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Upland cotton (*Gossypium hirsutum* L.) genotypes characterized by Biochemical traits

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Abstract
Fifty elite lines of upland cotton were evaluated at the Farm Research Area of Cotton Section, Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar during 2021. Gossypol content (%) ranged from 0.22 to 0.53. Marginal variation from 0.17 to 0.40 exhibited by Phenol content (%) along with less changes in Protein content (%) as 0.62 to 0.85 only. Tannin content (%) expressed changes from 0.26 to 0.98 while Sugar content (%) deviated from 0.28 to 0.98 in this set of cotton genotypes. Gossypol indicated high heritability with genetic advance % mean the presence of additive gene action while Protein content expressed high heritability with moderate genetic advance. High heritability coupled with high genetic advance, indicating the preponderance of additive gene action for sugar contents. Principal components analysis observed significant of first two components as accounted for 39% variation among the traits with 21.1%, 17.8% of respective contributions. Phenol, sugar, Tannin placed together with seed index in graphical representations. Multivariate hierarchical clustering as per Ward's method seen Seed expressed as point of dissection of quality traits as Gossypol, Protein, Phenol, Sugar, Tannin in one while other comprises of weight of cotton seed, cotton seed yield.

Keywords: Gossypol, tannin, phenol, biplot analysis, multivariate hierarchical clustering

Introduction
Cotton has been well established as the most important fiber and cash crop in world market (Iqbal *et al*., 2022) [6] and played significant role in the economy of the India. Besides providing the raw material to textile industry it supports the livelihood to 6 million farmers (Meena *et al*., 2022) [11]. Nearly 40 -50 million people of populations have been employed in cotton trade and its processing. Upland Cotton (*G. Hirsutum* L.) is extensively cultivated due to its wide adaptability to the environment, high production, and better yield potential, which fulfils over 95% of the output of global cotton yield (Balakrishnan *et al*., 2020) [2]. Cotton has many important biochemical compounds or secondary metabolites which may be studied as soluble sugar, phenol, terpenoids, gossypol, soluble protein, fatty acids and so on (Fatima *et al*., 2021) [5]. These are present in abundance in the seeds, leaves, stalks, bolls and stem or distributed throughout the plant (Zafar *et al*., 2022) [16]. These secondary metabolites proved very effective in defence mechanism and value addition of crop as gossypol having contraceptive properties, phenols and tannins are being insecticidal and herbicidal in nature, and cotton fibre itself composed of cellulose makes it convenient in defence mechanism of crop (Kumar *et al*., 2019) [10]. Though the yield is the major component in terms of production (Bhatti *et al*., 2020) [3] and for an effective improvement in yield and quality, it is necessary to have knowledge about the mutual relationship between yield and its component characters (Kakar *et al*., 2021) [9]. The present study exploited principal component analysis and multivariate hierarchical clustering mechanism to explore the inter relationship among quality and yield traits of upland cotton genotypes.

Method and materials
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 station located in the semi-arid 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 were followed to raise a good crop stand.

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In the present study, biochemical traits were taken into account i.e. reducing sugar content, phenol content, gossypol content, tannin content and protein content in samples of seed taken from 50 elite upland cotton planted into three Replication. Seeds were separated from fibre after ginning, then delinting of cotton seed performed. Delinting can be defined as the process of separation of fuzz from seeds of cotton. Delinting was performed with the help of concentrated sulphuric acid @ 100 ml/kg of fuzzy cotton-seed. Then air drying of seed was performed. Air-dried seeds crushed to convert them into powder form and kept in oven for further drying. Different quantity of powdered seed was taken for different biochemical analysis.

