***Original Research Article***

**Morphological and Quantitative traits based Genetic diversity analysis of Sesame (*Sesamum indicum* L.) Genotypes Released in India**

**Abstract**

**Aims:**Sesame is an important high-value oilseed crop. India is very rich in the wild and cultivated sesame, offers a rich load of genetic variability for breeding. Recognizing and utilizing this genetic diversity holds significant importance in devising efficient breeding programs aimed at enhancing the yield potential of various genotypes.

**Study design:** The experimental design adopted was Randomized Complete Block design with two replications.

**Place and Duration of Study:** The field experiment was conducted in the Summer 2021 at the Research Farm, Indian Institute of Oilseeds Research (IIOR), Narkhoda, Hyderabad, Telangana, India.

**Methodology:** In this study, 70 released sesame varieties of India were characterized for 12 morphological and 14 quantitative characters and subjected it to genetic divergence (UPGMA hierarchial clustering) analysis.

**Results:** From divergence analysis for morphological characters, these cultivars were grouped into seven clusters at the genetic distance of 10 using Ward’s minimum variance method and Gower’s method of genetic distance. Selection of the genotypes present in different clusters having more genetic distance, preferably belonging to different geographical origin may result in more heterotic effects in the hybridization programme. Good recombinants can be obtained by mating between clusters I and VII for genotypes viz., Vinayak, RT-103, CUMS-17, TKG-308 with JLT-7, Amrit, Phule Til-1, YLM-11 for morphological characters, as they have maximum genetic distance between them. From the divergence analysis for quantitative characters, 70 cultivars were grouped into 7 clusters based on divergence analysis at the genetic distance of 10 using Ward’s minimum variance method and Euclidean method of genetic distance. Good recombinants can be obtained on mating between the clusters I and VII for lines *viz.,*Amrit, TKG-308, JTS-8, HT-1, Phule Til-1 with Vinayak, CUMS-17, JLT-7, YLM-11 for quantitative characters, as they have maximum genetic distance between them. Most of the characters recorded high mean values in cluster VII for quantitative characters. Hence, for breeding of these traits, the genotypes present in cluster VII can be selected as parents.

**Conclusion:** Based on both morphological and quantitative characters, the following superior and complementary genotype pairs: Vinayak and CUMS-17 with Amrit and Phule Til-1 respectively could be served as parents in the breeding program.

**Keywords:** Sesame, Diversity, Cluster, UPGMA, recombinants

**1. INTRODUCTION**

Sesame (*Sesamum indicum* L.) is one of the ancient oilseed crop, originated and domesticated in India, is widely cultivated across tropical and subtropical regions (Bedigian, 2003). Sesame, commonly called as ‘Til’ is also known as ‘benni seed’ and ‘gingelly’; classified under the order Tubiflorae and family Pedaliaceae. Sesame is diploid possessing 26 chromosomes (2n=26), and a genomic size estimated at approximately ~369Mb (Zhang *et al*., 2013). Sesame oil is extensively used in various industries, not just for cooking. It is a primary component in the manufacture of soaps, perfumes, paints, pharmaceuticals, insecticides.Moreover, it plays a crucial role in Ayurvedic medicine, serving as a base for many traditional remedies. Sesame meal is used as feed for poultry and livestock.

Sesame seed possess excellent nutritional properties, comprising 50% oil, 23% protein and 15% carbohydrate. In the presence of lignans (sesamolin, sesamol, sesamin) and tocopherols, sesame seed oil has remarkable antioxidant properties and long shelf life. These seeds are abundant in protein and essential amino acids, such as methionine and tryptophan. The oil primarily contains 85% unsaturated fatty acids, especially linoleic acid, which is very stable, helps lower cholesterol, and aids in preventing cardiovascular diseases. It has rich source of vitamins A, B complex, E, niacin and minerals *viz.,* phosphorous, iron, calcium, copper, zinc, magnesium and potassium. Considering these benefits, sesame is often called as queen of oil seeds.

