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Genetic diversity studies for yield traits in upland cotton (*G. hirsutum* L.)

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Abstract

A total of 320 cotton germplasm collections developed in various breeding schemes, commercially released varieties, exotic and indigenous germplasm collections were utilized to study the genetic variations by evaluated with five checks viz., Sahana, Surbi, MCU-5, DS-28 and ARBH-813. The germplasm lines recorded high genetic and phenotypic coefficient of variation across five environments. Correlation among the yield component traits indicates their dependence on each other. Present study also estimated genetic divergence based on D^2 values, 320 germplasm lines including five checks were grouped into eighteen clusters based on morphological and yield contributing traits indicating high amount of divergence. Among the eighteen clusters, cluster XVI was the largest with 37 germplasm lines followed by cluster II with 31 germplasm lines and cluster XII is the smallest with 7 germplasm lines. Number of monopodia contributed 30.58 per cent to the total divergence followed by seed index (13.36%), plant height (13.16%), ginning outturn (13.09%) and it was observed that genotypes grouped under cluster III, II and VI ranked first by having four characters at desirable direction and selection of genotypes under these cluster would be useful to generate desirable genetic resource on inter crosses.

Keywords: Germplasm, genetic variation, divergence, heritability and upland cotton

Introduction

The genus *Gossypium* consists of 45 diploid species divided into 8 subgenomes (A-G and K) and five tetraploids (AD). Of all the *Gossypium* species, two tetraploids (*G. hirsutum* and *G. barbadense*; new world cotton, $2n=4x=52$) and two diploid species (*G. arboreum* and *G. herbaceum*; old world or Asiatic cotton, $2n=2x=26$) are commercially grown for natural fiber. *G. hirsutum* (upland cotton, medium and long staple cotton or Mexican cotton) and *G. barbadense* (Sea Island cotton, extra long staple cotton, American Pima or Egyptian cotton) being natural allopolyploids are derived from an interspecific hybridization of African-Asian A-subgenome (*G. herbaceum* var. *africanum*) and an American D-subgenome (*G. raimondii*) species followed by chromosome doubling (Wendel and Cronn, 2003) [23]. Upland cotton (*G. hirsutum*) dominates the production of most-utilized natural textile fiber crop and accounts for 95% of the world's total production of cotton. Cotton fiber is primarily used in textile industries providing highest employment during production, processing, spinning, weaving and marketing throughout the world. Due to technology upgradation in textile industry in terms of ginning machinery efficiency, quality of cotton should also be improved in the same phase to meet the requirement of textile industry. However, fiber quality has a negative genetic correlation with lint yield, which has long been a major problem in cotton breeding. Progress in cotton improvement programme depends mainly on the genetic diversity in the metric traits of the base population. For the selection of superior parents for hybridization programme, it is necessary to measure the genetic diversity among the set of genotypes as genetic diversity plays an important role in generating heterosis in hybrids between genotypes. Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for different breeding programmes. Therefore, the present investigation was undertaken to study the nature and magnitude of genetic divergence in 320 genotypes of upland cotton.

Materials and methods

The present experiment was conducted in two locations during 2013-14 viz. Agricultural Research Station, Dharwad Farm and Agricultural Research Station, Bagalakot utilizing 320 diverse cotton germplasm collections (breeding lines developed in various breeding schemes, commercially released varieties, exotic and indigenous germplasm collections) evaluated with five checks viz., Sahana, Surbi, MCU-5, DS-28 and ARBH-813. The experiments were laid in alpha lattice designs with two replications. Each replication was subdivided into 16 blocks and each block containing 20 entries.

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Yield characters *viz.*, plant height (cm), number of monopodia per plant, number sympodia per plant, number of bolls per plant, number of fruiting bodies per plant, days to 50 per cent flowering, days to 50 per cent boll opening, mean boll weight (g), ginning out turn (%), seed index (g), lint index (g) and seed cotton yield per ha (kg) were measured on five plants average. Phenotypic data were analyzed using REML procedure (Residual Maximum Likelihood) implemented in Cropstat 7.2 software. The least mean squares were obtained after removing the block effects were used in further analysis. The estimates of covariance and variances were utilized in computing genotypic and phenotypic correlation coefficient and correlation coefficient was worked out using the formula suggested by Hazel *et al.* (1943) [14]. The data was also subjected to randomized complete block design analysis and Mahalanobis's D² statistic (1936) extended by Rao (1952) [17] using software, Windostat version 9.1. Based on D² values the genotypes were clustered into different groups following Tocher's method (Rao, 1952) [17]. Frequency distribution curves were obtained using SPSS version 16.0 software.

