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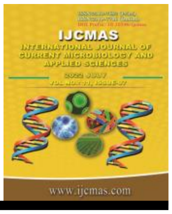

Original Research Article

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Study of Environmental Influence on Genetic Diversity Estimates (D^2) of Parental Lines in Upland Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

Keywords

Cotton, D^2 analysis, Dendrogram, Genetic distance, Genetic Diversity and *G. hirsutum*

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The hereditary parenthood of genepool plays important role in crop improvement. D^2 statistics is a powerful estimating the magnitude of genetic diversity. Comparative study was conducted to estimate the genetic distances among ten parental lines of upland cotton in two different sets of environments indicated the varying pattern of genetic distances along with varying pattern of dendograms revealed the role of environmental factors controlling expression of quantitative characters and subsequent magnitude of genetic diversity estimates. Clustering based on D^2 analysis provides a statistical tool for selecting the diverse parents for hybridization program. The D^2 distances matrix calculated for Environment (E_1), Environment (E_2) and average (E_1 & E_2) shown mean genetic distances of 15.38, 14.83 and 14.15 respectively. Comparing D^2 matrices among E_1, E_2 and average of environments (E_1 & E_2) revealed the significant effect of environment on genetic distances with mean values 0.56 (E_1 vs E_2), 0.82 (E_1 vs Avg [E_1 & E_2]) and 0.62 (E_2 vs Avg.[E_1 & E_2]). The average deviation of 0.82 was estimated for genetic diversity estimates over the environments. The recent techniques of molecular techniques (MAS) should be used for precise estimation of genetic diversity followed by clustering pattern for effective selection of diverse parents for exploitation of phenomenon of heterosis.

Introduction

Amongst the fibers, cotton is under cultivation from ancient period as a source of a fiber in India. Indian agriculture provides around 58% of livelihood to Indians and is the primary source of income for half of the population that contributed 17% to 18% to their GDP (Anonymous, 2021). Cotton has a vital role in the national economy, being an important source of raw material (85 per cent) to textile industry. During the year 2020-21, the total acreage in India was around 129 lakh ha and production is expected to be around 371 lakh bales of 170 kg with a productivity of 485 kg lint/ha (Anonymous, 2021).

Cotton refers to those species of genus *Gossypium* that bears the spinnable seed coat fibers. There are about forty-two species of this genus, out of which only four species viz., *Gossypium arboreum, G. herbaceum*, *G.hirsutum* and *G.barbadense* are cultivated and rest are recognized as wild. The first two species i.e. *G. arboreum* and *G. herbaceum* are cytologically diploid (2n=2x=26) and native of Old World, termed as either *Desi* or Asiatic cotton. The remaining two i.e. *G.hirsutum* (American/Upland cotton) and *G.barbadense* (Sea land/ Egyptian or Tanguish cotton) are cytogentically tetraploids (2n=4x=52) and referred as New World Cotton.

The knowledge of genetic variation existing in germplasm is an important and essential aspect for initiating any crop breeding program as the hybrids between lines of diverse origin generally display greater heterosis than those between closely related parents (El-Moghny *et al.,* 2015). The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits (Jyothi *et al.*, 2021 and Bhimate *et al.,* 2019). The crosses combinations which are planned based on genetic distances may be advanced in further generations for development of superior genotypes (Ujjainkar and Patil, 2021).

The individual organism in natural population highly experiences environmental heterogeneity over temporal and spatial scales, which has significant evolutionary implications through influences on patterns of selection and subsequent expression of variation at genetic level (Weinig and Schmitt, 2004). Whereas, the environmental heterogeneity has important role in process of determination of evolutionary dynamics of phenotypic traits that are governed by polygenes and also helpful for maintenance of genetic variation within population.