On a global scale, sesame stands as the sixth most produced oilseed, behind soybean, groundnut, cottonseed, sunflower, linseed, and rapeseed. Sesame ranks fourth among oilseed crops in India in terms of area (16,27,040 ha), production (7,88,740 metric tonnes), and productivity (484.8 kg/ha). Despite having a sizable area under cultivation, India's overall productivity and production are fairly low (484.8 kg/ha) compared to the global average (525.2 kg/ha) (FAOSTAT, 2022). The reason for sesame's lower productivity compared to other oilseed crops lies in its cultivation on marginal lands with inadequate management practices. Furthermore, the non-availability of improved cultivars suitable for diverse agro-climatic conditions and deficiencies in the seed supply system exacerbate the problem of poor yield.

The presence of genetic variation is a fundamental requirement for any crop improvement programme. Recognizing and utilizing this genetic diversity holds significant importance in devising efficient breeding programs aimed at enhancing the yield potential of various genotypes. Exploiting genetic variation necessitates the characterization of germplasm, which involves assessing primary variables like the agro-morphological traits of sesame genotypes. These traits serve as crucial indicators for measuring phenotypic variation. However, the characterization using agro-morphological traits “is simple and requires relatively lower cost which makes it an interesting tool for studying genetic diversity but” is affected by environment (Banerjee and Kole 2009; Tabatabaei *et al*., 2011) and has the problems of low heritability and time consuming. Despite its limitations, this approach remains widely utilized “for assessing genetic diversity. The genotypes that are genetically distant for traits, contributes genetic divergence, are expected to generate a wide range of genetic variation in recombination breeding and pave the way for greater scope for the recovery of transgressive segregants” (Sharma *et al*., 2008).

“The successful recovery of heterosis has been reported in crosses involving genetically diverse parents” (Singh *et al*., 2007 in mustard; Dong *et al*., 2003 in soybean; Pasquet *et al.,* 2002 in groundnut; Khan *et al.,* 2013 in linseed; and Yousuf *et al.,* 2011 in rapeseed). The understanding of genetic diversity and phylogenetic relationships among sesame cultivars is essential for selecting appropriate genotypes for crop improvement in adverse conditions. Therefore, an attempt has been made to to measure the level of genetic divergence between each pair of test genotypes and identify those significantly divergent. This is aimed at customizing desirable gene combinations through recombination breeding.

**2. MATERIAL AND METHODS**

**2.1 Experimental site**

The field experiment was conducted in the Summer 2021 at the Research Farm, Indian Institute of Oilseeds Research (IIOR), Narkhoda, Hyderabad, Telangana, India. The research plot in Narkhoda, Hyderabad was situated at 17. 25’ N latitude and 78.32’ E longitude at an altitude 542 meter above the sea level. The soil type is sandy clay loam. It falls in sub-tropical southern Telangana agroclimatic zone.

**2.2 Experimental material and design**

The plant material utilized in the experiment consisted of 70 released sesame varieties of India obtained from IIOR and AICRP, Sesame and Niger**.** The experimental design adopted was Randomized Complete Block design with two replications. Row length adopted is 4 m and allotted 2 rows per genotype. Row to row distance is 45cm and plant to plant distance is 15cm.

**Table 1: Details of the experimental material**

|  |  |  |
| --- | --- | --- |
| 1.AKT-101 | 25.N-32 | 49.TKG-22 |
| 2.AKT-64 | 26.Nirmala | 50.TKG-306 |
| 3.Amrit | 27. Phule Til-1 | 51.TKG-308 |
| 4.B-67 | 28. Paiyur | 52.TKG-55 |
| 5.Chandana | 29. PKDS-11 | 53.TMV-3 |
| 6.CUMS-17 (Suprava) | 30. PKDS-8 | 54.TMV-4 |
| 7.DS-5 | 31.Prachi | 55.TMV-6 |
| 8.DSS-9 | 32.Pragati | 56.TMV-7 |
| 9.E-8 | 33.Punjab Til-1 | 57.TSS-6 |
| 10.GJT-5 | 34. Punjab Til-2 | 58. Tarun |
| 11.GT-1 | 35. Rajeshwari | 59. Thilak |
| 12.GT-10 | 36. Rama | 60. Thilottama |
| 13.GT-2 | 37. RT-103 | 61.Thilarani |
| 14.GT-3 | 38. RT-125 | 62.Uma |
| 15.GT-4 | 39. RT-127 | 63.Usha |
| 16.HT-1 | 40. RT-346 | 64.VRI-1 |
| 17.HT-2 | 41. RT-351 | 65.VRI-2 |
| 18.Hima | 42. RT-372 | 66.VRI-3 |
| 19.IIOS-1101 | 43. RT-46 | 67.Vinayak |
| 20.JLT-408 | 44.Savitri | 68.YLM-11 |
| 21.JLT-7 | 45.Shubra | 69.YLM-17 |
| 22.JTS-8 | 46.Smarak | 70.YLM-66 |
| 23.Kanak | 47.Swetha Til |  |
| 24.Krishna | 48.T-78 |  |

