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Generation of potential genetic variability from interspecific (*G. hirsutum* × *G. barbadanse*) hybrid derived lines

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Abstract

Limited genetic variability in the upland cotton (*Gossypium hirsutum* L.), has stagnated the further genetic improvement in various traits. Many reports suggested for interspecific hybridization for enhancing genetic variability. The present study hence, evaluated RILs (F16 and F17) derived from interspecific hybridization (*Gossypium hirsutum* cv. DS-28 x *Gossypium barbadense* cv. SBYF425) during 2020-21 at ARS Dharwad and at ARS Dharwad & at MARS Raichur during 2021-22 for yield and plant architectural traits. The recorded range *i.e.*, number of times the trait variation greater than the minimum trait value for plant height (0.96), number of monopodia plant⁻¹ (11.88), number of sympodia plant⁻¹ (0.71), number of bolls plant⁻¹ (2.50), fruiting points plant⁻¹ (2.36), internodal distance (1.59), inter boll distance (4.33), sympodial angle at 50% plant height (1.04), sympodial length at 50% plant height (3.20), plant diameter (5.41) and seed cotton yield plant⁻¹ (8.22) indicates the presence high genetic variability. And, the presence of high heritability (> 60%), for all these traits suggests for involving these lines for commercial varietal development. The compact architectured lines, RIL-160, RIL-120, RIL-117, and RIL-167 have yielding ability numerically lower than normal best yield parent DS -28 but could be potential lines for high-density planting which intern enhance productivity.

Keywords: Cotton, recombinant inbred lines, interspecific cross, GCV, PCV, heritability, principal component analysis, path analysis

Introduction

Cotton is a fiber, oil, and protein-yielding crop of global significance, cultivated in over 105 countries. Due to its importance in agriculture as well as in the industrial economy, it is known as "white gold". The cotton with 51 species, only four are cultivated and two among them are tetraploids (G. hirsutum and G. barbadense) and another two are diploids (G. arboreum and G. herbaceum). However, G hirsutum, upland cotton occupies >95% of the cultivated area in the world. The remaining three species together occupied 5% area (Katageri et al., 2020) [17]. The world cotton area is 32.20 Mha with a production of 31.09 Mt and productivity of 766 kg ha⁻¹. Three countries India (12.86 Mha & 17.73 Mt), China (3.25 Mha & 29.50 Mt), and USA (3.52 Mha & 9.73 Mt) share 60.96% area of the world, contributing 50.70% of world production (Anon, 2020)^[1]. Even though G. hirsutum has occupied > 95% global cotton area; the extent of genetic variability for economic traits is limited. For any crop improvement breeding program the basic requirement is to have sufficient genetic variability for targeted traits. Different approaches like plant introduction, mutation, polyploidization, hybridization, and genetic engineering approaches have been suggested for generating genetic variability. But, among them through the shuffling of two different species' genomes, interspecific hybridization will produce various combinations of genes which intern generate huge genetic variability for all the traits. Among the seven tetraploid species, G. barbadanse is the best species with its genome comparatively good compatible with G. hirsutum. In the present study, the male parent G. barbadanse cv. SBYF 425 is compact as its fruiting bodies beared on the main stem, lowering the plant diameter, contrasting the female parent, DS-28 (G. hirsutum) a normal branching with a higher diameter. Hence, the SBYF 425 involved interspecific hybrid-derived lines are the potential variability sources for plant architectural traits. The majority of cotton genotypes grown in India are robust types that require greater three-

dimensional space to reach their full genetic potential. These require lower planting densities, intensive plant protection measures, and higher input levels. The "Compact" plant type, in contrast to such robust types, is small and erect, taking up less space in three dimensions.

As a result, such compact genotypes are suited for planting in large densities and can easily be harvested by machines. The cotton lower leaves must receive enough light to meet the requirement of photosynthesis to produce photosynthates required for the initial growing fruits (Mauney, 1987; Wullschleger and Oosterhuis, 1990, Heitholt et al., 1999)^{[21,} ^{29, 13]}. Consequently, crops with dense canopies as like in robust type may either produce few, or small fruits under high density (Constable, 1986)^[8]. Similarly, the robust type variety had higher nutrient concentrations in its leaves and stems after harvest, which was not used for reproductive growth; hence it may affect fruit development in robust types (Bhatt and Appukutan *et al.*, 1971)^[3]. And another important thing is in indeterminate robust cotton genotypes' maturation was delayed by an increase in plant density from 10 to 15 plants per square meter, but the shorter determinate compact genotypes were unaffected (Kerby et al., 1990)^[18]. Hence, early maturity is an additional benefit of compact cotton varieties, making cotton a member crop in multiple cropping systems where other crops are planted in succession to the cotton crop for sustainable agriculture (Jatoi et al., 2008, Kumar et al., 2020)^[15, 19]. Keeping all the importance of plant architecture and yield potentiality in mind, 198 recombinant inbred lines derived from the interspecific hybrid (Choudki et al., 2012a: Choudki et al., 2012b)^[6-7] were evaluated to assess the level of genetic variability.