The plants in the segregating population that have the suitable genes combinations are the important component of plant breeding. Once the markers tightly linked to the genes have been detected, breeders may use particular DNA marker to identify the plants carry the genes. The effectiveness and cost of MAS are influenced by the marker technique; therefore, it must be selected carefully. With the rapid development of genomics, many functional genes have been targeted. Molecular marker assisted selection can accelerate the breeding process by linking selection to functional genes (Ujjainkar and Patil, 2020). Further, mapping quantitative trait loci has long application history in field of agricultural and allied application studies. Recent studies, the application of QTLs has found its suitability to identify the specific loci underlying trait variation over range of environments, facilitates for measurement of environmental variation in natural selection on those loci and testing of assumption models regarding the maintenance of genetic variations subjected to environmentally heterogeneous selection (Weinig and Schmitt, 2004). In present investigation, the fluctuations in genetic diversity estimates were tested over environments indicating varying pattern of genetic distances due to change in environment for same set of germplasm.

Materials and Methods

The experimental material comprises of ten elite parental lines collected from major cotton growing states of India (Table 1) grown in RBD design over two sets of environment. The observations were recorded on yield contributing traits and fibre quality traits viz., days to 50% flowering, plant height (cm), monpodia per plant, sympodia per plant, bolls per plant, boll weight (g), seeds per bolls, ginning outturn (%), seed index (g), lint index (%), 2.5 % span length (mm), fibre strength (g/tex), micronaire value (ug/inch) and seed cotton yield per plant (g).

Genetic Distances (D^2)

The inverse matrix of original genotypic variance covariance matrix was computed to derive the relationship by which the original character mean ($X_1 - X_{14}$) were transformed to an uncorrelated set of variables $Y_1 - Y_{14}$. In term of variance and covariance, the D^2 values were obtained as follows (Mahalanobis, 1936)

$$D^2_P = \sum_{i=1}^{P} \sum_{j=1}^{P} W_{ij} \left[\bar{X}^1_i - \bar{X}^2_i\right] \left[\bar{X}^1_j - \bar{X}^2_j\right]$$

Where

$\left[\bar{X}^1_i - \bar{X}^2_i\right]$ = the mean of i^th^ character in the first and second genotype, respectively

W_{ij} = Inverse of variance and covariance matrix

The D^2 value obtained for a pair of population is taken as the calculated value of χ^2 and is tested against the tabulated value of χ^2 for 'p' degrees of freedom, where 'p' is the number of characters. Further, the D^2 distances matrix calculated for Environment (E_1), Environment (E_2) and average (E_1 & E_2) and comparisons were made among all possible pairs of environments to record the changes in genetic distances due to environmental factors.

Results and Discussion

In cotton hybrid breeding program, the genetic diversity of parental lines is one of the pre-requisites for getting higher degree of heterosis. In the present investigation the parents differed significantly for all the traits, indicating presence of sufficient variability (Table 2). Among the parents AKH –91 showed the maximum mean for seed cotton yield per plant along with for number of bolls per plant, boll weight, number of seeds per boll, ginning outturn, seed index, lint index and fibre strength. The genotypes LRA – 5166, AH – 107 and AKH – 84635 exhibited high magnitude of seed cotton yield per plant along with better performance for the most of the quantitative traits studied. The parent AH – 107 though recorded high yield potential and performed good for most of yield contributing traits, the parent was unable to produce promising hybrid which indicated that only parents having high mean do not result in to better cross combination. The parents showed notable differences for means in E_1, E_2 and average of both environments, indicating the high degree of environmental influence. The genetic distances (D^2) for E_1, E_2 and average of both environments indicated the varying degree of deviations among parental lines due to influence of environmental factors. (Table 3, 4 and 5). The range of genetic distances (D^2) estimated were 26.97 – 6.64 (E_1), 23.20 – 5.40 (E_2) and 24.78 – 7.60 (average of both environments), whereas the mean genetic distances were estimated were 15.38 (E_1), 14.83 (E_2) and 14.15 (average of both environments) indicating the deviations in diversity estimates of same set of cotton genotypes due to environments. The dendrograms based on genetic distances exhibits varying pattern of relatedness among the genotypes drawn based on morphological performances in E_1 (Fig.1), E_2 (Fig.2) and average of both environments (Fig.3) respectively. Moreover, at individual genotype comparison also indicated the deviations for genetic distances as shown in Table 6 (E_1Vs E_2), Table 7 (E_1Vs average of environments), Table 8 (E_2Vs average of environments).

