GENETIC DIVERSITY STUDIES IN LOCAL GERMPLASM OF SESAME(*Sesamum indicum* L.)

ABSTRACT: The objective of the current study, "Genetic diversity studies in local germplasm of sesame (*Sesamum indicum* L.)," was to determine the type and degree of genetic diversity between traits that contribute to seed yield. Using a Randomized Block Design with two replications, 36 sesame genotypes were assessed for 10 distinct features at the Botany section farm, College of Agriculture, Dhule, in the summer of 2023. The genotypes were divided into fourteen clusters based on the D^2 value. In addition to providing options for achieving a high heterotic effect and upgrading the base population, inter-crossing between them would also restore suitable transgressive segregants and a wide range of diversity in succeeding generations. The study found that local germplasm*viz.*, JLS-1414-21-2 for number of primary branches per plant, number of seeds per capsule, oil content (%), and seed yield, and TS-14 for plant height, number of primary branches, number of capsules per plant, number of seeds per capsule, 1000 seed weight, and seed yield per plant found superior and can be used for further breeding methodologies. Genotypes JLT-408 and AVTS-2001 were shown to be superior for protein content, DS-10 for earliness, TKG-22 for oil content, TS-16 for earliness, and DLS-12 for plant height, number of capsules per plant, and 1000 seed weight.

KEYWORDS: Genetic diversity, sesame, cluster, genotypes, D^2 value.

INTRODUCTION: In this study, thenature and magnitude of divergence among the local germplasm of sesame was explored.Genetic diversity refer to variation within a species due to genetic factors. It is apotent source for heritable crop improvement. Genetic diversity may develop as aresult of geographical separation, spontaneous mutation or hurdles in crossability (Shete*et al.*, 2023).Breeders have long recognized the importance of genetic variety in crop development and its critical role in determining the success of hybridization programs. Evaluation of germplasm to local conditions is crucial because polygenes affect yield and yield contributing traits, and the environment has a significant impact. Exploring genetic variability in available germplasm is a prerequisite.

One of the first oilseed crops that has been grown since ancient times is sesame(*Sesamumindicum* L.). Despite 5–10% cross-pollination by insects and other pollinating agents, sesame is a self-pollinating plant. The crop has somatic chromosome number 26 and is a member of the order Tubiflorae and family Pedaliaceae. Grown in tropical and subtropical regions, primarily between latitudes 400 N and 400 S, sesame is a significant oil seed crop. With an annual rainfall of roughly 500 mm, it has spread to elevations of 1200 m on the plains. 25–27˚C is the ideal temperature range for quick germination, early growth, and flower formation.With an average yield of 248.5 kg/ha, Maharashtra produced 2700 tonnes of sesame on 10,700 hectares in 2022–2023. Maharashtra's main sesame-producing regions include Jalgaon, Latur, Nanded, Yavatmal, Akola, Beed, Buldhana, Sambhajinagar, Vidarbha, and a portion of Khandesh.

Because to its high oil content (38–54%), protein (18–25%), carbohydrate (16–18%), calcium, phosphorus, oxalic acid, and superior seed oil properties, sesame is known as the "queen of oilseeds."Total seed production of sesame reached 6,741,479 tonnes. Historically, total sesame seed production reached an alltime high of 6,811,362 tonnes in 2019 and analltimeslow 1,419,988 tonnes in 1961 (FAOSTAT, 2022).The likelihood of heterotic F_1s and a wide range of diversity in segregating generations increases with the number of parents within the overall limit of fitness (Arunachalam, 1981; Falconer, 1989). Therefore, accessing genetic diversity is the initial step in any crop breeding program is very helpful and it is exploited in this study.

MATERIALS AND METHODS: Thirty six local germplasm's of sesamum made up the experimental material for this study. Five competitive plants per genotype in each replication were chosen at random to record observations on various characters (apart from days to 50% flowering and days to maturity), and the averages of these observations were used in the statistical analysis. Seeds from the 5 observational plants per genotype were bulked, these seeds were used for oil and protein analysis. The oil and protein content was estimated on NIR Spectrometer facilities available at AannasahebShinde, College of Engineering and Technology, M. P. K.V., Rahuri.

