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Correlation and association studies for yield contributing traits and fibre quality traits in GMS based interspecific cotton hybrids (*Gossypium hirsutum L.* x *Gossypium barbadense L.*)

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Abstract
The present study was focused on the relationship between the yield and fibre quality traits to select the best GMS based hybrids. Thirty five GMS based interspecific tetraploid hybrids were raised from 5 lines (GMS14, GMS17, GMS19, GMS21, GMS27) and 7 testers (CCB26, CCB51, DB1901, CCB2, CCB6, CO18, SUVIN) in Line x Tester design and were evaluated for days to first flowering, days to 50% flowering, days to first bursting, plant height, boll weight, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, ginning outturn, seed index, lint index, upper half mean length, uniformity index, bundle strength, elongation percentage and fiber fineness. The study of correlation on seed cotton yield for 18 traits reported that number of sympodia per plant, boll weight, ginning outturn, lint index, seed index, upper half mean length, uniformity index, bundle strength, elongation percentage and fiber fineness showed significant positive association with the seed cotton yield per plant. The path analysis resulted boll weight, ginning outturn, upper half mean length, elongation percentage, fibre fineness were exhibited positive direct effects on the seed cotton yield per plant. Hence, the above mentioned traits could be considered for further breeding programme.

Keywords: Cotton, GMS based interspecific tetraploid hybrids, correlation, path analysis

Introduction

Cotton is also called as "white gold".According to the ICAC Journal "Cotton This Month" – 1st June 2023, worldwide cotton output for the current season was 24.51 million tonnes (1481 lakh bales) which is 2.8% lesser than the last year, while global cotton consumption is predicted to be 23.79 million tonnes (1399 lakh bales), which is 8% lesser than the last year. India took first place in the world in cotton acreage. Almost 67% of India's cotton is grown on rain-fed land, while 33% is farmed on irrigated land. India ranks 39th in productivity with a yield of 447 kg/ha. For cotton season, 2022-2023 world scenarios, China tops the list for cotton productivity with 1993 kgs/ha, followed by Brazil. But India ranks second for the production of the world cotton with a yield of 5.84 million metric tonnes.

Cotton is an often cross pollinated crop belongs to *Malvacaea* family of the genus *Gossypium*, includes about 50 species. Among these, only 4 species are commercially cultivated worldwide. They are classified into old world or diploid cotton and new world or tetraploid cotton. The most commonly cultivated allotetraploid species are *Gossypium hirsutum L.* and *Gossypium barbadense L. i.e.,* new world cotton introduced to India during 17th century and 18th centuries, contained A genome from the old-world diploid cotton and D genome from a taxon of the American diploid cotton. After polyploidization, *Gossypium hirsutum* evolved to produce a higher fibre yield and survive better in harsh environment than other species and *Gossypium barbadense* evolved to produce superior quality fibre traits like Upper Half Mean Length (mm), bundle strength, fibre fineness (micronaire), uniformity ratio and elongation percentage.

The pollen sterility that is created by nuclear genes is termed as genetic male sterility (Singh *et al.*, 2002) [3]. Male sterility is responsible for the outbreeding. Hence, there is an important role for the genetic male sterility in the development of hybrids. The large number of GMS based parents can be used in crosses, because all the genotypes have dominant genes responsible for male sterility. To produce a hybrid cotton with high yield and superior fibre quality doak's method of emasculation is employed.

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This increases the problem of labour shortage and cost of expenses. In order to reduce these risks the GMS is the best suited tool for producing the best hybrids.

Due to its economic and industrial importance for the quality fiber cotton yield, this study contributes to know the association and its direction of the effect for the seed cotton yield which is considered to be dependent trait.

