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## Assessment of genetic diversity using $D^2$ analysis among $F_3$ progenies derived from $F_2$ populations of intra-hirsutum cotton hybrids (*Gossypium hirsutum* L)

**Suman Parre and Rajesh S Patil**

### Abstract

To inquest the genetic divergence for yield attributing traits among selected  $F_2$  ( $F_3$ ) populations of intra-hirsutum cotton hybrids, an appraisal was conducted encompassing 86 lines of the  $F_3$  population. The experiment was comprehended with progeny rows in the  $F_3$  population with five checks, laid out in augmented design. Compilation of data and its analysis depicted that there is significant variation among the different genotypes for the different characters studied. Mahalanobis  $D^2$  - statistic was used for assessing the genetic divergence among the  $F_3$  segregants lines of the experiment.  $D^2$  values were clustered using Tocher's method Genotypes were grouped onto 9 clusters. Cluster I (53) contain the maximum number of genotypes followed by cluster II (19) and cluster III (8). The remaining clusters depicted that they were solitary. Among the cluster distances inter-cluster distances were wide-ranging when compared to intracluster distances stipulating that there was wider genetic diversity. The maximum inter-cluster distance was between the clusters VIII and IX and the minimum between VI and VII. Plant height, number of seeds per boll number of nodes per plant and number of seeds per boll had contributed much for divergence. The genetic diversity results have shown that clusters VI, VII, VIII and IX can be crossed for isolating promising segregants or can be further advanced to the next generation for the development of suitable inbred lines.

**Keywords:** cotton (*Gossypium hirsutum*) genetic diversity, intra-hirsutum cotton hybrids, cluster means, yield attributing traits of cotton

### Introduction

Cotton is a significant fibre crop grown all over the world accounting for 50% of all the fibres used in the textile industry (Fryxell 1992) [3]. This crop became the major source to meet the clothing needs of millions. Cotton had played a significant role in the social and economic structure of many countries and also assisted in shaping the history of certain parts of the world (Ranganatha *et al.* 2013) [7]. Though several natural and synthetic fibers are at hand, the outstanding qualities and properties offered by cotton lint have made it to be chosen over all other fibers (Rajan *et al.* 2018) [5]. India being the first largest producer of cotton, produced 5.77 million metric tonnes of cotton (www.statista.com). For the improvement of production and productivity in cotton, isolation of suitable inbred lines and assessment of genetic divergence is a must. As most of the farmers in India were small and marginal, developing cultivars that yield as good as commercial hybrids is a primary thrust. So that the farming community may have good returns. Genetic divergence among the  $F_3$  population assists in isolating segregants that are as good as parental lines and also suitable segregants with new gene combinations that perform well when compared to parental genotypes. Genetic variability, divergence and genetic potential play a significant role in developing new promising cultivars. Hence studying the genetic divergence magnitude among the  $F_3$  population from different crosses will assist in understanding the  $F_3$  individual's diversity concerning one another.

### Materials and Methods

The experiment was conducted at agricultural research station Hebballi, under the University of Agricultural Sciences Dharwad. Selected  $F_2$  populations advanced to  $F_3$  generation; 86 lines were studied for the assessment of genetic diversity. The lines were sown in Augmented design. Total 115 lines were sown in five blocks each with 23 lines. Each progeny was sown as a single row, 5meters in length with a spacing of 90 centimetres between each row. Five

