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Genetic Diversity and Association Studies in Asian Cotton (*Gossypium arboreum* L.)

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ABSTRACT: Thirty diverse accessions of asian/*desi* cotton (*Gossypium arboreum*) were evaluated for 15 quantitative traits, during *Kharif* - 2021-22 at Regional Cotton Research Station, Anand Agricultural University to study the genetic variability, heritability, genetic advance as percent of mean, correlation and path coefficient analysis. The analysis of variance revealed significant differences among genotypes for all the characters under investigation. The magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits. High heritability coupled with high genetic advance as per cent of mean were recorded for the characters *viz.,* monopodia per plant, sympodia per plant, bolls per plant, boll weight, seed cotton yield per plant, lint yield per plant, ginning out turn, seed index and fibre fineness suggesting the major role of additive gene action in the inheritance of these traits. Among all characters studied sympodia per plant, bolls per plant and lint yield per plant showed positive and significant correlation with seed cotton yield per plant at both genotypic and phenotypic levels. The results of path analysis indicated that lint yield per plant, bolls per plant, fibre fineness, days to maturity and plant height exerted a strong positive direct effect on seed cotton yield.

Keywords: Asian cotton, genetic variability, heritability, Genetic advance, Correlation coefficient, Path analysis.

INTRODUCTION

Cotton is well known as the "King of Fibre Crops" and also "White Gold". Looking at the botanical hierarchy, cotton belongs to family *malvaceae* and tribe *Gossypieae*, among the eight recognized genera of the tribe, cotton comes under genus *Gossypium*. Cotton possesses a broad genetic diversity with the genus *Gossypium* and constitutes more than 50 species of which 46 are diploids and 7 are tetraploids. Among those, only four are cultivated throughout the world. All four cultivated species of cotton *viz., Gossypium arboreum*, *G. herbaceum*, *G. hirsutum* and *G. barbadense* are raised in India. The first two species *viz., G. arboreum* and *G. herbaceum* are diploid ($2n = 2x = 26$) in nature having A_1 and A_2 genomes, respectively and are called old world cottons. They are also known as Asian cottons because they are cultivated only in Asia. On the other hand, the remaining two species namely *G. hirsutum* and *G. barbadense* are tetraploid ($2n = 4x = 52$) in nature having $(AD)_1$ and $(AD)_2$ genomes, respectively and are referred to as new world cottons. 98 per cent of world's cotton production is achieved from the tetraploid species *G. hirsutum* and *G. barbadense* and just two percent (2%) by diploid species *G. arboreum* and *G. herbaceum* (Shim *et al.,* 2018).

Asian cotton (*G. arboreum* L.) commonly known as tree cotton is native to the Indian subcontinent. The races evolved from *G. arboreum* are *indicum*, *burmanicum, sinense, sudanense, cernuum* and *bengalense*. Historically, India was famous for the world's finest cotton cloth produced from its fibre. Asian cotton ruled the cotton area and production in India prior to Independence. Introduction of upland cotton in 1790s, development of hybrid cotton since 1970s and commercial approval of *Bt* cotton since 2002 has led to drastic reduction in area under *desi* cotton (Santosh *et al.,* 2021). The diploid species of cotton, have an inherent ability to resist various biotic and biotic stress however, these two species suffer with poor fiber quality (Parekh *et al.,* 2016). Although the diploid species share just 2% of the world cotton but are the vital source of important biotic and abiotic resistant genes. *Desi* cotton is cultivated on large scale in India due to its good genetic and agronomic base, suitability to rainfed conditions, resistance to pests and diseases and drought tolerance. With the increasing menace of pink bollworm across cotton growing states and Whitefly-Cotton Leaf Curl Virus complex in northern states and unpredictable climatic vagaries increasingly and adversely affecting cotton production in India, there is a renewed interest in *desi* cotton. Contrary to *Bt* hybrids (*G. hirsutum*), *G. arboreum* cotton is sturdy, tolerant to various biotic (whiteflies and leaf hoppers) and abiotic stresses (drought and waterlogging), immune to dreaded 'cotton leaf curl virus' disease, and require very fewer chemical inputs such as fertilizers or insecticides (Blaise *et al.,* 2020). Because of lesser cost of production, higher net returns and climate resilience, *desi* cotton is expected to play a crucial role in the long-term sustainability of higher cotton yields in India. Cotton lints are short fibres left after removal of long fibres, these are yet another important by product as they are a source of purest cellulose. Usually, *desi* cotton contains 4.30% to 5.90% of cellulose. Hull, the seed coat, constitutes about 37% of the seed weight (Sagar*et al.,* 2022). *G. arboreum* is a perennial, usually 6 to 10 feet in height, having long trailing thin branches, stems and more especially the young branches, petioles, peduncles and bracteoles of a deep glossy purple colour, a peculiarity sometimes even possessed by the young leaves, especially on the under surface. Leaves of a thick and leathery consistence, gland dotted, sub-glabrous or having short, abortively stillate hairs on the blade, especially more under surface, and a few younger spreading hairs on the petiole and young shoots, blade of the leaf mostly five lobed. Flowers yellow with purplish red petal spot. Capsules round to tapering with 3-4 loculi (Gotmare *et al.,* 2001).

