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Study of Genetic Divergence Analysis in Sesame (*Sesamum indicum* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Aim: To determine the extent of genetic divergence (D^2 statistics) present in sesame genotypes for different traits.
Study Design: The experiment was conducted in Augmented Block Design (ABD).
Place and Duration of Study: The experiment was laid out in *kharif* 2020 at BSP (Groundnut) Research Farm, JNKVV, Jabalpur (M.P.).
Methodology: Total 160 sesame genotypes and 5 checks *viz.,* RT346, PBTil2, GT10, TMV-7 and VRI-1 were used for diversity analysis for twelve quantitative traits for selection of diverse parents. The 165 genotypes were grouped into eight clusters based on the Mahalanobis D^2 values following Tocher's methods.

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Results: Maximum inter cluster distance (63.235) was exhibited between cluster III and cluster VIII and intra cluster distance (28.509) was in cluster VII. The lowest inter cluster divergence (15.881) was noticed between cluster III and V indicating that the genotypes included in them were closely related. Relative contribution of different characters to total divergence was assessed through comparison of actual D2 values for individual characters over all possible combinations. Cluster III had highest mean value for plant height (126.609), days to flower initiation (34.308), days to 50% flowering (37.462), and oil content (44.715). Cluster VII reported to be days to maturity (91.750), number of primary branches per plant (3.833) and number of secondary branches per plant (2.625) and in cluster V had capsule length (2.651). cluster VI reported for number of capsules per plant (59.484) and seed yield per plant (9.168), number of seeds per capsule (58.533) and thousand seed weight (2.848). It was revealed that number of primary branches per plant (11.32%) followed by oil content (11.06%) and number of capsules per plant (11.05%) contributed maximum to total divergence and minimum contributed by days to flower initiation (3.49%).

Conclusion: So, it is expected that crosses between genotypes of cluster III with genotypes of cluster VIII will give rise to high yielding sergeants as high inter cluster distance and those clusters has recorded good mean values can be preferred in selecting germplasm lines for respective traits.

Keywords: Genetic diversity; D2 analysis; Clustering pattern; Sesamum.

1. INTRODUCTION

"Sesame (*Sesamum indicum* L.) is a significant oilseed *kharif* crop categorized under the order Lamiales and the family Pedaliaceae. It goes by various names such as benne, gingelly, simsim and til. It has a long history of cultivation, dating back to ancient times, and it thrives in regions with tropical to temperate climates. The diploid chromosome number of sesame is 2n=26, while its origins can be traced to Sub-Saharan Africa, the cultivated variety of sesame is believed to have originated in India. Sesame stands out as a drought-resistant plant, particularly during its vegetative growth stage, because of its extensive root system. Sesame is known as the "queen of oilseeds" due to its high oil content, mild flavour, and pleasant edible oil" [1]. According to Anilakumar et al. [2], sesame has a high nutritional energy value of 6,355 kcal/kg and comprises 50–60% oil, 18–25% protein, 23-25% carbohydrate, and 5% ash. Due to their high nutritional content, which includes minerals like Fe, Mg, Mn, Cu, and Ca as well as vitamins like thiamine, riboflavin, niacin, folic acid, and tocopherol as well as beneficial polyunsaturated fatty acids (PUFA), sesame seeds are also known as a "health-food" in traditional cultures [3]. The highest amount of antioxidants is found in sesame oil, which also contains a number of fatty acids, including oleic acid (43%), linoleic acid (35%), palmitic acid (11%), and stearic acid (7%).