Material and Method

As much as 198 advance generation recombinant inbred lines from an interspecific cross between DS-28 (G. hirsutum) and SBYF-425 (G. barbadense) were evaluated along with checks (DS-28, SBYF-425, MCU-5, Sahana, CNH120MB, and Suraj) in augmented design with nine blocks, each block containing twenty-eight lines (RILs +checks), among them RILs were not replicated and checks were replicated across the blocks, the block measured 6.1 meters in length, and spacing of 0.20 meters between plants and 0.90 meters between the rows was followed. Experiments were conducted during Kharif 2020-21 (F₁₆ RILs) at the Agricultural Research Station, University of Agricultural Sciences, Dharwad, and during Kharif 2021-22 (F17 RILs) two experiments, were at Agricultural Research Station, Dharwad and Main Agricultural Research Station (MARS), University of agricultural sciences, Raichur. The plant height in centimeters, the number of monopodial branches, the number of sympodial branches, fruiting points plant⁻¹, number of bolls plant⁻¹, Inter nodal distance (cm), Inter boll distance (cm), sympodial angle at 50% plant height, sympodial length at 50% plant height (cm), seed cotton yield plant⁻¹ were recorded. Total seed cotton harvest from a single line was used to calculate per plant seed cotton yield in grams. At 50% of the plant height using the scale internodal distance on the main stem, Inter boll distance on sympodia and sympodial length were measured. By protractor sympodial angle from the main stem was measured in degrees. Further, plant diameter was calculated using sympodial length at 50% plant height and the sympodial angle at 50% plant height. The sympodial angle in degrees was converted to radian using the formula, Radian = [Sympodial angle x 3.14159] / 180, this radian was converted into Sine of radian and then into radius using the formula Radius = [Sine (Radian) x Sympodial length at 50% plant height], then diameter was obtained by doubling the radius and expressed in cm.

The augmented RCBD R package (Aravind et al., 2022)^[2] was used in R-Studio for statistical analysis of the augmented design. The pooled adjusted mean values were further used for downstream analysis like variability statistics, principal component analysis, correlation, and path analysis using the R program. The genetic variability parameters like the genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were calculated by the formula given by Burton (1952)^[4]. Since RILs are stabilized lines, broad sense heritability (%) was calculated using the formula suggested by Lush (1949)^[20]. The prcomp function was used to perform principal component analysis (PCA), and the biplot function was used to plot PC1 vs PC2, ward's D² analysis was performed using the dist and hclust functions. Correlation analysis was performed using the RStudio corrplot package, and all the non-significant correlations at 0.05 level of significance were cross-marked in the correlation plot.

Results and Discussion

Globally, even though India stands first with respect to cotton area, the productivity levels are 30 to 50% lower than the world's average. Hence, there is huge scope to change the world cotton economy by enhancing Indian productivity levels. So, it's time to consider some other options to enhance cotton productivity. Generally, there are two ways to increase cotton productivity *i.e.* increasing plant yield per se through the development of potential genotypes, and exploitation of heterosis. Another way is through an increasing number of plants per unit area through high-density planting of compact genotypes. But the presence of low genetic variability in G. hirsutum cotton, occupying 95% of the cultivating area, the plateau in yield level has been seen these days. Among the different approaches, interspecific hybridization is known to generate high genetic variability in many crops (Niemann et al., 2012, Kamiński et al., 2020 and Raveendran et al., 2000) ^[24, 16, 26], including cotton (Gowda et al., 2021, Gopikrishnan *et al.*, 2013)^[11, 10], therefore an attempt was made to generate recombinant inbred lines from a well known interspecific hybrid, DCH 32 (Jayalakshmi), which was released in 1980 and has been under cultivation for nearly 25 years in almost 25% of the Indian cotton area. Its male parent happens to be compact type as its fruiting bodies directly originate from the main stem, as expected potential genetic variability has been observed for plant architecture as well, along with yield and yield contributing traits.

