi *et al.*, 2015 [15] and Nikhil *et al.*, 2018 [14]. Seed index exhibited a positive and highly significant correlation with lint index at both genotypic and phenotypic levels. Similar findings were reported by Khan *et al.*, 2010; Farooq *et al.*, 2014 and Nikhil *et al.*, 2018 [14]. Lint index exhibited positive and non significant correlations only at phenotypic level and negative and non significant correlation only at genotypic level with fibre fineness. Similar finding was confounded by Nawaz *et al.*, 2019 [13]. Oil content possessed positive and non significant correlation with fibre strength and fibre fineness. Similar finding was reported by Tuleja *et al.*, 2006 [21]. 2.5% Span length recorded positive and highly significant association with fibre strength. Similar findings were observed by Sambamurthy *et al.*, 2006 [19]; Tuleja *et al.*, 2006; Leela Pratap *et al.*, 2006 [21, 10]; Dahiphale *et al.*, 2015 [4] and Reddy *et al.*, 2015 [18]. Fibre strength recorded negative and highly significant association with fibre fineness. Similar findings were reported by Katageri *et al.*, 2015 [6]; Khokhar *et al.*, 2017 [8] and Nikhil *et al.*, 2018 [14].

Path coefficient analysis

Genotypic path coefficient analysis

Ginning percentage (Latif *et al.*, 2015) [9], boll weight (Asha *et al.*, 2015 and Nikhil *et al.*, 2018) [2, 14] and seed index (Leela Pratap *et al.*, 2006; Vinodhana *et al.*, 2013; Padmavathi *et al.*, 2015 and Nawaz *et al.*, 2019) [10, 22, 15, 13] exhibited very high and positive direct effects on seed cotton yield per plant. Number of bolls per plant (Pujer *et al.*, 2014; Asha *et al.*, 2015; Dahiphale *et al.*, 2015 and Nawaz *et al.*, 2019) [17, 2, 4, 13] and lint index (Asha *et al.*, 2015) [2] exhibited high and negative direct effect towards seed cotton yield per plant. These traits turned out to be major components of seed cotton yield for direct selection.

Days to flowering (Reddy *et al.*, 2015) [18] had positive direct effect of moderate magnitude on seed cotton yield per plant. Days to boll opening, plant height (Latif *et al.*, 2015 and Nikhil *et al.*, 2018) [9, 14] and fibre strength (Reddy *et al.*, 2015 and Nikhil *et al.*, 2018) [18, 14] exhibited low and negative direct effects towards seed cotton yield per plant. Number of sympodia per plant (Leela Pratap *et al.*, 2006; Dahiphale *et al.*, 2015 and Padamavathi *et al.*, 2015) [10, 4], 2.5% span length (Sambamurthy *et al.*, 2006) [19] and fibre fineness (Nawaz *et al.*, 2019) [13] had positive direct effect of negligible magnitude on seed cotton yield per plant. Number of monopodia per plant (Latif *et al.*, 2015 and Reddy *et al.*, 2015) [9, 18] and oil content (Ashokkumar and Ravikesavan, 2010) [3] had negative direct effect of negligible magnitude on seed cotton yield per plant.

Phenotypic path coefficient analysis

Number of bolls per plant (Ashokkumar and Ravikesavan 2010; Pujer *et al.*, 2014; Asha *et al.*, 2015; Dahiphale *et al.*, 2015 and Nawaz *et al.*, 2019) [3, 17, 2, 4, 13] and boll weight (Vinodhana *et al.*, 2013 and Nikhil *et al.*, 2018) [22, 14] exhibited very high and positive direct effects on seed cotton yield per plant. These traits turned out to be major components of seed cotton yield for direct selection. Ginning percentage (Latif *et al.*, 2015) [9], 2.5% span length (Sambamurthy *et al.*, 2006) [19], fibre fineness (Nawaz *et al.*, 2019) [13] and days to boll opening exhibited low and positive direct effect on seed cotton yield per plant. Lint index (Pujer *et al.*, 2014 and Asha *et al.*, 2015) [17, 2] and days to flowering (Reddy *et al.*, 2015) [18] exhibited low and negative direct effect on seed cotton yield per plant.

Seed index (Leela Pratap *et al.*, 2006; Padmavathi *et al.*, 2015 and Nawaz *et al*., 2019) [10, 15, 13], oil content (Ashokkumar and Ravikesavan, 2010) [3] and number of sympodia per plant (Tuleja *et al.*, 2006; Leela Pratap *et al.*, 2006; Dahiphale *et al.*, 2015 and Padamavathi *et al.*, 2015) [21, 4, 10] had positive direct effect of negligible magnitude on seed cotton yield per plant. Number of monopodia per plant (Latif *et al.*, 2015 and Reddy *et al.*, 2015) [9, 18], fibre strength (Reddy *et al.*, 2015 and Nikhil *et al.*, 2018) [18, 14] and plant height (Latif *et al.*, 2015 and Nikhil *et al.*, 2018) [9, 14] had negative direct effect of negligible magnitude on seed cotton yield per plant.