Although variations in climatic and edaphic conditions influence sesame yields and performance, according to Muhamman and Gungula [4], "the major constraints of sesame cultivation in most countries are yield instability, a lack of wider adaptability, drought, non-synchronous maturity, poor stand establishment, a lack of response to fertiliser application, profuse branching, a lack of seed retention, a low harvest index, and susceptibility to insect pests and pathogens". The leading sesame producing countries are India, China, Burkina Faso, Ethiopia, Central African Republic and Cameroon. Asia has the largest sesame production which comprises nearly 67.22% of the world production area and 70% of the world production followed by Africa, shares 26% of the world production. India possesses second rank in the production of sesame seeds in the world, which account for 13.7% of the total world production of the sesame seeds. In India, sesame is cultivated in 1625 thousand hectare with production of 812 thousand tonnes and productivity of 500 kg/ha [5]. Madhya Pradesh contributes 19.4% and 16.86% share of country's area (315 thousand ha) and production (126 thousand tonnes), respectively and ranked second in area and production. In India, major area and more than 85% production of sesame comes from the states Rajasthan, Gujarat, Madhya Pradesh, Andhra Pradesh, West Bengal and Telangana.

"It is usually self-pollinated although cross-pollination is reported ranging from 5 to over 50%" [6]. As a result, the crop is categorised as

often cross-pollinated. Consequently, a high degree of genetic variation may be anticipated in this crop. The crossing programme involving genetically varied parents is likely to be expected in the segregating generations. Genetic difference among parents is important to generate significant heterotic effects and higher variability Different gene frequencies between populations/genotypes are indicated by genetic diversity. Multivariate analysis employing the Mahalanobis D^2 statistical method [7] has been utilised "in numerous crops to find such varied parents for crossing. This is a widely using tool to study genetic divergence at inter varietal and sub-species level in classifying the crop plants".

"Genetic diversity of crops plays an important role in sustainable development and food security , as it allows the cultivation of crops in the presence of various biotic and abiotic stresses" [8]. Genetic diversity is an inherited variation among and between population, created, activated and maintained by evolution. It plays an important role in the selection of parents among the genotypes having wider variability for different traits and ultimately for the most efficient use of genetic resources for use in hybridization to create new variability. Mahalanobis D^2 statistics has been demonstrated to be a substantial tool for measuring genetic divergence in a stated population. Keeping these point bin view, the present study was carried out to assess the genetic diversity among 165 genotypes for twelve quantitative traits in sesame germplasm.

2. MATERIALS AND METHODS

The experiment was laid out in *kharif* 2020 at BSP (Groundnut) Research Farm, JNKVV, Jabalpur (M.P.) Jabalpur district situated under Kymore plateau and Satpura hills agroclimatic zone. The soil of the experiment was sandy loam with uniform topography and free from water logged conditions. The average rainfall recorded about 1200-1400 mm. The experimental material consisted of 160 indigenous sesame accessions and 5 checks varieties RT346, PBTil2, GT10, TMV-7 and VRI-1 were collected from NBPGR. The total 165 sesame genotypes including 5 checks were sown on 1st july 2020 in Augmented Block Design (ABD) randomized in 8 blocks. Each genotype was sown by dibbling the seeds adopting the spacing of 40 cm between rows and 10 cm plant to plant. Thinning of seedling was carried out after 10 days of sowing by keeping one seedling per hill. The recommended cultural practices were adopted in respect of irrigation, weeding and fertilization. Plant protection measures were taken up as and when required. The genotypes were harvested as when they attained physiological maturity. Biometrical observations were taken with five randomly selected plants in each accession line for 12 quantitative traits namely days to flower initiation, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, capsule length (cm), days to maturity, number of seeds per capsule, thousand seed weight (g) and seed yield per plant (g). The mean values were utilized for statistical analysis.

2.1 Statistical Analysis

The data was subjected to genetic diversity analysis by using Mahalanobis D^2 statistic [7]. Character means were transformed condensation of common dispersion matrix according to Rao [9]. In all the D^2 combination, the characters were ranked on the basis of their contribution to D^2 and grouping of genotypes into various cluster were carried out utilizing Tocher's method (Rao,1952) using the INDOSTAT software.