Table.1 Details of experimental material

Sr. No.	Genotype	Geographical Origin	Sr. No.	Genotype	Geographical Origin
1.	AKH 84635	Akola (Maharashtra)	6.	AKH62	Akola (Maharashtra)
2.	JLH 1594	Jalgaon (Maharashtra)	7.	AH 107	Akola (Maharashtra)
3.	KH-118	Khandwa (Madhya Pradesh)	8.	AKH 44	Akola (Maharashtra)
4.	NH 545	Nanded (Maharashtra)	9.	AKH 24	Akola (Maharashtra)
5.	AKH 91	Akola (Maharashtra)	10.	LRA 5166	Coimbatore (Tamil Nadu)

Table.2 Mean performance of parental lines in Environment (E_1)

Parent	Env	DF	PH	MONO	SYMP	BOLL	BW	SPB	GOT	SI	LI	SL	FS	MV	SCY
AKH84635	E_1	68.0	99.8	3.3	14.4	24.7	3.5	18.3	37.4	8.1	4.9	25.0	18.6	4.7	52.4
	E_2	74.3	83.2	2.8	8.6	17.5	3.0	17.9	31.9	7.7	3.6	21.2	10.8	2.6	29.4
	Avg	71.2	91.5	3.1	11.5	21.1	3.3	18.5	34.6	7.9	4.3	23.1	14.7	3.6	40.9
JLH 1594	E_1	73.7	100.9	3.1	14.3	18.3	3.0	21.1	30.6	7.6	4.9	23.2	15.4	3.7	45.7
	E_2	78.0	87.7	3.2	8.1	10.3	3.0	20.7	27.4	7.2	2.7	22.1	8.9	2.0	24.5
	Avg	75.8	94.3	3.2	11.2	14.3	3.0	20.7	29.0	7.4	3.9	22.7	12.1	2.8	35.1
KH118	E_1	74.3	76.7	2.8	16.8	26.0	2.9	22.7	37.0	8.2	3.4	23.7	18.3	4.0	41.7
	E_2	78.7	69.9	2.8	10.1	20.3	2.9	22.7	31.5	7.8	3.6	22.6	10.6	2.2	22.8
	Avg	76.5	73.3	2.8	13.4	23.2	2.9	22.7	34.3	8.0	3.5	23.1	14.5	3.1	32.3
NH545	E_1	77.3	102.3	3.3	14.9	25.7	3.3	17.1	35.5	8.3	4.6	22.3	15.9	4.3	38.0
	E_2	80.7	91.8	2.5	8.9	19.0	2.8	16.8	30.2	8.0	3.5	23.8	9.1	2.4	26.3
	Avg	79.0	97.1	2.9	11.9	22.4	3.0	16.9	32.9	8.0	4.0	23.0	12.5	3.3	32.2
AKH91	E_1	73.7	91.1	3.3	14.3	23.7	3.4	22.6	37.0	7.5	4.5	21.6	18.7	4.1	46.3
	E_2	75.7	78.1	4.0	8.8	16.1	2.9	22.2	31.5	7.1	3.3	22.2	16.9	2.3	36.5
	Avg	74.7	84.6	3.7	11.6	19.9	3.1	22.4	34.3	7.3	3.9	21.9	17.5	3.2	41.4
AKH62	E_1	73.0	92.3	2.9	16.7	28.3	3.0	17.1	34.7	8.1	4.4	23.7	22.1	4.5	50.7
	E_2	76.7	84.3	2.4	9.3	20.6	2.6	16.8	29.6	7.7	3.3	22.6	12.9	2.5	28.6
	Avg	74.8	88.3	2.7	13.0	24.5	2.8	16.9	32.1	7.9	3.8	23.1	17.8	3.5	39.7
AH107	E_1	76.0	87.9	2.7	18.1	28.7	3.5	19.9	33.7	8.0	4.1	24.0	21.6	4.6	52.9
	E_2	80.3	76.3	2.5	10.7	25.4	3.0	19.5	28.7	7.6	3.1	22.8	12.6	2.6	29.6
	Avg	78.2	82.2	2.6	14.4	27.1	3.3	19.7	31.2	7.8	3.6	23.4	17.1	3.6	41.2
AKH44	E_1	79.0	93.2	3.2	14.8	23.4	2.8	18.1	37.7	7.7	4.7	24.3	14.7	4.3	47.6
	E_2	79.7	90.4	3.3	8.9	15.9	2.3	17.8	32.1	7.3	3.5	20.6	8.4	4.0	27.2
	Avg	79.3	91.4	3.3	11.8	19.7	2.5	17.9	34.9	7.7	4.1	22.4	11.6	4.4	37.4
AKH24	E_1	74.7	93.1	3.0	13.0	19.1	3.3	22.6	38.8	8.4	5.4	23.2	15.2	4.2	44.3
	E_2	81.3	83.9	2.3	7.7	10.5	2.8	22.2	33.5	7.9	4.1	22.1	8.7	2.4	25.7
	Avg	78.0	88.5	2.7	10.4	14.8	3.0	22.4	36.2	8.2	3.3	22.7	12.0	3.3	35.0
LRA5166	E_1	75.0	83.4	2.8	14.8	26.1	3.6	15.6	35.2	6.8	3.7	22.4	19.4	3.6	46.3
	E_2	77.3	73.6	2.2	8.4	19.9	3.1	15.3	30.6	6.5	2.9	20.8	11.3	2.1	36.3
	Avg	76.2	78.5	2.5	11.6	23.0	3.3	15.4	32.9	7.0	3.3	21.6	15.4	2.8	41.3
MEAN	E_1	**74.5**	**92.1**	**3.1**	**15.2**	**24.4**	**3.2**	**19.5**	**35.8**	**7.9**	**4.5**	**23.3**	**18.0**	**4.2**	**46.6**
	E_2	**78.3**	**81.9**	**2.8**	**8.9**	**17.6**	**2.8**	**19.2**	**30.7**	**7.5**	**3.4**	**22.1**	**11.0**	**2.5**	**28.7**
	Avg	**76.4**	**87.0**	**2.9**	**12.1**	**21.0**	**3.0**	**19.4**	**33.2**	**7.7**	**3.8**	**22.7**	**14.5**	**3.4**	**37.6**
SD	E_1	**2.9**	**8.0**	**0.2**	**1.5**	**3.5**	**0.3**	**2.6**	**2.4**	**0.5**	**0.6**	**1.0**	**2.6**	**0.4**	**4.7**
	E_2	**2.3**	**7.3**	**0.6**	**0.9**	**4.6**	**0.2**	**2.7**	**1.8**	**0.5**	**0.4**	**1.0**	**2.6**	**0.6**	**4.6**
	Avg	**2.5**	**7.4**	**0.4**	**1.2**	**4.0**	**0.3**	**2.6**	**2.1**	**0.4**	**0.3**	**0.6**	**2.4**	**0.5**	**3.8**

