Electronic Journal of Plant Breeding, 9 (2) : 631-637 (June 2018) DOI: 10.5958/0975-928X.2018.00077.7
ISSN 0975-928X

**Research Article**

# Assessment of genetic diversity among identified testers aids in development of hybrids in sesame (*Sesamum indicum*.L)

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(Received:20 Mar 2018; Revised:10 Apr 2018; Accepted:12 Apr 2018)

**Abstract**
Diversity analyses on ninety two genotypes of sesame using ten morphological characters were studied. Results indicated that ten clusters were formed wherein maximum inter cluster distance was observed between cluster IX and X (239.87). Simultaneously crossing of these 90 genotypes with Co-1 and TMV-5 was carried out. The 180 hybrids generated using two lines (CO 1 and TMV 5) with these 90 genotypes, upon evaluation, indicated five elite hybrids namely TMV 5 X bardur local (B)(217.49 percent), TMV 5 X bardur local (W) (198.38 percent), CO 1 x RT 172 (163.47 percent), TMV 5 x Rama (161.04 percent) and TMV 5 x MT-10-23-3 (155.57 percent) significantly yielded than the standard check TMV 7 and their male parents were found to be from the cluster I which were moderately divergent (19.09) among them.

**Key words**
*Sesamum, Diveristy and Heterosis*

## Introduction

*Sesamum indicum* L (2n= 26), an annual plant belonging to Pedaliaceae family is considered as the queen of the oilseeds originated from Africa. Kobayashi(1983). Its seed comprises 50 per cent oil with monounsaturated fatty acids especially oleic acid Gandhi(2009) that helps to keep the LDL lower. Sesame is rich in sesamol and sesaminol that eliminates harmful free radicals and the oil fraction shows a remarkable stability to oxidation. It is also a good source of B-complex such as niacin, folic acid, thiamine pyridoxine and riboflavin Borchani *et al.(*2010). India ranks second in production after China with a productivity of 413 kg/ha, cultivated in an area of 17.90 lakh hectares with production of 8.02 lakh tonnes NMOOP (2017). In India, West Bengal is the leading producer followed by Assam and Tamil Nadu. Despite the health benefits and highest area under cultivation, sesame ranks sixth in the world's production of oilseeds and twelfth for vegetable oil production Weiss(2001). This leaves a hope of improving sesame crop which can be attempted through heterosis breeding.

Information on genetic diversity and relationship among populations is important for plant breeding programs as it helps to select the right genetic material to be used Ganesh and Thangavelu, (1995). The analysis of genetic diversity using $D^2$ statistics enables one to discriminate between different cultivars according to the diversity present Mahalanobis (1936). Based on the magnitude of variation present in the population, individual character's contribution to the total spectrum of variability differs. Number of capsules per plant and seed yield contributed mostly to divergence in many of the studies carried out Arriel *et al*.(2007). Sesame being a less explored crop when compared to the rest of the oilseeds need to be well studied and inculcating the production of hybrids may foster the productivity. In order to exploit the variability existing in the crop and produce superior hybrids this study was taken up by utilizing the diverse parents with good combiners of yield.

## Materials and Methods

The experimental material consisted of 90 genotypes of sesame collected from different research stations all over India. These genotypes were utilized as male parents with two lines namely CO 1 and TMV 5 as female parents. Crossing programme was taken up in a Line x Tester fashion. All the 92 lines were first planted in two replications in Randomised Block Design and $D^2$ Mahanalobis (1936) analysis was done. Simultaneously, these 90 lines were crossed with CO1 and TMV 5 and their $F_1$'s were estimated for standard heterosis with TMV 7. Hybridisation was carried out by using the standard method of emasculation and dusting of pollens Ganesh and thangavelu (1995) in Line x Tester mating design. Ten characters namely days to first flowering, distance from base to capsule, number of branches, number of capsules in main stem, number of capsules in branches, capsule length, number of seeds per capsule, single plant yield, days to maturity and thousand seed weight were observed.