3. RESULTS AND DISCUSSION

Genetic divergence among 165 genotypes was determined for seed yield, its attributing characters and quality traits. The significance estimates of 'V' statistics during the analysis revealed significant differences among mean values of different correlated variables, thus analysis of genetics divergences among the tested sesame germplasm was considered to be relevant, indicating the existence of variability among the genotypes for the character studied. Hierarchical cluster analysis based on Tocher's method allotted the 165 genotypes into 8 clusters in Table 1. Out of the all clusters, cluster VI was the largest among all clusters comprising (31) genotypes, followed by cluster III having (26) genotypes, cluster II (25) genotypes, cluster V (23) genotypes, cluster IV (21) genotypes, cluster I (18) genotypes, cluster VII (16) genotypes and cluster VIII had the lowest (5) genotypes suggestion the existence of the high degree of heterogenesity among the genotypes. Similar finding were recorded by Baraki et al. [10], Iqbal et al. [11], Soundharya et al. [12] and Mohanty et al. [13] for cluster IV, V and VI containing the highest and lowest number of genotypes though

Table 1. Distribution of 165 sesame genotypes in different clusters

Name of cluster	Numbers of genotypes	Genotypes
I	18	IC0129282,IC0129308,IC0129318,IC0129334 ,IC0129336,IC0129370,IC0129372,IC0129383, IC0129510,IC0129514,IC0129630,IC0129657, IC0129689,IC0129714,IC0129778,IC0129862, IC0129976,IC0129990
II	25	IC0129293,IC0129295,IC0129574,IC0129593, IC0129596,IC0129604,IC0129611,IC0129649, IC0129653,IC0129664,IC0129669,IC0129677, IC0129698,IC0129724,IC0129727,IC0129731, IC0129733,IC0129749,IC0129750,IC0129759, IC0129770,IC0129777,IC0129780,IC0129782 ,IC0129966,IC0129968
III	26	IC0129289,IC0129311,IC0129314,IC0129316, IC0129342,IC0129350,IC0129382,IC0129395, IC0129443,IC0129810,IC0129812,IC0129879, IC0129897,IC0129898,IC0129902,IC0129942, IC0129942,IC0129943,IC0129944,IC0129947, IC0129969, RT 346, PB Til 2,GT10,PB, TMV 7, VRI 1
IV	21	IC0129293,IC0129295,IC0129574,IC0129596, IC0129604,IC0129611,IC0129653,IC0129669, IC0129677,IC0129698,IC0129724,IC0129727, IC0129731,IC0129733,IC0129749,IC0129770, IC0129777,IC0129780,IC0129782,IC0129966, IC0129968.
V	23	IC0129299,IC0129306,IC0129312,IC0129313, IC0129320,IC0129332,IC0129335,IC0129480, IC0129481,IC0129494,IC0129533,IC0129755, IC0129757,IC0129816,IC0129856,IC0129876, IC0129889,IC0129891,IC0129925,IC0129954, IC0129984,IC0129987,IC0129814,
VI	31	IC0129339,IC0129375,IC0129380,IC0501143, IC0129404,IC0129418,IC0129421,IC0129422, IC0129453,IC0129458,IC0129482,IC0129498, IC0129499,IC0129513,IC0129515,IC0129516, IC0129517,IC0129555,IC0129571,IC0129576, IC0129614,IC0129715,IC0129758,IC0129808, IC0129832,IC0129870,IC0129931,IC0129939, IC0129940,IC0129956,IC0129989,
VII	16	IC0129354,IC0129374,IC0129376,IC0129394, IC0129396,IC0129518,IC0129550,IC0129572, IC0129795,IC0129865,IC0129910,IC0129915, IC0129960,IC0129364,IC0129909,IC0129479
VIII	5	IC0129593,IC0129649,IC0129664,IC0129750,IC0129759

the number of clusters differed depending on the number of genotypes and character studied.