Abbreviations used : DF – Days to 50% flowering, PH- Plant height (cm), MONO – Monpodia per plant, SYMP – Sympodia per plant, BOLL – Bolls per plant, BW – Boll weight (g) SPB – Seed per bolls, GOT – Ginning OutTurn, SI – Seed Index (g), LI – Lint Index (%), SL – 2.5 % span length (mm), FS – Fibre Strength (g/tex), MV – MicronareValue (ug/inch) and SCY – Seed Cotton yield per plant (g)

Table.3 Genetic Distances (D^2) of parental lines in Environment (E_1)

Parental lines	JLH 1594	KH 118	NH 545	AKH 91	AKH 62	AH 107	AKH 44	AKH 24	LRA 5166
AKH 84635	13.74	26.85	17.96	13.34	11.24	16.21	14.40	15.00	19.55
JLH 1594		26.94	13.12	13.58	16.90	20.02	13.41	11.74	21.00
KH 118			26.97	15.73	19.53	17.12	19.37	18.86	11.41
NH 545				15.93	18.25	22.30	13.99	14.93	21.21
AKH 91					10.03	11.49	8.90	7.21	11.09
AKH 62						6.64	11.81	15.46	11.16
AH 107							13.11	17.25	10.62
AKH 44								8.66	12.72
AKH 24									15.42