**Results and Discussion**

The morphological observations of 92 genotypes were analysed for their variability and diversity by Mahanolobis (1936). The plant morphological characters observed showed considerable variation for all the traits (Table 5). The genotypes were grouped into ten clusters and their grouping depended on percentage contribution of characters wherein 59 per cent was contributed by number of capsules in main stem and 11.79 per cent by days to first flowering as shown in Table 2. The distribution pattern of genotypes indicated that genetic divergence was not based on their geographical differentiation as in accordance with Bandila *et al.(*2011).

According to Ghadri *et al*. (1984), increasing the parental distance implies a great number of contrasting alleles at the desired loci. Maximum genetic recombination is expected from the hybridization of the parents selected from distant groups. In the 10 clusters, the maximum inter cluster distance was observed between cluster IX and X (239.87) followed by cluster VII and IX (226.91) as reported in Table 3.

Hence, genotypes from clusters IX (China and LT 8), X (CO 1) and VII (JCS 2454) were highly diverse genotypes and crossing between them may yield hybrids.

Regarding the intra cluster values, Cluster IX had the maximum intra cluster (45.91) distance as compared to cluster I and III (Table 3). Although only two genotypes were found to be in the cluster, these genotypes China and LT 8( cluster IX) varied in number of capsules in main stem and flowering which was found to contribute more towards divergence. The cluster means for 10 characters spatially varied among genotypes and clusters, the maximum mean values were observed in cluster VII with high values for number of capsules in main stem and branches, number of branches, number of seeds per capsule, single plant yield and thousand seed weight (Table 4).

Cluster VII had a single genotype JCS 2454 and this genotype was found to be completely deviant from other clusters indicating its potential use as a parent in hybridization programmes for realizing higher single plant yield (20.80) and early duration (99) on an average. Though 77 genotypes clustered in single cluster, their mean performance compared to the other clusters were poor indicating the grouping of poor performers under a single cluster. The cluster VII (JCS 2454), IV (JCS 2498) and V (CST-2008-2) had higher cluster means for single plant yield as well as thousand seed weight and hence could be used in improvement of yield parameters. The cluster IX comprised China which is a monostem variety with highest capsule length and number of seeds per capsule coupled with higher number of capsules, could be used as a parent in hybridization for breeding monostem varieties with moderate yield. Although Variety Co 1 in cluster X showed highest mean for duration, number of capsules in branches, capsule length it had moderate values for single plant yield indicating that the shattering losses while harvesting as a constraint.

This study revealed high variability for ten characters studied with maximum genotypic and phenotypic variations for number of capsules in branches followed by distance from base to first capsule and number of seeds per capsule as mentioned in Table 6. As these characters recorded high GCA coupled with GA, selection for these characters would be effective as they are controlled by additive gene action Burton & Devane (1953). These similar results were also found in the findings of Tripathi *et al*.(2013) and Parimala *et al*.(2013).

Kiranmayi *et.al.* (2014) stated that the difference between GCV and PCV indicates the level of environmental influence whereas this experiment showed narrow differences for all 10 traits. Therefore, high genetic variability present for these characters in the given population can be ardently exploited for breeding sesame with more number of capsules in branches along with more seeds per capsule.

GCV coupled with high heritability would be more valuable in selection programmes Burton & Devane(1953). Number of capsules in branches, distance from the base to first capsule, number of capsules in main stem, seed yield per plant and days to first flowering exhibited high heritability and GCV indicating the predominance of additive gene action and selection for these characters is effective to improve seed yield by practicing simple selection. Genetic advance has considerable importance as it indicates the magnitude of the expected genetic gain from one cycle of selection Burton & Devane (1953). In the present investigation, all the traits except days to maturity, capsule length and number of seeds per capsule recorded high genetic advance as percent of mean indicating the scope of selection for all these characters.

Among the 180 crosses obtained, five of them exhibited heterosis against the standard check TMV 7 (Table 6). The female parent of four of these hybrids is TMV 5 inferring the potential of TMV 5 as a general good combiner for seed yield which was also acclaimed by Vidhyavathi *et al.* (2005).

The elite hybrids possesed TMV 5 as their female and male parents from the clusters I, II and X. Although their genetic distance were not found to be wider, it exhibited heterosis for yield which might be due to combination of favourable alleles from the parents.