Results and discussion

Genetic variation in seed cotton yield and component traits in upland cotton germplasm

The data on components of variation among 14 yield and yield component traits of 320 genotypes pooled over five environments were presented in table 1 and performance of check over five environments were presented in table 2 separately. The germplasm lines recorded high genetic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance for seed cotton yield and boll weight across environments suggesting additive gene effects may act to control of these two traits, simple selection based on these traits could yield high since farmer is directly related to development of superior lines for seed cotton yield and latter are preferred because of ease in hand picking. It also helps in reducing cost and time involved in manual harvesting. Tuteja *et al.* (2006) [20], Gitte *et al.* (2007) [10], Kulkarni *et al.* (2011) [13], Vinodhana *et al.* (2013) [22], Erande *et al.* (2014) [9] and Ahsan *et al.* (2015) [11] reported high GCV and PCV with high heritability, genetic advance for these trait in their study. Moderate GCV and high PCV, heritability and GAM were recorded for number of sympodia across the environments. However low heritability was observed in E4 (49.06%) and E5 (46.80%) for this trait which indicates the presence of higher genetic variability for sympodia per plant in these germplasm lines and the possibility of improving this trait by simple selection helps to improve the seed cotton yield since braches which bear bolls or squares are the sympodia and hence directly influence the seed cotton yield. Vinodhana *et al.* (2013) [22] recorded low GCV and moderate PCV, heritability for this trait in their study. Moderate GCV (17.91%), heritability (57.15%) and high PCV (23.40%), high genetic advance over mean (28.65%) were recorded for number of bolls per plant over environments suggesting variation and existence of non additive gene action which cannot be improved through simple selection. However it recorded high GCV in E1 (20.09%), E2 (22.14%) and E3 (20.06%) and moderate GCV in E4 (13.48%) and E5 (13.87%). Dinakaran *et al.* (2012) [8], Vinodhana *et al.* (2013) [22], Erande *et al.* (2014) [9] and Ahsan *et al.* (2015) [11] recorded high GCV, PCV, heritability and genetic advance for this trait. Tuteja *et al.* (2006) [20] reported high genetic advance as per cent mean for number of bolls in *G. hirsutum*. The germplasm lines recorded moderate genetic variability GCV,

PCV with moderate heritability and genetic advance for plant height and number of monopodia suggesting moderate response to selection. Ali *et al.* (2009) [2] and Tuteja *et al.* (2008) [21] in their experiment, they recorded low to moderate variability with low heritability. Seed index recorded moderate GCV (11.41%), PCV (13.595) and GAM (19.77%) across the environments except E3 and E5 where it recorded low GCV (9.48% and 9.59%) in these two environments respectively. However, high GAM was recorded in E1 (25.62%) and E2 (20.45%) and high heritability exhibited by this trait in all environments indicating that the selection for this trait will be effective to some extent. Gitte *et al.* (2007) [10] and Erande *et al.* (2014) [9] recorded low to moderate genetic variability for seed index. Moderate GCV (13.25%), PCV (17.95%), heritability (55.66%) and high GAM (20.28%) were exhibited by number of fruiting points in four environments except E4 where it recorded high PCV (22.44%), high heritability in E2 (63.15%), E5 (69.72%) and high GAM in E2 (23.85%), E4 (21.06%) and E5 (21.42%) suggesting moderate response to selection. Moderate GCV (13.33%), PCV (15.92%) and high heritability (68.42%), GAM (23.43%) were recorded for lint index over five environments whereas in E1, E2, E4 and E5 it recorded moderate GCV (19.06%, 17.54%, 10.46%, 10.02%) and moderate PCV (19.97%, 18.22%, 14.86%, 13.33%) respectively, however in E3 low GCV (9.55%) and moderate PCV (13.21%) was recorded for this trait. High heritability and GAM were recorded for lint index in E1 (92.66% and 34.78%) and E2 (91.1% and 37.48%) respectively showing narrow variability exist and existence of additive gene action. Vinodhana *et al.* (2013) [22] recorded moderate PCV, heritability, genetic advance and Choudki *et al.* (2012) [6] recorded moderate GCV, heritability and high PCV with high genetic advance. Genetic variation for ginning outturn was low as indicated by low GCV (5.15%), PCV (7.83%), GAM (7.01%) but this trait had moderate heritability (44.15%) suggesting low variability for this trait among the genotypes studied. Similar results were obtained by Tuteja *et al.* (2006) [20] and Vinodhana *et al.* (2013) [22], Erande *et al.* (2014) [9] and Dhivya *et al.* (2014) [7] in their study, where they recorded low GCV, PCV and moderate heritability for this trait.

