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Research Article

Evaluation on genetic variability and trait association in naturally coloured cotton (*Gossypium hirsutum* L.)

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Abstract
A study was carried out to understand the genetic variability and trait association in a set of 30 naturally coloured cotton hybrids along with their parents (five colour cotton and six white cotton parents). The Analysis of Variance revealed the significance of the mean square for most of the traits studied. The phenotypic coefficient of variation was more than that of the genotypic coefficient of variation for all the traits. High PCV and GCV were recorded for the traits number of monopodia and single plant yield. The heritability and genetic advance as percentage of mean (GAM) were high for the traits plant height, number of monopodia, number of bolls per plant, single boll weight, bundle strength, fibre fineness and single plant yield. The Number of sympodia, number of bolls per plant and boll weight were observed to have significant genotypic and phenotypic correlation with single plant yield, while upper half mean length was observed to have significant genotypic and phenotypic correlation with bundle strength and fibreelongation. Path analysis revealed that seed index and ginning out turn recorded very high direct effect with single plant yield.

Keywords: Colour cotton, GCV, PCV, heritability, correlation, path analysis

INTRODUCTION

Cotton is the leading cash crop in the world. In India, it is cultivated in an area of 120.69 lakh hectares with a production of 262.18 lakh bales and a productivity of 510 kg lint/ha (https://www.texmin.nic.in/sites/default/files/Cotton%20Sector.pdf). Among the different cultivated species of cotton, namely, *Gossypium hirsutum, G.barbadense, G.herbaceum,* and *G.arboreum, G.hirsutum* is the dominant species, with the lint being the predominant product of economic importance. Though the lint colour of cotton is white, several naturally coloured forms of different shades varying from brown, green are available. Among them, brown colour is more predominantly cultivated and is more stable (Zhou and Ye, 2022). The colour of the lint is a genetically controlled character. The genes responsible for the brown colour are Lc_1 and Lc_2 and the green colour is constituted by the gene *Lg* (Kohel, 1985). The colouration in lint is because of the accumulation of proanthocyanin or their derivative synthesised in the phenylpropanoid pathway (Jie Sun *et al*., 2021). Since Naturally Coloured Cotton (NCC) possesses colour inherently, they don't need artificial dying, thus minimizing the problems of pollution due to dying industries.But the cultivation of NCC is not widespread as compared to the white forms.One of the reasons for the low area of cultivation of NCC is its relatively low fibre quality. Hence it is imperative to improve the fibre quality of NCC to increase its amount. This can be achieved by hybridizing the NCC

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genotypes with superior white cotton genotypes. For the achievement of tangible results in any breeding program, the information on the availability of genetic variation among the parental genotypes is of paramount importance. The genetic variability parameters like Genotypic Coefficient of Variance (GCV) and Phenotypic Coefficient of Variance (PCV) provide information on the existing variability but the extent of heritable proportion of variability is provided by the estimates of Heritability (h^2) and Genetic Advance as percentage of Mean (GAM). Several studies on the variability and heritability of traits in white-linted cotton have been carried (Abasianyanga and Balu,2017;Sri Subalakhshmi *et al.*, 2022; Mawblei *et al.*,2022;Gnanasekaran *et al.*, 2020 and Nandhini *et al.*, 2019). Though selection could be made based on heritability, the efficiency of selection could be enhanced by availability of information on association among the different traits at the genotypic and phenotypic levels. Studies on the association of traits in cotton have been carried out by Chapepa *et al.*, (2020) and Shruti *et al.*, (2020), among others. Considering the above, the present study was carried out to analyse the genetic variability, heritability and character association in NCC genotypes involving 30 hybrids and their parents.

MATERIALS AND METHODS

A total of five NCC genotypes, six white-lined genotypes, listed in **Table 1**, and 30 F_1s generated by crossing the parents in Line x Tester fashion were raised in the Department of Cotton, Tamil Nadu Agricultural University during Winter, 2022-23. The experiment was laid out in a Randomized Block Design with two replications and each entry was raised in two-row plots of 1.08 sqm size.