The Panse and Sukhatmate (1995) approach was used to perform the analysis of variance. Analysis of variance for the individual characters studied was worked out as per RBD to test the significance among the genotypes.The D^2 Statistic of Mahalnobis (1936), as explained by Rao (1952), was used to analyse divergence, and Tocher's technique, as explained by Rao (1952), was used to generate clusters. In accordance with Arunachalam and Bandopadhyaya (1984), the potential boundaries of parental divergence where heterosis was likely to occur were computed.Transformation was done by using the pivotal condensation method. The coefficients for the transformation were obtained by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements.

RESULTS AND DISCUSSION: Table 1 shows the results of the analysis of variance for ten quantitative characters, which showed very significant differences among the genotypes for all the characters. This suggests that there is a great amount of variability among the genotypes for the characters under study. Heritable improvement is based on genetic divergence, which is caused by genetic variables. Therefore, the high degree of variation in agricultural plants has long captivated plant breeders. Therefore, accurate genetic divergence information is essential for a successful breeding effort. High heterotic effects are known to be produced by genetically different parents, which results in favourable recombinants in the breeding material.

The maximum inter-cluster distance between cluster VIII and XIV (33.99) was found in the current study (Table 2 and Fig. 1), indicating that the genotypes included in cluster VIII may have a completely different genetic architecture than the genotypes included in cluster XIV. This suggests that the genotypes in these clusters have a significant degree of genetic divergence. Manivannan and Ganesan (2000), Solanki and Gupta (2002), Narayanan and Murugan (2013), and Mohammed and Firew (2015) have all observed similar findings. Clusters IV and XIV (D^2=28.04), V and VIII (D^2=27.14), VIII and XII (D^2=26.45), XIII and XIV (D^2=26.33), VII and VIII (D^2=23.84), III and XIV (D^2=23.15), and IV and V (D^2=22.87) had the next highest D^2values. This demonstrated that the greatest genetic variation was seen in these genotypes.

The cluster means for seed yield per plant ranged from 5.03 g (cluster V) to 15.80 g (cluster XIII). The cluster XIII (15.80 g) exhibited the highest cluster mean followed by cluster VIII (13.86 g), X (12.68 g), VI (11.03 g), and VII (10.02 g). While for cluster V (5.03 g) exhibited lowest followed by cluster IX (6.08 g), III (6.083), XIV (6.62 g) than cluster average (9.24g).

Cluster means were highest in cluster XIII, X, VIII for plant height at maturity, number of primary branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight and seed yield per plant. The results are confirmation with the findings of Gupta *et al.* (2001), Parameshwarappa*et al.* (2010), Kindeya(2017), Swathy*et al.* (2018) and Swapna *et al.* (2023).

The highest cluster mean for seed yield per plant, recorded by cluster XIII (15.80 g), appeared to be caused by the contribution of component characters, specifically plant height at maturity (135.70 cm), days to maturity (97.60 days), days to 50% flowering (42.90 days), oil content (46.95%), number of capsules per plant (93.52), number of seeds per capsule (68.78), 1000 seed weight (5.37 g), number of branches per plant (4.8), and protein content (19.72%), according to the cluster mean performances of the clusters for ten characters (Table 3).The least yielder was determined to be Cluster V. In comparison to other genotypes from other clusters, it consisted of two genotypes, DLS-14 and DLS-7, which had late maturity, fewer primary branches, fewer capsules per plant, and lower plant height. These genotypes' low seed output per plant can be ascribed to their late maturity (99.25 days), fewer branches per plant (1.19), and fewer capsules per plant (37.04).The results are confirmation with the findings of Mohammed and Firew (2015),Kindeya(2017), Swathy*et al.* (2018) and Swapna*et al*. (2023).

Table 4 showed that the number of branches per plant (37.93%) contributed most to genetic divergence, making the characteristics' relative contribution to the divergence the largest. This was followed by the following: days to 50% flowering (4.13%), days to maturity (4.13%), oil content (1.90%), number of seeds per capsule (0.79%), plant height at maturity (11.26%), number of capsules per plant (7.62%), protein content (6.66%), 1000 seed weight (4.60%), and seed yield per plant (20.95%). Greater share of overall divergence Additionally, Sudhakar (2003) reported on the number of capsules per plant and the number of days until 50% flowering; Gangadharao (2004) reported on the number of capsules per plant, the 1000 seed weight, and the seed yield per plant; Parameshwarappa*et al*. (2010) reported on the 1000 seed weight, the number of capsules per plant, and the seed yield; Narayanan and Murugan (2013) reported on the number of capsules per plant, the number of days until 50% flowering; Chandra (2014) reported on the number of capsules per plant; Mohammed and Firew (2015) and Rahna*et al.* (2023) reported on the seed yield per plant and the 1000 seed weight.On the basis of divergence classes (DC) crosses of genotypes from different clusters can formulated for next programme and this was grouped on that crosses present between differentclusters and separated by moderate genetic distance would gave yield with heterotic effect of $F_1$and transgressive segregants in advance generation.

