Biological Forum – An International Journal **14(3): 1461-1468(2022)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Characterization of upland Cotton Genotypes as per PPV&FR Guidelines via Important Morphological Traits

Himanshi Saraswat, Sonika*, Omender Sangwan and Ajay Verma
Department of Genetics & Plant Breeding,
College of Agriculture CCS Haryana Agricultural University, Kaul,
ICAR-Indian Institute of Wheat & Barley Research, Karnal (Haryana), India.

(Corresponding author: Sonika)*

(Received 14 July 2022, Accepted 24 August, 2022)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: In the present investigation, characterization of 50 elite lines of cotton was carried out during kharif 2021 at CCSHAU, Kaul for better documentation and utilization in breeding programmes. Significant differences were observed among cotton genotypes for morphological traits. Vales of treatments Mean sum of squares were large as compared to error mean sum of squares for all the traits. Values of critical differences varied from 0.003 to 14.55 for Tannin and seed cotton per plants. Plant height of genotypes expressed variation from 123 to 225 while growth habit showed 46.4 to 76 values. Maximum divergence observed for Cotton seed per plant as values deviated from 65.4 to 234.4 whereas seed weight per boll registered change from 3.2 to 4.9. Values of seed index exhibited change from 44 to 8.9 and ginning (%) ranged from 19.6 to 43.3 and number of bolls per plant maintained deviation from 15.6 to 55.3 while monopods per plant expressed variation from 1.2 to 3.6 only among the genotypes. Marginal variation from 3.0 to 5.0 exhibited by number of locules per boll along with less changes in seeds per locule as 5.0 to 7.6 only. Days to first flower expressed changes from 51.6 to 66.6 while lint index deviated from 1.6 to 6.4 in this set of cotton genotypes. Cotton seed yield and Weight of seed cotton/boll expressed high Heritability with high genetic advance as % mean for additive gene action. Biplot analysis observed 40.3% variation accounted by first two components with 22.5 %, 17.8% contributions. Cotton seed yield, Number of bolls per plant, Lint index, Seed index, Number of monopods contributed more in first Principal component whereas Ginning, Locules per boll, Lint index, Number of monopods, Plant height contributed more to second one.

Keywords: Upland cotton, PCA, Biplot analysis, Multivariate Hierarchical clustering.

INTRODUCTION

Cotton (White Gold) has been established as the most significant cash crop and the backbone of the global textile industry (Zafar *et al.*, 2022). Cotton crop has boosted Indian economy by providing raw material for manufacturing sector, and generating employment directly or indirectly for 60 million people (Saritha and Patil 2020). Cotton seed yield depends on contributing traits and better understanding aids to researchers to minimize the yield penalty factors. The total variability had been partitioned by Analysis of variance (ANOVA) into heritable and non-heritable components with the help of Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) (Shaheen *et al.*, 2021). More influence of the environmental factors on traits judged by large magnitude of PCV as compared to GCV values. Nature of gene action involved can be determined with the help of heritability and genetic advance (Bhatti *et al.*, 2020). Heritability is a good indicator of the transmission of characters from parents to their offspring. Presence of genetic variability with high heritability indicates phenotypic selection which is very effective in improvement of traits (Kakar *et al.*, 2021). High genetic advance along with high heritability provides better response to selection rather than individual high heritability effects (Balakrishnan *et al.*, 2020). High genetic advance coupled with high heritability indicates the presence of additive gene action, which is a prerequisite for selection to proceed (Fatima *et al.*, 2021). Genetic diversity for morphological traits has been estimated using principal component analysis, which lead to identification of phenotypic variability in cotton (Jarwar *et al.*, 2018; Karena *et al.*, 2021; Iqbal *et al.*, 2022). In present study genotype-by-traits (GT) biplot analysis has been exploited to study the nature of association among the traits, evaluation of genotypes based on multiple traits.

MATERIALS AND METHODS

The present investigation was carried out during kharif 2021 at the Farm Research Area of Cotton Section, Department of Genetics & Plant Breeding, CCS Haryana Agricultural University Hisar. The experimental material for the present research work consists of 50 genotypes of upland cotton (*Gossypium hirsutum* L.). The research centre is located in the semiarid sub-tropical area at 290-100N latitude and 750 - 460 E longitude with an elevation of 215.52 m above mean sea level. There was one row of each genotype with row length of 6.0 m, row to row distance of 67.5 cm and, plant to plant distance of 30 cm. All the necessary recommended package of practices was followed to raise a good crop stand. Observations recorded on Plant height(cm), Plant growth habit, Seed cotton yield/plant (g), Weight of seed cotton/boll (g), Ginning (%), Seed index(g), Number of bolls per plant, Number of locules/boll, Number of seeds/locule, Lint index(g), Days to first flower, Number of monopods/plants subjected to further statistical analysis.