Materials and Methods

The current experiment was done during September 2022 and February 2023 at Department of Cotton, Center of Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. During September 2022, five GMS based *G. Hirsutum* genotypes *viz.*, GMS14, GMS17, GMS19, GMS21 and GMS27 were used as lines, received from CICR- Nagpur and seven *G. Barbadense* genotypes *viz.*, CCB26, CCB51, DB1901, CCB2, CCB6, CO18 and Suvin were used as testers were raised separately in the crossing block. Since the lines were genetic male sterile lines there were no necessity for emasculation. The pollen was dusted to each lines from all the testers to produce 35 GMS based F_1 hybrids. The parents were raised in 6m ridge with a plant spacing of 120 x 60 cm. appropriate agronomic practices and crop protection method as per the crop production guide were followed. Sufficient crossed bolls were obtained. The selfed bolls also obtained by selfing the parents by clay smearing technique and thread method. During the month of February 2023, 35 GMS-based hybrids were examined, together with their 5 lines, 7 testers and a standard check (DCH 32). A Randomized Block Design (RBD) with two replications was used to estimate the test. Two rows of each entry were grown. To keep 10 plants in a row, the spacing was 90 x 45 cm. All agronomic techniques were employed in well-fertilized and irrigated circumstances to obtain the very good yield. From each genotype in each replication, five plants were randomly chosen for biometrical observations, including days to first flowering (DF), days to 50% flowering (DFF), days to first bursting (DFB), plant height (PH), boll weight (BW), number of monopodia/plant (NMPP), number of sympodia/plant (NSPP), number of bolls/plant (NBPP), ginning outturn (GOT), seed index (SI) and lint index (LI). Lint samples were ginned to assess the properties of the fiber, including upper half mean length (UHML), uniformity index (UI), bundle strength (STR), elongation percentage (EL), and fibre fineness (MIC). The characteristics of the fibre were measured using 10 g of lint sample and the High-Volume Instrument (HVI) 900 classic.

The PB-Perfect program was used to analyze the phenotypic and genotypic correlation and its association investigations.

Results and Discussion
Correlation studies

To improve the quality traits in high yielding *G.hirsutum* lines it was essential to know the relationship between the yield traits and quality traits. The genotypic and phenotypic correlation given in the Table 1 and Fig.1

The SCYPP (g) was positively correlated with the following traits *viz.*, NSPP, BW (g) (Palabiyik *et al.*, 2022) [15], GOT (%), LI (g), SI (g), UHML (mm), UI (%), STR (g/tex), EL and MIC. Similar results obtained by Lekshmi *et al.*, (2023) [8] found that expect seed index (g). The findings of Mawblei *et al.* (2022) [12] found SCYPP (g) was positively correlated with NSPP and BW (g). DF demonstrated non significance to all the traits except DFF which was highly positive significance

for both genotypic and phenotypic correlation.

DFB showed positively significance to SI and also showed negatively significance to SCYPP (g), GOT (%) for both levels. PH (cm) exhibits non significance for SCYPP (g), DF, DFB, NMPP, NSPP, BW (g), GOT (%), LI (g), SI (g) and all other quality traits at both levels. NMPP exhibited negatively significance to the NSPP.

NSPP was positively significance for SCYPP (g), NBPP, BW (g), GOT (%), LI (g), UHML (mm), UI (%), STR (g/tex), EL and MIC similar results were obtained by Monicashree and Balu (2018) [10]. NBPP showed significance to the SCYPP (g), GOT (%), LI (g) and MIC. Similar results obtained by Arunkumar and Murthy (2020) [16]. BW (g) exhibited positive significance to GOT (%), LI (g) (Nikhil *et al.*, 2018) [11], UHML (mm) (Subhashini *et al.*, 2022) [7], UI (%), STR (g/tex), EL and MIC. NSPB showed negative significance to the LI (g), UHML (mm), UI (%), STR (g/tex), EL at both level.