Cotton is mainly grown for its fibre in the different parts of the world; besides this, it is also an important source of edible oil (15-25%). The leading cotton growing countries in the world are China, India, United States, Brazil and Pakistan. India has the distinction of having the largest area under cotton cultivation which is about 40% of the world area. While in terms of production India ranks second with a contribution of 23% of the world production of cotton. In India, there are 10 major cotton growing states which are divided into three zones *viz*., north zone, central zone and south zone. North zone consists of Punjab, Haryana and Rajasthan. Central zone includes Madhya Pradesh, Maharashtra and Gujarat. South zone comprises of Andhra Pradesh, Telangana, Karnataka and Tamil Nadu (Anon., 2021-22).

The nature and extent of genetic variability is one of the most important criteria in formulating an efficient breeding programme and knowledge of Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) is much helpful in predicting the amount of variation present in a given assemblage of genotypes. However, with the help of GCV alone, the heritable variation cannot be measured (Singh and Nandpuri 1974). Genetic variability along with heritability should be considered for assessing the maximum and accurate effect of selection (Burton, 1952). Thus, estimation of heritable variability and its genetic components such as GCV, genetic advance is essential in planning and executing a breeding programme for improving quantitative attributes.

Estimation of genotypic and phenotypic correlation among various characters may provide information necessary in a breeding programme when selection is based on two or more characters simultaneously. Selection of one trait results in correlated response in several other traits. Path analysis is simply standardized partial regression co-efficient which splits the correlation coefficient into the measures of direct and indirect effects of a set of independent variables on the dependent variable. The knowledge of the association of one or more characters with yield is useful in selecting high yielding individuals based on their phenotypic values for the improvement of any crop.

The concept of correlation was put forward by Galton (1889) and later elaborated by Fisher (1918). It is an index of the proportion of causes common in the genesis of two variables to the total, not the causes themselves. The study of correlation is very useful to plant breeder for selecting suitable plant type.

Path coefficient analysis originally developed by Wright (1921) is capable of providing a measure of direct and indirect effect of the characters influencing yield and indicates their relative significance in selection for yield more precisely. Dewey and Lu (1959) demonstrated the validity of path analysis in effective plant selection that results in selection of desirable genotypes.

MATERIALS AND METHODS

The present experimental study was conducted at Regional Cotton Research Station, Anand Agricultural University, Anand, Gujarat during *Kharif* 2021-22.30 diverse *desi* cotton genotypes (Table 1) were planted in randomized complete block design with three replications. The spacing among the plants was of 120 × 30 cm. Five competitive plants from each entry were tagged for recording the observations.

In total fifteen characters were considered for the study of which 11 were morphological characters *viz.,* days to 50% flowering (DFF), days to maturity (DM),plant height (PH), monopodia per plant(MP), sympodia per plant(SP), bolls per plant(BP), boll weight(BW), seed cotton yield per plant(SCYP), lint yield per plant(LYP), ginning out turn (GOT) and seed index (SI), three were fibre quality parameters *viz.,* upper half mean length (UHML), fibre strength(FS), fibre fineness(FF) and a single biochemical parameter *viz.,* oil content (OC).

Broad sense heritability is the ratio of genotypic variance to the phenotypic variance and expressed in per cent. It is a standard index of the transmission of characters from parents to their offspring (Falconer, 1989). It was computed in per cent using the formula given by Allard (1960). Heritability percentage was categorized as demonstrated by Robinson *et al*. (1949).