RESULTS AND DISCUSSION

A. Descriptive analysis

The recorded data on studied traits were subjected to analysis of variance (ANOVA) technique. Significant differences were observed among genotypes for studied morphological traits as evident from ANOVA (Kumar *et al.*, 2019). The descriptive statistics observed sufficient magnitude of variability for the studied traits among the cotton genotypes. Values of treatments Mean sum of squares were large as compared to error mean sum of squares for all the traits (Pinki *et al.*, 2018). Values of critical differences varied up to 14.55 for cotton seed per plants. Plant height of genotypes expressed variation from 123 to 225 while growth habit showed 46.4 to 76 values. Maximum divergence observed for Cotton seed per plant as values deviated from 65.4 to 234.4 whereas seed weight per boll registered change from 3.2 to 4.9. Values of seed index exhibited change from 44 to 8.9 and ginning (%) ranged from 19.6 to 43.3 and number of bolls per plant maintained deviation from 15.6 to 55.3 while monopods per plant expressed variation from 1.2 to 3.6 only among the genotypes. Marginal variation from 3.0 to 5.0 exhibited by number of locules per boll along with less changes in seeds per locule as 5.0 to 7.6 only. Days to first flower expressed changes from 51.6 to 66.6 while lint index deviated from 1.6 to 6.4 in this set of cotton genotypes.

B. Heritability and Genetic advance

Plant height(cm). The overall mean of the character found was 183.56 with a range of variation from lowest by C 2-3 genotype (123.33 cm) to highest by PIL 8-5 genotype (225.67). The magnitude of GCV (12.49%) and PCV (13.01%) showed by character was moderate in nature. Smaller difference observed between GCV and PCV values indicating the little influence of environment on the inheritance of the trait. Heritability (92.18%) with genetic advance % mean (24.72%) was very high and high respectively indicating the presence of additive gene action, which responds to selection for the inheritance of the trait.

Plant growth habit. The overall mean of the character found was 61.14 with a range of variation from lowest by N 46 genotype (52 cm) and highest by S 344 genotype (76 cm). The GCV (9.68%) and PCV (10.23%) values showed by the character was low and moderate respectively. Heritability (89.61%) with genetic advance % mean (18.89) was very high and moderate respectively showing the preponderance of additive gene action, which is pre-requisite for selection to proceed further (Dahiphale *et al.*, 2018).

Seed cotton yield/plant (g). The overall mean of the character found was 131.65 with a range of variation from lowest by Dunn genotype (65.42 g) and highest by AR 37 genotype (234.35 g). The GCV (29.12%) and PCV (29.91%) values showed by the character was high and comparable, indicating little influence of environment on the trait. Heritability (94.79%) with genetic advance as % mean (58.40%) was very high and high respectively, indicating that high heritability is due to additive gene action and selection will be rewarding for the improvement of trait (Gnanasekaran *et al.*, 2018).

Weight of seed cotton/boll (g). The overall mean of the character found was 3.96 with a range of variation from lowest by GTSV 337 genotype (3.22g) and highest by Combed Seed genotype (4.90g). The GCV (11.02%) and PCV (11.29%) values showed by the character was moderate in nature. Heritability (95.21%) with the genetic advance % mean (22.15%) was very high and high respectively, indicating the presence of additive gene action, which responds to selection (Hamidi *et al.*, 2018).

Ginning (%). Ginning can be defined as the process of separation of fibre from seed cotton. Ginning out turn can be defined as the percentage of lint obtained from seed cotton. The overall mean of the character found was 39.75 with a range of variation from lowest by Tx ORSC78 genotype (19.63) and highest by genotype EL505 (42.73). The GCV (8.59%) and PCV (10.14%) values showed by the character was low in nature, indicating low magnitude of genetic variability were present among the genotypes. The magnitude of PCV was higher than GCV indicating the influence of environment over the trait. Heritability (71.79%) with the genetic advance as % of mean (15.00) was high and moderate respectively, which indicates that selection can be used for the improvement of the trait.

Seed index (g). Seed index is the weight of 100 cotton seed, which was collected from five average sized bolls. It was classified as very small, small, medium, bold and very bold. Most of the genotype had small seed index while nine genotype had medium seed index. The overall mean of the character found was 6.46 with a range of variation from lowest by Dunn 119 genotype (4.40) and highest by GTSV 337-1 genotype (8.90). The GCV (15.03%) and PCV (15.97%) values showed by the character was moderate and low in nature. Heritability (96.81%) with the genetic advance % mean (30.49%) was very high and high respectively, indicating the presence of additive gene action, which is a prerequisite for selection.