Genetic diversity

In the present study, D^2statistics estimated on 50 cotton genotypes for 15 characters. On the basis of D^2 values, twelve clusters were formed from 50 genotypes. The cluster I having largest number of genotypes (20) followed by cluster III (12), cluster V (5) and cluster X (5). On the other hand, cluster II, cluster IV, cluster VI, cluster VII, cluster VIII, cluster IX, cluster XI and cluster XII are solitary clusters. The intra cluster distance (D) ranged from 9.67 (cluster I) to 13.63 (cluster X). High intra cluster distance indicated about the wider genetic diversity among the genotypes which could be used in yield improvement of cotton. The maximum inter cluster distance was found between clusters XI and XII (D = 26.21) followed by that between clusters VI and XII (D = 25.88), II and XII (D = 23.03), VIII and XII (D = 22.02), VII and XI (D = 21.93), III and XII (D = 21.63), IV and XII (D = 21.46) and VI and VII (D = 20.74). The minimum inter cluster distance was found between clusters II and VIII (D=8.60). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates or to exploit maximum level of hybrid vigour in cotton.

In present investigation, wide range of variation for several characters among multi genotypic clusters was observed. Fibre fineness (23.02%), number of monopodia per plant (19.10%) and boll weight (18.20%) were the main contributors to the total divergence. These three characters accounted for 60.32% of total divergence. A considerable diversity of 60.32% was observed due to these three characters. Hence, selection for divergent parents based on these three characters would be useful for heterosis breeding in cotton. Fibre strength (7.84%), 2.5% span length (7.59%) and days to flowering (7.10%) were other contributors towards the total divergence. Adsare *et al.*, 2017 also reported higher genetic diversity due to boll weight. Adsare *et al.*, 2017 and Malathi and Patil, 2019 supported that more divergence was found due to days to flowering. Ashokkumar and Ravikesavan, 2010 [3]; Dahiphale *et al.*, 2015 [4] and Nikhil *et al.*, 2018 [14] also reported higher genetic diversity due to number of monopodia per plant. Khan *et al.*, 2010; Katageri *et al.*, 2015 [7, 6]; Padmavathi *et al.*, 2015 [15] and Nawaz *et al.*, 2019 [13] supported that more divergence was found due to fibre fineness, fibre strength and 2.5% span length. The contribution of oil content (4.41%), seed cotton yield (3.43%), number of bolls per plant (3.10%), ginning percentage (2.69%), seed index (1.71%), lint index (0.98%), number of sympodia per plant (0.73%) and plant height (0.08%) were negligible. Low genetic diversity for these traits in such diverse group of genotypes may also suggest high degree of consistency and moderate to low heritability of these traits. On other hand, days to boll opening (0.00) have no contribution.

The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used either for direct adoption as improved varieties or for hybridization to exploit heterosis breeding. In the present study, the cluster IX differed from other clusters in respect of days to flowering and cluster XII differed from other clusters in respect of days to boll opening, while cluster IV had desirable rating for plant height, number of sympodia per plant, number of bolls per plant and seed cotton yield per plant. The cluster VIII had the highest mean values for seed index, lint index and oil content. The maximum mean values for boll weight was observed in cluster XI. Therefore, intercrossing of such genotypes involved in these clusters would be useful for inducing variability in the respective characters and their rational improvement for increasing seed cotton yield.

Table 1: Estimates of Genotypic (r_g) and phenotypic (r_p) correlation coefficients among 15 characters of cotton

Characters		DF	DB	PH	MP/P	SP/P	BP/P	BW	GP	SI	LI	OC	FL	FS	FF
SCY	r_p	0.1044	0.2014	0.1797	-0.0646	0.2010	0.5545**	0.0753	0.1087	0.0380	0.1092	0.0588	0.0218	-0.1546	0.1346
	r_g	0.1193	0.2360	0.2275	-0.0718	0.2186	0.6392**	0.0916	0.1082	0.0279	0.1046	0.0693	0.0354	-0.1736	0.1435
DF	r_p		0.9310**	0.1078	0.0217	0.3667**	-0.0328	0.1580	-0.0627	-0.0174	-0.0479	0.2635	-0.0547	-0.0577	0.1639
	r_g		0.9484**	0.1084	0.0256	0.3991**	-0.0279	0.1674	-0.0537	-0.0139	-0.0389	0.2825*	-0.0568	-0.0590	0.1725
DB	r_p			0.1970	0.0436	0.4038**	0.0517	0.1410	-0.0315	-0.0502	-0.0480	0.2821*	-0.1707	-0.1108	0.2303
	r_g			0.2135	0.0483	0.4642**	0.0671	0.1567	-0.0286	-0.0478	-0.0414	0.2981*	-0.1855	-0.1200	0.2463
PH	r_p				0.0924	0.6412**	0.1937	-0.0264	0.0523	0.0062	0.0538	-0.1349	-0.1921	-0.1937	0.0882
	r_g				0.1239	0.7926**	0.2513	-0.0108	0.0478	0.0075	0.0596	-0.1591	-0.2055	-0.2313	0.0927
MP/P	r_p					-0.1401	0.0089	-0.0148	0.0164	-0.1989	-0.1421	0.1352	0.0562	0.0967	0.0888
	r_g					-0.1486	0.0001	-0.0121	0.0201	-0.2553	-0.1746	0.1355	0.0586	0.1068	0.0868
SP/P	r_p						0.2349	-0.1004	0.1069	-0.0706	0.0128	0.1070	-0.2237	-0.2230	0.0866
	r_g						0.2578	-0.1079	0.1363	-0.0958	0.0212	0.1340	-0.2469	-0.2484	0.0884
BP/P	r_p							-0.7055**	0.1520	0.0367	0.1203	0.0718	0.0602	0.1085	0.0109
	r_g							-0.7405**	0.1712	0.0181	0.1251	0.0767	0.0616	0.1251	0.0096
BW	r_p								-0.1694	0.0403	-0.0636	-0.0390	-0.0553	-0.1999	0.0477
	r_g								-0.1810	0.0703	-0.0558	-0.0391	-0.0630	-0.2110	0.0541
GP	r_p									-0.0417	0.6492**	-0.1886	-0.1781	-0.0709	-0.0083
	r_g									-0.0489	0.6955**	-0.1973	-0.1875	-0.0807	-0.0085
SI	r_p										0.7299**	-0.0742	-0.0838	0.0106	0.0158
	r_g										0.6813**	-0.1162	-0.1047	-0.0050	0.0125
LI	r_p											-0.1888	-0.1792	-0.0462	0.0009
	r_g											-0.2337	-0.2067	-0.0702	-0.0037
OC	r_p												-0.0971	0.1258	0.2038
	r_g												-0.0894	0.1415	0.2076