**2.3 Observations recorded**

In this study, morphological characterization was conducted, focusing on the botanical and morphological traits of plants and their parts. The characters under study adhered to DUS guidelines with 12 different morphological categories viz., petal color, petal hairiness, leaf margin, capsule hairiness, branching pattern, capsule shape, stem hairiness, leaf lobes, capsule number per leaf axil, capsule arrangement and seed coat color and also 14 quantitative characters like days to emergence, days to 50% flowering, days to flower cessation (completion), days to maturity, length to first capsule (cm), plant height, primary branches per plant, secondary branches per plant, capsule number per plant, number of leaf axils on main stem, capsule length(cm), test weight (g), oil content (%) and seed yield per plant (g). Observations on the above traits were recorded on the five random competitive plants, except for the traits days to emergence, days to 50% flowering, days to flowering cessation (completion), days to maturity, which were recorded on plot basis.

**2.4 Method**

The study evaluated the genetic dissimilarity among 70 sesame genotypes by considering morphological and quantitative characters. These traits were then used as inputs for UPGMA (Unweighted Pair Group Method with Arithmetic Mean) cluster analysis. The UPGMA is a simple agglomerative (bottom-up) hierarchical clustering method attributed by Sokal and Michener (1958).

**2.5 Statistical analysis**

**2.5.1 Genetic diversity analysis using morphological characters:**

UPGMA clustering is done using Ward’s minimum variance method and Gower’s method of genetic distance (Gower, 1971) The UPGMA dendrogram is constructed using R software version 4.1.0.

Gower’s method of genetic distance:

(x1, x2)= 1- () where, x1, x2 are nominal variables

**2.5.2 Genetic diversity analysis using quantitative traits:**

UPGMA clustering is done using Ward’s minimum variance method and Euclidean method of genetic distance. The UPGMA dendrogram is constructed using R software version 4.1.0.

Euclidean method of genetic distance:

d (x,y) = where, x, y are ordinal variables

**3. RESULTS AND DISCUSSION**

The choice of parents is of paramount importance in any hybridization breeding programme but it is a difficult task for a plant breeder. Understanding the nature and magnitude of genetic divergence is essential for effective planning of hybridization programme. Genetic divergence studies play a crucial role for evaluating genotypes for variability which helps the breeder to plan for selection of genotypes as parents for breeding programme. Crosses between genetically divergent parents typically result in a more pronounced heterotic effect compared to those involving closely related individuals.

**3.1 Genetic diversity analysis using morphological characters**

In this study, genetic divergence of 70 sesame genotypes was assessed by employing nominal variables of morphological characters. These variables served as input for the UPGMA (unweighted pair group method with arithmetic mean) cluster analysis in which clustering was done using Ward’s minimum variance method and Gower’s method of genetic distance was derived. The dendrogram was constructed by using R software ver. 4.1.0.

**3.1.1 Grouping of genotypes into different clusters**

In this study, 70 genotypes were grouped into 7 clusters based on divergence analysis at the genetic distance of 10 (Table 1) (Fig. 1). Clustering of genotypes was mainly due to their morphological differences. Cluster VII was the largest among all clusters comprising 16 genotypes. Cluster V has 13 genotypes, Cluster VI has 11 genotypes, Cluster I has 10 genotypes, Cluster III has 9 genotypes, Cluster IV has 6 genotypes and Cluster II has 5 genotypes.

The maximum genetic distance was present between genotypes of cluster I and VII followed by cluster II and VII. So, the good recombinants can be obtained on mating between the clusters I and VII; II and VII for lines *viz.,*Vinayak, RT-103, CUMS-17, TKG-308 with JLT-7, Amrit, Phule Til-1, YLM-11

Out of 70 genotypes, only 40% of genotypes were clustered according to geographical origin (Table 2). The results of UPGMA dendrogram are compared according to geographical origin and following inferences are drawn.