Results and Discussion
Descriptive analysis
The recorded data on studied traits were subjected to analysis of variance (ANOVA) technique. Significant differences were observed among genotypes for quality traits as evident from ANOVA (Aarthi *et al*., 2018) [1]. 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 (Dahiphale and Deshmukh, 2018) [4]. 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 (Figure 1). Values of seed index exhibited change from 4.4 to 8.9 and Gossypol content (%) ranged from 0.22 to 0.53. Marginal variation from 0.17 to 0.40 exhibited by Phenol content (%) along with less changes in Protein content (%) as 0.62 to 0.85 only. Tannin content (%) expressed changes from 0.26 to 0.98 while Sugar content (%) deviated from 0.28 to 0.98 in this set of cotton genotypes (Jarwar *et al*., 2018) [7].

Heritability and Genetic advance
Gossypol content (%)
The overall mean of the character found was 0.341 with a range of variation from lowest 0.22 to highest 0.54. The GCV (28.14%) and PCV (28.74) values showed by the genotypes were high and moderate indicating sufficient amount of genetic variability was present among the genotypes. Heritability (95.85%) with genetic advance % mean (56.75) was very high, indicating the presence of additive gene action (Vekariya *et al*., 2017) [15]. Selection will be beneficial for the improvement of the trait.

Protein content (%)
The overall mean of the character found was 0.72 with a range of variation from lowest (0.62) to highest (0.85). The GCV (8.54%) and PCV (8.96%) values showed by the character was low in magnitude indicating the narrow range of genetic variability among the genotypes (Saritha and Patil, 2020) [14]. Heritability (96.07%) with genetic advance % mean (16.78%) was very high and moderate in nature.

Sugar content (%)
The overall mean of the character found was 0.59 with a range of variation from lowest 0.62 to highest 0.85. The GCV (27.84%) and PCV (28.41%) values showed by the character were high and comparable indicating that enough magnitude of genetic variation was present among the genotype and little influence of environment over the trait. Heritability (96.07%)

with genetic advance % mean (56.22%) was very high and high in magnitude (Ramani *et al*., 2017) [13]. High heritability coupled with high genetic advance, indicating the preponderance of additive gene action.

Phenol content (%)
The overall mean of the character found was 0.25 with a range of variation from lowest 0.17 to highest 0.40. The GCV (20.59%) and PCV (20.71%) values shown by the character was moderate and comparable in nature, indicating the little influence of environment on the trait. Heritability (98.78%) with genetic advance % mean (42.16%) was very high and high in magnitude (Pinki *et al*., 2018) [12]. Very high heritability coupled with high genetic advance % mean, indicating the preponderance of additive gene action, which is highly suitable for selection.

Tannin content (%)
The overall mean of the character found was 0.73 with a range of variation from lowest 0.26 to highest 0.98. The GCV (28.843%) and PCV (28.848%) values shown by the character were high and moderate in magnitude. Heritability (99.96%) with genetic advance % mean (59.40%) was very high and high in magnitude respectively (Karena *et al*., 2021) [8]. Very high heritability coupled with high genetic advance % mean, indicating the preponderance of additive gene action, which is highly suitable for selection.

Principal components analysis (PCA)
Results of the principal component analysis (PC) indicated that the first two components were important in explaining the 39% variation among the quality traits of 50 genotypes evaluated under field trials with 21.1%, 17.8% respective contributions of principal components (Table 3). The variations in Tannin (%), Cotton seed weight and yield, Sugar, Phenol contributed more in first Principal component. Traits including Gossypol, Cotton seed weight and yield, Tannin (%), Protein (%) contributed more to second PC (Saritha and Patil, 2020) [14]. Biplot analysis revealed significant positive associations among Tannin, Phenol, Sugar, seed index. Cotton seed yield expressed positive association with weight of cotton seeds (Zafar *et al*., 2022) [16]. The correlation between Gossypol and Protein was negative. GT-biplot represents multivariate analyses with graphical display that encompass relations between traits (Figure 3). Phenol, sugar, Tannin placed together with seed index. First quadrant observed grouping of weight of cotton seed with cotton seed yield. Lastly Protein and Gossypol observed as outliers in different quadrants.

