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Characterization of elite Asiatic cotton (*Gossypium arboreum)* lines on the basis of DUS traits

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ABSTRACT : Field studies were carried out to study the varietal characterization of various DUS characters of 40 elite lines of Asiatic cotton. The experiment was conducted in the experimental area of the Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar in *kharif,* 2015 in a randomized block design with three replications. results revealed that hypocotyl pigmentation, leaf shape, leaf petiole pigmentation, leaf nectarines, leaf pubescence, leaf colour, plant stem pigmentation, plant stem hairiness, flower male sterility, pollen colour, flower petal spot, anther filament colouration, flower stigma position, flower petal colour, days to first flower, boll shape, boll surface, boll opening, prominence of tip in boll, boll weight, boll colour,seed fuzz colour, seed fuzz, seed size or seed index, ginning out turn , fibre strength, fibre uniformity (%), fibre length, fibre fineness, fibre colour and fibre maturity proved to be useful and stable diagnostic characters which could classify the genotypes based on the phenotypic traits. This investigation reveals that classification of genotypes on the basis of DUS traits provided identification of key characteristics of various genotypes which can be used to distinguish them from others and also further investigation of these characters may help in crop improvement programme.

Key words : Asiatic cotton, DUS, morphological characters

Cotton is the most important commercial crop in the world and is also known as 'white gold'. The genus *Gossypium* comprises 50 species. There are four cultivated species of cotton *viz., Gossypium arboreum, G. herbaceum, G. hirsutum* and *G. barbadense*. *Gossypium arboreum* and *G. herbaceum,* species are diploid (2n=26) and commonly known as old world cotton. The *G. hirsutum* and *G. barbadense* species are tetraploid (2n=52) and referred as new world cottons Descriptors of varieties of crop species are required for characterization of varietal identity, determine varietal purity, and establish the distinctiveness of new variety from existing varieties and documentation of genetic resources. In early days, all over the world, a small list of descriptors was sufficient to distinguish between crop varieties in use. However, in the recent decades, the world witnessed the emergence of large and highly competitive variety development programmes, particularly in the developed countries and also in some of the developing countries. Characterization of cultivars is required for their protection under PPV and FR Act 2001. Registration and protection can be granted to a variety only if it conforms to the criteria of distinctness, Uniformity and Stability. It means that the new variety has to be distinct uniform stable (DUS) in its characteristics. In India,

certain diagnostic features released for notified crop varieties and hybrids are used in seed certification. A variety is eligible for registration and release if it possesses novelty, distinctiveness, uniformity and stability (DUS) characteristics. DUS is a test procedure for descriptive assessment, morphological characterization and identification of a new variety using morphological, biochemical, molecular and other characteristics. DUS Testing of cultivars is one of the requirements for granting Plant Breeders Rights (PBR) and it is conducted according to national guidelines prepared on the basis of UPOV guidelines. A strict maintenance breeding for genetic purity of all the example varieties is warranted for a valid DUS testing for proper implementation of PPV and FR Act (Chakrabarty *et al.,* 2012).