Hays and Johansson (1939) and East and Hays (1942) obtained maximum heterosis from crosses between diverse parent than those between closely related ones. Bhatt (1970) advocated the use of multivariate analysis for the selection of parents.Considering all of the aforementioned factors, the following genotypes from the current study are worthy of being regarded as powerful parents for next crossing programs aimed at increasing seed yield and yield-contributing traits.

1. TS-14
2. JLS-1414-21-2
3. DLS-12
4. TS-16
5. JLS-1411-1-1
6. TKG-22
7. DS-10
8. JLT-408
9. AVTS-2001

The aforementioned genotypes may be used in future breeding programs to create the maximum spectrum of variability for various yield contributing characters, taking into account the inter-cluster distance, cluster means, per se performance of genotypes, and divergence class.

This will make it easier to develop superior genotypes with multiple characters and also make it possible to improve multiple characters at once.

More diversity increases the likelihood of choosing suitable genotypes for hybridization. The ability to estimate parental diversity may be aided by direct chemical examination of genetic material or gene products (Thorat*et al.*, 2023).This study is beneficial for identifying suitable local germplasm based on individual plant characters. The study showed the best possible local genotypes that could be exploited in further research programs for developing particular quantitative or qualitative traits in the plant. The details of this is mentioned in the table 5.

SUMMARY AND CONCLUSIONS: The genotypes under study exhibit significant genetic variability which were divided into fourteen clusters. Cluster II had the most genotypes, with nine, followed by cluster IV with seven, I with four, and III with three. Clusters V, VI, and VII each had two genotypes, and the remaining clusters, VIII, IX, X, XI, XII, XIII, and XIV, were unique because they each had only one genotype. These genotypes can be categorized as promising since they were unique and varied.The genotypes, namely TS-14 for plant height, number of primary branches, number of capsules per plant, number of seeds per capsule, 1000 seed weight, and seed yield per plant, JLS-1411-1-1 for earliness and number of seeds per capsule, JLS-1414-21-2 for number of primary branches per plant, number of seeds per capsule, oil content (%), and seed yield, were evaluated based on inter-cluster distances, cluster mean and per se performance, and divergence class noted in the current study. Genotypes JLT-408 and AVTS-2001 were found to be superior for protein content, whereas DLS-12 was superior for plant height, number of capsules per plant, and 1000 seed weight; TS-16 was superior for earliness; TKG-22 was superior for oil content; and DS-10 was superior for earliness. These genotypes can be categorized as promising since they were unique and varied. Inter-crossing these genotypes can produce heterosis and greater sesame variety.

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.

Option 2:

Author(s) hereby declare that generative AI technologies such as Large Language Models, etc. have been used during the writing or editing of manuscripts. This explanation will include the name, version, model, and source of the generative AI technology and as well as all input prompts provided to the generative AI technology

Details of the AI usage are given below:

1. No generative AI technologies were used for the preparation of this manuscript.

2.

3.

REFERENCES:

Arunachalam, V. (1981). Genetic distances in plant breeding. *Indian Journal of Genetics*, 41:226-236.

Arunachalam, V. and A. Bandyopadhyay.(1984). Limits to genetic divergence for occurrenceofheterosis experimental evidence from crop plants. *Indian Journal of Genetics*, 44(3):548-554.

Bhatt, G. M. (1970). Multivariate analysis approach to selection of parents for hybridization,assuming of yield improvement in self-pollinated crops. *Australian Journal ofAgricultureResearch*, 21: 1-17.

Chandra, M. (2014). Variability and genetic divergence in sesame (*Sesamum indicum* L.).*International Journal of Applied Biology and Pharmaceutical Technology*, 5 (3):0976-4550.