The composition of cluster and values of inter and intra clusters distances age give in the tables respectively. The results revealed that the inter cluster distance in most cases was larger than intra cluster distance suggesting wider diversity among the germplasm of different groups. The range of inter and intra cluster distance was 15.88 to 63.23 and 12.92 to 28.50 respectively (Table 2). The highest inter cluster distance was highest between the clusters III and VIII (63.235) followed by clusters V and VIII (53.666), clusters VII and VIII (56.929), clusters IV and VII (49.113) This indicates the high divergence between these clusters. When the inter-cluster distance between clusters is higher, the genotypes in

those clusters would be more diverse. Genotypes from these diverse clusters may be selected for crossing programme as parents in order to have high heterotic effects in the hybrid combinations and the lowest inter clusters distance was observed between cluster III and V (15.881), indicating that the genotypes included in them were closely related. The maximum intra cluster distance was recorded in cluster VII (28.509) followed by cluster IV (27.914), cluster V (26.420), cluster III (26.129), cluster VI (23.933), cluster I (23.701), cluster II (14.472) and lowest in cluster VIII (12.929). It indicates that the germplasm lines of cluster VII were more diverged than any other cluster. The germplasm lines belonging to the distant clusters could be used in hybridization programme for obtaining a wider range of variability. Similar finding was recorded by Baraki et al. [10] for clusters II and III whereas, the lowest distance was found between clusters I and III; Dash et al. [14] for clusters II and IV; Swathy et al. [15] highest for clusters IX and V and lowest for clusters VIII and II.

Cluster means of germplasm for twelve characters in sesame (Table 3.) revealed that cluster III had highest mean value for plant height (126.609), days to flower initiation (34.308), days to 50% flowering (37.462), and oil content (44.715). Cluster VII reported to be days to maturity (91.750), number of primary branches per plant (3.833) and number of secondary branches per plant (2.625) and in cluster V had capsule length (2.651). cluster VI reported for number of capsules per plant (59.484) and seed yield per plant (9.168), number of seeds per capsule (58.533) and thousand seed weight (2.848). These clusters can be preferred in selecting germplasm lines for respective traits as they recorded good mean values. The lowest cluster mean values were recorded in cluster II for the traits days to flower initiation (31.280), days to 50% flowering, days to maturity (88.720), number of secondary branches per plant (1.573), number of seeds per capsule (29.360) and seed yield per plant (5.312). Cluster VIII had plant height (69.667), number of primary branches per plant (3.166) and capsule length (2.366). Cluster VII consisted of number of capsules per plant (42.583) and thousand seed weight (2.617). Cluster I included oil content (31.944). Similar results were recorded by Tripathi et al. [16] for days to 50% flowering contributing highest towards genetic divergence; Bamrotiya et al. (2016) for height to first capsule followed by number of capsules per leaf axil, length of capsule, seed yield per plant and number of seeds per capsule; Swathy et al. [15] for number of capsules per plant and seed yield per plant in cluster IX and oil content and days to 50% flowering in cluster III.

The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times, each of the yield component character appeared first in rank and its respective percent of contribution towards genetic divergence was presented in (Table 4). The results showed that number of primary branches per plant (11.32%) contributed highest towards genetic divergence by taking 1532 times first rank, followed by oil content (11.06%) by 1496 times, number of capsule per plant (11.05%) by 1145 times, number of secondary branches per plant (10.45%) by 1414 times, days to maturity (10.30%) by 1393, plant height (9.76%) by 1321 times, capsule length (8.46%) by 1145 times, seed yield per plant (6.99%) by 946 times, number of seeds per capsule (6.09%) by 824 times and thousand seed weight (5.97%) by 808 times. On the other hands, least variation was recorded for days to 50% flowering (5.06%) by 684 times and days to flower initiation (3.49%) by 472 times. Showing comparatively less contribution of these characters towards

Table 2. Inter and intra cluster distance D^2 values among 8 cluster in Sesame genotypes