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 (Meena *et al*., 2022) [11]. Fifty evaluated genotypes were divided into six different clusters based on quality traits. The respective number of genotypes in different clusters varied from 9, 7, 12, 4, 12, 6 genotypes (Figure 4). Seed expressed as point of dissection of quality traits as Gossypol, Protein, Phenol, Sugar, Tannin in one while other comprises of weight of cotton seed, cotton seed yield.

**Table 1:** Details of evaluated upland cotton genotypes

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

Table 2: ANOVA, GCV, PCV & heritability of quality traits

	Minimum	Maximum	Mean Sum of Squares	Mean	GCV	PCV	Broad sense Heritability	GA as % of mean
Gossypol content (%)	0.22	0.54	0.146**	0.341	28.14	28.74	95.85	56.75
Protein content (%)	0.62	0.85	0.141**	0.72	8.54	8.96	96.07	16.78
Sugar content (%)	0.28	0.98	0.192**	0.59	27.4	28.41	96.07	56.22
Phenol content (%)	0.17	0.4	0.193**	0.25	20.59	20.71	98.78	42.16
Tannin content (%)	0.26	0.98	0.177**	0.73	28.843	28.848	99.96	59.4
Seed cotton yield/plant	65.42	239.55	10,092.2**	3.93	29.12	29.91	94.79	58.4
Boll weight(g)	3.22	4.9	10,918.5**	3.93	11.02	11.29	95.21	22.15
Seed index(g)	4.4	8.9	12,289.6**	11.31	15.03	15.97	96.81	30.49

