Morphological, biochemical and molecular characterization of Asiatic cotton (*Gossypium arboreum* L.)

By
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CERTIFICATE-I

This is to certify that this thesis entitled, "**Morphological, biochemical and molecular characterization of Asiatic cotton (*Gossypium arboreum* L.)**" submitted for the degree of **Doctor of Philosophy** in the subject of **Genetics and Plant Breeding** to Chaudhary Charan Singh Haryana Agricultural University, Hisar, is a bonafide research work carried out by **Mr. Deepak Kumar**, Admission No. **2019A44D** under my supervision and that no part of this thesis has been submitted for any other degree.

The assistance and help received during the course of investigation have been fully acknowledged.

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CERTIFICATE-II

This is to certify that the thesis entitled **"Morphological, biochemical and molecular characterization of Asiatic cotton (*Gossypium arboreum* L.)"** submitted by **Mr. Deepak Kumar,** Admn. No. **2019A44D** to Chaudhary Charan Singh Haryana Agricultural University, Hisar in partial fulfillment of the requirement for the degree of Doctor of Philosophy in the subject of **Genetics and Plant Breeding** has been approved by the Student's Advisory Committee after an oral examination on the same in the collaboration with an External Examiner.

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MAJOR ADVISOR

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ABBREVIATIONS

Short form	**Full form**
ANOVA	Analysis of variance
Cm	Centimeter
CV	Coefficient of variation
DFF	Days to first flower
D.F	Degree of freedom
et al.	*et alia* (and other)
GCV	Genotypic coefficient of variance
PCV	Phenotypic coefficient of variance
PH	Plant height
BW	Boll weight
S.E.	Standard error
NS/B	Number of seeds per boll
SCY	Seed cotton yield
viz.	Likely
NM/P	Number of monopods per plant
GOT	Ginning out turn
NB/P	Number of bolls per plant
SSR	Simple sequence repeats
Bp	Base pair
QTL	Quantitative trait loci
CTAB	Cetyl trimethyl ammonium bromide
DNA	Deoxyribonucleic acid
dNTP	Deoxyribose nucleoside triphosphate
EDTA	Ethylene diamine tetra acetic acid
Hb	Heritability (broad sence)
UPGMA	Unweighted pair group methods with arithmetic average
SI	Seed Index
NTSYS-PC	Numerical taxonomy and multivariate analysis system Programme
PCR	Polymerase chain reaction
RNase	Ribonuclease
SSR	Simple sequence repeats
Taq	Thermus aquaticus
TBE	Tris Boric EDTA
TE	Tris EDTA
Tris	2 amino-2(hydroxymethyl)-1, 3-propanediol

CHAPTER-I

INTRODUCTION

Cotton is one of the most important fibre crops which is grown mainly for its lint, textile raw materials, seeds, seed oil and protein. It is popularly known as ‘White Gold’ or “King of Fibres”. It is extensively cultivated throughout the country and plays an important role in national economy in terms of providing employment, contribution in trade, industrial activities and earning foreign exchange in India. Cotton is one of the sources of natural fibre. Furthermore, cotton seed has also additional economic importance as it has major contribution in edible oil, protein and other by- products (Harijan *et al.,* 2016). Cotton seed oil is used for preparation of alkyl resins for interior paints, special bio-lubricants and soft soaps in industries (Saxena *et al.,* 2011). Cotton seed contains 23% high quality protein (Lusas and Jividen, 1987). Its seed meal is used as a protein concentrate feed for livestock production. “Gossypol” is an important biochemical component which provide defense against insect-pests and diseases to cotton crop. Ruminant animals can tolerate the gossypol, but it is toxic to non-ruminants. Presence of gossypol toxicity make it unfit for human consumption.

Cotton is grown in tropical and subtropical regions of more than 80 countries of the world. The major cotton producing countries are India, China, USA, Pakistan, Uzbekistan, Turkey, Brazil, Greece, Argentina and Egypt which contribute about 85 % of the world's cotton production. Among the major cotton exporting countries in the world, India occupied 3rd position with 5.5 million bales (USA–16.25 million bales and Brazil –10.70 million bales) (USDA, 2020-21).

India is the native home of old cultivated cotton and there is wide diversity in agro-climatic conditions for cotton cultivation. Major cotton growing states of India are divided into three zones *viz.* the North Zone (Punjab, Haryana and Rajasthan), the Central Zone (Maharashtra, Madhya Pradesh and Gujarat) and the Southern Zone (Andhra Pradesh, Karnataka, Telangana and Tamil Nadu) (Cotton Corporation of India, 2021). In India, largest cotton producing state is Gujarat followed by Maharashtra. In India, nearly 65 % of the cotton crop is grown under rainfed conditions. About 2/3rd of the cotton production in India comes from the states of Maharashtra, Gujarat, Andhra Pradesh, and Telangana collectively known as “Cotton Basket of India”. In Haryana, cotton cultivation is progressing rapidly in five districts *viz.* Sirsa, Hisar, Fatehabad, Jind and Bhiwani. Being an important cash crop, it has profound impact on the economy and social affairs of the world. During 2021-2022, production of cotton in India was 340 lakh bales cultivated under an area of 123 lakh hactares with a productivity of 469 kg/ha (Cotton Corporation of India, 2021). In Haryana, cotton was grown in an area of 6.48 lakh ha with a production of 19 lakh bales and a productivity of 497 kg/ha lint (CCI Report, 2022).

Cotton belongs to genus "*Gossypium*" and family "Malvaceae" and comprises about 50 species, out of which only four are cultivated *viz. arboreum, herbaceum, hirsutum* and *barbadense* (Fryxell *et al.* 1992). *Gossypium hirsutum* is an upland cotton and it is native to Central America, Mexico, Caribbean and Southern Florida (90% of world production). *Gossypium barbadense* is known for its extra-long staple and native to tropical South America (8% of world production). *Gossypium arboreum* (tree cotton) is native to India and Pakistan (less than 2% of world production) and *Gossypium herbaceum* is known as Levant cotton and it is native to Southern Africa and Arabian Peninsula (less than 2% of world production) (Edwards and Mirza, 1979). Based on chromosomal similarities, *Gossypium* species are commonly grouped into eight diploid genomic groups (A to G and K) and one tetraploid genomic group (Edwards and Mirza, 1979 and Stewart, 1995). *G. arboreum* and *G. herbaceum* ($2n=2x=26$) are diploids while *G. hirsutum* and *G. barbadense* ($2n=4x=52$) are tetraploid and mostly domesticated because of their good fibre quality (Mishra *et al*., 2013). Cotton lint is a fluffy fibre which is the extensions of the seed coat made up of almost pure cellulose and aid in seed dispersal (Basra and Malik, 1984). Asiatic cotton (*G. arboreum)* is mostly grown under poor crop management conditions but its yield potential is not being utilized fully yet. This species of cotton has some special desirable attributes like hardiness, earliness, tolerance to drought and insect pests which results in low cost of production. Its maturity period varies from 156 to 180 days. Generally, it has coarse and short fibre as well as high degree of resistance against disease and insect pests.

Breeders establish target for developing superior varieties based on the uses or demands, such as improving fibre qualities in the textile industries and increasing oil content with high oleic content and less gossypol in the oil sector. Major breeding objectives of cotton crop include good quality lint fibre, high quality seed production, early maturity and resilience to biotic and abiotic stresses. In terms of nutrition, decreased gossypol content in seeds is thought to be beneficial for boosting the quality of cotton meal. Unsaturated fatty acid content of cotton seed oil has to be reduced and Mono-Unsaturated Fatty Acid (MUFA) and Polyunsaturated Fatty Acid (PUFA) contents are to be increased for good quality oil. Also, there is need to increase oil content above 25% as presently cultivars possess only 16–18% oil content (Zhao *et al.,* 2019). Plant breeders can achieve all of these goals by assessment of variability followed by development of effective breeding techniques based on genetic variability of yield and its related traits available in gene pool.

Selection is effective only when magnitude of variability is high enough in the breeding population. A wider range of variability helps in selecting a desirable elite genotype. Substantial genetic variances along with high heritability estimates revealed that characters could be improved through selection from segregating populations (Baloch and Baloch, 2004). It is important to know that how much part of this variability is heritable which is prerequisite for any breeding programme. Therefore, it becomes necessary to split the total variability into heritable and non-heritable components with the help of certain genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). To achieve various breeding objectives; understanding of the genetic mechanism controlling various quantitative and qualitative characters under different environmental conditions become essential (Ahsan *et al*., 2015). Heritability coupled with genetic advance helps in predicting the gene action controlling the concerned trait. The genetic variability along with heritability of a trait will indicate how much improvement is possible through selection on the basis of phenotype (Magadum *et al*., 2012). It is observed that heritability estimate alone may not clearly indicate the breeding value (Mishra *et al*., 2015). Thus, genetic advance over means should also estimate for more effective prediction of effects of selection (Ramanjinappa *et al.*, 2011; Eswari *et al.*, 2018). High genetic advance coupled with high heritability estimates provides a more effective response to selection (Larik *et al*., 1997). From the above discussed facts, it is clear that information based on different genetic parameters *viz.* variability, heritability and genetic advance are very important to predict the performance of the parents which are to be utilized in breeding programme for achieving high yielding cultivars.

After the evaluation of genetic parameters, we have understood the importance of selection, also they aid in deciding the breeding method to be followed for the same. But in the field it is not that easy, as yield is complex trait. Since, fibre quality and seed cotton yield are complex quantitative characters, direct selection may not be effective because they are influenced by number of environmental factors. Breeders need to know more about inter-relationship among different traits for effective selection. Otherwise, improvement in one trait may lead to deterioration in another due to negative correlation among them. Hence, in order to amplify the yield potential of the cotton varieties, knowledge on relationship among different characters is important (McCarty *et al*. 2008). The inter-relationships between yield and its contributing traits are estimated by correlation coefficient analysis. Such association studies provide information on nature of extent and direction of selection. The correlation analysis reveals the changes occurring in dependent variable (yield) at the expanse of the proportionate change among component traits. It measures the relationship between various traits and determines the component characters on which selection depends for genetic improvement (Salahuddin *et al.*,2010). In case of cotton, seed cotton yield is dependent on several contributing traits *viz*. number of sympodial branches, number of monopodial branches, number of bolls per plant and boll weight (Adsare and Salve, 2017). Therefore, during selection not only the yield but other traits also should be considered. Hence, correlation studies provide the information about the nature of association which is often incomplete even sometimes unrelated traits also show correlation. Additional influences from other traits may skew the results in either direction which is not taken care of in correlation analysis. On the other hand, path coefficient analysis is an efficient statistical tool specially designed to quantify the inter-relationship among different components and their direct and indirect effects on yield. So it's important to know more about the traits which contribute to the yield and their direct and indirect association for successfully design an effective breeding programme. It is helpful in the procedure of selection and empowers the breeders to select the genotypes on the basis of two or more traits simultaneously (Salahuddin *et al*., 2010).

Plant breeding programmes aim at developing varieties superior to the existing ones. This is achieved by combining desirable traits such as yield, resistance to insects and diseases, tolerance to abiotic stresses and good quality traits etc. Crop improvement programmes in India have generated large number of varieties in the major field and vegetable crops. With the proliferation of newly developed varieties in important cultivated crops, the task of establishing the identity of these varieties and of maintaining their seed lots has become a major concern since the variety attains acceptance only when farmers get genetically pure seeds of high standards. Characterization of varieties is thus of significance for the purpose of assessment of varietal purity for seed production and certification. Assessment of genetic diversity of the elite germplasm has been sought and used by plant breeders for numerous reasons, *e.g*., genetic relationships, parent selection, germplasm management and protection among others (Lee, 1998; Parihar, 2022).

Recently, molecular markers are found to be more useful for analyzing genetic diversity and molecular characterization. Molecular markers such as RFLP, RAPD, AFLP, SSRs, ISSR and SRAP are available for genetic diversity analysis. Of these marker types, Simple Sequence Repeats (SSRs) have been reported to be more advantages due to high polymorphism, co-dominance, good reproducibility, and easy to use (Qian, *et al.*, 2022:, Xiong, *et al.*,2022). SSRs have been successfully used for genetic diversity analysis, QTL mapping, and cotton DNA fingerprinting (Iqbal *et al.*, 2021; Li *et al.*, 2019; Kumar *et al.*, 2021). This has managed to improve the protection of cotton germplasm resources and made it possible for cotton varieties to be genetically improved. In cotton, DNA fingerprinting using PCR-based molecular markers had been reported. Using RAPD markers, cotton genotypes were clustered according to whether their lint was white or colored, and it was found that coloured and white-linted genotypes were clearly separated from one another (Punitha, and Raveendran, 2010). The genetic diversity of 27 cotton accessions from 2009 to 2010 was analyzed by Han *et al.* (2011) using SSR markers to create fingerprints. By studying the genetic diversity in the main cotton varieties using SSR markers, Kuang *et al.*

(2014) discovered a correlation between cultivars and geographical origins. Li *et al.* (2011) employed 20 pairs of SSR primers to create fingerprints of the Baimian cotton series.

Due to narrow genetic base of cotton germplasm, plant breeders need to put an emphasis on its characterization and conservation. If the germplasm does not have information on characterization, evaluation and biochemical analyses, their utilization is very limited in crop improvement. In earlier times, entire world uses a small list of descriptors to distinguish between cultivated crop varieties. However, in 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. Continuous improvement in plant breeding activities results in development of considerable number of new candidate varieties on a global scale, emphasizing the importance of defining their distinct diagnostic characteristics for better differentiation between them. Farmers recognize the variety and hybrids only on receiving quality seeds of high genetic purity. To ensure this purpose, each cultivar should be characterized with defined descriptors, for better identification during seed production through field inspection and certification.

Characterization of any variety or hybrid is of utmost importance to know its novelty, distinctiveness, uniformity, and stability for the registration and notification. DUS testing helps to distinguish between a newly bred variety and existing varieties of the same species. Novelty refers to the newness of a variety. Distinctiveness means a variety should be clearly distinguishable from previously released varieties. Uniformity refers to the same type of population to a variety and stability means a variety should give stable performance generation after generation over a wide range of environmental conditions. The characterization of cultivars is essential to be protected under PPV&FR Act 2001.

Characterization of the germplasm by using biochemical markers has got a special attention. Researchers and plant breeders can use this information to make decisions regarding the choice for selecting the superior genotypes for further improvement or to be used as parents for the development of future cultivars through hybridization. Cotton has many important biochemical compounds or such as soluble sugar, phenol, terpenoids, gossypol, soluble protein, fatty acids and so on distributed throughout the plant on seeds, leaves, stalks, bolls and stem. Abundance of these secondary metabolites in cotton plant brings forward various novel techniques for the isolation of these valuable biochemicals to convert them into valuable products. Gossypol has contraceptive properties, phenols and tannins being insecticidal and herbicidal in nature, cotton fibre itself composed of cellulose proved very efficient in defense mechanism and value addition of crop.

Keeping the above facts in mind the present study "Morphological, biochemical and molecular characterization of Asiatic cotton (*Gossypium arboreum* L.)" was undertaken to characterize the germplasm lines with the following objectives:

1. Morphological characterization of *desi* cotton germplasm on the basis of DUS traits
2. To study correlation and path analysis among various yield contributing traits
3. Biochemical characterization of *desi* cotton germplasm using different seed quality traits
4. To analyze molecular diversity using SSR markers

CHAPTER-II

REVIEW OF LITERATURE

A lot of relevant studies related to different aspects of present investigation have been done; some of them are reviewed briefly are under. The available literature is dealt under the following broad headings.

2.1 Characterization of germplasm lines
2.2 Variability, heritability and genetic advance
2.3 Correlation and Path analysis
2.4 Genetic diversity studies

2.1 Characterization of germplasm lines:

Protection of Plant Varieties and Farmers' Rights Act, 2001 has been enacted in India to provide better establishment of system for protection of plant varieties, rights of farmers, plant breeders and to encourage the development of new varieties of crop plants. All these objectives can be fulfilled by characterization of plant varieties for Distinctness (D), Uniformity (U) and Stability (S) together called as DUS characters. Such protection can accelerate the growth of the seed industry which will ensure the availability of high quality seeds to the farmers. PPV & FRA has listed 31 DUS traits for diploid cotton. A lot of work has already been published for the objective which has been reviewed below:

Begum and Hossain (2011) studied twelve cotton genotypes and found that all genotypes under study except SR-05 showed short hair. All the genotypes produced fuzzy seed and white coloured lint. The only genotype, SR-05 produced okra leaf type leaves whereas others had palmate types and the genotypes, SR-05 and SR-12 produced the highest seed cotton yield (2634.73 and 2632.59 kg ha-1). Superior performance of SR-05 was mainly due to its highest seed cotton yield and average weight of seed cotton per ten bolls.

Aruna *et al*. (2012) Characterized six hybrids and their twelve parental lines on the basis of morphological traits *viz*. leaf size, leaf shape, pigmentation, flower colour, anther colour, hairiness, etc. Out of all, two genotypes CSH 8 and LD 327 were found to be unique possessing early days to 50% flowering and digitate leaf shape respectively.

Balakrishna *et al.* (2016) observed seven lint descriptors on 65 *Gossypium hirsutum* L. genotypes. Out of which two genotypes (MCU 5, L 604) showed extra-long fibre and 21 genotypes had long fibre length. Medium strength was shown by 17 genotypes, 43 genotypes exhibited fine fibre and 49 lines exhibited excellent fibre uniformity. Thus observations would be made useful for selecting superior parental lines in intra-specific hybridization.

Pooja *et al*. (2016) during their experiment noticed that maximum variation among the morphological characters studied was present in hypocotyl pigmentation, leaf petiole pigmentation, leaf hairiness, leaf colour, leaf size, plant stem hairiness, plant height (cm), plant growth habit, days to 50% flowering, flower petal colour, boll shape, prominence of tip in boll, boll opening, number of locules/boll and seed fuzz density an all proved to be stable and useful diagnostic characters and helps in classifying the genotypes based on the phenotypic traits.

Sangwan *et al.* (2016) characterized 4 interspecific hybrids and their parents for varietal identification and observed that variation among the genotypes was observed majorly for two characters namely; stem pigmentation and petal colour. Only one genotype (GCW136) had frego type bract which makes it distinct from others. Thus such traits are highly useful for identification of genotypes.

Anjani *et al.* (2018) worked on 40 genotypes and found that many descriptors did not had any variation like leaf colour, leaf shape, leaf pubescence, nectarines, stem hairiness, bracts, flower petal spot, anther filament colouration, boll bearing habit, boll colour and boll opening. But eight descriptors had significant variations in them (petiole pigmentation, flower petal colour, stigma position, colour of pollen, boll shape and tip prominence) and thus they can apply for characterization and identification of genotypes.

Hamidi *et al*. (2018) evaluated three genotypes of cotton (GT40, TBL60 and SKT134) for DUS testing by studying 39 morphological traits. GT40 genotype was distinct from TBL60 and SKT134 genotypes based on yellow pollen colour, exerted stigma, small leaf size, stem pubescence, dwarf plants and early boll time of opening. TBL60 genotype was different from other two due to non-clustered type of flowering. Therefore these traits can be used as descriptors.

Hoffmann *et al*. (2018) studied ex situ morphological analysis which showed that *G. barbadense* plants from the Amazonas state presented higher similarity to cotton plants from other northern Brazilian states, and were grouped separately from those of other northern Brazilian states by descriptor analysis. This study indicates the distinctiveness of Amazon cottons, and contributes to demonstrate the discrimination power of multi categorical traits.

Rathinavel (2019) observed 26 qualitative and 14 quantitative morphological traits in upland cotton. The findings showed no variation for gossypol glands, male sterility, anther filament colouration, boll bearing habit and boll opening. Whereas traits like germination percent, seed vigour index, seed cotton yield/plant and fibre strength possessed maximum variation and genotypes can be characterized on the basis of these traits.

Krishnamoorthi *et al.* (2020) investigated 155 *desi* cotton genotypes for six qualitative traits: petal colour, plant body colour, leaf form, anther colour, boll shape, and hairiness. Plant body colour, 96 genotypes (61.93%) were greenish purple, 51 genotypes

(32.9%) were green, and eight genotypes (ClSA1793, DW1601, PA839, ARBAS138, CJSA101, LD0995, RG385, CNA1039) displayed red colour with a frequency of 5.16%. For petal colour characteristic, five separate groups were detected with a greater frequency of 49.03% for light yellow colour in 76 genotypes followed by yellow colour 51 genotypes with 32.9% frequency. On the other hand, 17 genotypes were white, eight genotypes (DSV1202, AKA2006, PA852, CSA1105, RG763, CNA2030, PA841, CNA2036) were creamy, and three genotypes were yellow.

Karena *et al.* (2021) characterized 50 genotypes of upland cotton on the basis of various morphological traits as per the guidelines of DUS testing. Observations were recorded for hypocotyl pigmentation, leaf shape, leaf petiole pigmentation, flower petal colour, pollen colour, boll colour, boll shape, boll opening and seed fuzz. Hypocotyl pigmentation was present in 9 genotypes and absent in remaining 41 genotypes. All the 50 genotypes showed palmate or normal leaf shape. Flower petal colour is one of the most important parameters for characterization of cotton genotypes. Three genotypes (GP Hir.48, GP Hir.49 and GP Hir.82) had white petal colour, 33 had cream and 15 genotypes had yellow petal colour.

2.2 Variability, heritability and genetic advance:

For efficient selection, it is necessary to have knowledge about the variability present in the genetic material. More specifically genetic variability should be present which can be passed to next generation. Substantial genetic coefficient of variance and high heritability estimates implies that characters can be improved through selection from segregating populations (Baloch and Baloch, 2004). Along with the presence of variability and heritability, genetic advance also plays a major role in deciding which selection procedure will be more effective. High genetic advance coupled with high heritability estimates offers a most effective response to selection (Larik *et al.*, 1997). Thus in light of the above the many studies have already been performed some of them are being highlighted below.

Pujer *et al.* (2014) evaluate 68 diverse genotypes of *Gossypium hirsutum* L. by studying 13 quantitative and fibre quality traits. High PCV and GCV were observed in number of balls per plant and seed cotton yield. Number of balls per plant, boll weight and plant height possessed high heritability coupled high genetic advance hence they are easy to select and improve.

Farooq *et al*. (2014) investigated 53 cotton genotypes and the variability studies showed that CLCuV (Cotton Leaf Curl Virus) and seed cotton yield had maximum value of GCV and PCV. Heritability in broad sense was found maximum in traits like fibre strength (99%) followed by boll weight (98%), ginning out turn percentage (97%) and fibre fineness (96%).

Dhivya *et al*. (2014) assessed variability in *Gossypium hirsutum.* The high PCV and GCV were observed in plant height, lint index, seed index, and boll weight. Number of sympodia branch per plant, yield per plant, seed index and fibre strength have high broad sense heritability coupled with genetic advance. Accessions MCU5, TCH1715, TCH1716 and Gcot16 based on their performance were identified as donors for yield per plant (g), number of bolls per plant, 2.5% span length (mm) and fibre strength (g/tex) hence can be used in breeding programme.

Ahsan *et al*. (2015) found that highest genotypic and phenotypic coefficient of variation were exhibited by the number of bolls per plant, lint index and seed cotton yield of single plant. Also these three traits showed high heritability and high genetic advance. This combination provides information of the trait in the selection process.

Khan *et al*. (2015) estimated level of variation among 50 cotton genotypes by recording 14 morphological traits. GCV and PCV values differed less from each other suggesting low level of environmental effects. High expected genetic advance and high heritability were observed for plant height, boll weight, number of bolls per plant and seed cotton yield per plant that means additive gene action is predominant and hence selection will be productive.

Aarthi *et al.* (2018) studied three hundred and ninety nine germplasm lines of upland cotton (*Gossypium hirsutum* L.) for fifteen traits. High estimates of PCV and GCV were observed for number of monopodia and seed cotton yield. While lowest estimates of PCV and GCV were observed for days to 50% flowering, seed index, uniformity and elongation percent. High heritability coupled with high genetic advance as percent of mean was observed for number of monopodia, number of sympodia, boll weight, lint index, micronaire value and seed cotton yield and these characters were controlled by additive gene effects, hence selection of genotypes based on these characters would be effective in the improvement of yield.

Chaudhari *et al.* (2017) recorded data in forty genotypes of cotton (*Gossypium hirsutum* L.) and obtained high genotypic and phenotypic coefficient of variation for number of sympodia per plant, number of boll per plant, seed cotton yield per plant, gossypol content, phenol content and reducing sugar content.

Gnanasekaran *et al*. (2018) determined genetic variability, heritability and genetic advance estimates in 42 improved *Gossypium hirsutum* genotypes for eleven characters. The difference between the estimates of PCV and GCV were low for all the characters except number of monopodia per plant, number of sympodia per plant and number of bolls per plant thereby indicating that lesser role played by the environment in the expression of these characters. High heritability coupled with high genetic advance as a percent of mean was recorded for boll weight, seed cotton yield and micronaire value indicated the major role of additive gene action in the inheritance of these characters.

Hasan and Latha (2017) studied 144 *Gossypium arboreum* genotypes. Most of the traits exhibited high genetic advance with high heritability *viz*. seed cotton yield (kg/ha), plant height, number of bolls per plant, boll weight except number of monopodial branches per plant and number of sympodial branches per plant with low heritability coupled with high genetic advance indicates prevalence of additive gene effects.

Jarwar *et al.* (2018) observed that the largest phenotypic and genotypic coefficient of variation was displayed by the seed cotton yield per plant, number of bolls per plant and seed index. Highest amount of heritability and uttermost genetic advance was found in the seed cotton yield per plant, number of bolls per plant and lint index. Hence these three traits can easily be improved through selection.

Kumar and Katageri (2017) observed more than 20 % PCV and GCV for number of monopods per plant (46.08 and 26.09), number of sympods per plant (27.86 and 21.99), boll weight (25.69 and 22.99) and seed cotton yield (32.80 and 20.51). High heritability (> 60 %) was observed for plant height, number of sympodia per plant, seed index, ginning outturn, lint index, boll weight and seed cotton yield per plant. Whereas, days to first flowering, number of monopodia per plant and number of bolls per plant were recorded with moderate (30 - 60 %) heritability. Similarly, Genetic advance over mean was high for plant height, number of monopodia per plant, number of sympodia per plant, lint yield per plant, lint index, boll weight and seed cotton yield per plant.

Monisha *et al.* (2018) evaluated F_1 generation synthesized using six lines (four compact and two non-compact) with nine non-compact testers in line × tester fashion for seed cotton yield and fibre quality traits. High PCV and GCV were obtained for number of monopodial branches per plant and yield per plant. High heritability coupled with high genetic advance (as per cent of mean) was observed for number of sympodial branches per plant, number of monopodial branches per plant, number of bolls per plant and single plant yield.

Nikhil *et al.* (2018) evaluated 96 cotton germplasm collections for genetic variability, heritability and genetic advance for fifteen quantitative traits. The results showed high GCV and PCV for number of monopodia and number of bolls per plant. High heritability coupled with high genetic advance as percent of mean was observed for all the traits which indicated that selection could be effective for improvement in these traits except for fibre quality characters, ginning outturn and seed cotton yield per plant.

Manonmani *et al.* (2019) recorded high PCV and GCV for number of monopodia and plant yield. High heritability coupled with high genetic advance recorded for most of the characters except for uniformity ratio and bundle strength.

Nandhini *et al.* (2019) characterized 220 RILs developed from MCU 5 and TCH1218 on the basis of morphological and fibre quality traits. Number of monopodia had high PCV and GCV while number of bolls per plant exhibit moderate GCV and high PCV. Except five almost all traits followed similar trend for GCV and PCV indicating less environment effects. High Genetic Advance of 5% mean along with high heritability was possessed by boll weight, number of monopodia per plant, lint index, and fibre fineness. Hence have additive gene action is present.

Krishnamoorthi *et al.* (2020) characterized 155 *desi* cotton accessions (*Gossypium arboreum* L.) using six qualitative features. For each genotype, the distribution of genotypes classified by the selected attributes and their states was computed. PCA showed three principal components accounting for 56.91% of the variability in the *arboreum* germplasm, with PC 1 accounting for 20.51% and PC 2 accounting for 18.62%. The results of the eigen vectors of six qualitative qualities suggested that anther colour, plant body colour, and boll form could serve as identifiable morphological markers for genotype classification of *G. arboreum*.

2.3 Correlation and path analysis

Seed cotton yield cannot be selected alone because of the complexity of the trait; in such condition correlation studies are very helpful. The inter-relationships between yield and yield contributing traits are estimated by correlation co-efficient analysis. Since, seed cotton yield is a complex quantitative character; direct selection is not a reliable approach as it is influenced by environmental factors. So it is important for breeders to know more about direct and indirect effects among different traits while selection. Path coefficient analyses parts the correlation into direct and indirect components and thus provide an effective aid in selection. It is important to know about the traits which contribute more to the yield and their direct and indirect association to successfully design a breeding programme. Some of the studies of correlation and path analysis have been discussed below:

Babu *et al*. (2017) studied 14 characters in 54 genotypes of *Gossypium hirsutum*. The correlation studies revealed that plant height, number of sympodia per plant, number of bolls per plant, boll weight, seed index, GOT and micronaire value showed significant positive association with seed cotton yield per plant. Further dividing the correlation coefficients into direct and indirect effects presented that plant height, number of monopodia per plant, number of sympoida per plant, boll weight, seed index and lint index had direct positive effect on seed cotton yield per plant. These studies clearly indicate that direct selection based on number of bolls per plant, boll weight and seed index may be helpful for developing high yielding varieties.

Hasan and Latha (2017) together found the genotypic and phenotypic correlation coefficient estimates were very strong for number of bolls per plant and boll weight with total seed cotton yield. Path coefficients also showed that number of bolls per plant and boll weight possess positive direct and indirect effects at both genotypic and phenotypic level. Thus these two traits are most important for selecting high yielding plants.

Chaudhari *et al.* (2017) revealed that number of sympodia per plant, number of bolls per plant and oil percentage exhibited high positive correlation at both genotypic and phenotypic levels with seed cotton yield per plant whereas, days to 50% flowering expressed negative and highly significant association. Besides this, fibre quality traits and biochemical traits like gossypol content, phenol content, protein content and reducing sugar content were not significantly correlated with seed cotton yield. The path analysis showed that number of bolls per plant and boll weight had high direct effect on seed cotton yield per plant. On contrary cotton yield per plant was not much affected by fibre quality and bio chemical traits.

Ul-Allah *et al.* (2017) developed five F_3 populations from five diverse crosses to analyze genetic association within-boll yield components. The highest genotypic correlation was observed between seed cotton yield per locule and number of seeds per boll. All traits within-boll yield components had highly significant positive correlation with seed cotton yield except number of seeds per locule and lint percentage. Path coefficient analysis divulged that number of seeds per boll had a maximum direct effect on yield ranging from 0.776 to 0.895 for different crosses. The study showed that number of locules per boll, seed cotton yield per locule, number of seeds per boll and seed cotton yield per boll can be used as efficient selection criteria for the improvement in seed cotton yield.

Dahiphale and Deshmukh (2018) worked on fifteen diverse genotypes of cotton (*Gossypium hirsutum* L.). In their findings seed cotton yield was positively and significantly correlated with number of monopodial branches, sympodial branches, ginning outturn (%) and fibre length. Lint kg/ha exhibited the highest magnitude of direct effects on seed cotton yield, followed by fibre length, plant height, bolls and sympodia/plant. Selection could be made on the basis of results.

Nikhil *et al.* (2018) performed correlation and path coefficient analysis for 15 quantitative traits of yield and fibre quality in 96 diverse genotypes. Seed cotton yield per plant was found positively correlated with number of monopodia, number of bolls per plant, boll weight and lint index at phenotypic level. The path analysis indicated that number of bolls per plant and boll weight had highest direct effect on seed cotton yield, on the contrary traits like plant height, fibre strength and lint index had direct negative effect on yield revealing that weightage should be given to more number of bolls per plant and more boll weight and these can be considered as principal yield determining components.

Pinki *et al*. (2018) studied three cultivars of upland cotton grown in six environments in which they found that Traits *viz.* plant height, seeds/boll, bolls/plant, GOT and lint yield/plant had positive correlation with seed cotton yield/plant. Similarly, path coefficient analysis unravels that bolls/plant, seeds/boll, monopods/plant and ginning outturn exerted positive and high direct effect on seed cotton yield and can be utilized while selecting for higher seed cotton yield.

Chinchane *et al.* (2018) investigated that there was significant and positive genotypic and phenotypic correlation of seed cotton yield with number of bolls per plant, whereas, there was negative association of seed cotton yield with both days to 50 percent flowering and days to maturity. The highest direct effect on seed yield was shown by ginning out turn (%) followed by number of sympodia per plant, number of bolls per plant, staple length (mm) and 100 seed weight. Whereas, days to maturity showed highest negative direct effect on seed yield followed by plant height, boll weight, days to 50 per cent flowering and number of monopodia per plant.

Kumar *et al*. (2019) conducted an experiment on 33 cotton genotypes to study the association among the seed cotton yield and 13 contributing traits. The studies revealed that plant height, number of bolls per plant, number of sympodial branches per plant and single boll weight exhibited significant positive association with seed cotton yield. Further portioning into direct-indirect effects highlighted the importance of number of bolls per plant, single boll weight and lint index which exerted high positive direct effect towards seed cotton yield.

Reddy *et al.* (2019) conducted an experiment comprised of 40 elite genotypes of upland cotton with one check (H 1098i). The association studies divulge that seed cotton yield per plant is highly significant and positive with all the important yield contributing traits. In the path-coefficient analysis lint yield per plant and seed index were considered as they exhibited high positive direct effects on seed cotton yield per plant. Hence, selections based on these two traits will result in genotypes with high seed cotton yield.

Manonmani *et al*. (2019) conducted a trial for estimation of genotypic correlation and path analysis in parents and F_1's of 4 (lines) × 8 (testers) and one check hybrid (Bunny) in intra-specific crosses of cotton (*Gossypium hirsutum* L.). Days to first flowering, number of monopodia, number of bolls per plant and number of sympodia on per plant displayed very high direct effect in the results. Association analysis revealed that plant yield exhibited significant positive correlation with days to first flowering, no. of sympodia, no. of bolls, boll weight, seed index, lint index, ginning out turn and fibre fineness and hence, selection for these characters will help in selecting genotypes with high yield.

Arunkumar and Murthy (2020) revealed that plant height, number of sympodia, inter nodal length, number of bolls per plant and seed index had significant positive correlation with seed cotton yield whereas, traits fibre strength and micronaire value exhibited negative correlation with seed cotton yield. Similarly, path coefficient analysis revealed that number of sympodia exhibited maximum direct effect on yield.

Gnanasekaran *et al.* (2020) observed high PCV and GCV for seed cotton yield per plant. High heritability was observed for the number of monopodia per plant, the number of bolls per plant, seed index, lint index, ginning percentage, 2.5% span length, uniformity ratio, and seed cotton yield per plant. The correlation study revealed that plant height, the number of monopodia per plant, the number of sympodia per plant and the number of bolls per plant had a significant positive association with seed cotton yield per plant. Path analysis indicated that the number of bolls per plant and seed index have maximum positive direct effect on seed cotton yield per plant.

Rai and Sangwan (2020) observed that seed cotton yield expressed a significant positive association with the plant height (0.2458 and 0.4348), the number of monopods per plant (0.2821 and 5.9365), the number of bolls per plant (0.8606 and 0.8558), boll weight per boll (0.5077 and 0.5137), lint index (0.3382 and 0.4409), ginning out turn (0.2794 and 0.4566), seed index (0.1826 and 0.2117), the number of seeds per locule (0.1826 and 0.2117) at genotypic and phenotypic levels. Number of locules per boll (1.5872) showed a significant correlation at the genotypic level with seed cotton yield. A significant negative correlation was observed with days to 50% flowering (-0.2222 and -0.2931) at both levels.

Satish *et al.* (2020) revealed that plant height, number of sympodia per plant, number of bolls per plant and boll weight had significant positive association with seed cotton yield per plant. Mahdy *et al.* (2021) found that the reduction percent caused by drought stress in SCY/P (seed cotton yield per plant) ranged from 31.44 to 39.39 with an average of 33.93. The correlation of SCY/P under normal irrigation was high with LY/P (lint yield/ plant), Lint percent, NB/P (number of bolls per plant), LI (lint index) and BW (boll weight), moderate with NS/B (number of seeds per boll) and upper half mean length, and low with DFF (days to first flower), Pressley index and negative with micronaire reading.

Krishnamoorthi *et al.* (2020) divided 155 *G. arboreum* accessions into five distinct clusters, with Cluster V having the most genotypes. The results of cluster analysis identified DWDA 1701, GAM2 60, TAS 130, CISA 1793, and RG 690 as prospective genotypes with the highest degree of divergence for future desi cotton breeding research.

Sakthivel and Somasundaram (2021) revealed that no. of bolls had significant positive association with seed cotton yield. Path analysis revealed the highest positive direct effects for plant height and number of bolls per plant in majority of crosses. The positive indirect effect for seed cotton yield was observed for number of bolls per plant.

Jangid *et al*. (2022) study used 30 elite genotypes of *desi* cotton. The genotypes were planted at Sirsa Cotton Research Station. The examination of correlation coefficients revealed a highly substantial positive association between seed cotton yield and yield contributing variables. The most favourable and significant correlations with seed cotton yield were lint yield, number of bolls per plant, boll weight, and gossypol content. According to the path-coefficient analysis, the number of bolls per plant, boll weight, and lint production were significant because they had a positive direct influence on seed cotton yield per plant. As a result, genotypes with high seed cotton yield will arise through selection based on the aforementioned qualities.

2.4 Genetic diversity studies

Cotton germplasm resources contain beneficial alleles that can be exploited to develop germplasm adapted to wide environmental and climate conditions. Germplasm lines have traditionally been characterized based on phenotypes, but phenotypic profiles are limited by the cost, time, and space required to make visual observations and measurements. With advances in molecular methods, genotypic profiles are increasingly able to identify differences among accessions due to the larger number of genetic markers that can be measured. A combination of both methods would greatly enhance our ability to characterize germplasm resources.

Singh *et al.* (2016) assessed the genetic diversity of a group of 64 genotypes of *G. arboreum* using a variety of quantitative traits, including seed cotton yield, boll weight, bolls/plant, lint percentage, lint yield, seed index, seeds/locule, days to 50% flowering, days to boll opening, plant height, chlorophyll content, leaf area index, lint index, span length, fibre strength, and fibre fineness. Based on the Mahalanobis D^2 analysis, the genotypes were divided into six clusters. Clusters I and V as well as II and III had the largest (97.85) and smallest (32.59) inter-cluster distances, respectively. Clusters V and VI's intra-cluster distance values ranged from 0 to 30.68. (Cluster I). Similar to this, a number of morphological characteristics, including plant body colour, petal colour, leaf shape, and the presence or absence of a leaf nectary, had no bearing on how cotton genotypes clustered. Some of the lines found in this investigation can be a part of the *desi* cotton core collection. From this collection of attractive cotton genotypes, potential donors may be chosen to serve as parents for the creation of varieties with desired character combinations.

Kumar *et al.* (2018) divided the genotypes studied into five distinct clusters, with each cluster receiving the whole collection. No correlation between geographic and genetic divergence was found. For each character under study, there was a sizable difference in cluster means. Crosses between the genotypes of Clusters III, IV, and V may result in heterotic hybrids and a broad spectrum of variability in later segregating generations, taking into account the level of variety among the genotypes and cluster means for different traits. It was discovered that the genotypes GJHV 503 and CSH 2810 could serve as parents in a future cotton breeding programme.

Mahesh *et al.* (2021) in order to investigate the correlation, path coefficient, and D^2 analysis in *desi* cotton during Kharif 2019, the material was tested in a Randomized Block Design (RBD) with three replications. Association analysis demonstrated a substantial positive correlation between seed cotton output per plant and the number of sympodia and bolls per plant in this experiment. The direct correlation demonstrated that the number of sympodia and bolls per plant had a significant direct effect on seed cotton yield per plant. This demonstrated that, in order to boost seed cotton yield through a selection programme, more focus should be placed on these traits. D^2 study revealed greater genetic variety across fifty cotton genotypes classified into four groupings. Cluster II and IV had the greatest inter-cluster distance (D^2) (21.32), followed by Cluster III and IV (19.01).

Bilval *et al.* (2017) analyzed genetic diversity using a total of 25 RAPD, 22 ISSR and 16 SSR primers, UPGMA analysis was performed based on combined pooled data, which revealed the genetic similarities ranged from 0.74 to 0.93 per cent. Dendrograms clustered the nine genotypes into two major clusters (A and B) showing affinity at genus level; most of the genotypes (five out of nine) falling into cluster A. Maximum similarity (93%) was found between the genotype DELTA-15 and KH-19; followed by 92 per cent similarity among GSHV-93/13 and DELTA-15; and GSHV97/1016 and Kh-119. On the other hand, least similarity of 0.72 was recorded among GJHV-337 with GSHV-97/1016; GISV8/1029; DELTA-15 and KH-119. The results indicate that the genotypes can be separated from each other at the molecular level.