Table1. Lines and testers used in the experiment

Lines	Testers(White linted)
HC (Brown linted)	KC 3
P15 – 1 (Brown linted)	MCU 7
EC 34 (Brown linted)	CO 17
P15 (Green linted)	SVPR 6
EC 25 (Green linted)	CO 14
	MCU 5

All the recommended cultivation practices were followed for better crop stand. Observations on quantitative traits namely, plant heightin centimeter (PH), number of monopodia (NM), number of sympodia (NS), number of bolls/plant (NB), single boll weightin grams (SBW) and single plant yield in grams (SPY) were recorded in five plants per entry in each replication. The traits days to 50% flowering (DFF), seed index, lint index (LI) and ginning outturn in percentage (GO)were recorded on a plot basis in each replication. The qualitative traits namely upper half mean length in mm (UHML), BS(Bundle strength) in g/tex, MIC (micronaire value – fibre fineness) in µg/inch, uniformity index in percentage (UI) and elongation in percentage (EL) were assessed in the high-volume instrument (Statex Engineering, Coimbatore, India) in the Department of Cotton. The mean of observations for each trait was used for statistical analysis.

The Analysis of variance (ANOVA) was carried out as per Kempthorne (1957). Estimation of GCV and PCV was done as per Burton and De Vane (1953) and it was categorized as low (< 10%), moderate (10% to 20%) and high (> 20%) as proposed by Sivasubramanian and Madhava Menon (1973). The broad sense heritability (h^2) was worked out as per the formula proposed by Lush (1949) and classified as low (< 30%), moderate (30% to 60%) and high (>60%) as proposed by Johnson *et al*.,(1955). The GAM was calculated and designated as low (<10%), moderate (10% to 20%) and high (> 20%) as per Johnson *et al*.,(1955). Phenotypic and genotypic correlation coefficients were computed from variance and covariance components based on the method described by Singh and Chaudhury (1996). The estimates of direct and indirect effects of traits on the dependent trait, single plant yield, were obtained by path coefficients analysis as proposed by Dewey and Lu (1959). The effects were categorized as negligible (0.00 to 0.09), low (0.10 to 0.19), moderate (0.20 to 0.29), high (0.3 to 1.0) and very high (>1) as per Lenka and Mishra (1973). The above statistical analyses were performed using R STUDIO with R packages “variability” and “corrplot”.

RESULTS AND DISCUSSION

The mean sum of squares derived from the ANOVA (**Table 2**) among the lines, testers and off springs were significant for all the traits indicating the existence of sufficient variability among them, thus providing ample chance for selection. The performance *per se* of the NCC hybrids and their parents, for different traits and the estimates of genetic variability parameters are furnished in **Table 3**.

The mean DFF was observed to be 61.93 days. The hybrids P15-1 x CO17, EC34 x SVPR6 and P15 x MCU7 were found to be early flowering (57 days), while the hybrid EC 25 x CO 14 was observed to be late flowering (76.00). The mean PHwas observed to be 131.57 cm and the maximum plant height was recorded by the combination HC x MCU5 (160.00 cm). The mean NM was 1.50 with a maximum value of 3.33 in the hybrid HC x CO14. NS was maximum in the hybrid HC x CO14 (20.00). The mean of NB was observed to be 31.87 with a maximum value of 44.50 for the cross P15 x MCU5.The hybrid HC x MCU5 was observed to be of bigger boll type with a mean boll weight of 5.99g as compared to the mean which was 4.67g.The mean for 100SW was 14.43g with the cross HC x CO14 having bold type seeds with mean 100SW of 17.80g. The mean for LI was 4.61g and the lint index was high for the hybrid P15 x CO14 with the mean value of 5.89g. The hybrid P15 x MCU7(38.34%) had a high GO. The mean value for UHML was 26.82 and the hybrid P15