0-30 % = Low
30-60 % = Moderate
60 % and above = High

The expected genetic advance was calculated for each character by adopting the procedure as suggested by Allard (1960). The genetic advance as per cent was categorized as demonstrated by Johnson *et al*. (1955).

<10% = Low
>20% = High

The correlation coefficients were worked out as per procedure suggested by Hazel (1943) to discover association of seed cotton yield per plant with its component traits at both genotypic (r_g) as well as phenotypic (r_p) levels. The path coefficient analysis was carried out according to the method suggested by Wright (1921) and used by Dewey and Lu (1959). The scale for direct or indirect effect was utilized as proposed by Lenka and Mishra (1973).

Values for direct or indirect effect	Rate or Scale
0.00-0.09	Negligible
0.10-0.19	Low
0.20-0.29	Moderate
0.30-0.99	High
> 1.00	Very High

RESULT AND DISCUSSION

A. Variance Components

The estimates of GCV and PCV were high (>20%) for monopodia per plant (26.09 and 27.77), sympodia per plant (25.91 and 27.51), boll weight (21.46 and 23.69), seed cotton yield per plant (19.10 and 23.42) and lint yield per plant (24.77 and 28.79). High GCV values with marginally high PCV values indicated that inter-accession variations were high and that the expression of these characters was less influenced by the environment. The results are in close agreement with the reports of Panhwar *et al.* (2020); Mawblei *et al.* (2022) for monopodia per plant, Kumar and Katageri (2017) for sympodia per plant, boll weight and int yield per plant and Anjani *et al.* (2020) for seed cotton yield per plant. Low GCV and PCV (<10%) was recorded for days to 50% flowering, days to maturity, plant height, upper half mean length, fibre strength and oil content. Low PCV values with marginally low GCV values in these characters indicated less variability for these traits in the genotypes studied and thereby less chances of improvement through selection. Similar results were obtained by Gnanasekaran *et al.* (2018) for days to 50% flowering and plant height, Jogender *et al.* (2023) for oil content. Rest of the characters *viz.,* ginning out turn, seed index and fibre fineness showed moderate (10-20%) estimates of GCV and PCV, which are in line with findings of Joshi and Patil (2018) for ginning out turn and seed index and Gnanasekaran *et al.* (2018); Premalatha *et al.* (2020) for fibre fineness (Table 2).

Knowledge of heritability is important to a plant breeder since it indicates the possibility and extent to which improvement is possible through selection. High heritability estimates were observed for DFF (87.33%), DM (62.92%), MP (88.25%), SP (88.72%), BP (62.89%), BW (82.08%), SCYP (66.52%), LYP (73.99%), GOT (84.90%), SI (82.17%), UHML (79.61%), FS (66.72%), FF (85.51%) and OC (77.30%). High heritability estimates for majority traits indicating major contribution of genetic variance to phenotypic variance and thereby little role of environment on their expression.

Moderate estimates of heritability were obtained for PH (50.98%) which indicated that selection based on phenotypic performance would be rewarding on the partitioning of environmental variances.

The heritability estimates along with genetic advance are more useful than the former alone in predicting the best individuals. High heritability coupled with high genetic advance as per cent of mean were observed for monopodia per plant, sympodia per plant, bolls per plant, boll weight, seed cotton yield per plant, lint yield per plant, ginning out turn and seed index and fibre fineness which indicated better scope of their improvement through selection, as these characters were predominantly governed by additive genetic action (Table 3). Similar results were obtained by Khokhar *et al.* (2017); Mawblei *et al.* (2022) for monopodia per plant and bolls per plant, Kumar and Katageri (2017) for sympodia per plant, boll weight and ginning out turn, Anjani *et al.* (2020) for seed cotton yield per plant, Erande *et al.* (2014) for lint yield per plant and Gnanasekaran *et al.* (2018) for fibre fineness.

Characters namely days to 50% flowering, UHML, FS and OC had high heritability but moderate value of genetic advance as a per cent of mean. The results are in harmony with Premalatha *et al.* (2020) for DFF, and Erande *et al.* (2014) for oil content.

Only one character *viz.,* days to maturity, had high heritability coupled with low genetic advance as a per cent of mean. This clearly indicated the existence of non-additive gene action in the expression of these traits.