The genotypes belonging to Gujarat state (GJT-5, GT-2, GT-3, GT-4, GT-10, GT-1) are grouped in one cluster (cluster 4) except for genotypes like GT-3 and GT-10 due to white petal color, one capsule per axil, alternate capsule arrangement. GT-3 is different from others in dense petal hairiness while, GT-10 has tapered capsule shape and black seed coat color.

The genotypes belonging to Madhya Pradesh state (JTS-8, TKG-306, TKG-22, TKG-308, TKG-55, PKDS-11, PKDS-8, N-32) are clustered in cluster 1 except for genotypes JTS-8, PKDS-8, PKDS-11 and N-32. The similarity of genotypes in cluster 1 is due to light purple petal color, top branching pattern, sparse stem hairiness, slightly lobed leaf lobes, weak leaf margin, one capsule number per leaf axil, four locule number per capsule, broad oblong capsule shape, opposite capsule arrangement and white seed coat color.

The genotypes belonging to Karnataka (DS-5, DSS-9 and E-8) are grouped in cluster 3 except for genotype E-8 is due to sparse hairiness, top branching pattern and alternate capsule arrangement**.**

The genotypes belonging to Kerala (Thilothama, Thilak, Thilarani) are grouped in cluster 6 except for genotype Thilarani because it has dense stem hairiness.

The genotypes belonging to other states are grouped in different clusters is due to difference in various morphological characters.

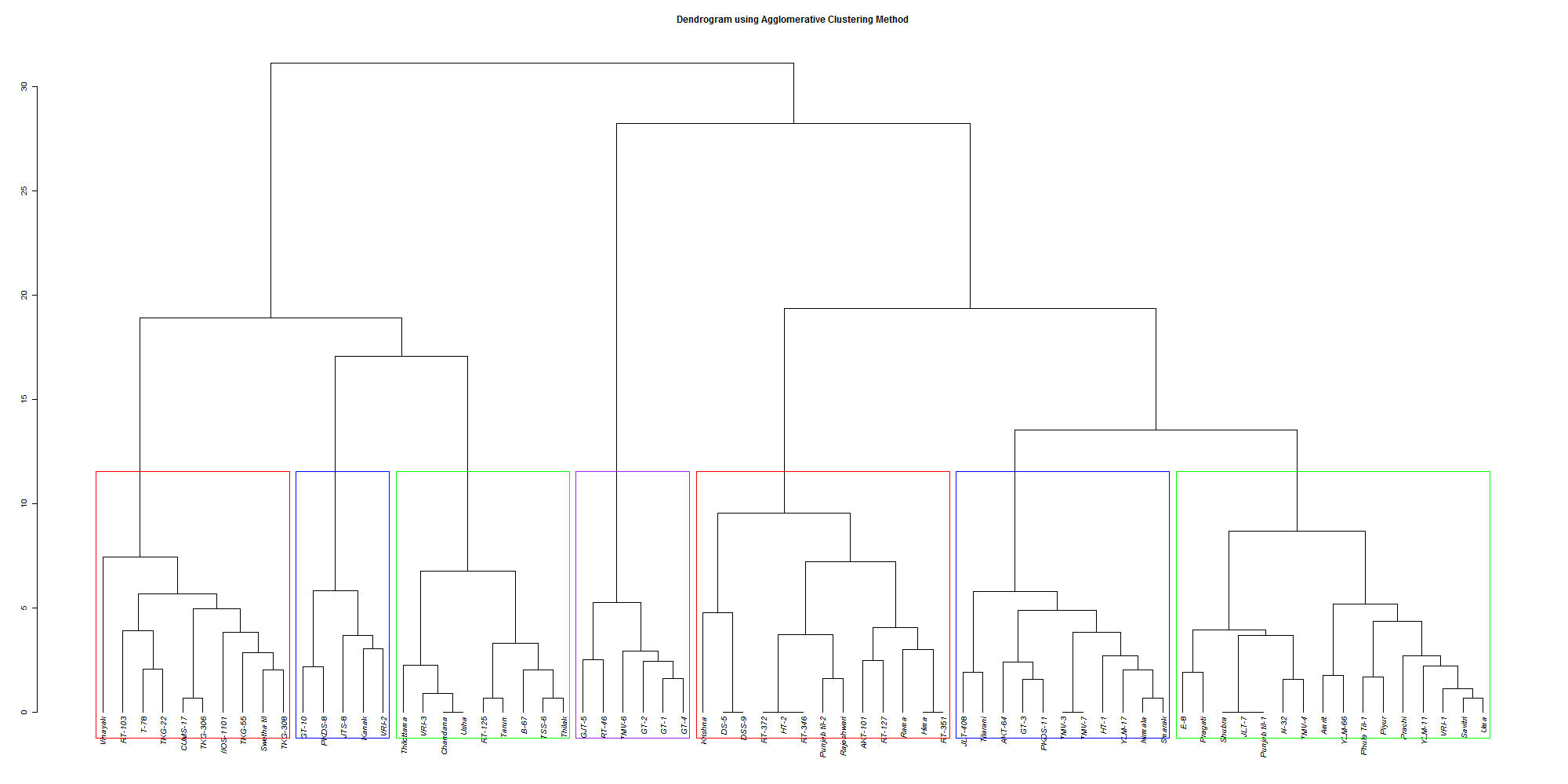
Hence, selection of genotypes present in different clusters having more genetic distance, preferably belonging to different geographical origin may result in more heterotic effects in hybridization programme.