FL	r_p													0.3180*	-0.6058**
	r_g													0.3384*	-0.6240**
FS	r_p														-0.3857**
	r_g														-0.4002**

*, ** Significant at 5 and 1% levels, respectively

DF=Days to flowering, DB=Days to boll opening, PH=Plant height (cm), MP/P=No. of monopodia per plant, SP/P=No. of sympodia per plant, BP/P=No. of bolls per plant, BW=Boll weight (g), SCY=Seed cotton yield per plant (g), GP=Ginning percentage (%), SI=Seed index (g), LI=Lint index (g), OC=Oil content (%), FL=2.5% Span length (mm), FS=Fibre strength (g/tex), FF=Fibre fineness (mv)

Table 2: Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed cotton yield per plant in 50 genotypes of cotton

Characters	DF	DB	PH	MP/P	SP/P	BP/P	BW	GP	SI	LI	OC	FL	FS	FF	SCY
DF	0.1323	-0.1944	-0.0206	-0.0014	0.0219	-0.0481	0.2381	-0.0768	-0.0170	0.0725	-0.0049	-0.0039	0.0077	0.0139	0.1193
DB	0.1254	-0.2050	-0.0405	-0.0026	0.0254	0.1156	0.2228	-0.0410	-0.0587	0.0771	-0.0052	-0.0129	0.0155	0.0198	0.2360
PH	0.0143	-0.0438	-0.1898	-0.0066	0.0434	0.4331	-0.0154	0.0684	0.0092	-0.1112	0.0028	-0.0143	0.0298	0.0074	0.2275
MP/P	0.0034	-0.0099	-0.0235	-0.0529	-0.0081	0.0001	-0.0173	0.0288	-0.3131	0.3257	-0.0023	0.0041	-0.0137	0.0070	-0.0718
SP/P	0.0528	-0.0951	-0.1504	0.0079	0.0548	0.4444	-0.1534	0.1951	-0.1175	-0.0395	-0.0023	-0.0171	0.0320	0.0071	0.2186
BP/P	-0.0037	-0.0138	-0.0477	0.0000	1.7236	-1.0530	-1.0530	0.2450	0.0222	-0.2352	-0.0013	0.0043	-0.0161	0.0008	0.6392**
BW	0.0221	-0.0321	0.0021	0.0006	-0.0059	-1.2763	1.4221	-0.2591	0.0862	0.1041	0.0007	-0.0044	0.0272	0.0043	0.0916
GP	-0.0071	0.0059	-0.0091	-0.0011	0.0075	0.2950	-0.2574	1.4315	-0.0600	-1.2972	0.0034	-0.0130	0.0104	-0.0007	0.1082
SI	-0.0018	0.0098	-0.0014	0.0135	-0.0053	0.0312	0.1000	-0.0700	1.2261	-1.2707	0.0020	-0.0073	0.0006	0.0010	0.0279
LI	-0.0051	0.0085	-0.0113	0.0092	0.0012	0.2174	-0.0793	0.9955	0.8353	-1.8652	0.0040	-0.0143	0.0090	-0.0003	0.1046
OC	0.0974	-0.0611	0.0302	-0.0072	0.0073	0.1322	-0.0556	-0.2824	-0.1425	0.4359	-0.0173	-0.0062	-0.0182	0.0167	0.0693
FL	-0.0075	0.0380	0.0390	-0.0031	-0.0135	0.1061	0.0896	-0.2684	-0.1284	0.3856	0.0015	0.0694	-0.0436	-0.0501	0.0354
FS	-0.0079	0.0246	0.0439	-0.0056	-0.0136	0.2157	-0.3001	-0.1156	-0.0061	0.1310	-0.0024	0.0235	-0.1287	-0.0321	-0.1736
FF	0.0228	-0.0505	-0.0176	-0.0046	0.0048	0.0165	0.0770	-0.0122	0.0153	0.0069	0.0036	-0.0433	0.0515	0.0803	0.1435

*, ** Significant at 5% and 1% levels, respectively (Residual effect = 0.2010)