East, E. M. and Hays, H. K. (1942). Heterozygosis in evolution and plant Breeding U.S.D.A Bureau of plant Industry Bulletin, 243:1-58.

Falconer, D. S. (1989). An introduction to Quantitative Genetics. Longman, New York.

FAOSTAT (2022). Food and Agriculture Organization.

Gangadharao, R. (2004). Genetic divergence in sesame(*Sesamum indicum* L.). *Journal ofOilseeds Research*, 21(2): 336-337.

Gupta,R.R., Parihar, B. M. S. and Gupta, P. K. (2001). Genetic diversity for some metric characters in sesame (*Sesamum indicum* L.). *Crop Research*, 21(3): 350-354.

Hays, H. K. and Johnson, I. J. (1939). The breeding of self-improved lines of corn. *Journal ofAmerican Society of Agronomy*, 31: 710-724.

Kindeya, Y. B. (2017). Correlation and cluster analysis of white seeded sesame (*Sesamumindicum* L.) genotypes oil yield in northern Ethiopia. *African Journal of AgriculturalResearch*, 12(12): 970-978.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *proceedings of theNational Academy of Science*, 2:55-79.

Manivannan, N. and Ganesan, J. (2000). D statistics in sesame (*Sesamum indicum* L.). *Madras Agriculture Journal*, 87: 278-280.

Mohammed, A. and Firew, M. (2015). Study on genetic divergence in low-altitude sesame (*Sesamum indicum* L.) germplasm of Ethiopia based on agro morphological traits. *Journal of Advanced Studies in Agriculture, Biological and Environmental Science*, 2:2394-2606.

Narayanan, R. and Murugan, S. (2013). Studies on genetic diversity and heritability insesamum. *International Journal of current Agriculture Research*, 2(11):52-55.

Narayanan, R. and Murugan, S. 2013. Studies on genetic diversity and heritability insesamum. *International Journal of current Agriculture Research*, 2(11):52-55.

Parmeshwarappa, S.G.,Palkashappa, M.G., Salimath, P.M. and Parmeshwarappa, K.G. (2010). Analysis of genetic divergence in sesame, (*Sesamum indicum* L) *Karnataka JournalofagricultureScience*, 23(2): 227-230.

Rahna, K., Kalaiyarasi, R., Umadevi, M., Senthil, and Sudha, M. (2023). Genetic variability and diversity analysis in sesame (*Sesamumindicum* L.) germplasm. *Electronic Journal of PlantBreeding*, 14(3):1055-1062.

Rao, C. R. (1952). *Advanced Statistical Methods in Biometrical Research*. John Willey and Sons, New York.

Shete R. R., Borale, S. U., Thorat, V. V., Shaniware, Y. A. and Girase, V. S. (2023) Identifying Promising Genotypes for Genetic Divergence and Path analysis in Soybean [*Glycine max* (L.) Merr.]. *International Journal of Agriculture Sciences*, Volume 15, Issue 11, pp: 12763-12766.

Solanki, Z.S. and Gupta, D. (2002). Genetic divergence for seed yield and other characteristics in sesamum (*Sesamum indicum* L.). *Journal of Oilseed Research*,19(1):35-37.

Sudhakar, N. (2003). Studies on genetic diversity in sesame (*Sesamum indicum* L). *M.Sc.*

(Agri.)Thesis,University of Agricultural Science, Dharwad.

Swapna, B., Thippani, S., Donda, P. And Nayak, S. S. (2023). Genetic diversity for yield and yield contributing characters in sesame (*Sesamum indicum* L.). *International JournalofEnvironment and Climate Change*, 13(8):1717-1725.

Swathy, V., Premnath, A., Viswanathan, P. L., Raveendran, M. and Manonmani,S. (2018). Determination of genetic divergence based on morphological traits in sesame(*Sesamum indicum* L.). *Electronic Journal of Plant Breeding*. 9(2): 747 - 752.

Thorat, V. V., Borale, S. U., Shaniware, Y. A., Goykar,M. B. and Girase V. S. (2023). To study genetic diversity among different traits in soybean [*Glycine max* (L). Merrill]. *The Pharma Innovation Journal*, 12(12): 1704-1709.