**Table 2: Distribution of sesame genotypes into different clusters (morphological characters)**

|  |  |  |
| --- | --- | --- |
| **Name of Cluster** | **No.of Genotypes** | **Genotypes** |
| **I** | 10 | Vinayak, RT-103, T-78, TKG-22, CUMS-17, TKG-306, IIOS-1101, TKG-55, Swetha Til, TKG-308 |
| **II** | 5 | GT-10, PKDS-8, JTS-8, Kanak, VRI-2 |
| **III** | 9 | Thilothama, VRI-3, Chandana, Usha, RT-125, Tarun, B-67, TSS-6, Thilak |
| **IV** | 6 | GJT-5, RT-46, TMV-6, GT-2, GT-1, GT-4 |
| **V** | 13 | Krishna, DS-5, DSS-9, RT-372, HT-2, RT-346, Punjab Til-2, Rajeshwari, AKT-101, RT-127, Rama, Hima, RT-351 |
| **VI** | 11 | JLT-408, Thilarani, AKT-64, GT-3, PKDS-11, TMV-3, TMV-7, HT-1, YLM-17, Nirmala, Smarak |
| **VII** | 16 | E-8, Pragati, Shubra, JLT-7, Punjab Til-1, N-32, TMV-4, Amrit, YLM-66, Phule Til-1, Paiyur, Prachi, YLM-11, VRI-1, Savitri, Uma |

**Table 3: Clustering of genotypes in accordance to geographical origin**

| **Geographical origin** | **Genotypes** | **Cluster** |
| --- | --- | --- |
| Gujarat | GT-2, GT-4, GT-1, GJT-5 | Cluster 4 |
| GT-10 | Cluster 2 |
| GT-3 | Cluster 6 |
| Rajasthan | RT-372, RT-351, RT-346, RT-127 | Cluster 5 |
| RT-125 | Cluster 3 |
| RT-46 | Cluster 4 |
| RT-103 | Cluster 1 |
| Maharashtra | AKT-64, JLT-408 | Cluster 6 |
| Phule Til-1, JLT-7 | Cluster 7 |
| AKT-101 | Cluster 5 |
| Madhya Pradesh | TKG-306, TKG-22, TKG-55, TKG-308 | Cluster 1 |
| JTS-8, PKDS-8 | Cluster 2 |
| PKDS-11 | Cluster 6 |
| N-32 | Cluster 7 |
| Andhra Pradesh | YLM-66, YLM-11 | Cluster 7 |
| Hima, Rajeshwari | Cluster 5 |
| Chandana | Cluster 3 |
| Swetha Til | Cluster 1 |
| YLM-17 | Cluster 6 |
| Uttar Pradesh | Tarun | Cluster 3 |
| Pragati | Cluster 7 |
| T-78 | Cluster 1 |
| West Bengal | Savitri | Cluster 7 |
| CUMS-17 | Cluster 1 |
| Rama | Cluster 5 |
| B-67 | Cluster 3 |
| Tamil Nadu | TMV-4, VRI-1, Paiyur | Cluster 7 |
| TMV-7, TMV-3 | Cluster 6 |
| VRI-3, TSS-6 | Cluster 3 |
| VRI-2 | Cluster 2 |
| TMV-6 | Cluster 4 |
| Bihar | Krishna | Cluster 5 |
| Karnataka | DS-5, DSS-9 | Cluster 5 |
| E-8 | Cluster 7 |
| Kerala | Thilothama, Thilak | Cluster 3 |
| Thilarani | Cluster 6 |
| Punjab | Punjab Til-1 | Cluster 7 |
| Punjab Til-2 | Cluster 5 |
| Odisha | Amrit, Shubra, Uma, Prachi | Cluster 7 |
| Smarak, Nirmala | Cluster 6 |
| Vinayak | Cluster 1 |
| Kanak | Cluster 2 |
| Usha | Cluster 3 |
| Haryana | HT-1 | Cluster 6 |
| HT-2 | Cluster 5 |
| Telangana | IIOS-1101 | Cluster 1 |

