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DUS characterization of upland cotton (*Gossypium hirsutum* L.) elite genotypes by qualitative characters

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Abstract

Characterization of any variety or hybrid is must to know its novelty for the registration and notification. In the present investigation, experiment consisting of 86 genotypes was carried out during *kharif* 2017 at Cotton Research Area, Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar. Observations were recorded for qualitative traits of cotton on the basis of guidelines provided by PPV and FRA for DUS testing. Twenty morphological characters were studied out of which only nine characters *i.e.* leaf colour, leaf hairiness, leaf appearance, stem hairiness, flower petal colour, flower stigma, pollen colour, boll shape, boll tip showed significant variation and no variation is recorded for remaining eleven characters. On the basis of nine traits all the genotypes were clustered intro six groups. Out of those, cluster I (27) and cluster II (33) are the major clusters with 70 genotypes in them while cluster IV and VI had only three genotypes each. The variability in these characters can be used in hybridization program for selection of desirable parents.

Keywords: DUS, qualitative character, variation, PCA, cluster

Introduction

Cotton is the ruling fibre crop grown in many countries and it is also a major source of oil, feed with worlds utilization of approximate 27mt per year (Chen *et al*., 2007) [1]. There are two cultivated species of Gossypium namely New world and Old world cotton. Old world cotton includes two species *Gossypium arboreum* and *Gossypium herbaceum* with ploidy level of 2n=2x=26 (diploid, AA) and commonly called as desi cotton or Asiatic cotton. New world cotton are *Gossypium hirsutum* and *Gossypium barbedense* with a ploidy level of 2n=4x=52 (tetraploid, AADD). Yield is the major target of all breeding programmes but due to genetic erosion there is a massive decline in genetic diversity of cotton varieties over last decade (Meredith, 2000) [4]. So due to its narrow genetic base characterization of cotton germplasm, plant breeders need to put emphasis on its characterization and conservation. PPVFR, Act enacted in the year 2001 in India to facilitate the protection of plant varieties and farmers rights. According to this Act DUS testing is necessary for a variety to be released or protected. This act provides good quality seeds and planting stock to the farmers and encourage the farmers, breeders and private industries to develop new varieties. Distinctiveness, Uniformity and Stability (DUS) testing is obligatory for characterization and documentation of different traits of cotton varieties and parental lines in PPVFR, Act 2001. The variety to be protected must be unquestionably distinguishable by atleast one essential character form other varieties. DUS characterization of cotton lines can be used for crop improvement by selection of better parents with specific trait which could be used in breeding programme. There are total 37 DUS characters for tetraploid cotton including fibre characters. Out of these 37 characters the present was conducted for DUS testing of cotton lines for 20 different morphological traits or morphological markers using DUS testing manual of protection of plant variety & farmers rights authority, India.

Material and Methods

Morphological evaluation of 86 cotton lines was carried out at cotton research area, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (India) during kharif 2017 in a randomized block design with 3 replications. All cultivation practices were performed as directed by the agronomist of cotton section. Twenty morphological markers/ qualitative characters were used for characterization of these cotton lines. The qualitative traits used were namely, leaf nectarines, leaf petiole pigmentation, leaf shape, stem hairiness, stem pigmentation, bract type, flower petal colour, flower petal spot, flower stigma, flower anther filament colour, pollen colour, boll bearing habit, boll colour, boll shape, boll surface, boll tip. Scores were assigned for these characters as per the guidelines provided by DUS testing manual Table 1.