Table 1: Analysis of variance for different characters in sesame

Sr.No.	Characters	Mean sum of square		
		Replications	Genotypes	Error
1	Days to 50% flowering	0.98	17.3954**	1.2303
2	Days to maturity	0.933	20.1247**	1.332
3	Plant height	0.2048	494.04**	21.781
4	Number of branches/plant	0.0018	2.1839**	00.0477
5	Number of capsules /plant	2.3907	681.36**	17.20
6	Number of seeds/capsule	13.615	60.76**	12.33
7	1000 seed weight	0.0107	0.732**	0.0790
8	Oil content	4.59045	7.588**	2.6254
9	Protein content	0.00133	2.411**	0.4683
10	Seed yield /plant	0.0002	13.795**	0.678

*,** Indicates significance at 5% and 1% level, respectively.

Table 2: Average intra and inter-cluster distance (D^2) value for ten characters in sesame

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	6.39	12.73	11.41	11.20	18.01	10.52	10.91	17.42	19.57	11.45	12.98	14.34	11.99	21.11
II		8.25	10.53	16.96	9.71	13.93	14.81	21.33	11.97	16.46	13.32	11.59	15.90	17.47
III			7.45	13.47	14.62	16.11	17.78	17.58	13.96	17.83	13.93	16.21	14.69	23.15
IV				7.48	22.87	17.31	17.47	10.49	20.85	14.54	12.10	20.66	11.01	28.04
V					6.92	17.15	17.97	27.14	10.80	20.64	17.06	11.40	21.70	14.52
VI						7.80	8.51	22.87	21.17	9.50	16.03	12.11	14.96	16.39
VII							7.32	23.84	22.28	10.65	15.01	10.36	16.43	15.33
VIII								0	22.23	18.25	15.54	26.45	11.56	33.99
IX									0	21.20	14.22	17.58	20.68	21.86
X										0	12.70	16.06	13.58	20.90
XI											0	14.87	14.31	20.93
XII												0	19.18	9.23
XIII													0	26.33
XIV														0