Table 1: Augmented ANOVA f	or interspecific hybrid lines,	, evaluated during Kharif	2020-21 at ARS Dharwad.
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	DF	Plant height (cm)	Number of monopodia plant ⁻¹	Number of sympodial plant ⁻¹		Fruiting points plant ⁻¹	Inter nodal distanc e (cm)	Inter boll distance (cm)	Sympodial angle at 50% plant height (Degrees)	Sympodial length at 50% plant height (cm)	Plant diameter (cm)	Seed cotton yield plant ⁻¹ (g)
Block (Eliminating Treatment effect)	8	153.8	0.14	2.22	3.78	28.26	0.49	0.69	5.83	4.22	4.71	7.51
Treatment (Eliminating Block effect)	203	294.92 **	0.3 **	4.25 *	7.11 **	87.13 **	2.11 **	1.51 **	110.83 **	29.11 **	31.97 **	20.9 **
Checks	5	702.57	1.5 **	9.02 **	41.56 **	255.19 **	2.65 **	4.21 **	679.86 **	19.82 *	100.17 *	138.62 *
RILs	197	342.88 **	0.29 **	5.38 **	8.62 **	112.25 **	2.5 **	1.6 **	95.83 **	28.65 **	29.02 **	19 **
Checks vs RILs	1	128.32	0.34	2.35	2.35	9.7	0.01	0.09	469.07 **	209.05 **	314.18 **	6.72
Error	40	120.93	0.11	2.29	2.06	32.63	0.53	0.4	11.65	5.82	6.22	4.73
CV (%)	-	9.26	28.57	9.48	16.94	16.36	9.65	9.65	4.76	7.15	7.85	17.72
CD @ 1%	-	45.43	1.36	6.26	5.93	23.6	2.6	2.6	14.1	10.3	9.96	8.98
CD @ 5%	-	33.95	1.02	4.68	4.43	17.64	1.94	1.94	10.54	7.45	7.7	6.71

*- Significant at 0.05 probability level, ** - Significant at 0.001 probability level

Table 2: Augmented ANOVA for interspecific hybrid lines, evaluated during Kharif 2021-22 at ARS Dharwad

	DF		Number of monopodia plant ⁻¹			noints	nodal	Inter boll distance (cm)	angle at 50% plant	Sympodial length at 50% plant height (cm)	Plant	Seed cotton yield plant ⁻¹ (g)
Block (Eliminating Treatment effect)	8	53.04	0.22 *	6.12 *	7.16	15.59	0.59	0.45	3.64	7.73	5.52	9.9
Treatment(Eliminating Block effect)	203	176.6 **	0.31 **	6.88 **	17.85 **	49.28 **	1.64 **	2.27 **	74.35 **	31.54 **	32.74 **	62.21 **
Checks	5	275.68	1 **	15.04 **	30.97 **	42.23 *	2.65 **	11.76 **	1320.34 **	19.09 *	130.41 *	130.64 *
RILs	197	177.75 **	0.28 **	7.26 **	18.36 **	48.81 **	1.7 **	2.09 **	43.12 **	32.54 **	30.31 **	61.79 **
Checks vs RILs	1	12.58	5.06 **	25.95 **	4.79	963.69 **	0.6	0.00033	267.5 **	104.53 **	192.71 **	73.56 **
Error	40	72.75	0.09	2.74	7.63	12.4	0.38	0.74	7.45	7.74	7.2	9.87
CV (%)	-	7.85	21.65	9.35	20.11	14.89	9.35	12.16	3.81	9.4	9.63	14.64
CD @ 1%	-	35.23	1.27	6.84	11.41	14.55	2.54	3.55	11.28	11.49	11.09	12.98
CD @ 5%	-	26.33	0.95	5.11	8.53	10.87	1.9	2.65	8.43	8.59	8.29	9.7

*- Significant at 0.05 probability level, ** - Significant at 0.001 probability level

Table 3: Augmented ANOVA for interspecific hybrid lines, evaluated during Kharif 2021-22 at UAS Raichur