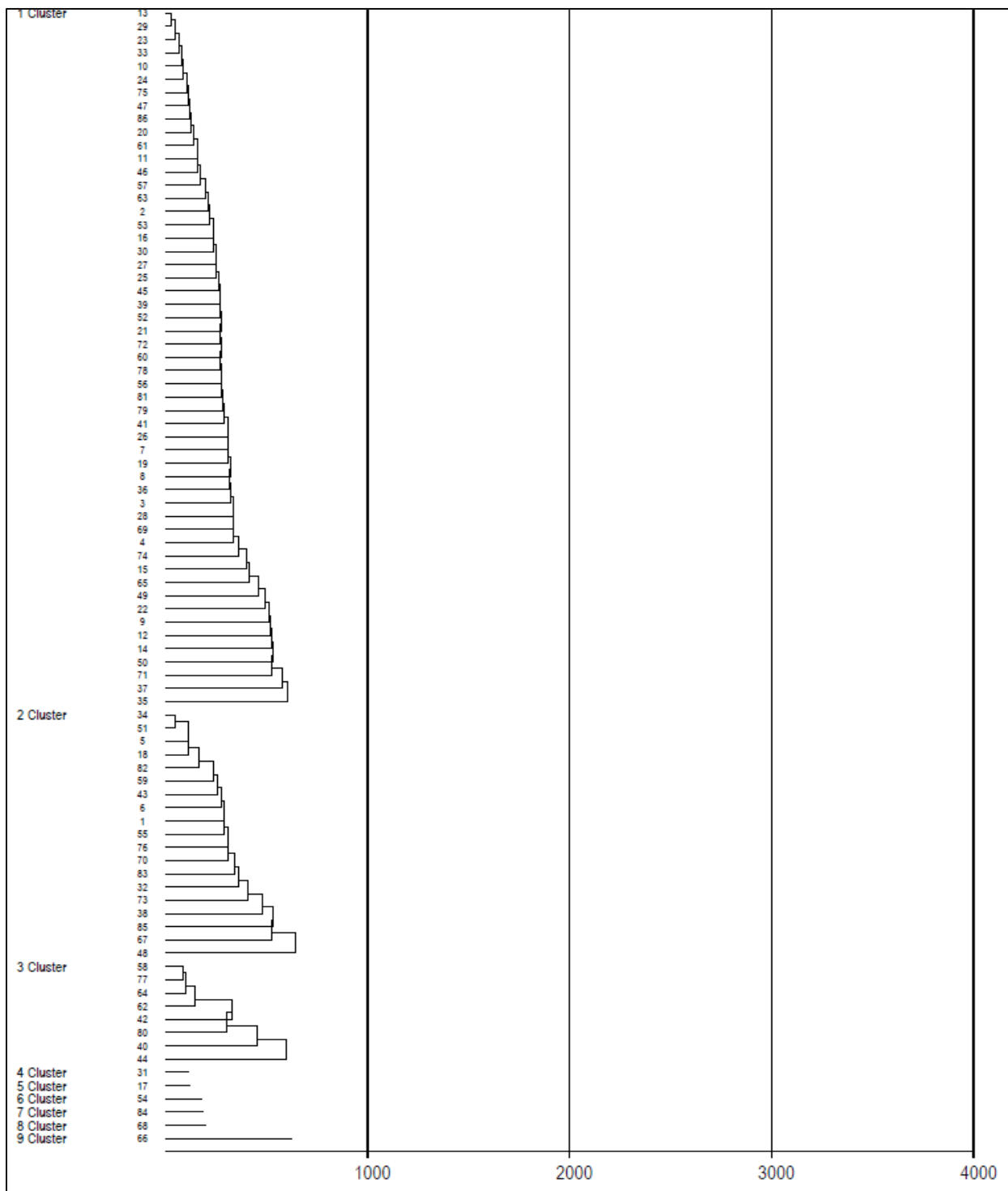
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checks were used for the comparison of performance RAH 100, RAH 221, Sahana, ABHR- 813, LRA-5166 with five replications. All intercultural operations were carried out according to the prescribed standards. Data was recorded on 15 yield attributing characters such as Plant height, Monopodia per plant, Sympodia per plant, Sympodial length at 50% plant height, Number of nodes per plant, Sympodial angle, Number of bolls, Stem girth, Boll weight, Seed cotton yield/plant, Halo length, Number of seeds per boll, Seed index, Lint index and Ginning out turn respectively. Statistical analysis was performed with WINDOSTAT 2.1 version. D<sup>2</sup>-statistic developed by Mahalonobis (1936) [4] was used for assessing the diversity among the F<sub>3</sub> population. D<sup>2</sup> values were calculated with Tocher's method, outlined by Rao

(1952) [8]. Intra and inter-cluster distances were calculated by the method given by Singh and Chaudhary (1977) [9]. Nearest cluster and farthest cluster from each other based on D<sup>2</sup> values, the percentage contribution of different characters to divergence, average intra and inter-cluster D<sup>2</sup> values were calculated for the nine clusters. Mean values for each cluster calculated.

**Results and discussion**

Dendrogram derived from the study of divergence of different yield attributing traits acceded the 86 individuals into nine groups (Figure 1), implying that there was significant variability among the individuals under study. Genetic variability was essential for.