Fig. 1: Cluster diagram of thirty-six sesame genotypes

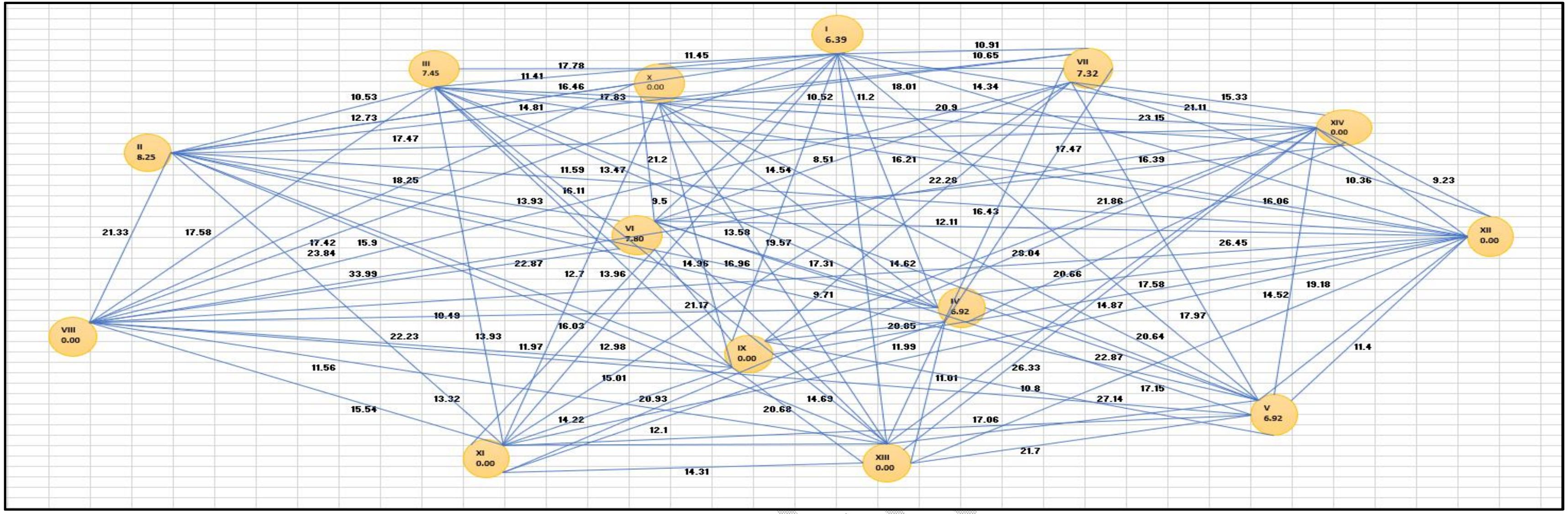

Table 3: Cluster mean of thirty-six sesame genotypes

Sr. No.	Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	Average
1.	Days to 50% flowering	43.47	46.88	46.53	42.10	49.05	47.15	42.20	44.80	50.80	48.3	42.40	42.50	42.90	43.70	45.19
2.	Days to maturity	93.05	97.30	96.70	91.87	99.25	96.00	93.10	94.00	96.30	92.40	89.20	96.50	97.60	94.20	94.81
3.	Plant height (cm)	115.40	95.13	89.25	105.85	84.41	128.87	123.85	116.40	80.60	133.65	103.00	110.00	135.70	116.25	109.88
4.	No. of primary branches/plant	3.75	2.19	2.75	3.98	1.19	3.79	3.26	4.59	1.36	4.05	2.72	2.09	4.80	1.76	3.02
5.	No. of capsules/plant	78.11	53.18	47.75	77.74	37.04	82.31	84.34	84.46	29.44	90.58	57.35	54.83	93.52	49.56	65.73
6.	No. of seeds / capsule	56.77	60.65	58.75	64.94	60.90	61.98	55.57	70.97	60.58	65.43	67.95	60.29	68.78	62.38	62.56
7.	1000 seed wt. (g)	4.46	3.60	3.54	4.20	3.25	4.67	4.13	4.79	3.33	4.80	3.65	3.38	5.37	3.71	4.06
8.	Oil content (%)	49.55	47.58	48.62	48.68	47.28	44.95	47.96	52.05	49.28	48.82	49.07	50.54	46.95	45.99	48.38
9.	Protein content (%)	20.41	20.25	20.50	19.48	19.15	18.60	18.96	19.14	19.07	17.83	18.17	18.34	19.72	17.82	19.10
10.	Seed yield/ plant (g)	9.63	7.21	6.08	10.05	5.03	11.03	10.02	13.86	6.08	12.68	8.46	6.89	15.80	6.62	9.24

Table 4: Relative per cent contribution of different characters towards total genetic divergence in sesamum.

Sr. No.	Characters	Times ranked 1st	Per cent contribution
1	Days to 50% flowering	26	4.13
2	Days to maturity	26	4.13
3	Plant height at maturity (cm)	71	11.26
4	Number of branches per plant	239	37.93
5	Number of capsules per plant	48	7.62
6	Number of seeds per capsule	5	0.79
7	1000 seed weight (g)	29	4.60
8	Oil content (%)	12	1.90
9	Protein content (%)	42	6.66
10	Seed yield per plant (g)	132	20.95
	Total	630	100

Table 5: Tentative suggested crossing programme in future

Sr. No.	Characters to be improved	Cluster combination with inter-cluster distance	Genotypes possible	Crosses
1	50% flowering, days to maturity (Earliness)	IV x VII = 17.47	TS-16, JLS-1411-1-1, DS-10,	TS-16 x DS-10 TS-16 x JLS-1411-1-1
2	Plant height (tall)	XIII x X = 13.58	TS-14, DLS-12	TS-14 x DLS-12
3	Number of primary branches (maximum)	XIII x VIII = 11.56	TS-14, JLS-1414-21-2	TS-14 x JLS-1414-21-2
4	Number of capsules per plant (maximum)	XIII x X = 13.58	TS-14, DLS-12	TS-14 x DLS-12
5	Number of seeds per capsule (maximum)	VIII x XIII = 11.56	JLS-1414-21-2, TS-14	JLS-1414-21-2 x TS-14
6	1000 seed weight (g) (maximum)	XIII x X = 13.58	TS-14, DLS-12	TS-14 x DLS-12
7	Oil content (%) (maximum)	VIII x I =17.42	JLS-1414-21-2, TKG-22	JLS-1414-21-2 x TKG-22
8	Protein content (%) (maximum)	II x I = 12.73	AVTS-2001, JLT-408	AVTS-2001 x JLT-408
9	Seed yield per plant (g) (maximum)	XIII x VIII = 11.56	TS-14, JLS-1414-21-2	TS-14 x JLS-1414-21-2