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
Cluster1	23.701	26.741	34.000	31.990	25.053	18.182	25.421	35.937
Cluster2		14.472	27.773	20.806	18.558	25.320	33.063	42.043
Cluster3			26.129	46.966	15.881	24.898	18.321	63.235
Cluster4				27.914	34.806	35.054	49.113	28.989
Cluster5					26.420	19.030	23.975	53.666
Cluster6						23.933	22.077	45.138
Cluster7							28.509	56.929
Cluster8								12.929

Table 3. Cluster mean for yield and yield attributing traits in Sesame genotypes

Characters	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8
Days to flower initiation	31.333	31.280	34.308	31.666	32.130	31.613	32.125	31.800
Days to 50% flowering	34.778	34.480	37.462	34.714	35.739	35.258	35.688	34.600
Days to maturity	89.722	88.720	90.500	90.190	89.043	90.613	91.750	89.600
Plant height (cm)	103.611	99.413	126.609	80.460	114.986	111.591	125.396	69.666
No. of primary branches/plant	3.630	3.306	3.410	3.349	3.333	3.656	3.833	3.166
No. of secondary branches/plant	2.000	1.573	2.585	1.873	2.058	2.398	2.625	1.600
No. of seeds per capsule/capsule	52.741	29.360	31.977	33.714	32.181	58.533	48.063	48.780
Capsule length(cm)	2.511	2.476	2.619	2.398	2.651	2.556	2.421	2.366
No. of capsules/ plant	46.944	49.906	50.500	55.460	54.638	59.484	42.583	46.000
Thousand seed wt. (g)	2.658	2.818	2.952	2.650	2.765	2.848	2.617	2.775
Oil content (%)	31.944	43.500	44.715	38.952	35.239	41.500	43.031	42.100
Seed yield/plant (g)	7.980	5.312	6.204	6.147	6.127	9.168	6.617	8.969

Table 4. Relative contribution of different characters to genetic diversity in sesame genotypes

Source	Times ranked 1st	Contribution %
Days to flower initiation	472	3.49
Days to 50% flowering	684	5.06
Days to maturity	1393	10.30
Plant height (cm)	1321	9.76
Number of primary branches per plant	1532	11.32
Number of secondary branches per plant	1414	10.45
Number of capsules per plant	1495	11.05
Capsule length (cm)	1145	8.46
Number of seeds per capsule	824	6.09
Thousand seed weight (g)	808	5.97
Oil content (%)	1496	11.06
Seed yield per plant (g)	946	6.99

the genetics divergence. These results are in agreement with those given by Jadhav and Mohrir [17] for oil content trait; Kumhar et al. [18] for number of primary branches per plant; Narayanan and Murugan [19] reported that seed yield contributed the most towards the divergence of genotypes followed by number of pods per plant, days to 50% flowering and plant height; Bamrotiya et al. [20] for number of capsules per leaf axil, length of capsule, seed yield per plant and number of seeds per capsule. [21] It indicates that these characters contribute towards the genetic divergence in the present germplasm lines [22].

4. CONCLUSION

The present study provides information for most of the characters and their possible use in hybridization programme, genetic diversity

directly contributes to the creation of variability. Crosses can be made between genotypes of cluster III and genotypes of cluster VIII followed by clusters V and VIII, followed by cluster VII and VIII to isolate desirable high yielding segregants as it exhibit the highest inter cluster distance should be used rather than the genotypes of clusters having low divergences. Crossing two parents with highly divergent genotypes, however, may result in a situation where the harmonious functioning of alleles is somewhat disturbed, and as a result, the physical functions are not as efficient as they would be if the alleles were exposed to similar selection pressure. This suggests that crossing between most divergent genotypes may not yield a proportionate heterotic response. While several researchers have suggested employing D^2 analysis to select parents for hybridization, there aren't many reports on comparative empirical verification, like the one conducted in this study.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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