	DF		Number of monopodia plant ⁻¹			noints	nodal	Inter boll distance (cm)	Sympodial angle at 50% plant height (Degrees)	Sympoular length at	diameter	Seed cotton yield plant ⁻¹ (g)
Block (Eliminating Treatment effect)	8	28.48	0.08	5.98	4.58	5.39	0.44	1.74	11.21	10.48	6.08	80.94
Treatment(Eliminating Block effect)	203	1712.15 **	0.48 **	7.7 *	17.77 **	37.1 **	2.17 **	7.36 **	48.82 **	78.27 **	78.83 **	307.45 **
Checks	5	862.45	1.95 **	8.42	179.46 **	78.71 **	3.17 **	75.84 **	726.23 **	32.93 *	183.68 *	2854.2 *
RILs	197	1810.89 **	0.46 **	7.97 *	14.57 **	37.14 **	2.38 **	5.23 **	31.47 **	78.89 **	74.45 **	257.29 **
Checks vs RILs	1	14.16	0.55	11.07	37.99 **	1.64	3.24 *	77.3 **	464.46 **	349.43 **	608.68 **	534.9 **
Error	40	155.09	0.16	4.59	3.98	9.79	0.49	1.45	7.71	13.26	9.1	54.13
CV (%)	-	8.47	23.34	10.95	15.86	8.7	9.28	14.56	4.33	9.61	8.85	20.07
CD @ 1%	-	51.45	1.63	3.27	8.24	12.93	2.9	4.97	4.24	15.04	12.46	11.24
CD @ 5%	-	38.45	1.22	6.61	6.16	9.66	2.16	3.71	8.57	11.24	9.31	22.71

*Significant at 0.05 probability level, ** - Significant at 0.001 probability level

	Plant height (cm)	Number of monopodia plant ⁻¹	Number of sympodial plant ⁻¹	Number of bolls plant ⁻¹	Fruiting points Plant ⁻¹	Inter nodal distance (cm)	Inter boll distance (cm)	Sympodial angle at 50% plant height (Degrees)	Sympodial length at 50% plant height (cm)	Plant diameter (cm)	Seed cotton yield plant plant ⁻¹ (g)
Mean	112.41	1.15	15.88	11.42	31.85	6.94	7.37	69.75	34.14	63.44	29.09
Minimum	89.03	0.17	12.52	6.31	15.71	4.48	2.33	44.60	16.75	20.69	4.51
Maximum	174.66	2.19	21.40	22.08	52.84	11.59	12.41	91.20	70.35	132.70	41.58
Number of times the variation is greater than the minimum trait value	0.96	11.88	0.71	2.50	2.36	1.59	4.33	1.04	3.20	5.41	8.22
h2	77.67	85.49	63.17	74.56	76.27	83.11	86.25	93.11	79.70	84.53	81.46
GV	97.28	0.09	1.43	2.52	24.81	0.77	1.19	29.61	22.83	24.79	31.35
PV	125.26	0.10	2.27	3.38	32.54	0.93	1.38	31.80	28.65	29.33	38.48
GCV (%)	8.77	25.44	7.54	13.90	15.64	12.67	14.78	7.80	14.00	15.69	19.25
PCV (%)	9.96	27.52	9.48	16.09	17.91	13.89	15.92	8.09	15.68	17.07	21.32
ECV (%)	4.70	10.48	5.76	8.12	8.72	5.71	5.90	2.12	7.06	6.71	9.18
DS-28	125.54	1.33	15.05	10.22	32.08	7.08	7.19	72.34	32.64	72.43	32.6
SBYF-425	119.53	0.45	15.35	10.60	24.83	6.09	2.23	46.98	29.34	18.80	7.82
MCU-5	129.12	1.16	15.40	11.65	29.10	7.32	7.05	71.62	32.23	73.14	32.09
Sahana	129.14	1.32	16.38	11.62	32.01	7.52	7.95	72.52	33.17	70.07	37.72
CNH120MB	125.59	1.18	16.50	13.70	32.15	6.58	7.73	68.33	31.28	66.14	32.29
Suraj	122.44	1.12	16.29	11.23	30.37	6.79	7.63	68.96	33.25	67.42	30.78
CV (%)	4.71	10.59	5.76	8.11	8.82	5.72	5.97	2.14	7.15	6.83	9.13

Table 4: Measures of genetic variability for the pooled data of three seasons

Table 5: Eigenvectors of the principal components obtained for yield and plant architectural traits