Bourgou *et al*. (2017) studied genetic diversity of 121 accessions of the collection using SSR markers polymorphism which clearly identified the three different species, *G. arboreum*, *G. barbadense* and *G. hirsutum*. The perennials and annuals forms were also separated. The farmer’s varieties cultivated anciently by villagers are remarkable and fairly unique. This genetic resource could have promising attributes like environmental adaptation or traditional uses and needs to be properly characterized and preserved.

El-Moghny *et al.* (2017) assessed genetic diversity among the newly identified drought tolerant lines. Jaccard coefficient-based dissimilarity index ranged from 0.18 to 0.82 among the genotypes indicating presence of wide variation at the DNA level. Cluster and factorial analyses had clearly distinguished the drought tolerant and susceptible cotton genotypes. The clustering pattern was in congruence with the pedigree of genotypes. The information can be utilized for molecular mapping and marker assisted breeding to achieve drought tolerance in cotton.

Javaid *et al.* (2017) screened 30 simple sequence repeat primers to estimate genetic divergence among 22 cotton accessions for drought stress tolerance. Genetic similarity coefficients ranged from 0.87-1.00. PCA confirmed the clustering of 21 genotypes in two groups leaving one genotype (CIM-109) ungrouped. Overall, genetic diversity among the genotypes was low.

Saif *et al*. (2017) characterized five Egyptian cotton varieties Giza(G)86, Giza(G)87, Giza(G)88), Giza(G) 92 and Giza(G) 93 at molecular level using ISSR; SSR and RAPD-PCR markers. The phylogenetic relationships of the five Egyptian cotton varieties indicated two groups with 56% similarity; the first group had (G88); However, G93 and G86 with homology percentage of 81%, and both of them in relation to G87 variety with approximately 65.5% similarity.

Kumbhalkar *et al*. (2018) performed molecular profiling of 15 cotton genotypes using 104 SSRs primers. Average polymorphic information content values were, 0.210 and 0.345, respectively for fibre length and fibre strength. Dendrograms for fibre properties comprising six main groups for the fibre length and five clusters' groups for the fibre strength. The study revealed that parents AKH 10-2, AKH 84635 and SURAJ for fibre length and parents AKH 84635, AKH 09-5 and SURAJ for fibre strength were grouped different cluster and found to be most diverse. The identified polymorphic markers could be used for the MAS to develop of cotton hybrids having longer fibre length and high strength by incorporation of genetically diverse parents.

Kusuma *et al.* (2018) used SSR markers which were linked to high yield and high oil seed content against 22 genotypes of cotton. The genetic tree and phenotypic tree were concurrent with each other which explained that broad genetic diversity appears to exist among tested accessions.

Seyoum *et al.* (2018) recorded genetic distances in the whole cotton germplasm ranged from 0.451 to 0.052, indicating relatively wider genetic diversity range. Chinese originated germplasm showed the highest level of polymorphisms (gene diversity = 0.268), compared with American-origin with highest mean genetic distance (0.274). The SSRs displayed moderate level of genetic diversity at DNA level and identified three structured subpopulations, which suggests a potential use of these markers for genome wide association mapping.

Shekhawat and Tomar (2018) estimated genetic distance and genetic purity of five cotton hybrids, *viz*. ZCH 501 BGII, ZCH 541 BGII, PCHH 4 BGII, PCHH 6 BGII and PCHH 560 BGII using ten primers namely, NAU1048, BNL530, NAU1369, NAU895, BNL2590, NAU1103, NAU2083, BNL1053, NAU1190 and BNL1672. Amplicon size ranged from 100 to 300 bp. Different hybrids showed variable amplification at base pair which could be the key to identification of the cotton hybrids, genetic purity, analyzing genetic distance and IPR protection.

Gawande *et al.* (2019) investigated polymorphism between the three diverse cotton genotypes *i.e.,* MCU5, PKV Rajat and AKH-081 popular university varieties of *Gossipium hirsutum*. 116 SSR markers were used for detecting variation. Out of 116 SSR, 64 markers showed polymorphism between the parents PKV Rajat, AKH-081 and MCU-5.

Chavhan *et al.* (2021) used 20 SSRs markers to assess parental polymorphism and genetic diversity, with seven SSRs confirmed to be polymorphic. Using Jaccard's similarity coefficient, a dendrogram was created, and genotypes were divided into three clusters depending on the SSR profile. P1 and D1 had the lowest similarity coefficient value (0.80), indicating that they had substantial genetic diversity. The maximum similarity coefficient value (0.90) was found in P2 and D2, showing limited diversity between them. Only BNL-

3580 has the highest level of polymorphism (94%) among SSRs. SSR genotyping identified 18 single cross hybrids as true hybrids out of 55 successful hybrids, confirming SSRs as good genomic tools for parentage confirmation and hybridity determination.

Santosh *et al.* (2022) used 300 genome-wide SSR markers to profile 24 prominent Asiatic cotton cultivars. Of these, 48 were recognised as clearly polymorphic, with a total of 124 alleles discovered ranging from 2 to 5 alleles per locus, with an average of 2.58. The genetic dissimilarity between 24 *G. arboreum* varieties ranged from 0.27 to 0.53, with an average of 0.42 indicating that Indian *arboreum* cultivars have considerable genetic diversity. The clustering pattern was discovered to be incompatible with their known origin or ancestry. We propose a set of eight informative SSR markers for variety identification in diploid cotton, and a DNA fingerprint of 24 Asiatic cotton types was created using those markers. They propose a set of eight informative SSR markers for variety identification in diploid cotton, and a DNA fingerprint of 24 Asiatic cotton types was created using those markers. The produced DNA fingerprint was robust and reliable, with a very low probability of identical match (2.68 10-6) and a goodness of fit of 0.65. The information obtained in this work about the pattern of variability among popular Asiatic cotton varieties in India and the found polymorphic markers will be extremely useful in the preservation of valued *desi* cotton varieties and marker assisted breeding.

CHAPTER-III

MATERIALS AND METHODS

The experimental material for the present study comprised of one hundred fifty germplasm lines of Asiatic cotton *Gossypium arboreum* (Table 3.1) grown in *Kharif* 2020-21 and 2021-22 at Research area of Department of Genetics and Plant Breeding CCS-HAU, Hisar. The experiment material was raised in augmented design along with three check varieties *i.e.*, HD 432, HD 324 and HD 123 sown after every 15 genotypes in a single row of 6 m length, distance between rows and plants was 1.35 m and 30 cm respectively. All the recommended cultural package of practices was followed from sowing to harvesting the crop.

Table 3.1 List of 153 germplasm lines of *desi* cotton used in the experiment

Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype
1	S 302	**31**	S351	**61**	HD 328-1
2	FFS1	**32**	S479	**62**	FFS16
3	HD 404	**33**	S479 I	**63**	CISA 21
4	HD 514	**34**	DS 1	**64**	PA 405
5	HD 372	**35**	AC 33	**65**	CINA 329
6	HD 408	**36**	H 52 -519	**66**	FFS19
7	FFS2	**37**	AC-8	**67**	RG 255
8	HD 379	**38**	FFS8	**68**	LD 814
9	FFS3	**39**	FFS9	**69**	RG 260
10	Arlano	**40**	FFS10	**70**	LD 805
11	B 2-16-2	**41**	FFS11	**71**	LD 713
12	B-4	**42**	D 462-1-1 P3	**72**	AKA 9410
13	HD 392	**43**	D 462-1-1 P4	**73**	DLSA 17
14	BHO 5 VIII	**44**	D 462-1-1 P5	**74**	HD 418
15	BH 30	**45**	AC 41	**75**	G. Cot 19
16	BH 41	**46**	Malvi 12	**76**	HD 107
17	BH 92	**47**	P 248	**77**	CISA 6
18	BH 102	**48**	P 485	**78**	AH 11
19	FFS4	**49**	P 489	**79**	AKA 210
20	BPS	**50**	JL 60	**80**	AKA 315
21	FFS5	**51**	M 53070	**81**	AKA 9623-2
22	D 43-21	**52**	Jubli	**82**	RG 395
23	D 48-154-1	**53**	H 248	**83**	HD 453
24	D 462-1-1	**54**	H 174	**84**	FFS21
25	DC-93	**55**	H 460	**85**	PSRV 12489
26	DC 108	**56**	LD 327	**86**	CINA 347
27	EB 31-1	**57**	Vira 6	**87**	S7060
28	G 20	**58**	79/Lohit	**88**	PSRSV 12516
29	G 23	**59**	Petaloidy	**89**	S7060 A
30	Gao-16 LB VI	**60**	AC3376	**90**	S6071

91	Garovilli	**112**	AC3212	**133**	S6799
92	GOV 6	**113**	AC3377	**134**	HD 521
93	H 1	**114**	AC3269	**135**	HD 524
94	H 476-5	**115**	AC3233	**136**	FFS17
95	HD 6	**116**	AC3252	**137**	FFS18
96	HD 10	**117**	FFS12	**138**	HD 503
97	HD 3	**118**	DS 5-2	**139**	HD 543
98	HD 20	**119**	DS 5-3	**140**	HD 542
99	N-W-1	**120**	DS 5-4	**141**	HD 550
100	PL 735	**121**	FFS13	**142**	HD 551
101	PL 735	**122**	30822 BLL	**143**	HD 544
102	RA 1	**123**	Sanguinum	**144**	HD 535
103	Y-1	**124**	AC S 3028	**145**	HD 541
104	35/5 B	**125**	HD 369	**146**	HD 545
105	FFS6	**126**	AC 3347	**147**	HD 548
106	S2204	**127**	S3031	**148**	HD 549
107	S2446	**128**	CC1-1-3-41	**149**	HD 555
108	FFS7	**129**	FFS15	**150**	HD 556
109	DS-5	**130**	NGPA 1-9-1	**C1**	HD432
110	DS 5-1	**131**	FFS14	**C2**	HD324
111	S5278	**132**	HD328	**C3**	HD123

3.1: Recording of experimental data

Five random competitive plants were selected from each genotype to record various quantitative and qualitative characters as mentioned in Table 3.2. Data were recorded for following morphological traits described by PPV&FR Authority, India.

Table 3.2: List of various phenotypic traits recorded on field of 153 germplasm lines

Sr. No.	Trait	Sr. No.	Trait
1	Hypocotyl pigmentation	**19**	Prominence of tip in boll
2	Leaf colour	**20**	Boll opening
3	Leaf pubescence	**21**	Boll weight (g)
4	Leaf nectarines	**22**	Seed fuzz colour
5	Leaf petiole pigmentation	**23**	Seed index
6	Leaf shape	**24**	Ginning out turn %
7	Plant stem hairiness	**25**	Fibre colour
8	Plant stem pigmentation	**26**	Fibre length (2.5% span length) (mm)
9	Plant height (cm)	**27**	Fibre strength (g/tex)
10	Days to first flower	**28**	Fibre fineness (µ/inch)
11	Flower petal colour	**29**	Fibre uniformity (%)
12	Flower petal spot	**30**	Fibre maturity (%)
13	Flower stigma	**31**	Number of bolls per plant
14	Anther filament colouration	**32**	Number of locules per boll
15	Pollen colour	**33**	Number of seeds per boll
16	Boll colour	**34**	Number of monopods per plant
17	Boll shape	**35**	Seed cotton yield per plant (g)
18	Boll surface		

Brief description of all the morphological parameters recorded:

A. LEAF CHARACTERISTICS

1) **Hypocotyl pigmentation**: Hypocotyl is the part of stem of embryo beneath the stalk of seed leaves or above the root. The hypocotyl pigmentation was observed at 14thday after sowing under light condition for all the genotypes and classified by visual assessment. On this basis genotypes were classified as present or absent.

2) **Leaf colour**: 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.

3) **Leaf hairiness**: 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.

4) **Leaf nectaries**: 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.

5) **Leaf petiole pigmentation**: 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.

6) **Leaf shape**: 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).

B. STEM CHARACTERISTICS

1) **Stem hairiness:** 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.

2) **Sstem pigmentation**: The plant stem pigmentation was recorded on visual assessment basis at peak flowering stage. On the basis of plant stem pigmentation genotypes were classified as present or absent.

3) Plant height (cm)

The height of plant was measured in centimeter (cm) from base to apex of the main stem at maturity.

C. FLOWER CHARACTERISTICS

1) **Days to first flower**: On the basis of days to 50% 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).

2) **Flower petal colour**: The flower petal colour was recorded on visual assessment basis at peak flowering stage. On the basis of flower petal colour genotypes were classified as white, cream, yellow, pink, red and variegated.

3) **Flower petal spot**: The flower petal spot was recorded on visual assessment basis at peak flowering stage. On the basis of flower petal spot genotypes were classified as present or absent.

4) **Flower stigma position**: At the time of Peak flowering, the position of stigma in the flower was observed visually. On the basis of flower stigma position genotypes were classified as embedded and exerted.

5) **Anther filament colouration**: The anther filament colouration was recorded on visual assessment basis at peak flowering stage. On the basis of flower anther filament colouration genotypes were classified as present or absent.

6) **Pollen colour**: The anther colour was recorded on visual assessment basis at peak flowering stage. On the basis of flower pollen colour genotypes were classified as cream and yellow.

D. BOLL CHARACTERISTICS

1) **Boll colour**: The boll colour was observed visually before boll bursting stage. On the basis of boll colour genotypes were classified as green or red.

2) **Boll shape**: The shape of boll was observed visually. On the basis of boll shape (longitudinal section) genotypes were classified as rounded, ovate and elliptic.

3) **Boll surface**: The surface of fully mature boll (pre-busting stage) was observed visually. On the basis of boll surface appearance genotypes were classified as smooth or pitted.

4) **Prominence of tip in boll**: On the basis of prominence of boll tip genotypes were classified as blunt or pointed.

5) **Boll opening**: On the basis of boll opening genotypes were classified as semi-open, open and close.

6) **Boll weight (g)**: 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 (<2.0g), large (>3.0g) and medium (2.0-3.0g).

E. SEED CHARACTERISTICS

1) **Seed fuzz colour**: On the basis of seed fuzz colour genotypes were classified as white, grey and brown.

2) **Seed size or Seed index**: It is weight of seed obtained from 100 seeds in grams. Genotypes based on the seed index (one hundred healthy seeds were counted from each of five plants selected for data, weighed on an electrical balance in grams and averaged) 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).

F. FIBRE CHARACTERISTICS

1) **Ginning out turn (%):** It is defined as the ratio of lint percentage to the seed cotton expressed in percentage. On the basis of ginning out turn (%) genotypes were classified as very low (< 30),low (31-32), medium (33-34), high (35-36) and very high (>37)

2) **Fibre uniformity (%):** It is ratio of 50% span length to 2.5% 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).

3) **Fibre strength (g/tex):** It is capacity of fibre that how much force it can tolerate before breaking. 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).

4) **Fibre length (mm):** It is the distance between the two ends of fibre when substantially free from any external restraints. Span length means extent exceeded by stated proportion of cotton fibre. 2.5% span length means length exceeded by 2.5% of fibres by number. It was determined by digital fibrograph. 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). The observations in the present study were recorded on the basis of UHML.

5) **Fibre fineness:** This is a relative measurement of the diameter, linear density, and fineness of the fibres. The fineness was measured using a device called a "Sheffield micronaire" and was expressed in micrograms per inch. The micronaire instrument works on the basis of airflow resistance via a plug of fibres. It was calculated by compressing a 3.24 g sample of lint to a predetermined volume in the specimen holder. The plug was forced to pass through air at a predetermined pressure. The location of the float in the vertical tube attached to the compression chamber serves as a gauge for the quantity of flow. On the micronaire scale, fineness is measured directly. 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).

6) **Fibre colour**: The colour of the fibre was observed visually. On the basis of seed fibre colour genotypes were classified as white, cream, green and brown.

7) **Fibre maturity (%)**: It denotes the relative degree of thickening of wall. A tweezer was used to arrange about 100 fibres on a slide so that they are roughly parallel to one another from an aligned end of the sliver. The fibres were covered with a cover slip and irrigated with a caustic soda solution that contained 18% caustic. In order to see the centre of the fibres beneath the objective lens, the mounted slide was set on the microscope stage. The microscope's stage was moved in a transverse direction as each

fibre was examined individually. The following formula was then used to compute the maturity co-efficient.

$$Mc = \frac{(M + 0.6\,H + 0.4\,I)}{10}$$

Where, M denotes the mature fibre, H denotes the half mature fibre and I denotes the immature fibre. It denotes the matured fibres in a sample and was classified as

a. Very immature (<31)
b. Immature (32-49)
c. Average (50-65)
d. Good (66-80)
e. Very good (>81)

G. Others characters:

1. **Number of bolls per plant:** Number of bolls per plant was recorded from randomly selected five plants that contributed to seed cotton yield by counting the number of fully opened bolls during harvesting and averaged.
2. **Number of locules per boll:** The number of locules of a boll was counted after the boll opening.
3. **Number of seeds per boll:** The number of seeds in all the locules of a boll was counted.
4. **Number of monopods per plant:** Monopods are the vegetative branches *i.e.*, branches that are not bearing bolls, are lateral and axillary in position, present on main stem. These branches were counted at maturity stage and then mean value was calculated.
5. **Seed cotton yield per plant (g):** Total weights of seed cotton obtained from five randomly selected plants of each genotype were recorded in grams and then mean value was calculated.

3.2 Biochemical parameters

Sample preparation:

After ginning, 100 g cotton seeds of each of 150 distinct *desi* cotton genotypes as well as checks were rinsed with concentrated sulphuric acid (H_2SO_4) to remove fuzz of seeds. The cotton seeds were rinsed under running tap water to eliminate any dirt or chemicals and then dried in the open air for 30 minutes. After this, seeds were oven dried at 40-50^{o}C for few minutes. On the next day, dried seeds were crushed to prepare powdered samples and samples of each genotype were wrapped in aluminium foil and placed in an oven at 30-35^{o}C for further use. Following that, the dried powder samples were used to calculate crude protein, seed oil and gossypol using following techniques:

Crude Protein Content (%):

The Micro- Kjeldahl method was used for analyzing crude protein content in cotton seeds.

Reagent used:

1. Conc. H_2SO_4
2. Catalyst: Mixture of K_2SO_4 and $CuSO_4.5H_2O$ in the ratio of 5:1
3. 40% NaOH
4. 2% Boric acid
5. Standard HCl solution (0.01N)

250 mg of cotton seed powder was mixed with 10 ml of conc. H_2SO_4 and a catalyst combination of 500 mg (K_2SO_4 and $CuSO_4.5H_2O$ in the ratio of 5:1) in a long neck digestion flask. Sample was digested on Kjeldahl heating unit until the solution become clear. Then the digested sample was cooled and it was diluted with distilled water to reach a final amount of 100 ml. A blank was made by taking 10 ml of acid (without the sample) and digesting it in the same manner as that of sample. In a 100 ml conical flask, pour 25 ml of boric acid solution. This receiving flask was placed in such a manner that the condenser of the micro- Kjeldahl distillation apparatus's outlet dipped into the boric acid solution. 10 ml acid digested samples were transferred to the steam chamber of the micro- Kjeldahl apparatus. To the aliquot of the digested material, add 25 ml of 40% NaOH. Close the stopcock immediately and pass the steam through the steam chamber to the distilled ammonia until around 30-40 ml of distillate was collected in the receiving boric acid flask. Then the receiving flask was removed from apparatus and titrated the contents against 0.1 N HCl until the colour changed from blue green to pink. Blank solution was also titrated and subtracted the titration volume from sample titration value. The crude protein content was calculatedusing following calculations:

$$\textbf{Protein (\%)} = \frac{0.0014\ (y-x) \times 100 \times 1000 \times 100 \times 6.25}{10 \times 250}$$

Weight of sample taken = 250 mg

Final volume made to = 100 ml

Volume of the sample taken for the distillation = 10 ml

1 ml of 0.01 N HCl used for blank = x ml

Let volume of 0.01 N HCl used for sample = y ml

Actual volume of 0.01 N HCl used for sample= y-x ml

Seed oil content (%):

Seed oil content was calculated by using Soxhlet Extraction method.

Material used:

1. Soxhlet apparatus
2. Thimble
3. Drying oven
4. Weighing balance
5. Petroleum ether

Procedure:

Firstly, all the glass beakers were cleaned using petroleum ether, then the empty beakers were dried in the oven and weighted. After this, 1 g cotton seed powder was weighed in a thimble. The thimble was then placed in a glass beaker and slowly poured 100 ml petroleum ether into the beaker. In the thimble containing the sample, a small quantity of petroleum ether was also added. After that, beaker was placed in the Soxhlet's apparatus and it was run for approximately an hour and a half. The beaker was then removed from Soxhlet's apparatus and dried in the oven overnight before being weighed with oil. Crude oil content was calculated using for formula:

$$\textbf{Crude Oil (\%)} = \frac{W_2 - W_1}{W_3} \times 100$$

Where,

W_1 = Weight of empty beaker

W_2 = Weight of beaker and extracted oil (g)

W_3 = Sample weight (g)

Gossypol content (%):

Extraction:

500 mg powdered leaf sample was taken in a plastic centrifuge tube and 5 ml ethanol (80%) was added in it. Then, the tube was placed in a water bath and heated to 80°C for 20 minutes before being shaken over vortex. The same procedure was carried out twice and the supernatants were collected in a tube. The homogenate was centrifuged at 4000 rpm for 15 minutes after cooling and the supernatant was collected in a separate tube. After adjusting the pH of the extract to 3.0 with 0.1 N HCl, 15 ml of diethyl ether was added to the contents. On a hot plate, the ether 16 phase was evaporated. In a known volume (3 ml) of 95 % ethanol, the residue was redissolved.

Estimation:

The gossypol content in cotton seeds was calculated using the Bell method (1967). One ml of aliquots, 0.5 ml of phlorglucinol reagent and 1 ml of conc. HCl was added in each tube. The samples were then incubated at room temperature for 30 minutes and final volume was made of 10 ml with 80 % ethanol. At 550 nm, the absorbance was measured against a reagent blank. Concentration of gossypol was determined by using gossypol acetate (10-100 µg/ml) as standard.

3.3 Statistical Analysis for morpho-biochemical and fibre traits

The data for various characters was analysed on the mean basis. The analysis was carried out using the software R studio. The data was subjected to following statistical analysis.

3.3.1 Analysis of Variance (ANOVA)

Data with respect to check varieties were subjected to analysis of variance as per Augmented design (Federer 1956) to obtain adjusted trait values for 3 checks as well as for 150 test genotypes. To obtain the estimate of error, following ANOVA was used (Table 3.3 & 3.4).

Table 3.3: A two-way Table of check genotypes for each character

Check varieties	**Blocks**				
	B_1	**B_2 ---------**	**B6**	**Total**	**Mean**
C1	X11	X12 --------	X1**6**	C1	X 1
C2	X21	X22 --------	X2**6**	C2	X 2
Total	B.1	B.2--------	B.6		M

Where,

C1 and C2 stand for Kent and UPO-212 respectively.

Xij = character value of i^{th} check in j^{th} block

B.j = $\sum X_{ij}$ = sum over checks in j^{th} block.

Ci. = $\sum X_{ij}$ = sum of i^{th} check over all the blocks.

G = $\sum C_{i.} = \sum B_{.j}$ = grand total of all checks.

XI = C_i. / b = mean of the i^{th} check

M = $\sum X_{\,i}$ = G/b = sum of all check means

b = number of blocks

c = number of checks

Table 3.4: Analysis of variance for an Augmented block design used in the present experiment

Source of Variation	**d.f.**	**Sum of squares**	**Mean squares**
Total	bc-1	SST	MST
Blocks	b-1	SSB	MSB
Checks	c-1	SSC	MSC
Error	(b-1)(c-1)	SSE	MSE

$$SST = \sum_{i=1}^{c}\sum_{j=1}^{b} x^2\, ij - G^2/bc$$

$$SSB = \left(\frac{1}{c}\right)\sum_{j=1}^{b} B^2\, j - G^2/bc$$

$$SSC = \left(\frac{1}{b}\right)\sum_{i=1}^{c} c^{2i} - G^2/bc$$

SSE = SST – (SSB + SSC)

$$MSE = SSE/ (b-1) (c-1)$$

The further analysis was performed on the adjusted means for all the genotypes towards each character, which were calculated as follows:

$$Yi = Yij - rj$$

Where,

Yi = adjusted mean of the character for *ith* genotypes in the *jth* block

X ij = unadjusted mean of the character for *ith* genotype in the *jth* block

r j = block effect for *jth* block, and is estimated as mentioned below:

r j = 1/c (Bj-M)

Parameters of Variability

Mean ($\overline{X}$)

Mean value of each character was calculated by dividing the total sum of observations by corresponding number of observations.

$$\overline{X} = \frac{\sum X_{ij}}{N}$$

Where,

X_{ij} = Any observation in i^{th} treatment and j^{th} replication

N = Number of observations

Standard error of mean [S.E. (m)]

Standard error of mean was calculated by using error mean squares value from ANOVA Table using formula:

$$\textbf{S.E. (m)} = \frac{\sqrt{MS_e}}{r}$$

Where,

MS_e = Error mean sum of squares

r = Number of replications

Critical difference (CD)

For every character, critical difference (*i.e* difference of any two mean values) was calculated in order to compare the treatment means using following formula:

$$\textbf{S.E. (d)} = \frac{\sqrt{2MS_e}}{r}$$

$$\textbf{C.D. at 5 or 1 \%} = \frac{\sqrt{2MS_e}}{r} \times 't'$$

Where,

't' is the tabulated value at error degree of freedom at 5 or 1 % level of significance.

Range

The minimum and maximum values of each character were recorded as range of that character.

Coefficient of variation (C.V.)

The coefficient of variation is a standardized form of variance which is useful for comparing the extent of variance between different characters. According to Burton and de Vane (1953), genotypic and phenotypic coefficients of variation were estimated based on the estimates of genotypic and phenotypic variances.

$$\textbf{Genotypic coefficient of variation (GCV \%)} = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

$$\textbf{Phenotypic coefficient of variation (PCV \%)} = \frac{\sqrt{\sigma^2 P}}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = General mean of a particular character

σ^2_g= Genotypic variance

σ^2_p= Phenotypic variance

GCV and PCV were grouped according to the method suggested by Sivasubramanian and Menon (1973):

0-10 % = Low

10- 20 % = Moderate

>20 = High

Heritability (broad sense)

Heritability in terms of broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and it was expressed in percentage:

$$\textbf{Heritability } (h^2) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

The calculated heritability was categorized into three groups as suggested by Johnson *et al.* (1955):

0-30%	:	Low
30-60%	:	Moderate
>60%	:	High

Genetic advance (GA)

Genetic advance was calculated using formula given by Johnson *et al.* (1955):

$$\textbf{GA} = k \times h^2 \times \sqrt{\sigma^2 p}$$

Where,

h^2 = Heritability in broad sense

k = Selection differential, which is equal to 2.06 at 5% intensity of selection (Lush, 1949)

$\sqrt{\sigma^2 p}$ = Phenotypic standard deviation

Genetic advance as percent of mean

Genetic advance as percent of mean for each character was calculated by using formula given by Johnson *et al.* (1955):

$$\textbf{Genetic advance as percent of mean} = \frac{\mathbf{GA}}{\bar{\boldsymbol{X}}} \times \mathbf{100}$$

Where,

GA = Genetic advance

$\bar{X}$ = General mean

Genetic advance as percent of mean was classified as per formula suggested by Johnson *et al.* (1955).

0-10 % = Low

10- 20 % = Moderate

>20 % = High

3.4 Correlation coefficient analysis

The correlation coefficients among all possible character combination at phenotypic ‘r (p)’ and genotypic ‘r (g)’ level were calculated using formulae suggested by Al- Jibouri *et al.* (1958):

$$\textbf{Genotypic correlation } \mathbf{r_{xy}}\ \textbf{(G)} = \frac{\boldsymbol{CoV_{xy}(G)}}{\sqrt{\boldsymbol{V_x(G) \times V_y(G)}}}$$

$$\textbf{Phenotypic correlation } \mathbf{r_{xy}}\ \textbf{(P)} = \frac{\boldsymbol{CoV_{xy}(P)}}{\sqrt{\boldsymbol{V_x(P) \times V_y(P)}}}$$

Where,

CoV_{xy} (G) = Genotypic co- variance between character ‘x’ and ‘y’

CoV_{xy} (P) = Phenotypic co- variance between character ‘x’ and ‘y’

V_x (G) = Genotypic variance of character ‘x’

V_x (P) = Phenotypic variance of character ‘x’

V_y (G) = Genotypic variance of character ‘y’

V_y (P) = Phenotypic variance of character ‘y’

The significance of correlation was tested against standardized tabulated values with (n-2) d.f., where ‘n’ is the number of genotypes.

3.5 Path coefficient analysis

The path coefficient analysis was performed according to the formula given by Wright (1921) and adopted by Dewey and Lu (1959). Standard path coefficients, which are also known as standardized partial regression coefficients, were calculated. These values were obtained by solving the following set of ‘p’ simultaneous equations using INDOSTAT software.

$$P_{01} + P_{02}\, r_{12} + \text{-------------} + P_{0P}\, r_{1P} = r_{01}$$

$$P_{01} + P_{12}\, r_{02} + \text{-------------} + P_{0P}\, r_{2P} = r_{02}$$

$$\downarrow$$

$$P_{01} + r_{1P} + P_{02}\, r_{2P} + \text{-------------} + P_{0P} = r_{0P}$$

Where,

P_{01}, P_{02}, ------------ P_{0P} are the direct effects of variables 1,2, ------------, p on the dependent variable 0 and r_{12}, r_{13}, ---------- r_{1P}----------- r $_{P\,(P-1)}$ are the possible correlation coefficients between various independent variables and r_{01}, r_{02}, r_{03}, -------, 3_{0P} are the correlations between dependent and independent variables.

The indirect effects of ith variable via jth variable are attained as ($P_{oj}\times r_{ij}$). The contribution of remaining unknown factor is measured as the residual factor, which is calculated as given below:

$$\mathbf{P^2_{0X} = 1- [P^2_{01}+ 2P_{01}P_{02}r_{12}+ 2P_{01}P_{03}r_{13}+ ---------- + P^2_{02} + 2P_{02}P_{03}r_{23}+------+ P^2_{0P}]}$$

$$\textbf{Residual factor} = \sqrt{(\boldsymbol{P^2ox})}$$

3.6 Genetic diversity

Mahalanobis D^2 analysis

Mahalanobis (1936) D^2 analysis was used for assessing the genetic divergence among the test genotypes involving quantitative characters. The generalized distance between any two populations is given by the formula:

$$D^2 = \sum\sum \lambda_{ij}\, \sigma_{ai}\sigma_{aj}$$

Where,

D^2 = Square of generalized distance

λ_{ij} = Reciprocal of the common dispersal matrix

σ_{ai} = $(\mu_{i1}\text{-}\mu_{i2})$

σ_{aj} = $(\mu_{j1}\text{-}\mu_{j2})$

μ = General mean

Since the calculation's formula requires for the inversion of a higher order component, the initial correlated un-standardized characters (Xs) were changed into standardised uncorrelated variables (Ys) to make the computation process simpler. The sum of squares of the differences between pairs of corresponding uncorrelated (s) values of any two uncorrelated genotypes was used to get the D^2 values (Rao, 1960).

Ward's Minimum Variance Method

The clustering method was originally developed by Ward (1963). Several authors independently proposed its names as *Minimum Variance Clustering*, *Sum of Squares* method (Orloci, 1967) and *Incremental Sum of Squares* method (Burr, 1968). The years, *i.e.,*, the objects, have been grouped based on a specific criterion, which is presumed to be measuring the similarity between the years. Once the clusters have been formed, the objects and their respective distances are represented in the form of a tree diagram, termed as dendrogram. Here, on X-axis, the objects are shown in the same order, as they are included in the clusters and the ‘stem’ or links between the clusters (and the objects) are drawn on Y-axis whose height relies upon the average distance between the clusters. This technique involves fusion of clusters from the matrix of inter-year distances provided as under:

To start with, the squared distances of objects ½ d^2_{ij} (ij = 1,….,n) are computed corresponding to all possible pairs of objects. These distances from the matrix Do. Form Do, the pair of objects having the least ½ d^2ij is grouped to form the initial cluster, say C (1). D_1 represents the *Increase in the total* within cluster sum of square of the distances from the centroids of the C (1) with the other objects, in addition to ½ d^2ij values of the objects, which are not clustered. The search for new clusters is again carried out on the least values of D_1.

The procedure of revising the matrix D_i [i = 1,…..] based on D (1) and the search for the fusion clusters is continued until the fusion of clusters is combined into a single cluster. The values of D_i during each step of fusion provide ‘links’ or distances between the clusters and the objects through which the dendrogram can be constructed. During every step of fusion, the matrix D is revised in terms of an Index I, which can computed as follows:

$$1\,[C\,(i), C\,(j)] = \frac{n(i)\,n(j)}{n(i) + n(j)}[x\,(i) - x\,(j)]^{2}$$

Where,

x(i) and x(j) are respectively the centroids of the clusters C (i) and C (j), which consist of n(i) and n(j) objects. This method of clustering has been used in present investigation.

Cluster mean value

The cluster mean of a particular character is the summation of mean values of genotypes included in a cluster, divided by number of genotypes in the same cluster.

3.7: Assessing genetic diversity among parents using SSR markers

3.7.1 Plant Material

Young leaves from 4-5 week old seedling of 48 selected genotypes were collected for DNA extraction during 2019-20 for the present study.

3.7.2 Chemicals and reagents

All the Chemicals used for DNA extraction and PCR amplification were purchased from Sigma-Chemicals Co. USA, Promega corporation and Thermo Fisher Scientific. All other chemicals used in the present investigation were of molecular grade.

3.7.3 Glasswares

Glasswares used in the present investigation, were of the borosilicate quality. Oven dried (180°C) conical flasks, bottles, pipettes, beakers, volumetric flasks, measuring cylinders of different sizes (50 ml; 100 ml; 150 ml; 500 ml; 1000 ml) were used for reagents/solutions.

3.7.4 Methods

3.7.4.1 Genomic DNA isolation

Genomic DNA was isolated from young leaves of cotton plants by Cetyl Trimethyl Ammonium-Bromide (CTAB) extraction method (Saghai-Maroof *et al.*, 1984).

3.7.4.2 DNA Extraction

Reagents

Following reagents were used to isolate genomic DNA from the cotton leaves:

1) **CTAB extraction buffer:** It was prepared fresh every time by mixing the reagents given below (except β-mercaptoethanol and PVP) in double distilled water. The mixed buffer reagents were then incubated at 65ºC for 1 hour.

   Tris (pH 8.0) : 1 M
   NaCl : 5 M
   EDTA (pH 8.0) : 0.5 M
   CTAB : 2 % (w/v)
   PVP : 2 % (w/v)
   ß-mercaptoethanol : 2% (v/v) (added just before use)

2) **Tris-EDTA (TE) buffer:** Prepared by mixing Tris (pH 8.0), 10mM and EDTA (pH 8.0), 1mM and then autoclaved it.

3) **DNA extraction procedure:**

1. One gram of the leaf tissue was homogenized in liquid nitrogen to convert it into a fine powder using sterilized mortar and pestle.
2. The leaf tissue was then transferred in the extraction buffer (mentioned above) and were thoroughly mixed by gently inverting the tubs and subjected to incubation in water bath at 65ºC for 60 minutes. Mixing was done by gently inverting the tubes at an interval of 10-15 min.
3. Samples were then cooled to room temperature and 2.5 ml chloroform : isoamylalcohol (24:1) solution was added. Samples were centrifuged for about 15 minutes at 10,000 rpm.
4. After centrifugation, the upper aqueous phase was transferred to another centrifuge tube and again samples were washed with 2.5 ml of CI by centrifugation at 8,000 rpm for 10 minutes.
5. The upper aqueous phase was transferred to another centrifuge tube with tapering end and equal volume was of pre-chilled iso-propanol was added and kept at 4ºC for 30 minutes for precipitation of DNA.
6. The pellet was extracted into 1.5 ml centrifuge tube and the solution was centrifuged at 10,000 rpm for 5 minutes for settling down of DNA in bottom and upper solution was removed.

7. The DNA pellet was washed with 70 per cent ethanol for 10 minutes. After which the pellet was air dried.
8. The dried pellet was dissolved in 70 µl of TE buffer and allowed for complete suspension of DNA.

3.2.4.3 RNase Treatment

1. To the extracted genomic DNA samples RNase treatment was given at concentration of 1µl of RNase per 20 µl DNA sample to remove RNA contamination and then samples were incubated in water bath at 37ºC for 5 hours.
2. After incubation, washing with CI solution and precipitation of DNA was done following steps mentioned in DNA extraction method.

3.7.4.4 Quantitative and Qualitative determination of DNA

Quantity and quality of the isolated genomic DNA was estimated by Nanodrop. Readings on 260 nm and 280 nm were self-recorded by the instrument. Quality and quantity of DNA was measured on the bases of absorbance of the two wavelengths. Samples with ratio (O.D 260/O. D 280) 1.8 are considered as pure DNA and above this represents RNA contamination, also below this value represents protein contamination. We received readings ranged from 1.75-1.87, which can be used for PCR reaction. Agarose Gel Electrophoresis method was also done by comparing samples with 50 nm concentration λ DNA. It is just to confirm the Nanodrop readings because sometimes presence of sheared DNA and other chemicals such as chloroform that may contribute to UV absorbance at 260 nm.

Reagents used for electrophoresis were:

1) Agarose (Low melting Temperature)

2) 10X TBE buffer (Autoclaved)

Tris	108.0 g
Boric acid	55.0 g
EDTA	4.6 g
Final volume	1000 ml

3) 6X Loading dye

Sucrose	4.0 g
Bromophenol blue	0.025 g
Xylene cyanol	0.025 g
Final volume	10 ml

Loading dye solution was stored at 4^0C in the refrigerator.

Procedure

1. Agarose solution was prepared by adding 0.8 g agarose in 100ml of 0.5X TBE and then melting it.

2. It is then cooled down to bearable temperature under tap water and ethidium bromide was added in the gel at the rate of 2µg/ 50ml.
3. The gel was poured in gel casting plate inserted with comb of required well number and size.
4. After setting of gel, combs were removed and it was submerged into 0.5X TBE buffer.
5. DNA samples were mixed with double distilled water and 6X loading dye solution (2:7:1) and loaded into the wells along with λ-DNA, using micropipette.
6. Electrophoresis was carried out at voltage of 3 volt/cm of the gel.
7. The samples were visualized under UV light and photographed using BIO RAD gel documentation system.

3.7.5 Polymerase Chain Reaction (PCR) Amplification

Thermo Scientific Themocycler was used for PCR amplification. The optimization of PCR reaction was done by using varying concentrations of template DNA (25-100 ng), dNTPs mix (100-300 µM), $MgCl_2$ (2-2.5 mM), primers (0.1- 0.8 µM) and *Taq* DNA Polymerase (0.2-2 units) in a reaction volume of 20 µl. The optimized reaction mixture (20 µl) contained:

DNA template : 50 ng
dNTPs mix : 250 µM
$MgCl_2$: 2.5 mM
Primers : 0.4 µM
Taq DNA Polymerase : 0.3 µl

A total of 100 SSR markers were used for PCR amplification of the template DNA (Table 3.3). The PCR reaction (20 µl) was set up in thin walled 0.2 µl PCR tubes under following reaction conditions:

i) 94°C for 4:00 minutes (initial denaturation)
ii) 94 °C for 1:00 minute (denaturation)
iii) 50-63°C for 1:00 minute (primer annealing)
iv) 72 °C for 1:00 minutes (primer extension)
v) 72°C for 5 minutes (final primer extension)
vi) Hold at 4ºC for infinity

The amplification reaction was set to repeat the steps (ii) to (iv) for 30 times and the product was kept at 4°C till further use.

3.7.7 Allele scoring

The banding pattern for each marker was scored for 153 cotton genotypes. The presence of an amplified band was scored as 1 and the absence as 0. The size of the amplified bands in base pairs was determined based on its relative migration to 100 bp DNA ladder.