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C-I

C-II

C-III

C-IV

C-VI

C-VII

**Fig. 1: Agglomerative hierarchical cluster analysis [using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) procedure] of 70 sesame genotypes using morphological characters at the genetic distance of 10**

**3.2 Genetic diversity analysis using quantitative characters**

In this investigation, the genetic divergence among 70 sesame genotypes was assessed using ordinal variables of quantitative characters. These variables were utilized as input for UPGMA (unweighted pair group method with arithmetic mean) cluster analysis, employing Ward’s minimum variance and Euclidean method of genetic distance was derived. The dendrogram was constructed by using R software ver. 4.1.0.

**3.2.1 Grouping of genotypes into different clusters**

In the present study, 70 genotypes were grouped into 7 clusters based on divergence analysis at the genetic distance of 10 (Table 3) (Fig.2). Clustering of genotypes was mainly due to their ordinal variables of quantitative differences. Cluster II is the largest among all clusters comprising 22 genotypes. Cluster VII has 13 genotypes, Cluster VI and Cluster I has 11 genotypes each, Cluster IV has 5 genotypes, Cluster III and Cluster V has 4 genotypes each.

The maximum genetic distance was present between genotypes of cluster I and VII followed by cluster II and VII. So, the good recombinants can be obtained on mating between the clusters I and VII; II and VII for lines *viz.,*Amrit, TKG-308, JTS-8, HT-1, Phule Til-1 with Vinayak, CUMS-17, JLT-7, YLM-11 while, the minimum genetic distance was present between genotypes of cluster IV and V followed by cluster VI and VII. Hence, selecting genotypes from different clusters with higher genetic distance can result in increased heterotic effects in hybridization programs.