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Plant diameter (cm)	-0.39	0.45	-0.01	0.01	-0.29	0.05	-0.09	0.04	-0.10	0.09	-0.72
Plant height (cm)	-0.29	-0.24	0.33	-0.31	0.23	-0.39	-0.35	0.46	-0.09	0.33	0.00
Number of monopodia plant ⁻¹	-0.24	-0.26	0.16	0.56	0.16	0.47	-0.32	0.18	-0.30	-0.24	0.01
Number of sympodia plant ⁻¹	-0.31	-0.26	0.37	-0.22	-0.23	-0.26	0.13	-0.43	-0.24	-0.52	0.00
Number of bolls plant ⁻¹	-0.11	-0.46	-0.35	-0.21	-0.49	0.22	0.34	0.42	-0.16	0.05	0.00
Fruiting points plant ⁻¹	-0.34	-0.23	0.35	0.26	-0.11	0.15	0.28	-0.18	0.59	0.38	0.01
Inter nodal distance (cm)	-0.25	0.02	-0.07	-0.50	0.50	0.52	0.17	-0.27	-0.18	0.17	-0.02
Inter boll distance (cm)	-0.37	0.14	-0.23	-0.02	0.34	-0.12	0.22	0.36	0.43	-0.54	0.02
Sympodial angle at 50 per cent plant height (Degrees)	-0.31	0.00	-0.34	0.41	0.21	-0.42	0.34	-0.16	-0.40	0.29	0.10
Sympodial length at 50 per cent plant height (cm)	-0.36	0.49	0.04	-0.07	-0.34	0.13	-0.14	0.06	-0.07	0.06	0.68
Seed cotton yield plant ⁻¹ (g)	-0.24	-0.28	-0.55	-0.07	-0.09	-0.06	-0.58	-0.36	0.26	0.02	0.01
Standard deviation	1.93	1.26	1.09	1.04	0.98	0.82	0.74	0.71	0.62	0.59	0.07
Proportion of variance	0.34	0.14	0.11	0.10	0.09	0.06	0.05	0.05	0.04	0.03	0.00
Cumulative proportion of variance	0.34	0.48	0.59	0.69	0.78	0.84	0.89	0.93	0.97	1.00	1.00

Table 6: Direct and indirect effects of different yield and plant architectural traits on plant diameter

	Plant Height (cm)	Number of monopodia plant ⁻¹	Number of sympodia plant ⁻¹	Number of	noints	Inter nodal distance (cm)	Inter boll distance (cm)	Sympodial angle (Degree)	Sympodial length (cm)	Seed cotton yield plant ⁻¹ (g)	Plant diameter (cm)
Plant Height (cm)	0.0022	0.0015	0.0016	-0.0005	0.0050	-0.0083	0.0099	0.0230	0.1696	0.0032	0.207**
Number of monopodia plant ⁻¹	0.0005	0.0068	0.0007	-0.0004	0.0066	-0.0026	0.0067	0.0439	0.1024	0.0033	0.168*
Number of sympodia plant ⁻¹	0.0011	0.0015	0.0031	-0.0011	0.0070	-0.0061	0.0064	0.0259	0.2517	0.0035	0.293**
Number of bolls plant ⁻¹	0.0002	0.0006	0.0007	-0.0051	0.0022	-0.0018	0.0016	0.0105	-0.0385	0.0065	-0.023
Fruiting points plant ⁻	0.0008	0.0033	0.0016	-0.0008	0.0135	-0.0046	0.0088	0.0438	0.2608	0.0028	0.330**
Inter nodal distance (cm)	0.0007	0.0006	0.0007	-0.0003	0.0023	-0.0276	0.0121	0.0022	0.2356	0.0035	0.247**
Inter boll distance (cm)	0.0007	0.0015	0.0007	-0.0003	0.0040	-0.0112	0.0298	0.0726	0.4125	0.0052	0.515**
Sympodial angle (Degree)	0.0004	0.0021	0.0006	-0.0004	0.0041	-0.0038	0.0151	0.1435	0.2255	0.0059	0.393**
Sympodial length (cm)	0.0004	0.0008	0.0008	0.0002	0.0038	-0.0070	0.0132	0.0347	0.9323	0.0022	0.981**
Seed cotton yield plant ⁻¹ (g)	0.0004	0.0013	0.0007	-0.0020	0.0023	-0.0057	0.0091	0.0498	0.1177	0.0170	0.191**