3.7.8 Data analysis:

3.2.8.1 Polymorphic Information Content (PIC)

Polymorphic information content (PIC) was calculated, using the formula:

$$\mathrm{PICi} = 1 - \sum_{j=1}^{n} \mathrm{Pij}^2$$

Where,

PICi is the polymorphic information content of a marker i,

Pij is the frequency of the j^{th} pattern for marker i, and

The summation extends over n patterns

CHAPTER-IV

RESULTS

The experimental material for the present study comprised of one hundred fifty germplasm lines of asatic cotton *Gossypium arboreum* grown in *Kharif* 2020-21 and 2021-22 at Research area of Department of Genetics and Plant Breeding CCSHAU, Hisar. The experiment material was raised in augmented design with three check varieties *i.e.*, HD 432, HD 324 and HD 123 sown after every 15 genotypes in a single row of 6m length, along with row-to-row distance of 1.35 m and plant to plant distance of 30 cm. The pooled data have been subjected to various analyses and mean Table of pooled data of seasons one (*Kharif* 2020-21) and two (*kharif* 2021-22) is provided in Table 4.34. On the basis of the observations that were noted, the results of recorded parameters were explained under following subheads:

4.1 DUS characterization of germplasm
4.2 ANOVA (Analysis of variance)
4.3 Mean, range and other genetic parameters of various quantitative traits
4.4 Association studies
4.5 Diversity analysis
4.6 Molecular analysis on the basis of SSR markers

4.1 DUS characterization of germplasm

A DUS test is used to identify a genotype and to protect the farmers and plant breeder's rights. It is also conducted so that a new variety can enter the market legally. The morphological characterization of reported genotypes serves as the basis for a substantial portion of the registration process for new variety. According to the requirements of the Protection of Plant Varieties & Farmers Right Authority, 150 cotton germplasm lines and three checks were classified in the current study on the basis of 30 DUS (Distinctness, Uniformity, and Stability) traits that were observed in the field at various phases of plant growth. Using morphological traits to characterise cultivars extends the use of traditional taxonomic methods from species to cultivars. Numerous investigations have been done to find stable morphological features for differentiating crop varieties in the present study the data was collected across two successive seasons (*kharif* 2020-21) and (*kharif* 2021-22) and there was no change in the qualitative traits, indicating that the characters remained stable throughout both the seasons. Quantitative traits showed some heterogeneity, but it was nonetheless within the grouping range that the authority had indicated in the cotton DUS traits. On the basis of DUS traits, the study material was morphologically described as follows:

4.1.1 Hypocotyle pigmentation

On the basis of hypocotyle pigmentation, 153 germplasm of *desi* cotton were characterized into two categories *i.e.,* absent and present. Twenty genotypes were found in which the hypocotyle pigmentation was absent and 133 genotypes showed hypocotyle pigmentation. The classification of *desi* cotton genotypes have been presented in Table 4.1 and plate 4.1.

Table 4.1: Classification of 153 *desi* cotton genotypes on the basis of hypocotyl pigmentation

Code	Genotype number	Genotypes
Absent (1)	20	HD 372, HD 392, BH 30, FFS9, D 462-1-1 P3, BH 102, D 43-21, HD 6, HD 324, HD 20, S2204, DS 1, D 462-1-1 P5, AC3269, DS 5-4, RG 260, LD 805, LD 713, CINA 347 and S7060
Present (9)	133	S 302, FFS1,HD 404, HD 514, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, BHO 5 VIII, BH 41, BH 92, FFS4, BPS, FFS5, D 48-154-1, , DC-93, DC 108, EB 31-1, G 20, G 23, Garovilli, GOV 6, H 1, H 476-5, HD 10, HD 3, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, AC 33, H 52 -519, AC-8, FFS8, FFS10, FFS11, D 462-1-1 P4, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, S7060, PSRSV 12516, S7060 A, S6071, S6799, HD521, HD 524, FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549, HD 555,HD 432 HD123 and HD 556

4.1.2 Leaf colour

On the basis of leaf colour *desi* cotton genotypes were categorized into light green, green, and pink. 127 genotypes showed light green colour leaf and 26 genotypes were having green colour leaf. The classifications on the basis of leaf colour have been presented in Table 4.2 and plate 4.2.

4.1.3 Stem hairiness

The 153 *desi* cotton genotypes were classified into three categories on the basis of stem hairiness *i.e.,* sparse, medium and dense. 36 genotypes were under sparse, 85 under medium and 32 were having dense stem hairiness. The classifications on the basis of stem hairiness were presented in Table 4.3 and plate 4.3.

Table 4.2: Classification of 153 *desi* cotton genotypes on the basis of leaf colour

Code	Genotype number	Genotypes
Light Green (1)	127	HD 432, HD 123, FFS1,HD 404, HD 514, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, BHO 5 VIII, BH 30, BH 41, BH 92, FFS4, BPS, FFS5, D 43-21, D 48-154-1, DC-93, DC 108, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 10, HD 3, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, AC 41, Malvi 12, P 248, P 485, JL 60, M 53070, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3377, AC3233, AC3252, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, PSRSV 12516, S7060 A, S6071, S6799, HD 524, FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549, HD 555 and HD 556
Green (2)	26	HD 324, S 302, HD 372, HD 392, BH 102, D 462-1-1, EB 31-1, HD 6, HD 20, S2204, DS 1, D 462-1-1 P4, D 462-1-1 P5, P 489, Jubli, AC3212, AC3269, FFS12, RG 260, LD 805, LD 713, FFS21,, PSRV 12489, CINA 347, S7060, and HD521

Table 4.3: Classification of 153 *desi* cotton genotypes on the basis of stem hairiness

Code	Genotype number	Genotypes
Sparse (3)	36	S 302, FFS1, HD 514, HD 372, HD 408, HD 379, Arlano, B 2-16-2, BH 30, G 23, Gao-16 LB VI, GOV 6, H 1, H 476-5, PL 735, Y-1, S2204, S2446, D 462-1-1 P4, Malvi 12, RG 395, P 489, H 174, FFS12, CISA 6, AC 3347, FFS14, NGPA 1-9-1, FFS15, CINA 329, FFS19, PSRSV 12516, S7060 A, S6071, HD 524,
Medium (5)	85	HD 432, HD 123, , HD 324, HD 404, FFS2, FFS3, B-4, , BH 92, BPS, FFS5, D 48-154-1, D 462-1-1, DC-93, DC 108, G 20, Garovilli, HD 3, HD 20, RA 1, 35/5 B, FFS 6, S5278, S351, S479, S479-1, DS 1, H 52 -519, AC-8, FFS9, FFS10, D 462-1-1 P3, D 462-1-1 P5, AC 41, P 248, P 485, M 53070, Jubli, H 248, H 460, LD 327, 79/Lohit, Petaloidy, AC3376, AC3212, AC3269, AC3233, AC3252, DS 5-2, DS 5-3, DS 5-4, 30822 BLL, AC S 3028, HD 369, S3031, CC1-1-3-41, HD 328-1, FFS16, CISA 21, PA 405, RG 255, , RG 260, LD 805, LD 713, AKA 9410, DLSA 17, G. Cot 19, AH 11, AKA 210, A KA 315, AKA 9623-2, HD 453, FFS21,, PSRV 12489, CINA 347, S7060, FFS 17, HD 503, HD 543, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 549, and HD 556
Dense (7)	32	HD 392, BHO 5 VIII, BH 41,BH 102, FFS4, D 43-21, EB 31-1, HD 6, HD 10, N-W-1, PL 735-1, FFS7, DS-5, DS 5-1, AC 33, FFS11, FFS8, JL 60, Vira 6, AC3377, FFS13, Sanguinum, HD 328, LD 814, HD 418, HD 107, S6799, HD521, FFS18, HD 542, and HD 555

4.1.4 Leaf hairiness

On the basis of leaf pubescence 153 *desi* cotton genotypes were classified into three categories *i.e.,* sparse, medium and dense. Thirty five genotypes were in category sparse, 87 were in medium category and 31 genotypes were having dense leaf pubescence as represented in Table 4.4 and plate 4.4.

Table 4.4: Classification of 153 *desi* cotton genotypes on the basis of leaf hairiness

Code	Genotype Number	Genotypes
Sparse (1)	35	S 302, FFS1, HD 514, HD 372, HD 408, HD 379, Arlano, B 2-16-2, BH 30, G 23, Gao-16 LB VI, GOV 6, H 1, H 476-5, PL 735, Y-1, S2204, S2446, D 462-1-1 P4, Malvi 12, RG 395, P 489, H 174, FFS12, CISA 6, AC 3347, FFS14, NGPA 1-9-1, FFS15, CINA 329, FFS19, PSRSV 12516, S7060 A, S6071 and HD 524
Medium (5)	87	HD432, HD324, HD 123, HD 404, FFS2, FFS3, B-4, , BH 92, BPS, FFS5, D 48-154-1, D 462-1-1, DC-93, DC 108, G 20, Garovilli, HD 3, HD 20, RA 1, 35/5 B, FFS 6, S5278, S351, S479, S479-1, DS 1, H 52 -519, AC-8, FFS9, FFS10, D 462-1-1 P3, D 462-1-1 P5, AC 41, P 248, P 485, M 53070, Jubli, H 248, H 460, LD 327, 79/Lohit, Petaloidy, AC3376, AC3212, AC3269, AC3233, AC3252, DS 5-2, DS 5-3, DS 5-4, 30822 BLL, AC S 3028, HD 369, S3031, CC1-1-3-41, HD 328-1, FFS16, CISA 21, PA 405, RG 255, , RG 260, LD 805, LD 713, AKA 9410, DLSA 17, G. Cot 19, AH 11, AKA 210, A KA 315, AKA 9623-2, HD 453, FFS21,, PSRV 12489, CINA 347, S7060, FFS 17, HD 503, HD 543, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 549, and HD 556
Dense (9)	31	HD 39 2, BHO 5 VIII, BH 41,BH 102, FFS4, D 43-21, EB 31-1, HD 6, HD 10, N-W-1, PL 735-1, FFS7, DS-5, DS 5-1, AC 33, FFS11, FFS8, JL 60, Vira 6, AC3377, FFS13, Sanguinum, HD 328, LD 814, HD 418, HD 107, S6799, HD521, FFS18, HD 542, and HD 555

4.1.5 Leaf nectaries

On the basis of leaf nectaries, 153 germplasm of *desi* cotton were characterized into two categories *i.e.,* absent and present. Out of total, 25 genotypes were found in which the leaf nectaries was absent and 128 genotypes were having leaf nectaries. The classification of *desi* cotton genotypes have been presented in Table 4.5 and plate 4.5.

4.1.6 Petiole pigmentation

On the basis of leaf colour *desi* cotton genotypes were categorized into two categories *i.e.,* absent and present. In 136 genotypes, petiole pigmentation was absent and only 17 genotypes were having petiole pigmentation. The classifications on the basis of petiole pigmentation have been presented in Table 4.6 and plate 4.6.

Table 4.5: Classification of 153 *desi* cotton genotypes on the basis of leaf nectaries

Code	Genotype Number	Genotypes
Absent (1)	25	S 302, FFS1, HD 514, HD 372, HD 408, FFS2, HD 379, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, DC-93, DC 108, EB 31-1, G 20 and GOV 6
Present (9)	128	HD 404, , FFS3, BH 41, D 462-1-1G 23, Gao-16 LB VI, Garovilli, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, CINA 347, S7060, PSRSV 12516, S7060 A, S6071, S6799, HD521, HD 524, FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD432, HD 324, HD 123, HD 541, HD 545, HD 548, HD 549, HD 555 and HD 556

Table 4.6: Classification of 153 *desi* cotton genotypes on the basis of petiole pigmentaion

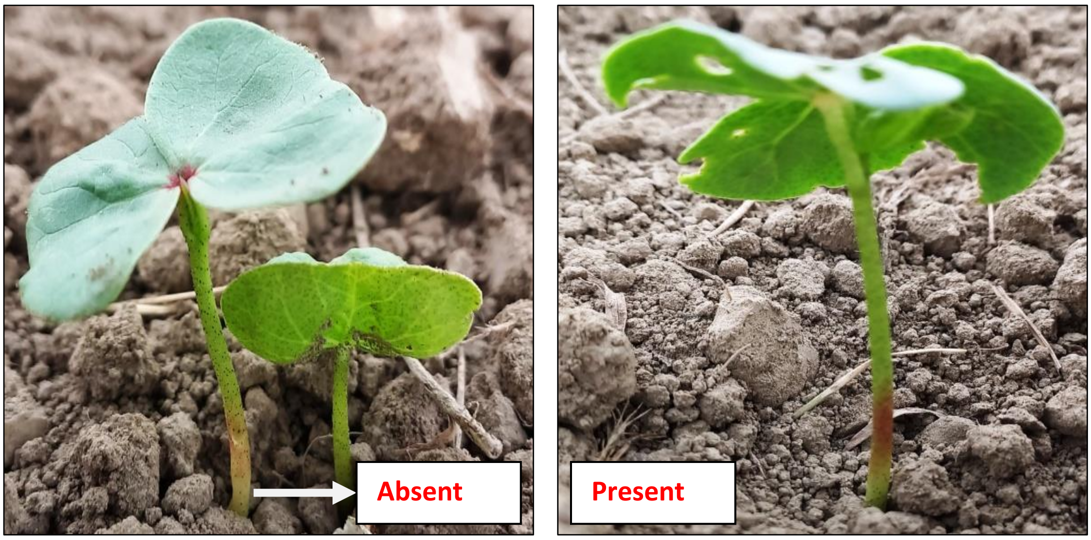
Code	Genotype Number	Genotypes
Absent (1)	136	S 302, FFS1,HD 404, HD 514, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, BHO 5 VIII, BH 41, BH 92, FFS4, BPS, FFS5, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 10, HD 3, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, PSRSV 12516, S7060 A, S6071, S6799, HD521, HD 524, FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549, HD 555, HD 432, HD 123 and HD 556
Present (9)	17	HD 324, HD 372, HD 392, BH 30, BH 102, D 43-21, HD 6, HD 20, S2204, DS 1, D 462-1-1 P5, AC3269, RG 260, LD 805, LD 713, CINA 347 and S7060

4.1.7 Leaf shape

On the basis of leaf shape, *desi* cotton genotypes were classified as okra, semi-okra and normal type. Eight genotypes were under the normal category and 145 genotypes were having okra type of leaf while no any genotype was found in category semi-okra type of leaf. The different group of genotypes were presented in Table 4.7 and plate 4.7.

Table 4.7: Classification of 153 *desi* cotton genotypes on the basis of leaf shape

Code	**Genotype Number**	**Genotypes**
Normal (1)	8	FFS1, EB 31-1, HD 6, HD 20, S2204, S479, AC3212, and AC 41
Okra (3)	145	HD 404, HD 514, HD 408, FFS2, FFS3, B 2-16-2, B-4, BHO 5 VIII, BH 30, BH 92, FFS4, FFS5, D 43-21, DC 108, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H HD 3, PL 735-1, RA 1, 35/5 B, FFS 6, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, Malvi 12, P 485, P 489, Jubli, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, CINA 347, S7060, PSRSV 12516, S6071, S6799, HD521, HD 524, FFS 17, FFS18, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549, HD 555 and HD 556, S 302, HD 372, HD 379, Arlano, HD 392, BH 41, BH 102, BPS, D 48-154-1, D 462-1-1, DC-93, 476-5, HD 10, N-W-1, PL 735, Y-1, P 248, JL 60, M 53070, AC3376, AC3377, HD 432, HD 324, HD 123, AC S 3028, S7060 A, and HD 503
Semi-okra (6)	0	-



(a) (b)

Plate 4.1 Hypocotyle pigmentation: (a) Absent (b) Present

(a) Light Green **(b) Green**

Plate 4.2 Leaf colour: (a) Light Green (b) Green

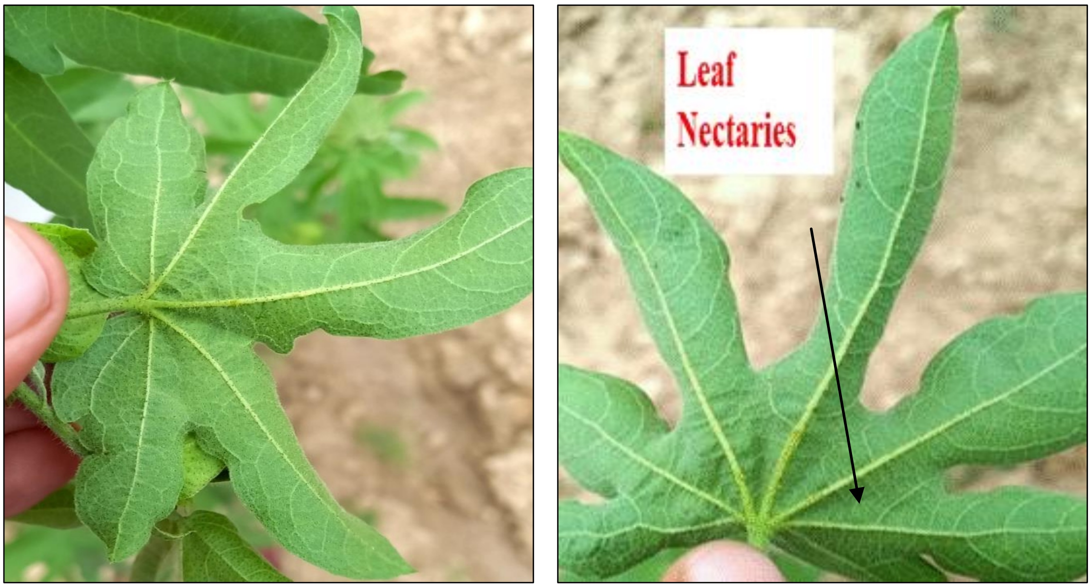
(a) Dense (b) Sparse (c) Medium

Plate 4.3 Stem Hairiness: (a) Dense (b) Sparse (c) Medium

(a) Sparse **(b) Medium**

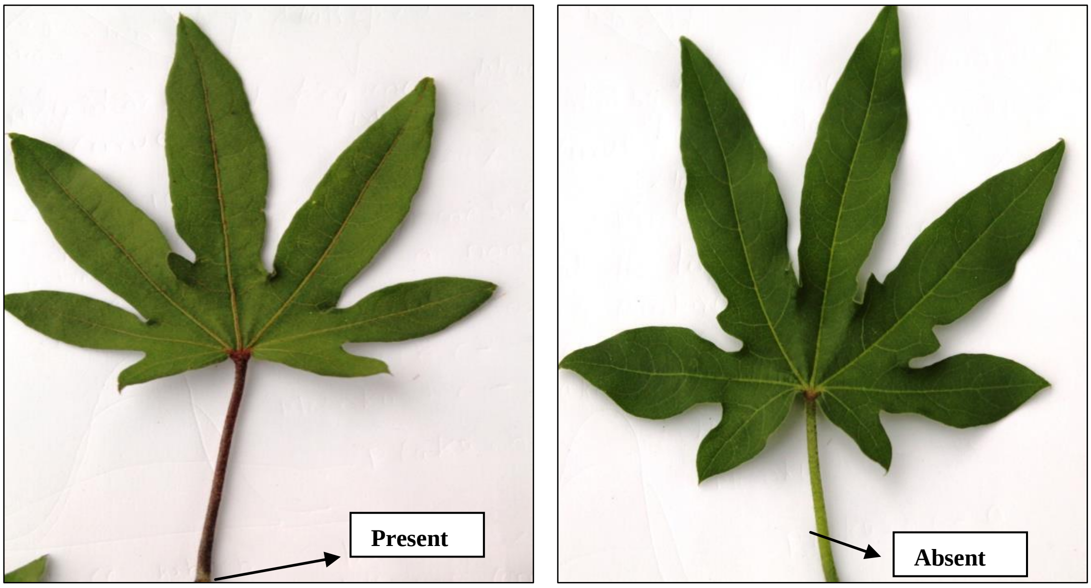
(c) Dense

Plate 4.4 Leaf Pubescence: (a) Sparse (b) Medium (c) Dense



(a) Absent **(b) Present**

Plate 4.5 Leaf Nectaries: (a) Absent (b) Present



(a) Present **(b) Absent**

Plate 4.6 Petiole Pigmentaion

Complete plant view of Palmate type leaf plant

Complete Plant view of Okra type leaf plant

Plate 4.7 Leaf Shape: (a) Palmate type (b) Okra type

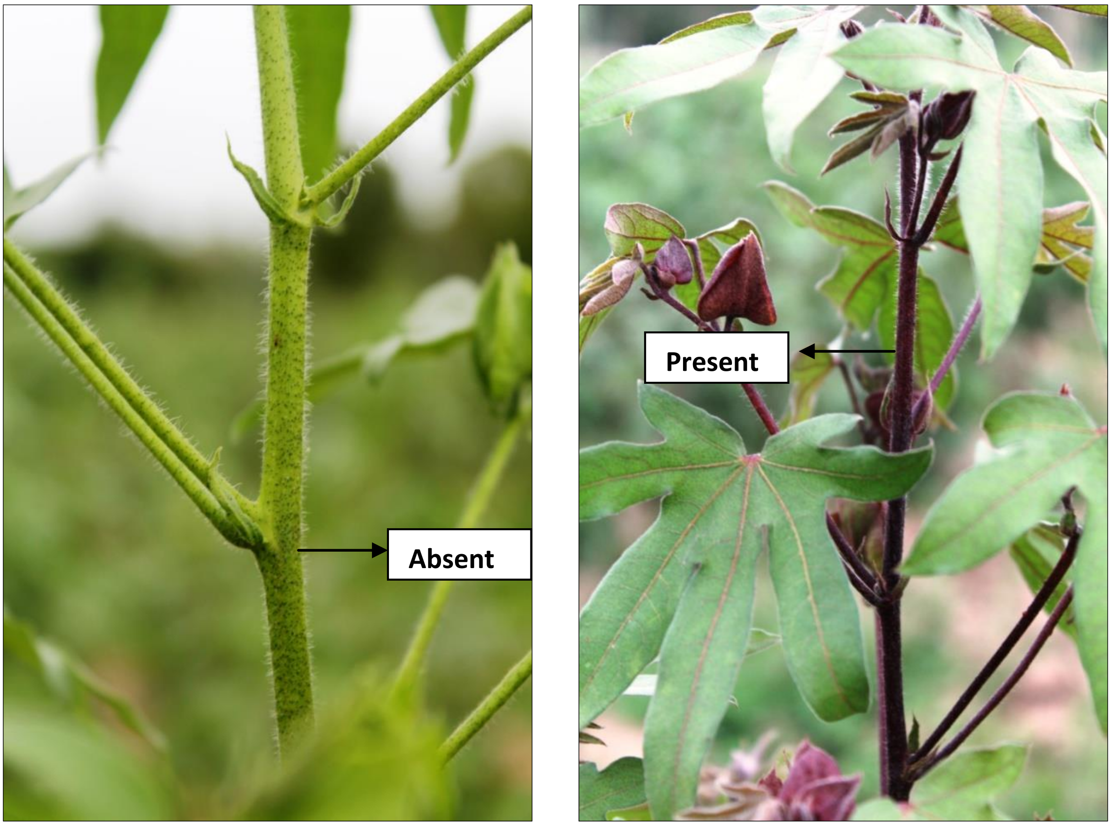


Plate 4.8 Stem pigmentation: (a) Absent (b) Present

4.1.8 Stem pigmentation

On the basis of stem pigmentation, 153 genotypes of *desi* cotton were classified into two categories *i.e.,* absent and present. Only 17 genotypes were having stem pigmentation and in 136 genotypes the stem pigmentation was absent as represented in Table 4.8 and plate 4.8.

4.1.9 Flower petal colour

On the basis of flower petal colour, 153 genotypes of *desi* cotton were classified into six categories *i.e.*, white, pink, red, yellow, cream and variegated. Among 153 genotypes, 76 genotypes were white, 10 cream, 49 yellow, 14 pink and one genotype have red flower petal colour. None of the genotype was found in category of variegated flower petal colour. The classifications of different groups were represented in Table 4.9 and plate 4.9.

4.1.10 Flower petal spot

On the basis of flower petal spot, 153 genotypes of *desi* cotton were classified into two categories *i.e.,* absent and present. All the 153 genotypes were having flower petal spot. No any genotype was found in which flower petal spot was absent. Various groups of the genotypes on the basis of flower petal spot were represented in the Table 4.10 and plate 4.10.

Table 4.8: Classification of 153 *desi* cotton genotypes on the basis of stem pigmentation

Code	Genotype Number	Genotypes
Absent (1)	136	S 302, FFS1,HD 404, HD 514, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, BHO 5 VIII, BH 41, BH 92, FFS4, BPS, FFS5, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 10, HD 3, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, PSRSV 12516, S7060 A, S6071, S6799, HD521, HD 524, FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549, HD 555, HD 432, HD 123 and HD 556
Present (9)	17	HD324, HD 372, HD 392, BH 30, BH 102, D 43-21, HD 6, HD 20, S2204, DS 1, D 462-1-1 P5, AC3269, RG 260, LD 805, LD 713, CINA 347 and S7060

Table 4.9: Classification of 153 *desi* cotton genotypes on the basis of flower petal colour

Code	Genotype Number	Genotypes
White (1)	76	S 302, FFS1, HD 408, HD 379, Arlano, FFS3, BHO 5 VIII, B 2-16-2, BH 92, BH 41, BH 102, FFS4, D 462-1-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, HD 10, HD 3, PL 735, PL 735-1, RA 1, 35/5 B, DS-5, DS 5-1, S5278, H 52 -519, AC-8, FFS8, P 489, AC3376, AC3212, AC3377, AC3269, AC3233, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC 3347, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, LD 814, HD 418, CISA 6, AKA 9623-2, RG 395, HD 453, FFS21, PSRV 12489, PSRSV 12516, S6071, S6799, HD521, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 545, HD 548, HD 555 and HD 556
Cream (2)	11	HD 404, HD 514, N-W-1, FFS9, H 248, H 174, HD 107, S7060, HD 503, HD 123 and HD 541
Yellow (3)	50	FFS2, B-4, BPS, FFS5, DC-93, DC 108, EB 31-1, H 476-5, Y-1, FFS 6, S2446, FFS7, S351, S479, S479-1, AC 33, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, JL 60, M 53070, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3252, AC S 3028, HD 369, S3031, CC1-1-3-41, FFS14, AKA 9410, DLSA 17, G. Cot 19, AH 11, AKA 210, AKA 315, S7060 A, HD 524, FFS 17, FFS18, HD432 and HD 549
Pink (4)	15	HD 372, HD 392, BH 30, D 43-21, D 48-154-1, HD 6, HD 20, DS 1, Jubli, RG 255, RG 260, LD 805, LD 713, HD 324 and CINA 347
Red (5)	1	FFS12
Variegated (6)	0	-

Table 4.10: Classification of 153 *desi* cotton genotypes on the basis of flower petal spot

Code	Genotype Number	Genotypes
Absent (1)	-	-
Present (9)	153	S 302, FFS1,HD 404, HD 514, HD 372, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-RA 1, Y-1, 35/5 B, FFS 6, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, CINA 347, S7060, PSRSV 12516, S7060 A, S6071, S6799, HD521, HD 524, FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549, HD 555, HD 432, HD 324, HD 123 and HD 556

(a) **Red**

(b) White

(c) Yellow

(d) Pink **(e) Cream**

Plate 4.9 Flower Petal colour: (a) Red (b) White (c) Yellow (d) Pink (e) Cream

Plate 4.10 Flower petal spot: Present

(a) (b)

Plate 4.11 Flower stigma: (a) Exerted (b) Embeded

(a) (b)

Plate 4.12 Anther filament colouration: (a) Absent (b) Present

4.1.11 Flower stigma

On the basis of flower stigma, 153 *desi* cotton genotypes were classified into two categories *i.e.,* embedded and exerted. Five genotypes were having embedded stigma in flower and 148 genotypes were having exerted stigma. The classifications on the basis of flower stigma were presented in Table 4.11 and plate 4.11.

4.1.12 Anther filament colouration

On the basis of anther filament colouration, *desi* cotton genotypes were classified into absent and present category. One thirty-four genotypes had no any colouration on anther filament while 19 genotypes had anther filament colouration. The classifications of different categories were represented in Table 4.12 and plate 4.12.

Table 4.11: Classification of 153 *desi* cotton genotypes on the basis of flower stigma

Code	Genotype Number	Genotypes
Embeded (3)	5	H 460, Vira 6, FFS11, D 462-1-1 P3 and LD 713
Exerted (5)	148	S 302, FFS1,HD 404, HD 514, HD 372, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, LD 327, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, CINA 347, S7060, PSRSV 12516, S7060 A, S6071, S6799, HD521, HD 524, FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 432, HD 324, HD 123 HD 535, HD 541, HD 545, HD 548, HD 549, HD 555 and HD 556

Table 4.12: Classification of 153 *desi* cotton genotypes on the basis of anther filament colouration

Code	Genotype Number	Genotypes
Absent (1)	134	S 302, FFS1,HD 404, HD 514, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, P 248, JL 60, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3233, AC3252, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, LD 814, AKA 9410, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, PSRSV 12516, S7060 A, S6071, S6799, HD521, HD 524, FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 432HD 123, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549, HD 555 and HD 556
Present (9)	19	HD 372, HD 392, RG 255, RG 260, LD 805, LD 713, CINA 347, S7060, AC 41, Malvi 12, HD 324, DLSA 17, P 485, P 489, M 53070, Jubli, H 248, AC3269 and FFS12

4.1.13 Pollen colour

On the basis of pollen colour *desi* cotton genotypes were classified into two categories *i.e.,* cream and yellow. 134 *desi* cotton genotypes were found in which pollen colour is cream while 19 genotypes showed yellow coloured pollen as represented in Table 4.13 and plate 4.13.

Table 4.13: Classification of 153 *desi* cotton genotypes on the basis of pollen colour

Code	**Genotype Number**	**Genotypes**
Cream (1)	134	S 302, FFS1,HD 404, HD 514, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, P 248, JL 60, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3233, AC3252, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, LD 814, AKA 9410, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, PSRSV 12516, S7060 A, S6071, S6799, HD521, HD 524, FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 432HD 123, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549, HD 555 and HD 556
Yellow (9)	19	HD 372, HD 392, RG 255, RG 260, LD 805, LD 713, CINA 347, S7060, AC 41, Malvi 12, HD 324, DLSA 17, P 485, P 489, M 53070, Jubli, H 248, AC3269 and FFS12

4.1.14 Boll colour

On the basis of boll colour *desi* cotton genotypes were classified into two categories *i.e.,* green and red. One thirty eight *desi* cotton genotypes were found in which boll colour is green while 15 genotypes showed red coloured boll as represented in Table 4.14 and plate 4.13.

4.1.15 Boll shape

On the basis of boll shape, out of 153 *desi* cotton genotypes, 23 genotypes were having round bolls, 67 have ovate and 63 were having elliptical type boll shape. The classifications of different groups were represented in Table 4.15and plate 4.14.

Table 4.14: Classification of 153 *desi* cotton genotypes on the basis of boll colour

Code	Genotype Number	Genotypes
Green (3)	138	S 302, FFS1,HD 404, HD 514, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, BHO 5 VIII, BH 30, BH 41, BH 92, FFS4, BPS, FFS5, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS13, NGPA, 1-9-1, FFS14, HD 328, HD 328, FFS15, CISA 21, PA 405, CINA 329, FFS19, LD 814, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, PSRSV 12516, S7060 A, S6071, S6799, FFS 18, FFS17, HD 521, HD 524, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 432, HD 123 HD 541, HD 545, HD 548, HD 549, HD 555 and HD 556
Red (5)	15	HD 372, HD 324, HD 392, BH 102, D 43-21, DS 1, D 462-1-1 P5, Jubli, AC3269, RG 255, RG 260, LD 805, LD 713, CINA 347 and S7060

Table 4.15: Classification of 153 *desi* cotton genotypes on the basis of boll shape

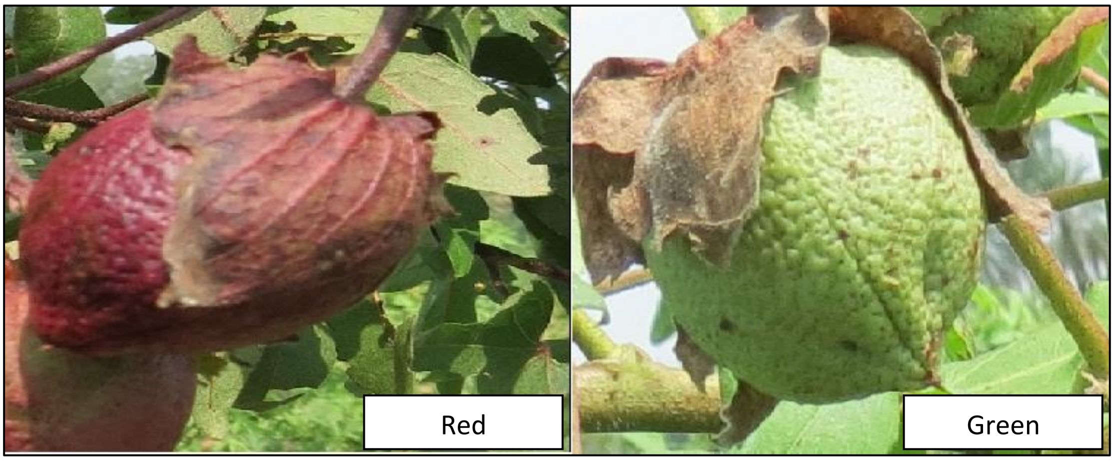
Code	Genotype Number	Genotypes
Round (3)	23	HD 379, Arlano, D 462-1-1, RA 1, AC-8, FFS8, FFS9, DS 1, DS-5, S5278, AC 41, P 485, P 489, Petaloidy, AC3377, NGPA 1-9-1, HD 328, HD 328, PA 405, RG 260, CINA 347, S6799 and HD 544
Ovate (5)	67	S 302, HD 514, FFS2, B 2-16-2, B-4, HD 392, BH 30, BH 41, D 48-154-1, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, 35/5 B, AC 33, S479, FFS7, DS 5-1, 0S479, D 462-1-1 P3, D 462-1-1 P4, JL 60, Jubli, H 460, 79/Lohit, AC3233, AC3252, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC 3347, S3031, FFS16, CISA 21, FFS19, RG 255, LD 805, HD 418, FFS21,, HD 453, S7060, FFS18, HD 524, HD 432, HD 324, HD 123, HD 503, HD 542, HD 535, HD 545, HD 548, HD 549, and HD 556
Elliptic (7)	63	FFS1,HD 404, HD 372, HD 408, FFS3, BHO 5 VIII, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, DC-93, DC 108, Y-1, FFS 6, S2204, S2446, S351, S479-1, H 52 -519, FFS10, FFS11, D 462-1-1 P5, Malvi 12, P 248, M 53070, H 248, H 174, LD 327, Vira 6. AC3376, AC3212, AC3269, FFS12, DS 5-2, DS 5-3, AC S 3028, HD 369, CC1-1-3-41, FFS14, FFS15, CINA 329, LD 814, LD 713, AKA 9410, DLSA 17, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, PSRV 12489, PSRSV 12516, S7060 A, S6071, FFS 17, HD 521, HD 543, HD 550, HD 551, HD 541 and HD 555

4.1.16 Boll surface

On the basis of boll surface, *desi* cotton genotypes were categorized into two groups *i.e.,* smooth and pitted. In 123 genotypes pitted type bolls were present while in 30 genotypes were having smooth type boll. Classification of boll surface was represented into Table 4.16 and plate 4.15.

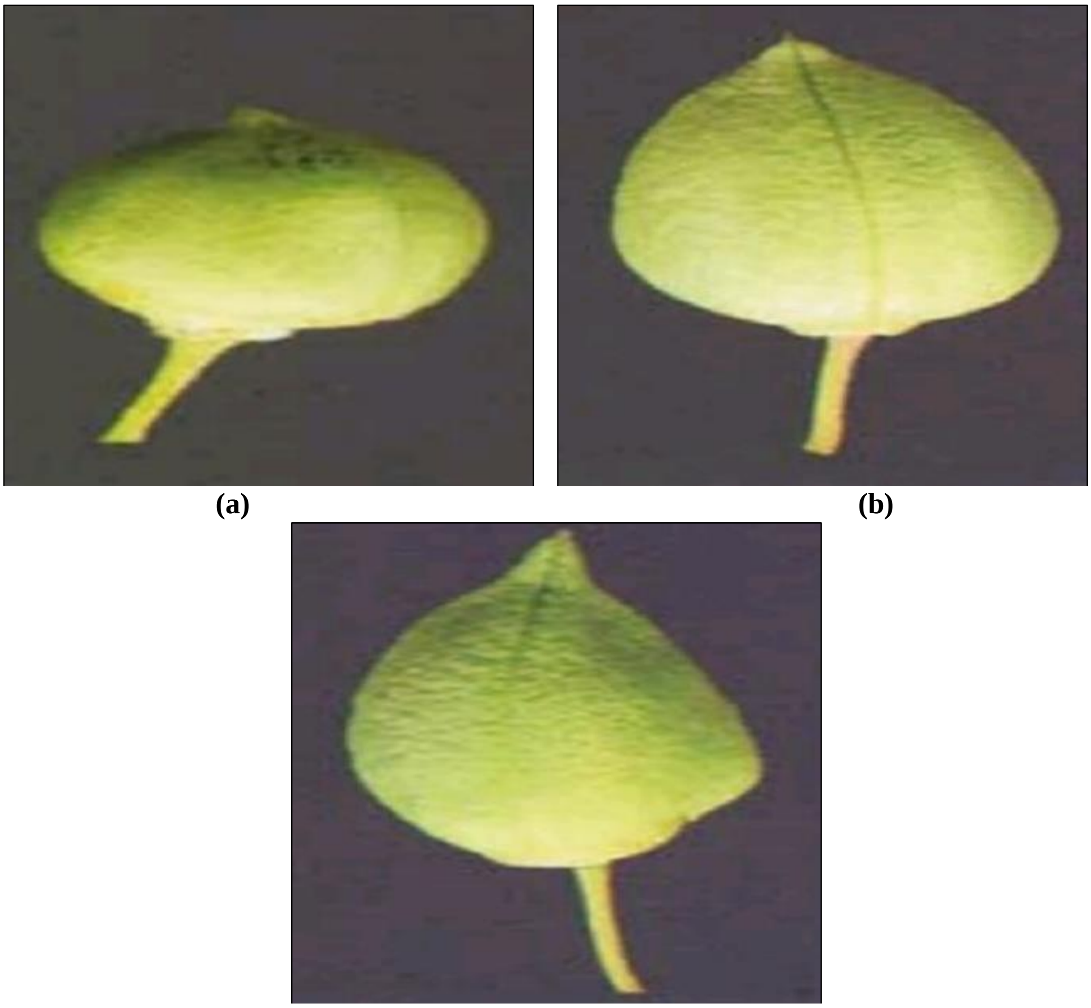
Table 4.16: Classification of 153 *desi* cotton genotypes on the basis of boll surface

Code	Genotype Number	Genotypes
Smooth (1)	30	PL 735-1, 35/5 B, FFS 6, FFS7, DS-5, S351, S479, S479-1, DS 1, FFS8, FFS9, D 462-1-1 P3, P 485, P 489, H 248, H 460, LD 327, AC3377, AC3269, FFS13, , HD 369, AC 3347, S3031, CC1-1-3-41, PA 405, CISA 6, AKA 315, FFS21, HD 542 and HD 535
Pitted (9)	123	S 302, FFS1,HD 404, HD 514, HD 372, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, RA 1, Y-1, S2204, S2446, DS 5-1, S5278, AC 33, H 52 -519, AC-8, FFS10, FFS11, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, JL 60, M 53070, Jubli, H 174, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028NGPA, 1-9-1, FFS14, HD 328, HD 328, FFS15, CISA 21, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, AH 11, AKA 210, AKA 9623-2, RG 395, HD 453, PSRV 12489, CINA 347, S7060, PSRSV 12516, S7060 A, S6071, S6799, FFS 18, FFS17, HD 521, HD 524, HD 503, HD 543, HD 550, HD 324, HD 123HD 551, HD 544, HD 541, HD 545, HD 548, HD 549, HD 555 and HD 556



(a) (b)

Plate 4.13 Boll colour: (a) Red (b) Green



(a) (b)

(c)

Plate 4.14 Boll shape: (a) Round (b) Ovate (c) Eliptical

(a) (b)

Plate 4.15 Boll Surface: (a) Smooth (b) Pitted

(a) (b)

Plate 4.15 Boll: Prominence of tip: (a) Pointed (b) Blunt

(a) (b)

Plate 4.16 Boll: opening: (a) Semi open (b) Open

4.1.17: Boll: Prominence of tip

On the basis of prominence of boll tip, *desi* cotton genotypes were classified into blunt and pointed types of boll. Among the *desi* cotton 19 genotypes were having blunt bolls and 134 genotypes were having pointed types bolls. The classifications of different groups were presented in Table 4.17 and plate 4.16.