**Table 3:** Loading of quality traits of cotton genotypes

| Traits	Principal Component 1	Principal Component 2
Gossypol content (%)	-0.0785	0.4383
Protein content (%)	0.2908	0.2020
Sugar content (%)	0.3832	-0.1535
Phenol content (%)	0.3241	-0.1536
Tannin content (%)	0.5664	-0.2776
Seed cotton yield/plant	-0.3030	-0.4086
Boll weight(g)	-0.4073	-0.5634
Seed index(g)	0.2808	-0.3981
% contribution of components (Total 39.02%)	21.14%	17.88%
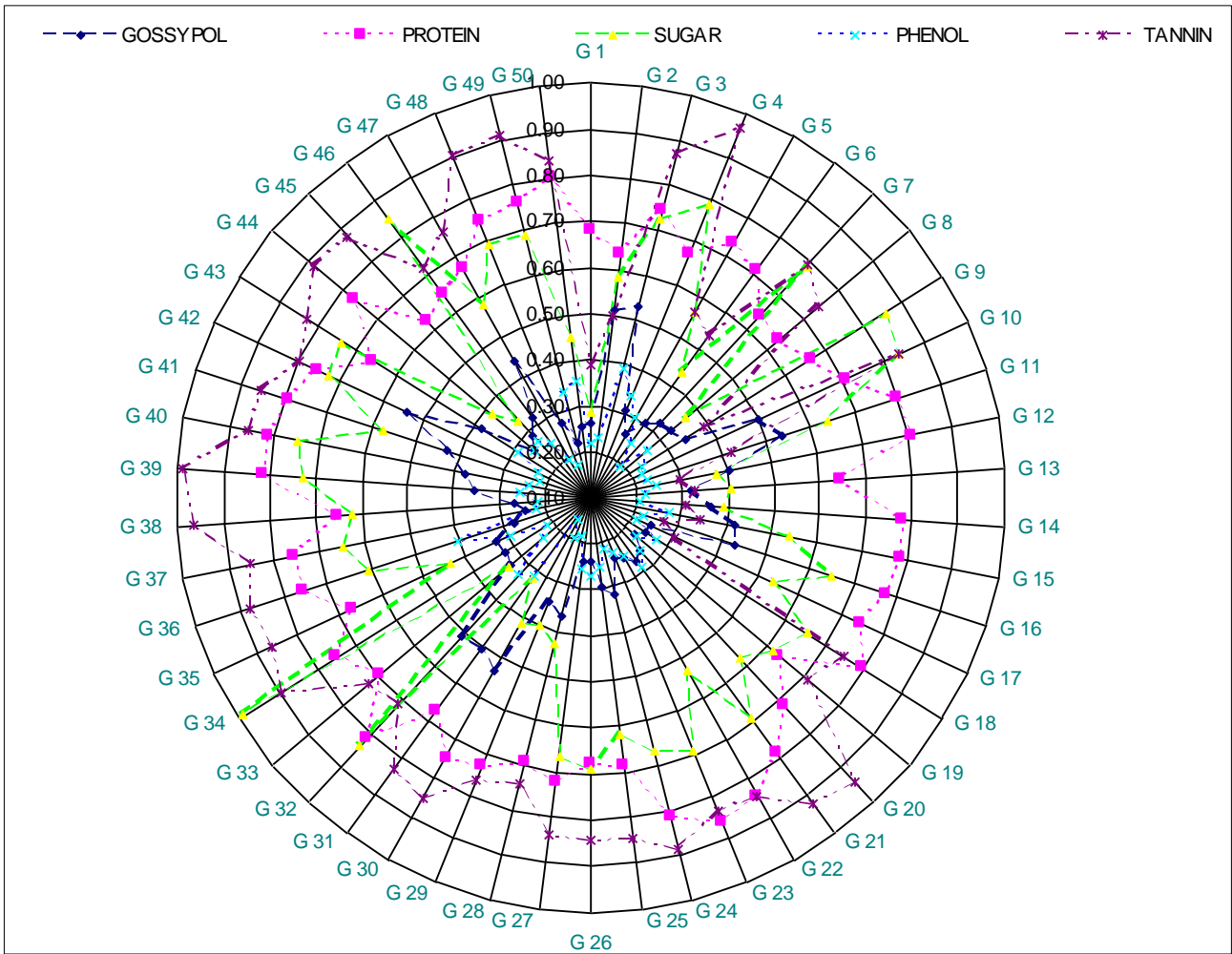
Fig 1: Divergence among quality traits for evaluated cotton genotypes
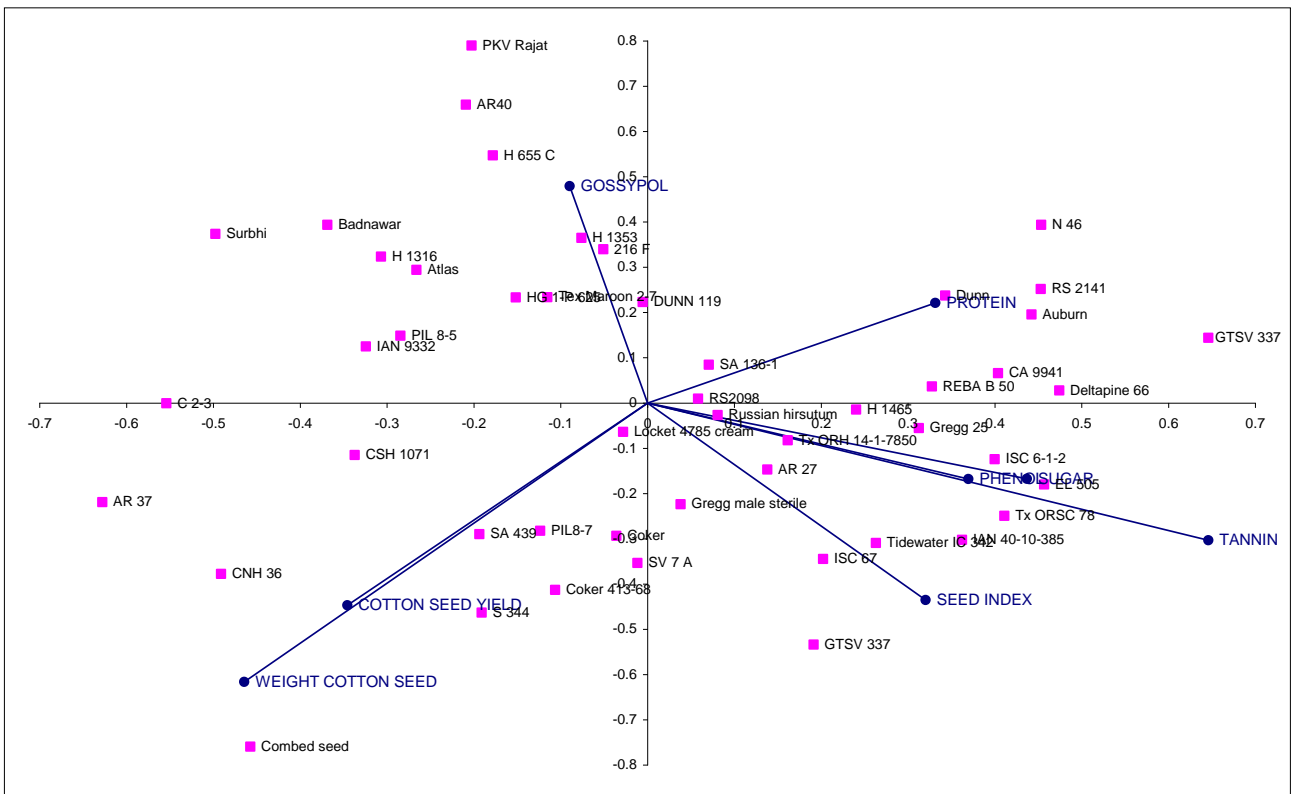