The present investigation was carried out in the Research Area of Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *kharif* 2015. Forty elite lines of desi cotton genotypes were used as experimental material. The seeds for present investigation were collected from Cotton Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar. These plants were used for recording of data for given various characters. Data were recorded for following morphological traits described by PPV and FR Authority**.** Forty elite lines HD 123, HD 324, HD 432, HD 418, HD 503, HD 514, HD 509, HD 521, HD 302, HD 372, HD 408, 302, D-43-21, D462-1-1, EB 31-1, HD 6, . HD 20, 2446, DS-5, DS 1, AC 33, D462-1-1 P5, Jubli, FFS, AC 3028, FFS 105, PA 405, RG 295, AKA 9410, CINA 347, 7060 A, CINA 348, . P 536, P 551, . P 555, HD 426, . P 397, HD 442, DA-2/02, HD 357 were used for present study**.** Randomized block design was used as a statistical layout for the present investigation. Layout plan include three replications with row length 6.0 m, plant to plant distance 30 cm and row to row distance 90 cm. Five randomly selected plants were used for recording data. Qualitative morphological characters listed by national DUS test guidelines descriptors for cotton were used for characterization. Hypocotyl is the part of stem of embryo beneath the stalk of seed leaves or above the root. The hypocotyl pigmentation were observed at 14th day after sowing under light condition for all the genotypes and classified by visual assessment. On this basis genotypes were classified as present or absent. The leaf shape of the fourth leaf of main stem from the top of the plant was recorded on visual assessment basis at peak flowering stage for all the genotypes. According to the leaf shape genotypes were classified as palmate (normal), semi digitate (semi okra) and digitate (okra). The leaf petiole pigmentation was recorded on visual assessment basis at peak flowering stage for all the genotypes**.** On the basis of leaf petiole pigmentation genotypes were classified as present or absent. Nectaries are present on the underside of foliage leaf located on the midpart of largest vein and appears black so known as black gland. The fourth leaves from top of plants were observed visually at peak flowering stage for their nectaries for all the genotypes. On the basis of leaf nectaries genotypes were classified as present or absent. The leaf pubescence on the fourth leaf of main stem from the top of the plant was recorded at peak flowering stage. On the basis of leaf pubescence genotypes were classified as sparse, medium, dense and absent.

The leaf colour of the fourth leaf of main stem from the top of the plant was recorded on visual assessment basis**.** On the basis of leaf colour genotypes were classified as: light green, green, light red and dark red. On the basis of plant stem pigmentation genotypes were classified as present or absent. The plant stem pigmentation was recorded on visual assessment basis at peak flowering stage**.** On the basis of plant stem hairiness genotypes were classified as absent, sparse, medium and dense. On the basis of flower male sterility genotypes were classified as present or absent. flower pollen colour genotypes were classified as cream and yellow. flower petal spot genotypes were classified as present or absent. flower anther filament colouration genotypes were classified as present or absent. On the basis of flower stigma position genotypes were classified as embedded and exerted. On the basis of flower petal colour genotypes were classified as white, cream, yellow, pink, red and variegated. On the basis of days to 50 per cent flowering (50% of the plants with at least one opened flower) genotypes were classified as early (<50 days), medium (50-60 days) and late (>60 days). On the basis of boll shape (longitudinal section) genotypes were classified as rounded, ovate and elliptic. On the basis of boll surface appearance genotypes were classified as smooth or pitted. for boll opening characteristics genotypes were classified as semi open, open and close. On the basis of prominence of boll tip genotypes were classified as blunt or pointed. On the basis of boll weight (five well opened bolls were picked from each five selected plant, weighed in grams and averaged) genotypes were classified as small (< 2.0), large (>3.0) and medium (2.0-3.0). The boll colour was observed visually before boll bursting stage. On the basis of boll colour genotypes were classified as green or red. On the basis of seed fuzz colour genotypes were classified as white, grey and brown. On the basis of seed fuzz genotypes were classified as medium and dense. Genotypes based on the seed index were classified as very small (<3 g), small (3- 5 g), medium (5.1- 7 g), bold (7.1- 9g) and very bold (>9 g). On the basis of ginning outturn (%) genotypes were classified as very low (< 30), low (31-32), medium (33-34), high (35-36) and very high (>37). It is ratio of 50 per cent span length to 2.55 span length. On the basis of fibre uniformity genotypes were classified as poor (< 42), fair (42-43), average (44-45), good (46-47) and excellent (> 47). On the basis of their tenacity genotypes were classified as very weak (<16), weak (17.0- 20.0), medium (21.0-24.0), very strong (>29.0) and strong (25.0 - 28.0). On the basis of fibre length genotypes were classified as very short (< 20mm), short (20.5-24.5mm), medium (25-29mm), long (29.5-33.5mm) and extra long (>33.5mm). 2.5% span length is the old term and now modified into upper half mean length (UHML). On the basis of fibre fineness genotypes were classified as very coarse (> 6), coarse (5- 5.9), medium (4- 4.9), fine (3- 3.9) and very fine (< 3). On the basis of seed fibre colour genotypes were classified as white, cream, green and brown. Fibre maturity was classified as very immature (<31), immature (32-49), average(50-65), good (66-80) and very good (>81).