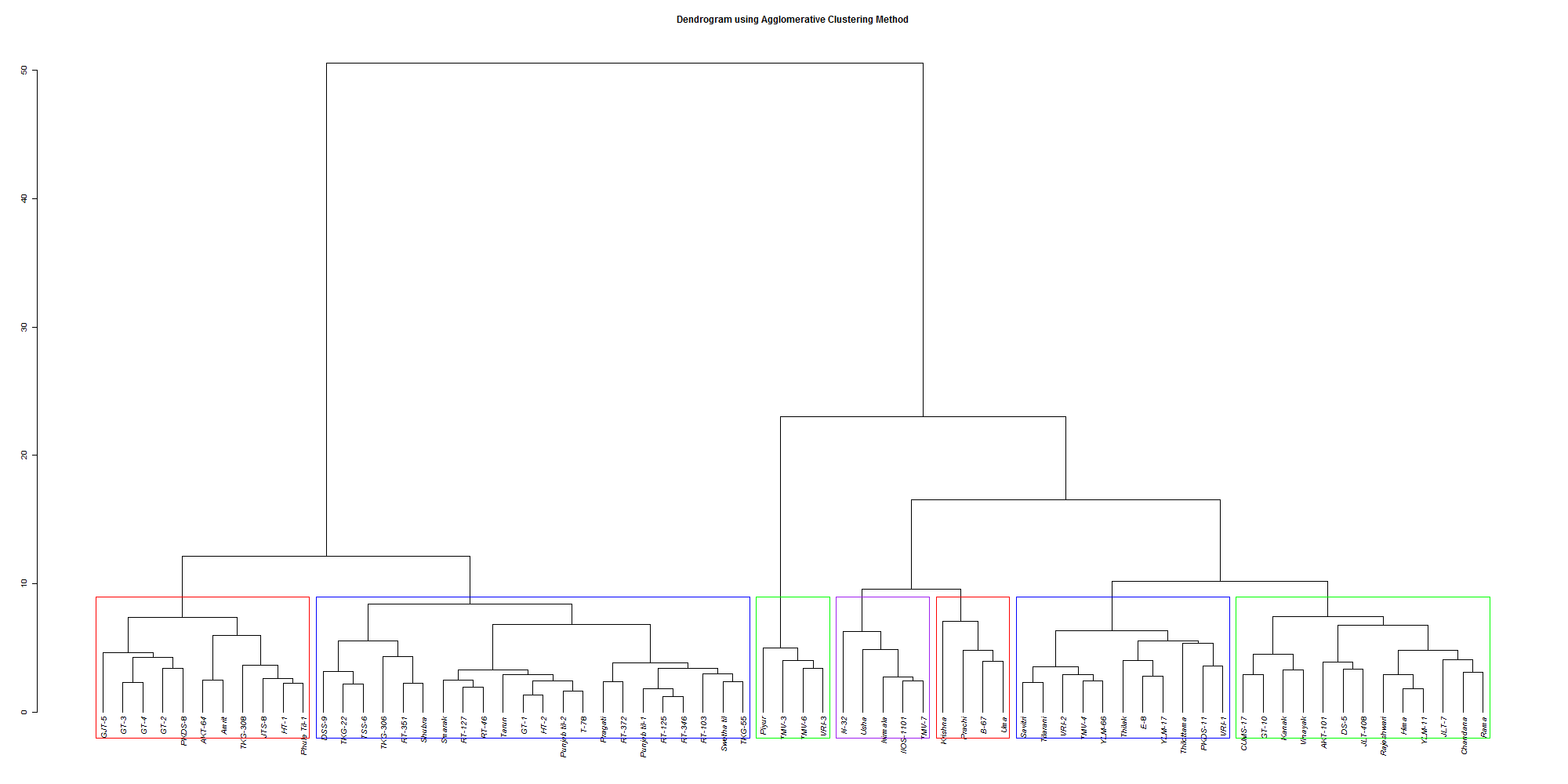
**Table 4: Distribution of sesame genotypes into different clusters (quantitative characters)**

|  |  |  |
| --- | --- | --- |
| **Name of Cluster** | **No.of Genotypes** | **Genotypes** |
| **I** | 11 | GJT-5, GT-2, GT-4, GT-3, PKDS-8, AKT-64, Amrit, TKG-308, JTS-8, HT-1, Phule Til-1 |
| **II** | 22 | DSS-9, TKG-22, TSS-6, TKG-306, RT-351, Shubra, Smarak, RT-127, RT-46, Tarun, GT-1, HT-2, Punjab Til-2, T-78, Pragati, RT-372, Punjab Til-1, RT-125, RT-346, RT-103, Swetha Til, TKG-55 |
| **III** | 4 | Paiyur, TMV-3, TMV-6, VRI-3 |
| **IV** | 5 | N-32, Usha, Nirmala, IIOS-1101, TMV-7 |
| **V** | 4 | Krishna, Prachi, B-67, Uma |
| **VI** | 11 | Savitri, Thilarani, VRI-2, TMV-4, YLM-66, Thilak, E-8, YLM-17, Thilothama, PKDS-11, VRI-1 |
| **VII** | 13 | CUMS-17, GT-10, Kanak, Vinayak, AKT-101, DS-5, JLT-408, Rajeshwari, Hima, YLM-11, JLT-7, Chandana, Rama |

The cluster mean values of different characters are presented in Table 4. In cluster I and III, none of the characters recorded the highest cluster mean value whereas, in cluster II, highest cluster mean values were recorded for Capsule length. In cluster IV, highest cluster mean value was recorded for days to emergence and test weight whereas, in cluster V, highest cluster mean value was recorded for primary branches per plant. In cluster VI, highest cluster mean value was recorded for days to flower session whereas, in cluster VII, highest cluster mean values were recorded for the characters days to 50% flowering, days to maturity, length to first capsule, plant height, secondary branches per plant, capsule number per plant, number of leaf axils in main stem and oil content. Most of characters recorded high mean values is in cluster VII. Therefore, for breeding for these traits, it is desirable to select genotypes that are present in cluster VII as one of the parents