B. Correlation Coefficients Analysis

The estimates of genotypic correlation coefficient were in general similar in direction but higher in magnitude than their corresponding phenotypic correlation coefficients which indicate strong association between pair of characters (Table 3 and 4). However, in some cases the values of phenotypic correlation were slightly higher than their genotypic counterpart, which indicate non-genetic causes expanded the value of genotypic correlation because of the interaction with environments.

Correlation study revealed that amongst the fourteen characters, eight showed positive correlation whereas, six character sportrayed negative correlation with seed cotton yield per plant. Amongst these, three characters *viz.,* sympodia per plant (r_g = 0.838**, r_p = 0.685**), bolls per plant (r_g = 0.898**, r_p = 0.823**) and lint yield per plant (r_g = 0.908**, r_p = 0.917**) exhibited highly significant positive correlation on the contrary four characters *viz.,* days to 50% flowering (r_g = -0.624**, r_p = -0.483**), days to maturity (r_g = -0.598**, r_p = -0.346**), monopodia per plant (r_g = -0.514**, r_p = -0.364**) and seed index (r_g = -0.750**, r_p = -0.493**) showed highly significant negative association with seed yield per plant at both genotypic and phenotypic levels. Characters ginning out turn(r_p = 0.275**) and fibre strength (r_p = 0.222*) had significant and positive correlation with seed cotton yield per plant at phenotypic level only.

Results obtained are in accordance with the reports of Dinakaran *et al.* (2012) for lint yield per plant, Chaudhari *et al.* (2017); Kumar *et al.* (2019b) for days to 50% flowering, Ali *et al.* (2020) for bolls per plant, Premalatha *et al.* (2020); Mawblei *et al.* (2022); Sainath *et al.* (2022) for sympodia per plant and bolls per plant, Satish *et al.* (2020) for days to 50% flowering, monopodia per plant and seed index, Mahesh *et al.* (2021) for fibre strength and Aishwarya *et al.* (2022); Gurmessa *et al.* (2022) for ginning out turn.

A positive association indicates that the selection for improvement in one of the yield components would result in concomitant increase in one or more components. Correlation studies revealed that seed yield per plant was strongly and positively associated with sympodia per plant, bolls per plant and lint yield per plant at genotypic and phenotypic levels signifying that selection for these characters can increase seed cotton yield.

Days to 50% flowering and days to maturity had significant and negative association with sympodia per plant, bolls per plant, seed cotton yield per plant, lint yield per plant and fibre strength at both genotypic and phenotypic levels indicating yield can improved with earliness in flowering and maturity. Monopodia per plant and seed index also portrayed significant and negative correlation with seed cotton yield per plant indicating lower number of monopodial branches and lesser seed weight would be fruitful for the improvement in terms of seed cotton yield.

None of the quality parameters showed direct significant association with seed cotton yield per plant, but upper half mean length and fibre strength had significant positive association with characters such as sympodia per plant and bolls per plant which in turn had highly significant and positive association with seed cotton yield, this indirect relation indicates that improvement in upper half mean length and fibre strength could be simultaneously achieved along with improvement in seed cotton yield.

C. Path Coefficient Analysis

Path analysis was carried out at genotypic level considering seed cotton yield per plant as dependent variable and the remaining 14 traits as the independent variables. Each component has two kinds of effects in path analysis *viz.,* direct effect on seed cotton yield and indirect effect through other components which are not explained by correlation studies. The results of genotypic path coefficient analysis are presented in Table 5 and Fig. 1. The path coefficient analysis revealed the cause-and-effect relationship which is shown at genotypic level.

Highest positive direct effect on seed cotton yield was registered by lint yield per plant (0.687) followed by bolls per plant (0.658), fibre fineness (0.608), days to maturity (0.360) and plant height (0.163). Similar findings were reported by Reddy *et al.* (2019) for lint yield per plant, Jangid *et al.* (2022); Mawblei *et al.* (2022) for bolls per plant, Sainath *et al.* (2022) for monopodia per plant and Erande *et al.* (2014) for fibre fineness and plant height. Remaining characters *viz.,* days to 50% flowering (-0.485), sympodia per plant (-0.123), boll weight (-0.067), ginning out turn (-0.980), seed index (-0.240), upper half mean length (-0.274), fibre strength (-0.016) and oil content (-0.129) exerted direct negative effect on seed cotton yield per plant. It was noteworthy that sympodia per plant which showed highly significant positive correlation with seed cotton yield per plant gave the negative direct effect. Reason being the indirect influence *via* bolls per plant, lint yield per plant and days to 50% flowering suggesting sympodia per plant is a desirable parameter for improving seed cotton yield. Similar results were obtained by Mawblei *et al.* (2022).