The results obtained in the present investigation have been presented in the Table 1. Hypocotyl pigmentation was absent in 27 genotypes and in rest of 13 genotypes hypocotyl pigmentation was present. Similar results were carried out by Rai *et al.,* (2016) and

Jain. (2017). Leaf colour was present in majority of genotypes *i.e.* 33 green leaves were observed while seven were of light green leaves Jain (2017). Presence of hairs on leaves is also a common characteristic. Observation recorded for leaf hairiness indicated twenty genotypes were medium hairs and twenty with dense leaf hairiness. Similar results were obtained in investigaton by Aruna *et al.,* (2012), Rai *et al.,* (2016) and Jain (2017). Out of total genotypes studied 35 were found without nectaries and in remaining five nectaries on leaves were observed Jain (2017). Twenty eight genotypes showed absence leaf petiole pigmentation whereas rest 12 genotypes had leaf petiole pigmentation. Similar results were recorded in studies by Rai *et al.,* (2016) and Jain (2017). Thirty three genotypes had okra type leaves while rests were having semi-okra leaf. Similar results were obtained in studies of Begum and Hossain (2011), Sangwan *et al.,* (2016) and Jain (2017). Majority of genotypes *i.e.* 27 found to have strong leaf hairiness while 13 fell in medium leaf hairiness category. Similar results were obtained by Aruna *et al.*, (2012), Rai *et al.,* (2016) and Jain (2017). Twenty six genotypes had absence of stem pigmentation and fourteen were having presence of stem pigmentation and resuls are in accordance with Pujer *et al.,* (2014) and Jain (2017). Twenty eight genotypes were grouped in medium (50-60 days) while rest 12 were in late (>60 days) duration group. Similar results were studied by Rai *et al.,* (2016). Plant height showed variations among genotypes. Thirty genotypes were very tall and rests ten were in tall height class. observed that both additives and dominance type of gene action for plant height. Fifteen genotypes were yellow, eleven were pink, eight were cream, five were white and one was red flower as per observations recorded. Similar studies on flower petal were conducted by Rai *et al.,* (2016) and Jain (2017). Presence of flower petal spot is a common characteristic feature in desi cotton. Absence of petal spot in *desi* cotton is a morphological marker character and can be used for identification of varieties. Thirty eight genotypes were found with flower petal spot and two (P 536 and P551) were with spotless. Presence or absence of petal spot is genetic effect which is controlled by polygenes having cumulative effect and generally dominant genes were present. Similar results were found in study done by Rai *et al.,* (2016), Jain (2017) and Rathinavel (2018) who have differentiated the *Gossypium hirsutum* and *Gossypium arboretum* genotypes using the leaf characters like leaf shape, leaf initiation, leaf hairiness etc. On the basis of position of stigma 38 genotypes were grouped in exerted type of stigma while only two genotypes (302, AKA9410) were in embedded type of stigma. Similar results were observed by Rai *et al.,* (2016), Jain (2017) and Rathinavel (2018). Hypocotyl pigmentation (HP) absent=1, present=9; Leaf colour (LC) light green=1, green=2, dark red=4; Leaf pubescence (LP) medium=5, strong=9;Leaf nectarines (LN) absent=1, present=9; Leaf petiole pigmentation (LPP) absent=1, present=9; Leaf shape (LS) palmate (normal)=1, digitate (okra)=3, lanceolate (super okra)=4; Plant stem hairiness (PSH) medium=5, strong=7; Plant stem pigmentation (PSP) absent=1, present=9; Days to 50% flower (DFF) medium (50-60 days)=5, late (>60 days)=7; Flower petal colour (FPC) cream=1, yellow=2, purple=4; Flower petal spot (FPS) absent=1,