4.1.18 Boll opening

When roughly 20% of the bolls were open during the first picking, the opening of the boll was noted. On the basis of boll opening, genotypes were categorized into two groups *i.e.*, semi-open and open. When a boll develops cracks but does not fully open, the condition is known as a semi-open boll. In the current study, 89 genotypes exhibited open-type boll opening, while 65 genotypes exhibited semi-open type. Table 4.17 and plate 4.17 represents the grouping of genotypes based on the opening of the boll.

Table 4.17: Classification of 153 *desi* cotton genotypes on the basis of boll prominence of tip

Code	Genotype Number	Genotypes
Blunt (1)	19	S 302, HD 408, FFS2, B 2-16-2, G 23, DS-5, FFS8, FFS9, D 462-1-1 P5, P 485, P 489, H 460, FFS13, HD 418, HD 453, S7060 A, S6071, S6799 and HD 555
Pointed (9)	134	FFS1,HD 404, HD 514, HD 372, HD 379, FFS3, Arlano, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2204, S2446, FFS7, DS 5-1, S5278, S351, S479, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, AC 41, Malvi 12, P 248, JL 60, M 53070, Jubli, H 248, H 174, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA, 1-9-1, FFS14, HD 328, HD 328, FFS15, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, AKA 9410, DLSA 17, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, FFS21,, PSRV 12489, CINA 347, S7060, PSRSV 12516, FFS 18, FFS17, HD 521, HD 524, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549, HD 324, HD 123and HD 556

Table 4.18: Classification of 153 desi cotton genotypes on the basis of boll opening

Code	Genotype Number	Genotypes
Open (3)	88	HD 20, HD 404, N-W-1, PL Y-1, 35/5 B, S479, H 174, , 79/Lohit, AC3269, PA 405, AKA 9410, HD 514, , HD 408, FFS2, BH 92, BH 102, Garovilli, GOV 6, H 1, H 476-5, , PL 735, PL 735-1, RA 1, FFS 6, S2204, DS 5-1, S5278, S351, DS 1, AC 33, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, H 460, Vira 6, Petaloidy, AC3212, AC3377, AC3233, AC3252, DS 5-4, Sanguinum, AC S 3028, AC 3347, CC1-1-3-41, FFS14, NGPA 1-9-1, HD 328, FFS16, CISA 21, FFS19, RG 255, RG 260, LD 805, DLSA 17, HD 418, AKA 210, AKA 315, AKA 9623-2, G. Cot 19, CISA 6, HD 453, PSRV 12489, PSRSV 12516, S7060 A, S6799, HD 521, FFS 17, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 545, HD 324, HD 123 and HD 548
Semi open (5)	65	S 302, FFS1, HD 379, FFS3, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, HD 372, HD 6, HD 10, HD 3, S2446, FFS7, DS-5, S479-1, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, P 489, JL 60, M 53070, Jubli, H 248, LD 327, AC3376, FFS12, DS 5-2, DS 5-3, FFS13, 30822 BLL, HD 369, S3031, FFS15, HD 328, CINA 329, LD 814, LD 713, AH 11, HD 107, RG 395, FFS21, CINA 347, S7060, S6071, HD 524, FFS18, HD 541, HD 549, HD 555 and HD 556

4.1.19 Seed fuzz density

Seeds were first separated from lint with the process called ginning. After separation of seeds they had hair like structures on seed coat called as fuzz. The quantity of this fuzz present on the seed coat is termed as seed fuzz density and it was recorded after ginning. Density of fuzz on seed is grouped in three categories *viz*. sparse, medium and dense. Most of the genotypes were under dense category *i.e.,*146 and other 7 showed medium fuzz density. The categorization of genotypes on the basis of seed fuzz density is presented in Table 4.19 and plate 4.18.

Table 4.19: Classification of 153 *desi* cotton genotypes on the basis of seed fuzz

Code	Genotype Number	Genotypes
Medium (3)	7	FFS7, PL 735, S2446, S479, FFS14, CC1-1-3-41 and FFS18
Dense (5)	146	S 302, FFS1,HD 404, HD 514, HD 372, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2204, DS-5, DS 5-1, S5278, S351, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21,, PSRV 12489, CINA 347, S7060, PSRSV 12516, S7060 A, S6071, S6799, HD521, HD 524, FFS 17, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549, HD 555, HD 324, HD 123 and HD 556

4.1.20 Seed fuzz colour

Variation is not only present in seed fuzz density but also the colour of the fuzz also varies. The colour of seed fuzz found in *desi* cotton genus were; grey and brown. The fuzz colour was noticed grey in all the genotypes in present investigation except for genotype S7060A which was brown in colour. The colour of seed fuzz was recorded after final harvest and ginning. The classification of different seed fuzz colour is presented in Table 4.20.

4.1.21 Fibre colour

Fibre may have colour variation like grey, green and brown. Fibre is the extension of seed coat which is made up of cellulose. In present research, 152 genotypes had grey colour fibre and genotype S7060 A had brown colour fibre. It was recorded at the time final picking. The classification and different types of fibre colour were represented in Table 4.21 and plate 4.19.

Table 4.20: Classification of 153 *desi* cotton genotypes on the basis of seed fuzz colour

Code	Genotype Number	Genotypes
Grey (1)	152	S 302, FFS1,HD 404, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, DLSA 17, HD 418, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, FFS21,, PSRV 12489, CINA 347, S7060, PSRSV 12516, S6071, S6799, HD521FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 548, , HD 555, HD 324, HD 123 16 LB VI, FFS9, Vira 6, 79/Lohit, FFS14, AKA 9410, G. Cot 19, HD 453, , HD 524 and HD 549 and HD 556
Brown (2)	1	S7060 A

Table 4.21: Classification of 153 *desi* cotton genotypes on the basis of fibre colour

Code	Genotype Number	Genotypes
Grey (1)	152	S 302, FFS1,HD 404, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, DLSA 17, HD 418, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, FFS21,, PSRV 12489, CINA 347, S7060, PSRSV 12516, S6071, S6799, HD521FFS 17, FFS18, HD 503, HD 543, HD 542, HD 550, HD 551, HD 544, HD 535, HD 541, HD 545, HD 548, , HD 555, HD 324, HD 123 16 LB VI, FFS9, Vira 6, 79/Lohit, FFS14, AKA 9410, G. Cot 19, HD 453, , HD 524 and HD 549 and HD 556
Green (3)	0	-
Brown (4)	1	S7060 A

4.1.22 Days to first flower

Days to first flower was noted when 50% of plants with at least one open flower. On the basis of days to first flower *desi* cotton genotypes were classified into early, medium and late category. Among 153 genotypes, 34 were early and 119 genotypes were in medium category. No any genotype exhibited late flowering. The classification of different groups is described in the Table 4.22.

Table 4.22: Classification of 153 *desi* cotton genotypes on the basis of days to first flower (50% of plants with at least one open flower)

Code	Genotype Number	Genotypes
Early (<50) (3)	34	FFS6, S479-1, P 485, 79/Lohit, NGPA 1-9-1, FFS15, FFS16, PA 405, RG 255, LD 814, LD 805, LD 713, AKA 9410, HD 418, HD 107, CISA 6, AKA 210, AKA 315, AKA 9623-2, HD 453, FFS21, CINA 347, S7060, PSRSV 1516, HD 521, HD 524, FFS17, FFS18, HD 543, HD 544, HD 535, HD 541, and HD 548
Medium (50-60) (5)	119	S 302, FFS1, HD 404, HD 514, HD 372, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, HD 328, HD 328-1, CISA 21, CINA 329, FFS19, RG 260, DLSA 17, G. Cot 19, AH 11, RG 395, PSRV 12489, S7060 A, S6071, S6799, HD 503, HD 542 , HD 550 , HD 551, , HD 545, HD 549, HD 555, HD 556, HD 432, HD 324 and HD 123
Late (>60) (7)	-	

4.1.23 Seed Index

Seed index is referred as 100 seed weight of cotton seed measured in grams. It is divided into various groups *viz.* very small when 100 seed weight is less than 3g, small (3-5g), medium (5.1-7g), bold (7.1-9g) and very bold (more than 9g). Out of 153 genotypes no any genotype fell into very small group, 88 genotypes in small group and 65under medium group. No genotypes were found with bold or very bold type seeds, the same has been shown in Table 4.23, where genotypes have been characterized on the basis of seed index.

Table 4.23: Classification of 153 *desi* cotton genotypes on the basis of seed index

Code	Genotype Number	Genotypes
Very small (<3.0) (1)	-	
Small (3.0-5.0) (3)	88	S 302, HD 404, HD 514, HD 408, HD 379, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, FFS5, D 43-21, DC-93, DC 108, EB 31-1, G 20, GOV 6, Gao-16 LB VI, HD 6, HD 3, HD 20, PL 735, RA 1, 35/5 B, S2204, S2446, DS-5, DS 5-1, S5278, S351, S479, S479-1, , AC 33, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, JL 60, H 24879/Lohit DS 5-2, DS 5-3, Sanguinum, AC S 3028, HD 369, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, HD 328, FFS16, CINA 329, RG 255, LD 814, LD 805, LD 713, AKA 9410, DLSA 17, HD 418, CISA 6, AH 11, AKA 315, RG 395, HD 453, PSRV 12489, CINA 347, S7060, PSRSV 12516, S7060 A, S6071, S6799, FFS18, HD 542, HD 544 , HD 535, HD 541, HD 545, HD 548, HD 549, HD 555, HD 556, HD 432, HD 324 and HD 123
Medium (5.1-7.0) (5)	65	FFS1, HD 372, FFS2, FFS3, BH 41, BH 92, BH 102, FFS4, BPS, D 48-154-1, D 462-1-1, G 23,Garovilli, H 1, H 476-5, HD 10, N-W-1, PL 735-1, Y-1, FFS6, FFS7, DS 1, H 52 -519, AC-8, FFS8, FFS9, FFS10, P 485, P 489, M 53070, Jubli, H 174, H 460, LD 327, Vira 6, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5, FFS13, 30822 BLL, AC 3347, FFS15, HD 328-1, CISA 21, PA 405, FFS19, RG 260, G. Cot 19, HD 107, AKA 210, AKA 9623-2, FFS21, HD 521, HD 524, FFS17, , HD 503, HD 543 and HD 550
Bold (7.1-9.0) (7)	-	
Very bold (>9.0) (9)	-	

4.1.24 Boll weight (g)

Boll weight was categorized on the basis of a single boll weight in grams. The categories made were; small, medium and large on the basis of boll weight. Five genotypes fall under small category with weight of boll being less than 2 gram. Ninty five genotypes had boll weight between 2-3 g and come under medium category. Fifty three genotypes had boll weight more than 3 gram and fall in large category. Characterization of genotypes based on boll weight has been shown in Table 4.24.

4.1.25 Ginning out turn (%)

Ginning out turn is the total amount of lint in gram extracted. The percentage of lint (a white, fluffy fibre) recovered from a yield of 100 grams of seed cotton is known as ginning percent. It has been classified as very low (<30%), low (31-32%), medium (33–34), high (35–36), and very high (more than 36). Only two genotypes (EB 31-1, and AC3212) had very low ginning percentages, eight genotypes had low ginning percentages, thirty belonged to the medium group, thirty five had high ginning percentage and the majority of genotypes, 95 genotypes had recovered lint greater than 36%, placing them in the very high group. Table 4.25 represents the grouping of genotypes based on various ginning % groups.

Table 4.24: Classification of 153 *desi* cotton genotypes on the basis of boll weight (g)

Code	**Genotype Number**	**Genotypes**
Small (<2) (1)	5	FFS1, D 48-154-1, DC 108, DS 5-1 and S479
Medium (2-3) (3)	95	S 302,HD 404, HD 514, HD 372, HD 408, FFS2, HD 379, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 41, BH 102, D 462-1-1, DC-93, EB 31-1, G 23, Gao-16 LB VI, Garovilli, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS6, S2204, DS-5, S5278, S351, S479-1, DS 1, AC 33, H 52 -519, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, DS 5, Sanguinum,FFS14,HD 328-1, FFS16, PA 405, CINA 329, FFS19, RG 260, LD 805, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, RG 395, PSRV 12489, S6071, HD 524, FFS17, HD 543, HD 542 , HD 548, HD 555, HD 556, HD 432, HD 324 and HD 123
Large (>3) (5)	53	FFS3, BH 30, BH 92, FFS4, BPS, FFS5, D 43-21, G 20, GOV 6, S2446, FFS7, AC-8, FFS8, FFS9, AC3252, FFS12, DS 5-2, DS 5-3, FFS13, 30822 BLL, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, NGPA 1-9-1, FFS15, HD 328, CISA 21, RG 255, LD 814, LD 713, AKA 9410, AKA 315, AKA 9623-2, HD 453, FFS21, CINA 347, S7060, PSRSV 12516, S7060 A, S6799, HD 521, FFS18, HD 503, HD 550 , HD 551, HD 544 , HD 535, HD 541, HD 545, HD 549

Table 4.25: Classification of 153 *desi* cotton genotypes on the basis of ginning out turn (%)

Code	Genotype Number	Genotypes
Very low (<30) (1)	2	EB 31-1 and AC3212
Low (31-32) (3)	8	G 20, DC 108, N-W-1, 35/5 B, H 460, AC3233, LD 805 and HD 555
Medium (33-34) (5)	13	D 48-154-1, HD 10, HD 3, PL 735-1, FFS7, DS 5-1, 79/Lohit, P 489, DS 5-2, DLSA 17, G. Cot 19, PSRV 12489 and HD 379
High (35-36) (7)	35	HD 514, Arlano, BH 92, BH 102, FFS5, D 43-21, DC-93, G 23, Gao-16 LB VI, H 1, H 476-5, PL 735, RA 1, Y-1, HD 20, S5278, S479, AC 41, Malvi 12, JL 60, Petaloidy, AC3376, AC3269, FFS12, DS 5, FFS13, NGPA 1-9-1, CISA 21, RG 260, HD 107, RG 395, PSRSV 12516, S6799, HD 521, HD 543 ,HD 551
Very high (>37) (9)	95	S 302, FFS1, HD 404,HD 372, HD 408, FFS2, FFS3, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, FFS4, BPS, D 462-1-1, Garovilli, GOV 6, HD 6, FFS6, S2204, S2446, DS-5, S351, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, P 248, P 485, M 53070, Jubli, H 248, H 174, LD 327, Vira 6, AC3377, AC3252, DS 5-3, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, FFS15, HD 328, HD 328-1, FFS16, PA 405, CINA 329, FFS19, RG 255, LD 814, LD 713, AKA 9410, HD 418, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, HD 453, FFS21, CINA 347, S7060, S7060 A, S6071, HD 524, FFS17, FFS18, HD 503, HD 542 , HD 550 , HD 544 , HD 535, HD 541, HD 545, HD 548, HD 549, HD 556, HD 432, HD 324 and HD 123

4.1.26 Fibre length (2.5% span length) (mm)

The distance spanned by 2.5% of the fibre in the sample being tested when the fibre strands are parallelized and randomly dispersed is referred to as the 2.5% fibre span length and is measured in millimetres. It is divided into four length categories: short (20mm), medium (20.5-24.5mm), medium long (27.5-32 mm) and long (32.5 mm). The length of the fibre increases as the 2.5% fibre travels a greater distance. Only 43 genotypes had short fibre length, 97 genotypes had medium long fibre length, and 13 genotypes had long fibre length, as represented in Table 4.26.

Table 4.26: Classification of 153 *desi* cotton genotypes on the basis of fibre: length (2.5% span Length) (mm)

Code	Genotype Number	Genotypes
Short (1)	43	S 302, FFS1, FFS3, HD 392, D 462-1-1, GOV 6, H 1, HD 10, DS 5-1, S5278, DS 1, P 485, P 489, Jubli, H 460, AC3269, DS 5-3, DS 5, FFS13, 30822 BLL, Sanguinum, AC 3347, NGPA 1-9-1, FFS15, FFS16, PA 405, LD 805, CISA 6, RG 395, PSRSV 12516, CINA 347, S7060, HD 503, HD 550 , HD 535, HD 541, HD 545, HD 548, HD 549, HD 556 , HD 432, HD 324 and HD 123
Medium (3)	97	HD 404, HD 514, HD 372, HD408, HD 379, Arlano, B 2-16-2, B-4, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, FFS5, D 43-21, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, H 476-5, HD 6, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, S2204, S2446, FFS7, DS-5, S351, S479, AC 33, H 52 -519,AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, JL 60, M 53070, H 174, , LD 327, Vira 6, 79/Lohit, AC3376, AC3212, AC3377, AC3252, FFS12, DS 5-2, AC S 3028, HD 369, S3031, CC1-1-3-41, HD 328, HD 328-1, CISA 21, FFS19, RG 255, LD 814, RG 260, LD 713, HD 418, G. Cot 19, HD 107, AH 11, AKA 315, AKA 9623-2, HD 453, FFS21, PSRV 12489, S7060 A, S6071, HD 521, HD 524, FFS17, FFS18, HD 543, HD 542, HD 551 , HD 544 and HD 555
Medium Long (5)	13	FFS2, BPS, FFS6, S479-1, H 248, Petaloidy, AC3233, FFS14, CINA 329, AKA 9410, DLSA 17, AKA 210, S6799
Long (7)	-	
Extra-long (9)	-	

4.1.27 Fibre Strength (g/tex)

Fibre strength, also referred to as bundle strength, is a measurement that determines how strong a fibre is. It is the amount of force necessary to break a fibre with a unit linear density. Based on fibre strength, genotypes can be categorised into five groups, ranging from very weak to very strong. Thirty three genotypes were found in weak category (17-20.0), 100 genotypes had medium fibre strength (21.0-24.0) and 20 genotypes had strong (25.0-28.0) fibre strength (Table 4.27). No any genotype show very poor as well as very strong fibre strength.

Table 4.27: Classification of 153 *desi* cotton genotypes on the basis of fibre strength (g/tex)

Code	Genotype Number	Genotypes
Very weak (<16) (1)	-	-
Weak (17-20.0) (3)	33	P 489, Jubli, H 460, AC3212, AC3269, DS 5-3, DS 5, FFS13, 30822 BLL, Sanguinum, AC 3347, NGPA 1-9-1, FFS15, FFS16, PA 405, LD 805, RG 395, CISA 6, PSRV 12489, CINA 347, S7060, HD 503, HD 550, HD 544 , HD 535, HD 541, HD 545, HD 548, HD 549, HD 556, HD 432, HD 324 and HD 123
Medium (21.0 – 24.0) (5)	100	S 302, FSS1, HD 514, HD372, HD379, FSS3, HD 408, B 2-16-2, HD 392, BH 30, BH 41, BH 92, BH 102, FFS5D 43-21, D 48-154-1, D 462-1-1, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, HD 6, HD 10, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, , S2446, DS-5, DS 5-1, S5278, S351, S479, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, JL 60, M 53070, H 248, H 174, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3377, AC3252, FFS12, DS 5-2, AC S 3028, HD 369, S3031, CC1-1-3-41, FFS14, HD 328, HD 328-1, CISA 21, FFS19, RG 255, LD 814, RG 260, LD 713, DLSA 17, HD 418, G. Cot 19, HD 107AH 11, AKA 210, AKA 315, AKA 9623-2, HD 453, FFS21, PSRSV 12516, S7060 A, S6071, S6799, HD 521, HD 524, FFS17, FFS18, HD 543, HD 542 , HD 551 , HD 555
Strong (25.0 – 28.0) (7)	20	HD 404, HD 514, FFS2, Arlano, B-4, BHO 5 VIII, FFS4, BPS, DC-93, H 476-5, HD 3, 35/5 B, FFS6, FFS7, S479-1, FFS10, AC3233, CINA 329, AKA 9410
Very strong (>29.0) (9)	-	

4.1.28 Fibre Uniformity (%)

On the basis of fibre maturity, *desi* cotton genotypes were classified into five classes *i.e.*, poor, fair, average, good and excellent. All the studied genotypes possessed excellent fibre uniformity *i.e.*, more than 47%. No any genotype was in poor, fair, average and good category of fibre uniformity as classified in Table 4.28.

Table 4.28: Classification of 153 *desi* cotton genotypes on the basis of fibre uniformity

Code	Genotype Number	Genotypes
Poor (<42) (1)	–	–
Fair (42-43) (3)	–	–
Average (44-45) (5)	–	–
Good (46-47) (7)	–	–

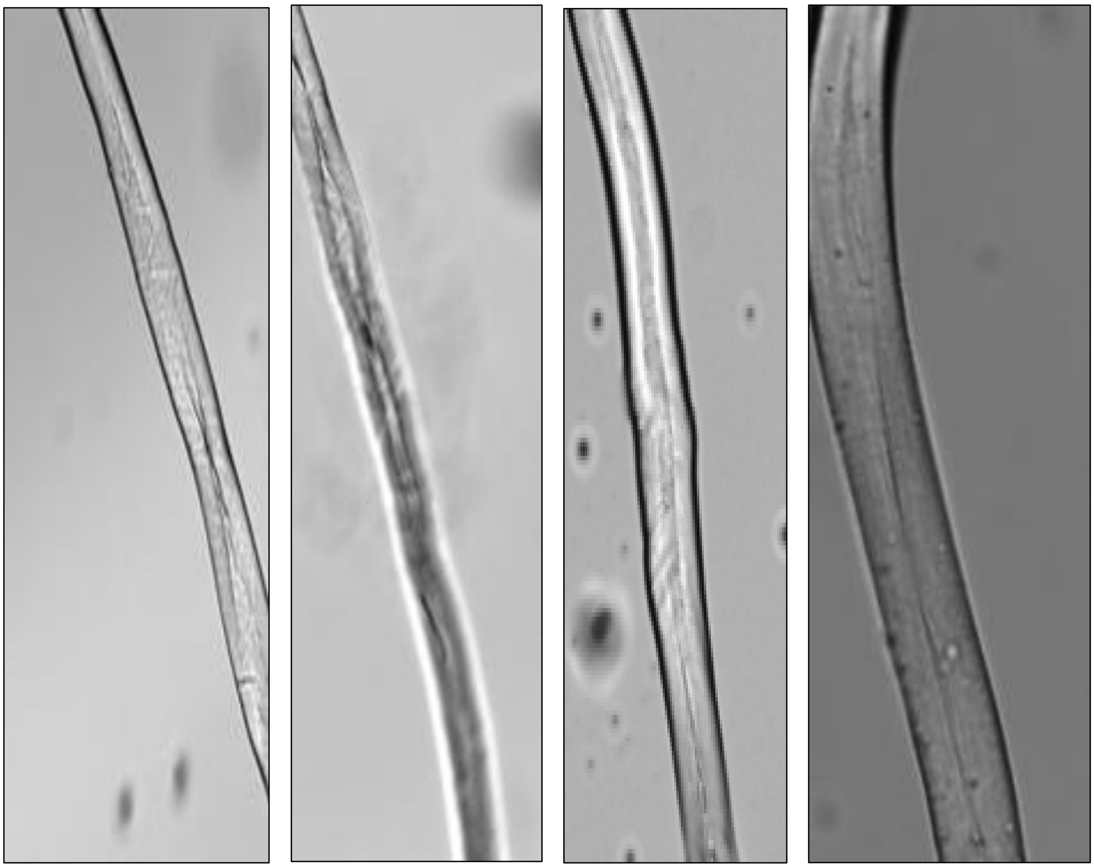
Excellent (>47) (9)	153	S 302, FFS1, HD 404, HD 514, HD 372, HD 408, FFS2, HD 379, FFS3,, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS6, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21, PSRV 12489, CINA 347, S7060, PSRSV 12516, S7060 A, S6071, S6799, HD 521, HD 524, FFS17, FFS18, HD 503, HD 543, HD 542 , HD 550 , HD 551, HD 544 , HD 535, HD 541, HD 545, HD 548, HD 549, HD 555, HD 556, HD 432, HD 324 and HD 123

(a) **(b)**

Plate 4.17 Seed fuzz density: (a) Dense (b) Medium

(a) (b)

Plate 4.18 Fibre colour: (a) Brown (b) Grey



(a) (b) (c) (d)

Plate 4.19 Fibre maturity: (a) & (b) Immature fibre (c) & (d) Mature fibre

4.1.29 Fibre maturity (%)

Fibre maturity is a fibre quality feature that expresses the relative level of fibre wall thickening. Thick walls are a sign of mature fibre. It is expressed as a percentage and divided into 5 categories: very immature (cell wall thickening less than 31%), immature (32–49%), average (50–65%), good (66–80%), and very good (more than 81%). All the genotypes possessed the very good fibre maturity. The distribution of genotypes according to fibre maturity is shown in Table 4.29 and differentiation of mature and immature fibre as shown in plate 4.20.

Table 4.29: Classification of 153 *desi* cotton genotypes on the basis of fibre maturity

Code	Genotype Number	Genotypes
Very immature (<31) (1)	-	-
Immature (32-49) (3)	-	-
Average (50-65) (5)	-	-
Good (66-80) (7)	-	-
Very Good (>81) (9)	153	S 302, FFS1, HD 404, HD 514, HD 372, HD 408, FFS2, HD 379, FFS3,, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, BPS, FFS5, D 43-21, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 6, HD 10, HD 3, HD 20, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS6, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, DS 1, AC 33, H 52 -519, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3269, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1, FFS16, CISA 21, PA 405, CINA 329, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, AKA 9410, DLSA 17, HD 418, G. Cot 19, HD 107, CISA 6, AH 11, AKA 210, AKA 315, AKA 9623-2, RG 395, HD 453, FFS21, PSRV 12489, CINA 347, S7060, PSRSV 12516, S7060 A, S6071, S6799, HD 521, HD 524, FFS17, FFS18, HD 503, HD 543, HD 542 , HD 550 , HD 551, HD 544 , HD 535, HD 541, HD 545, HD 548, HD 549, HD 555, HD 556 ,HD 432, HD 324 and HD 123

4.1.30 Fibre fineness (µ/inch)

The resistance to air flow provided by a specific amount of cotton fibre, also known as fibre fineness or micronaire, is measured in micrograms per inch (g/inch). When the micronaire number is greater than 6, the fibre is considered to be extremely coarse. When it is between 4.0 and 4.9, it is considered coarse. When it is between 3.0 and 3.9, it is considered fine. When it is less than 3, it is considered very fine. Among 153 *desi* cotton genotypes neither a genotype with very fine nor fine fibre was found. One genotype (BPS) had medium type of fibre fineness, 63 genotypes had coarse fineness of the fibre, and 89 genotypes had very coarse type of fibre. Table 4.30 represented the characterization of genotypes based on fibre fineness.

Table 4.30: Classification of 153 *desi* cotton genotypes on the basis of fibre Fineness (µ/inch)

Code	Genotype Number	Genotypes
Very coarse (>6) (1)	89	FFS1, HD 372, FFS3, D 48-154-1, D 462-1-1, DC-93, DC 108, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, HD 6, HD 10, HD 20, N-W-1, PL 735, PL 735-1, RA 1, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, H 52 -519, AC-8, FFS8, D 462-1-1 P5, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, Vira 6, AC3212, AC3377, AC3269, FFS12, DS 5-2, DS 5-3, DS 5, FFS13, 30822 BLL, Sanguinum, AC 3347, NGPA 1-9-1, FFS15, HD 328-1, FFS16, PA 405, FFS19, RG 255, LD 814, RG 260, LD 805, LD 713, HD 107, CISA 6, AKA 9623-2, RG 395, HD 418, PSRV 12489, CINA 347, S7060, FFS17, FFS18, HD 503, HD 543, HD 550 , HD 551, HD 544 , HD 535, HD 541, HD 545, HD 548, HD 549, HD 556, HD 432, HD 324 and HD 123
Coarse (5.9-5.0) (3)	63	S 302, HD 404, HD 514, HD 408, FFS2, HD 379, Arlano, B 2-16-2, B-4, HD 392, BHO 5 VIII, BH 30, BH 41, BH 92, BH 102, FFS4, FFS5, D 43-21, EB 31-1, H 1, H 476-5, HD 3, Y-1, 35/5 B, FFS6, S351, S479, S479-1, DS 1, AC 33, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, 79/Lohit, Petaloidy, AC3376, AC3233, AC3252, AC S 3028, HD 369, S3031, CC1-1-3-41, FFS14, HD 328, CISA 21, CINA 329, AKA 9410, DLSA 17, G. Cot 19, AH 11, AKA 210, AKA 315, HD 453, FFS21, PSRSV 12516, S7060 A, S6071, S6799, HD 521, HD 524, HD 542 and HD 555
Medium (4.9-4.0) (5)	1	BPS
Fine (3.9-3.0) (7)	-	-
Very fine (<3.0) (9)	-	-

4.2 Analysis of variance (ANOVA)

The data collected for morphological, biochemical and fibre traits with three check varieties and 150 genotypes sowed in augmented block design for *desi* cotton during *kharif* 2020 and *kharif* 2021 were used in the analyses of variances Table 4.31, 4.32, 4.33 and 4.34. For consistent and more reliable results, the combined (pooled) data from both seasons were used. Mean sum of square for treatment (adjusted) (Table 4.31 and Table 4.32) and blocks (adjusted) (Table 4.33 and Table 4.34) were significant for boll weight, days to first flower, plant height, number of seed per boll, ginnining out turn, number of bolls per plant, number of monopods per plant, oil content, gossypol content, protein content, seed cotton yield, fibre strength, fibre length, fibre uniformity and fibre maturity which indicated that sufficient variability is present among genotype. Whereas, mean sum of square was found non-significant in both the conditions for seed index and number of locules per boll demonstrating that not sufficient variability was found for these traits. In order to evaluate the experimental data in terms of variance between checks (controls), between test genotypes (treatments), and between test genotypes and checks, additional analysis was computed. Under both the condition [treatment (adjusted) and blocks (adjusted)] mean sum of square for checks was found significant for boll weight, plant height, number of bolls per plant, number of locules per boll, seed cotton yield, fibre maturity and fibre fineness which indicates that significant difference was present among three checks for these traits. While very less or no any variability was found for the traits *viz* number of seed per boll, ginning out turn, number of monopods per plant, seed index, oil content, gossypol content, protein content, fibre strength, fibre length, fibre uniformity and days to first flower among three checks. For treatment *vs* checks under both the condition non-significant mean sum of square was found for seed index, number of locules per boll and gossypol content while for rest of the studied traits significant differences was found for test treatments and checks. These results indicate that for these traits genotypes were significantly different from the three checks. The block effect when the treatment effect is eliminated was found non-significant for all the studied traits except days to first flower which demonstrated that blocks have significant effect on the trait days to first flower.

Table 4.31: Pooled analysis of variance of nine quantitative traits for 153 genotypes when treatment is adjusted

Source	DF	DFF	BW	PH	NOS	GOT	SI	NOB	NOL	NOM
Block (ignoring Treatments)	9	48.03 **	1.04 **	3379.94 **	21.56 **	20.58 **	0.42 ns	548.09 **	0.17 ns	0.53 **
Treatment (eliminating Blocks)	152	11.03 **	0.22 **	790.55 **	23.15 **	7.28 **	0.42 ns	91.56 **	0.16 ns	0.22 **
Treatment: Check	2	4.43 ns	0.57 **	753.52 *	1.96 ns	2.82 ns	0.59 ns	148.6 **	0.57 **	0.02 ns
Treatment: Test and Test vs. Check	150	11.11 **	0.22 **	791.05 **	23.43 **	7.34 **	0.42 ns	90.79 **	0.16 ns	0.22 **
Residuals	18	1.66	0.03	183.11	2.25	2.08	0.28	5.69	0.1	0.08

ns – Non Significant, ** Significant at 1% level DFF- Days to first flower, BW- Boll weight (g), PH- Plant height (cm), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NOB- No. of bolls per plant,, NOL- No. of locules per boll, NOM-Number of monopods per plant.

Table 4.32: Pooled analysis of variance of seed cotton yield, biochemical anf fibre traits when treatment is adjusted

Source	DF	OIL	GC	PC	SCY	FF	FS	FL	FU	FM
Block (ignoring Treatments)	9	2.99 **	0.0039 *	6.82 **	2484.27 **	0.29 **	19.13 **	2.73 **	5.91 **	17.94 **
Treatment (eliminating Blocks)	152	0.53 *	0.0022 ns	4.71 **	656.59 **	0.14 **	3.1 **	4.34 **	1.02 **	21.63 **
Treatment: Check	2	0.12 ns	0.0016 ns	3.33 ns	843.62 **	0.07 **	0.06 ns	0.13 ns	7.72 ns	138.12 **
Treatment: Test and Test vs. Check	150	0.54 *	0.0022 ns	4.73 **	654.07 **	0.14 **	3.14 **	4.4 **	1.04 **	20.06 **
Residuals	18	0.27	0.0014	1.62	14.21	0.01	0.39	0.27	0.02	0.23

ns – Non Significant, ** Significant at 1% level OIL-Oil content (%), GC- Gossypol Content (mg/g), PC- Protein Content (%), SCY- Seed Cotton Yield, FF- fibre fineness (µ/inch), FS- fibre strength (g/tax), FL- fibre Length (2.5% span length) (mm), FU- fibre uniformity (%) and FM- fibre maturity (%)

Table 4.33: Pooled analysis of variance of nine quantitative traits when blocks are adjusted

Source	DF	DFF	BW	PH	SI	GOT	NOB	NOL	NOM	NOS
Treatment (ignoring Blocks)	152	13.53 **	0.28 **	983.43 **	0.44 ns	8.38 **	123.68 **	0.17 ns	0.25 **	24.19 **
Treatment: Check	2	4.43 ns	0.57 **	753.52 *	0.59 ns	2.82 ns	148.6 **	0.57 **	0.02 ns	1.96 ns
Treatment: Test vs. Check	1	123.92 **	2.7 **	225.98 ns	0.23 ns	27.72 **	615.5 **	0.4 ns	2.46 **	157.11 **
Treatment: Test	149	12.9 **	0.26 **	991.71 **	0.44 ns	8.32 **	119.99 **	0.16 ns	0.24 **	23.59 **
Block (eliminating Treatments)	9	6.26 **	0.06 ns	165.3 ns	0.14 ns	2.36 ns	12.76 ns	0.06 ns	0.03 ns	4.14 ns
Residuals	18	1.66	0.03	183.11	0.28	2.08	5.69	0.1	0.08	2.25

ns – Non Significant, ** Significant at 1% level BW- Boll weight (g), DFF- Days to first flower, PH- Plant height (cm), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NOB- No. of bolls per plant, NOM-Number of monopods per plant, NOL- No. of locules per boll, and NOS- No. of Seeds per Boll.

Table 4.34: Pooled analysis of variance of seed cotton yield, biochemical anf fibre traits when blocks are adjusted

Source	DF	OIL	GC	PC	SCY	FF	FS	FL	FU	FM
Treatment (ignoring Blocks)	152	0.7 **	0.0023 ns	4.91 **	804.46 **	0.16 **	4.25 **	4.51 **	1.38 **	22.68 **
Treatment: Check	2	0.12 ns	0.0016 ns	3.33 ns	843.62 **	0.07 **	0.06 ns	0.13 ns	7.62 ns	138.12 **
Treatment: Test vs. Check	1	4.86 **	0.0025 ns	48.47 **	756.84 **	0.94 **	143.84 **	134.77 **	3.77 **	161.58 **
Treatment: Test	149	0.68 **	0.0023 ns	4.64 **	804.25 **	0.16 **	3.36 **	3.68 **	1.38 **	20.16 **
Block (eliminating Treatments)	9	0.17 ns	0.0012 ns	3.45 ns	19.85 ns	0.01 ns	0.01 ns	0.05 ns	7.8e ns	0.54 ns
Residuals	18	0.27	0.0014	1.62	14.21	0.01	0.39	0.27	0.02	0.23

ns – Non Significant, P > 0.05; * P <= 0.05; ** P <= 0.01 OIL-Oil content (%), GC- Gossypol Content (mg/g), PC- Protein Content (%), SCY- Seed Cotton Yield (g), FF- fibre fineness (µ/inch), FS- fibre strength (g/tax), FL- fibre Length (2.5% span length) (mm), FU- fibre uniformity (%) and FM- fibre maturity (%

4.3 Mean, range and other genetic parameters of various traits

The mean value of all the quantitative, biochemical and fibre quality traits for 150 genotypes and three checks were given in Table 4.35 and Table 4.36 showing their critical differences and coefficients of variation. Other genetic parameters like GCV (genotypic coefficient of variation), phenotypic coefficient of variation (PCV), heritability (H^2b) and genetic advance as per cent of mean has been provided in Table 4.37 and showing by figure 4.1, 4.2 and 4.3.

4.3.1 Days to first flower

Days to first flower were ranged from 44.78 (HD 556) o 59.28 (RA 1) and the mean was found 52.45 days. Low GCV (6.39%) and PCV (6.85%) were noted for days to first flower. It also exhibited high heritability *i.e.,* 87.11% and medium (12.31%) genetic advance as per cent of mean.

4.3.2 Plant height (cm)

Maximum plant height was observed for the genotype DS-5 *i.e.,* 293.97 and lowest for the genotype S351 *i.e.,* 150.93 and average height of the genotypes was 223.61 cm. Plant height exhibited medium GCV (12.72 %) and PCV (14.08 %). High heritability *i.e.,* 81.54 % coupled with high genetic advance as per cent of mean recorded for plant height.

4.3.3 Boll weight (g)

Weight of single boll measured in grams is called boll weight. Maximum boll weight was observed for the genotype HD 521 *i.e.,* 4.1700 g and minimum were observed for the genotype FFS 1 *i.e.,* 1.74 g. Average boll weight of all the genotypes was 2.8 g. Boll weight shows medium GCV (17.15 %) and PCV (18.15). It showed high heritability *i.e.,* 89.86 % as well as high genetic advance as percent of mean *i.e.,* 33.42 %.

4.3.4 Seed index

Seed index was found highest for the genotype HD 107 *i.e.,* 6.5 % and lowest by the genotype DS-5 *i.e.,* 3.2 %. The average seed index of all the genotype was 4.96 %. Seed index posses' low GCV *i.e.,* 8.18 and medium PCV *i.e.,* 13.38 as well as medium heritability (37.41%) and genetic advance as per cent of mean (10.33 %).

4.3.5 Number of bolls per plant

Genotype P 485 has highest number of bolls per plant *i.e.,* 67.16 whereas AH 11 has lowest number of bolls per plant *i.e.,* 9.87 (Table 4.35). The average number of bolls for all the genotypes was recorded as 34.92. Number of bolls per plant shows high GCV (30.92 %) and PCV (31.68 %) as well as high heritability (95.26 %) and genetic advance as per cent of mean (62.26 %).

4.3.6 Ginning out turn

The minimum ginning percentage was recorded as 29.1% in genotype EB 31-1 and the maximum ginning percentage value was 44.03% in HD 545. The average value of the trait was 37.35% which falls under very high category according to DUS traits grouping. GCV and PCV values for ginning percent were found as low as 6.69% and 7.72% respectively. On the other hand, magnitude of heritability was high (75.04%) accompanied with medium genetic advance as percent of mean (11.96%).

4.3.7 Number of seeds per boll

The range of seeds per boll was recorded 39.15 (AKA 9623-2) to 20.83 (DFFS-5) and the average number of seeds per boll recorded are 30.05 (Table 4.36). Number of seeds per boll exhibited medium GCV *i.e.,* 15.37 % and PCV *i.e.,* 16.16 %. High heritability *i.e.,* 67.99 % and genetic advance as per cent mean *i.e.,* 40.01% were also recorded for this trait.

4.3.8 Number of locules per boll

The highest number of locules per boll (4.68) was possessed by AKA 9623-2 whereas the least number of locules per boll (2.36) were in FFS-2. The average of the trait was recorded as 3.65 locules per boll. It also shows low GCV (7.01 %) and medium PCV (11.01%) which revealed that number of locules per boll did not have much variation. Similarly, this trait has medium heritability *i.e.,* 40.48 % with low genetic advance as percent of mean (9.20 %).

4.3.9 Number of monopods per plant

The range of monopods per plant was recorded 2.8 (B 2-16-2) to 0.85 (DS-5) and the average number of monopods recorded were 1.71 (Table 4.36). Number of monopods per plant exhibited high GCV *i.e.,* 23.52 % and PCV *i.e.,* 28.52 % as well as high heritability *i.e.,* 67.99 % and genetic advance as per cent of mean *i.e.,* 40.01%.