The residual effect was observed low (-0.015) through various characters which are not considered under study, it indicating that there was no considerable effect *via* such traits which are not considered under investigation. The negative sign indicates that the correlations between estimated values of some of the traits is found very high.

The path coefficient analysis revealed that lint yield per plant and bolls per could be considered as major yield components and should be given due weightage while exercising selection for improvement in terms of seed cotton yield as they had high positive direct effect as well as positive correlation with seed cotton yield.

Table 1: List of Asian cotton genotypes used in the study procured from RCRS, Viramgam.

J.Tapti	AKA 7	CNA 1054
CINA 310	GSav-1056	PAIG 377
AKA 9431	SRT GMS-1	PA 826
PAIG 8/1	PA 741	CNA 1065
PAIG 27	PA 778	PA 873
DLSA 17	PAIG 373	PAIG 379
DLSA 24	PA 796	PA 869
PA 255	PA 812	CINA 1068
824	PA 833	CINA 1069
Cernuum	PA 842	CINA 1067

Table 2: Estimates of genetic parameters for different characters in *desi* cotton.

Sr. No.	Characters	GCV (%)	PCV (%)	h^2_b (%)	GA % Mean
1.	Days to 50% flowering	7.40	7.92	87.33	14.25
2.	Days to maturity	2.07	2.61	62.92	3.39
3.	Plant height	8.49	11.89	50.98	12.49
4.	Monopodia per plant	26.09	27.77	88.25	50.49
5.	Sympodia per plant	25.91	27.51	88.72	50.27
6.	Bolls per plant	16.81	21.20	62.89	27.46
7.	Boll weight	21.46	23.69	82.08	40.06
8.	Seed cotton yield per plant	19.10	23.42	66.52	32.09
9.	Lint yield per plant	24.77	28.79	73.99	43.89
10.	Ginning out turn	10.84	11.77	84.90	20.58
11.	Seed index	12.14	13.40	82.17	22.68
12.	Upper half mean length	7.98	8.95	79.61	14.67
13.	Fibre strength	7.42	9.08	66.72	12.48
14.	Fibre fineness	19.39	20.97	85.51	36.93
15.	Oil content	6.54	7.44	77.30	11.85

Table 3: Estimates of genotypic correlation coefficients (r_g) among 15 characters of *desi* cotton.

Characters	DFF	DM	PH	MP	SP	BP	BW	LYP	GOT	SI	UHML	FS	FF	OC	SCYP
DFF	1	1.057**	-0.196	0.378*	-0.760**	-0.735**	0.228	-0.567**	-0.230	0.592**	-0.367*	-0.548**	0.213	0.249	-0.624**
DM		1	-0.119	0.343	-0.678**	-0.610**	0.145	-0.547**	-0.229	0.510**	-0.318	-0.475**	0.147	0.186	-0.598**
PH			1	0.256	0.543**	0.562**	-0.932**	0.162	-0.206	0.020	0.492**	0.584**	-0.784**	-0.162	0.300
MP				1	-0.415*	-0.354	-0.437 *	-0.588**	-0.456*	0.533**	0.079	-0.077	-0.412*	0.248	-0.514**
SP					1	0.911**	-0.265	0.734**	0.231	-0.708**	0.411*	0.536 **	-0.361	-0.3253	0.838**
BP						1	-0.345	0.830**	0.361*	-0.779**	0.398*	0.536 **	-0.363*	-0.394*	0.898**
BW							1	0.121	0.219	-0.007	-0.540**	-0.537**	0.913**	0.265	0.057
LYP								1	0.691**	-0.801**	-0.103	0.150	0.163	-0.417*	0.908**
GOT									1	-0.533**	-0.561**	-0.201	0.491**	-0.636**	0.330
SI										1	-0.216	-0.395*	0.044	0.554**	-0.750**
UHML											1	0.869**	-0.700**	0.121	0.195
FS												1	-0.563**	-0.077	0.317
FF													1	0.152	-0.042
OC														1	-0.170
SCYP															1

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

DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height, MP = Monopodia per plant, SP = Sympodia per plant, BP = Bolls per plant, BW = Boll weight, SCYP = Seed cotton yield per plant, LYP = Lint yield per plant, GOT = Ginning out turn, SI = Seed index, UHML = Upper half mean length, FS = Fibre strength, FF = Fibre fineness, OC = Oil content.