present=9; Flower stigma position (FSP) embedded=3, exerted=5; Anther filament colouration (AFC) absent=1, present=9; Flower pollen colour (PC) cream=1, yellow=9; Flower male sterility (FMS) absent=1, present=9; Boll colour (BC) green=3, red=5; Boll shape (longitudinal section) (BSh) round=3, ovate=5, elliptic=7; Boll surface (BSf) smooth=1, pitted=9; Prominence of tip in boll(PTB) blunt =1, pointed=2; Boll opening (BO) semiopen=3, open=5; Seed cotton boll weight (SCBW) small (<2.0)=1, medium (2-3)=3, large (>3)=5; Seed fuzz (SF) medium=3, dense=5; Seed fuzz colour (SFC) grey=1, brown=2; Seed index (SI) very small (<3)=1, small (3-5)=3, medium (5.1-7)=5, bold (7.1-9)=7, very bold (>9)=9; Ginning outturn (GOT) very low (<30)=1, low(31-32)=3, medium (33-34)=5, high (35-36)=7, very high (>37)=9; Fibre colour (FC) cream=2, green=3, brown=4; Fibre length (FL) short (<20)=1, medium (20.5-24.5)=3, medium long (25-27)=5, long (27.5-32)=7, extra long (>32.5)=9; Fibre strength (FS) very weak (<16)=1, weak (17-20)=3, medium (21-24)=5,strong (25-28)=7, very strong (>29)=9; Fibre fineness (FF) very coarse (>6)=1, coarse (5.9-5)=3, medium (4.9-4)=5, fine (3.9-3)=7, very fine (<3)=9; Fibre uniformity (FU) poor(<42)=1, fair (42-33)=3, average (44-45)=5, good (46-47)=7, excellent (>47)=9; Fibre maturity (FM) very immature (<31)=1, immature (32-49)=3, average (50-65)=5, good (66-80)=7, very good(>81)=9. In thirty seven genotypes anther filament colouration was absent while it was present in only three genotypes. Thirty three genotypes were found with yellow pollen colour while seven genotypes with purple pollen colour (Sangwan *et al.,* 2016), Jain. (2017) and Rathinavel (2018). Boll colour was classified as green and red. Thirty one genotypes had green colour bolls while nine genotypes had red colour boll. Similar results observed by Sangwan *et al.,* (2016) and Jain (2017). Fifteen genotypes were having round shape boll, thirteen were of elliptic and twelve were ovate shaped bolls. On the basis of surface of boll genotypes were either smooth or pitted. Smooth boll surface was observed in twenty eight genotypes while rest twelve were having pitted boll surface. Generally pointed tip was present in most of the genotypes *i.e.* thirty three while blunt boll observed in seven genotypes. Similar results were observed by Rai *et al.,* (2016), Jain (2017) and Rathinavel (2018). On the basis of opening of boll genotypes were classified as open and semi open. Thirty eight genotypes had open boll type of opening and remaining two (302, DS-5) were of semi opening of bolls. Similar results were observed in studies by Rai *et al.,* (2016), Sangwan *et al.,* (2016), Jain (2017) and Rathinavel (2018). Boll weight was generally small for all the 40 genotypes. Thirty seven genotypes had below three number of monopods and remaining three genotypes had monopods above 4. Seed size was small in 26 genotypes, very small in nine and five were of medium seed size. Medium ginning out turn was observed in 17 genotypes, low in three, high in ten and very high in rest of ten genotypes. Fibre length categorised genotypes in very small, small, medium and large category. Twenty two genotypes had short fibre length, 16 were having very small whereas medium in two genotypes Rai *et al.,* (2016) and Rathinavel, (2018). Fibre strength was generally strong in majority of genotypes *i.e.* thirty eight and strong in rest of two genotypes. Fibre fineness was mostly very coarse in 38 genotypes and coarse in remaining