Number of bolls per plant. Boll shape (longitudinal section) were classified as round, ovate or elliptic. The overall mean of the character found was 33.12 with a range of variation from lowest by PIL 8-5 genotype (16.33) and highest by genotype EL 505 (55.33). The GCV (27.16%) and PCV (28.05%) values showed by the character was high and moderate in nature.

Heritability (93.75%) with genetic advance % mean (54.18) was very high and high respectively, indicating that high heritability is due to additive gene action and selection will be rewarding for the improvement of the trait (Aarthi *et al.,* 2018).

Number of locules/boll. The overall mean of the character found was 3.91 with a range of variation from lowest (3.0) and highest (5.0) value. The GCV (12.88%) and PCV (16.96%) values showed by the character was moderate and low in nature indicating little amount of genetic variability were present among the genotypes, also high magnitude of PCV than GCV indicates the influence of environment over the trait. Heritability (57.59%) and genetic advance % mean of (20.16%) of the character was moderate in nature respectively. This trait showed the lowest value of heritability among all the morphological traits under study.

Number of seeds/locule. Seed cotton yield per plant or single plant yield (g) was the yield obtained 77 from single plant of cotton. Seed cotton yield/plant being the most important parameter which can be classified into low, medium and high. The overall mean of the character found was 6.38 with a range of variation from lowest (5.0) to highest (7.67) value. The GCV (9.01%) and PCV (11.20%) values showed by the character was low in magnitude, indicating little amount of genetic variability was present among the genotypes for this trait. Heritability (64.65%) with genetic advance % mean (14.92%) was high and moderate in nature respectively (Shaheen *et al.,* 2021).

Lint index (g). Lint index can be defined as the ratio of lint weight to the seed cotton. Lint index can be classified as low medium and high and all the genotype under study showed sufficient amount of variation in this character. The overall mean of the character found was 4.3 with a range of variation from lowest by PIL 8-5 genotype (1.60) to highest by genotype EL 505 (6.32). The GCV (19.53%) and PCV (21.20%) values showed by the character were moderate in nature, indicating sufficient magnitude of genetic variability was present among the genotypes for the trait. Heritability (84.84%) with genetic advance % mean (37.06%) was very high and high respectively, indicating the preponderance of additive gene action (Saritha and Patil 2020).

C. Principle components analysis (PCA)

Results of the principal component analysis (PC) indicated that the first two components were important in explaining the 40.3% variation among the morphological traits of 50 genotypes evaluated under field trials and respective contributions were 22.5 %, 17.8% (Table 4). It illustrated the variations in Cotton seed yield, Number of bolls per plant, Lint index, Seed index, Number of monopods contributed more in first Principal component. Traits including Ginning, Locules per boll, Lint index, Number of monopods, Plant height contributed more to second PC. The traits are positively correlated if the angle among their vectors is less than 90° and negatively correlated if angle among trait vectors are more than 90°. While trait vectors that are approximately at right angle behave independently (Zafar *et al.,* 2022). Biplot analysis revealed significant positive associations among growth habit, Number of monopods, number of cotton seeds per plant and cotton seed yield. Seeds per locule expressed positive association with Locules per boll of the evaluated genotypes. Similar kind of association was observed among plant height, ginning, lint index, seed index, weight of cotton seed (Shaheen *et al.,* 2021). The correlation between number of monopods with seeds per locule and locules per boll was negative (Fig. 4). As a graphical display of a multivariate analyses, the GT-biplot represents a tool that combine several advantages from analyses that encompass relations between traits (Fig. 5), demonstrating the usefulness of this analysis. Number of monopods placed together with number of bolls per plant, growth habit, cotton seed yield. Next quadrant observed grouping of weight of cotton seed with seed index, days to first flower, plant height whereas nearby placed lint index and ginning in other group. Lastly seeds per locule showed affinity with locules per boll in last group.