Table 2. ANOVA for 15 characters of NCC genotypes

Source	df	DFF	PH	NM	NS	NB	SBW	SI	LI
Replication	1	10.97	7.01	0.03	1.43	0.47	0.013	0.06	0.002
Genotypes	40	49.77**	1196.57**	0.50**	15.37**	85.03**	0.83**	4.52**	0.36**
Cross	29	27.78**	597.16**	0.46**	7.53**	51.75**	0.72**	3.85**	0.32**
Line (c)	4	26.10**	1033.98**	0.32**	13.26**	64.16**	0.83**	2.81**	0.40**
Tester (c)	5	20.26**	526.49**	0.70**	8.07**	58.07**	0.60**	1.30^{NS}	0.20*
Line cross tester	20	30.00**	527.47**	0.42**	6.25**	47.69**	0.73**	4.70**	0.34**
Parent	10	112.82**	557.99**	0.60**	31.77**	98.61**	1.02**	6.91**	0.50**
Line (p)	4	97.60**	430.97**	0.25^{NS}	3.15^{NS}	20.96**	1.13**	8.44**	0.74**
Tester (p)	5	129.53**	541.55**	0.81**	19.83**	49.90**	1.07**	5.41**	0.112^{NS}
Lines (P)vs Testers (P)	1	90.20**	1148.32**	0.96*	205.96**	652.80**	0.36^{NS}	8.29**	1.38**
Cross vsParents	1	57.18**	24964.98**	0.69*	78.81**	914.24**	2.01**	0.16^{NS}	0.18^{NS}
Error	40	2.15	4.30	0.13	1.93	3.36	0.13	0.65	0.07

Table 2. Continued.

Source	df	GO	UHML	BS	MIC	UI	EL	SPY
Replication	1	1.09	2.63	0.94	0.02	0.0001	0.07	0.08
Genotypes	40	11.38**	13.66**	24.47**	0.73**	1.80*	0.12**	3096.76**
Cross	29	11.71**	8.04**	19.80**	0.79**	1.28^{NS}	0.11**	2069.60**
Line (c)	4	12.68**	13.90**	58.66**	3.12**	2.62*	0.35**	4396.08**
Tester (c)	5	9.55**	9.09**	13.27**	0.92**	1.02^{NS}	0.08*	445.93**
Line cross tester	20	12.05**	6.61**	13.67**	0.29**	1.08^{NS}	0.07^{NS}	2010.22**
Parent	10	11.20**	31.32**	38.55**	0.62**	2.91**	0.12**	2418.69**
Line (p)	4	4.59*	12.57**	22.53**	0.46**	3.09*	0.06^{NS}	1507.17**
Tester (p)	5	17.52**	23.43**	29.98**	0.87**	0.36^{NS}	0.07^{NS}	1384.50**
Lines (P)vs Testers (P)	1	6.01^{NS}	145.79**	145.42**	0.008^{NS}	14.94**	0.59**	11235.76**
Cross vsParents	1	3.77^{NS}	0.01^{NS}	19.08*	0.0003^{NS}	5.49*	0.36**	39665.14**
Error	40	1.72	1.81	3.55	0.09	0.86	0.02	6.84

* - Significant @5% ;** - Significant @1%

DFF : Days to 50% flowering
PH : Plant height in cm.
NM - Number of monopodia
NS - Number of sympodia
NB - Number of bolls/plants
SBW - Single boll weight in g.
Seed Index
LI - Lint index
GO - Ginning outturn in %
UHML - Upper half mean length in mm.
BS - Bundle strength in g/tex.
MIC - micronaire – fibre fineness in µg/inch.
UI - Uniformity index in %.
EL – Elongation percentage in %.
SPY - Single plant yield in g.

x CO14(32.30) was observed to havea high fibre length. The bundle strength of the fibre was found to be high in the hybrid P15 x CO14 with a value of 35.10mm, while the overall mean for the trait was 27.67mm.The hybrid EC25 x SVPR6 was observed to be very fine with MIC value of 2.55µg/inch, while the mean MIC value was 3.76µg/inch. The hybrid with a high uniformity index was observed to be HC x CO17(82.80%). The elongation of fibre was high for the hybrid P15 x SVPR6 (6.7%) and the mean elongation percentage was 6.05%. Among the different cross combinations, the hybrid HC x CO14 recorded a maximum SPY (230.84g), while the mean SPY was 153.13g.