DF=Days to flowering, DB=Days to boll opening, PH=Plant height (cm), MP/P=No. of monopodia per plant, SP/P=No. of sympodia per plant, BP/P=No. of bolls per plant, BW=Boll weight (g), SCY=Seed cotton yield per plant (g), GP=Ginning percentage (%), SI=Seed index (g), LI=Lint index (g), OC=Oil content (%), FL=2.5% Span length (mm), FS=Fibre strength (g/tex), FF=Fibre fineness (mv)

Table 3: Phenotypic path coefficient analysis showing direct (diagonal and bold) indirect effects of different characters on seed cotton yield per plant in 50 genotypes of cotton

Characters	DF	DB	PH	MP/P	SP/P	BP/P	BW	GP	SI	LI	OC	FL	FS	FF	SCY
DF	-0.1188	0.1001	-0.0030	-0.0019	0.0021	-0.0386	0.1449	-0.0127	-0.0012	0.0066	0.0086	-0.0075	0.0047	0.0211	0.1044
DB	-0.1106	0.1075	-0.0055	-0.0037	0.0023	0.0609	0.1294	-0.0064	-0.0033	0.0066	0.0092	-0.0235	0.009	0.0296	0.2014
PH	-0.0128	0.0212	-0.0279	-0.0079	0.0037	0.2280	-0.0242	0.0106	0.0004	-0.0074	-0.0044	-0.0265	0.0157	0.0114	0.1797
MP/P	-0.0026	0.0047	-0.0026	-0.0857	-0.0008	0.0105	-0.0136	0.0033	-0.0133	0.0196	0.0044	0.0078	-0.0078	0.0114	-0.0646
SP/P	-0.0436	0.0434	-0.0179	0.0120	0.0057	0.2765	-0.0921	0.0216	-0.0047	-0.0018	0.0035	-0.0308	0.0180	0.0112	0.2010
BP/P	0.0039	0.0056	-0.0054	-0.0008	0.0013	1.1773	-0.6472	0.0307	0.0024	-0.0166	0.0023	0.0083	-0.0088	0.0014	0.5545**
BW	-0.0188	0.0152	0.0007	0.0013	-0.0006	-0.8306	0.9173	-0.0342	0.0027	0.0088	-0.0013	-0.0076	0.0162	0.0061	0.0753
GP	0.0074	-0.0034	-0.0015	-0.0014	0.0006	0.1789	-0.1554	0.2018	-0.0028	-0.0897	-0.0061	-0.0246	0.0057	-0.0011	0.1087
SI	0.0021	-0.0054	-0.0002	0.0170	-0.0004	0.0432	0.0370	-0.0084	0.0666	-0.1008	-0.0024	-0.0116	-0.0009	0.0020	0.0380
LI	0.0057	-0.0052	-0.0015	0.0122	0.0001	0.1416	-0.0583	0.1310	0.0486	-0.1381	-0.0061	-0.0247	0.0037	0.0001	0.1092
OC	-0.0313	0.0303	0.0038	-0.0116	0.0006	0.0845	-0.0357	-0.0381	-0.0049	0.0261	0.0325	-0.0134	-0.0102	0.0262	0.0588
FL	0.0065	-0.0183	0.0054	-0.0048	-0.0013	0.0709	-0.0507	-0.0360	-0.0056	0.0247	-0.0032	0.1378	-0.0257	-0.0780	0.0218
FS	0.0069	-0.0119	0.0054	-0.0083	-0.0013	0.1277	-0.1834	-0.0143	0.0007	0.0064	0.0041	0.0438	-0.0808	-0.0497	-0.1546
FF	-0.0195	-0.0248	-0.0025	-0.0076	0.0005	0.0129	0.0438	-0.0017	0.0011	0.0001	0.0066	-0.0835	0.0312	0.1288	0.1346

*, ** Significant at 5% and 1% levels, respectively (Residual effect = 0.4720)

DF=Days to flowering, DB=Days to boll opening, PH=Plant height (cm), MP/P=No. of monopodia per plant, SP/P=No. of sympodia per plant, BP/P=No. of bolls per plant, BW=Boll weight (g), SCY=Seed cotton yield per plant (g), GP=Ginning percentage (%), SI=Seed index (g), LI=Lint index (g), OC=Oil content (%), FL=2.5% Span length (mm), FS=Fibre strength (g/tex), FF=Fibre fineness (mv)