Residual effects = 0.0098

Table 7: Best performing RILs in three seasons for yield and plant architectural traits, in the G. hirsutum cv DS-28 x G. barbadense cv SBYF-425 hybrid derived lines

	DII «	PD	PD	PD	PD	PH	PH	PH	PH	SCY	SCY	SCV D(2022)	SCY
	RILs	D(2021)	D(2022)	R(2022)	Mean	D(2021)	D(2022)	R(2022)	Mean	D(2021)	D(2022)	SCY R(2022)	Mean
	RIL-160	33.66	41.06	11.08	28.60	110.00	100.41	97.81	102.74	17.2	28.2	40.42	28.60
Compact	RIL-120	51.26	42.92	59.74	51.31	120.00	86.99	97.87	101.62	14.8	32.83	36.99	28.20
	RIL-117	54.96	52.88	54.46	54.10	117.00	85.79	94.67	99.15	10.00	20.66	34.97	25.54
Tall compact	RIL-167	58.18	59.80	52.28	56.75	128.01	128.01	120.51	125.51	15.23	12.93	69.19	33.78
	RIL-147	72.86	70.13	74.9	72.63	126.06	111.20	136.38	124.55	30.71	19.61	80.29	43.54
	RIL-98	70.24	62.96	80.52	71.24	120.25	102.58	145.50	122.78	29.74	36.94	64.7	43.79
	DS-28	74.20	68.80	74.28	72.43	131.15	102.36	143.10	125.54	28.4	36.2	33.2	32.6
	SBYF-425	18.05	20.45	17.90	18.80	117.67	106.51	134.40	119.53	5.91	10.81	6.75	7.82
High yielding robust	MCU-5	69.67	76.85	72.91	73.14	110.64	112.93	163.80	129.12	12.04	39.62	44.62	32.09
High yielding tobust	Sahana	71.83	65.14	73.23	70.07	125.93	113.23	148.25	129.14	15.39	40.64	57.14	37.72
	CNH120MB	65.28	63.92	69.23	66.14	125.50	103.65	147.61	125.59	14.46	32.77	49.64	32.29
	Suraj	69.65	62.33	70.28	67.42	109.62	115.40	142.30	122.44	16.32	30.73	45.30	30.78
	CD @1%	19.92	14.55	12.46	8.8	45.43	35.23	51.45	51.45	8.98	12.98	11.24	30.39
	CD @5%	15.4	10.87	9.31	6.58	33.95	26.33	38.45	16.33	6.71	9.7	22.71	8.25

Note: D(2021): Dharwad 2021 Experiment; D(2022): Dharwad 2022 experiment; R(2022): Raichur 2022 experiment

PH: Gossypium height (cm), PD: Plant diameter (cm), SCY: Seed Gossypium yield plant⁻¹ (g)

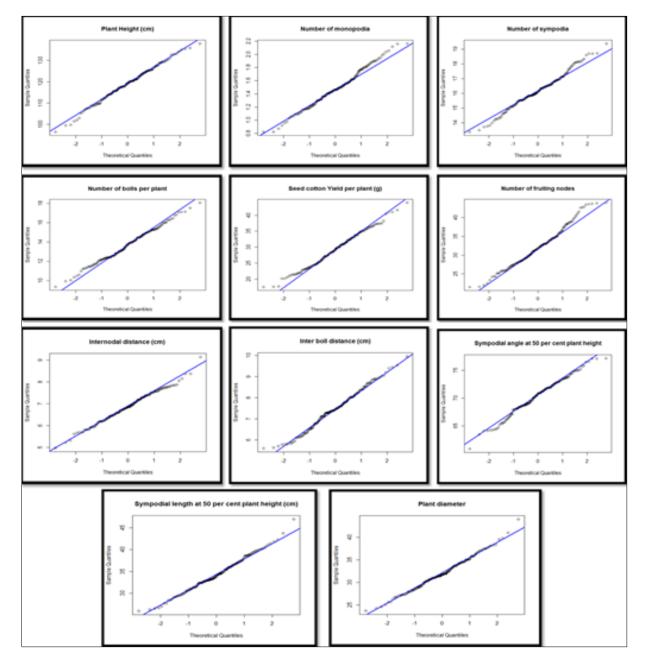


Fig 1: Quantile- Quantile (QQ) plots showing normal distribution and continuous variation for productivity and plant architectural traits