D^2 (Mean) = 15.38

Table.4 Genetic Distances (D^2) of parental lines in Environment (E_2)

Parental lines	JLH 1594	KH 118	NH 545	AKH 91	AKH 62	AH 107	AKH 44	AKH 24	LRA 5166
AKH 84635	12.00	16.52	11.80	11.80	5.54	13.03	9.79	11.82	12.95
JLH 1594		21.23	11.51	18.99	13.31	20.42	9.38	8.42	21.94
KH 118			23.20	17.94	17.00	11.75	22.26	17.88	16.18
NH 545				20.53	9.82	17.86	5.72	13.45	21.53
AKH 91					13.23	14.13	18.75	16.99	11.12
AKH 62						10.59	10.23	14.09	13.69
AH 107							18.40	18.77	11.25
AKH 44								10.32	20.25
AKH 24									19.80

D^2 (Mean) = 14.83

Table.5 Genetic Distances (D^2) of parental lines in Environment (Average E_1 & E_2)

Parental lines	JLH 1594	KH 118	NH 545	AKH 91	AKH 62	AH 107	AKH 44	AKH 24	LRA 5166
AKH 84635	12.44	21.47	13.44	9.38	7.60	14.15	9.65	12.59	14.71
JLH 1594		23.92	11.07	15.09	14.94	19.91	10.06	9.78	20.53
KH 118			24.78	15.46	18.21	14.26	20.25	18.18	13.06
NH 545				18.03	13.63	19.14	8.67	13.57	21.27
AKH 91					8.80	9.93	11.91	11.46	10.33
AKH 62						8.30	10.45	14.61	10.84
AH 107							14.60	17.48	8.41
AKH 44								8.13	15.28
AKH 24									16.93

D^2 (Mean) = 14.15

Table.6 Deviation in Genetic Distances (D^2) of parental lines over Environments (E_1 Vs E_2)

Parental lines	JLH 1594	KH 118	NH 545	AKH 91	AKH 62	AH 107	AKH 44	AKH 24	LRA 5166
AKH 84635	1.75	10.33	6.16	1.54	5.70	3.18	4.61	3.18	6.59
JLH 1594		5.71	1.61	-5.41	3.59	-0.40	4.03	3.31	-0.94
KH 118			3.77	-2.20	2.53	5.37	-2.88	0.98	-4.77
NH 545				-4.59	8.42	4.44	8.26	1.48	-0.32
AKH 91					-3.20	-2.63	-9.85	-9.79	-0.03
AKH 62						-3.95	1.58	1.37	-2.53
AH 107							-5.28	-1.52	-0.62
AKH 44								-1.66	-7.53
AKH 24									-4.38

D^2 (Mean) = 0.56

Table.7 Deviation in Genetic Distances (D^2) of parental lines over Environments (E_1 Vs [Average E_1 & E_2])

Parental lines	JLH 1594	KH 118	NH 545	AKH 91	AKH 62	AH 107	AKH 44	AKH 24	LRA 5166
AKH 84635	1.30	5.38	4.52	3.96	3.64	2.06	4.76	2.41	4.84
JLH 1594		3.01	2.05	-1.51	1.96	0.11	3.35	1.96	0.46
KH 118			2.19	0.27	1.32	2.86	-0.88	0.68	-1.65
NH 545				-2.10	4.62	3.17	5.32	1.36	-0.06
AKH 91					1.22	1.56	-3.01	-4.26	0.76
AKH 62						-1.66	1.36	0.85	0.32
AH 107							-1.48	-0.23	2.22
AKH 44								0.53	-2.56
AKH 24									-1.51

D^2 (Mean) = 1.23

Table.8 Deviation in Genetic Distances (D^2) of parental lines over Environments (E_2 Vs [Average E_1 & E_2])