Table 4.35: Pooled mean Table of various traits in 153 genotypes of *desi* cotton

Treatment	DFF	PH	BW	SI	GOT	NOB	NOL	NOM	NOS	OIL	GC	PC	SCY	FS	FL	FU	FM	FF
S2204	47.95	228.61	2.4	4.4	39.22	34.99	3.94	1.08	32.55	14.8	0.29	20.09	88.42	23.16	20.97	76	95.28	6.28
S2446	55.95	236.95	3.27	3.65	38.93	31.98	3.41	1.41	33.83	15.25	0.25	19.82	94.93	24.26	22.17	77	93.33	6.08
S 302	53.12	167.73	3.44	4.89	41.47	56.11	3.94	2.13	35.71	12.78	0.22	19.36	155.74	22.29	20.33	75	84.07	5.88
S3031	47.78	227.36	3.44	4.74	36.64	23.15	4.27	1.4	27.63	15.73	0.33	8.29	88.84	22.03	22.4	78	84.32	5.78
30822 BLL	57.28	215.69	3.4	4.34	37.82	31.99	3.8	2.07	28.63	14.96	0.26	20.51	81.33	19.83	19.6	78	91.72	6.48
35/5 B	58.78	239.95	2.13	4.92	32.23	33.21	3.89	1.74	33.16	15.24	0.25	20.17	67.56	25.99	23.83	78	88.79	5.98
S351	54.95	150.93	2.3	4.65	37.73	54.92	3.98	1.91	34.88	14.77	0.27	14.09	107.23	25.16	23.67	78	93.3	5.88
S479	49.2	210.22	2.1	3.8	36.11	57.9	3.74	1.9	27.77	14.99	0.29	16.45	102.3	22.81	24.62	79	94.74	5.48
S5278	50.45	246.95	2.51	3.65	35.98	41.82	4	1.24	30.27	15.07	0.34	20.75	92.5	22.76	19.87	75	94.28	6.38
S6071	55.12	217.55	2.42	4.37	38.5	25.41	3.07	1.4	28.31	15.49	0.27	19.59	55.4	20.56	22.17	78	85.33	5.88
S6799	55.62	182.55	3.7	4.97	36.19	17.41	3.62	1.24	30.31	15.54	0.39	17.93	54.15	23.06	24.57	79	84.41	5.78
S7060	50.62	202.55	3.36	5.12	39.01	26.07	3.06	1.9	27.81	15.74	0.34	19.46	71.69	19.76	19.87	78	92.43	6.48
S7060 A	51.62	222.55	3.13	4.97	37.87	17.24	3.12	2.24	28.81	14.89	0.24	19.51	57.75	20.56	22.17	78	87.83	5.38
79/Lohit	46.28	165.84	2.1	4.8	34.06	49.53	4.06	2.07	34.17	15.27	0.23	17.57	110.66	22.56	23.93	79	84.92	5.88
AC-8	51.95	189.95	3.57	5.78	36.96	51.31	3.92	2.23	30.27	15.02	0.23	15.8	155.12	21.46	21.27	78	92.63	6.28
AC S 3028	56.78	260.69	3.9	4.34	39.26	31.32	3.74	1.57	28.13	15.33	0.27	19.51	100.4	22.43	23.4	79	95.82	5.68
AC 33	51.95	195.15	2.45	4	37.83	50.31	3.44	2.07	25.27	14.97	0.27	20.14	100.98	22.96	22.87	78	92.8	5.58
AC 3347	58.28	249.03	2.76	4.64	41.15	33.81	3.28	1.57	22.63	15.53	0.33	20.04	83.21	20.23	19.9	78	92.83	6.28
AC 41	57.12	257.67	1.93	4.1	36.31	55.18	3.33	1.46	28.33	14.65	0.23	21.34	96.08	21.53	21.7	78	84.22	5.98
AC3212	56.28	235.63	1.95	5.2	30.05	38.36	3.6	1.74	27.66	14.72	0.27	24.54	68.58	20.46	21.53	78	92.91	5.98
AC3233	55.28	253.13	2.12	5.05	31.97	28.36	3.09	1.07	26.16	14.32	0.38	22.59	69.01	25.76	25.43	79	88.82	5.38
AC3252	51.28	250.63	3.06	4.9	36.46	26.53	3.63	1.24	27.16	14.92	0.38	22.06	72.39	23.06	24.43	79	83.92	5.78
AC3269	54.28	228.13	2.7	5.15	35.61	33.03	3.11	1.24	28.16	15.12	0.3	21.19	79.69	19.66	18.93	77	89.91	6.28
AC3376	53.78	237.3	2.33	4.95	35.62	26.53	3.61	1.07	25.16	14.87	0.18	21.74	70.84	22.46	23.43	79	89.92	5.48
AC3377	53.78	217.3	2.36	5.15	37.63	33.86	3.31	1.4	30.16	15.72	0.32	24.72	74.7	21.06	21.53	78	95.92	5.98
AH 11	53.62	280.64	2.23	4.2	37.81	9.87	3.93	1.13	30.83	15.18	0.16	19.86	38.02	24.16	24.33	79	82.82	5.78
AKA 210	48.12	239.22	2.79	5.42	39.8	32.07	3.1	2.07	28.31	14.99	0.23	22.59	92.59	23.76	24.97	79	86.43	5.48

AKA 315	49.62	188	3.34	5.12	42.49	34.91	4.14	2.4	36.92	15.14	0.27	19.15	122.21	22.66	23.67	79	89.33	5.58
AKA 9410	50.12	281.47	3.11	5.15	39	26.87	3.98	2.3	31.83	14.33	0.24	21.85	79.95	24.86	26.23	79	92.92	5.48
AKA 9623-2	50.62	257.55	2.97	5.42	43.44	48.24	4.16	2.74	39.15	15.19	0.25	22.55	149.36	20.76	21.37	78	95.83	6.28
Arlano	56.62	254.4	2.3	4.69	34.1	26.61	3.85	1.8	24.34	14.83	0.22	22.09	63.85	24.59	22.93	77	93.82	5.88
B-4	51.62	252.73	2.6	4.14	35.92	35.61	2.9	1.63	22.97	15.58	0.28	22.11	86.95	24.89	23.33	78	85.68	5.88
B 2-16-2	52.62	226.9	2.66	4.99	37.26	35.22	3.88	2.8	28.97	15.58	0.21	20.71	85.52	23.09	21.43	76	95.77	5.98
BH 102	53.95	247.73	2.96	5.5	33.73	34.05	3.9	1.08	27.33	12.59	0.35	14.44	100.46	23.36	21.47	76	96.32	5.78
BH 30	50.12	170.6	3.28	4.39	37.89	40.17	3.91	2.46	36.04	12.62	0.25	15.88	111.76	22.89	21.23	76	92.02	5.78
BH 41	54.45	171.1	2.86	5.35	38.08	53.55	3.95	1.9	34.44	11.24	0.26	16.03	117.13	22.56	20.47	76	86.63	5.68
BH 92	55.45	211.9	3.34	6	34.01	21.22	3.86	1.23	28.83	14.14	0.34	19.06	65.66	23.16	21.87	77	89.32	5.78
BHO 5 VIII	54.12	206.06	2.52	5.09	37.23	36.61	2.91	1.13	24.97	14.73	0.33	21.06	83.42	25.59	24.03	78	90.12	5.88
BPS	55.95	251.9	4.1	5.5	37.01	32.89	3.86	1.91	33.1	11.09	0.24	16.89	105.12	25.26	25.87	80	84.33	4.88
CC1-1-3-41	47.28	167.92	3.16	5.44	38.55	34.65	4.16	2.07	30.33	14.88	0.3	18.46	108.15	22.83	24	79	81.42	5.78
CINA 329	57.62	215.64	3.32	4.4	36.72	36.05	3.97	1.3	29.83	14.91	0.24	18.02	99.34	25.76	26.03	79	96.23	5.28
CINA 347	48.12	191.55	3.07	4.22	39.7	26.07	3.65	1.57	27.31	15.24	0.28	19.11	78.51	19.56	18.97	77	94.86	6.68
CISA 21	51.28	227.36	3.11	5.44	38.8	25.65	4.28	1.57	25.13	14.48	0.41	19.9	87.7	20.13	21.2	78	95.93	5.78
CISA 6	49.62	218.97	2.2	5.1	38.21	36.22	3.92	1.8	29.27	14.88	0.27	18.35	61.39	19.36	18.43	77	84.23	6.78
D 43-21	48.95	231.9	3.2	4.3	33.05	28.39	3.83	0.91	29.33	14.39	0.34	19.63	56.87	23.86	22.37	77	82.5	5.38
D 462-1-1	52.95	168.77	3.02	5.5	40.01	49.72	3.96	2.21	34	15.09	0.24	15.73	127.93	22.46	20.37	76	82.32	6.48
D 462-1-1 P3	56.12	189.75	2.48	4.68	39.96	48.68	3.34	2.46	34.94	14.73	0.24	16.82	111.9	21.43	21.9	78	85.12	5.88
D 462-1-1 P4	56.12	245.17	2.47	4.6	37.6	49.02	3.76	1.96	26.33	15.05	0.26	16.96	101.22	23.03	23.4	79	87.12	5.78
D 462-1-1 P5	56.12	258.5	2.41	4.05	38.05	42.35	3.3	1.79	26.33	15.05	0.2	16.7	95.71	20.83	21	78	90.22	6.68
D 48-154-1	49.45	247.73	1.84	5.5	32.01	20.72	2.85	1.07	23.33	14.79	0.31	19.79	57.34	22.26	19.77	75	84.52	6.18
DC-93	47.95	258.68	2.7	5.05	35.11	40.22	3.94	1.58	29.83	15.44	0.31	18.39	86.39	24.66	22.17	77	91.42	6.18
DC 108	48.95	236.4	2.12	5.3	31.01	33.55	2.95	0.91	25.33	14.64	0.37	19.09	50.67	24.36	22.97	78	81.33	6.28
DLSA 17	52.62	259.8	2.53	4.9	34.31	20.37	3.95	1.3	30.83	14.93	0.22	19.75	63.87	22.96	24.63	79	94.23	5.48
DS-5	47.95	236.11	2.26	3.2	37.84	33.64	3.98	0.9	29.77	14.77	0.33	18.13	72.57	22.36	20.47	76	86.32	5.98
DS 1	50.95	185.82	2.5	5.6	40.56	58.92	3.93	2.58	29.77	15.27	0.3	14.72	131.77	20.26	20.27	78	94.98	5.78
DS 5-1	51.95	230.28	2.04	3.5	33.76	42.14	3.43	1.07	32.21	14.82	0.25	16.2	85.94	22.56	19.77	75	89.3	6.48

DS 5-2	51.78	277.3	3.05	4.6	34.4	30.7	3.09	1.24	25.16	14.47	0.31	22.76	73.25	20.76	20.83	78	86.92	5.98
DS 5-3	50.78	282.3	3.13	4.8	37.67	25.36	3.12	1.24	24.16	14.82	0.2	21.71	67.22	19.56	19.03	77	87.92	6.58
DS 5-4	51.28	293.97	2.84	5.3	36.18	25.03	4.07	1.24	29.9	15.52	0.29	20.31	61.52	19.76	19.53	78	83.82	6.38
EB 31-1	56.95	241.9	2.28	4.3	29.10	19.89	2.91	1.24	23.33	14.44	0.31	22.27	45.33	24.86	22.87	78	89.44	5.78
FFS	50.78	178.31	3.33	4.14	39.08	34.81	3.31	2.07	22.63	14.98	0.33	19.16	117.74	23.23	25.4	79	83.51	5.68
FFS1	51.12	175.58	1.74	5.99	37.23	61.53	3.89	1.3	35.01	12.68	0.26	15.69	113.1	21.79	18.73	74	82.9	6.28
FFS10	54.62	190.75	2.28	4.95	40.7	57.46	3.28	1.96	31.83	14.23	0.23	19.27	119.53	24.93	24.5	79	90.32	5.88
FFS11	56.12	256.83	2.34	4.75	37.82	26.84	3.25	1.79	30.33	14.98	0.27	16.03	88.84	22.03	23	78	92.21	5.78
FFS12	49.78	283.13	3.18	5.75	35.55	28.53	4.06	1.24	30.16	15.22	0.25	20.31	79.58	21.86	21.83	78	85.92	5.98
FFS13	51.28	186.9	3.3	4.14	41.48	38.65	4.25	2.07	34.74	14.56	0.31	16.7	134.19	19.63	19.1	77	92.82	6.78
FFS14	49.28	249.03	2.83	4.84	38.6	50.16	4.26	1.4	26.13	15.13	0.29	23.8	127.62	19.73	19.8	78	88.92	6.58
FFS16	51.28	221.53	2.74	4.98	38.57	42.65	4.3	1.57	28.63	15.18	0.26	21.65	96.23	19.53	19.1	77	94.9	6.58
FFS17	50.28	189.83	2.67	5.12	39.98	28.17	3.65	1.85	32	15.84	0.22	19.02	154.28	20.96	21.57	78	89.63	6.08
FFS18	49.78	181.08	3.14	4.97	40.7	24.84	3.62	1.85	27	14.59	0.29	21.2	116.6	21.76	21.87	78	94.33	5.98
FFS19	47.12	229.8	3	5.7	41.21	21.37	3.97	1.96	32.33	14.47	0.29	17.58	71.15	20.76	21.03	78	84.92	6.28
FFS2	57.62	251.73	2.18	5.14	36.04	21.78	2.36	1.13	24.03	15.23	0.24	21.08	43.59	24.79	26.53	80	95.02	5.28
FFS20	51.78	197.92	3.58	6.06	36.64	28.98	3.78	1.24	27.74	15.13	0.34	19.69	91.06	20.83	22	78	92.92	5.88
FFS21	46.62	190.05	3.49	6.02	37.47	34.24	3.64	1.4	25.81	15.44	0.25	16.22	93.93	22.56	23.57	79	95.41	5.88
FFS3	53.62	192.58	3.06	5.82	38.79	43.61	3.87	2.13	39.97	12.11	0.24	16.51	105.56	21.99	18.83	74	92.88	6.28
FFS4	54.45	180.48	3.64	6.1	38.01	37.81	3.96	2.41	32.07	15.29	0.24	15.16	131.22	25.16	24.07	78	93.42	5.88
FFS5	51.95	288.56	3.44	5.2	35.01	27.72	2.87	1.58	20.83	13.79	0.34	20.26	72.6	23.16	23.47	78	88.63	5.38
FFS6	46.78	233.28	2.6	5.32	36.51	30.37	2.91	1.08	30.22	15.64	0.15	21.83	83.64	24.89	25.23	79	93.82	5.88
FFS7	56.95	276.95	3.37	4.8	34.94	36.99	3.96	1.91	33.78	15.1	0.22	17.69	101.66	25.36	22.97	78	92.23	5.98
FFS8	48.45	203.61	3.65	6.19	40.56	40.48	3.94	2.58	33.83	15.07	0.3	14.09	157.1	21.06	20.87	78	86.63	6.18
FFS9	49.45	173.82	3.58	5.54	43.89	57.26	3.96	1.4	35.78	15.42	0.22	18.13	182.5	22.36	21.97	78	88.43	5.88
G 20	54.45	198.21	3.22	4.27	30.01	21.72	3.99	1.41	26.33	14.34	0.36	18.42	66.15	23.26	21.47	76	90.43	5.98
G 23	49.45	218.56	3.12	5.7	34.01	33.89	2.92	2.23	27.33	14.39	0.31	22.97	89.62	23.06	21.27	76	94.85	5.98
G. Cot 19	55.62	268.14	2.74	6.36	35.28	28.21	3.95	1.3	31.33	14.93	0.29	20.54	50.77	22.66	24.23	79	85.92	5.78
Gao-16 LB VI	57.45	206.06	3.12	4.55	34.13	36.05	2.95	1.41	27.33	14.59	0.21	19.47	87.6	24.06	21.47	76	96.43	6.18

Garovilli	49.78	203.64	2.64	6.02	41.24	44.79	3.92	2.24	32.22	15.63	0.31	14.51	124.93	22.89	20.93	76	94.82	6.38
GOV 6	55.78	259.95	3.31	5.17	38.44	35.03	3.79	1.91	31.2	15.22	0.28	16.35	104.75	22.39	20.23	75	95.9	6.28
H 1	55.78	223.28	2.77	5.43	34.96	32.2	3.45	1.58	30.66	15.12	0.26	17.75	94.58	22.49	20.23	75	93.82	5.88
H 174	48.12	203.86	3.18	5.56	40.63	48.18	3.32	1.96	33	14.75	0.24	21.34	127	21.13	22.3	78	92.02	6.38
H 248	49.62	170.74	2.19	4.45	41.35	40	3.67	2.29	30.83	15.3	0.27	15.8	139.63	23.93	25.9	79	95.22	5.98
H 460	50.28	210.8	3.26	5.6	32.08	31.2	3.55	1.74	32.66	16	0.23	21.91	86.74	19.66	19.03	77	89.92	6.88
H 476-5	52.78	255.78	2.75	5.62	35.34	39.03	3.43	0.91	24.66	14.94	0.25	18.33	90.97	26.99	23.73	78	92.92	5.58
H 52 -519	56.95	205.62	2.88	5.65	42.22	45.64	3.98	1.91	36.88	14.62	0.3	17.86	148.5	21.26	21.07	78	96.3	6.18
HD 10	54.78	224.95	2.41	5.72	32.4	25.21	3.46	1.24	29.16	14.74	0.36	21.48	57.3	22.79	20.43	75	94.8	6.38
HD 107	48.12	279.47	2.42	6.5	35.92	25.55	3.44	1.13	30.83	14.48	0.24	18.09	77.13	21.76	21.33	78	82.92	6.28
HD 20	50.78	226.61	2.3	5.02	35.78	33.7	3.9	0.91	31.16	14.84	0.3	19.07	74.3	23.29	20.93	76	87.81	6.68
HD 3	53.78	222.45	2.52	4.92	32.8	25.2	3.43	1.08	24.16	15.09	0.37	22.18	58.81	24.69	23.03	78	92.81	5.88
HD 328-1	49.28	255.69	2.72	5.54	38.79	42.99	4.3	2.4	29.63	15.18	0.31	19.2	106.96	21.33	22	78	94.23	6.08
HD 369	58.78	232.53	3.27	4.24	37.13	30.98	3.28	1.24	23.13	15.13	0.42	19.51	101.06	22.83	23.2	78	91.77	5.38
HD 372	49.62	194.57	2.54	5.74	35.48	51.78	3.8	2.13	31.73	12.43	0.25	20.41	105.52	23.39	21.53	76	93.12	6.08
HD 379	49.62	205.53	2.16	4.24	31.89	32.94	2.83	1.13	28.41	15.13	0.32	20.41	72.57	22.59	20.53	76	95.92	5.98
HD 392	49.62	185.8	2.9	4.24	40.4	44.11	3.93	2.8	29.72	12.73	0.24	15.08	102.23	22.29	20.03	75	87.81	5.98
HD 404	50.12	184.58	2.64	5.09	37.87	48.11	3.97	2.63	34.04	12.44	0.25	16.21	110.61	25.09	23.63	78	86.12	5.98
HD 408	54.62	226.06	2.3	4.44	35.69	30.44	3.87	1.13	26.97	14.63	0.35	23.04	51.16	24.09	22.43	77	94.12	5.88
HD 418	49.12	222.3	2.61	4.9	37.63	34.21	3.92	2.13	35.33	15.18	0.26	19.49	93.73	21.96	21.93	78	91.23	6.08
HD 453	49.12	201.22	3.16	4.62	40.76	30.91	4.19	1.4	31.31	14.99	0.29	16.6	94.39	20.56	21.37	78	94.33	5.78
HD 503	52.78	196.23	2.98	5.64	43.62	49.67	4.29	2.02	28	15.59	0.2	19.71	163.58	19.66	20.17	78	98.43	6.18
HD 514	51.12	185.73	2.26	4.89	34.77	44.11	2.84	2.13	31.68	11.33	0.24	14.76	105.6	23.59	21.73	77	89.9	5.28
HD 521	50.62	188.2	4.17	5.27	35.91	26.57	3.99	2.57	32.31	14.89	0.19	17.76	138.93	21.66	22.47	78	82.33	5.48
HD 524	49.12	189.2	2.59	5.77	39.83	38.07	3.63	2.74	32.31	15.54	0.28	17.27	108.1	21.16	22.87	78	83.43	5.88
HD 541	49.78	256.29	3.54	4.52	42.3	26.34	3.67	1.85	36.57	15.54	0.29	20.61	110.04	19.76	19.87	78	81.43	6.58
HD 542	56.78	204.62	2.76	4.82	39.53	27.17	3.58	1.85	26.5	15.29	0.32	18.96	99.28	20.96	21.67	78	86.43	5.88
HD 543	51.78	195.94	2.77	5.52	37.6	34.84	3.63	2.18	27	15.99	0.3	18.88	104.29	23.66	23.27	79	93.74	6.38
HD 544	50.28	211.29	3.31	4.37	41.04	17.01	3.6	1.18	29	15.24	0.32	19.93	79.95	20.36	22.17	78	86.74	6.08

HD 545	55.28	212.96	3.44	4.02	44.03	18.67	3.64	1.52	29.5	15.99	0.31	21.87	60.37	19.96	19.57	78	89.43	5.98
HD 548	50.78	226.29	2.8	4.92	41.96	17.01	3.6	1.52	31	15.79	0.32	22.65	76.87	19.56	19.37	78	88.74	6.18
HD 549	52.28	249.62	3	4.05	41.52	27.17	4.17	1.52	36	15.29	0.29	20.46	62.73	19.76	20.07	78	86.74	6.48
HD 550	54.28	210.46	2.99	5.67	39.45	40.29	3.62	2.02	27	15.44	0.39	19.14	102.11	19.86	19.87	78	88.74	6.28
HD 551	53.78	252.96	2.83	5.67	36.72	23.84	3.61	1.68	26.5	15.89	0.34	19.4	74.08	20.56	20.57	78	89.96	6.48
HD 555	58.8	262.96	2.48	3.32	32.66	15.34	4.12	0.85	32.45	15.84	0.28	17.31	43.99	20.56	20.97	78	94.44	5.88
HD 556	59.28	243.79	2.57	3.86	42.11	20.01	3.59	1.35	32	15.29	0.3	18.1	54.91	19.96	19.87	78	95.74	6.28
HD 6	54.78	244.95	2.36	3.72	40.05	37.54	3.39	0.91	22.66	15.29	0.39	19.45	64.58	22.59	20.73	76	93.82	6.08
HD123	55.05	218.92	2.86	4.67	37.84	34.16	3.92	2.03	33	15.35	0.27	21.16	96.82	19.78	19.5	78	88.65	6.2
HD328	54.95	236.03	3.19	4.8	38.42	27.81	3.9	2.05	32.34	15.15	0.3	20.86	81.49	19.64	19.3	78	93.73	6.34
HD432	53.85	224.91	3.32	5.14	38.9	27.2	3.5	1.96	32.15	15.34	0.3	20.05	80.39	19.76	19.5	78	95.89	6.2
JL 60	57.12	206.83	1.79	3.85	36.54	35.5	3.64	1.63	29.33	14.95	0.25	20.81	88.67	22.73	22.8	78	96.02	5.98
Jubli	54.62	227.67	2.37	5.57	38.84	44.18	3.74	2.29	34.94	15.05	0.31	17.57	100.74	19.73	19.2	77	94.12	6.78
LD 327	53.78	250.63	2.34	5.5	37.35	46.59	4.08	1.9	34.66	15.45	0.31	23.57	83.95	22.46	23.13	79	89.02	6.18
LD 713	51.12	228.97	3.26	4.15	38.43	29.87	3.96	2.46	33.83	14.53	0.25	21.84	82.93	20.66	20.53	78	95.92	6.48
LD 805	48.62	238.97	2.85	4.7	32.97	21.21	3.46	1.63	25.83	15.38	0.31	20.75	64.46	20.06	20.23	78	93.92	6.78
LD 814	49.12	222.3	3.43	4.74	39.69	22.71	4.03	1.8	28.33	14.48	0.26	17.9	77.7	21.46	22.23	78	83.92	6.58
M 53070	46.12	190.75	2.78	5.82	40.24	66	2.79	2.63	36.57	14.45	0.26	15.78	181.02	21.23	21.6	78	93.22	6.48
Malvi 12	50.17	231	2.33	4.65	35.69	41.01	3.8	1.96	30.57	14.3	0.21	19.59	99.23	22.03	22.6	78	87.12	6.28
N-W-1	56.78	211.61	2.3	5.52	32.2	34.36	2.93	1.24	23.66	14.74	0.28	22.88	81.15	22.89	20.83	76	95.81	6.38
NGPA 1-9-1	54.28	196.01	2.92	5.24	38.47	38.99	4.32	2.4	30.38	15.18	0.31	20.91	106.37	19.73	19.6	78	86.92	6.58
P 248	54.12	227.67	1.85	3.75	39.36	35.18	2.37	1.46	30.83	15.35	0.3	18.45	71.24	21.13	21.4	78	93.12	5.98
P 485	49.62	203.75	1.94	4.85	40.37	67.16	3.29	2.29	34.94	14.35	0.26	15.45	127.37	20.43	20.2	78	95.02	6.78
P 489	55.62	256	1.99	5.68	34.63	56.35	3.32	1.63	27.33	14.75	0.3	20.37	84.66	19.13	18	77	97.12	6.78
PA 405	56.12	274.8	3.45	4.4	41.26	19.71	3.4	1.8	34.83	15.11	0.25	18.98	98.01	19.26	18.73	77	94.12	6.68
Petaloidy	53.28	232.3	2.27	5.2	34.96	47.03	4.11	1.24	35.16	15.17	0.28	25.41	87.93	23.36	26.43	79	87.72	5.08
PL 735	54.78	227.87	2.63	5.67	34.34	31.95	3.92	1.32	28.18	15.39	0.27	20.73	86.6	23.29	21.43	76.5	83.29	6.43
PSRSV 12516	49.62	214.22	3.34	4.37	36.42	14.57	4.09	1.24	31.31	15.04	0.28	19.33	53.88	21.66	21.67	78	88.43	5.78
PSRV 12489	57.38	220.88	2.77	4.12	35.44	14.91	4.11	1.57	30.81	14.89	0.26	18.5	49.77	19.46	19.97	78	92.42	6.18

RA 1	44.78	246.61	2.29	5.22	34.64	30.54	2.91	0.91	24.66	15.39	0.3	19.2	84.78	24.29	22.43	77	85.79	6.28
RG 255	49.62	255.64	3.21	5.04	39.68	29.54	3.43	1.63	29.33	14.48	0.23	20.8	94.47	20.36	20.13	78	82.02	6.58
RG 260	54.62	258.97	2.53	6.17	36.95	25.87	3.16	2.3	28.83	14.68	0.25	18.95	69.55	20.86	20.73	78	86.23	6.18
RG 395	53.12	229.22	2.68	4.82	35.73	32.07	3.64	2.4	26.31	14.74	0.39	19.14	83.16	19.96	19.87	78	96.43	6.18
Sanguinum	50.78	197.81	3.44	6.09	38.56	28.66	3.73	2.07	33.64	15.16	0.25	17.97	118.07	19.53	19.1	77	93.72	6.28
Vira 6	53.28	217.3	2.14	5.1	37.97	27.2	3.58	1.74	25.66	14.91	0.28	22.52	68.83	21.86	22.13	78	87.92	5.98
Y-1	57.78	227.45	2.71	5.32	35.28	30.86	3.9	1.57	25.16	15.24	0.29	22.97	76.49	24.19	23.33	78	86.8	5.98
Max.	59.28	293.97	4.17	6.5	44.03	67.16	4.32	2.8	39.15	16	0.42	25.41	182.5	26.99	26.53	80	98.43	6.88
Min.	44.78	150.93	1.74	3.2	29.10	9.87	2.36	0.85	20.83	11.09	0.15	14.09	38.02	19.13	18	74	81.33	4.88

DFF- Days to first flower, PH- Plant height (cm), BW- Boll weight (g), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NOB- No. of bolls per plant,, NOL- No. of locules per boll, NOM-Number of monopods per plant, OIL-Oil content (mg/g), GC- Gossypol Content (%), PC- Protein Content (%), SCY- Seed Cotton Yield, FF- fibre fineness (μ/inch), FS- fibre strength (g/tax), FL- fibre Length (2.5% span length) (mm), FU- fibre uniformity (%) and FM- fibre maturity (%)

Table 4.36: Showing the Critical differences and coefficient of variation possessed by different traits

Comparison	**DFF**	**PH**	**BW**	**SI**	**GOT**	**NOB**	**NOL**	**NOM**	**NOS**	**OIL**	**GC**	**PC**	**SCY**	**FF**	**FS**	**FL**	**FU**	**FM**
A Test Treatment and a Control Treatment	3.26	34.18	0.42	1.33	3.64	6.03	0.78	0.7	3.79	1.31	0.1	3.22	9.52	0.24	1.57	1.31	0.4	1.22
Control Treatment Means	1.2	12.62	0.16	0.49	1.34	2.23	0.29	0.26	1.4	0.48	0.04	1.19	3.52	0.09	0.58	0.48	0.15	0.45
Two Test Treatments (Different Blocks)	4.39	46.09	0.57	1.79	4.91	8.13	1.06	0.94	5.11	1.76	0.13	4.34	12.84	0.32	2.11	1.76	0.54	1.65
Two Test Treatments (Same Block)	3.8	39.92	0.49	1.55	4.25	7.04	0.91	0.81	4.43	1.53	0.11	3.76	11.12	0.28	1.83	1.53	0.47	1.43
CV	2.44	6.04	5.86	8.62	3.84	7.03	8.45	8..73	4.94	3.47	3.39	6.52	9.15	1.56	2.86	2.42	0.2	0.53

DFF- Days to first flower, BW- Boll weight (g), PH- Plant height (cm), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NOB- No. of bolls per plant,, NOL- No. of locules per boll, NOM-Number of monopods per plant, OIL-Oil content (mg/g), GC- Gossypol Content (%), PC- Protein Content (%), SCY- Seed Cotton Yield, FF- fibre fineness (μ/inch), FS- fibre strength (g/tax), FL- fibre Length (2.5% span length) (mm), FU- fibre uniformity (%) and FM- fibre maturity (%)

Table 4.37: Showing the mean, GCV, PCV, heritability (H^2b) and genetic advance per cent of mean for different studied traits

Trait	Mean	GCV	GCV Category	PCV	PCV Category	H^2b	H^2b Category	GAM	GAM. Category
DFF	52.45	6.39	Low	6.85	Low	87.11	High	12.31	Medium
SI	4.96	8.18	Low	13.38	Medium	37.41	Medium	10.33	Medium
BW	2.8	17.15	Medium	18.15	Medium	89.26	High	33.42	High
PH	223.61	12.72	Medium	14.08	Medium	81.54	High	23.69	High
NOB	34.57	30.92	High	31.68	High	95.26	High	62.26	High
GOT	37.35	6.69	Low	7.72	Low	75.04	High	11.96	Medium
NOS	30.05	15.37	Medium	16.16	Medium	90.46	High	30.16	High
NOL	3.65	7.01	Low	11.01	Medium	40.48	Medium	9.2	Low
NOM	1.71	23.52	High	28.52	High	67.99	High	40.01	High
OIL	14.84	4.34	Low	5.57	Low	60.82	High	6.99	Low
GC	0.28	10.86	Medium	17.29	Medium	39.43	Medium	14.07	Medium
PC	19.34	8.98	Low	11.13	Medium	65.03	High	14.94	Medium
FL	21.71	8.51	Low	8.83	Low	92.72	High	16.9	Medium
FU	77.62	1.5	Low	1.51	Low	98.19	High	3.07	Low
FS	22.08	7.81	Low	8.3	Low	88.53	High	15.16	Medium
FF	6.06	6.35	Low	6.54	Low	94.23	High	12.71	Medium
FM	90.26	4.95	Low	4.97	Low	98.84	High	10.14	Medium
SCY	91.59	30.69	High	30.96	High	91.23	High	62.75	High

DFF- Days to first flower, BW- Boll weight (g), PH- Plant height (cm), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NOB- No. of bolls per plant,, NOL- No. of locules per boll, NOM-Number of monopods per plant, OIL-Oil content (mg/g), GC- Gossypol Content (%), PC- Protein Content (%), SCY- Seed Cotton Yield, FF- fibre fineness (μ/inch), FS- fibre strength (g/tax), FL- fibre Length (2.5% span length) (mm), FU- fibre uniformity (%) and FM- fibre maturity (%)

4.3.10 Oil content

Average oil content was recorded 14.84%. Highest oil content was recorded 16% (H 460) and lowest was 11.09% (BPS). Oil content possessed low GCV (4.34%) and PCV (5.57%) which indicated that very less variation was present among the genotype for the selection. This trait had high heritability *i.e.,* 60.82% but had low genetic advance as per cent of mean *i.e.,* 6.99 indicating that there was influence of environment interaction on this trait.

4.3.11 Gossypol content

Average gossypol content was recorded 0.28%. Highest gossypol content was recorded 0.42% (HD 369) and lowest was 0.15% (FFS 6). Gossypol content possessed medium GCV (10.86%) and PCV (17.29%) which indicated that little variation was present among the genotype for the selection. This trait also had medium heritability *i.e.,* 39.43% but as well as medium genetic advance as per cent of mean *i.e.,* 14.07% indicating that there was little influence of environment interaction on this trait.

4.3.12 Protein content

Highest protein content was observed in genotype Petaloidy *i.e.,* 25.41% and the lowest was observed in genotype FFS 8 *i.e.,* 14.09%. Average protein content of all the genotypes was 19.34%. This trait possessed low GCV (8.98%) and high PCV (11.13%). High heritability (65.03 c %) and moderate genetic advance as per cent of mean (14.94%) was recorded for this character.

4.3.13 Seed cotton yield

The lowest seed cotton yield per plant was 38.02 g (AH 11) while the maximum yield was 182.5 g (FFS 9), showing their huge difference between the least and maximum values of seed cotton yield. The average yield of seed cotton per plant was 91.59 g. The seed cotton yield showed high variability, with GCV and PCV values of 30.69% and 30.96%, respectively. Heritability and genetic advance as per cent of mean was found to be under high category *i.e.,* 91.23%, and 62.75%.

4.3.14 Fibre strength

Maximum fibre strength was observed for the genotype H 476-5 *i.e.,* 26.99 g and minimum was observed for the genotype P 489 *i.e.,* 19.13. Average fibre strength of all the genotypes was 22.08. Fibre strength exhibited low GCV (7.81 %) and PCV (8.3%) but exhibited high heritability *i.e.,* 88.53 % and medium genetic advance as percent of mean *i.e.,* 15.16 %.

4.3.15 Fibre length

The lowest fibre length was 18 mm (P 489), while the maximum was 26.53 mm (FFS 2. The average fibre length is 21.71 mm. The fibre length showed low variability, with GCV and PCV values of 8.51% and 8.83%, respectively. Heritability and genetic advance per cent of mean was found to be under high category *i.e.,* 92.72% and 16.90%.

4.3.16 Fibre fineness

Maximum fibre fineness was observed for the genotype H 406 *i.e.*, 6.88 µ and minimum was observed for the genotype BPS *i.e.*, 4.88 µ. Average fibre fineness of all the genotypes was 6.06 m µ. Fibre strength showed low GCV (6.35 %) and PCV (6.54%). It also exhibited high heritability *i.e.*, 94.23 % but medium genetic advance as percent of mean *i.e.*, 12.71%.

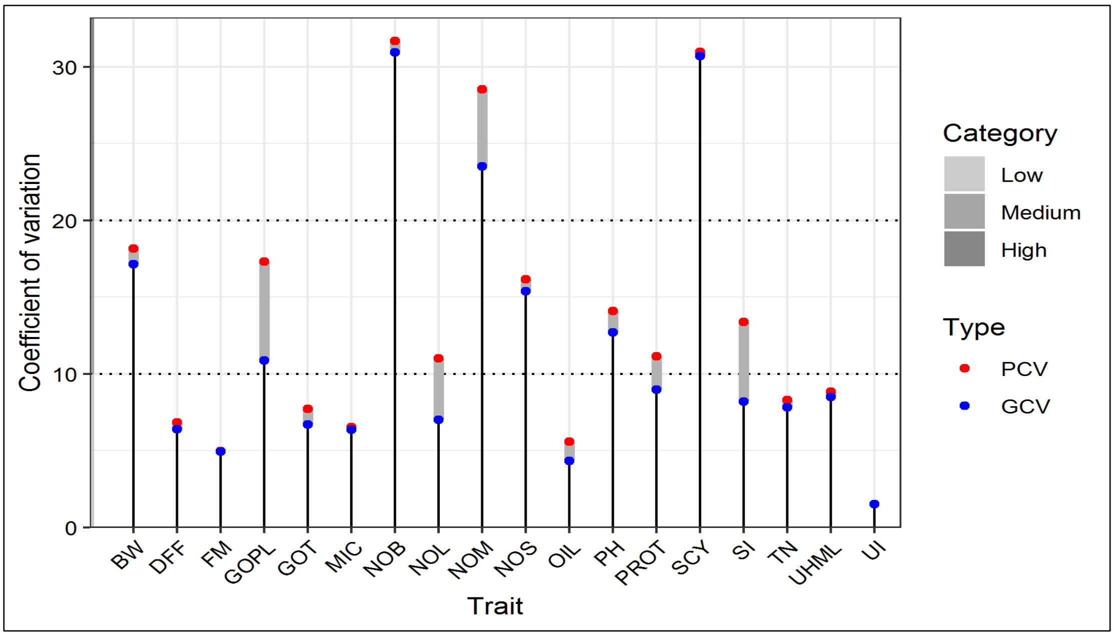
4.3.17 Fibre uniformity

The lowest fibre uniformity was 74% (FFS 1), while the maximum was 80% (FFS 2). The average fibre uniformity was 77.62%. The fibre uniformity showed low variability, with GCV and PCV values of 1.50% and 1.51%, respectively. It showed high heritability *i.e.*, 98.19 % but low genetic advance as percent of mean *i.e.*, 3.07%.

4.3.18 Fibre maturity

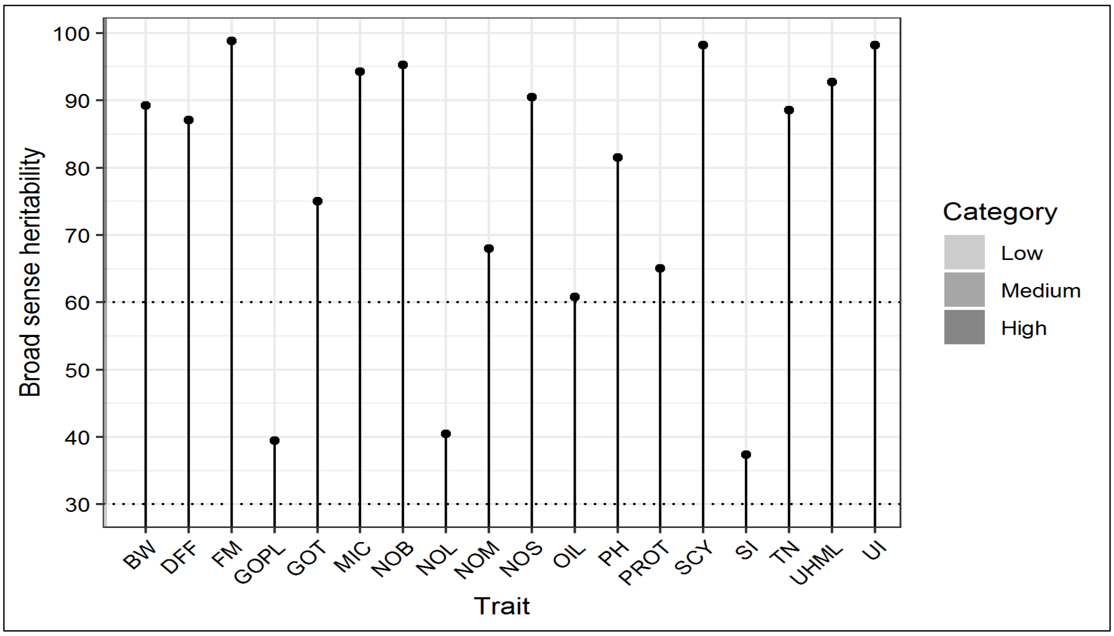
Maximum fibre maturity was observed for the genotype HD 503 *i.e.*, 98.43% and minimum was observed for the genotype DC 108 *i.e.*, 81.33%. Average fibre maturity of all the genotypes was 90.26%. Fibre maturity exhibited low GCV (4.95 %) and PCV (4.97%). It also showed high heritability *i.e.*, 98.84 % but medium genetic advance as percent of mean *i.e.*, 10.14%.