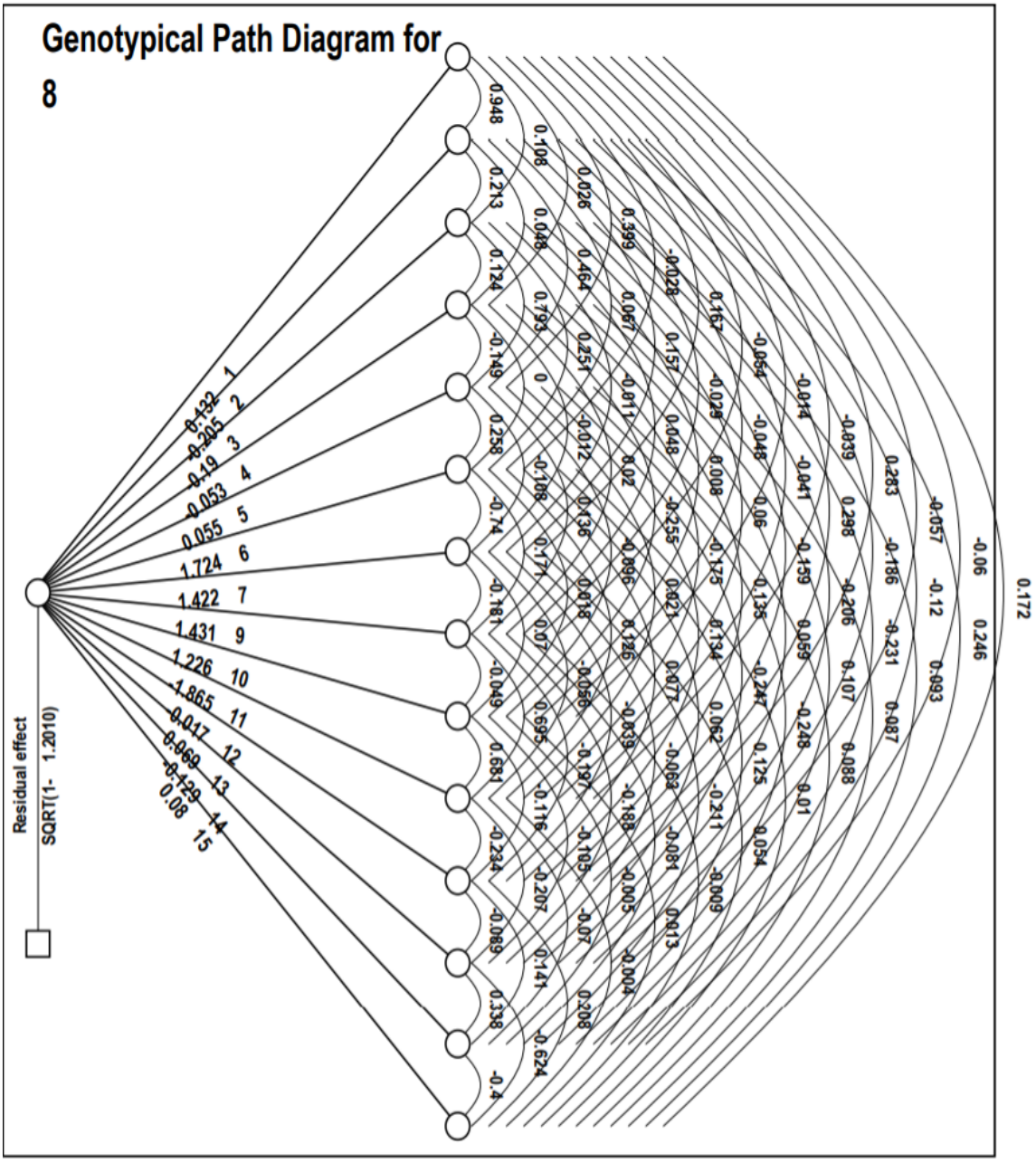

Fig 1: Diagrammatic representation of genotypic path analysis using 15 characters of cotton 1. Days to flowering 2. Days to boll opening 3. Plant height (cm) 4. Number of monopodia per plant 5. Number of sympodia per plant 6. Number of bolls per plant 7. Boll weight (g) 8. Seed cotton yield per plant (g) 9. Ginning percentage (%) 10. Seed index (g) 11. Lint index (g) 12. Oil content (%) 13. 2.5% Span length (mm) 14. Fibre strength (g/tex), 15. Fibre fineness (mv)