**Table 5: Cluster mean values for fourteen traits in sesame genotypes**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Character** | **Cluster1** | **Cluster2** | **Cluster3** | **Cluster4** | **Cluster5** | **Cluster6** | **Cluster7** |
| **Days to emergence** | 5 | **4.59** | 5.62 | **6.43** | 6.14 | 5.90 | 5.25 |
| **Days to 50% flowering** | 42.81 | **40.18** | 47.12 | 42.27 | 46.23 | 47.80 | **49.62** |
| **Days to flower session** | 69.46 | **67.68** | 76.25 | 69.02 | 72.41 | **80.30** | 79.12 |
| **Days to maturity** | 96.62 | 94.18 | 99.12 | **92.32** | 99.73 | 97.80 | **100.12** |
| **Length to first capsule** | 22.59 | 20.56 | 24.5 | **19.38** | 30.97 | 27.77 | **45.92** |
| **Plant height** | 91.46 | 86.85 | 112.83 | **83.67** | 92.70 | 103.63 | **121.21** |
| **Primary branches per plant** | 5.23 | **4.45** | 5.5 | 4.59 | **6.45** | 6 | 6.25 |
| **Secondary branches per plant** | 4.73 | 1.77 | 3 | **0.45** | 5.09 | 3.4 | **9** |
| **Capsule number per plant** | 80.96 | **64.77** | 66 | 74.27 | 77.05 | 128.30 | **185.25** |
| **Number of leaf axils in main stem** | 94.38 | **67.27** | 79.62 | 86.77 | 89.55 | 140.8 | **200.88** |
| **Capsule length** | 2.50 | **2.74** | 2.48 | 2.67 | **2.39** | 2.73 | 2.56 |
| **Test weight** | 3.43 | 3.44 | **2.48** | **3.59** | 3.32 | 2.96 | 3.39 |
| **Oil content** | 47.98 | 48.82 | **44.13** | 48.81 | 47.56 | 45.24 | **49.88** |
| **Seed yield per plant** | 7.81 | 5.92 | 6.12 | **5.84** | 7.87 | **9** | 7.51 |

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C-V

C-VI

C-VII

C-IV

C-III

C-II

C-I

**Fig. 2: Agglomerative hierarchical cluster analysis [using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) procedure] of 70 sesame genotypes using quantitative characters at the genetic distance of 10.**

Based on both morphological and quantitative characters, the following superior and complementary genotype pairs: Vinayak and CUMS-17 with Amrit and Phule Til-1 respectively can be served as parents in the breeding program. .

Similarly, diverse clustering pattern in sesame were reported by Kumhar and Solanki (2009) has clustered 82 genotypes of sesame into eight clusters; Pham *et al.* (2011) has grouped the twelve sesame population into three clusters based on 10 agro-morphological characters; Pandey *et al.* (2015) has clustered 60 genotypes for 37 characters into two main clusters and eleven sub clusters at the genetic distance of 1.58; Swapan *et al.* (2016) has grouped the genotypes into six clusters for 14 agro-morphological characters using Euclidean genetic distance; Ramprasad *et al*. (2017) has grouped the 41 sesame genotypes into four clusters; Bhattacharjee *et al*. (2019) has clustered 30 genotypes for 12 characters into five clusters at the genetic distance of 0.52; Ramya *et al.* (2020) has clustered 110 genotypes for 30 morphological characters and 10 agronomic characters into 7 clusters.

**4. CONCLUSION:**

The genetic diversity analysis present in the Indian sesame varieties using agro-morphological traits is aimed at customizing desirable gene combinations through recombination breeding which is essential for breeding of new sesame varieties and selection of parental lines. From the study, the following superior and complementary genotype pairs: Vinayak and CUMS-17 with Amrit and Phule Til-1 respectively can be served as parents in the breeding program. Further research on these selected germplasm will save a lot of time for the breeder in future. Agro-morphological traits have some shortcomings in evaluating genetic diversity as these are phenotypic markers and genetically distant germplasm may be morphologically similar. Further research should be done with molecular markers which can be used to determine genetic distance easily and successfully. DNA markers should provide more accurate measures of genetic similarity.

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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