**Fig 1:** Clustering using D<sup>2</sup> analysis in 86 F<sub>3</sub> progenies

**Table 1:** Diversity analysis and clustering in the F<sub>3</sub> progenies derived from Line X tester crosses

Clusters	Number of F <sub>3</sub> progenies	Name of F <sub>3</sub> progenies								
I	53	L2T1-3	L3T2-9	L3T2-3	L4T4-4	L1T1-10	L3T2-4	L8T4-7	L6T4-1	L9T4-8
		L7T1-7	L2T1-10	L2T1-1	L5T3-10	L7T1-3	L7T2-1	L1T1-2	L6T4-7	L2T1-6
		L4T4-1	L3T2-7	L3T2-5	L5T3-9	L5T3-3	L6T4-6	L3T2-1	L8T4-4	L7T1-6
		L8T4-10	L7T1-2	L9T4-3	L9T4-1	L5T3-5	L3T2-6	L1T1-7	L2T1-9	L1T1-8
		L4T4-7	L1T1-3	L3T2-8	L8T4-1	L1T1-4	L8T4-6	L2T1-5	L7T2-3	L6T4-3
		L3T2-2	L1T1-9	L2T1-2	L2T1-4	L6T4-4	L8T4-3	L5T3-1	L4T4-6	
II	19	L4T4-5	L6T4-5	L1T1-5	L2T1-8	L9T4-4	L7T1-5	L5T3-7	L1T1-6	L1T1-1
		L7T1-1	L8T4-8	L8T4-2	L9T4-5	L4T4-3	L8T4-5	L5T3-2	L9T4-7	L7T2-5
		L6T4-2	L7T1-4	L8T4-9	L7T2-2	L7T1-8	L5T3-6	L9T4-2	L5T3-4	L5T3-8
III	8	L7T1-4	L8T4-5	L8T4-9	L7T2-2	L5T3-6	L9T4-2	L5T3-4	L5T3-8	L7T1-4
IV	1	L4T4-2								
V	1	L2T1-7								
VI	1	L6T4-8								
VII	1	L9T4-6								
VIII	1	L7T2-6								
IX	1	L7T2-4								

practicing the selection to advance to the next generation. The highest number of individuals, in cluster I constituted 53 individuals or 61.62 % of the assessed individuals. cluster II consists of 19 individuals or 22.09% of the total individuals assessed. Cluster III with 8 individuals. The remaining six clusters were with a single genotype each (Table 1). Among the sixteen traits studied, the maximum contribution to diversity was due to plant height succeeded by the number of nodes per plant sympodial length at 50 per cent plant height, number of seeds per boll monopodia, stem girth, sympodial angle, number of bolls, seed index and harvest index (Table 2). These observations were as per earlier workers for plant height (Singh and Singh, 1984) [11], for plant height and seed cotton yield per plant (Singh and Bains, 1968; Dani, 1985; Rajendra Kumar *et al.*, 2000) [10]. The contribution of different traits for the diversity was remarkably pronouncing. Tocher's method of clustering for yield attributing traits in the F<sub>3</sub> population generated nine distinct groups. Groups with single individuals indicate that their characteristics were unique when compared to others (Vasconcelos *et al.*, 2007) [12]. The formation of many clusters indicates that the individuals are heterogenous for the population analyzed and

the yield attributing characters studied (Cruz & Regazzi 1997). According to the previous research reports, maximum heterosis is manifested in a particular cross combination where the parental individuals selected are highly divergent. Intra ad inter-cluster distances were recorded. The maximum inter-cluster distance was between the clusters V and IX (64.95) and the minimum between the clusters VI and VII (13.71) (Table 3) which indicated that divergent genotypes produced variability which is a broad spectrum in nature enabling further improvement over selection. Intra cluster distance was found to be maximum in cluster III followed by cluster two and one.

### Conclusion

To achieve maximum genetic advance, a high degree of genetic divergence among the members of the cluster is necessary for producing advantageous breeding materials. A high magnitude of heterosis and transgressive segregants can be obtained if crosses from divergent clusters are made. Crossing individuals from distant clusters will lead to superior segregants in the advanced generations.

**Table 2:** Per cent contribution of characters towards divergence

Sl. No.	Source	Times ranked first	Contribution (%)
1	Plant height	2314	35.30 %
2	Monopodia per plant	15	0.23 %
3	Sympodia per plant	0	0.00 %
4	Sympodial length at 50% plant height	38	0.58 %
5	Number of nodes per plant	1348	20.56 %
6	Sympodial angle	127	1.94 %
7	Number of bolls	114	1.74 %
8	Stem girth	333	5.08 %
9	Boll weight	15	0.23 %
10	Seed cotton yield/plant	5	2.35 %
11	Halo length	0	0.00 %
12	Number of seeds / bolls	2033	31.01 %
13	Seed index	64	0.98 %
14	Lint index	0	0.00 %
15	Ginning out turn	0	0.00 %

**Table 3:** Nearest cluster and farthest cluster from each other

Cluster number	Nearest cluster with D <sup>2</sup> value	Farthest cluster with D <sup>2</sup> value
I	IV (25.18)	IX (38.57)
II	V (28.61)	IX (53.96)
III	I (31.88)	VII (58.70)
IV	VIII (17.64)	IX (48.42)
V	VIII (22.83)	IX (64.95)
VI	VII (13.71)	III (53.19)
VII	VI (13.71)	III (58.70)
VIII	IV (17.64)	IX (56.51)
IX	I (38.57)	V (64.95)

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