Table 1: Morphological traits recorded for cotton germplasm and their scoring as per DUS guidelines

S. No.	characteristics	State	Score
1	Leaf colour	Light Green Green Light Red Dark Red	1 2 3 4
2	Leaf hairiness	Absent Medium Strong	1 5 9
3	Leaf appearance	Cup Flat	1 2
4	Leaf gossypol glands	Absent Present	1 2
5	Leaf nectarines	Absent Present	1 9
6	leaf shape	Palmate (Normal) Semi-digitate (Semi-okra) Digitate (Okra) Lanceolate (Super-okra)	1 2 3 4
7	leaf petiole pigmentation	Absent Present	1 9
8	Stem hairiness	Absent Sparse Medium Strong	1 3 5 7
9	Stem pigmentation	Absent Present	1 9
10	Bract type	Normal Frego	1 2
11	Flower petal spot	Absent Present	1 9
12	Flower petal colour	White Cream Yellow Pink Red Bicolour	1 2 3 4 5 6
13	Flower stigma	Embedded Exerted	1 2
14	Flower anther filament colour	Absent Present	1 2
15	Pollen colour	White Cream Yellow Purple	1 2 3 4
16	Boll bearing habit	Solitary Cluster	1 2
17	Boll colour	Green Red	1 2
18	Boll shape	Rounded Ovate Elliptical	1 2 3
19	Boll surface	Smooth Pitted	1 2
20	Boll tip	Blunt Pointed	1 2

Statistical analysis of the scored observation for principal component analysis was carried out by PAST software and clustering of the genotype was done by unweighted pair-group average agglomeration method on similarity basis by XLSTAT software.

Result and discussion

Twenty qualitative character were recorded for the present study. Out of two twenty traits eleven traits had no variation among all genotypes those characters are leaf gossypol gland, leaf nectarines, leaf petiole pigmentation, leaf shape, stem pigmentation, bract type, flower petal spot, flower anther filament color, boll bearing habit, boll color, boll surface. Nine characters which has shown variation are leaf colour, leaf hairiness, leaf appearance, stem hairiness, flower petal colour, flower stigma, pollen colour, boll shape, boll tip Table 2. So further analysis of the study was carried out using only these nine traits.

Principle component analysis of the accessions showed that the first four PCs (PC1 to PC4) having eigenvalues > 1.0 and cumulatively accounted for 67.55% of the total variation (Table 3). The first PC axes accounted for 20.64% of the total variation, whereas the second PC explained 19.194% and the third PC accounted for 14.45% of variation. The cumulative proportion of the variation reached 55.03% in the first three PC axes, and 67.55% in the all four axes. The high level of variation in all four PC axes showed a high level of variation for these characters. The variation in PC1 was largely correlated with leaf appearance, flower petal colour, flower stigma, and pollen colour, boll shape and boll tip; in PC2 with leaf colour, leaf hairiness, leaf appearance, stem hairiness, flower petal colour and boll shape; PC3 was mainly associated with leaf colour, leaf hairiness, leaf appearance, stem hairiness, flower stigma, boll shape and boll tip, and in the fourth PC variation was mainly correlated with leaf appearance and boll shape. Traits with high coefficients in the PC1 to PC2 should be considered as more significant because these axes explain more than 50% of the whole variation (Fig.1a). Principal component analysis indicated that stem hairiness, leaf hairiness, boll tip and pollen colour were among the most important traits which accounted for most of the all phenotypic variation revealed in this cotton germplasm collection (Fig. 1b). It is suggested that research on these trait will save a lot of time for the identification of variant cotton germplasm. According to Düzyaman (2005) [2] there are no procedures to find out the significance of a coefficient, that is eigenvector. On the other hand higher coefficients for some traits designated the relatedness of that character to relevant PC axes (Sneath & Sokal, 1973) [7].