Fig. 4.1: Depicting phenotypic and genotypic coefficient of variation possessed by different traits



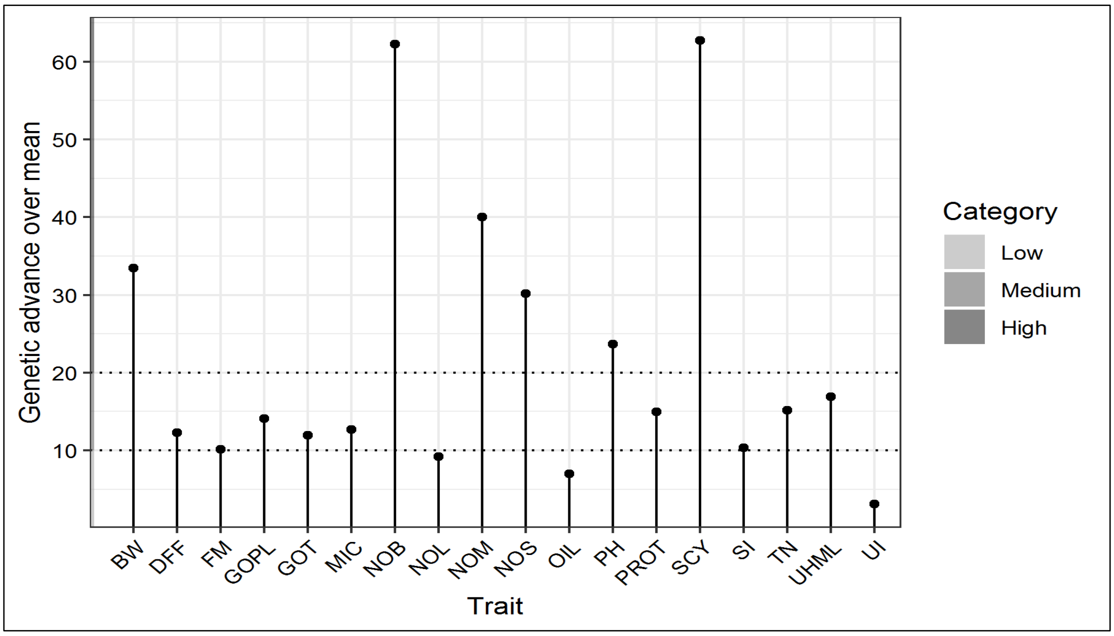
BW- Boll weight (g), DFF- Days to first flower, PH- Plant height (cm), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NB- No. of bolls per plant, NOM-Number of monopods per plant, NOL- No. of locules per boll, NOS- No. of Seeds per Boll, OIL-Oil content (%), GOPL- Gossypol Content (mg/g), PROT- Protein Content, SCY- Seed Cotton Yield, MIC (FF)- fibre fineness (µ/inch), TN (FS)- fibre strength (g/tax), UHML (FL)- fibre Length (2.5% span length) (mm), UI (FU)- fibre uniformity (%) and FM- fibre maturity (%)

Fig. 4.2: Estimated broad sense heritability of different trait



BW- Boll weight (g), DFF- Days to first flower, PH- Plant height (cm), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NB- No. of bolls per plant, NOM-Number of monopods per plant, NOL- No. of locules per boll, NOS- No. of Seeds per Boll, OIL-Oil content (%), GOPL- Gossypol Content (mg/g), PROT- Protein Content, SCY- Seed Cotton Yield, MIC (FF)- fibre fineness (μ/inch), TN (FS)- fibre strength (g/tax), UHML (FL)- fibre Length (2.5% span length) (mm), UI (FU)- fibre uniformity (%) and FM- fibre maturity (%)

Fig. 4.3: Estimated genetic advance as percent of mean of different traits



BW- Boll weight (g), DFF- Days to first flower, PH- Plant height (cm), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NB- No. of bolls per plant, NOM-Number of monopods per plant, NOL- No. of locules per boll, NOS- No. of Seeds per Boll, OIL-Oil content (%), GOPL- Gossypol Content (mg/g), PROT- Protein Content, SCY- Seed Cotton Yield, MIC (FF)- fibre fineness (μ/inch), TN (FS)- fibre strength (g/tax), UHML (FL)- fibre Length (2.5% span length) (mm), UI (FU)- fibre uniformity (%) and FM- fibre maturity (%)

4.4 Association studies

4.4.1 Correlation coefficient

Yield is a complex trait highly influenced by genotype-environment interaction. Thus a direct selection based on yield *per se* will not be effective. Under such conditions, selection may be based on simple traits which showed a positive association with yield. Correlation coefficient studies estimate the nature and extent of relationship of different traits with yield and among themselves. Table 4.38 depicts the relationship of different traits and their level of significance. Similarly correlogram (Graph 4.4) represents the intensity of the association among different studied characters.

4.1.1.1 Days to first flower

Days to first flower were significant and positively correlated with protein content (0.171), fibre strength (0.195) and fibre maturity (0.199), while significantly negative correlated with boll weight (-0.198), ginning out turn (-0.221) and seed cotton yield (-0.226).

4.1.1.2 Seed index

Seed index was positive and significant correlated with number of bolls per plant (-0.26), number of seed per boll (0.171), number of monopods per plant (0.229) and seed cotton yield (0.353).

4.1.1.3 Boll weight

Boll weight exhibited significant positive correlation with ginning out turn (0.S351), number of monopods per plant (0.248), fibre uniformity (0.171) and seed cotton yield (0.288), while, it was found significantly negative correlated with numbers of bolls per plant (-0.225) and fibre strength (-0.258).

4.1.1.4 Plant height

Plant height was significant and positively correlated with oil content (0.309), protein content (0.403) and fibre uniformity (0.223) but significantly negative correlated with number of bolls per plant (-0.441), ginning out turn (-0.272), number of seeds per plant (-0.201), number of locule per plant (-0.165), number of monopods per plant (-0.406) and seed cotton yield (-0.521).

4.1.1.5 Number of bolls per plant

Number of bolls per plant exhibited significant and positive correlation with ginning out turn (0.361), number of locule per plant (0.205), number of monopods per plant (0.462) and seed cotton yield (0.714), while significantly negative correlated with oil content (-0.259), protein content (-0.201) and gossypol content (-0.248).

4.1.1.6 Ginning out turn

Ginning out turn showed significant and positive correlation with number of seeds per boll (0.350), number of locule per plant (0.214), number of monopods per plant (0.447) and seed cotton yield (0.576), while significant negative correlated with protein content (-0.241), gossypol content (-0.164), fibre length (-0.165) and fibre strength (-0.279).

4.1.1.7 Number of seed per boll

Number of seed per boll exhibited significant and positively correlation with seed index (0.171), number of bolls per plant (0.365), ginning out turn (0.350), number of locule per plant (0.436), number of monopods per plant (0.374) and seed cotton yield (0.448), while significant negative correlated with protein content (-0.185), gossypol content (-0.260) and plant height (-0.201).

4.1.1.8 Number of locule per boll

Number of locule per boll exhibited significant and positive correlation with number of bolls per plant (0.205), ginning out turn (0.214), number of seeds per boll (0.436), number of monopods per plant (0.252) and seed cotton yield (0.250), while, it was significantly negative correlated with protein content (-0.185) and plant height (-0.201).

4.1.1.9 Number of monopods per plant

Number of monopods per plant showed significant and positive correlation with seed index (0.299), boll weight (0.248), number of bolls per plant (0.462), ginning out turn (0.447), number of seeds per boll (0.374), number of locule per plant (0.252), and seed cotton yield (0.631), while, it exhibited significant negative correlation with plat height (-0.406), protein content (-0.311), gossypol content (-0.223), and fibre strength (-0.175).

4.1.1.10 Oil content

Oil content exhibited significantly positive correlation with protein content (0.306), fibre uniformity (0.309), fibre fineness (0.283), plant height (0.309) but significantly negative correlated with seed cotton yield (-0.200).

4.1.1.11 Gossypol content

This trait showed significant negative correlation with number of bolls per plant -0.248), ginning out turn (-0.164), number of seeds per boll (-0.260), number of monopods (-0.233), and seed cotton yield (-0.334).

4.1.1.12 Protein content

Protein content exhibited positive correlation with days to first flower (0.171), plant height (0.403), but significantly negative associated with boll weight (-0.175), number of bolls per plant –0.201), ginning out turn (-0.241), number of seeds per boll (-0.185), number of locules per boll (-0.202), number of monopods (-0.311), and seed cotton yield (-0.333).

4.1.1.13 Fibre length

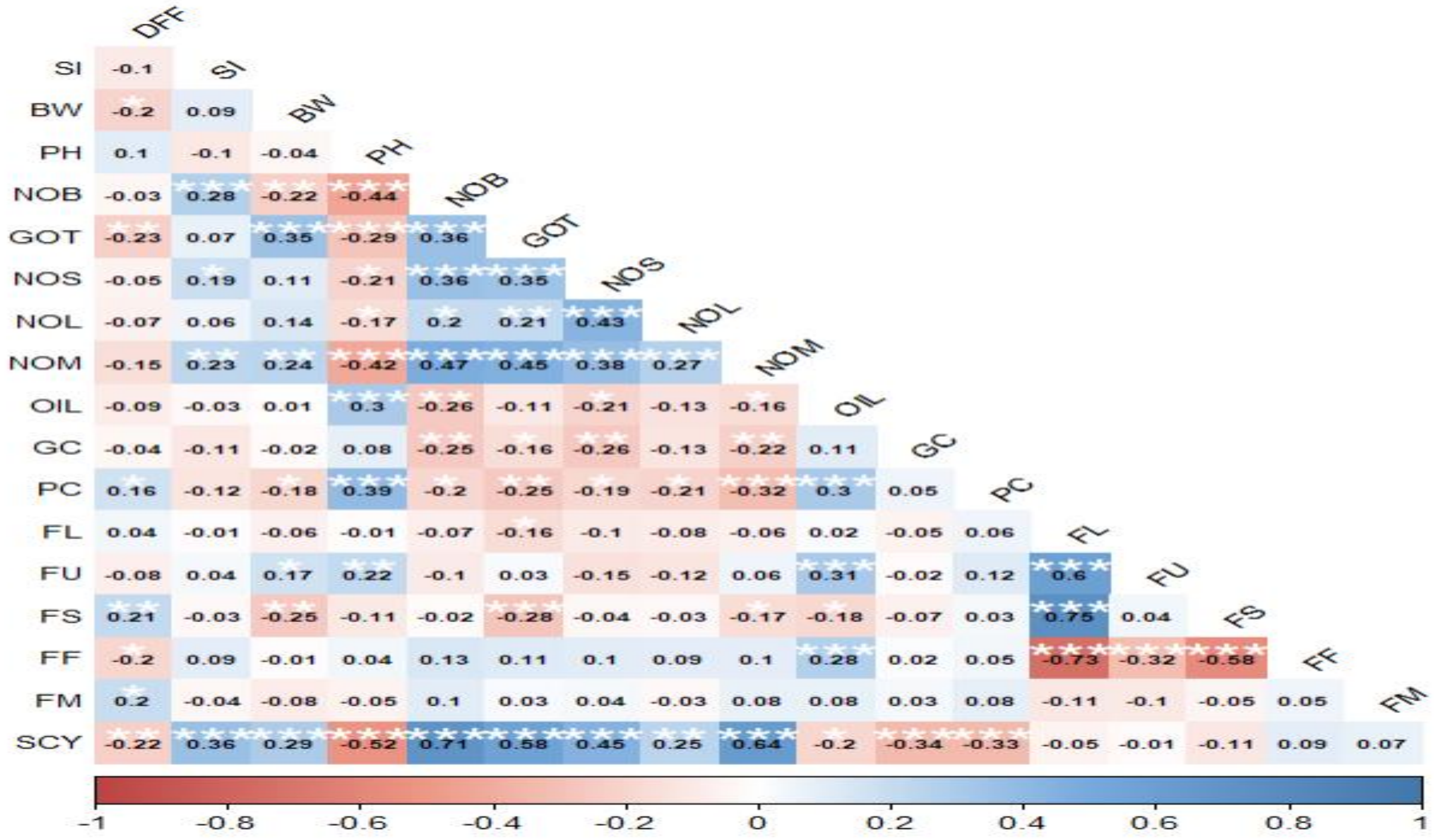
This trait exhibited significantly negative correlated with only ginning out turn (-0.165) and fibre fineness (-0.730) and significant positive association with the traits fibre strength (0.754) and fibre uniformity (0.580).

Table 4.38: Pooled Correlation studies of various characters with seed cotton yield

Traits	DFF	SI	BW	PH	NOB	GOT	NOS	NOL	NOM	OIL	GC	PC	FL	FU	FS	FF	FM	SCY
DFF	1																	
SI	-0.091	1																
BW	-0.198*	0.098	1															
PH	0.111	-0.109	-0.031	1														
NOB	-0.036	0.268**	-0.225**	-0.441**	1													
GOT	-0.221**	0.065	0.S351**	-0.272**	0.361**	1												
NOS	-0.052	0.171*	0.103	-0.201*	0.365**	0.350	1											
NOL	-0.069	0.038	0.127	-0.165*	0.205*	0.214**	0.436**	1										
NOM	-0.151	0.229**	0.248**	-0.406**	0.462**	0.447**	0.374**	0.252**	1									
OIL	-0.084	-0.039	0.008	0.309**	-0.259**	-0.104	-0.203*	-0.131	-0.155	1								
GC	-0.039	-0.097	-0.019	0.069	-0.248**	-0.164*	-0.260**	-0.128	-0.223**	0.102	1							
PC	0.171*	-0.129	-0.175*	0.403**	-0.201*	-0.241**	-0.185*	-0.202*	-0.311**	0.306**	0.043	1						
FL	0.029	-0.001	-0.071	-0.033	-0.06	-0.165*	-0.096	-0.069	-0.075	0.008	-0.041	0.035	1					
FU	-0.075	0.037	0.171*	0.223**	-0.098	0.029	-0.148	-0.123	0.059	0.309**	-0.02	0.123	0.580**	1				
FS	0.195*	-0.022	-0.258**	-0.131	-0.007	-0.279**	-0.038	-0.017	-0.175*	-0.188*	-0.054	0.013	0.754**	0.034	1			
FF	-0.195*	0.086	-0.004	0.055	0.128	0.116	0.103	0.087	0.105	0.283**	0.011	0.056	-0.730**	-0.314**	-0.581**	1		
FM	0.199*	-0.026	-0.072	-0.043	0.093	0.028	0.03	-0.045	0.087	0.08	0.031	0.089	-0.128	-0.097	-0.064	0.057	1	
SCY	-0.226**	0.353**	0.288**	-0.521**	0.714**	0.576**	0.448**	0.250**	0.631**	-0.200*	-0.334**	-0.333**	-0.046	-0.013	-0.102	0.087	0.067	1

DFF- Days to first flower, BW- Boll weight (g), PH- Plant height (cm), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NOB- No. of bolls per plant,, NOL- No. of locules per boll, NOM-Number of monopods per plant, OIL-Oil content (%), GC- Gossypol Content (mg/g), PC- Protein Content (%), SCY- Seed Cotton Yield, FF- fibre fineness (µ/inch), FS- fibre strength (g/tax), FL- fibre Length (2.5% span length) (mm), FU- fibre uniformity (%) and FM- fibre maturity (%)

Fig. 4.4: Correlogram showing the intensity of correlation among various characters of *desi* cotton



	DFF	SI	BW	PH	NOB	GOT	NOS	NOL	NOM	OIL	GC	PC	FL	FU	FS	FF	FM
SI	-0.1																
BW	* -0.2	0.09															
PH	0.1	-0.1	-0.04														
NOB	-0.03	*** 0.28	** -0.22	*** -0.44													
GOT	** -0.23	0.07	*** 0.35	*** -0.29	*** 0.36												
NOS	-0.05	* 0.19	0.11	* -0.21	*** 0.36	*** 0.35											
NOL	-0.07	0.06	0.14	* -0.17	* 0.2	** 0.21	*** 0.43										
NOM	-0.15	** 0.23	** 0.24	*** -0.42	*** 0.47	*** 0.45	*** 0.38	*** 0.27									
OIL	-0.09	-0.03	0.01	*** 0.3	** -0.26	-0.11	* -0.21	-0.13	* -0.16								
GC	-0.04	-0.11	-0.02	0.08	** -0.25	* -0.16	** -0.26	-0.13	** -0.22	0.11							
PC	* 0.16	-0.12	* -0.18	*** 0.39	* -0.2	** -0.25	* -0.19	* -0.21	*** -0.32	*** 0.3	0.05						
FL	0.04	-0.01	-0.06	-0.01	-0.07	* -0.16	-0.1	-0.08	-0.06	0.02	-0.05	0.06					
FU	-0.08	0.04	* 0.17	** 0.22	-0.1	0.03	-0.15	-0.12	0.06	*** 0.31	-0.02	0.12	*** 0.6				
FS	** 0.21	-0.03	** -0.25	-0.11	-0.02	*** -0.28	-0.04	-0.03	* -0.17	* -0.18	-0.07	0.03	*** 0.75	0.04			
FF	* -0.2	0.09	-0.01	0.04	0.13	0.11	0.1	0.09	0.1	*** 0.28	0.02	0.05	*** -0.73	*** -0.32	*** -0.58		
FM	* 0.2	-0.04	-0.08	-0.05	0.1	0.03	0.04	-0.03	0.08	0.08	0.03	0.08	-0.11	-0.1	-0.05	0.05	
SCY	** -0.22	*** 0.36	*** 0.29	*** -0.52	*** 0.71	*** 0.58	*** 0.45	** 0.25	*** 0.64	* -0.2	*** -0.34	*** -0.33	-0.05	-0.01	-0.11	0.09	0.07

4.1.1.14 Fibre uniformity

This trait exhibited significantly positive association with boll weight (0.171), plant height (0.2323), oil content (0.309) and fibre length (0.580), whereas, it was negative and significant correlation with only fibre fineness (-0.314).

4.1.1.15 Fibre strength

Fibre strength exhibited significant and positive association with days to first flower (0.195) and fibre length (0.754).

4.1.1.16 Fibre fineness

Fibre fineness exhibited significant and positive association with oil content (0.283), whereas, it exhibited significant negative correlation with days to first flower (-0.195), fibre length (-0.730), fibre uniformity (-0.314) and fibre strength (-0.581).

4.1.1.17 Fibre maturity

Fibre maturity exhibited significantly positive correlation with days to first flower (0.199) only but no any trait found with which fibre maturity exhibited significant negative association.

4.1.1.18 Seed cotton yield per plant

Seed cotton yield per plant exhibited positive correlation with almost all the morphological traits except for days to first flower, oil content, gossypol content, protein content, fibre length, fibre uniformity and fibre strength. Seed cotton yield showed significant negative correlation with days to first flower (-0.226), plant height (-0.521), oil content (-0.2), gossypol content (-0.33) and protein content (-0.33) but non-significant negative correlation with fibre length (-0.046), fibre uniformity (-0.013) and fibre strength (-0.102). Highest association with seed cotton yield was established by number of bolls per plant with value 0.714 followed by number of monopods per plant (0.631) , ginning out turn (0.576), number of seed per boll (0.448), seed index (0.353), boll weight (0.288), number of locule per boll all at p=0.01(1% significance level). Thus to increase seed cotton yield per plant selection for these traits will be effective. The positive association shows when these traits will be selected for higher value the seed cotton yield per plant will also increase. Days to first flower and plant height showed significant negative association with seed cotton yield, hence they can’t be selected directly. Taking the fibre quality parameters into account, 2.5% fibre span length (-0.046), fibre uniformity (-0.013) and fibre strength (-0.102) showed negative but non-significant association with seed cotton yield, while fibre maturity (0.067) and fibre fineness (0.087) established positive and non-significant relation with seed cotton yield. This demonstrated that we cannot select for quality traits or enhance seed cotton yield because quality and quantity have a negative correlation with one another.

4.4 Path coefficient analysis

Path coefficient analysis was used for evaluation of direct and indirect effects of different traits on seed cotton yield per plant considering seed cotton yield per plant as dependable variable and remaining traits as independent variables. For this, correlation matrixes at phenotypic level were taken into consideration. The results have been presented in Table 4.39.

4.4.1 Direct effects

Path coefficient analysis revealed that diagonal values of independent traits have direct effect on dependent trait. The maximum positive direct effect was exhibited by number of bolls per plant (0.570) followed by boll weight (0.334), ginning out turn (0.114) and number of monopods (0.107). Whereas maximum negative direct effect was exhibited by plant height (-0.114) followed by gossypol content (-0.122), days to first flower (-0.088), number of locules per boll (-0.055) and protein content (-0.029) (Table 4.38).

4.4.2 Indirect Effect

Days to first flower showed indirect negative effects through boll weight (-0.063), ginning out turn (-0.028) and seed index (-0.011). Seed index exhibited positive indirect effect *via* number of bolls per plant (0.154), boll weight (0.027) and number of seed per boll (0.016), Whereas, it revealed negative indirect effects through number of locules per boll, oil content, fibre uniformity, fibre fineness and fibre fineness though the effects were very small.

Boll weight exhibited positive indirect effect on seed cotton yield *via* ginning out turn (0.040) and number of monopods per plant (0.026), but negative indirect effect through number of bolls per plant (-0.131) and number of locules per boll (-0.008). Plant height had negative indirect effect on seed cotton yield *via* number of bolls per plant (-0.256) and ginning out turn (-0.031) (Table 4.38).

Number of bolls per plant had positive indirect effect through plant height (0.065), ginning out turn (0.040), number of monopods per plant (0.049), number of seed per boll (0.031) and seed index (0.025). Number of seed per boll had positive indirect effect through ginning out turn (0.040), number of monopods per plant (0.041), boll weight (0.037), plant height (0.027) and seed index (0.016), whereas this trait exhibited negative indirect on seed cotton yield effect *via* number of locules per boll (-0.024) and oil content (-0.016) (Table 4.38). Ginning out turn, number of locules per boll and number of monopods had positive indirect effect on seed cotton yield through number of bolls per plant, boll weight, seed index, plant height, number of seed per boll but had negative indirect effect *via* oil content and fibre length. The maximum contribution towards seed cotton yield by number of bolls per plant followed boll weight.

4.4.3 Residual effect

Residual effect was observed 0.18 which revealed that there were some other traits or factors besides these studied traits which were having effects on dependable variable *i.e.,* seed cotton yield per plant. It is denoted by “R” (Table 4.39).

Table 4.39: Pooled direct (diagonally) or indirect (off the diagonal) effects of various traits contributing to seed cotton yield

	DFF	SI	BW	PH	NOB	GOT	NOS	NOL	NOM	OIL	GC	PC	FL	FU	FS	MIC	FM	SCY
DFF	**-0.088**	-0.011	-0.063	-0.014	-0.006	-0.028	-0.005	0.004	-0.017	-0.007	0.006	-0.005	0.001	0.004	0.003	0.009	0.008	-0.226
SI	0.011	**0.091**	0.027	0.016	0.154	0.009	0.016	-0.004	0.027	-0.003	0.013	0.003	0.000	-0.002	0.000	-0.005	-0.002	0.353
BW	0.017	0.007	**0.334**	0.003	-0.131	0.040	0.010	-0.008	0.026	0.001	0.001	0.005	-0.001	-0.008	-0.003	0.000	-0.002	0.288
PH	-0.009	-0.010	-0.007	**-0.144**	-0.256	-0.031	-0.017	0.009	-0.044	0.025	-0.010	-0.011	-0.001	-0.009	-0.002	-0.003	-0.002	-0.521
NOB	0.001	0.025	-0.077	0.065	**0.570**	0.040	0.031	-0.011	0.049	-0.021	0.032	0.005	-0.001	0.004	0.000	-0.005	0.004	0.714
GOT	0.022	0.007	0.117	0.039	0.199	**0.114**	0.031	-0.011	0.048	-0.009	0.018	0.007	-0.003	-0.001	-0.003	-0.006	0.001	0.576
NOS	0.005	0.016	0.037	0.027	0.199	0.040	**0.089**	-0.024	0.041	-0.016	0.030	0.005	-0.002	0.007	-0.001	-0.005	0.001	0.448
NOL	0.007	0.006	0.047	0.024	0.114	0.023	0.038	**-0.055**	0.027	-0.011	0.015	0.006	-0.001	0.005	0.000	-0.004	-0.001	0.25
NOM	0.014	0.023	0.080	0.059	0.262	0.051	0.034	-0.014	**0.107**	-0.012	0.026	0.009	-0.002	-0.002	-0.002	-0.005	0.003	0.631
OIL	0.007	-0.004	0.003	-0.045	-0.148	-0.012	-0.018	0.007	-0.016	**0.082**	-0.012	-0.009	0.000	-0.014	-0.002	-0.013	0.003	-0.2
GC	0.004	-0.010	-0.003	-0.012	-0.148	-0.017	-0.022	0.007	-0.022	0.008	**-0.122**	-0.001	-0.001	0.001	-0.001	-0.001	0.001	-0.334
PC	-0.015	-0.011	-0.060	-0.056	-0.108	-0.030	-0.017	0.012	-0.033	0.025	-0.006	**-0.029**	0.001	-0.005	0.000	-0.002	0.003	-0.333
FL	-0.005	-0.002	-0.020	0.004	-0.034	-0.019	-0.009	0.003	-0.009	0.002	0.007	-0.001	**0.019**	-0.027	0.009	0.034	-0.003	-0.046
FU	0.007	0.004	0.057	-0.030	-0.051	0.002	-0.013	0.006	0.005	0.025	0.002	-0.003	0.012	**-0.045**	0.001	0.015	-0.004	-0.013
FS	-0.020	-0.004	-0.083	0.019	0.000	-0.032	-0.004	0.001	-0.019	-0.015	0.009	-0.001	0.015	-0.003	**0.012**	0.027	-0.001	-0.102
MIC	0.018	0.009	0.000	-0.010	0.063	0.015	0.011	-0.004	0.012	0.023	-0.002	-0.001	-0.015	0.015	-0.007	**-0.046**	0.001	0.087
FM	-0.019	-0.005	-0.020	0.007	0.063	0.002	0.004	0.002	0.009	0.006	-0.002	-0.003	-0.002	0.004	0.000	-0.002	**0.037**	0.067

R= 0.18 DFF- Days to first flower, BW- Boll weight (g), PH- Plant height (cm), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NOB- No. of bolls per plant,, NOL- No. of locules per boll, NOM-Number of monopods per plant, OIL-Oil content (%), GC- Gossypol Content (mg/g), PC- Protein Content (%), SCY- Seed Cotton Yield, FF- fibre fineness (µ/inch), FS- fibre strength (g/tax), FL- fibre Length (2.5% span length) (mm), FU- fibre uniformity (%) and FM- fibre maturity (%).

All the biochemical traits had negative indirect effect on seed cotton yield *via* through number of bolls per plant, boll weight, seed index, plant height, number of seed per boll and number of monopods per plant, but had little positive indirect effect through number of locules per boll (Table 4.38).

Fibre length, fibre strength and fibre uniformity had negative indirect effect through number of bolls per plant, boll weight, ginning out turn and seed index but had little positive indirect effect *via* number of locules and fibre fineness. The highest indirect contribution of these traits was *via* boll weight. Fibre fineness and fibre maturity exhibited positive indirect effect on seed cotton yield through number of bolls per plant, ginning out turn, number of seeds per boll, number of monopods per plant and oil content but negative indirect effect *via* fibre length, gossypol content and protein content. Highest indirect contribution of fibre maturity and fibre fineness on seed cotton yield was *via* number of seeds per boll *i.e.*, 0.063 and 0.063 (Table 4.39).

4.5 Diversity analysis

Dendrogram based on the complete linkage and Squared Euclidean Distance was created by calculating the genetic divergence among 153 *desi* cotton genotypes (150 genotypes and three checks). There are nine clusters formed from all 153 genotypes. High genetic diversity was found in the germplasm collection, as evidenced by the careful inspection of clusters. In Table 4.40, the genotype clustering for each of the nine clusters was represented. Cluster analysis is a very useful and potentially powerful method for classifying the germplasm based on genetic similarity or dissimilarity. Plant breeding methods frequently include categorization of the germplasm as well as the use of efficient and diverse parents to enhance heterosis in crop improvement programmes. Based on the linked magnitude of several quantitative and quality parameters in Euclidean distance form, a dendrogram was produced for the genotypes of *desi* cotton under study. Nine clusters were formed for all the genotypes (Figure 4.6). In the dendrogram (Figure 4.6), clusters were represented by various colours. With 34 genotypes, cluster one was the largest cluster, followed by cluster four with 31 genotypes, cluster three with 26 genotypes and cluster seven with 18 genotypes. There were 12, 12, 10, 9 and one genotypes in Clusters V, VIII, VI, II, and VIV respectively (Table 4.40).

Mean value of 18 morphological, biochemical and fibre quality traits were also estimated for each cluster. Cluster mean values of all the clusters were represented in Table 4.41. Cluster one included the genotypes which were having high value for oil content and fibre fineness, while cluster three includes the genotypes with high value of gossypol content. Cluster five include the genotypes with high value of seed index, whereas, cluster six includes the genotypes with high value for fibre length, fibre strength and fibre uniformity.

Table 4.40: Details of 153 *desi* cotton genotypes distributed in nine clusters based on the diversity analysis on the basis of quantitative traits

Clusters	No. of Genotype	Name of Genotypes
C1	34	HD432, HD324, HD123, P 489, Jubli, H 460, FFS13, 30822 BLL, Sanguinum, AC 3347, NGPA 1-9-1, FFS15, FFS, FFS16, CISA 21, PA 405, FFS19, RG 255, LD 814, LD 805, LD 713, CISA 6, RG 395, HD 453, CINA 347, S7060, HD 550, HD 544, HD 535, HD 541, HD 545, HD 548, HD 549 and HD 556
C2	9	S 302, FFS1, HD 404, HD 514, HD 372, FFS3, HD 392, BH 30 and BH 41
C3	26	HD 408, FFS2, B-4, BHO 5 VIII, BH 92, BH 102, FFS5, D 43-21, D 48-154-1, DC 108, EB 31-1, G 20, HD 6, HD 3, RA 1, P 248, AC3233, AC3252, HD 369, S3031, G. Cot 19, PSRV 12489, PSRSV 12516, S6071, S6799, and HD 555
C4	31	HD 379, Arlano, B 2-16-2, G 23, Gao-16 LB VI, GOV 6, H 1, HD 10, HD 20, N-W-1, PL 735, PL 735-1, Y-1, 35/5 B, S2204, S2446, FFS7, DS-5, DS 5-1, S5278, S479, AC 33, D 462-1-1 P4, D 462-1-1 P5, AC 41, Malvi 12, JL 60, LD 327, AC3212, AC3377 and AC S 3028
C5	12	FFS4, D 462-1-1, Garovilli, DS 1, H 52 -519, AC-8, FFS8, FFS9, D 462-1-1 P3, P 485, M 53070 and HD 503
C6	10	BPS, H 476-5, FFS6, Petaloidy, AC3376, CINA 329, AKA 9410, DLSA 17, AH 11 and AKA 210
C7	18	DC-93, S351, S479-1, FFS10, H 248, H 174, 79/Lohit, CC1-1-3-41, FFS14, HD 328-1, HD 418, AKA 315, FFS21, HD 521, HD 524, FFS17, FFS18 and HD 543
C8	12	FFS11, Vira 6, AC3269, FFS12, DS 5-2, DS 5-3, DS 5-4, RG 260, HD 107, S7060 A, HD 542 and HD 551
C9	1	AKA 9623-2

Cluster four includes the genotype with high value for days to first flower. Cluster nine included the genotype with high value of boll weight, plant height, number of bolls per plant, ginning out turn, number of seeds per boll, number of locules per boll, number of monopods per boll, protein content, fibre maturity and seed cotton yield (Table 4.41).

The following aspects should be taken into consideration when selecting the desirable genotypes: Clusters displayed the greatest intra-cluster distance, clusters divided by their greatest inter-cluster distance and the genotypes performed good in selected cluster. Inter and intra cluster distances was represented in Table 4.42. The maximum intra-cluster distance was recorded by cluster eight (113.68) followed by cluster nine (99.08), cluster one (97.30), and cluster three (91.21). Least intra-cluster distance was shown by cluster two *i.e.,* 58.45 (Table 4.42). Maximum inter cluster distance was recorded between cluster five and cluster six (182.01) followed by cluster two and cluster six (172.0) and cluster three and five (171.39), which indicates that high genetic diversity between the genotypes of these clusters. Graph 4.5 represents the similarity index among different genotypes of *desi* cotton.

Fig. 4.5: Heatmap depicting similarity index of 153 genotypes of *desi* cotton

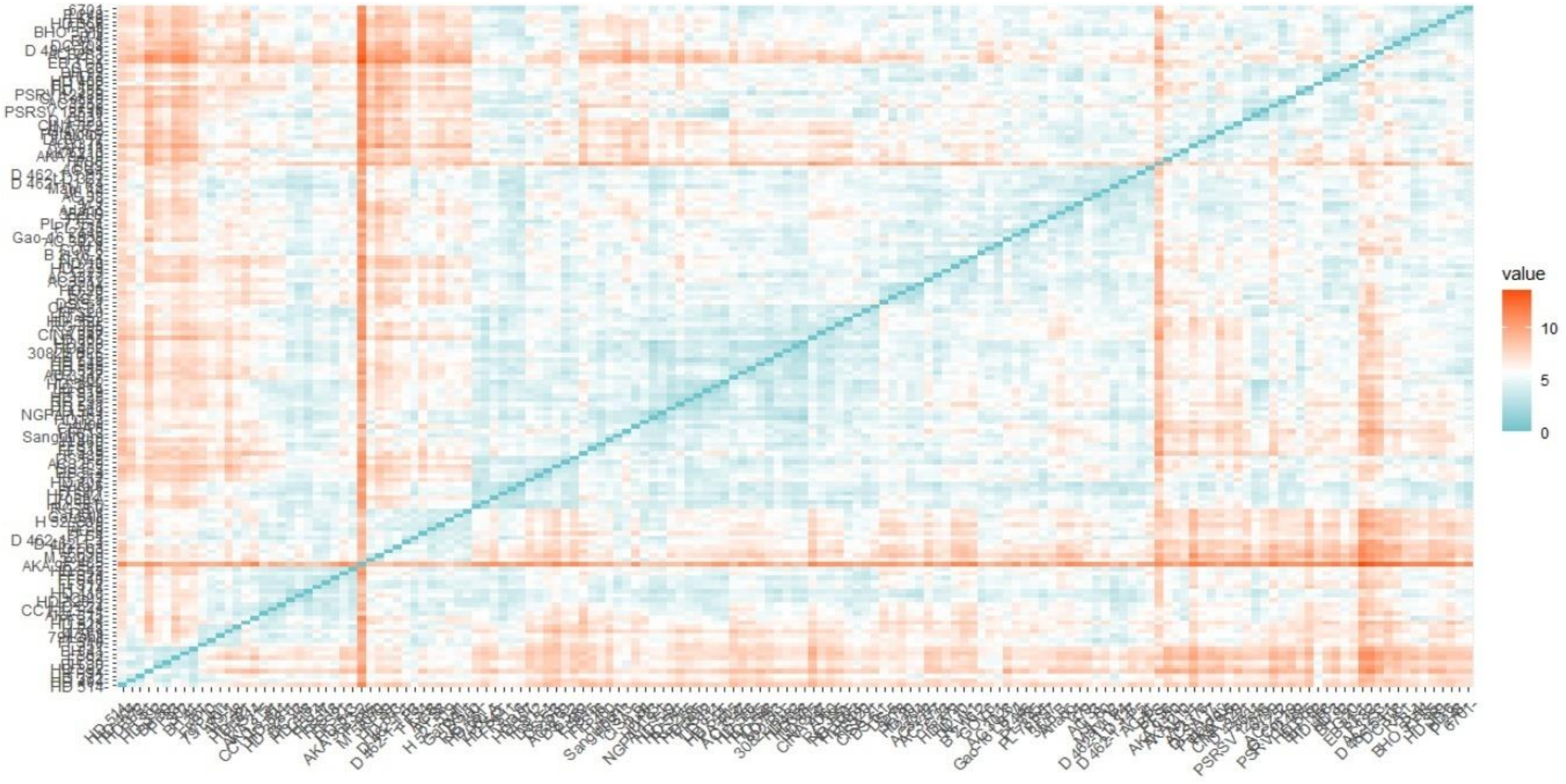


Table 4.41: Cluster mean for all the studied traits

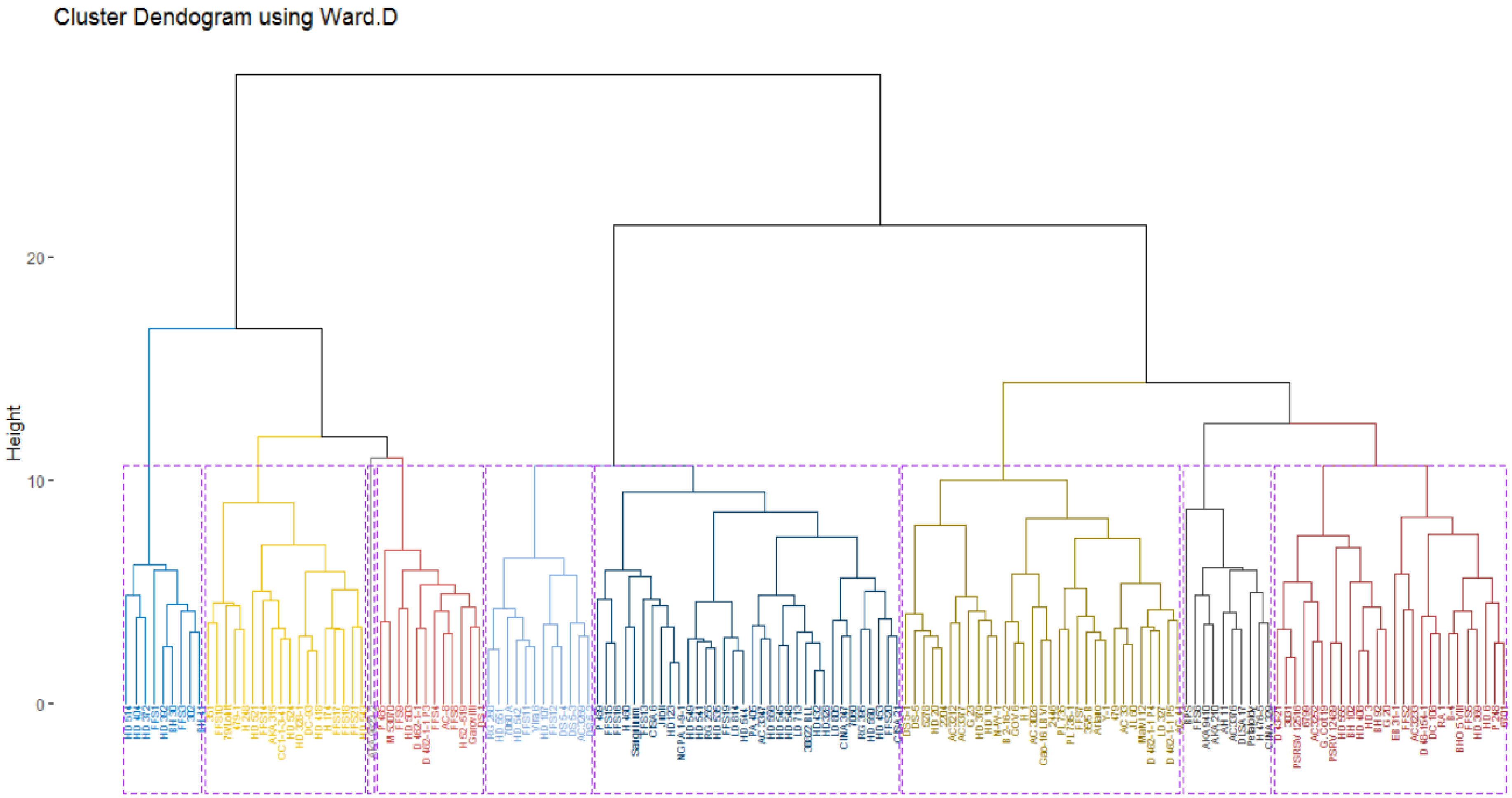
	DFF	SI	BW	PH	NOB	GOT	NOS	NOL	NOM	OIL	GC	PC	FL	FU	FS	FF	FM	SCY
C1	50.97	4.84	3.06	228.86	31.68	38.52	29.62	3.69	1.77	15.10	0.30	19.74	19.83	77.71	19.91	6.43	90.91	87.79
C2	52.33	5.09	2.70	175.13	47.22	39.38	34.86	3.90	2.07	12.24	0.25	16.26	20.71	75.67	22.89	5.84	88.66	115.03
C3	53.72	4.63	2.67	233.53	25.87	35.13	27.06	3.43	1.21	14.94	0.33	19.67	22.69	77.73	23.17	5.81	88.98	65.17
C4	54.99	4.76	2.51	230.33	36.36	35.82	29.82	3.67	1.62	15.01	0.26	20.72	21.72	76.97	22.86	6.09	91.67	84.97
C5	52.46	5.78	2.95	186.69	50.84	40.66	33.63	3.86	2.33	15.06	0.26	17.22	21.26	77.67	21.63	6.21	91.44	144.77
C6	52.20	4.97	2.77	248.25	29.93	36.60	29.78	3.70	1.39	14.75	0.23	20.32	25.09	79.00	24.48	5.44	90.36	79.92
C7	49.11	5.10	2.88	195.52	40.46	38.17	30.39	3.75	2.10	15.07	0.27	18.20	23.41	78.44	22.81	5.93	89.89	115.42
C8	52.79	5.39	2.84	260.18	26.83	36.57	27.40	3.38	1.54	15.00	0.27	18.94	20.98	77.83	20.88	6.12	87.43	75.42
C9	49.50	5.25	3.11	270.00	49.00	42.58	67.84	4.06	2.67	15.05	0.27	21.63	21.50	78.00	20.80	6.30	95.65	151.86

DFF- Days to first flower, BW- Boll weight (g), PH- Plant height (cm), NOS- Number of Seed per boll, GOT- Ginning out turn (%), SI- Seed index (g), NOB- No. of bolls per plant,, NOL- No. of locules per boll, NOM-Number of monopods per plant, OIL-Oil content (%), GC- Gossypol Content (mg/g), PC- Protein Content (%), SCY- Seed Cotton Yield, FF- fibre fineness (µ/inch), FS- fibre strength (g/tax), FL- fibre Length (2.5% span length) (mm), FU- fibre uniformity (%) and FM- fibre maturity (%).