D. Multivariate Hierarchical Cluster analysis

Multivariate statistical methods are appropriate tools for the analysis of the complex structure. Multivariate techniques have been used to estimate the genetic divergence between accessions, like biometric models estimated by the Euclidean Distance and hierarchical grouping methods (Kakar *et al.,* 2021). Multivariate clustering of genotypes based on studied traits had been carried out as per guidelines of popular Ward's method. Cluster analysis is a method that aims to clarify and classify a sample of objects (or subject) based on a set of deliberately chosen variables into a number of different groups keeping alike objects in the similar group. The cluster analysis has no mechanism for distinguishing irrelevant and relevant variables. Using cluster analysis, 50 cultivars were divided into six different clusters based on important morphological traits with respective membership of 7, 6, 9, 13, 14, 1 genotypes (Fig. 6). Growth habit expressed as point of dissection of studied traits as plant height, seeds per locule, Ginning, Locules per boll, days to first flower in one while other comprises of weight of cotton seed, cotton seed yield, number of bolls per plant, number of monopods, seed index with lint index.

Table 1: Details of evaluated upland cotton genotypes.

Gen 1	Acala 1517	Gen 18	Coker 413-68	Gen 35	ISC 67
Gen 2	Atlas	Gen 19	Combed seed	Gen 36	ISC 6-1-2
Gen 3	Auburn	Gen 20	Coker	Gen 37	Locket 4785 cream
Gen 4	GTSV 337	Gen 21	Deltapine 66	Gen 38	GTSV 337
Gen 5	AR 27	Gen 22	Dunn	Gen 39	CA 9941
Gen 6	CSH 1071	Gen 23	EL 505	Gen 40	N 46
Gen 7	RS2098	Gen 24	RS 2141	Gen 41	REBA B 50
Gen 8	CNH 36	Gen 25	DUNN 119	Gen 42	Russian hirsutum
Gen 9	PIL 8-5	Gen 26	Gregg 25	Gen 43	SV 7 A
Gen 10	PIL8-7	Gen 27	Gregg male sterile	Gen 44	SA 439
Gen 11	AR40	Gen 28	H 1353	Gen 45	SA 136-1
Gen 12	PKV Rajat	Gen 29	216 F	Gen 46	S 344
Gen 13	Surbhi	Gen 30	H 655 C	Gen 47	Tex Maroon 2-7
Gen 14	AR 37	Gen 31	HG 1-P 625	Gen 48	Tx ORH 14-1-7850
Gen 15	H 1316	Gen 32	H 1465	Gen 49	Tx ORSC 78
Gen 16	Badnawar	Gen 33	IAN 9332	Gen 50	Tidewater IC 342
Gen 17	C 2-3	Gen 34	IAN 40-10-385		

Table 2: Descriptive measures of morphological traits of evaluated cotton genotypes.

	Mean	**Range**	**Standard Error**	**Median**	**Sample Variance**	**Kurtosis**	**Skewness**	**Minimum**	**Maximum**
Plant Height(cm)	183.57	102.33	3.29	190.28	541.32	-0.35	-0.43	123.33	225.67
Growth Habit	61.14	29.56	0.85	62.11	36.45	-0.32	0.02	46.44	76.00
Number of Cotton Seeds /Plant	131.65	168.93	5.47	135.89	1496.80	-0.26	0.31	65.42	234.35
Weight of cotton seed /boll(g)	3.96	1.69	0.06	3.92	0.19	-0.91	0.17	3.22	4.91
Seed Index(g)	6.46	4.50	0.14	6.32	0.96	0.64	0.73	4.40	8.90
Ginning%	39.75	23.70	0.51	40.93	13.21	19.08	-3.84	19.63	43.33
Number of Bolls /Plant	33.13	39.67	1.29	33.17	82.78	0.18	0.28	15.67	55.33
Number of Monopod /Plant	1.97	2.33	0.07	2.11	0.24	1.05	0.68	1.22	3.56
Number of Locules /Boll	3.91	2.00	0.08	4.00	0.32	-0.51	-0.08	3.00	5.00
Number of Seeds /Locule	6.39	2.67	0.09	6.33	0.39	-0.11	-0.01	5.00	7.67
Lint Index(g)	4.30	4.81	0.12	4.31	0.75	1.58	0.03	1.61	6.42
Days to First Flower	60.67	15.00	0.53	62.00	14.18	0.00	-1.12	51.67	66.67

Table 3: ANOVA, GCV, PCV & heritability of morphological traits.