Among the five hybrids, TMV 5 x Bardur local (B) exhibited higher percentage of heterosis and overall performance of the successful hybrids as given in the table 7. These hybrids can be test verified further for stability of their performance over environments in future.

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**Table 1. List of parents and their place of collection**

| S.NO | PARENTS | PLACE | S.NO | PARENTS | PLACE |
|---|---|---|---|---|---|
| 1. | AT 178 | AMRELI | 48. | Jinbakkia | VRIDHACHALAM |
| 2. | AT 222 | AMRELI | 49. | OMT-30 | VRIDHACHALAM |
| 3. | AT 229 | AMRELI | 50. | ORM-17 | VRIDHACHALAM |
| 4. | AT 231 | AMRELI | 51. | KMR-77-1 | VRIDHACHALAM |
| 5. | AT 238 | AMRELI | 52. | NIC 8984 | VRIDHACHALAM |
| 6. | China | AMRELI | 53. | Nirmala | VRIDHACHALAM |
| 7. | Wild dhanuka | AMRELI | 54. | N 32 | VRIDHACHALAM |
| 8. | JR 22 | AMRELI | 55. | VS-07-023 | VRIDHACHALAM |
| 9. | RSS 106 | AMRELI | 56. | GPC-12-06 | JAGTIAL |
| 10. | RSE-3 | AMRELI | 57. | JCS 1020 | JAGTIAL |
| 11. | Shelna 5 | AMRELI | 58. | JCS 1942 | JAGTIAL |
| 12. | U-76-10 | AMRELI | 59. | JCS 1935 | JAGTIAL |
| 13. | IS 196 | AMRELI | 60. | JCS 2454 | JAGTIAL |
| 14. | B-90-1 | AMRELI | 61. | JCS 2498 | JAGTIAL |
| 15. | Vardi local | JALGAON | 62. | Madhavi | JAGTIAL |
| 16. | Amalgaon sel | JALGAON | 63. | JCS 1673 | JAGTIAL |
| 18. | JL-SG-06-6 | JALGAON | 64. | JCS 1860 | JAGTIAL |
| 19. | JLT 501 | JALGAON | 65. | JCS 2698 | JAGTIAL |
| 20. | JLS-510-3 | JALGAON | 66. | Chandhana | JAGTIAL |
| 21. | Gopi | JALGAON | 67. | Haryana til-2 | JABALPUR |
| 22. | NIC 7913 | JALGAON | 68. | PT 1 | JABALPUR |
| 23. | KMR 18 | JALGAON | 69. | Brijeshwari | JABALPUR |
| 24. | M-2 | JALGAON | 70. | T 78 | JABALPUR |
| 25. | JLS-110-12 | JALGAON | 71. | TC-289 | JABALPUR |
| 26. | IC 413187 | JALGAON | 72. | Amrit | JABALPUR |
| 27. | IC 204484 | DHARWAD | 73. | Usha | JABALPUR |
| 28. | E8 | DHARWAD | 74. | Kalaika | JABALPUR |
| 29. | TKG 377 | DHARWAD | 75. | TKG-306 | JABALPUR |
| 30. | DS 21 | DHARWAD | 76. | JT-7 | JABALPUR |
| 31. | DS 11 | DHARWAD | 77. | Thilathara | JABALPUR |
| 32. | DS 7 | DHARWAD | 78. | Rama | JABALPUR |
| 33. | RT 311 | MANDOR | 79. | Savitri | JABALPUR |
| 34. | RT 321 | MANDOR | 80. | Bardur local(W) | DHARWAD |
| 35. | RT 194 | MANDOR | 81. | Bardur local(B) | DHARWAD |
| 36. | RT 201 | MANDOR | 82. | MT-10-23-3 | DHARWAD |
| 37. | LT 8 | MANDOR | 83. | PKVNT 11 | DHARWAD |
| 38. | SI 3160 | MANDOR | 84. | Shekar | DHARWAD |
| 39. | CST-2001-1 | MANDOR | 85. | DS 3 | DHARWAD |
| 40. | CST-2008-2 | MANDOR | 86. | RT 172 | MANDOR |
| 41. | SP 44 | MANDOR | 87. | RT 180 | MANDOR |
| 42. | HT 9713 | MANDOR | 88. | RT 202 | MANDOR |
| 43. | PAIYUR 1 | VRIDHACHALAM | 89. | RT 209 | MANDOR |
| 44. | TNAU 64 | VRIDHACHALAM | 90. | RT 215 | MANDOR |
| 45. | Veppur local | VRIDHACHALAM | 91. | TMV 5 | VRIDHACHALAM |
| 46. | Thumkur local | VRIDHACHALAM | 92. | CO 1 | COIMBATORE |
| 47. | Cardeberga | VRIDHACHALAM | | | |