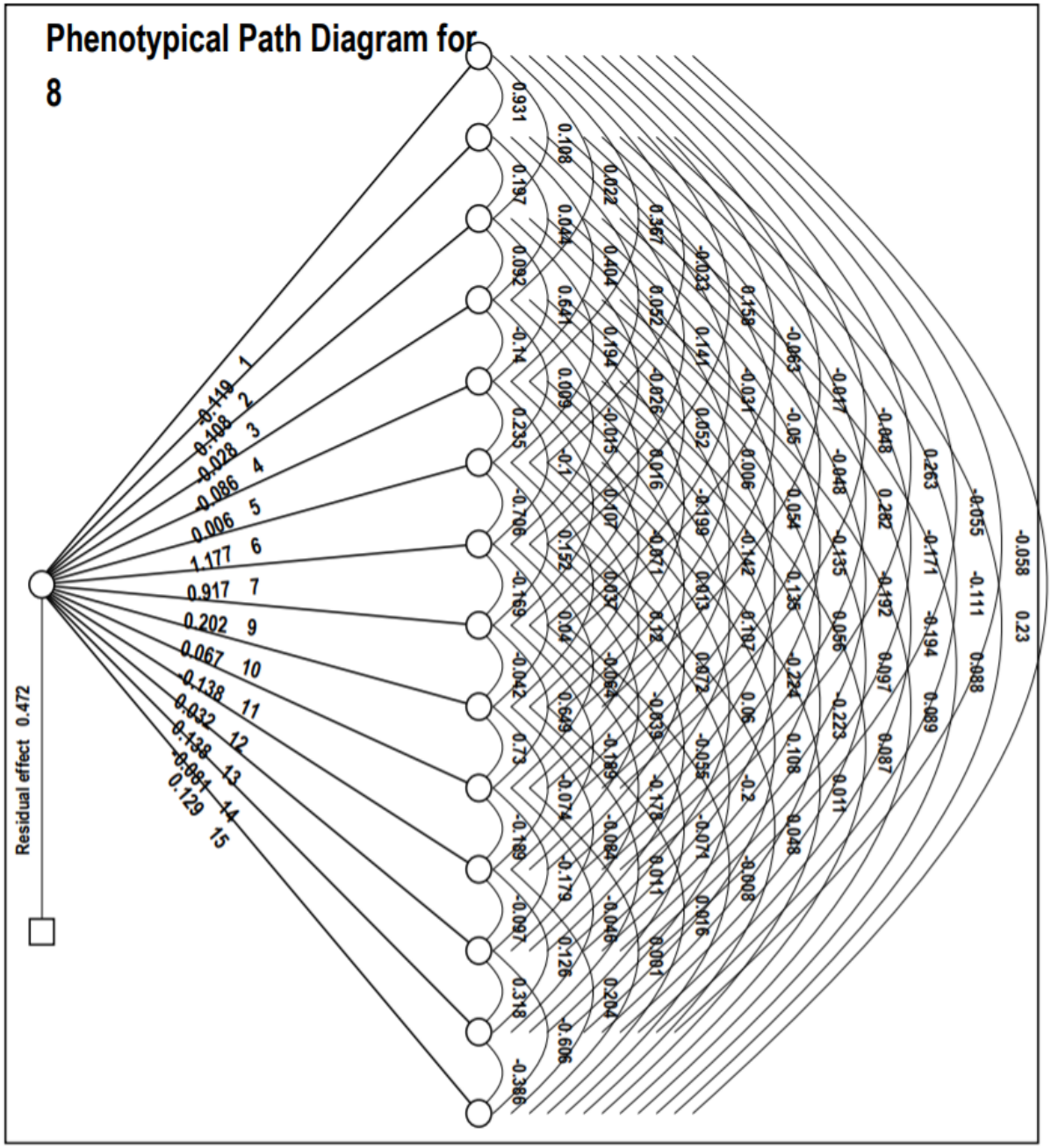

Fig 2: Diagrammatic representation of phenotypic path analysis using 15 characters of cotton 1. Days to flowering 2. Days to boll opening 3. Plant height (cm) 4. Number of monopodia per plant 5. Number of sympodia per plant 6. Number of bolls per plant 7. Boll weight (g) 8. Seed cotton yield per plant (g) 9. Ginning percentage (%) 10. Seed index (g) 11. Lint index (g) 12. Oil content (%) 13. 2.5% Span length (mm) 14. Fibre strength (g/tex), 15. Fibre fineness (mv)

Table 4: Grouping of 50 genotypes of cotton in various clusters on the basis of D^2 statistic

Cluster	No. of genotypes	Name of genotypes
I	20	G. P. Hir.-17, G. P. Hir.- 28, G. P. Hir.- 18, G. P. Hir.-32, G. P. Hir.-40, G. P. Hir.-25, G. P. Hir.-29, G. P. Hir.-21, G. P. Hir.-36, G. P. Hir.-37, GJ.Cot-102, G. P. Hir.-41, G. P. Hir.-4, G. P. Hir.-31, G. P. Hir.-27, G. P. Hir.-45, GJ.Cot-101, G. P. Hir.-26, G. P. Hir.-42, G. P. Hir.-3
II	1	G. P. Hir.-23
III	12	G. P. Hir.-6, G. P. Hir.-8, G. P. Hir.-9, G. P. Hir.-2, G. P. Hir.-7, G. P. Hir.-24, G. P. Hir.-15, G. P. Hir.-1, G. P. Hir.-47, G. P. Hir.-35, G. P. Hir.-11, G. P. Hir.-43
IV	1	G. P. Hir.-30
V	5	G. P. Hir.-22, G. P. Hir.-34, G. P. Hir.-5, G. P. Hir.-38, G. P. Hir.-44
VI	1	G.Cot-38
VII	1	G. P. Hir.-33
VIII	1	G. P. Hir.-39
IX	1	G. P. Hir.-19
X	5	G. P. Hir.-12, G. P. Hir.-13, G. P. Hir.-14, G. P. Hir.-20, G. P. Hir.-46
XI	1	G. P. Hir.-10
XII	1	G. P. Hir.-16