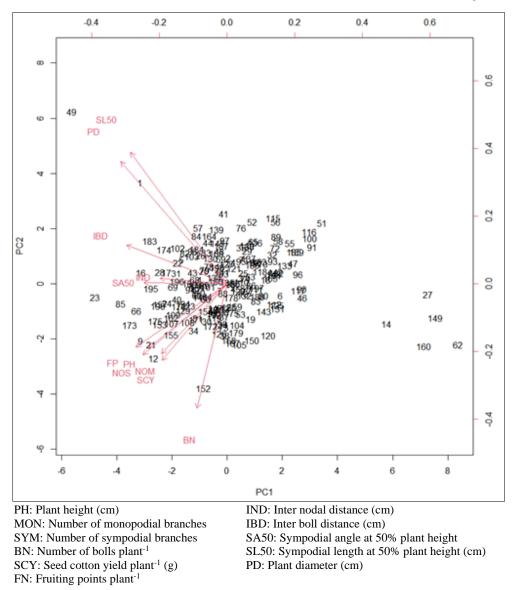


Fig 2: Scatter plot of PC1 Vs PC2 for yield and plant architectural traits for interspecific hybrid derived lines

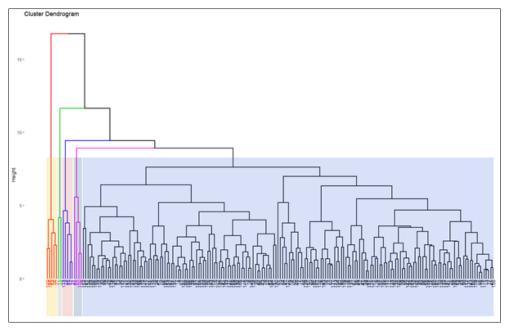


Fig 3: Clustering of interspecific hybrid-derived lines based on plant architectural traits

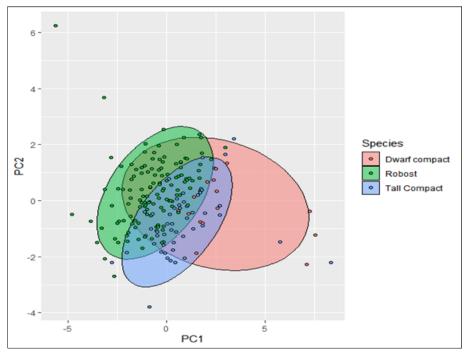


Fig 4: Biplot of PC1 Vs PC2 with superimposed clusters for plant architectural traits

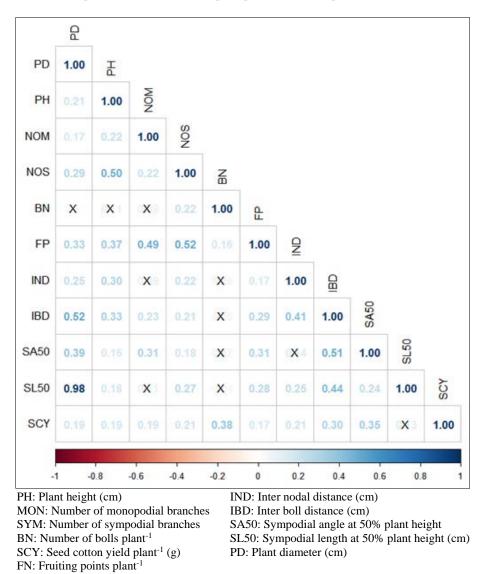


Fig 5: Correlation analysis between various plant architectural and yield traits in the *G. hirsutum* cv. DS-28 x G. *barbadense* cv. SBYF-425 hybrid derived lines