Table 2: Eigenvalues, proportion of variability and qualitative traits that contributed to the first four principal components of cotton genotypes

	PC1	PC2	PC3	PC4
Eigenvalue	1.8579	1.7947	1.3005	1.1267
Variability (%)	20.6435	19.9407	14.4500	12.5184
Cumulative %	20.6435	40.5842	55.0342	67.5526
Trait	Eigenvector			
leaf colour	-0.1393	0.2179	0.2333	-0.2624
leaf hairiness	-0.2207	0.5178	0.0273	-0.2772
leaf appearance	0.3692	0.1528	0.1109	0.4774
stem hairiness	-0.0857	0.6331	0.1458	-0.0748
flower petal colour	0.3282	0.2804	-0.5143	-0.3434
flower stigma	0.2396	-0.1780	0.5456	-0.4478
pollen colour	0.5522	-0.0484	-0.3653	-0.2584
boll shape	0.3279	0.3840	0.1441	0.4615
boll tip	0.4590	-0.0134	0.4415	-0.1505

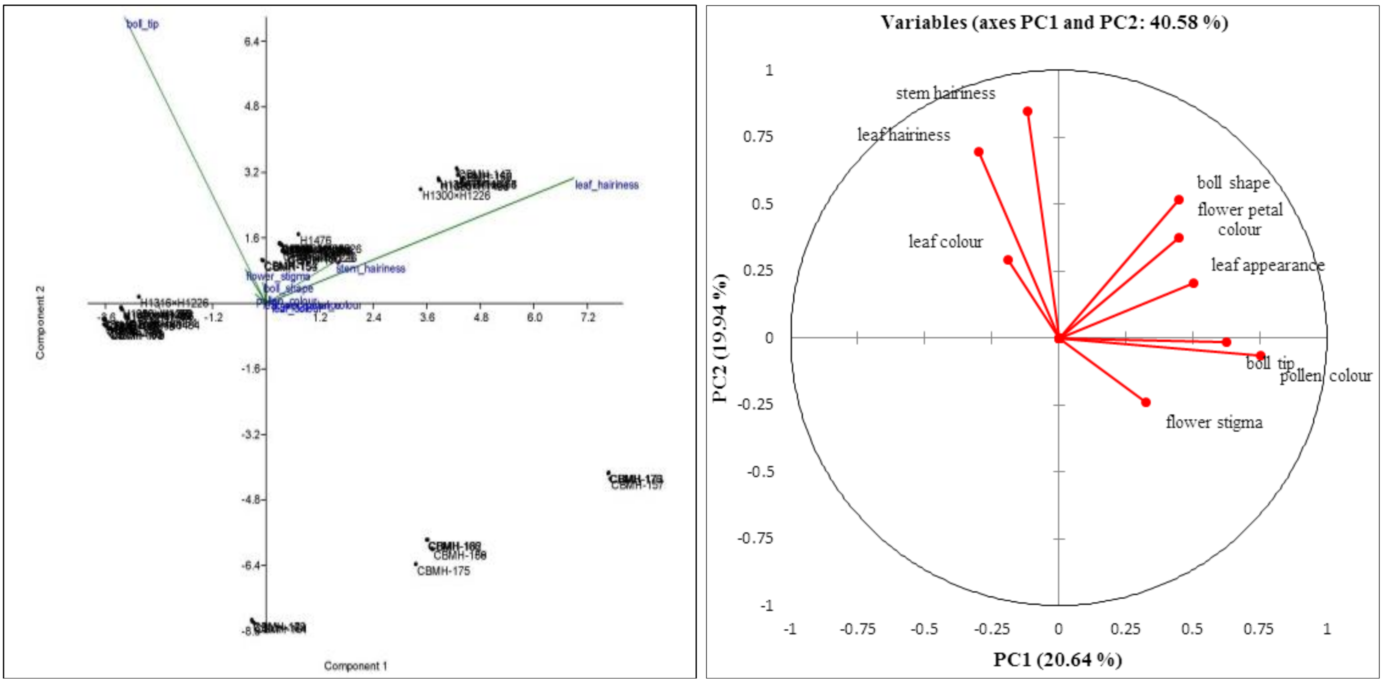

Fig 1: Scatter diagram of first two principal components based on mean values of qualitative traits in 86 accessions of cotton germplasm