Parental lines	JLH 1594	KH 118	NH 545	AKH 91	AKH 62	AH 107	AKH 44	AKH 24	LRA 5166
AKH 84635	-0.44	-4.95	-1.64	2.42	-2.06	-1.12	0.14	-0.78	-1.76
JLH 1594	0.00	-2.70	0.44	3.90	-1.63	0.50	-0.68	-1.35	1.41
KH 118		0.00	-1.58	2.47	-1.21	-2.51	2.01	-0.29	3.12
NH 545			0.00	2.49	-3.81	-1.28	-2.95	-0.12	0.25
AKH 91				0.00	4.43	4.19	6.85	5.53	0.79
AKH 62						2.29	-0.22	-0.52	2.86
AH 107							3.80	1.29	2.84
AKH 44								2.19	4.97
AKH 24									2.87

D^2 (Mean) = 0.62

Table.9 Average Deviation in Genetic Distances (D^2) of parental lines over Environments (E_1, E_2 and [Average E_1 & E_2])

Parental lines	JLH 1594	KH 118	NH 545	AKH 91	AKH 62	AH 107	AKH 44	AKH 24	LRA 5166
AKH 84635	0.87	3.59	3.01	2.64	2.43	1.37	3.17	1.60	3.22
JLH 1594		2.01	1.36	-1.01	1.31	0.07	2.23	1.31	0.31
KH 118			1.46	0.18	0.88	1.91	-0.58	0.45	-1.10
NH 545				-1.40	3.08	2.11	3.55	0.90	-0.04
AKH 91					0.82	1.04	-2.01	-2.84	0.51
AKH 62						-1.11	0.90	0.57	0.22
AH 107							-0.99	-0.15	1.48
AKH 44								0.35	-1.71
AKH 24									-1.01

D^2 (Mean) = 0.82

Fig.1 Dendrogram based on D^2 analysis of parental lines in Environment (E_1)

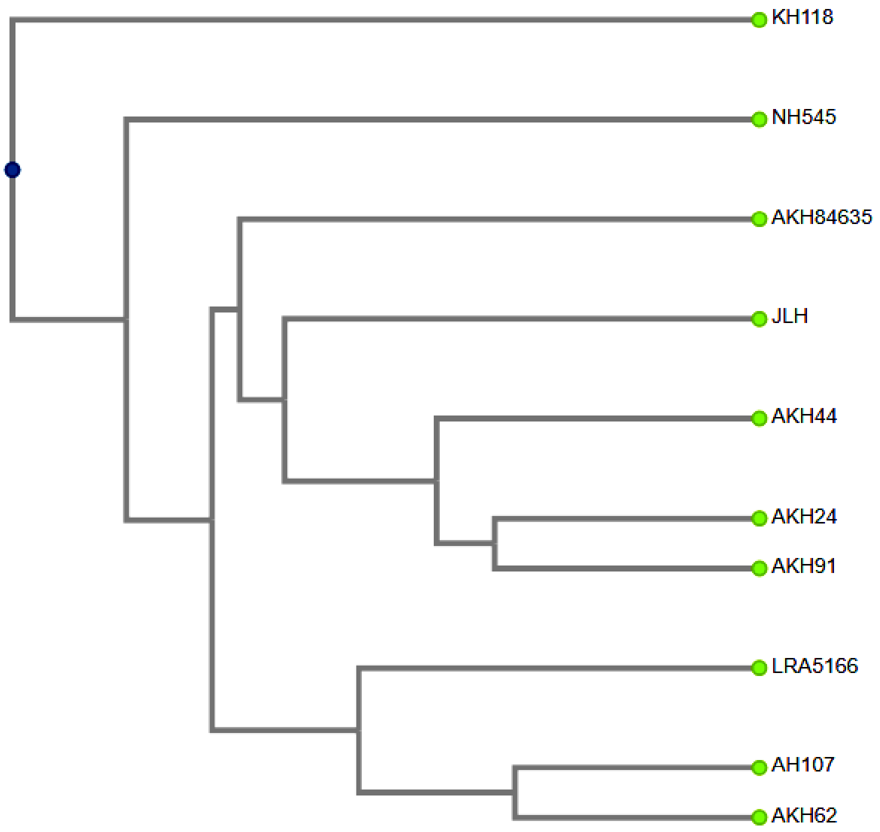


Fig.2 Dendrogram based on D^2 analysis of parental lines in Environment (E_2)