The augmented ANOVA of three experiments i.e., 2020-21 (ARS, Dharwad) and 2021-22 (ARS Dharwad and MARS Raichur) indicates the presence of significant difference at 0.05 level of confidence in the RILs. For all the traits the coefficient of variation was less than 20% indicating less influence of other factors on the experiment (Tables 1, 2, and 3). For the mean of three seasons, the range *i.e.*, number of times the trait variation greater than the minimum trait value for plant architectural traits such as plant height (0.96), number of monopodia plant⁻¹ (11.88), number of sympodia plant⁻¹ (0.71), number of bolls plant⁻¹ (2.50), fruiting points plant⁻¹ (2.36), Internodal distance (1.59), Inter boll distance (4.33), sympodial angle at 50% plant height (1.04), sympodial length at 50% plant height (3.20), plant diameter 5.41) and vield trait *i.e.*, seed cotton vield plant⁻¹ (8.22) indicates there is a high and continuous variation for yield and plant architectural traits in the interspecific hybrid derived lines (Table 4 and Fig 1). For the traits like number of bolls plant⁻¹, fruiting points plant⁻¹, internodal distance, inter boll distance, sympodial angle at 50% plant height, sympodial length at 50% plant height, plant diameter and seed cotton yield plant⁻¹ moderate GCV, PCV, and high heritability were observed. Similarly, the low GCV, PCV, and high heritability were noticed for plant height, number of sympodia plant⁻¹, and the sympodial angle at 50% plant height (Table 4). As the presence of additive gene effects for all these traits was evident due to high heritability (> 60%), the selection through the pedigree method will be effective in enhancing the potentiality of the plant genotypes. These kinds of observations were recorded by the studies of Soumya, 2017; Sowmya, 2020 [27].

The PCA analysis showed that the first five components out of 11 had a standard deviation equal to one and above with a cumulative proportion of 78% variance. The PC1 explained 34% of the total variation, the major contribution *i.e.*, major eigenvectors in the PC1 and PC2 were plant diameter, sympodial length at 50% plant height, inter boll distance, fruiting points plant⁻¹ and number of boll plant⁻¹ (Table 5). Similarly, the scatter biplot of PC1 vs PC2 depicts the magnitude of variability of each trait *i.e.*, eigenvector as red lines (Fig. 2). Based on the eigenvectors of the PC1 to PC5, hierarchical clustering was done and genotypes were split into five clusters (Fig. 3). Plotting of 198 RILs in the biplot of PC1 vs. PC2 indicated that the population has three well-defined clusters with a continuous link between them. The cluster in pale red color contains dwarf compact lines, clusters in blue were tall compact lines, and clusters with green had robust lines (Fig. 4). PCA suggested that the population structure is mainly explained by plant architectural traits by their higher eigenvalues unlike in many studies wherein the population structure is explained only by a few traits like boll weight, boll number plant⁻¹, and seed cotton yield plant⁻¹ (Isong *et al.*, 2017; Rathinavel 2018) [18, 25], inferring that this interspecific hybrid derived lines having high genetic variability. Because the parental lines are highly contrasting for plant architectural traits. Correlation and path analysis indicated that the important plant architectural trait, plant diameter was positively associated with inter boll distance, sympodial angle, and sympodial length with high direct effects (Table 6 and Fig. 5), indicates that while selecting for plant diameter one should also concentrate on direct effect traits (Mawblei et al., 2022, Sowmya, 2020) [22]. These close associations for plant architectural traits were in close agreement with

previous studies (Soumya, 2017; Sowmya, 2020) ^[27]. Similarly, the seed cotton yield plant⁻¹ was significantly positively associated with boll number plant⁻¹ (Table 6 and Fig. 4), so while selecting yield, one should concentrate on boll numbers plant⁻¹ (Monisha *et al.*, 2022; Gurmessa *et al.*, 2022; Chapepa *et al.*, 2020; Gauswami *et al.*, 2021)^[23, 12, 9].

Potential lines for yield and high-density planting

Even though we evaluated the interspecific hybrid derived lines in normal spacing, few lines had shown considerable compactness; probably they will perform well in high-density planting. Based on the three experimental mean phenotypic data, out of 198 RILs, four lines having good yield with plant architecture suitable for high-density planting were identified. The RIL-160, RIL-120, RIL-117, and RIL-167 had shown 60.51, 29.15, 25.30 and 21.64% reduced plant diameter as that of robust parent DS-28 respectively (Table 7). Except the RIL-167 remaining three lines *i.e.*, RIL-160, RIL-120, and RIL-117 showed 18.16, 19.05, and 21.02% reduced plant height compared to robust parent DS-28 respectively. RIL-167 showed on-par height with DS-28 and commercial checks. All four compact architectural lines had yield numerically lower than the best yield parent DS-28 and commercial checks, but this reduced yield will be compensated by the increased number of plants per unit area (Table 7). Similarly, as expected from interspecific hybridization, two transgressive segregants RIL-147 and RIL-98 were statistically superior over DS-28 and commercial checks for seed cotton yield plant⁻¹ were identified (Table 7). This studied population with large genetic variability with continuous variation is highly suitable for molecular linkage and QTL mapping in the future for plant architectural, yield, yield attributes, and fiber quality traits.

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