GOT (%) showed positively significance to the MIC, NMPP, STR (g/tex), BW (g), UHML (mm),NSPP, UI (%), EL and SCYPP (g). It was negatively significance to the seed index (g). Similar results were obtained by Satish *et al.*, (2020) [4] for seed index and similar results by Lekshmi *et al.*, (2023) [8] for UI (%), BW (g), UHML (mm), MIC, EL and STR (g/tex), LI was exhibiting positive significance to SCYPP (g), NSPP, NBPP, BW (g), GOT (%), (Monicashree and Balu 2018 [10]; Manonmani *et al.*, 2019; Satish *et al.*, 2020) [9, 4], UHML (mm), UI (%), STR (g/tex), EL and MIC. similar results by Lekshmi *et al.*, (2023) [8] and Jarwar *et al.*, (2019) [17] for STR (g/tex), BW (g), UHML (mm), MIC, EL and UI (%). SI had negatively significance to the SCYPP (g), BW (g), GOT (%), UHML (mm), UI (%), EL and MIC. It also had positive significance to the DFB.

UHML (mm) showed positively significance to SCYPP (g), BW (g), NSPP, EL, UI, GOT, MIC and STR and also exhibited negative significance to NSPB and SI at both levels. Similar results were obtained by Sathish *et al.*, (2020) for positive association trait. UI (%) exhibited positively significance to NSPB, BW (g), GOT (%), LI (g), STR (g/tex), MIC, UHML and EL. STR (g/tex) showed positively significance to UHML (mm), EL (%), GOT, BW (g), NSPP AND MIC at both genotypic and phenotypic correlation.

EL showed positively significance to GOT (%), MIC, UI (%), EL, STR (g/tex) and UHML (mm) and also negatively significance for SI (g) and NSPB at both levels. MIC had positive significance to UI (%), GOT (%), BW (g), SCYPP (g), NSPP, NBPP, LI (g), EL, UHML (mm) and STR (g/tex). It also had negative significance with SI (g).

Hence by this correlation studies the significant positive association traits with yield and quality trait are considered for the selection to enhance the yield and quality traits for further breeding programs. The traits *viz.*, NSPP, BW (g), GOT (%), LI (g), SI (g), UHML (mm), UI (%), STR (g/tex), EL (%) and MIC exhibited positive significant association with seed cotton yield. Hence these traits were used for selecting the high yield with improved fibre quality hybrids.

Path analysis

The path analysis studies enable the breeder to focus on the traits which are positive direct effect on the seed cotton yield (Table 2, figure 2). Thus, the path coefficient was partitioned into direct and indirect effect. It was found that BW (g) (1.095), GOT (%), (8.449), UHML (mm), (1.932), EL (0.964)

and MIC (1.602) were exhibited positive direct effect on the SCYPP. Similar results by Chaudhry *et al.*, (2022) [5, 6]; Lekshmi *et al.,* (2023) [8] for BW (g) (Hampannavar *et al.,* 2020) [13], (Parre *et al.,* 2021) [18], GOT (%), (Gurumessa *et al.,* 2022) and UHML (mm). The traits *viz.,* NSPP (-1.456) (Satish *et al.,* 2020) [4], LI (g) (-7.170), STR (g/tex) (-1.449) and UI (%) (-1.681) (Monicashree and Balu 2018 [10]; Nikhil *et al.,* 2018) [11] Were showing negative direct effect on SCYPP (g). The interrelationship between the yield and quality traits was always given the most importance for

selecting the best hybrids.

The reciprocal effect also considered to select the yield attributing characters indirectly. NSPP was exhibiting high positive indirect effect on SCYPP (g) through NBPP (0.315), BW (0.711), and GOT (%) (5.227). BW was exhibited high positive indirect effect on SCYPP (g) via GOT (%) (8.102). Among all the quality traits, UI (%) exhibited high positive indirect effect on SCYPP (g) via GOT (%) (8.672), UHML (mm) (1.652), EL (0.820) and MIC (0.156).