Traits	**Blocks**	**Main Effects**	**Error**	**GCV**	**PCV**	**Heritability**	**GA**
Plant height(cm)	7.13	10,470.3**	14.72	12.49	13.01	92.18	24.72
Plant growth habit	153.2	10,247.5**	15.79	9.68	10.23	89.61	18.89
Number of bolls/plant	0.372	10,092.2**	3.93	29.12	29.91	94.79	58.4
Boll weight(g)	19.93	10,918.5**	3.93	11.02	11.29	95.21	22.15
Seed index(g)	42.79	12,289.6**	11.31	15.03	15.97	96.81	30.49
Ginning (%)	7.24	10.408.4**	24.28	8.59	10.14	71.79	15
Number of bolls/plant	28.03	9,809.1**	4.76	27.16	28.05	93.75	54.18
Number of locules/boll	17.89	7,160.20	10.86	12.88	16.6	57.69	20.16
Number of seeds/boll	15	10,099.4**	7.32	9.01	11.2	64.65	14.92
Lint index(g)	3.96	10,233**	11.01	19.53	21.2	84.84	37.06
Days to first flower	12.83	8,435.6**	7.26	6.15	6.3	95.25	12.37
Number of monopods/plant	3.8	10,226**	17.26	23.97	27.16	77.9	43.6

Table 4: Loading of morphological traits of cotton genotypes.

Traits	**Principal Component 1**	**Principal Component 2**	**Traits**	**Principal Component 1**	**Principal Component 2**
Plant height	0.0329	0.3197	Number of bolls per plant	0.4985	-0.1465
Growth habit	0.2227	-0.1126	Number of monopods	0.2492	-0.3238
Cotton seed yield	0.4993	-0.1294	Locules per boll	-0.0837	0.4627
Weight cotton seed	0.0941	0.0147	Seeds per locule	-0.1400	0.2838
Seed index	0.3816	0.1181	Lint index	0.4160	0.4011
Ginning	0.1801	0.4997	Days to first flower	0.0536	0.1505
40.26	22.47	17.79			

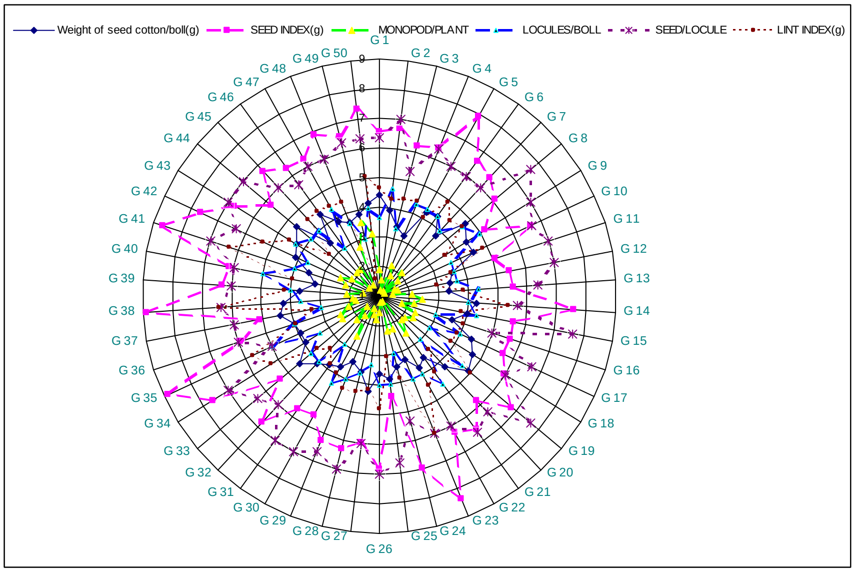

Fig. 1. Diversity in cotton genotypes for seed and lint values.

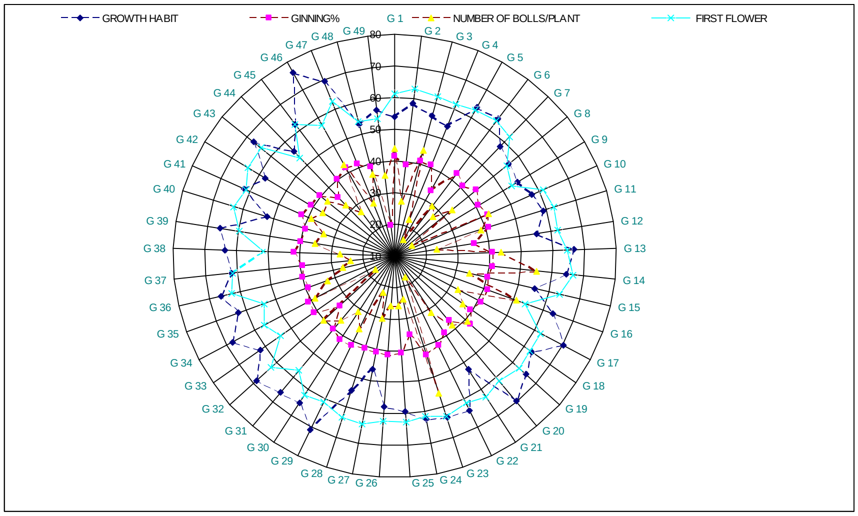

Fig. 2. Diversity of cotton genotypes for growth, ginning(%), number of bolls and days to first flower.