Phenotypic and genotypic correlations of seed cotton yield with yield component traits

Yield is the result of combined effect of several metric characters and environment. The present study estimated genotypic and phenotypic correlation coefficients among 14 characters of 320 genotypes from pooled data of five environments and worked out the association of seed cotton yield and yield component traits (Table 3). In the present study, seed cotton yield was positively influenced by number of yield component traits such plant height, number of monopodia, number of bolls, number of fruiting bodies, boll weight, ginning outturn and lint index which recorded significantly positive correlation at phenotypic and genotypic level. So improvement in any of these traits will improve seed cotton yield significantly by developmentally influenced functional relationships among these traits. Correlation among the yield component traits indicates their dependence on each other. Significant positive correlation among the component traits is desirable as improvement in one character influences other trait in positive direction, so these traits influence yield in positive direction. Salahuddin *et al.* (2010) [19] recorded positive phenotypic correlation among seed cotton yield, number of bolls, ginning outturn and boll weight, however

they also recorded positive phenotypic correlation among boll weight, sympodia and bolls per plant. Ginning outturn was significantly and positively associated with lint index and negatively with seed index whereas, seed index and lint index were positively correlated. Since seed cotton yield is positively correlated with ginning outturn and lint index, yield cannot be improved by simple selection. Hence we need generate the genetic material by breaking negative correlation between these traits either by biparental mating and triple test cross among these diverse germplasm lines. Similar results were reported by Vinodhana *et al.* (2013) [22] for ginning outturn, lint index and seed index at genotypic and phenotypic level.

Genetic diversity studies in upland cotton germplasm

The amount of diversity available in the crop decides the success of any crop improvement programme with manifold objectives. Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity. In the present investigation, 320 genotypes of cotton germplasm lines were considered for assessment of nature of genetic diversity by adopting Mahalanobis's (1936) [15] concept of generalized distance (D^2) considering ten characters.

Based on D^2 values, 320 germplasm lines including five checks were grouped into eighteen clusters based on morphological and yield contributing traits indicating high amount of diversity among the germplasm lines under study. Among the eighteen clusters, cluster XVI was the largest with 37 germplasm lines followed by cluster II with 31 germplasm lines and clusters VI and XVII with 26 and cluster XII is the smallest with 7 germplasm lines. The pattern of distribution of genotypes into various clusters is presented in Table 4. Basavaraddi and Katageri (2011) grouped 24 genotypes of F_8 generation of cross between *G.hirsutum* var. DS-28 and *G. barbadense* var. SB (YF)-425 into eight clusters based on plant morphological, yield and yield contributing characters.

Among the yield component traits studied, number of monopodia ranked first and contributed 30.58 per cent (Table 5) to the total divergence followed by seed index (13.36%), plant height (13.16%), ginning outturn (13.09%). The lowest contribution was from lint index (1.57%). Contrasting results were reported by Bourland and Jones (2010) [5] among different genotypes of *G. hirsutum*, where lint index contributes maximum to genetic diversity. Murthy *et al.* (2005) [16] reported number of bolls per plant contributed maximum towards divergence and Gururajan and Manickam

(2002) [12] ginning percentage recorded the maximum contribution for genetic divergence. However Basavaraddi and Katageri (2011) reported seed cotton yield was the major contributor to total divergence.