Table 1: Genotypic correlation (above diagonal) and phenotypic correlation (below diagonal)

	SCYPP	DF	DFF	DFB	PH	NMPP	NSPP	NBPP	BW	NSPB	GOT	LI	SI	UHML	UI	STR	EL	Mic
SCYPP	1	-0.25 *	-0.12	-0.38 **	-0.02	-0.12	0.64 **	0.19	0.56 **	-0.04	0.57 **	0.42 **	-0.29 *	0.62**	0.56 **	0.28*	0.58 **	0.51 **
DF	-0.2756	1	0.34 **	0.11	-0.21	0.05	0.03	0.06	0.09	0.19	-0.09	-0.09	0.06	-0.186	-0.09	0.04	-0.05	0.05
DFF	-0.15	0.44 **	1	-0.24 *	-0.09	0.01	-0.24 *	-0.09	-0.005	-0.02	0.01	-0.10	-0.14	0.076	0.001	-0.15	0.01	0.09
DFB	-0.39 *	0.10	-0.30	1	-0.08	0.04	-0.27 *	-0.05	-0.26 *	0.02	-0.33 **	-0.11	0.36 **	-0.13	-0.09	0.05	-0.11	-0.24 *
PH	-0.06	-0.28	-0.24	-0.09	1	-0.08	-0.11	-0.04	-0.02	0.05	0.009	-0.01	-0.04	0.001	0.004	-0.08	0.001	-0.06
NMPP	0.055	0.044	0.029	0.07	0.378	1	-0.04	0.10	-0.10	-0.01	0.002	0.03	0.01	0.02	-0.01	0.02	-0.17	-0.21
NSPP	0.77 **	0.01	-0.27	-0.34 *	-0.12	-0.33	1	0.30 *	0.51 **	0.03	0.44 **	0.36 **	-0.21	0.31 **	0.33 **	0.35 **	0.41 **	0.45 **
NBPP	0.20	0.05	-0.16	-0.05	-0.05	-0.09	0.4033 *	1	0.19	0.01	0.28 *	0.38 **	0.03	0.07	0.17	0.15	0.04	0.25 *
BW	0.59 **	0.11	-0.01	-0.29	-0.017	-0.06	0.64 **	0.19	1	-0.002	0.62 **	0.48 **	-0.33 **	0.43 **	0.51 **	0.32 **	0.51 **	0.59 **
NSPB	-0.11	0.42 *	-0.36 *	-0.007	-0.46 **	-0.02	0.03	-0.12	-0.10	1	-0.08	-0.22	-0.14	-0.15	-0.03	0.06	-0.10	-0.02
GOT	0.75 **	-0.05	0.06	-0.45 **	-0.02	-0.10	0.61 **	0.43 **	0.95 **	-0.32	1	0.81 **	-0.57 **	0.56 **	0.55 **	0.31 **	0.53 **	0.65 **
LI	0.63 **	0.04	-0.05	-0.16	-0.09	0.13	0.66 **	0.71 **	0.86 **	-0.45 **	0.82 **	1	-0.01	0.46 **	0.47 **	0.26 *	0.42 **	0.54 **
SI	-0.44 **	0.18	-0.18	0.56 **	-0.13	0.22	-0.17	0.10	-0.60 **	-0.04	-0.74 **	-0.24	1	-0.28 *	-0.24 *	-0.14	-0.25 *	-0.33 **
UHML	0.66 **	-0.19	0.11	-0.13 NS	-0.007	0.05	0.36 *	0.09	0.49 **	-0.54 **	0.69 **	0.63 **	-0.39 *	1	0.69 **	0.60**	0.77 **	0.47 **
UI	0.74 **	-0.11	-0.06	-0.13	-0.06	0.002	0.46 **	0.20	0.62 **	-0.80 **	1.02 **	0.96 **	-0.58 **	0.85 **	1	0.34 **	0.74 **	0.51 **
STR	0.50 **	0.05	-0.21	0.04	-0.13	-0.04	0.38 *	0.17	0.35 *	0.31	0.36 *	0.306	-0.24	0.62 **	0.40 *	1	0.51 **	0.35 **
EL	0.73 **	-0.06	-0.03	-0.12	0.01	-0.03	0.65 **	0.07	0.69 **	-0.38 *	0.85 **	0.81 **	-0.47 **	0.93 **	0.84 **	0.61 **	1	0.4617 **
Mic	0.64 **	0.09	0.1846	-0.3021	-0.2858	0.05	0.5843 **	0.3698 *	0.8425 **	-0.2042	1.0582 **	0.8872 **	-0.6978 **	0.6652 **	0.9783 **	0.4616 **	0.96 **	1