The PCV among the traits ranged from 4.22 (EL) to 36.49 percent (NM), while GCV ranged from 0.80 (UI) to 26.52 (NM). For all the traits studied, PCV was observed to be greater than GCV, indicating that environment plays a major role in the expression of the traits and selection may be misleading due to its influence. This is similar to the findings of Preetha and Raveendran (2006) and Mohan Kumar and Katageri, (2017) in cotton. High GCV and PCV were observed for the traits NM (26.52, 36.59) and SPY (20.97, 21.04). Estimate of GCV and PCV was moderate for PS (13.08, 13.19), NS (11.67,14.85), NB (15.42,16.49), SBW (11.88,13.82), BS (10.78,11.93) and MIC (15.68, 17.67). This is in tune with the findings of

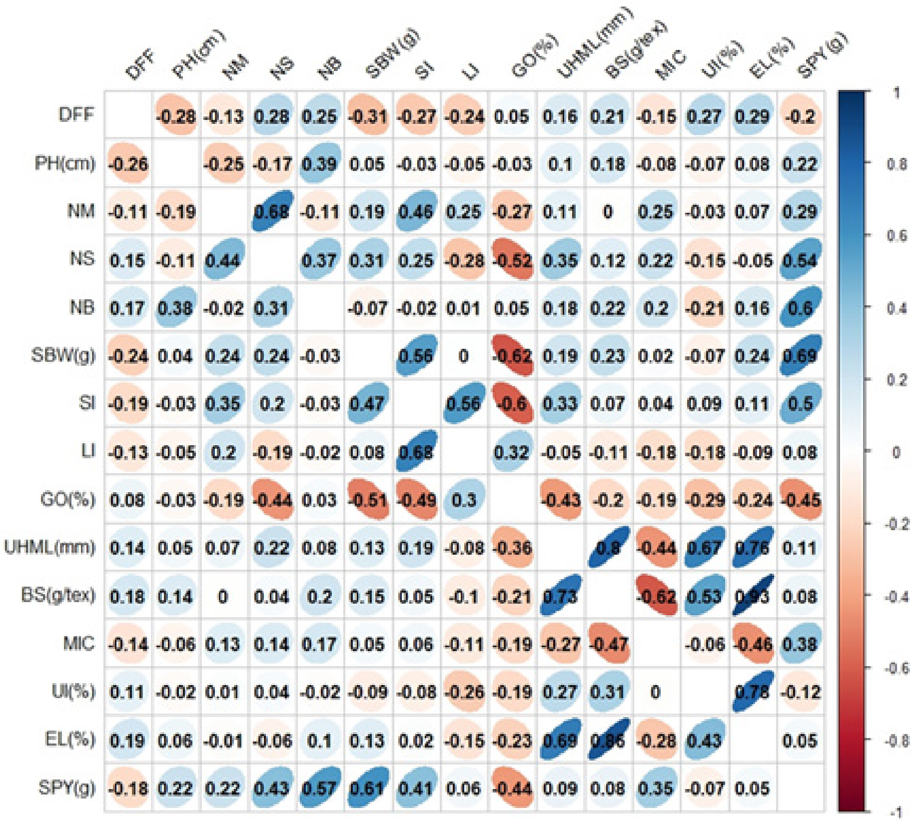
Table 3. Summary Statistics and genetic variability parameters for yield and fibre quality traits of NCC