In the present study, it was observed that germplasm lines grouped under cluster VIII were superior for five traits (number of monopodia, number of fruiting bodies, boll weight, lint index and seed cotton yield Kg/ha) (table 6) at desirable direction followed by germplasm lines under cluster IX for two traits (number of bolls and ginning outturn). Genotypes grouped under cluster XII recorded five traits in negative direction (number of fruiting bodies, boll weight, ginning outturn, lint index and seed cotton yield (Kg/ha). For seed cotton yield, lowest cluster mean value was recorded by cluster XII (844.1 kg/ha) and cluster VIII (2198.0 kg/ha) recorded highest cluster mean. The observed range of 770 to 906 kg/ha for cluster XII and 2125 to 2263 kg/ha for cluster VIII. It clearly shows that the germplasm lines grouped in VIII cluster are the highest yielding lines with one to two monopodia, 39 to 45 fruiting bodies, 35.5 to 38.5% ginning outturn and 4.8 to 5.7 g lint index. W247-85-T14-26 has recorded high seed cotton yield (2180 Kg/ha), even though they recorded less boll weight (3.85 g). Basavaraddi and Katageri (2011) reported cluster range from 1155 to 1808 kg/ha. Balu *et al.* (2011) [3] recorded cluster mean for seed cotton yield in the range of 735.2 to 1587.0 kg/ha. However Saeed *et al.* (2014) [18] recorded large difference in seed cotton yield with cluster mean of 297 to 2820 kg/ha.

Analysis of cluster means revealed the relative contribution of different traits to the total divergence by the different clusters. Based on range of means, it is possible to know the characters influencing divergence. It helps to identify clusters having different levels of variability for different characters, based on final ranks it is possible to identify clusters having higher and lesser diversity for more number of characteristics. Utilization of low ranked clusters in breeding programme are expected to yield desirable lines in advanced generation of selection. In the present investigation based on morphological and yield contributing traits, it was observed that genotypes grouped under cluster III, II and VI ranked first by having four characters (1-3 scores) at desirable direction followed by genotypes under cluster II with four and cluster VI with three characters. Therefore, selection of genotypes falling under cluster III, II and VI would be useful to generate desirable genetic resource on inter crosses.

Table 1: Estimates of genetic and phenotypic coefficient of variability, heritability and genetic advance in germplasm lines.

	Season	Plant height(cm)	Number of monopodia	Number of sympodia	Number of bolls	Number of fruiting points	Boll weight(g)	Ginning Outturn (%)	Seed index (g)	Lint index (g)	SCY (Kg/ha)
GCV (%)	E1	13.71	32.15	24.70	20.09	11.75	12.51	6.50	14.31	19.06	36.29
	E2	11.18	34.10	16.75	22.14	14.57	11.42	5.53	12.87	17.54	33.81
	E3	9.94	30.25	16.87	20.06	12.32	12.48	4.97	9.48	9.55	25.32
	E4	9.85	34.49	16.02	13.48	15.15	12.57	4.60	10.80	10.46	25.13
	E5	8.93	26.85	15.16	13.87	12.45	13.36	4.13	9.59	10.02	26.42
	Mean	10.72	31.57	17.90	17.91	13.25	12.47	5.15	11.41	13.33	29.39
PCV (%)	E1	19.23	36.47	30.51	21.68	16.96	16.69	10.38	16.46	19.97	37.86
	E2	14.93	35.99	20.97	28.24	18.34	14.79	8.61	16.68	18.22	35.77
	E3	13.91	35.60	21.69	25.56	17.10	13.47	6.48	11.35	13.21	28.47
	E4	13.57	39.67	22.87	20.86	22.44	13.53	7.25	12.33	14.86	27.58
	E5	14.65	31.01	22.16	20.68	14.92	14.85	6.44	11.13	13.33	28.58
	Mean	15.26	35.75	23.64	23.40	17.95	14.66	7.83	13.59	15.92	31.65
h ² (%) (broad)	E1	50.85	77.70	65.52	85.02	47.96	56.17	39.28	75.54	91.10	91.90
	E2	56.09	89.78	63.80	61.45	63.15	59.67	41.21	59.50	92.66	89.35