Table 4: Estimates of phenotypic correlation coefficients (r_p) among 15 characters of *desi* cotton.

Characters	DFF	DM	PH	MP	SP	BP	BW	LYP	GOT	SI	UHML	FS	FF	OC	SCYP
DFF	1	0.803**	-0.139	0.348**	-0.660**	-0.533**	0.186	-0.473**	-0.218*	0.535**	-0.320**	-0.444**	0.216*	0.1892	-0.483**
DM		1	-0.032	0.220*	-0.529**	-0.424**	0.149	-0.351**	-0.175	0.375**	-0.255*	-0.380**	0.137	0.08	-0.346**
PH			1	0.144	0.358**	0.209*	-0.607**	0.042	-0.118	-0.067	0.334**	0.367**	-0.550**	-0.135	0.096
MP				1	-0.345**	-0.194	-0.426**	-0.453**	-0.403**	0.446**	0.067	-0.031	-0.374**	0.180	-0.364**
SP					1	0.7522**	-0.245*	0.632**	0.204	-0.589**	0.358**	0.428**	-0.311**	-0.2623*	0.685**
BP						1	-0.258 *	0.773**	0.276**	-0.556**	0.260*	0.387**	-0.260*	-0.371**	0.823**
BW							1	0.091	0.165	-0.007	-0.438**	-0.404**	0.759**	0.203	0.041
LYP								1	0.627**	-0.593**	-0.116	0.110	0.125	-0.388**	0.917**
GOT									1	-0.474**	-0.479**	-0.160	0.431**	-0.537**	0.275**
SI										1	-0.178	-0.285**	0.031	0.435**	-0.493**
UHML											1	0.834**	-0.628**	0.0965	0.108
FS												1	-0.493**	-0.052	0.222*
FF													1	0.0978	-0.047
OC														1	-0.197
SCYP															1

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

DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height, MP = Monopodia per plant, SP = Sympodia per plant, BP = Bolls per plant, BW = Boll weight, SCYP = Seed cotton yield per plant, LYP = Lint yield per plant, GOT = Ginning out turn, SI = Seed index, UHML = Upper half mean length, FS = Fibre strength, FF = Fibre fineness, OC = Oil content.

Table 5: Path coefficient analysis showing direct (diagonal and bold) and indirect effect of different characters on seed cotton yield.

Characters	DFF	DM	PH	MP	SP	BP	BW	LYP	GOT	SI	UHML	FS	FF	OC	Genotypic correlation with yield
DFF	**-0.485**	0.381	-0.032	0.017	0.094	-0.483	-0.015	-0.390	0.226	-0.142	0.101	0.009	0.130	-0.032	-0.624**
DM	-0.512	**0.360**	-0.020	0.015	0.084	-0.402	-0.010	-0.376	0.224	-0.123	0.087	0.008	0.089	-0.024	-0.598**
PH	0.095	-0.043	**0.163**	0.011	-0.067	0.370	0.063	0.111	0.201	-0.005	-0.135	-0.009	-0.477	0.021	0.300
MP	-0.183	0.124	0.042	**0.044**	0.051	-0.233	0.029	-0.404	0.447	-0.128	-0.022	0.001	-0.250	-0.032	-0.514**
SP	0.368	-0.244	0.089	-0.018	**-0.123**	0.600	0.018	0.505	-0.226	0.170	-0.113	-0.009	-0.220	0.042	0.838**
BP	0.356	-0.220	0.092	-0.015	-0.112	**0.658**	0.023	0.571	-0.354	0.187	-0.109	-0.009	-0.220	0.051	0.898**
BW	-0.110	0.052	-0.152	-0.019	0.033	-0.227	**-0.067**	0.083	-0.215	0.002	0.148	0.009	0.555	-0.034	0.057
LYP	0.275	-0.197	0.026	-0.026	-0.091	0.546	-0.008	**0.687**	-0.677	0.192	0.028	-0.002	0.099	0.054	0.908**
GOT	0.112	-0.082	-0.034	-0.020	-0.029	0.238	-0.015	0.475	**-0.980**	0.128	0.154	0.003	0.298	0.082	0.330
SI	-0.287	0.184	0.003	0.023	0.087	-0.513	0.000	-0.551	0.522	**-0.240**	0.059	0.006	0.027	-0.071	-0.749**
UHML	0.178	-0.114	0.080	0.003	-0.051	0.262	0.036	-0.071	0.550	0.052	**-0.274**	-0.014	-0.426	-0.016	0.195
FS	0.266	-0.171	0.095	-0.003	-0.066	0.353	0.036	0.103	0.197	0.095	-0.239	**-0.016**	-0.342	0.010	0.317
FF	-0.103	0.053	-0.128	-0.018	0.045	-0.239	-0.062	0.112	-0.481	-0.010	0.192	0.009	**0.608**	-0.020	-0.042
OC	-0.121	0.067	-0.026	0.011	0.040	-0.259	-0.018	-0.287	0.624	-0.133	-0.033	0.001	0.093	**-0.129**	-0.170