Table 1. Distribution of morphological characters in different elite lines of upland cotton

	HP	LC	LP	LN	LPP	LS	PSH	PSP	FT	FPC	FPS	FS	FAFC	FPC	FMS	BC	BSh	BSf	BPT	BO	SCBW	SF	SFC	SI	GOT	FC	FL	FS	FF	FU	FM
1. HD 123	9	2	5	1	1	3	7	1	7	2	9	5	1	9	9	3	5	9	9	3	3	5	1	3	9	1	3	5	1	9	7
2. HD 324	9	2	9	9	9	3	7	1	7	4	9	5	1	9	9	5	5	9	9	3	3	5	1	5	5	1	1	5	1	9	7
3. HD 432	1	2	5	1	1	3	7	1	7	2	9	5	1	9	9	3	3	9	9	3	3	5	1	5	9	1	1	5	1	9	7
4. HD 418	1	1	5	1	1	3	5	1	5	2	9	5	1	9	9	3	5	9	9	3	3	5	1	3	5	1	3	5	1	9	7
5. HD 503	1	1	5	1	1	3	7	1	7	3	9	5	1	9	9	3	3	9	9	3	3	5	1	5	7	1	3	5	3	9	7
6. HD 514	1	2	9	1	1	3	7	1	7	3	9	5	1	9	9	3	5	9	9	3	3	5	1	3	7	1	3	5	1	9	7
7. HD 509	1	1	9	1	1	3	7	1	7	3	9	5	1	9	9	3	3	9	9	3	3	5	1	5	9	1	3	5	1	9	7
8. HD 521	1	2	5	1	1	3	7	1	7	3	9	5	1	9	9	3	5	9	9	3	3	5	1	5	5	1	3	5	1	9	7
9. HD 302	9	1	9	1	9	3	5	9	5	4	9	5	1	9	9	5	5	9	9	3	3	5	1	5	9	1	3	5	3	9	7
10. HD 372	9	2	9	1	9	3	7	9	7	4	9	5	9	1	9	5	5	9	9	3	3	5	1	5	7	1	1	5	1	9	7
11. HD 408	1	2	9	1	1	3	7	1	7	1	9	5	1	9	9	3	3	9	9	3	3	5	1	5	5	1	1	5	1	9	7
12. 302	1	2	9	1	1	3	7	1	7	1	9	3	1	9	9	3	3	9	1	5	3	5	1	5	5	1	1	5	1	9	7
13. D-43-21	9	2	9	1	9	3	7	9	7	4	9	5	9	9	9	5	5	9	9	3	3	5	1	5	5	1	1	5	1	9	7
14. D462-1-1	1	1	5	1	1	2	5	1	7	3	9	5	1	9	9	3	7	1	9	3	3	5	1	5	5	1	1	5	3	9	7
15. EB 31-1	1	1	9	1	1	2	5	1	5	3	9	5	1	9	9	3	7	1	9	3	3	5	1	5	9	1	3	7	3	9	7
16. HD 6	9	2	9	1	9	2	7	9	7	4	9	5	1	1	9	5	7	9	9	3	3	5	1	5	3	1	3	5	1	9	7
17. HD 20	9	2	5	1	9	2	7	9	5	4	9	5	1	1	9	5	7	9	9	3	3	5	1	5	5	1	1	5	1	9	7
18. 2446	1	2	5	1	1	3	5	1	7	3	9	5	1	9	9	3	7	9	9	3	3	5	1	5	5	1	3	5	1	9	7
19. DS-5	1	2	9	1	1	3	7	1	5	1	9	5	1	9	9	3	3	9	1	5	3	5	1	3	5	1	1	5	1	9	7
20. DS 1	9	2	5	1	9	2	5	9	5	4	9	5	1	1	9	5	3	1	9	3	3	5	1	3	5	1	1	5	1	9	7
21. AC 33	9	2	9	1	9	3	7	9	7	4	9	5	1	9	9	3	7	1	9	3	3	5	1	5	7	1	3	5	1	9	7