Characters	Mean	Range		GCV (%)	PCV (%)	Heritability (%)	GAM (%)
		Maximum	Minimum				
DFF	61.93	76.00	57.00	5.76	6.27	84	10.89
PH	131.57	160.00	94.00	13.08	13.19	98	26.72
NM	1.50	3.33	1.00	26.52	36.49	53	39.69
NS	14.53	20.00	10.00	11.67	14.85	62	18.92
NB	31.87	44.50	21.00	15.42	16.49	87	29.71
SBW	4.67	5.99	3.31	11.88	13.82	74	21.05
SI	14.43	17.80	10.83	8.69	10.47	69	14.86
LI	4.61	5.89	3.79	7.51	9.75	59	11.93
GO	32.04	38.33	26.38	7.32	7.78	88	14.18
UHML	26.82	32.20	22.80	6.46	8.37	59	10.26
BS	27.67	35.10	23.30	10.78	11.93	81	20.04
MIC	3.76	5.20	2.55	15.68	17.67	79	28.66
UI	80.51	82.80	78.60	0.80	1.16	47	1.13
EL	6.05	6.70	5.60	3.52	4.22	69	6.04
SPY	153.13	230.84	97.00	20.97	21.04	99	43.07

Preetha and Raveendran (2006), Sunayana *et al*., (2017), Sri Subalakhshmi *et al*., (2022), Mawblei *et al*., (2022), Gnanasekaran *et al*., (2020) and Nandhini *et al*., (2019) in cotton.The trait SI recorded low GCV (8.69) and moderate PCV (10.47), while low GCVand PCV were noted for the traits DFF (5.76, 6.27), LI (7.51, 9.75), GO (7.32, 7.78), UHML (6.46, 8.37), UI (0.80, 1.16) and EL (3.52, 4.22). The results are identical to the findings reported by Preetha and Raveendran (2006), Monisha *et al*.,(2018), Sri Subalakhshmi *et al*., (2022), Mawblei *et al*., (2022), Gnanasekaran *et al*., (2020) and Nandhini *et al*., (2019) in cotton. The trait SI recorded low GCV (8.69) and moderate PCV (10.47). The finding is concurrent with Mohan Kumar and Katageri, (2017). Low GCV estimates for some of the traits suggests the limited range of variability among the genotypes studied for the above traits, as reported by Hake and Bhoite, 2021, in rice. The GCV and PCV values were on par for the traits PH, NB, SBW, BS, MIC, and SPY. High heritability values were recorded for all the traits studied, except LI (59%), UHML (59%) and UI (47%) which recorded moderate heritability. High heritability coupled with genetic advance could be taken as a reliable index for the selection of a trait. In the present study, PH, NM, NB, SBW, BS, MIC and SPY recorded high values for the above components, suggesting the preponderant role of additive gene action for the inheritance of the traits and hence selection could be exercised based on these traits for development of better NCC genotypes. The findings are similar to Preetha and Raveendran (2006), Monisha *et al*., (2018), Sri Subalakhshmi *et al*., (2022), Mawblei *et al*., (2022), Gnanasekaran *et al*., (2020) and Nandhini *et al*., (2019) in cotton. Moderate heritability and genetic advance for the traits LI, UHML and UI could be due to the influence of environment on their inheritance. For traits such as DFF, NS, SI and GO, though heritability was high, genetic advance was moderate suggesting the influence of non-additive gene action. Improvement of these traits could be brought about by heterosis breeding.