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

DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height, MP = Monopodia per plant, SP = Sympodia per plant, BP = Bolls per plant, BW = Boll weight, SCYP = Seed cotton yield per plant, LYP = Lint yield per plant, GOT = Ginning out turn, SI = Seed index, UHML = Upper half mean length, FS = Fibre strength, FF = Fibre fineness, OC = Oil content.

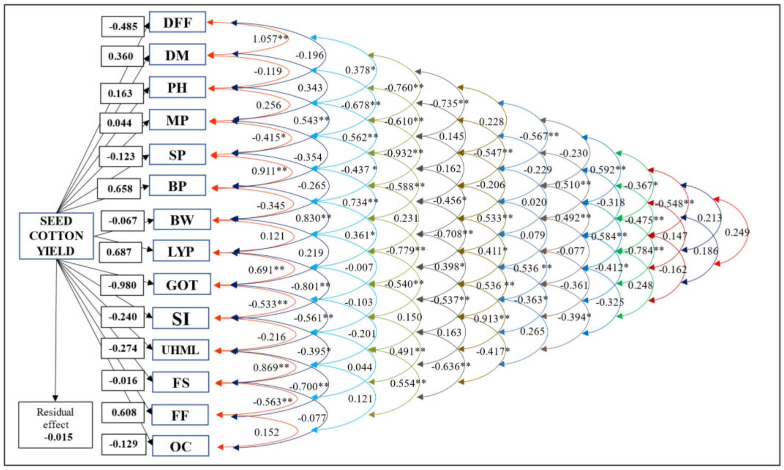

Fig. 1. Path diagram for 15 traits in *desi* cotton.

CONCLUSIONS

The findings of present experiment led to the conclusion that isolation of genotypes with higher seed cotton yield along with good quality is possible amongst the genotypes studied. The characters *viz.,* monopodia per plant, sympodia per plant, bolls per plant, boll weight, seed cotton yield per plant, lint yield per plant, ginning out turn, seed index and fibre fineness displayed sufficient variability, high heritability and high genetic advance. Hence, these characters were mainly governed by additive gene action and could be improved by selection.

The correlation study revealed the importance of characters sympodia per plant, bolls per plant and lint yield per plant for enhancing seed cotton yield. Further, path coefficient analysis discovered that lint yield per plant and bolls per plant could be considered as major yield components and should be given due weightage while exercising selection because of their high positive direct effect as well as positive correlation with seed cotton yield.

FUTURE SCOPE

Though asian/*desi* cotton is the least cultivated among all cultivated cotton species, it is of paramount importance for improvement of majorly cultivated cotton species. Genetic diversity study could provide a breakthrough scope for improvement by cisgenesis or distant hybridization. The lines identified as elite genotypes could be used as donors of genes for yield, fibre quality traits, biotic and abiotic stress in future breeding programme. The highly distinct and unique genotype like Cernuum could be conserved and used to improve specific traits and conserve the genetic diversity in nature.

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Conflict of Interest. None.

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