22. D462-1-1 P5	1	2	5	9	1	3	7	1	7	3	9	5	1	9	9	3	3	9	9	3	3	5	1	5	9	1	1	5	1	9	7
23. Jubli	9	2	5	1	9	2	5	9	7	2	9	5	9	1	9	5	5	9	9	3	3	5	1	5	5	1	1	5	1	9	7
24. FFS	1	1	5	1	1	3	7	1	5	5	9	5	1	9	9	3	7	9	9	3	3	5	1	3	7	1	3	5	3	9	7
25. AC 3028	9	2	5	1	1	3	7	1	7	3	9	5	1	9	9	3	3	1	1	3	3	5	1	7	3	1	3	5	3	9	7
26. FFS 105	1	2	5	9	1	3	5	1	7	2	9	5	1	9	9	3	3	9	9	3	3	5	1	7	3	1	1	5	1	9	7
27. PA 405	9	2	9	1	9	3	7	9	7	4	9	5	1	1	9	3	3	1	9	3	3	5	1	5	5	1	1	5	1	9	7
28. RG 295	1	2	5	1	1	3	5	1	7	4	9	5	1	9	9	3	7	1	9	3	3	5	1	5	9	1	3	5	1	9	7
29. AKA 9410	9	2	9	1	9	3	7	9	5	3	9	3	1	1	9	3	7	1	1	3	3	5	1	5	7	1	5	5	3	9	7
30. CINA 347	1	2	5	1	1	3	5	1	7	4	9	5	1	9	9	3	7	1	9	3	3	5	1	5	7	4	3	5	3	9	7
31. 7060 A	1	2	9	9	1	3	7	1	7	3	9	5	1	9	9	3	5	1	9	3	3	5	1	5	7	1	3	5	3	9	7
32. CINA 348	1	2	5	1	1	3	5	1	7	3	9	5	1	9	9	3	3	1	9	3	3	5	1	5	5	1	3	5	1	9	7
33. P 536	1	2	9	1	9	3	7	9	7	3	1	5	1	9	9	3	7	9	9	3	3	5	1	5	9	1	5	7	3	9	7
34. P 551	1	2	5	1	9	3	5	9	7	2	1	5	1	9	9	5	7	9	1	3	3	5	1	3	9	1	3	5	1	9	7
35. P 555	1	2	5	1	1	3	7	1	5	2	9	5	1	9	9	3	7	9	9	3	3	5	1	3	5	1	3	5	1	9	7
36. HD 426	1	2	5	1	9	3	5	9	5	2	9	5	1	9	9	3	3	9	9	3	3	5	1	7	7	1	3	5	3	9	7
37. P 397	1	2	9	9	1	2	7	1	5	3	9	5	1	9	9	3	5	1	9	3	3	5	1	5	7	1	1	5	3	9	7
38. HD 442	1	2	9	1	1	3	7	1	5	3	9	5	1	9	9	3	3	9	1	3	3	5	1	7	5	1	3	5	1	9	7
39. DA-2/02	1	2	9	1	1	3	7	1	7	3	9	5	1	9	9	3	5	9	9	3	3	5	1	5	9	1	1	5	1	9	7
40. HD 357	1	2	9	1	1	3	7	1	7	1	9	5	1	9	9	3	3	9	1	3	3	5	1	3	7	1	3	5	1	9	7

two genotypes. Fibre uniformity was observed excellent in all genotypes. Seed fuzz colour was generally white in all genotypes Jain (2017) and Rathinavel (2018). Fibre colour was also white in all genotypes Rathinavel (2018).

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