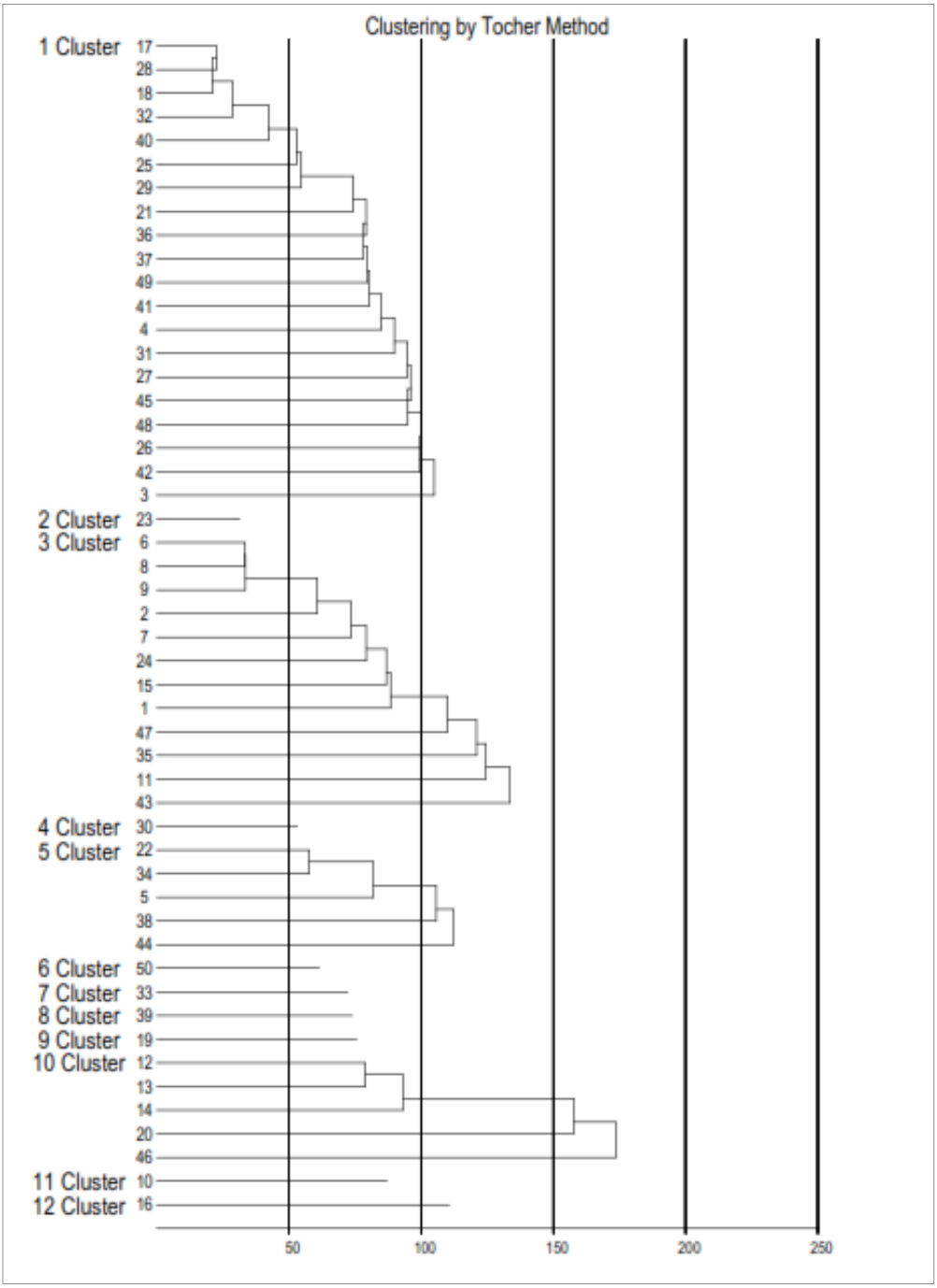

Fig 3: Dendrogram showing distribution of 50 cotton genotypes into 12 clusters

Table 5: Average intra and inter cluster distances between twelve clusters in cotton

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	9.67	12.68	13.08	11.69	12.34	14.26	13.13	13.78	12.93	14.02	16.24	18.84
II		0.00	10.39	14.98	12.76	7.85	19.46	8.60	14.14	15.63	12.52	23.03
III			10.81	14.72	13.85	12.58	17.77	12.23	15.44	14.06	15.21	21.63
IV				0.00	16.57	15.72	15.76	15.29	14.63	15.09	17.57	21.46
V					11.35	14.47	14.05	15.84	13.76	15.86	13.99	18.06
VI						0.00	20.74	11.56	16.03	16.59	10.70	25.88
VII							0.00	19.70	13.03	14.93	21.93	10.52
VIII								0.00	18.25	13.65	17.20	22.02
IX									0.00	17.34	18.56	18.21
X										13.63	19.36	17.63
XI											0.00	26.21
XII												0.00

Table 6: Cluster mean values of fifteen characters in twelve clusters of fifty genotypes in cotton

Sr. No	CH	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
1	DF	75.40	72.33	72.64	80.00	68.00	67.67	65.00	77.00	62.00	72.60	75.00	63.00
2	DB	116.25	110.33	113.61	122.33	105.93	110.33	102.33	117.67	108.67	114.20	118.00	99.67
3	PH	126.00	125.00	140.97	166.67	131.00	125.00	143.33	110.00	131.67	128.67	131.67	116.67
4	MP/P	2.64	2.80	1.80	2.80	2.63	2.53	1.87	1.60	3.73	0.73	2.93	1.13
5	SP/P	15.21	14.93	15.97	19.00	14.23	13.20	16.87	15.00	12.63	15.64	16.40	13.73
6	BP/P	35.93	25.67	31.00	56.07	23.77	23.40	44.40	32.20	42.40	38.16	19.20	49.07
7	BW	2.88	3.57	3.29	2.73	3.35	4.43	2.07	3.40	2.13	3.03	5.00	1.77
8	SCY	96.65	87.00	96.00	146.67	81.73	98.67	87.33	103.33	85.33	109.27	92.67	81.67
9	GP	33.72	30.50	34.42	32.13	34.62	32.40	34.97	30.30	31.90	32.93	33.30	31.30
10	SI	7.75	9.13	8.07	8.10	8.19	7.97	7.90	10.70	7.10	7.97	6.97	9.40
11	LI	3.95	4.01	4.26	3.84	4.35	3.81	4.26	4.67	3.32	3.91	3.49	4.27
12	OC	18.93	18.76	18.64	18.73	18.68	18.88	18.75	19.06	18.74	18.78	18.44	18.47
13	FL	28.27	26.52	26.01	28.30	28.03	26.64	28.10	27.51	25.30	27.41	27.08	30.01
14	FS	28.44	25.37	25.36	28.60	28.01	29.53	32.50	26.30	28.60	28.61	28.40	29.30
15	FF	4.99	5.55	5.30	5.28	4.52	5.58	4.32	5.45	5.18	4.80	4.56	3.58