**Table 2. Percentage contribution of characters**

| S.No | Character | Contribution (%) |
|---|---|---|
| 1 | Days to first flowering | 11.79 |
| 2 | Days to maturity | 9.01 |
| 3 | Distance from the base to first capsule | 0.15 |
| 4 | No. of primary branches | 5.19 |
| 5 | No. of capsules in main stem | 59.10 |
| 6 | No. of capsules in branches | 0.12 |
| 7 | Capsule length | 0.02 |
| 8 | No. of seeds per capsule | 0.02 |
| 9 | Seed yield /plant | 11.49 |
| 10 | Thousand seed weight | 3.10 |

**Table 3. Inter and intra cluster $D^2$ values and cluster distances**

| | I | II | III | IV | V | VI | VII | VIII | IX | X |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 19.09 | 25.63 | 37.24 | 25.98 | 58.01 | 36.88 | 76.26 | 41.39 | 160.70 | 88.80 |
| II | | 0 | 23.34 | 35.13 | 42.07 | 34.41 | 61.35 | 39.61 | 180.35 | 68.59 |
| III | | | 21.96 | 45.20 | 31.39 | 30.91 | 50.49 | 50.08 | 190.93 | 64.39 |
| IV | | | | 0 | 61.79 | 43.23 | 82.05 | 41.19 | 154.31 | 93.50 |
| V | | | | | 0 | 36.31 | 27.24 | 62.40 | 210.81 | 49.35 |
| VI | | | | | | 0 | 51.69 | 46.07 | 178.84 | 75.24 |
| VII | | | | | | | 0 | 82.58 | 226.91 | 54.83 |
| VIII | | | | | | | | 0 | 167.03 | 74.85 |
| IX | | | | | | | | | 45.91 | 239.87 |
| X | | | | | | | | | | 0 |

**Table 4. Cluster means for different characters of 90 Sesame lines**

| Cluster | DFF | DB | NPB | NMCP | NBRCP | CPL | NSCP | DM | SPYLD | TSDWT |
|---|---|---|---|---|---|---|---|---|---|---|
| **I** | 37.20 | 41.38 | 4.25 | 28.62 | 77.14 | 2.44 | 59.07 | 100.11 | 13.88 | 3.49 |
| **II** | 34.50 | 45.79 | 4.00 | 25.25 | 86.39 | 2.40 | 58.00 | 100.50 | 13.12 | 2.68 |
| **III** | 44.08 | 41.47 | 4.67 | 30.29 | 92.75 | 2.44 | 60.08 | 106.42 | 14.96 | 4.03 |
| **IV** | 40.00 | 46.92 | 3.50 | 28.61 | 73.11 | 2.55 | 60.00 | 114.00 | 23.13 | 3.20 |
| **V** | 47.00 | 44.79 | 4.50 | 41.94 | 104.29 | 2.81 | 71.50 | 119.00 | 20.47 | 3.11 |
| **VI** | 47.00 | 42.62 | 5.00 | 50.03 | 89.80 | 2.65 | 68.00 | 105.50 | 15.37 | 3.36 |
| **VII** | 34.50 | 34.71 | 5.25 | 53.53 | 115.22 | 2.80 | 76.00 | 99.00 | 20.80 | 4.20 |
| **VIII** | 45.00 | 82.22 | 4.75 | 32.28 | 79.39 | 2.85 | 69.00 | 112.00 | 11.53 | 3.55 |
| **IX** | 36.00 | 42.51 | 0.00 | 42.77 | 0.00 | 2.85 | 64.00 | 100.00 | 14.18 | 2.94 |
| **X** | 41.50 | 83.69 | 5.00 | 30.49 | 116.60 | 2.90 | 70.00 | 118.00 | 13.41 | 4.18 |