sense	E3	51.02	72.20	60.55	61.62	51.89	85.78	58.80	69.74	52.29	79.11
	E4	52.67	75.56	49.06	41.76	45.57	86.41	40.27	76.70	49.57	83.00
	E5	37.13	75.00	46.80	44.97	69.72	80.91	41.19	74.22	56.47	85.49
	Mean	49.55	78.05	57.15	58.96	55.66	73.79	44.15	71.14	68.42	85.77
Genetic advance (% of mean at 5%)	E1	20.14	58.38	41.18	37.98	16.76	19.31	8.40	25.62	37.48	71.66
	E2	17.25	66.57	27.56	35.75	23.85	18.18	7.31	20.45	34.78	65.84
	E3	14.62	52.94	27.05	32.44	18.28	23.81	7.85	16.30	14.23	46.39
	E4	14.72	61.76	23.11	17.95	21.06	24.07	6.01	19.49	15.18	47.16
	E5	11.20	47.91	21.36	19.16	21.42	24.75	5.47	17.01	15.51	50.33
	Mean	15.59	57.51	28.05	28.65	20.28	22.02	7.01	19.77	23.43	56.28
Genetic advance (% of mean at 1%)	E1	26.09	75.61	53.33	49.18	21.70	25.01	10.87	33.18	48.54	92.82
	E2	22.34	86.22	35.69	46.30	30.90	23.54	9.47	26.48	45.05	85.27
	E3	18.94	68.57	35.03	42.01	23.68	30.84	10.17	21.11	18.42	60.09
	E4	19.07	79.98	29.94	23.25	27.28	31.18	7.79	25.24	19.65	61.08
	E5	14.51	62.05	27.66	24.81	27.75	32.06	7.08	22.04	20.09	65.18
	Mean	20.19	74.48	36.33	37.11	26.26	28.52	9.08	25.61	30.35	72.89

E1-ARS, Dharwad (2011), E2- ARS, Dharwad (2012), E3 – ARS, Dharwad (2013), E4-MARS, Dharwad (2013) and E5 – ARS, Bagalkot(2013)

Table 2: Performance of *G. hirsutum* check lines varieties.

	Season	Plant height (cm)	Number of monopodia	Number of sympodia	Number of bolls	Number of fruiting points	Boll weight(g)	Ginning Outturn (%)	Seed index (g)	Lint index (g)	SCY (Kg/ha)
Sahana	E1	101.0	1.76	13.1	12.4	23.9	4.19	36.13	9.54	5.43	1625
	E2	62.2	1.81	17.2	6.1	22.4	4.00	35.00	7.35	3.97	364
	E3	103.5	1.90	13.3	16.6	37.8	4.29	38.80	10.25	5.74	2498
	E4	112.2	1.50	15.1	14.1	29.0	3.69	36.08	9.75	5.51	1350
	E5	121.5	2.40	16.3	13.9	40.4	4.55	37.89	9.75	5.95	2256
	Mean	100.1	1.87	15.0	12.6	30.7	4.14	36.78	9.33	5.32	1619
Surabi	E1	104.0	2.02	13.8	14.3	25.7	3.83	34.49	9.04	4.78	1708
	E2	69.2	1.81	23.2	12.5	24.2	2.98	34.76	7.35	3.93	848
	E3	106.2	2.10	12.3	13.8	32.0	3.94	34.73	9.75	5.19	2607
	E4	114.9	1.70	14.1	16.1	23.2	3.48	32.98	9.25	4.55	1464
	E5	124.2	3.05	15.3	16.1	44.6	4.68	35.83	8.75	4.89	1881
	Mean	103.7	2.14	15.7	14.6	29.9	3.78	34.56	8.83	4.67	1702
MCU 5	E1	88.1	1.94	14.2	14.2	42.0	3.94	36.62	7.68	4.49	1409
	E2	77.7	2.06	26.3	14.8	45.0	3.44	35.41	7.05	3.88	581
	E3	79.4	1.80	8.1	12.2	28.2	4.06	38.54	8.50	5.34	1841
	E4	88.0	1.40	7.4	14.5	19.3	3.49	36.01	8.00	4.49	1461
	E5	97.4	2.30	11.0	14.5	40.8	4.40	34.96	7.00	3.77	1739
	Mean	86.1	1.90	13.4	14.0	35.0	3.87	36.31	7.65	4.39	1406
DS 28	E1	92.1	1.97	15.1	14.7	36.5	4.47	37.25	8.18	4.84	1288
	E2	58.9	1.37	19.7	14.2	33.0	3.81	39.19	6.05	3.92	753
	E3	92.8	2.20	12.2	16.1	35.3	4.90	37.63	9.50	5.73	1568
	E4	101.4	1.80	13.0	11.1	26.4	4.11	36.95	8.75	5.13	1060
	E5	110.8	3.20	15.1	13.4	47.9	4.98	36.93	8.25	4.84	1859
	Mean	91.2	2.11	15.0	13.9	35.8	4.45	37.59	8.15	4.89	1305
ARBH 813	E1	97.5	2.39	16.1	20.7	67.3	4.31	37.16	7.44	4.40	1867
	E2	62.5	2.59	26.9	16.5	63.8	3.77	38.74	6.75	4.28	636
	E3	96.8	2.30	14.3	23.9	39.6	4.79	37.65	8.25	5.01	3127
	E4	105.5	1.90	11.1	18.9	30.8	4.27	35.27	7.75	4.25	1692
	E5	114.8	2.80	17.3	21.2	52.2	4.48	37.86	7.75	4.73	2150
	Mean	95.4	2.40	17.1	20.3	50.7	4.32	37.33	7.59	4.53	1894