Source: Data analysis from PB-Perfect
Significance levels: $p<.0001$ '****'; $p<.001$ '***', $p<.01$ '**', $p<.05$ '*'

Table 2: Genotypic path analysis for yield and quality attributing traits

	DF	DFF	DFB	PH	NMPP	NSPP	NBPP	BW	NSPB	GOT	LI	SI	UHML	UI	STR	EL	Mic	Correlations SCYPP
DF	0.320	-0.766	-0.094	0.050	0.007	-0.027	0.042	0.123	-0.017	-0.460	-0.309	1.018	-0.376	0.200	-0.073	-0.061	0.148	-0.275
DFF	0.140	-1.756	0.259	0.041	0.012	0.400	-0.128	-0.015	0.015	0.577	0.404	-1.016	0.221	0.117	0.307	-0.030	0.295	-0.152
DFB	0.035	0.528	-0.862	0.020	0.009	0.496	-0.045	-0.322	0.0003	-3.805	1.148	3.113	-0.269	0.230	-0.066	-0.122	-0.484	-0.395*
PH	-0.092	0.417	0.098	-0.176	-0.008	0.175	-0.040	-0.018	0.019	-0.201	0.661	-0.743	-0.0140	0.113	0.196	0.009	-0.458	-0.061
NMPP	0.051	-0.505	-0.177	0.033	-0.044	0.339	0.364	0.033	0.053	-7.020	3.022	5.243	-0.531	-0.258	-0.177	-0.526	-0.381	0.055
NSPP	0.005	0.482	0.294	0.021	-0.010	-1.456	0.315	0.711	-0.001	5.227	-4.789	-0.956	0.704	-0.783	-0.559	0.633	0.936	0.775**
NBPP	0.017	0.288	0.049	0.009	0.020	-0.587	0.782	0.213	0.005	3.678	-5.093	0.557	0.190	-0.343	-0.247	0.073	0.592	0.208
BW	0.036	0.024	0.254	0.003	0.001	-0.946	0.152	1.095	0.004	8.102	-6.199	-3.317	0.962	-1.054	-0.520	0.640	1.350	0.555**
NSPB	0.136	0.645	0.006	0.082	-0.057	-0.044	-0.099	-0.114	-0.041	-2.752	3.255	-0.269	-1.054	1.359	-0.457	-0.375	-0.327	-0.111
GOT	-0.017	-0.120	0.388	0.004	-0.037	-0.901	0.340	1.050	0.013	8.449	-5.929	-4.083	1.335	-1.725	-0.531	0.822	1.696	0.754**
LI	0.013	0.099	0.138	0.016	-0.018	-0.973	0.556	0.946	0.018	6.987	-7.170	-1.340	1.227	-1.627	-0.443	0.787	1.422	0.639**
SI	0.059	0.326	-0.491	0.023	0.042	0.254	0.079	-0.664	0.002	-6.308	1.757	5.468	-0.756	0.976	0.352	-0.453	-1.118	-0.448**
UHML	-0.062	-0.201	0.120	0.001	-0.012	-0.531	0.077	0.545	0.022	5.839	-4.553	-2.140	1.932	-1.437	-0.903	0.899	1.066	0.661**
UI	-0.038	0.122	0.118	0.011	0.006	-0.678	0.159	0.686	0.033	8.672	-6.939	-3.176	1.652	-1.681	-0.591	0.820	1.568	0.745**
STR	0.016	0.372	-0.039	0.023	0.005	-0.561	0.133	0.393	-0.013	3.095	-2.194	-1.329	1.203	-0.685	-1.449	0.588	0.739	0.300**
EL	-0.020	0.055	0.109	-0.001	-0.024	-0.956	0.059	0.727	0.016	7.200	-5.854	-2.572	1.800	-1.429	-0.884	0.964	1.544	0.735**
Mic	0.029	-0.324	0.260	0.050	-0.010	-0.851	0.289	0.922	0.008	8.940	-6.362	-3.816	1.285	-1.645	-0.669	0.929	1.602	0.641**