Cluster analysis is a biometrical tool used in grouping of genotypes in a manner that genotypes which belong to the same group are much more similarly compared to those of other groups or clusters. This helps to reveal the relationship between genotypes from varied origins and consequently extremely thorough identification of genotypes with valuable traits in the various clusters for hybridization. On the basis of relative magnitude, 86 genotypes were grouped in six major clusters in such a way that plants within each cluster had smaller value than those of between clusters as shown in Table 3. Cluster pattern revealed that, cluster II was the largest group consisting of 33 genotypes which was followed by cluster I (27 genotypes), these two cluster have about 75% percent of the total genotypes. The intra and inter cluster distances are given in Table 4. A maximum intra cluster difference was shown by cluster VI (4.00). This was followed by cluster III (3.42), cluster II (2.97), cluster V (2.93), cluster I (2.7) and Cluster IV (2.00). When diversity between clusters was studied, it ranged between 4.04 -11.74. Cluster III and cluster VI showed maximum inter cluster distance of (11.74), followed by cluster II and cluster IV (11.73). The minimum inter cluster distance was noticed between cluster I and cluster II (4.04), followed by clusters I and cluster III (4.11). Hence, the genotypes in these clusters may be used as parents for generation of new cultivars and hybrids. Gopinath *et al.* (2009) [3], Satish *et al.* (2009) [6] and Rathinavel *et al.* (2017) [5] have also clusted cotton genotypes in the same manners but for quantitative characters.

Table 3: Cluster composition of 84 cotton genotypes

Cluster	Total no of genotype	Genotypes
I	27	H1098i×H1300, H1098i×H1316, H1098i×H1226, H1098i×H1490, H1300×H1353, H1300×H1490, H1316×H1353, H1353×H1465, H1353×H1226, H1465×H1476, H1465×H1226, H1465×H1464, H1476×H1226, H1316, H1353, H1465, H1476, HHH223, CBMH-150, CBMH-151, CBMH-153, CBMH-154, CBMH-163, CBMH-165, CBMH-170, CBMH-171, CBMH-186
II	33	H1098i×H1353, H1098i×H1465, H1098i×H1476, H1098i×H1464, H1300×H1316, H1300×H1465, H1300×H1476, H1300×H1464, H1316×H1465, H1316×H1476, H1316×H1226, H1316×H1490, H1353×H1476, H1353×H1490, H1476×H1490, H1476×H1464, H1226×H1490, H1226×H1464, H1490×H1464, H1098i, H1226, CBMH-148, CBMH 149, CBMH-152, CBMH-160, CBMH-162, CBMH-168, CBMH-178, CBMH-17, CBMH-181, CBMH-183, CBMH-184, CBMH-185
III	14	H1300×H1226, H1316×H1464, H1353×H1464, H1465×H1490, H1300, H1490, H1464, CBMH-147, CBMH-155, CBMH-156, CBMH-167, CBMH-169, CBMH-17, CBMH-177
IV	3	CBMH-157, CBMH-173, CBMH-176
V	6	CBMH-158, CBMH-159, CBMH-166, CBMH-175, CBMH-180, CBMH-182
VI	3	CBMH-161, CBMH-164, CBMH-172

Table 4: Average intra (diagonal) and inter cluster distances in cotton

Cluster	I	II	III	IV	V	VI
I	2.17					
II	4.04	2.97				
III	4.11	8.13	3.42			
IV	9.36	11.73	8.26	2.00		
V	8.09	9.00	9.08	4.70	2.93	
VI	9.23	8.21	11.74	9.09	4.52	4.00