E1-ARS, Dharwad (2011), E2- ARS, Dharwad (2012), E3 – ARS, Dharwad (2013), E4-MARS, Dharwad (2013) and E5 – ARS, Bagalkot(2013)

Table 3: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficient for yield, yield component and fiber traits.

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
X1	1	0.068	0.387**	0.008	0.380**	0.054	-0.062	0.154**	0.088*	0.178**
X2	0.103**	1	-0.103**	0.150**	0.082*	0.136**	0.116**	-0.013	0.070	0.143**
X3	0.397**	-0.095*	1	0.136**	0.302**	0.133**	0.077	0.108**	0.039	0.036
X4	0.057	0.212**	0.241**	1	0.150**	0.083*	0.142**	-0.124**	0.007	0.193**
X5	0.499**	0.157**	0.486**	0.309**	1	0.052	-0.047	0.054	0.014	0.199**
X6	0.183**	0.200**	-0.174**	-0.171**	0.205**	1	0.008	0.196**	0.172**	0.209**
X7	-0.065	0.171**	-0.042	0.225**	0.020	0.061	1	-0.266**	0.522**	0.163**
X8	0.194**	-0.050	0.162**	-0.135**	0.023	0.315**	-0.346**	1	0.677**	0.029
X9	0.131**	0.084*	0.130**	0.067	0.045	0.324**	0.493**	0.642**	1	0.140**
X14	0.352**	0.236**	0.069	0.296**	0.407**	0.433**	0.276**	0.022	0.235**	1

*, ** -- Significant at 5% and 1% level of significance, respectively.

X1	Plant height (cm)	X5	No. of fruiting points	X9	Lint index (g)
X2	No. of monopodia	X6	Boll weight (g)	X10	Seed cotton yield (kg/ha)
X3	No. of sympodia	X7	Ginning Outturn (%)		
X4	No. of bolls	X8	Seed index (g)		

Table 4: Cluster-wise distribution of 320 *G. hirsutum* germplasm lines for yield and yield related traits.

Sl. No.	Cluster	No. of genotypes	Genotypes*
1.	I	11	6 25 31 51 54 118 190 216 228 239 310
2.	II	31	3 7 42 55 72 79 80 103 140 144 148 169 176 180 182 184 202 203 205 208 213 232 234 243 263 266 294 308 309 313 317
3.	III	18	12 16 23 40 52 68 113 122 172 173 181 196 248 267 271 278 283 312
4.	IV	20	34 48 114 131 150 154 158 163 164 179 192 207 210 223 233 237 280 285 291 311
5.	V	10	26 53 57 58 67 115 147 151 252 305
6.	VI	26	2 18 20 27 28 47 66 84 97 116 120 123 132 145 160 177 195 201 204 257 259 264 277 288 293 318
7.	VII	11	5 56 81 85 119 161 168 197 225 255 314
8.	VIII	8	9 38 41 46 63 71 75 235
9.	IX	16	39 50 62 65 70 78 87 93 94 108 124 191 226 254 258 262
10.	X	21	1 4 14 35 43 44 95 102 104 106 133 166 170 193 198 209 212 246 268 295 301
11.	XI	25	15 32 45 82 83 90 92 100 109 128 134 135 152 153 155 156 157 159 174 185 199 219 221 230 281
12.	XII	7	8 30 98 99 251 273 300
13.	XIII	14	11 13 74 96 110 125 126 136 175 189 206 298 319 320
14.	XIV	13	21 64 89 91 129 142 146 187 217 227 261 302 316
15.	XV	9	17 61 88 107 141 149 220 270 279
16.	XVI	37	10 29 33 36 49 59 60 69 73 77 101 105 117 127 167 178 194 214 218 222 236 240 241 245 247 249 250 265 269 275 284 286 287 296 297 307 315
17.	XVII	26	22 24 76 111 137 162 171 183 186 188 200 215 224 229 231 244 253 256 260 272 274 282 289 290 292 304
18.	XVIII	17	19 37 86 112 121 130 138 139 143 165 211 238 242 276 299 303 306

* Number indicates serial number of a germplasm line mentioned in Annexure-I

Table 5: Contribution of different traits towards genetic divergence in *G. hirsutum* germplasm lines for yield and yield related traits.