*DFF : DAYS TO FIRST FLOWERING

DB : DISTANCE FROM THE BASE TO FIRST CAPSULE (cm)
NPBR : NUMBER OF PRIMARY BRANCHES
NMCP : NUMBER OF CAPSULES IN MAIN STEM
NBRCP : NUMBER OF CAPSULES IN BRANCHES
CPL : CAPSULE LENGTH (cm)
NSCP : NUMBER OF SEEDS PER CAPSULE
SPYLD: SEED YIELD PER PLANT (g)
TSDWT: THOUSAND SEED WEIGHT (g)

**Table 5. ANOVA for the mean performance of 90 genotypes**

| Source of Variation | SS | Df | MS | F | P-value | F crit |
|---|---|---|---|---|---|---|
| Genotypes | 7706.856 | 89 | 86.59388 | 2.145296 | 3.68E-08 | 1.27805 |
| Traits | 928480.8 | 9 | 103164.5 | 2555.821 | 0 | 1.891552 |
| Error | 32332 | 801 | 40.36454 | | | |
| Total | 968519.6 | 899 | | | | |

**Table 6. Co-efficient of Variation, Heritability (broad sense) and Genetic advance in 92 sesame accessions**

| S.No | Characters | PCV% | GCV% | ECV% | $H^2$ (%) | GA | GA% |
|---|---|---|---|---|---|---|---|
| 1. | Days to first flowering | 29.73 | 28.67 | 1.05 | 96.44 | 10.83 | 28.54 |
| 2. | Days to maturity | 51.63 | 39.48 | 12.14 | 76.48 | 11.32 | 11.17 |
| 3. | Distance from the base to first capsule (cm) | 57.13 | 55.92 | 1.20 | 97.88 | 15.24 | 35.92 |
| 3. | No. of primary branches | 0.65 | 0.54 | 0.10 | 83.92 | 1.39 | 33.17 |
| 4. | No. of capsules in main stem | 30.40 | 29.70 | 0.69 | 97.71 | 11.09 | 37.32 |
| 5. | No. of capsules in branches | 214.31 | 214.03 | 0.28 | 99.87 | 30.11 | 38.68 |
| 6. | Capsule length (cm) | 0.13 | 0.07 | 0.05 | 58.41 | 0.43 | 17.70 |
| 7. | No. of seeds per capsule | 86.74 | 45.96 | 40.77 | 52.99 | 10.16 | 16.97 |
| 9. | Seed yield /plant (g) | 7.01 | 6.77 | 0.24 | 96.57 | 5.26 | 37.12 |
| 10. | Thousand-seed weight (g) | 0.41 | 0.36 | 0.04 | 88.91 | 1.18 | 33.65 |

PCV (%)-Phenotypic coefficient of variation
GCV (%)-Genotypic coefficient of variation
ECV (%)-Environmental coefficient of variation
$H^2$- Heritability
GA-Genetic advance
GA (%)-Genetic advance as percent of mean

**Table 7. Overall performance of superior five heterotic crosses for yield and other component characters**

| HYBRIDS | DFF | DB | NPB | NMCP | NBRCP | CPL | NSCP | TSWD | DM |
|---|---|---|---|---|---|---|---|---|---|
| TMV5 x Bardur local (B) | 2.47 | 29.64* | 0.00 | 22.72* | 33.77** | 16** | 28.57** | 11.89** | 2.40** |
| TMV5 x Bardur local(W) | 2.47 | 69.94** | 16.67** | 7.62 | 21.05* | 0.00 | 14.29** | -15.47* | 0.48 |
| CO1 x RT172 | 8.64** | 36.32* | 4.17 | 49.77* | -52.93* | 4.00* | 21.43** | 12.97** | 19.71** |
| TMV5 x Rama | 2.47 | 17.11 | 50.00** | 19.15* | 27.81 | 0.00* | 7.14 | -15.14** | 10.58 |
| TMV5 x MT 10-23-3 | 12.35** | 2.59** | 29.17* | 60.42* | 74.30* | -8.00 | -3.57 | 5.41 | 1.44 |