Table 4.42: Inter and Intra cluster distances of 153 genotypes clustered into nine clusters

	C1	**C2**	**C3**	**C4**	**C5**	**C6**	**C7**	**C8**	**C9**
C1	**97.30**								
C2	135.96	**58.45**							
C3	119.09	157.86	**91.21**						
C4	92.65	130.94	100.32	**83.60**					
C5	150.41	83.48	171.39	145.28	**83.60**				
C6	133.76	172.09	94.37	114.23	186.22	**83.60**			
C7	130.13	113.65	142.07	127.53	125.95	154.86	**83.60**		
C8	134.34	171.92	114.24	121.15	182.01	99.21	165.32	**113.68**	
C9	115.94	120.11	131.90	118.52	119.85	128.77	137.23	110.97	**99.08**

Fig. 4.6: Dendrogram showing the clustering pattern of 153 genotypes of *desi* cotton on the basis of morphological, biochemical and fibre traits



4.6 Molecular analysis among genotypes using SSR marker

Genetic diversity analyses the genotypes variability at DNA level. Diversity is prerequisite for both; selection for developing high yielding variety and choosing parents for heterosis breeding. High yield is the major breeding programme in the world of fast-growing population therefore in present investigation 153 *desi* cotton genotypes were analysed for genetic diversity studies. Genomic DNA was extracted by CTAB method (Saghai-Maroof *et al.* (1984), following polymerase chain reaction for amplification of SSR regions. The polymorphism was then checked on 2% agarose gel. A total of 100 SSR markers were used for screening 153 accession lines. Agarose gel showing allelic polymorphism among genotypes for SSR markers are shown in plate 4.18 & 4.19. Salient features of microsatellite marker analysis represented in Table 4.43:

Table 4.43: Allelic diversity in SSR Markers used to screen 153 genotypes of *desi* cotton

Number of genotypes	153
Number of markers used	100
Number of markers that show amplification	94
Number of markers that did not show amplification	6
Number of polymorphic markers	66
Number of monomorphic markers	28
Range of allele	1-5
Total number of alleles in polymorphic markers	182
Average number of alleles	2.73

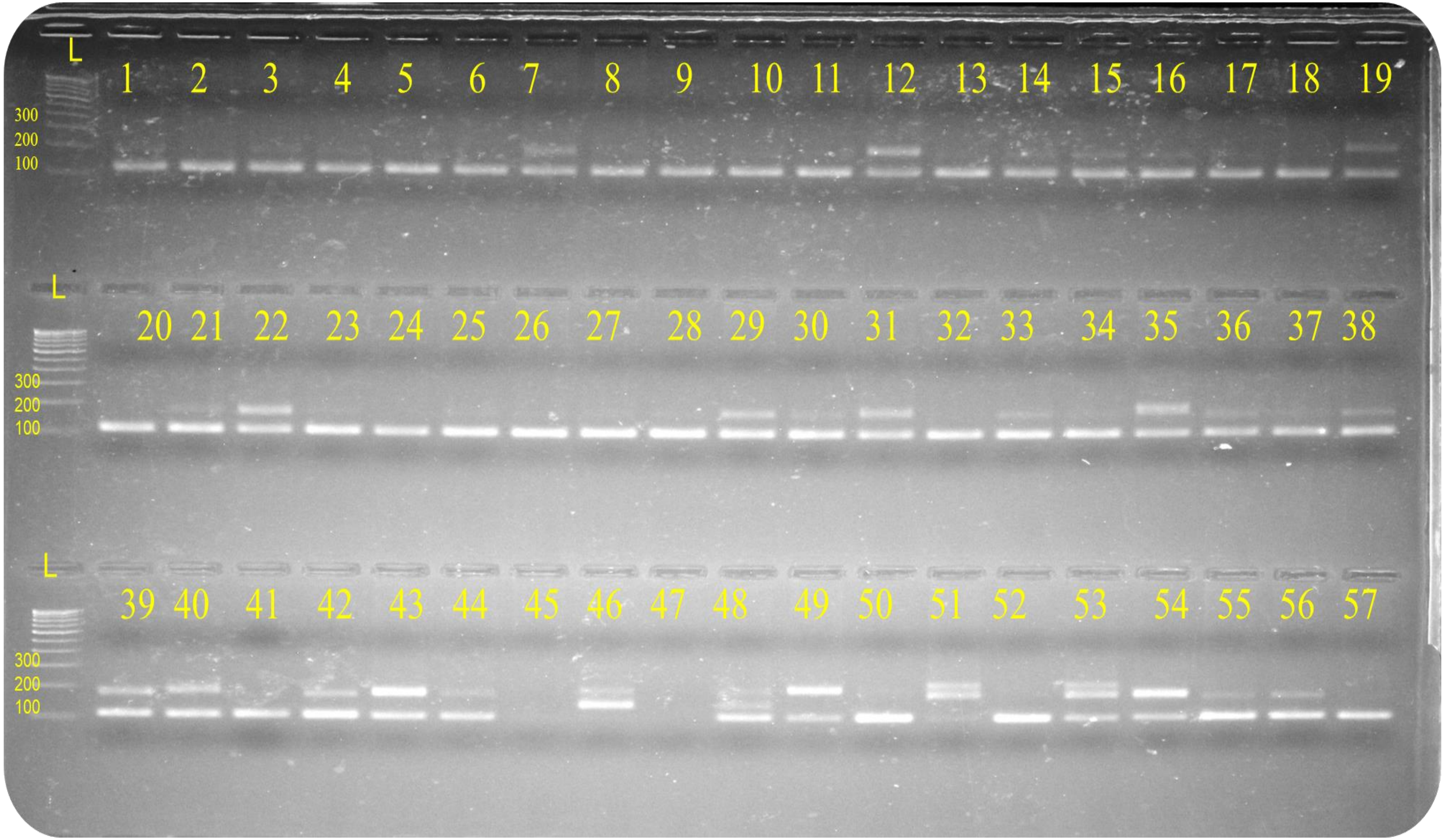
4.5.1 Variation in allelic profile for SSR marker

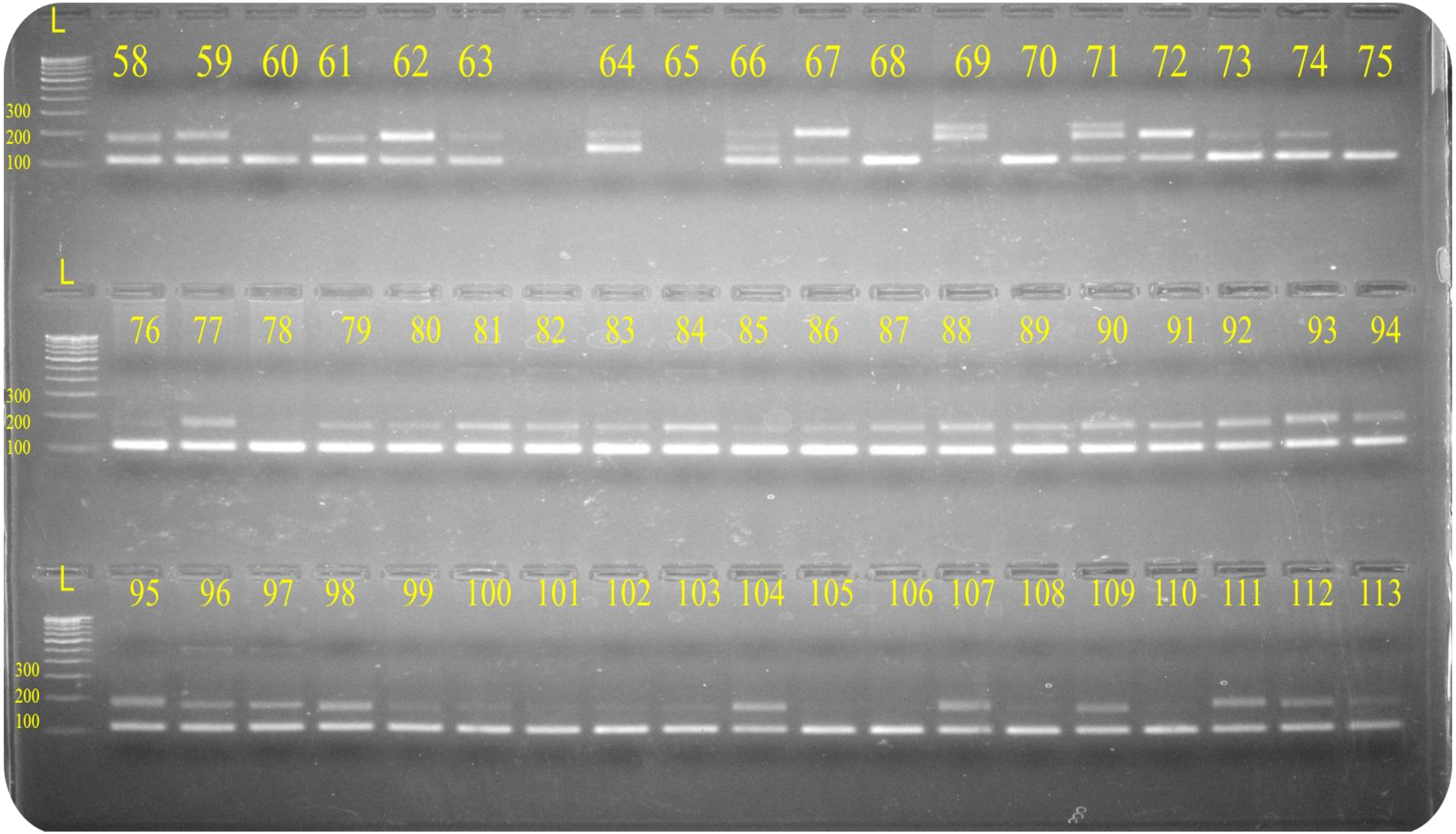
One hundred primers were used for diversity analysis of 153 selected germplasm lines, out of which 66 were found polymorphic, six did not amplified and 28 were monomorphic in nature. List of the 100 primers and there forward and reverse sequences is given in appendex I. One eighty-two distinguished alleles were produced by 66 polymorphic markers with average number of alleles being 2.73 per microsatellite. The range of allele per locus varied from 1 to 5 (Table 4.43). Majority of polymorphic markers displayed two alleles per locus. One type allele was found in all monomorphic primers hence no polymorphism was seen among the genotypes of these alleles. Five alleles were found only by four primers *i.e.,* BNL1679, BNL1017, NAU1167 and BNL2652. The PCR amplified product size varied from 100 base pairs to 800 base pairs, the shortest and longest both band belongs to MUSS599. Polymorphic information content (PIC) of the SSR microsatellite was also estimated to indicate the in formativeness of the marker. PIC ranged from 0.10 (MUSS083) to 0.676 (NAU1167) with an average of 0.38. High is the PIC value higher is the polymorphism detected by it among the genotypes and thus better allelic diversity information is provided by the primer. Markers with PIC value more than 0.5 are considered more informative. In present investigation marker like BNL-1434, BNL1017, BNL1679, MUSS422, BNL2652, MUSS123, MUSS026, NAU1167, NAU1046, NAU1182, NAU1278, BNL-2569, BNL448, BNL-580, BNL-2656, BNL-S3511, BNL-3992, NAU-5499, BNL2544 and BNL-1434 possessed polymorphism more than 50%. List of polymorphic markers along with their band size, allele number and PIC value have been given in Table 4.44.

4.5.2 Molecular marker based genetic diversity analysis

Sixty six polymorphic simple sequence repeats were used for genetic diversity analysis among 153 high yielding genotypes at molecular level. Darwin 6.0 software was used for constructing dendrogram on the basis of dissimilarity value calculated among the genotypes using binary code of polymorphic microsatellite. The UPGMA (unweighted pair group method of arithmetic average) algorithm was used to perform hierarchal cluster analysis and estimated the genetic diversity among genotypes. In the presented dendrogram (Fig 4.7 & 4.8) at dissimilarity value 0.07 formed five groups. In the starting point of forming dendrogram every individual genotype is considered in different cluster. Now as the dissimilarity value decreases the objects join in to form group on the basis of similarity between them. The largest groups were I and II with 93 and 57 genotypes respectively. AC 33, H 52-519 and Vira 6 were single in their respective groups namely III, IV and V and they can be counted as outliers (Table 4.45). Genotypes falling in same group show similarity in the banding patterns created by SSR markers thus they are less diverse from each other whereas genotypes in different clusters have polymorphism at molecular level and they can be selected for heterosis breeding in future programmes.

Plate 4.20: Electrophoretic agarose gel showing allelic polymorphism among 153 *desi* cotton genotypes using primer BNL-226

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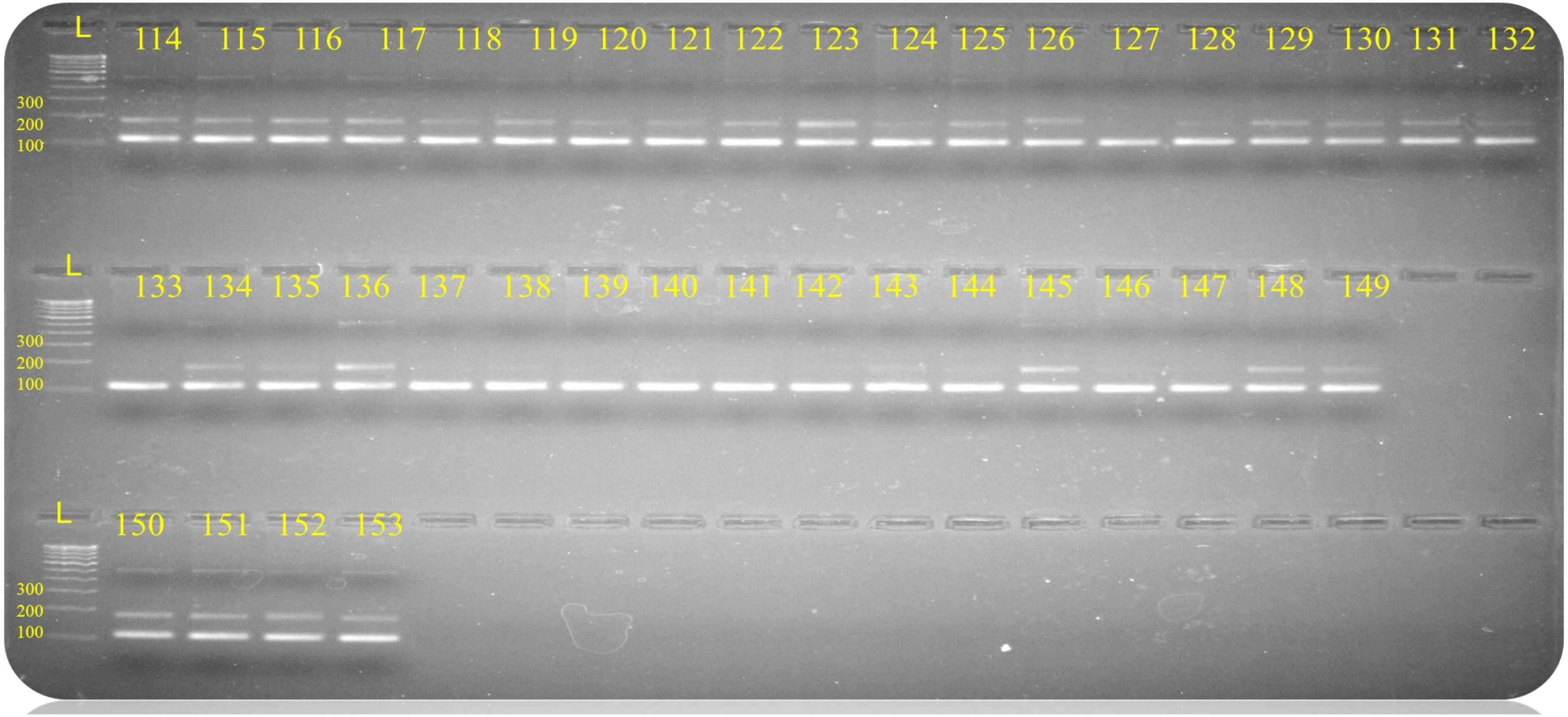
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Table 4.44: No. of alleles, band size, PIC value and H value of polymorphic markers

Sr. No.	Primer Name	No. of alleles	Size of amplified segment (bp)	PIC value	H value	Sr. No.	Primer Name	No. of alleles	Size of amplified segment (bp)	PIC value	H value
1	BNL-3580	2	300-500	0.12	0.13	21	BNL2652	5	150-600	0.69	0.73
2	BNL-3888	3	100-400	0.38	0.51	22	MUSS123	3	200-400	0.56	0.64
3	BNL-3090	3	100-250	0.37	0.49	23	MUSS026	3	200-300	0.55	0.63
4	BNL-3971	2	150-250	0.29	0.36	24	NAU1167	5	150-500	0.76	0.79
5	BNL-1434	3	250-650	0.59	0.61	25	NAU1046	3	150-400	0.59	0.66
6	BNL-3259	2	100-200	0.2	0.2	26	NAU1182	3	100-200	0.59	0.6
7	BNL-226	2	200-600	0.34	0.37	27	NAU1278	3	250-400	0.58	0.69
8	BNL-2443	2	300-500	0.12	0.13	28	NAU1141	2	200-600	0.36	0.48
9	BNL-1395	2	200-400	0.01	0.01	29	BNL-3359	2	300-700	0.32	0.4
10	BNL1604	3	100-400	0.12	0.12	30	BNL-2569	3	150-300	0.52	0.59
11	BNL3792	3	100-400	0.41	0.45	31	NAU1067	2	150-250	0.37	0.49
12	BNL1017	5	50-400	0.63	0.69	32	BNL448	4	150-300	0.68	0.73
13	BNL1672	2	400-500	0.37	0.49	33	BNL598	3	200-400	0.58	0.65
14	BNL4053	2	200-300	0.37	0.5	34	BNL632	2	300-500	0.12	0.13
15	BNL1404	2	300-500	0.37	0.49	35	BNL542	2	200-400	0.14	0.15
16	BNL1673	2	200-400	0.14	0.15	36	BNL834	2	100-200	0.37	0.49
17	BNL1679	5	150-450	0.67	0.72	37	BNL852	2	100-150	0.25	0.3
18	BNL2652	4	250-650	0.25	0.26	38	BNL946	2	100-150	0.12	0.23
19	MUSS422	4	150-300	0.68	0.73	39	BNL1162	2	200-300	0.17	0.19
20	MUSS599	4	100-800	0.67	0.72	40	BNL1395	2	100-200	0.31	0.39

Sr. No.	Primer Name	Size of amplified segment (bp)	No. of allele	PIC value	H value	Sr. No.	Primer Name	Size of amplified segment (bp)	No. of allele	PIC value	H value
41	BNL1408	2	100-150	0.19	0.2	54	BNL-3992	3	150-300	0.52	0.59
42	BNL1421	3	150-250	0.41	0.48	55	BNL-3241	2	150-250	0.34	0.4
43	MUSS026	3	100-200	0.35	0.41	56	NAU-5499	4	150-300	0.68	0.79
44	MUSS083	2	100-250	0.1	0.12	57	NAU4024	3	100-400	0.38	0.49
45	MUSS096a-b	3	120-200	0.47	0.56	58	BNL-3347	3	100-250	0.37	0.46
46	BNL-580	3	300-550	0.53	0.61	59	BNL-4049	2	150-150	0.29	0.36
47	BNL-3537	2	150-250	0.37	0.49	60	BNL2544	3	250-600	0.55	0.63
48	NAU-4024	3	150-450	0.4	0.51	61	NAU-1067	2	100-200	0.11	0.21
49	BNL-2656	3	150-400	0.59	0.66	62	BNL-1434	3	150-600	0.52	0.61
50	BNL-3347	3	100-200	0.41	0.47	63	BNL-4049	2	300-500	0.12	0.13
51	BNL-S3511	3	250-400	0.58	0.66	64	BNL-2572	2	200-400	0.01	0.02
52	BNL-448	2	200-600	0.36	0.48	65	MUSS-99	3	100-400	0.12	0.12
53	BNL-4049	2	300-700	0.32	0.4	66	BNL-3992	3	100-400	0.41	0.45

Fig. 4.7: Dendrogram showing the clustering pattern of 153 genotypes of *desi* cotton on the basis of SSR marker analysis

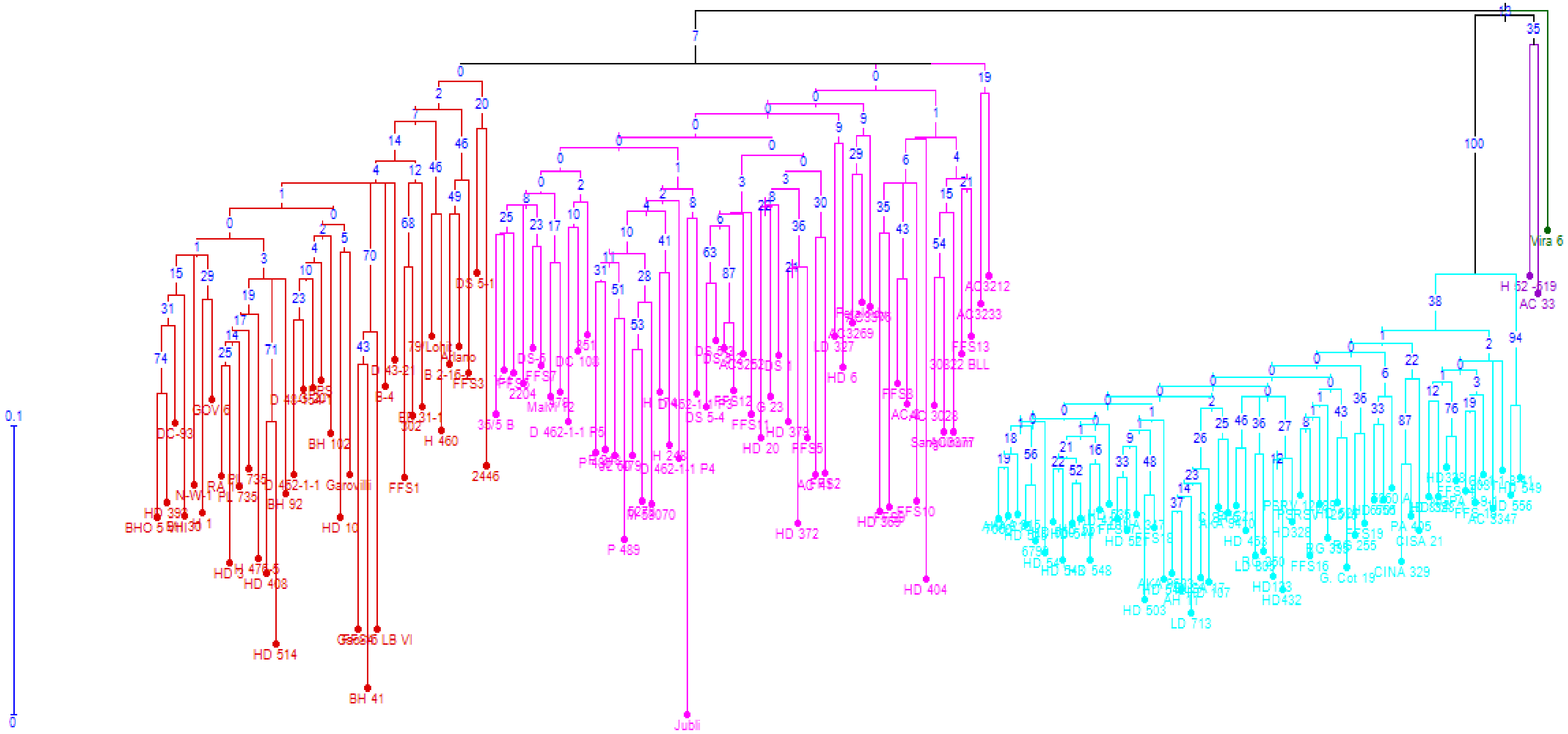

Fig. 4.8: Dendrogram representing genetic relationships among *desi* genotypes constructed using DARWIN

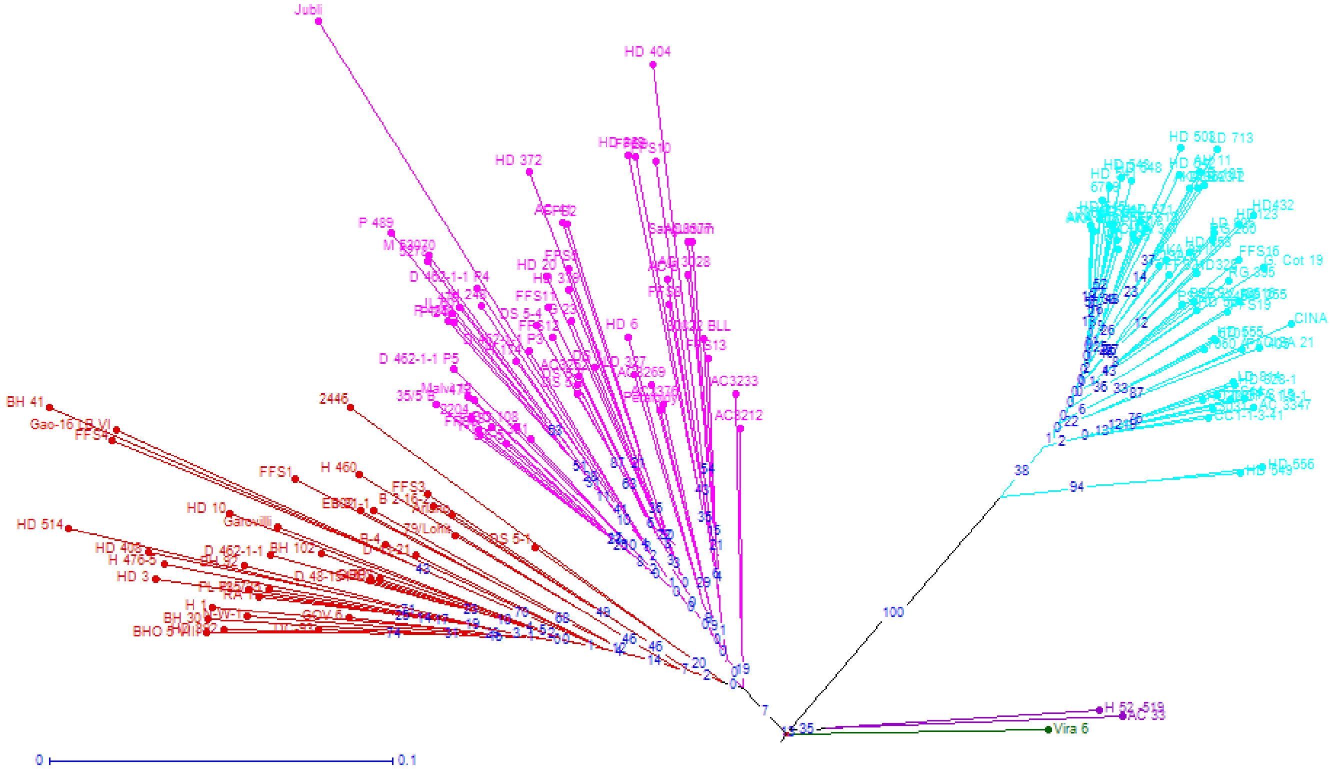

Fig. 4.8: Dendrogram representing genetic relationships among *desi* genotypes constructed using DARWIN

Table 4.45: Clustering of 153 genotypes of *desi* cotton on the basis of SSR marker analysis

Cluster	Genotype Number	Genotypes
C1	93	S 302, FFS1,HD 404, HD 514, HD 408, FFS2, HD 379, FFS3, Arlano, B 2-16-2, B-4, BHO 5 VIII, BH 41, BH 92, FFS4, BPS, FFS5, D 48-154-1, D 462-1-1, DC-93, DC 108, EB 31-1, G 20, G 23, Gao-16 LB VI, Garovilli, GOV 6, H 1, H 476-5, HD 10, HD 3, N-W-1, PL 735, PL 735-1, RA 1, Y-1, 35/5 B, FFS 6, S2446, FFS7, DS-5, DS 5-1, S5278, S351, S479, S479-1, AC-8, FFS8, FFS9, FFS10, FFS11, D 462-1-1 P3, D 462-1-1 P4, AC 41, Malvi 12, P 248, P 485, P 489, JL 60, M 53070, Jubli, H 248, H 174, H 460, LD 327, 79/Lohit, Petaloidy, AC3376, AC3212, AC3377, AC3233, AC3252, FFS12, DS 5-2, DS 5-3, DS 5-4, FFS13, 30822 BLL, Sanguinum, AC S 3028, HD 369, AC 3347, S3031, CC1-1-3-41, FFS14, NGPA 1-9-1, FFS15, HD 328, HD 328-1 and FFS16
C2	57	RG255, HD 542, FFS18, HD 503, LD 805, RG 260, AKA 9410, CISA 6, S6799, HD 535, HD 418, AKA 210, AKA 315, S7060, HD 543, HD 550, HD 544, HD 535, HD 548, HD 553, HD 395, FFS21, PSRV 12489, CINA 347, PSRV 12516, S7060A, HD 555, S6071, FFS 16, CISA 21, PA 405, LD 814, LD 713, DLSA 17, G. Cot 19, HD 107, AH 11, AK 9623-2, FFS 17, HD 541, HD 549, vira 6, CINA 329, HD 432, HD 324, HD 123 and HD 556
C3	1	H 52-519
C4	1	AC 33
C5	1	Vira-6

CHAPTER-V

DISCUSSION

Cotton is an important cash crop in India and is referred to as "white gold" because it plays a vital role in country's economy. It is grown for its fibre, which serves as a raw material for the textile, animal feed, oil, and timber industries. The recent rise of numerous variety development programmes around the globe has resulted in a market overflow with numerous variations and identification uncertainty due to the duplication of plant material. Therefore characterization of genotypes is required so that they can be easily protected and identified. To identify varieties, determine genetic purity and establish the distinctiveness of a new variety from current varieties, various crops need to have descriptors. These descriptors are enlisted by PPV & FRA for different crops which assist in testing varieties for Distinctness, Uniformity and Stability of traits.

Another significant issue is the exploitation of a limited narrow genetic base for producing hybrids or new varieties. Utilizing specific superior parents repeatedly for various breeding programmes has resulted in genetic erosion and yield plateau. DUS testing is useful for analysing the diversity of germplasm lines.

India is a rich source of cotton germplasm and characterization of this germplasm will help in in identifying suitable genotypes to be used as parents for further heterosis programme and creating variability using segregating population. Identification and diversity analysis based on DNA polymorphism and biochemical properties will further assist the breeding programmes. In present investigation efforts were made in characterization of 150 germplasm lines and three checks based on DUS testing, molecular markers and biochemical properties. The findings of the experiment are discussed below:

5.1 DUS characterization

Thirty five morphological traits were recorded on the experimental material for the identification of possible descriptors. Crop stage wise observations were collected and the results have been discussed below:

Hypocotyl pigmentation was observed at seedling stage after 5-6 days of sowing. It was categorized as green hypocotyl (pigmentation absent) and purple hypocotyl in which anthocyanin colouration was present. One thirty three genotypes showed presence of hypocotyl pigmentation whereas 20 genotypes were devoid of hypocotyl pigmentation. Similar studies were conducted by Ponnuswamy *et al.* (2003), Pooja *et al.* (2016), and Reddy *et al.* (2007), where they categorized different genotypes on the basis of hypocotyl pigmentation. It is an important morphological marker that is simple to observe.

Fifty percent flowering is the stage when at least one flower should have opened in 50% of the plant population in the line. Generally, crop attains 50% flowering from 50-60 days after sowing. On the basis of days to first flower *desi* cotton genotypes were classified into early, medium and late category. Among 153 genotypes, 34 were early and 119 genotypes were in medium category. No any genotype exhibited late flowering. Similar results were obtained by Mahesh *et al*. (2021). All the leaf and flower characteristics were recorded at this stage of crop which are discussed below:

On the basis of leaf colour genotypes were categorized as light green and green. One twenty seven genotypes were having light green leaf colour and 26 genotypes had green colour. Three types of leaf shapes were found in experimental material. Out of 153 genotypes, eight genotypes had palmate *i.e.*, normal type of leaf and 145 genotypes had okra type leaf. The leaf pubescence in cotton is classified as sparse, medium and dense. Thirty five genotypes showed sparse hair on leaf blade whereas, 87 genotypes showed presence of medium hair. Thirty seven genotypes were found with dense hair on the leaf. The next leaf character recorded was presence of nectaries. One twenty eight genotypes were found with leaf nectarines, whereas in 25 genotypes leaf nectarines were absent. The leaf characteristics were also studied by Aruna *et al*. (2012), Padmavathi *et al.* (2009), Pooja *et al.* (2016), Sangwan *et al*. (2016), Reddy *et al*. (2007) and Sangwan *et al*. (2021) and concluded that characters like leaf hairiness, leaf colour, leaf size are stable and uniform in performance thus act as useful diagnostic characters for identification. Whereas, Anjani *et al*. (2018) observes that leaf shape, leaf colour, leaf hairiness, gossypol glands and nectraies does not show much variation among the tested genotypes.

Same like hypocotyl anthocyanin pigmentation can be found on leaf petiole and stem of the cotton plant. The presence or absence of pigmentation in petiole and stem was recorded and 17 genotypes had pigmented petiole and stem whereas remaining 136 had green petiole and stem. Grouping of genotypes on the basis of pigmentation on petiole and stem is in conformity with the results of Aruna *et al*. (2012), Padmavathi *et al*. (2009), Sangwan *et al*. (2016), Krishnamoorthi *et al*. (2020) and Sangwan *et al*. (2021).

On the basis of petal colour; out of 153 germplasm lines 10 had cream petals, 14 had pink, 49 had yellow and 76 with white petals. Only one genotype (FFS12) possessed red petal flower. The stigma position in flower may be embedded or exerted. The stigma was exerted in 148 genotypes and five genotypes had embedded stigma, whereas petal spot was present in all genotypes. Variation in petal spot is due to genetic effect and it is due to polygenes which have cumulative effect and usually dominant genes are observed as observed by Jawaharlal (1994), Patil (1996) and Ezilkumar (1999). Purple colouration on stalk of the androecium was also recorded and 19 genotypes showed presence of colouration on anther filament and remaining 134 genotypes had no anther filament colouration. Floral traits are very important descriptors and are easy to score, they have been used by Aruna *et al*. (2012), Pooja *et al*. (2016), Reddy *et al*. (2007) and Sangwan *et al.* (2016), Balakrishnan *et al.,* (2020) and Karena *et al.,* (2021) for identification and characterization of different genotypes.

Boll bursting is the stage when a boll or capsule cracks and fibre comes out of it. Boll related characters were observed at this stage. All the germplasm lines except 13 genotypes had green boll colour in the investigation; only 13 genotypes possessed red boll colour as it had whole body of red colour. Boll surface also forms two groups *i.e.,* smooth or pitted. In 123 genotypes, pitted type bolls were present, while 30 genotypes were having smooth type boll. On the basis of boll shape, out of 153 *desi* cotton genotypes, 23 genotypes were having round bolls, 67 had ovate and 63 were having elliptical type boll shape. Tip prominence at the end was categorized as blunt (absence) or pointed (presence). Nineteen germplasm lines had blunt end and pointed tip bolls were found in 134 germplasm lines. Genotypes revealed a great variation in boll shape and tip prominence hence, these two traits are very important discriptors. Grouping on basis of boll shape, colour, surface and tip prominence was also performed by Aruna *et al*. (2012), Padmavathi *et al*. (2009), Pooja *et al*. (2016), Reddy *et al*. (2007), Balakrishnan *et al.,* (2020), Sagar *et al.,* (2019), Karena *et al.,* (2021) and Sangwan *et al.* (2021).

On the basis of boll opening 89 genotypes were grouped under open category while 65 genotypes under semi open category. Anjani *et al*. (2018) and Rathinavel *et al.* (2019) also reported that genotypes have sufficient variation for boll opening. Fibre colour of almost all the genotypes was observed as grey and except genotype S7060 which had brown fibre colour. Boll weight is categorized on the basis of a single boll weight in grams. The categories made were; small, medium and large on the basis of boll weight. Five genotypes were under small size category with weight of boll being less than 2 g. Ninty five genotypes had boll weight between 2-3 g and come under medium category. Fifty three genotypes had boll weight more than 3 g and were in large category. Begum and Hossain (2011) were able to find out a superior genotype mainly due to its high seed cotton yield and average weight of seed cotton per ten bolls; hence boll weight is a vital character for identification grouping of genotypes. Aruna *et al.* (2012), Padmavathi *et al*. (2009), Pooja *et al*. (2016) and Sangwan *et al.* (2016) also studied these traits in different genotypes and were able to characterize them.

After the crop was finally harvested in the month of October, seed and fibre quality parameters were examined. Seed fuzz is the fibre which remains on seed coat after ginning. In present study 152 genotypes had grey seed fuzz colour, whereas, genotype S7060 had brown colour seed fuzz. Seven genotypes (FFS7, PL 735, S2446, S479, FFS14, CC1-1-3-41 and FFS18) had medium fuzz density while 146 genotypes showed dense fuzz. Seed index or hundred seed weight is divided into various groups having weight between 3g to 9g. Out of 153 genotypes, 88 fell into small group in which weight recorded were 3g-5g and 65 under medium group with weight range 5.1-7 g. No genotype was found with bold or very bold type seeds and very small category. Variation in 100 seed weight may be due to inherent properties that were present during the period of crop growth, seed development and maturation. Embryo size and other food reserve materials with respect to genotypes can also alter seed weight and generates variation. Reddy *et al*., (2007) examined genotypes based on 100 seed weight. Ginning percentage is the amount of fibre extracted from seed cotton yield after ginning. Only two genotypes *i.e.,* EB 31-1 (29.10%), and AC3212q (30.05%) had very low ginning percentages, eight genotypes had low ginning percentages, thirty genotypes belonged to the medium group, thirty five had high ginning percentage and the majority of genotypes, 95, had recovered lint greater than 36%, placing them in the very high group. Similar findings were reported by Sagar *et al.,* (2019), Santhy *et al.,* (2020) and Sangwan *et al.* (2021).

Fibre quality traits are important to estimate as the major product of cotton crop is its fibre. Cotton is the second most developed sector in textile industry thus with high productivity and production, fibre quality also has to be maintained. Among the 153 examined genotypes, 43 genotypes had short fibre length (20 mm), 97 genotypes had medium fibre length (20.5-24.5 mm) and 13 genotypes showed medium long fibre length (27.5-32 mm). On the basis of fibre strength, 33 genotypes were found in weak category (17-20.0 g/tex), 100 genotypes had medium fibre strength (21.0-24.0) and 20 genotypes had strong (25.0-28.0 g/tex) fibre strength. No genotype showed very poor as well as very strong fibre strength. On the basis of fibre maturity *desi* cotton genotypes were classified into five classes *i.e.,* poor, fair, average, good and excellent. All the studied genotypes possessed excellent fibre uniformity *i.e.,* more than 47%. Fibre maturity is another index for fibre quality in which development of fibre walls are assessed. All the genotypes possessed very good fibre maturity. Observations recorded for fibre fineness revealed that among 153 *desi* cotton genotypes neither a genotype with very fine nor fine fibre was found. One genotype had medium type of fibre fineness, 63 genotypes had coarse (5.9-6.0 μ/inch) fineness of the fibre, and 89 genotypes had very coarse (>6 μ/inch) type of fibre fineness. Balakrishna *et al*. (2016) studied seven lint descriptors and were able to identify good fibre quality genotypes which had potential to be used as parents in further hybridization programme. Thus, fibre quality parameters are very important descriptors. Iqbal *et al*. (2015) characterized 26 accessions of *Gossypium arboreum* on basis of fibre quality traits.