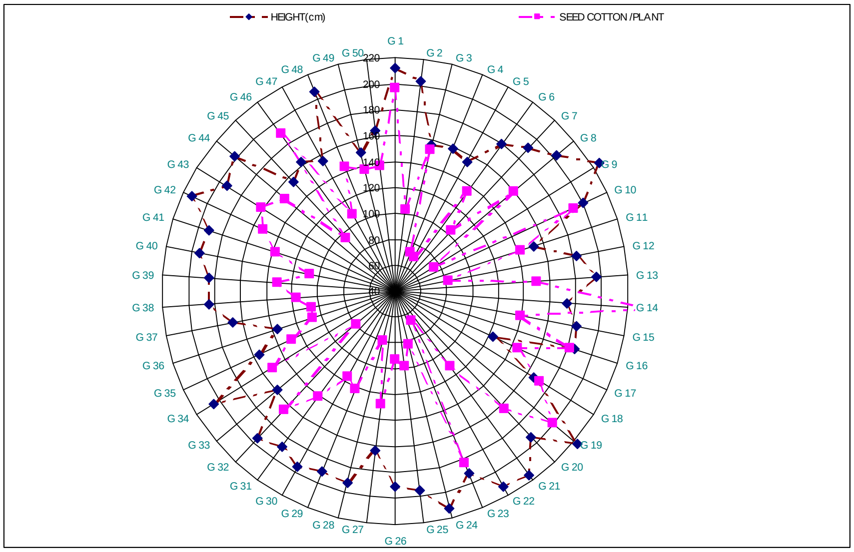

Fig. 3. Description of plant height and number of cotton seeds per plant.