Yield of seed cotton is variously influenced by several traits. Hence for improvement of seed cotton yield, knowledge of correlation of various component traits with yield is very important. In the present study, the level of genotypic and phenotypic correlations of different traits with seed cotton yield was analysed and the same is presented in **Fig. 1.** Among the traits, NS, NB, SBW, SI and MIC were observed to have high positive genotypic and phenotypic correlations with SPY. Hence, selection based on these traits could result in parallel improvement in yield of NCC. This is similar to the findings of Monisha *et al*., (2018) and AnandaLekshmi *et al*., (2023) in white linted cotton. Apart from yield, fibre length and strength are the two important quality traits that need improvement in NCC. In the present study, it was observed that UHML recorded a significant positive correlation with SI, BS, UI and EL. BS was observed to have significant positive correlation with UI and EL. The findings are parallel to AnandaLekshmi *et al*., (2023) and Nandhini *et al*., (2019) for UHML, BS, UI and EL in white-linted cotton. This could be because of the pleiotropic effects of the genes governing the above traits on fibre length. This suggests that improvement of fibre length and strength could be achieved by selecting genotypes with bold seeds, high bundle strength, high fibre elongation and uniformity.

Though correlation analysis gives information on the direct relationship between traits, the indirect effects of different traits on the dependent character can be accounted for by



	DFF	PH(cm)	NM	NS	NB	SBW(g)	SI	LI	GO(%)	UHML(mm)	BS(g/tex)	MIC	UI(%)	EL(%)	SPY(g)
DFF		-0.28	-0.13	0.28	0.25	-0.31	-0.27	-0.24	0.05	0.16	0.21	-0.15	0.27	0.29	-0.2
PH(cm)	-0.26		-0.25	-0.17	0.39	0.05	-0.03	-0.05	-0.03	0.1	0.18	-0.08	-0.07	0.08	0.22
NM	-0.11	-0.19		0.68	-0.11	0.19	0.46	0.25	-0.27	0.11	0	0.25	-0.03	0.07	0.29
NS	0.15	-0.11	0.44		0.37	0.31	0.25	-0.28	-0.52	0.35	0.12	0.22	-0.15	-0.05	0.54
NB	0.17	0.38	-0.02	0.31		-0.07	-0.02	0.01	0.05	0.18	0.22	0.2	-0.21	0.16	0.6
SBW(g)	-0.24	0.04	0.24	0.24	-0.03		0.56	0	-0.62	0.19	0.23	0.02	-0.07	0.24	0.69
SI	-0.19	-0.03	0.35	0.2	-0.03	0.47		0.56	-0.6	0.33	0.07	0.04	0.09	0.11	0.5
LI	-0.13	-0.05	0.2	-0.19	-0.02	0.08	0.68		0.32	-0.05	-0.11	-0.18	-0.18	-0.09	0.08
GO(%)	0.08	-0.03	-0.19	-0.44	0.03	-0.51	-0.49	0.3		-0.43	-0.2	-0.19	-0.29	-0.24	-0.45
UHML(mm)	0.14	0.05	0.07	0.22	0.08	0.13	0.19	-0.08	-0.36		0.8	-0.44	0.67	0.76	0.11
BS(g/tex)	0.18	0.14	0	0.04	0.2	0.15	0.05	-0.1	-0.21	0.73		-0.62	0.53	0.93	0.08
MIC	-0.14	-0.06	0.13	0.14	0.17	0.05	0.06	-0.11	-0.19	-0.27	-0.47		-0.06	-0.46	0.38
UI(%)	0.11	-0.02	0.01	0.04	-0.02	-0.09	-0.08	-0.26	-0.19	0.27	0.31	0		0.78	-0.12
EL(%)	0.19	0.06	-0.01	-0.06	0.1	0.13	0.02	-0.15	-0.23	0.69	0.86	-0.28	0.43		0.05
SPY(g)	-0.18	0.22	0.22	0.43	0.57	0.61	0.41	0.06	-0.44	0.09	0.08	0.35	-0.07	0.05	

Fig. 1. Genotypic and phenotypic correlation among the yield and quality traits in NCC

In the figure, above diagonalvalues indicate genotypic correlations and below diagonal values indicate phenotypic correlation