Residuals: 0.1468
Source: Genotypic Path - Data analysis for PB-Perfect

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SCYPP – Seed cotton yield per plant	DF – Days to first flowering
	DFF – Days to 50% flowering
	DFB-Days to first bursting
PH- Plant height	NMPP- No. of monopodia/ plant
	NSPP- No. sympodia/ plant
	NBPP- No. of bolls per plant
BW- Boll weight	NSPB- No. of seeds per boll
	GOT- Ginning outturn
	LI – lint index
SI- Seed index	UHML- upper half mean length
	UI – Uniformity index
	STR- Bundle strenght
EL- Elongation percentage	Mic- Fibre fineness
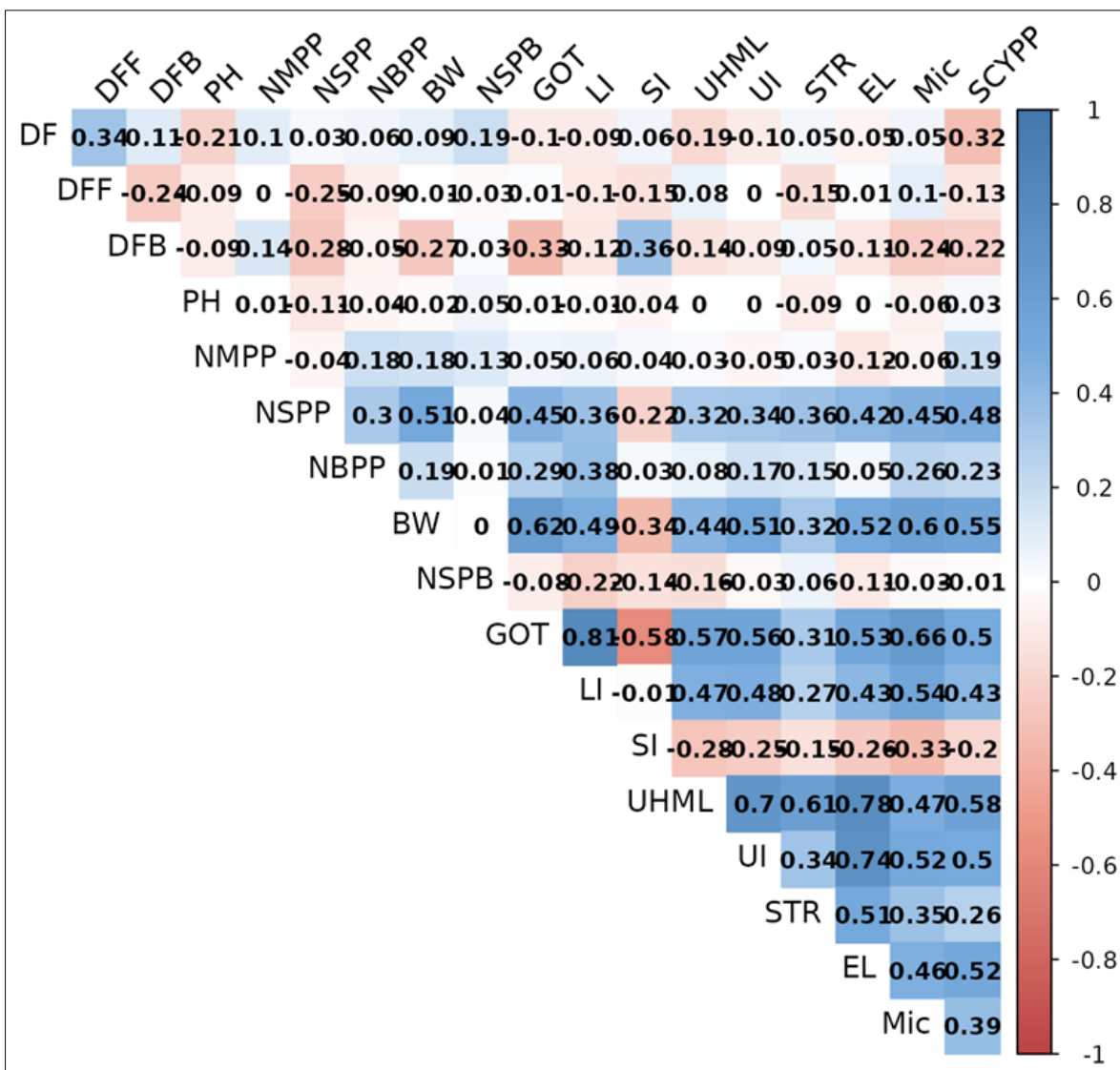
Fig 1: Correlation diagram representation
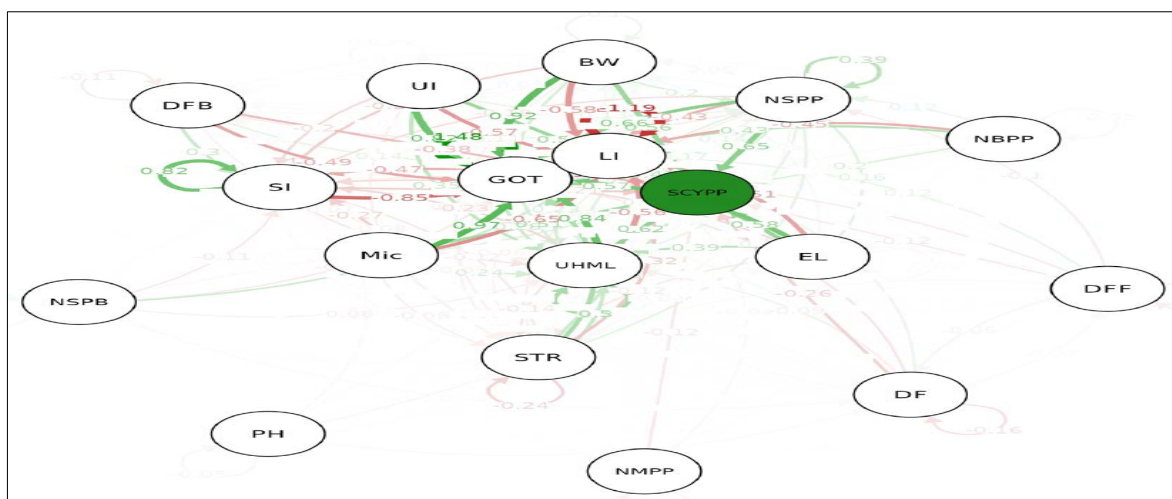
Fig 2: Genotypic path analysis diagram

Conclusion
In conclusion, the present study of correlation and path analysis for direct and indirect effect of the various traits on the seed cotton yield per plant paves the way to identify the interrelationship between and among the traits to select the

best hybrids. Based on the correlation studies, significant components *viz.,* NSPP, GOT (%), LI (g), UHML (mm), BW (g), STR (g/tex), EL, UI (%), MIC and SI (g) were used for selecting the best high yielding hybrids along with good quality trait. From the path analysis of direct effect, revealed

BW (g), UHML (mm), EL (%) and MIC showed positive direct effect on seed cotton. Hence, by improving on these traits *viz.,* BW (g), UHML (mm), EL (%) and MIC, the best commercial hybrids can be produced for the cotton farmers as well as for the textile industries.

Conflict of Interest: None.

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