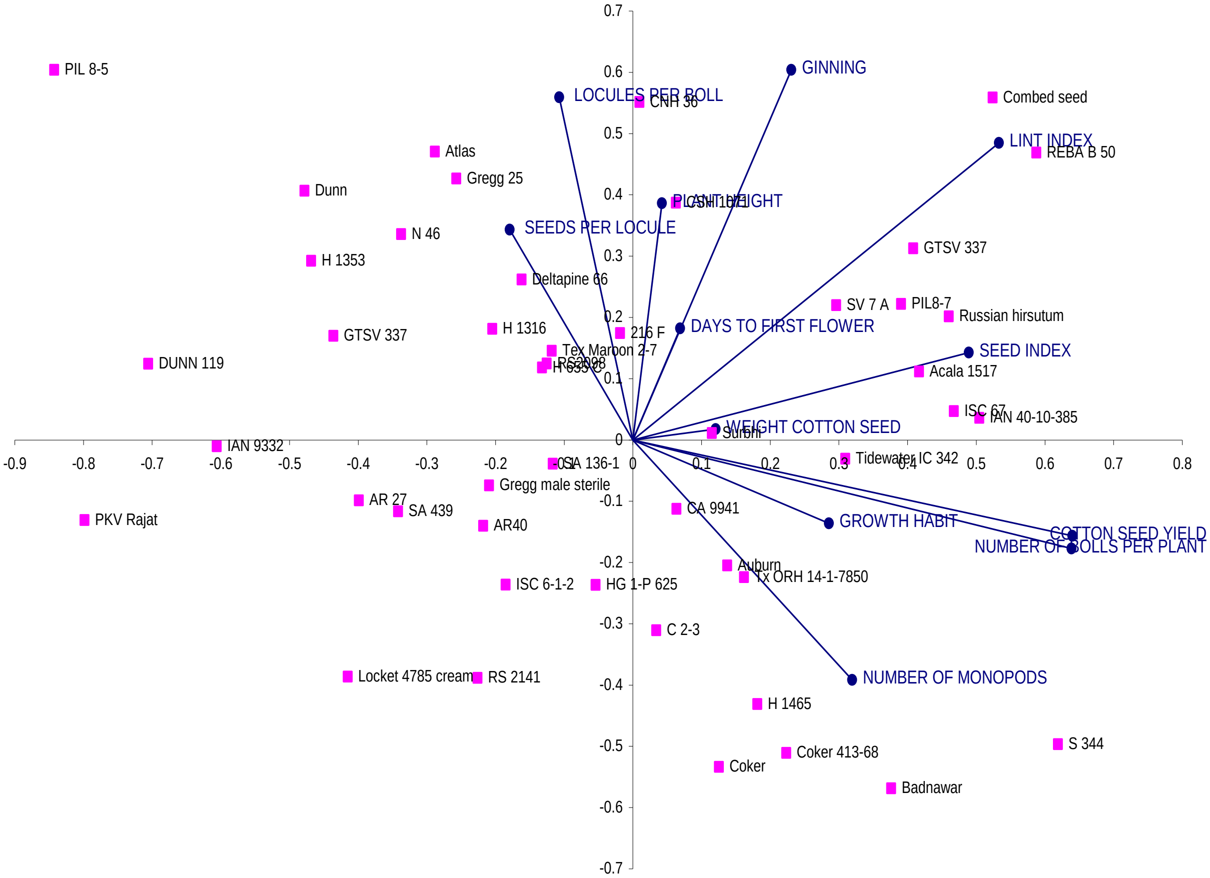

Fig. 4. Biplot analysis of morphological traits vis-à-vis genotypes.

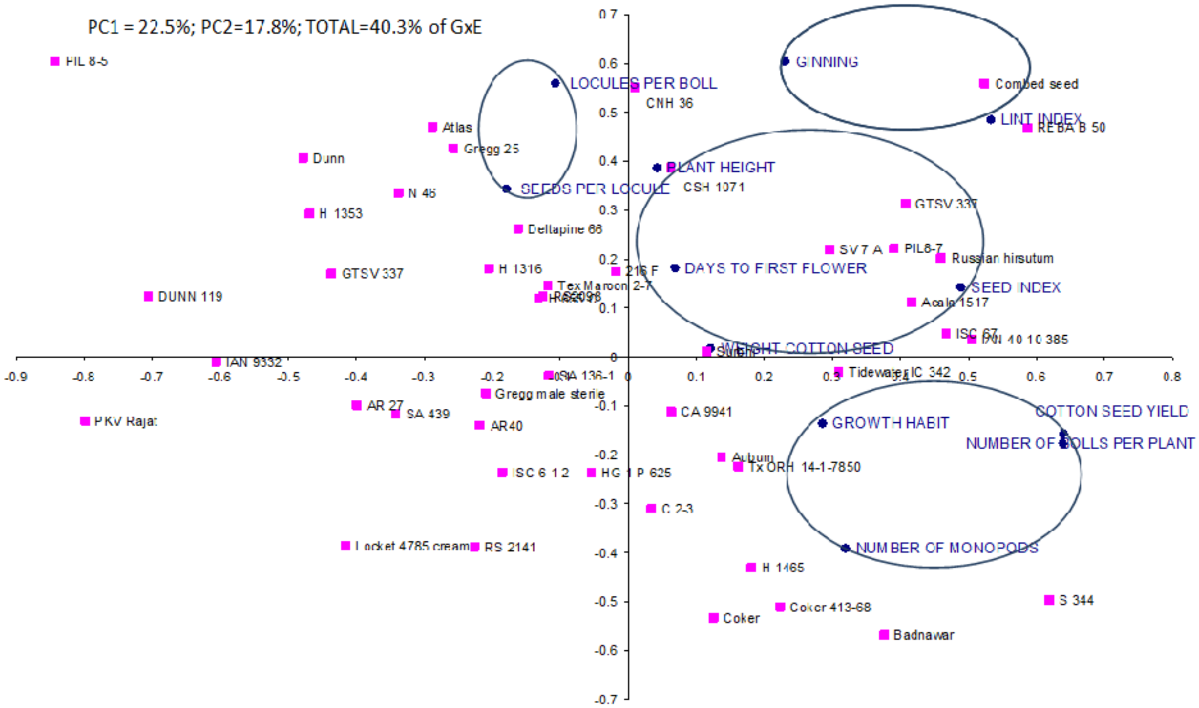

Fig. 5. Clustering pattern of morphological traits.