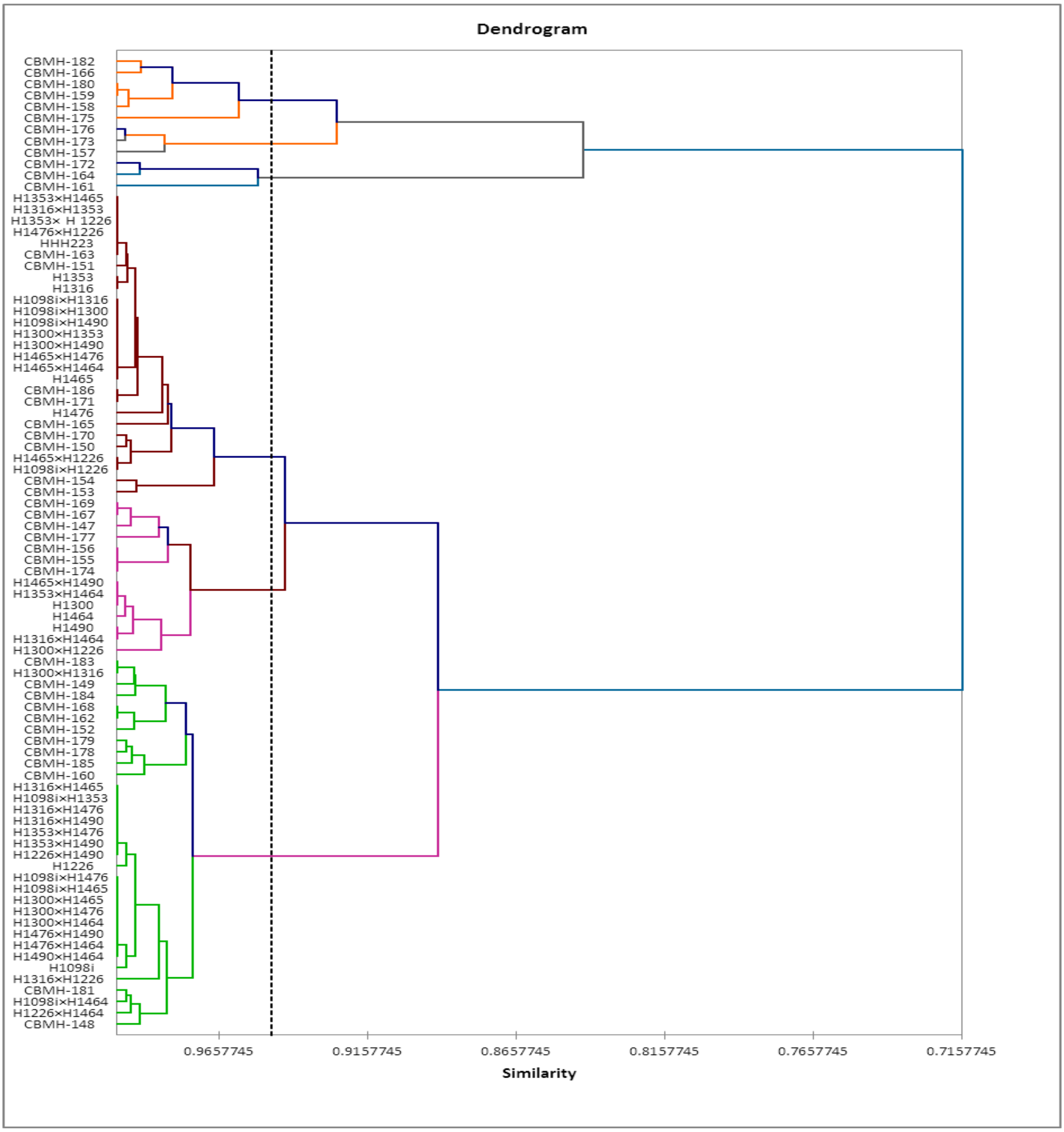

Fig 2: Dendrogram showing clustering pattern of 86 cotton genotypes

Conclusion

Out of 20 qualitative characters only 9 characters had recorded significant level of diversity in our study. Getting the correlation of these morphological traits with other agro-morphological traits will help in selection of desired plants in early stages of plants. Apart that, these qualitative characters can also be used as morphological markers for varietal identification. As the present era of crop research need to maintain the germplasm of any crop, these qualitative traits will help in avoiding germplasm duplication and even differentiating genotypes by their unique identification.

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