CH=Character, DF=Days to flowering, DB=Days to boll opening, PH=Plant height (cm), MP/P=No. of monopodia per plant, SP/P=No. of sympodia per plant, BP/P=No. of bolls per plant, BW=Boll weight (g), SCY=Seed cotton yield per plant (g), GP=Ginning percentage (%), SI=Seed index (g), LI=Lint index (g), OC=Oil content (%), FL=2.5% Span length (mm), FS=Fibre strength (g/tex), FF=Fibre fineness (mv)

Table 7: Contributions of various traits towards genetic divergence in cotton

Sr. No	Characters	Time ranked first	Contribution (%)
1	Days to flowering	87	7.10
2	Days to boll opening	0	0.00
3	Plant height (cm)	1	0.08
4	No. of monopodia per plant	234	19.10
5	No. of sympodia per plant	9	0.73
6	No. of bolls per plant	38	3.10
7	Boll weight (g)	223	18.20
8	Seed cotton yield per plant (g)	42	3.43
9	Ginning percentage (%)	33	2.69
10	Seed index (g)	21	1.71
11	Lint index (g)	12	0.98
12	Oil content (%)	54	4.41
13	2.5% Span length (mm)	93	7.59
14	Fibre strength (g/tex)	96	7.84
15	Fibre fineness (mv)	282	23.02

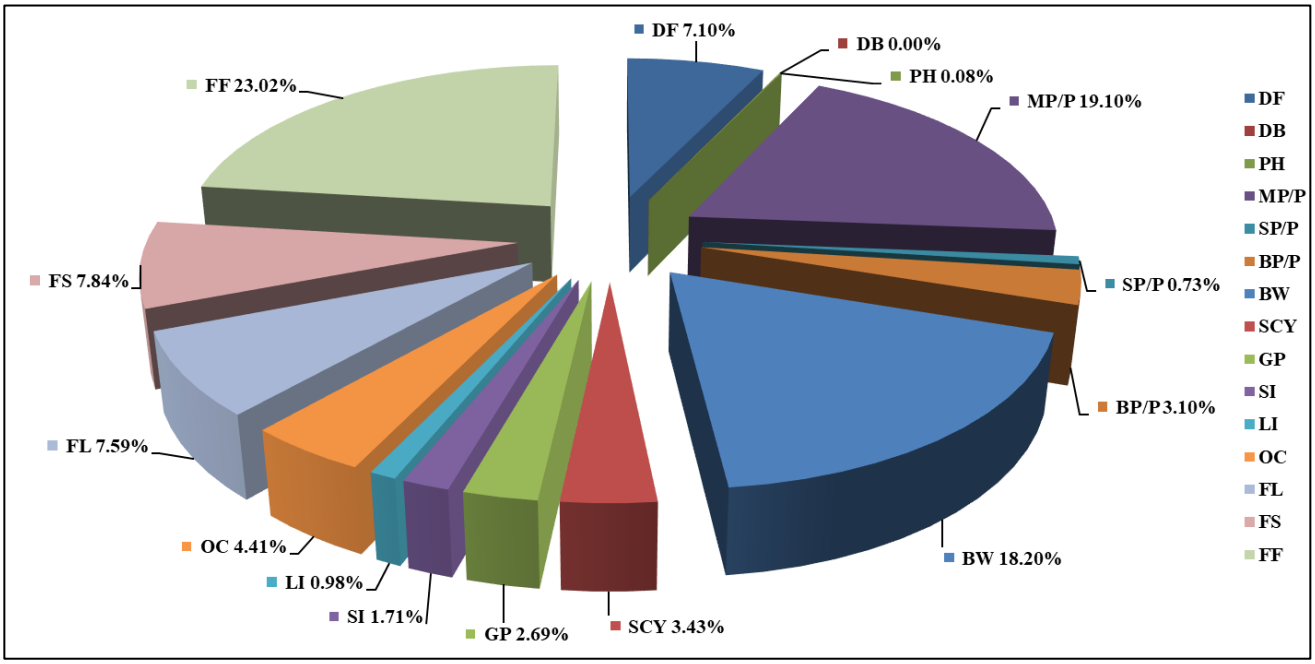

Fig 4: Relative contribution of different characters towards diversity

Conclusion

It could be concluded from the present findings that number of bolls per plant was highly significant and positively correlated at both phenotypic and genotypic levels with seed cotton yield per plant. This was most important attribute which contributed towards higher seed cotton yield. The path coefficient analysis revealed that days to boll opening, number of bolls per plant, boll weight, ginning percentage, 2.5% span length and fibre

fineness had the highest and positive direct effects on seed cotton yield per plant. This revealed that for improvement of seed cotton yield through selection programme, more emphasis should be given to these traits. Fibre fineness, number of monopodia per plant and boll weight had highest contribution towards total genetic divergence. Hence, selection for divergent parents based on these three characters would be useful for exploitation of heterosis breeding in cotton if commercially feasible. Therefore, due weightage should be given to these traits for genetic improvement in cotton.

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