Sl. No.	Characters	Per cent contribution
1	Plant height (cm)	13.16%
2	Number of monopodia	30.58%
3	Number of sympodia	6.19%
4	Number of bolls	5.35%
5	Number of fruiting points	5.16%
6	Boll weight (g)	4.03%
7	Ginning outturn (%)	13.09%
8	Seed index (g)	13.36%
9	Lint index (g)	1.57%
10	Seed cotton yield per hectare (g)	7.51%

Table 6: Performance of germplasm lines under cluster VIII on the basis of cluster mean

Gh AM	Germplasm	Seed cotton yield (Kg/ha)	Number of monopodia	Number of fruiting bodies	Boll weight (g)	Lint index (g)
75	EC296596	2263	2.26	37.8	4.39	4.85
71	128333-Acala-44	2258	1.82	32.9	4.31	5.54
63	543416A03N132	2250	1.68	44.8	4.94	5.61
235	HAGH-148	2220	1.75	41.3	4.62	5.22
38	W247-85-T14-26	2180	1.76	43.6	3.85	5.60
46	54335402A015	2160	1.71	62.9	4.21	5.74
41	490151-NM970513	2128	1.77	27.5	4.47	5.34
9	IC357226	2125	1.97	45.1	4.90	5.45
	Mean	2198	1.84	42.0	4.46	5.42
	Minimum	2125	1.68	27.5	3.85	4.85
	Maximum	2263	2.26	62.9	4.94	5.74
	ARBH 813	1894	2.40	50.7	4.32	4.53
	Surabhi	1702	2.14	29.9	3.78	4.67
	DS 28	1305	2.11	35.8	4.45	4.89
	Sahana	1619	1.87	30.7	4.14	5.32
	MCU 5	1406	1.90	35.0	3.87	4.39
	CD @5 %	341.58	0.53	8.73	0.61	0.79

Table 7: Performance of germplasm lines under cluster IX on the basis of cluster mean

Gh AM	Germplasm	Number of bolls	Ginning outturn (%)	Seed cotton yield (Kg/ha)
65	126663	17.6	37.17	1962
262	RDT-17	17.5	37.64	1937
254	NO-4	17.2	37.46	2044
124	FQT-38	16.9	39.22	1965
70	200759WIR7178	16.0	37.74	1930
39	477984-EMPIRE134	15.9	36.02	2048
93	EC560376	15.8	37.39	2005
108	EC560422	15.7	37.95	1985
50	543364A02N46	15.2	36.60	1962
258	RDT-3	15.0	38.40	2083
226	CPD-2007-4	14.9	36.91	1940
62	543403A03N106	14.8	37.09	1975
78	EC559012	14.6	38.66	1966
87	EC560354	14.0	39.08	1939
94	EC560377	13.0	38.27	1988
191	CPD-1002	12.9	34.74	2050
	Mean	15.4	37.52	1986
	Minimum	12.9	34.74	1930
	Maximum	17.6	39.22	2083
	DS 28	13.9	37.59	1305
	ARBH 813	20.3	37.33	1894
	CD @5 %	3.93	4.20	341.58

Table 8: Performance of germplasm lines under cluster XV on the basis of cluster mean.

Gh AM	Germplasm	Number of fruiting bodies	Boll weight (g)	Ginning outturn (%)	Lint index (g)	Seed cotton yield (Kg/ha)
8	IC357200	41.1	4.01	31.17	5.13	770
98	EC560387	32.8	4.47	34.43	5.11	811
251	CSHH-243F-Sirsa	40.4	3.66	34.83	4.67	822
300	CPD-469	27.2	3.83	36.84	4.45	844
273	CPD-436	29.3	4.18	36.98	5.46	874
30	EC143506	36.3	4.01	34.51	4.19	882
99	EC560391	26.0	4.28	32.37	4.01	906
	Mean	33.3	4.06	34.45	4.72	844.1
	Minimum	26.0	3.66	31.17	4.01	770
	Maximum	41.1	4.47	36.98	5.46	906

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