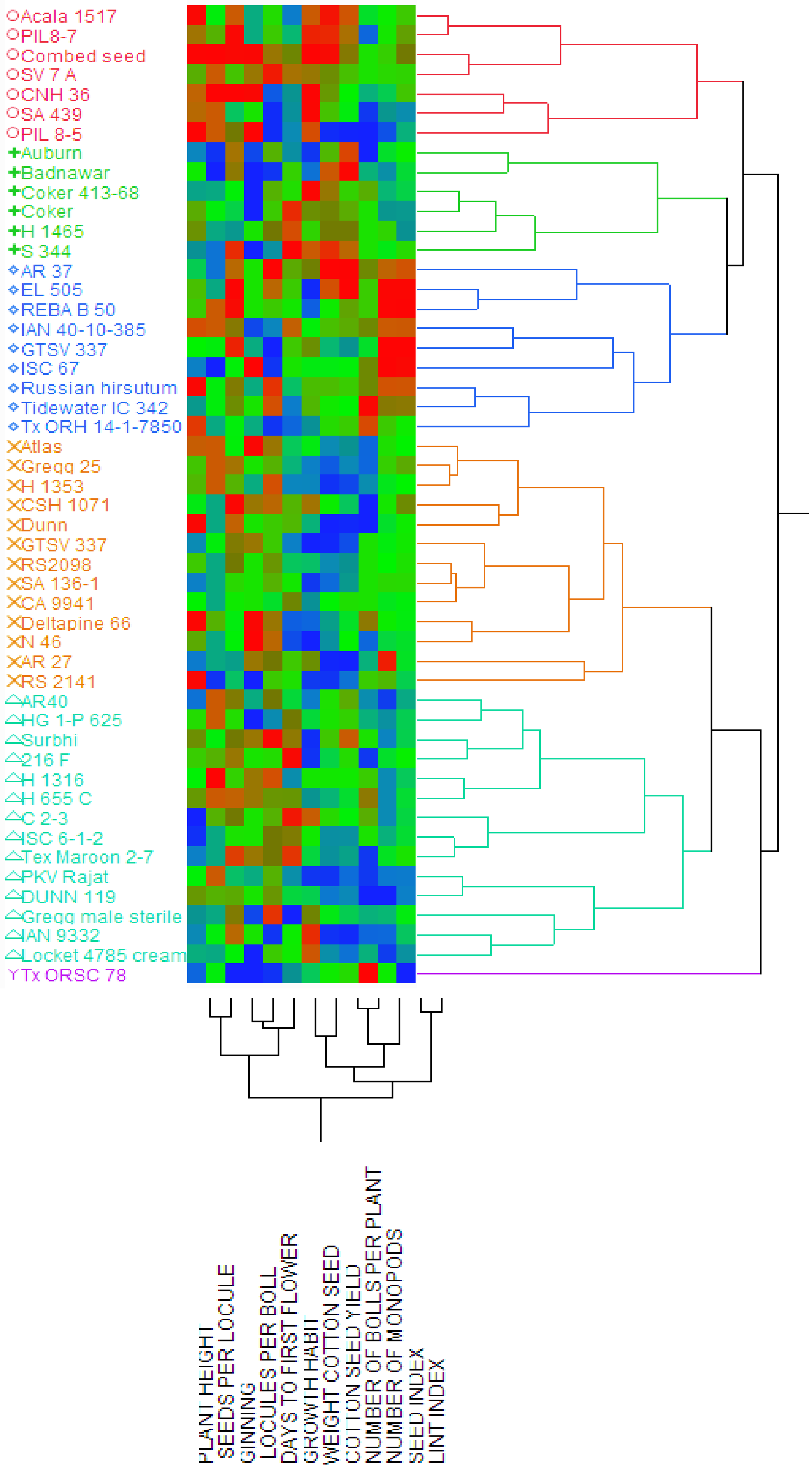

Fig. 6. Multivariate hierarchical clustering of genotypes vis-à-vis genotypes by Ward's method.

CONCLUSIONS

Evaluation of upland cotton genotypes expressed ample variability coupled with high heritability indicated, phenotypic selection would be very effective in improvement of morphological traits. High genetic advance along with high heritability expressed by Cotton Seed yield per plant, Number of bolls per plant, Seed index, Lint index ensured the better response to selection. Biplot analysis observed 40.3% variation accounted by first two components with 22.5 %, 17.8% contributions. Cotton seed yield, Number of bolls per plant, Lint index, Seed index, Number of monopods contributed more in first Principal component whereas Ginning, Locules per boll, Lint index, Number of monopods, Plant height contributed more to second one.

FUTURE SCOPE

Cotton Genotypes should be assessed based on Cotton seed yield, Number of bolls per plant, Lint index, Seed index, Number of monopods etc before recommendations for large scale cultivation.

Acknowledgements. First author sincerely acknowledge the hard work of field staff for the field evaluation of cotton genotypes along with the facilities of CCS HAU extended during the course of this study.
Conflict of Interests. None.

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How to cite this article: Himanshi Saraswat, Sonika, Omender Sangwan and Ajay Verma (2022). Characterization of upland Cotton Genotypes as per PPV&FR Guidelines via Important Morphological Traits. *Biological Forum – An International Journal*, *14*(3): 1461-1468.