Fig 2: Biplot analysis of quality traits vis-à-vis genotypes
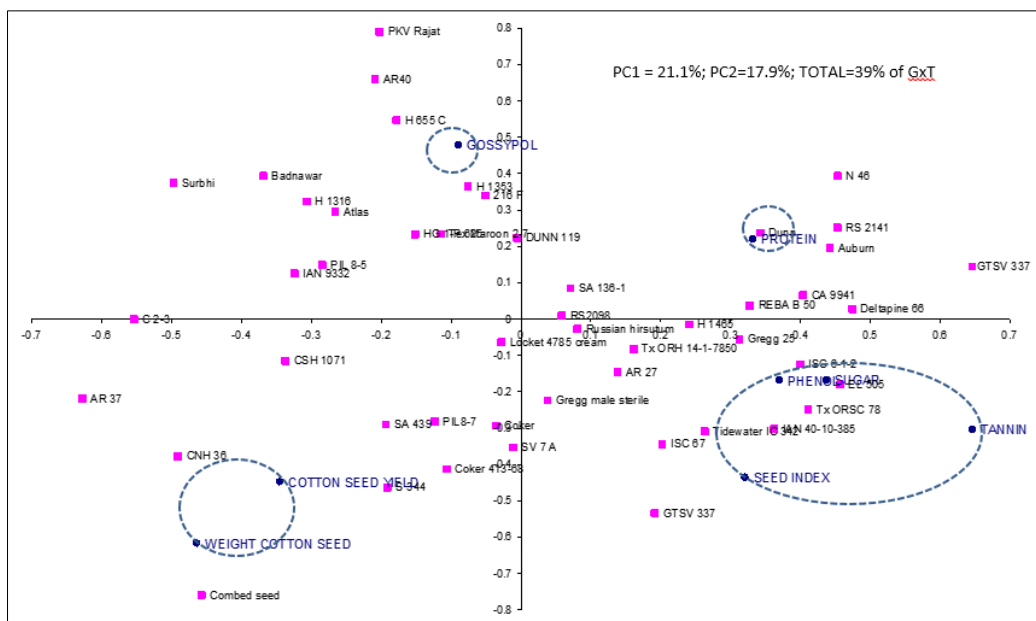
Fig 3: Clustering pattern of quality traits for evaluated cotton genotypes
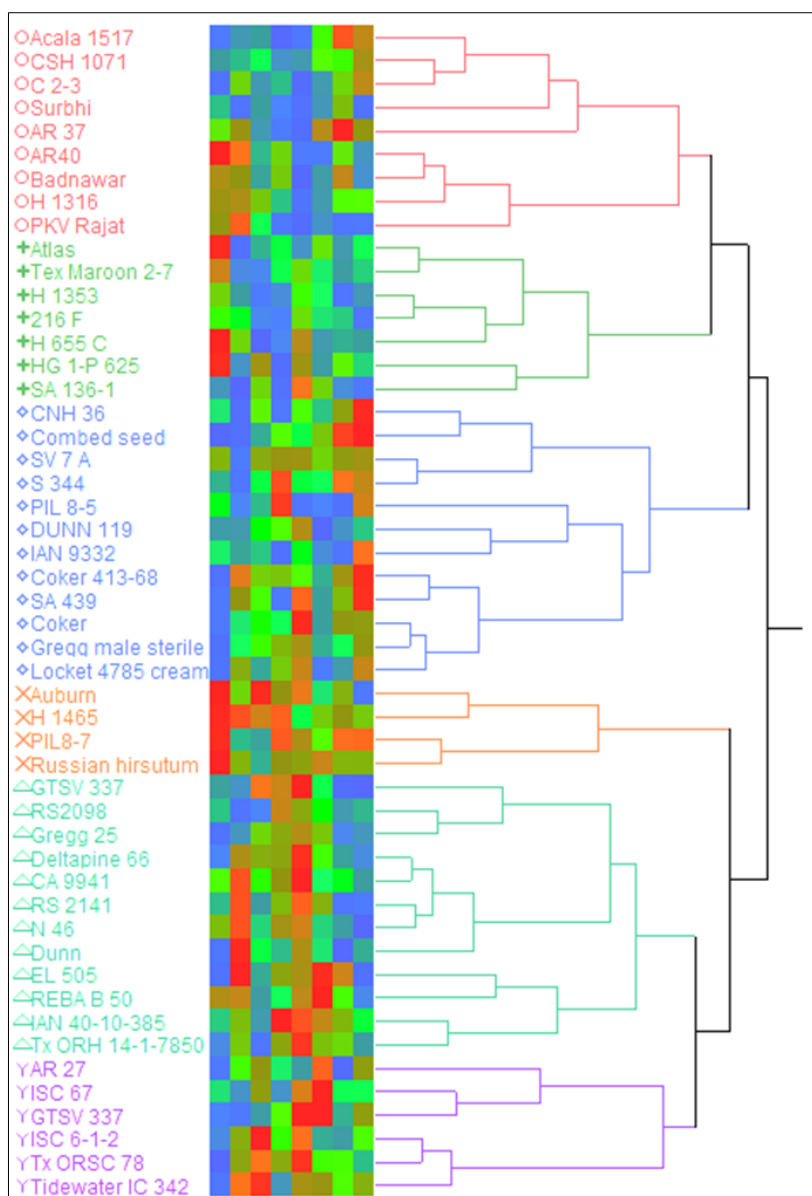
Fig 4: Multivariate hierarchical clustering of genotypes vis-à-vis genotypes by Ward's method

Conclusions

Gossypol indicated high heritability with genetic advance % mean the presence of additive gene action while Protein content expressed high heritability with moderate genetic advance. High heritability coupled with high genetic advance, indicating the preponderance of additive gene action for sugar contents. Principal components analysis observed significant of first two components as accounted for 39% variation among the traits with 21.1%, 17.8% of respective contributions. Phenol, sugar, Tannin placed together with seed index in graphical representations. Multivariate hierarchical clustering as per Ward's method seen Seed expressed as point of dissection of quality traits as Gossypol, Protein, Phenol, Sugar, Tannin in one while other comprises of weight of cotton seed, cotton seed yield.

Conflict of Interests: Authors declare no conflicts.

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