Table 4. Path analysis for 15 quantitative traits in NCC

	DFF	PH (cm)	NM	NS	NB	SBW (g)	SI	LI	GO (%)	UHML (mm)	BS (g/tex)	MIC	UI (%)	EL (%)	SPY (g)
DFF	**0.330**	-0.041	0.002	-0.087	-0.010	-0.107	-0.753	0.509	0.107	0.078	0.099	-0.144	-0.245	0.060	-0.201^{NS}
PH (cm)	-0.093	**0.144**	0.005	0.052	-0.015	0.016	-0.070	0.115	-0.070	0.050	0.085	-0.078	0.060	0.017	0.218^{NS}
NM	-0.042	-0.037	**-0.018**	-0.211	0.004	0.067	1.287	-0.516	-0.589	0.052	-0.001	0.244	0.030	0.016	0.287^{NS}
NS	0.092	-0.024	-0.012	**-0.312**	-0.014	0.108	0.690	0.587	-1.149	0.172	0.059	0.213	0.139	-0.010	0.538**
NB	0.084	0.056	0.002	-0.117	**-0.039**	-0.024	-0.065	-0.022	0.108	0.088	0.105	0.197	0.189	0.034	0.597**
SBW(g)	-0.102	0.007	-0.004	-0.097	0.003	**0.346**	1.563	0.000	-1.375	0.094	0.111	0.024	0.066	0.050	0.685**
SI	-0.089	-0.004	-0.008	-0.077	0.001	0.193	**2.802**	-1.187	-1.314	0.163	0.032	0.044	-0.081	0.024	0.498**
LI	-0.080	-0.008	-0.004	0.087	0.000	0.000	1.580	**-2.105**	0.714	-0.025	-0.051	-0.176	0.166	-0.019	0.079^{NS}
GO (%)	0.016	-0.005	0.005	0.163	-0.002	-0.216	-1.669	-0.681	**2.206**	-0.209	-0.095	-0.185	0.266	-0.049	-0.454*
UHML(mm)	0.053	0.015	-0.002	-0.110	-0.007	0.067	0.933	0.109	-0.943	**0.489**	0.383	-0.431	-0.610	0.159	0.105^{NS}
BS(g/tex)	0.068	0.026	0.000	-0.038	-0.008	0.081	0.187	0.227	-0.440	0.393	**0.477**	-0.604	-0.482	0.194	0.080^{NS}
MIC	-0.048	-0.011	-0.005	-0.068	-0.008	0.008	0.125	0.378	-0.417	-0.215	-0.294	**0.979**	0.057	-0.096	0.384*
UI (%)	0.089	-0.009	0.001	0.048	0.008	-0.025	0.251	0.386	-0.648	0.329	0.253	-0.061	**-0.907**	0.164	-0.120^{NS}
EL (%)	0.094	0.011	-0.001	0.015	-0.006	0.083	0.318	0.189	-0.521	0.370	0.441	-0.447	-0.708	**0.209**	0.047^{NS}

Residue : 0.184
Diagonal values indicate direct effect

path coefficient analysis. In the present study, the traits SI and GO were observed to have a very high positive direct effect on SPY (**Table 4**). Among the two traits, SI was also observed to have a significant positive correlation with SPY hence it could be considered as a reliable index for improvement of the dependent trait, SPY. In the case of GO, though the direct effect was very high, it was observed to have a significant negative correlation with SPY. This could be due to the high negative indirect effect exerted by SI through GO on SPY. This is also reflected in the negative correlation between the above traits. Thus, it could be concluded that the simultaneous improvement of SI and GO may not be possible in the current set of genotypes. Among the traits with high direct effect, MIC and SBW could be reliably employed for selection in view of the significant direct correlation of the traits with SPY. The residual value of the analysis was observed to be 0.184, suggesting that contribution to the level of 81.6 % by component traits to the dependent trait, SPY, has been accounted for.

Thus, based on the present study, it could be concluded that emphasis could be placed on SI, SBW and MIC for improvement of SPY in NCC. Improvement of SI could also result in a favourable shift in UHML of NCC.

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