5.2 Analysis of variance and other genetic parameters

Mean sum of square for treatment (adjusted) and blocks (adjusted) were significant for boll weight, days to first flower, plant height, number of seed per boll, ginnining out turn, number of bolls per plant, number of monopods per plant, oil content, gossypol content, protein content, seed cotton yield, fibre strength, fibre length, fibre uniformity and fibre maturity which indicated that sufficient variability is present among genotypes. Whereas mean sum of square was found non-significant in both the conditions for seed index and number of locules per boll demonstrating that not sufficient variability was found for these traits. In order to evaluate the experimental data in terms of variance between checks (controls), between test genotypes (treatments), and between test genotypes and checks, additional analysis was computed. Under both the condition [treatment (adjusted) and blocks (adjusted)] mean sum of square for checks was found significant for boll weight, plant height, number of bolls per plant, number of locules per boll, seed cotton yield, fibre maturity and fibre fineness which indicates that significant difference was present among three checks for these traits. While very less or no variability was found for the traits number of seed per boll, ginning out turn, number of monopods per plant, seed index, oil content, gossypol content, protein content, fibre strength, fibre length, fibre uniformity and days to first flower among three checks. For treatment *vs* checks under both the conditions non-significant mean sum of square was found for seed index, number of locules per boll and gossypol content while for rest of the studied traits significant differences was found for test treatments and checks. These results indicated that for these traits genotypes were significantly different from the three checks. The block effect when the treatment effect is eliminated was found non-significant for all the studied traits except days to first flower which demonstrated that blocks have significant effect on the trait days to first flower. Similar findings were reported by Manivanan *et al.* (2018) and Suman *et al*. (2021).

Genetic parameters, like coefficients of variation, heritability, genetic advance as percent of mean *etc.* helps breeder to select the appropriate breeding method. Coefficient of variation is further divided into genotypic and phenotypic coefficient of variation which provides the information about the heritable variability present in the material. Variability is a pre-requisite to start any breeding programme as selection will not be effective without genotypic variation. Heritability and genetic advance as percent of mean gives more insight into the gene action behind the trait which helps to improve precisely a specific trait in the material. In present investigation GCV, PCV, heritability and genetic advance as percent of mean were worked out, that is discussed below.

Days to first flower, ginning out turn (GOT %), oil content, fibre length, fibre uniformity, fibre strength and fibre fineness possessed low GCV and PCV values. Sundas *et al.* (2010) also found that days to 50% flowering had low GCV and moderate PCV. The GOT % had low GCV and PCV in the studies of Gururajan and Sunder (2004) and Gopikrishnan *et al*. (2013), which is in conformity with our results. Selection for these traits for improvement will not be effective as no significant variability was found for these in the examined 150 germplasm lines. Moderate GCV and PCV values were obtained for plant height, boll weight, number of seeds per boll and gossypol content. Preetha and Raveendran (2007), Kalapande *et al.* (2008) and Paramjeet *et al.* (2009) all reported moderate GCV and PCV for boll weight.

Dahiphale *et al.* (2015) reported moderate GCV and PCV values for plant height and seed index. Seed index, number of locule per boll and protein content had low GCV and medium PCV. Higher PCV values over GCV gives an indication of role of environment in creating variability, but when the difference between two is higher it means heritable variation is less and variability is caused by environmental effect thus trait cannot be improved. High variability was found in number of bolls per plant, seed cotton yield per plant and number of monopods per plant; hence presence of ample variability makes sure that selection for these traits will be effective. High PCV and GCV for number of bolls, number of monopods per plant and seed cotton yield were also reported by Aarthi *et al.* (2018) and Pujer *et al*. (2014). Devidas *et al*. (2017) also found that number of bolls possessed high GCV and PCV but seed cotton yield was found with moderate GCV and PCV.

Heritability was found high for all the traits *viz*. days to first flower, plant height, number of monopods per plant, number of seeds per boll, boll weight, number of bolls per plant, ginning out turn, oil content, protein content, fibre length, fibre uniformity, fibre strength, fibre fineness, fibre maturity and seed cotton yield per plant except seed index, number of locule per boll and gossypol content which exhibited medium heritability. High heritability and genetic advance as percent of mean for 50% flowering, boll weight and lint index was also observed by Sundas *et al*. (2010). Genetic advance as 5% over mean was high for plant height, number of monopods per plant, number of seeds per boll, boll weight, number of bolls per plant and seed cotton yield per plant. High genetic advance as percent of mean for plant height was in conformity with Ranganatha *et al.* (2013) and Vinodhana *et al.* (2013). Khokhar *et al*. (2017) revealed possession of high genetic advance as percent of mean by number of monopodial. Boll weight with high genetic advance as percent of mean value was also observed by Ranganatha *et al*. (2013), Pujer *et al.* (2014) and Vekariya *et al*. (2017). High genetic advance as percent of mean for seed and lint index was also reported by Ahsan *et al*. (2015), the same has been observed in present investigation.

Additive gene action was predominant in characters like plant height, number of monopods per plant, number of seeds per boll, boll weight, number of bolls per plant and seed cotton yield per plant as they possess high heritability paired with high genetic advance as percent of mean. High genetic advance as percent of mean along with high heritability was possessed by boll weight and number of monopodia per plant in the experiments conducted by Nandhini *et al.* (2019). These traits can be improved by direct selection in any breeding programme; also their association with yield is higher, so yield per plant will also improve simultaneously. Seed cotton yield per plant possessed high heritability and moderate genetic advance as per cent of mean in the investigation by Kalapande *et al.* (2008) and Paramjeet *et al*. (2009) whereas we received a combination of high heritability and high genetic advance. Ahsan *et al.* (2015), Dhivya *et al*. (2014), Jarwar *et al*. (2018), Pujer *et al*. (2014), Ranganatha *et al*. (2013) and Vekariya *et al*. (2017) also reported high heritability and high genetic advance for seed cotton yield, indicating additive gene action. This showed the complexity of the trait as different studies comes out with different conclusion. Nandhini *et al.* (2019) and Krishnamoorthi *et al.* (2020) also found high genetic along with high heritability by boll weight, number of monopodia per plant, lint index and fibre fineness.

5.3 Correlation and path studies

In any breeding programme, selection based on yield alone for evolving superior yielding genotypes may not be possible because yield is a complex trait. Characters which are highly correlated with yield are taken into account for selection which is estimated by correlation studies. Path analysis on other hand further divides this association into direct and indirect effects towards yield and hence gives a deeper insight for choosing traits in selection programme.

In the studied genotypes seed cotton yield per plant (dependent variable) exhibited positive correlation with almost all traits except days to first flower, plant height and biochemical as well as fibre quality traits. Highest association with seed cotton yield was shown by number of bolls per plant followed by number of monopods per plant. Hasan and Latha (2017) also reported highest association between number of bolls per plant and seed cotton yield. Other characters which revealed a positive association with yield were; boll weight, number of seeds per locule, seed index, number of monopods per plant and ginning out turn. This suggests that selection for improving these traits will also improve seed cotton yield of plant. Characters like number of bolls per plant, boll weight, seed index, and ginning out turn showed significant positive association with seed cotton yield per plant in the studies of Babu *et al.* (2017). Ul-Allah *et al*. (2017) found that number of seeds per boll was in positive and significant association with single boll yield but did not show significant association with total seed cotton yield, which is in disagreement with present results as here number of seeds per locule is positively related to seed cotton yield per plant. Positive association with different traits mentioned above was also reported by Asha *et al.* (2015), Javaid *et al.* (2017), Nikhil *et al*. (2018), Pinki *et al*. (2018), Rai and Sangwan (2020), Satish *et. al.* (2020), Sakthivel and Somasundaram (2021), Mahesh *et al.* (2021) and Jangid *et. al.* (2022).

On the other hand days to first flower and plant height did not possess any significant association with yield. Although days to first flower had negative values which shows its nature of relationship with seed cotton yield. A negative and non-significant association among days to first flowering and cotton yield was also reported by Kumar and Ravikesavan (2010). Chaudhari *et al*. (2017) also reported a negative but highly significant association, whereas Pujer *et al*. (2014) observed a positive relationship between flowering days and yield. Taking the fibre quality parameters into account, 2.5% fibre span length, fibre strength and fibre uniformity established a negative relation with seed cotton yield whereas fibre maturity and fibre fineness exhibited positive association but all of these have non-significant relationship. The negative association between quality and quantity suggests that selection has to be done very precisely as solely focusing on one trait will deteriorate other. The reason for negative association may be the linkage between loci of yield and quality traits. To break this linkage selection of outliers with better fibre and yield has to be made and then using these outlier lines in a recurrent selection programme is the suggested breeding scheme by Clement *et al*. (2012). Fibre quality traits did not significantly correlate with seed cotton yield according to the findings of Rai and Sangwan (2020), Gnanasekaran *et. al.* (2020), Satish *et. al.* (2020), Sakthivel and Somasundaram (2021) and Mahesh *et. al.* (2021) are in conformity with present findings. On the contrary Dahiphale and Deshmukh (2018) reported a positive association of fibre length and yield which is not in support with presented results.

Inter relationship among the traits was also examined and it was seen that number of bolls per plant showed positive correlation with number of seed per boll, ginning out turn and number of monopods per plant but negatively associated with fibre quality parameters. Patel *et al.* (2013), Salahuddin *et al.* (2010), Vinodhana *et al*. (2013) worked out that number of bolls per plant had strong positive association with number of monopods per plant, number of sympods per plant and plant height, same was reported in present experiment. Boll weight had a significantly high correlation with ginning out turn and number of monopods per plant. In the studies of Vinodhana *et al.* (2013) a positive relationship was noticed between boll weight and number of monopods per plant. It is obvious that when seed gets bolder and heavier it will also increase the single boll weight provided, whereas number of seeds per boll are not much affected. Quality parameters among themselves have positive association with each other. This implies that improving for one quality trait other traits may improve simultaneously and automatically. Nandhini *et al*. (2019) also encountered positive association among bundle strength, elongation percentage and uniformity ratio.

The path analysis estimated residual effect as low as 0.18. Residual effect measures the role of other independent variables on dependent variable which were not included in the studies. The results of the experiment revealed that maximum direct positive effect was exhibited by number of bolls per plant followed by boll weight, ginning out turn and number of monopods. Whereas maximum negative direct effect was exhibited by plant height followed by gossypol content, days to first flower, number of locules per boll and protein content. Hasan and Latha (2017), Chaudhari *et al*. (2017) and Mahdy *et al.* (2021) also reported high positive direct and indirect effects of number of bolls and boll weight on seed cotton yield. Plant height showed a positive direct effect in the studies of Dahiphale and Deshmukh (2018) but negative effect was also observed by Nikhil *et al*. (2018). Reddy *et al.* (2019) unravelled the seed index effect as positive in their studies. Manomani *et al*. (2019)

also reported a positive contribution of days to first flower towards seed cotton yield per plant, which is again in agreement with the results presented. Whereas traits like fibre maturity, number of monopods per plant, number of locules per boll, number of seeds per locule, ginning percentage, fibre length and fibre fineness possessed negative direct effect on seed cotton yield per plant.

Boll weight exhibited positive indirect effect on seed cotton yield *via* ginning out turn and number of monopods per plant, but negative indirect effect through number of bolls per plant (-and number of locules per boll. Plant height had negative indirect effect on seed cotton yield *via* number of bolls per plant and ginning out turn. Babu *et al.* (2017) also emphasizes on the number of bolls and boll weight for improving yield per plant.

Number of bolls per plant had positive indirect effect through plant height, ginning out turn, number of monopods per plant, number of seeds per boll and seed index. Number of seeds per boll had positive indirect effect through ginning out turn, number of monopods per plant, boll weight, plant height and seed index, whereas this trait exhibited negative indirect effect on seed cotton yield effect *via* number of locules per boll and oil content. Ginning out turn, number of locules per boll and number of monopods had positive indirect effect on seed cotton yield through number of bolls per plant, boll weight, seed index, plant height, number of seed per boll but had negative indirect effect *via* oil content and fibre length. The highest contribution was by number of bolls per plant followed by boll weight. Fibre quality parameter did not show any indirect large positive effect through any trait. Chaudhari *et al*. (2017) had similar finding where fibre quality traits do not much affect seed cotton yield directly or indirectly.

5.4 Diversity analysis

Genetic diversity is a crucial element of plant breeding that is required to accelerate the breeding programme in order to achieve the goals of crop improvement. Agro-ecological region-specific adaptive breeding strategies and methods for parent selection for hybrid development or recombination breeding can both be learned scientifically through the evaluation of germplasm. Plant breeders are motivated by the genetic diversity and broad genetic basis present in the germplasm to create new, high-yielding enhanced varieties that are tolerant of various environmental circumstances. Genetic diversity should be the only factor considered when choosing genotypes for hybridization. Due to the possibility of genetic drift brought by the frequent movement of breeding material between various centres, genotypes from diverse eco-geographic zones can be grouped together under the same cluster. The evaluation and use of the exchanged material in various geographic locations for hybridization may lead to the clustering of genotypes from various locations into a single cluster. In order to identify the diverse and desired genotypes in terms of inter and intra-cluster distance as well as the mean performance of traits, the cotton genotypes were grouped into several hierarchical clusters using squared Euclidean distance. The following factors should be taken into account when choosing the desirable genotypes *i.e* (i) Clusters with the greatest distance between them; (ii) Clusters with the greatest intra-cluster distance; and (iii) In a chosen cluster, genotypes performed well.

Bisht *et al*. (1998) stated that the availability of passport data for the evaluated gene pool, can be used effectively and efficiently to group them into several clusters. In addition, Knupffer and Van (1995) stated that clustering analysis using data from the core collection was used to examine genetic character data. Cluster analysis of 153 *desi* cotton genotypes (150 genotypes and three checks) with 18 quantitative, biochemical and fibre traits categorised these genotypes into nine clusters. With 34 genotypes, cluster one was the largest cluster, followed by cluster IV with 31 genotypes, cluster III with 26 genotypes and cluster VII with 18 genotypes. There were 12, 12, 10, 9 and one genotype in clusters V, VIII, VI, II and VIV respectively. The maximum intra-cluster distance was recorded by cluster VIII (113.68) followed by cluster VIV (99.08), cluster I (97.30), and cluster III (91.21). Least intra-cluster distance was shown by cluster II *i.e.*, 58.45. Maximum inter cluster distance was recorded between cluster V and cluster VIII (182.01) followed by cluster II and cluster VI (172.0) and cluster III and V (171.39), which indicated that high genetic diversity between the genotypes of these clusters.

The findings of the current study showed that there was greater genetic variability between cluster genotypes than within cluster genotypes, as evidenced by the observed inter-cluster distances being higher than the intra-cluster distances. To obtain a strong heterotic response and superior transgressive segregants, breeding programmes should explore hybridising the clusters with the highest inter-cluster distances (Murty and Arunachalam 1996). The genotypes included in the same cluster should not be included in the crossover programme due to the low level of intra-cluster distances, which showed narrow genetic variability within the clusters. The earlier research of Singh *et al.* (2016), Kumar *et al.* (2018) and Mahesh *et al.* (2021) were found to be in agreement with the current investigation.

5.5 Molecular analysis

In recent time, molecular markers have significantly complemented classical breeding. Markers help in identification of germplasm, estimate genetic diversity, genome mapping, population genetics and taxonomy. DNA based markers are the most powerful tool to uncover polymorphism and genomic variability. Selection of suitable molecular marker can successfully detect genetic diversity among the genotypes. In present studies, SSR markers were used as they are co-dominant in nature, hence can detect heterozygotes. SSR markers are reproducible, abundant and widely dispersed across the genome (Sharma *et al.* 2020). Genetic diversity analysis will support plant breeding programme as it helps in better organization of germplasm and efficient parental selection.

In present investigation a total of 100 SSR primer pairs were run over genomic DNA of 153 *desi* cotton genotypes. Sixty six markers showed polymorphism in the banding pattern of genotypes whereas 28 were monomorphic in nature. Gawande *et al.* (2019) used 116 SSR primers of estimating variation among three genotypes *i.e.,* MCU5, PKV Rajat and AKH-081 and got 64 polymorphic markers. A total of 182 unique alleles were produced by 66 polymorphic microsatellites with average number of alleles being 2.73 per microsatellite. These results were comparable with the studies of Kusuma *et al*. (2018); they reported average number of alleles as 3.3 and Tyagi *et al*. (2014) reported 3 alleles per locus. Bertini *et al*. (2006) evaluated 53 *desi* cotton accessions using 31 pairs of SSR primers which produced a total of 66 alleles with an average of 2.13 alleles per SSR locus which is comparable with present findings. The variation in number of alleles of each marker depends on two things; the marker and accession which is being genotyped (Lacape *et al*.; 2007).

The range of PCR amplified products varied from 100 base pairs to 360 base pairs belonging to BNL4028. Shekhawat and Tomar (2018) reported amplicon size range from 100 to 600 bp which is quite comparable with amplicon range. Different genotypes showed variable amplification which can be used in identification of cotton genotypes. The PCR amplified product size varied from 100 to 800 base pairs, the shortest and longest both band belongs to MUSS599. Polymorphic information content (PIC) of the SSR microsatellite was also estimated to indicate the informativeness of the marker. PIC value ranged from 0.10 (MUSS083) to 0.676 (NAU1167) with an average of 0.38. The present results are comparable with average PIC value 0.40 reported by Bertini *et al*. (2006). Moiana *et al*. (2015) diagnosed PIC range from 0.09 to 0.58 with an average number of alleles being 0.361 per locus, which is lower than presented results. Higher estimates (0.80) were reported by Zhang *et al*. (2011). Higher is the PIC value higher will be the polymorphism detected by it among the genotypes and thus better allelic diversity information will be provided by the primer. Markers with PIC value more than 0.5 are considered more informative. In present investigation markers like BNL-1434, BNL1017, BNL1679, MUSS422, BNL2652, MUSS123, MUSS026, NAU1167, NAU1046, NAU1182, NAU1278, BNL-2569, BNL448, BNL-580, BNL-2656, BNL-S3511, BNL-3992, NAU-5499, BNL2544 and BNL-1434 possessed polymorphism more than 50%.

Principal coordinate analysis (PCoA) and unweighted pair group method of arithmetic average (UPGMA) algorithm was used to estimate the genetic diversity among genotypes using Jaccard's dissimilarity values. In the presented dendrogram (Fig 1) at dissimilarity value 0.07, five groups were formed. The largest groups were I and II with 93 and 57 genotypes respectively. AC 33, H 52-519 and Vira 6 were single in their respective groups namely III, IV and V and they can be counted as outliers. The PCoA and UPGMA tree cluster analysis revealed that ample diversity is present among the genotypes. Genotypes in same group show similarity at DNA level thus they are less diverse whereas genotypes in different cluster exhibits more diversity and they can be selected as parents for hybridization programme. The clustering pattern by PCoA and UPGMA were almost similar with some minor differences. These differences occur because PCoA combines some of the factors and forms principal components and clustering is done on the basis of these principal components. Whereas UPGMA forms clusters on the basis of individual dissimilarity values without grouping them into principal components. Similar studies were done by Abbas *et al.* (2015), *et al.* (2013), El-Moghny *et al.* (2017), Kusuma *et al.* (2018), Mishra *et al.* (2013), Saif *et al*. (2017), Seyoum *et al*. (2018), Bilval *et al.* (2017), Bourgou *et al*. (2017), Kusuma *et al.* (2018), Shekhawat and Tomar (2018), Chavhan *et al.* (2021), Kumar *et al.* (2022) and Santosh *et al.* (2022) using microsatellites markers for assessment of genetic diversity among cultivars and their wild relatives in cotton. This study is helpful in assessing diveristy among the genotypes but is not a true picture as Zhang *et al*. (2005) stated that using less number of molecular markers cannot provide information of whole genome; however findings can be used in marker assisted selection.

CHAPTER-VI

SUMMARY AND CONCLUSION

The present study entitled "**Morphological, biochemical and molecular characterization of Asiatic cotton (*Gossypium arboreum* L.)**" was carried out in the research area of Cotton Section, Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar during *Kharif* 2020-21 and 2021-22. The objectives of this study were as follows:

1. Morphological characterization of *desi* cotton germplasm on the basis of DUS traits
2. To study correlation and path analysis among various yield contributing traits
3. Biochemical characterization of *desi* cotton germplasm using different seed quality traits
4. To analyze molecular diversity using SSR markers

The experimental material for the present study comprised of one hundred fifty germplasm lines of Asiatic cotton *Gossypium arboreum*. The experiment material was raised in augmented design with three check varieties *i.e.*, HD 432, HD 324 and HD 123 sown after every 15 genotypes in a single row of 6m length along with row to row distance of 1.35 m and plant to plant distance of 30 cm. All the recommended cultural package of practices were followed from sowing to harvesting the crop.

Five plants were selected randomly for each genotype and the observations were recorded for 35 traits *viz.* hypocotyl pigmentation, leaf colour, leaf pubescence, leaf shape, leaf nectaries, leaf petiole pigmentation, plant stem hairiness, plant stem pigmentation, days to first flower, flower petal colour, flower petal spot, flower stigma, anther filament colouration, pollen colour, plant height (cm), boll surface, boll shape, boll colour, boll opening, number of bolls per plant, number of locules per boll, number of seeds per boll, prominence of tip in boll, boll weight (g), seed fuzz colour, seed index, ginning out turn (%), fibre colour, fibre length (2.5% span length) (mm), fibre strength (g/tex), fibre fineness (μ/inch), fibre uniformity (%), fibre maturity (%), number of monopods per plant and seed cotton yield per plant (g).

One fifty germplasm lines and three checks were characterized based on DUS, seed quality and fibre traits and various statistical analysis were carried out like correlation studies by Karl Pearson, path analysis by Al-Jibouri (1958), GCV and PCV by Burton and Devane (1953), heritability and genetic advance by Allard (1960). Molecular diversity analysis was done using SSR markers. The findings of the experiment have been summarized and concluded below:

- On the basis of DUS characterization ample variation among genotypes was observed for hypocotyl pigmentation, leaf colour, leaf shape, leaf hairiness, flower stigma, leaf nectaries, stem hairiness, boll weight, petiole pigmentation, flower petal colour, boll shape, prominence of tip, plant height, boll opening, seed index, ginning percentage, fibre length, fibre strength and fibre fineness.

- Characters like boll colour, stem pigmentation, anther filament colouration and petiole pigmentation were seen less varied among the genotypes whereas traits *viz.* petal spot, seed fuzz colour, fibre colour and fibre maturity did not show any variations. All the qualitative traits were stable and uniform throughout, whereas, quantitative traits showed some variation as they have more environmental effects.
- Analysis of variance showed that all the traits except number of locules per boll and seed index were significant in both the treatment and block adjusted conditions. This showed all characters have ample amount of variability present among them and further analysis can be done for selection of traits.
- GCV and PCV were high for number of bolls per plant (30.92, 31.68) and seed cotton yield (30.69, 30.96), medium for plant height (12.72, 14.08), number of monopods (23.52, 28.52), single boll weight (17.15, 18.15), gossypol content (10.86, 17.29) and these parameters were found low in days to first flower (6.39, 6.58), seed index (8.18, 13.38), GOT (%) (6.69, 7.72), oil content (4.34, 5.57), fibre length (8.51, 8.83), fibre strength (7.83, 8.3), fibre uniformity (1.5, 1.51), fibre maturity (4.95, 4.97) and fibre fineness (6.39, 6.54).
- High heritability coupled with high genetic advance was observed for most of the traits *viz.* boll weight, plant height, number of monopods per plant, seed index, oil content, number of bolls per plant, fibre fineness, fibre strength and seed cotton yield per plant. This showed the dominance of additive gene action behind the traits hence direct selection will be effective for these traits.
- Correlation studies showed that seed cotton yield per plant was significantly and positively correlated with all the traits except days to first flower (-0.226) and plant height (-0.521) while, negatively correlated with biochemical and fibre quality traits. Thus improving other traits, seed cotton yield per plant will also increase. Fibre quality traits like fibre length was significantly positive (0.754) correlated with fibre strength but negative correlated with seed cotton yield, suggesting that quality and quantity cannot be improved simultaneously as one has to be compromised. Whereas, improving fibre length and fibre strength at a time is possible as they were in positive relationship.
- Path analysis also revealed that maximum contribution towards yield was by number of bolls per plant (0.57), boll weight (0.33), GOT (%) and number of monopods (0.10), hence these characters are important during selection and improvement of seed cotton yield per plant. Other traits like number of seed per boll have significant effect on seed

cotton yield *via* number of bolls per plant (0.19) whereas; fibre quality parameters did not show any significant contribution directly or indirectly with seed cotton yield.

- Cluster analysis of 153 *desi* cotton genotypes with 18 morphological, biochemical and fibre quality traits categorised these genotypes into nine clusters. The inter-cluster distance was observed maximum between cluster V and cluster VIII (182.01) and minimum inter cluster distance was recorded between cluster I and cluster IV (92.65). Intra-cluster distance recorded highest for cluster VIII (113.68) followed by VIV (99.08) whereas lowest intra-cluster distance was observed in cluster II (58.45).
- On the basis of biochemical characterization, the genotype FFS 9, M 53070 and S 302 were having highest protein content and H 460, H 551 and H 555 genotypes had high oil content while FFF, AH 11 and AC 3376 genotypes had lowest gossypol content among all the studied genotypes and at par than checks.
- On the basis of fibre quality parameters FFS2, FFS15, H476-5, FFS4 and CINA 329 were top five genotypes with long and strong fibres, good fibre maturity and medium fibre fineness.
- Molecular marker (SSR) based UPGMA clustering formed five groups of 153 genotypes in which cluster I contains 93 genotypes and cluster II contains 57 genotypes at 76% similarity index. AC 33, H 52-519 and Vira 6 were single in their respective groups namely III, IV and V and they can be counted as outliers. FFS15 and HD 328 or HD 551 and HD 544 showed 98% similarity index, which means they are the most similar genotypes and have similar genetic background whereas genotypes namely Vira 6 and BHO 5 VIII were the most dissimilar genotypes.
- Cluster analysis revealed that the genotypes FFS1 and FFS2 were the most diverse genotypes among all.

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APPENDIX I

Sr. No.	SSR Marker	Forward Primer sequence	Reverse Primer sequence	Tm
1	BNL-3580	CTTGTTTACATTCCCTTCTTTATACC	CAAAGGCGAACTCTTCCAAA	52
2	BNL-3888	GCCCACTTTGCCTCTTACAG	AGCTTTTCCCCTTTCACCAT	48
3	BNL-3090	GAAATCATTGGAAGAACATATACTACA	TTGCTCCGTATTTTCCAGCT	55
4	BNL-3971	CACATATTTTTGCCTCACGC	TGTGGACCCAAAAAGGAAGA	51
5	BNL-1897	TTAAAAGAAGATTGAGATGACATTATG	ATTTGTACTTAGATGTGCCAAATG	49
6	BNL-1434	AAATTCAAGAATCAAAAAACAACA	TTATGCCAAAGTATATGGAGTAACG	48
7	BNL-3259	TTTTGAAATTCCAGCGAAGG	GTCAATACCTGCTTCTCCACG	47
8	BNL-226	TTATTCTCACAGCCGGAACC	TTCACCCTCTCGCTTCTCAT	49
9	BNL-3441	CGTCATAAACCGTGCTTGTG	GGCCACTTTAAGGCTGTCAC	50
10	BNL-2443	TTTATTGGTCGGTCTTTGCC	TTAGGGTGTTCTTTGGGCAC	51
11	BNL-1395	AAGCAGCCAAGAAATACCGA	TCGATAACGGCTACAGTAATCT	50
12	BNL1604	AGAGGGAGTAAAGATTTGGGG	TCCAGTTCTTTTTGCCTTGG	48
13	BNL3792	TTCGAGATCCCCTGTTCTGA	CATATTCCAGTCAAACCAAACG	50
14	BNL3257	CAATCTGGGATCAAAAAAACC	GGTGAAACATAGCGTGTTGC	48
15	BNL1017	AGAAAAAAACTTCCTCATGAACC	GTTTCTCTCAGAATTTGTAGGCC	53
16	BNL1162	GCGCAAGCGTAGGAGTTTAC	TTGAACGATGAAAGGGAAGG	52
17	BNL1672	TGGATTTGTCCCTCTGTGTG	AACCAACTTTTCCAACACCG	51
18	BNL4053	TGAAGGCTTTGAAGCAAACA	AAGCAAGCACCAAGTTAGCC	52
19	BNL1404	CGAGAGCCCACTAACAGAAA	CCATTTGTTTTTTCCCCCTT	51
20	BNL1673	CTCTTAATGCTTGGCCTTGG	AGTACCGGACTCGGCACTAT	53
21	BNL1679	AATTGAGTGATACTAGCATTTCAGC	AAAGGGATTTGCTGGCAGTA	48
22	BNL3147	ATGGCTCTCTCTGAGCGTGT	CGGTTCAGAGGCTTTGTTGT	49
23	BNL3261	AAACGGAAACGAAGAAGGGT	CCCAAACCTGTCTCACCAAC	47
24	BNL2652	TTCATCATTCTAGCCTGAGTCC	GCGATAATCCTTCCAGGGAT	48
25	BNL4029	CGAGGGATAGAGAGGACGAA	GTTTGATTATTATGCTTGTAAAGTTACC	49
26	MUSS422	TGGTTTTGCCCATCTTTACG	GAAAGGGAAGATGAGGAGGG	54
27	MUSS073	TCTCCATGAAACCAAACAAACC	TTAATGCTATTTTCTCCGTCGC	53
28	MUSS599	AAATAACAGCCGAAGATGGG	CAAAAGCTAGCAACATTACAACTCC	55
29	MUSS207	TAGTTTCCTGCATTTTGCCC	TAGCTTCGACTTCGAGCAGC	54
30	MUSS192	GAGCGAAGGATGATCTCAGG	GCTGGAGGACATAACAAATATGC	48
31	MUSS172	TTTCTATCCCACCATTTTCCC	GTGTTTGTGTCACTGTGCCG	53
32	MUSS123	CAATTCCCAAACCTTCTTCTTC	GAAACCATTCTCCACTTCCTTG	47
33	MUSS068	CGAGCTGGTTTATAATATCCCC	GTGGCTGATGAGTTCTCTTGC	49
34	MUSS026	ACACGACTACATTTATCCGTTGG	GAAGAAGCATGATGTTTGAGATCC	48
35	NAU1167	CTGACTTGGACCGAGAACTT	AAGAGCCCTGGACAATGATA	59
36	NAU920	CATCCTAACCCAAAACAAGA	TTGGAGCATTGAAATTACCC	48
37	NAU1009	CATCGATCCAAGAGGAATTT	CAGACTCCATATATCAAGTTCAAGC	55
38	NAU1046	GAAAAAGAGAGGGCTGGTTT	GACCCAAATGCCAGAAATAC	49
39	NAU1182	TGGCTTTCATGTTCTTCAAC	ATGGTGTTTTCCGACAGTTT	48
40	NAU1162	CTGAGTGAGCCATGAAGTTG	TTCGGCTTCTGCTTTTACTT	47
41	NAU1278	ATCATGGAACCTGGTTGTTC	ATGAATTGCGGAGTCTAAGG	48
42	NAU1141	CCCCTCTCTCTGTTTCTCAA	AAGGGGTTTGAAGGGTTATC	58.
43	BNL-3359	TTGTTGTTGGGAATGATGGA	TGACCCTTCACCGACTTTCT	54
44	BNL-2569	CAGAGAGCCATTGTGAACGA	ATAATGCTAGGGCATGTGGC	51
45	BNL-1440	CCGAAATATACTTGTCATCTAAACG	CCCCCGGACTAATTTTTCAA	52
46	NAU1067	GATGCTTTTCTCACCCATTT	ACCATAGCCAAAACAAGGAA	48
47	BNL448	GCAGCTTGCTTTTCTGCTTC	ACGCAAGCTTGGTCAATACC	51
48	BNL530	CGTAGGATGGAAACGAAAGC	GCCACACTTTTCCCTCTCAA	49
49	BNL598	TATCTCCTTCACGATTCCATCAT	AAAAGAAAACAGGGTCAAAAGAA	50
50	BNL632	CAGTTTCCAAAACGGCGTAT	AAACCCTCACACACACTCCC	50.5
51	BNL542	TCGATCACATTTATAAGAACTATTGG	TTCATTTTGAACATTCGCCA	48

52	BNL834	TCGAGATTCATGGCTCTCCT	TGGCAAAAGTGGACATACCA	51.5
53	BNL852	TGCTTTCAGCCAATGACTTG	AACAATGCCCCCAATATTCA	48
54	BNL946	GCTGTTGCTCCACATCTCCT	GGGCAAACAGATAGGCAGAA	52.5
55	BNL1162	GCGCAAGCGTAGGAGTTTAC	TTGAACGATGAAAGGGAAGG	51
56	BNL1395	AAGCAGCCAAGAAATACCGA	TCGATAACGGCTACAGTAATCT	50
57	BNL1408	AAGGGAGAGAAACGGAGAGC	CATTTCACCTCTCCCACCAC	52
58	BNL1421	TGAAGATTTGGAGGCAATTG	GAAATCAAGCCTCAATTCGG	48
59	MUSS011	TGGTAAAGCATCAACATATGGG	CATGTAGGTACCAAAACAAGTCCC	50
60	MUSS026	ACACGACTACATTTATCCGTTGG	GAAGAAGCATGATGTTTGAGATCC	49
61	MUSS083	TCTCGGTTCTAGTTTCGTTTGG	CAATTCTCTTCCCTTGATGTGG	48.5
62	MUSS096a-b	TCTGATAAACAGCGACAAAAGG	AAGAAATGAACTCTCACATGGC	49.5
63	MUSS300	GCGTTGGAAATATTGATGGG	CATGCAAAAGCAATGACAGC	48
64	BNL-580	CTATGTTTGGCCTTGGCATT	TAGTGACAGATATCCCCGGC	50
65	BNL-3537	TGAAATGGACGTGACATGGT	TTGCAGGTTCTGATGAGCAG	51
66	NAU-4024	ACAAGCATCTTCATGGACCT	AGAAGGATGATGCAAAGAGG	49
67	BNL-3535	CTGGGATACATACCGTGGCT	ACTTTGCTGAATAAAGGTGAGTG	51
68	BNL-2656	AACCACAACCAAAATTTCACG	CTTTGGTTTCGTAGGGCTTG	53
69	BNL-3347	AGACTGACATGCAGCTTCCA	ATCTTAATTTTGAGTATAGGATAGGGG	53
70	BNL-3031	AGGCTGACCCTTTAAGGAGC	AACCAACTTTTCCAACACCG	52
71	BNL-3511	TAGAACATAGGGAGGCGTGG	AATGGAGAGACAATGATTTTTCG	53
72	BNL-448	GCAGCTTGCTTTTCTGCTTC	ACGCAAGCTTGGTCAATACC	52
73	BNL-4049	AGCTGTGGAACCAATTGACC	ATATCATTTTACTACTGCTTTTGTGTG	48
74	BNL-3992	CAGAAGAGGAGGAGGTGGAG	TGCCAATGATGGAAAACTCA	50
75	BNL-542	TCGATCACATTTATAAGAACTATTGG	TTCATTTTGAACATTCGCCA	48
76	BNL-3241	GTATTAAAATAATAAGAGTCTAATCTCCCC	GACCATGGACCGAGTTGAGT	51
77	NAU-5499	ATAAACTTTCCCGGCTGATT	CCAGCACAAGACTTGATTGT	48
78	NAU-2000	GAAAATGTTCCCCTCTTGTG	CTAAAGGGGACCAAAGCTG	48
79	NAU4024	ACAAGCATCTTCATGGACCT	AGAAGGATGATGCAAAGAGG	49
80	BNL-3347	AGACTGACATGCAGCTTCCA	ATCTTAATTTTGAGTATAGGATAGGGG	51.5
81	BNL-1694	CGTTTGTTTTCGTG AA AGG	TGGTGGATTCACATCCAAAG	48
82	BNL-4049	AGCTGTGGAACCAATTGACC	ATATCATTTTACTACTGCTTTTGTGTG	50
83	BNL-3580	CTTGTTTACATTCCCTTCTTTATACC	CAAAGGCGAACTCTTCCAAA	48
84	NAU-1067	GATGCTTTTCTCACCCATTT	ACCATAGCCAAAACAAGGAA	47
85	BNL-1434	AAATTCAAGAATCAAAAAACAACA	TTATGCCAAAGTATATGGAGTAACG	47
86	BNL-4047	CACCAAGGAGCTCTGCAAAT	ATCTGCAGCAAATAGTGACTCG	48
87	BNL-4049	AGCTGTGGAACCAATTGACC	ATATCATTTTACTACTGCTTTTGTGTG	49.5
88	BNL-2572	GTCCTATTACTAAAATTGTTAATTTAGCC	CGATGTTAAATCAATCAGGTCA	50
89	MUSS-99	CGGCACGAGCGACCTCCCTCC	GAATGATCAAGCACTGGGATGTC	53
90	BNL-3992	CAGAAGAGGAGGAGGTGGAG	TGCCAATGATGGAAAACTCA	54
91	NAU-934	TGCTTTCGTATCCTTTTTCC	ATTAGAGAAGCCAGGGAGGT	48
92	NAU-1151	TGGTTGCTTTGTATTGCTTG	CGTACTTGCGAAAGAGAACA	47
93	NAU-933	AGCATCAACATATGGGAGAA	GCCATGTAGGTACCAAAACA	50
94	BNL-1694	CGTTTGTTTTCGTGTAACAGG	TGGTGGATTCACATCCAAAG	47.5
95	BNL-686	ATTTTTCCCTTGGTGGTCCT	ACATGATAGAAATATAAACCAAACACG	49
96	BNL-1066	ACATTTCCACCCAAGTCCAA	ACTCTATGCCGCCTCTCGTA	55
97	BNL-1707	TCCTAGGCTGAGTGAGGGCT	AATGACGTCGTTTTATGCCC	47
98	NAU1067	GATGCTTTTCTCACCCATTT	ACCATAGCCAAAACAAGGAA	48.5
99	JESPR-185	CCCAAGCTACAGAGATAACC	CACACAAATTGGGTAAGAATAG	49
100	BNL1053	AGGGTCTGTCATGGTTGGAG	CATGCATGCGTACGTGTGTA	50

ABSTRACT

Title of thesis	:	**Morphological, biochemical and molecular characterization of Asiatic cotton (*Gossypium arboreum* L.)**
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Title of degree	:	Doctor of Genetics and Plant Breeding
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The present investigation “Morphological, biochemical and molecular characterization of Asiatic cotton (*Gossypium arboreum* L.)” was carried out at Chaudhary Charan Singh Haryana Agricultural University, Hisar in kharif 2019-2020 and 2020-21 with the objective of estimating diversity of 150 genotypes of *desi* cotton. Variation among genotypes was present for hypocotyl pigmentation, leaf colour, leaf shape, leaf hairiness, flower stigma, leaf nectaries, stem hairiness, boll weight, petiole pigmentation, flower petal colour, boll shape, prominence of tip, plant height, boll opening, seed index, ginning percentage, fibre length, fibre strength and fibre fineness. Analysis of variance revealed presence of variability for all the quantitative traits among the genotypes other than number of locules per boll and seed index. GCV and PCV were high for number of bolls per plant and seed cotton yield, medium for plant height, number of monopods, single boll weight, gossypol content and these parameters were found low in days to first flower, seed index, GOT (%), oil content, fibre length, fibre strength), fibre uniformity, fibre maturity and fibre fineness. High heritability coupled with high genetic advance was observed for most of the traits *viz.* boll weight, plant height, number of monopods per plant, seed index, oil content, number of bolls per plant, fibre fineness, fibre strength and seed cotton yield per plant. This shows the dominance of additive gene action behind the traits hence direct selection will be effective for these traits. Correlation studies showed that seed cotton yield per plant was significantly and positively correlated with all the traits except days to first flower, plant height and negatively correlated with biochemical and fibre quality traits. Thus, improving other traits, seed cotton yield per plant will also increase. Fibre quality traits like fibre length is significantly positive correlated with fibre strength but negative correlated with seed cotton yield thus suggests that quality and quantity cannot be improved simultaneously one has to be compromised. Whereas, improving fibre length and fibre strength at a time is possible as they are in positive relationship. Genetic diversity analysis was done using 100 SSR markers out of which 66 were found polymorphic with average number of alleles as 2.73 per locus. FFS15 and HD 328 or HD 551 and HD 544 showed 98% similarity index, which means they are the most similar genotypes and have similar genetic background whereas genotypes namely Vira 6 and BHO 5 VIII were the most dissimilar genotypes.

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