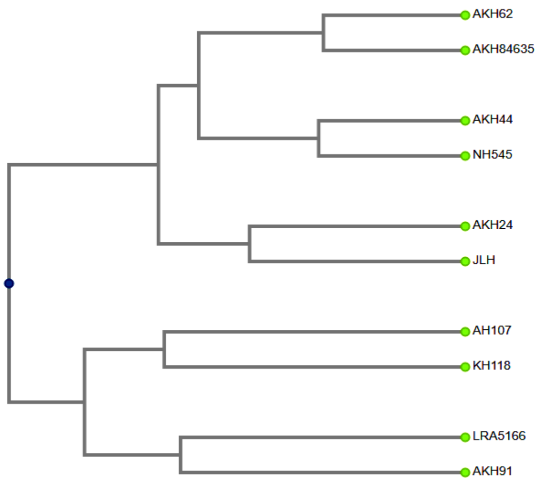
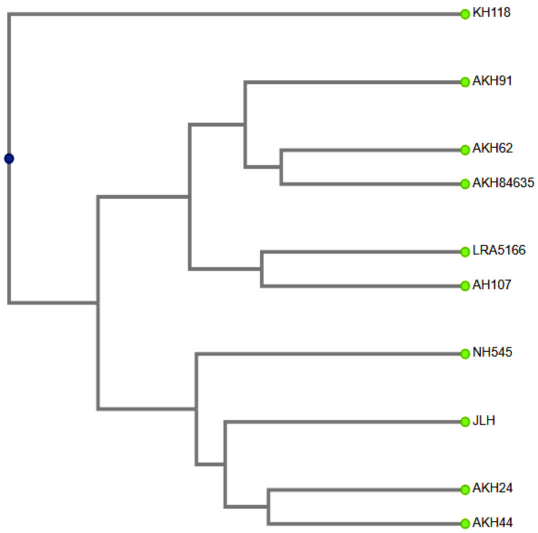


Fig.3 Dendrogram based on D^2 analysis of parental lines in Environment (Average of E_1 and E_2)



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The average deviations among genetic diversity estimates over different sets indicated the varying pattern (Table 9). Comparing D^2 matrices among E_1, E_2 and average of environments (E_1 & E_2) revealed the significant effect of environment on genetic distances with mean values 0.56 (E_1 vs E_2), 0.82 (E_1 vs Avg [E_1 & E_2]) and 0.62 (E_2 vs Avg.[E_1 & E_2]). The average deviation of 0.82 was estimated for genetic diversity estimates over the environments. In case of fibre quality traits in cotton, the improvement is one of challenge, as these fibre traits are controlled by multigenes and designated as complex quantitative traits having negative relationship with seed cotton yield resulting in low genetic gain in conventional phenotypic selection (Ijaz *et al.*, 2019).

It is revealed that selection of parents on the basis of *per se* performance will not always be useful in planning a breeding program. Therefore there is need to study of genetic architecture of parents involved in crossing program is necessary. Further, the genetic diversity estimates (D^2) of same parental set can fluctuate by environment.

So there is need to screen the genetypes by techniques which is less prone to environmental fluctuations. The recent advances avails the innovative tools for quick screen the diverse cotton population using biochemical markers along with precise DNA markers techniques can be deployed for speed-up the process of selection of parents in breeding program to build the platform of marker assisted breeding (Ujjainkar and Patil, 2020)

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Yield and its contributing characters are the polygenic trait and governed by minor genes having cumulative effects for expression which is highly influenced by environmental factors, to overcome this limitation the molecular markers may be employed for estimating the genetic diversity among parental lines to predict their potential for development of heterotic cross combinations.

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