RESEARCH PAPER

Genetic analysis, yield and other components uses for human life and industrial purposes of linseed

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Abstract

One significant crop in the world is linseed. It can be used as food and feed, as a raw, material for various medications, in industry, and for a variety of other purposes. It has oil and antioxidants, making it very nourishing for the human body. Because they shield cells from the harmful effects of free radicals, antioxidants are essential to the body. Oil, protein, dietary fiber, moisture and ash are all abundant in this medicinal plant. Alpha-linolenic and linoleic acid, two essential fatty acids that are very good for human health, are found in high concentrations in it. Oil industry-derived industrial waste products frequently contain valuable materials and elements with significant potential. The rich nutritional profile and health benefits of lignans, protein, vitamins and minerals make linseed a valuable functional food. Because of its versatility, the plant is used in many different industries, including paints and varnishes, oilcloth and linoleum, paper and textiles, bioproducts, animal feed and wood preservation and other coatings. The goal of linseed genetic analysis is to enhance yield and certain component qualities for a variety of uses in industrial, medical and human nutrition. The trial was carried out at the C.S.A. University of agriculture and Technology Kanpur, Department of Linseed Kanpur, during the winter cropping season of 2023-2024. Statistical techniques for data analysis. The genetic divergence between 26 linseed genotypes was evaluated using the Mahalanobis D_2 statistic. Similar genotypes were found to fall into fifteen clusters, indicating significant genetic diversity. The degree of variation within clusters was found to be lower, than that between clusters, indicating that the genotypes, genetic differentiation was significant.

Key word: Linseed, Mahalanobis D_2, clusters and versatility.

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Introduction

Linseed has been used for over 8000 years as a source of a raw materials for food, medicine and textiles, flax is regarded as a founder crop that is crucial to human welfare (Zeist and Bakker-Heeres, 1997). It has been suggested that flax originated in the middle east, the mediterranean basin, Ethiopia and India (Vavilov, 1926; Zohary and Hopf, 2000). Linseed is a good source of lignans that have anticancer properties (Westcott and Muir, 2003). The high content of Omega-3 fatty acid in the oil is the characteristic of flaxseed that make it distinct from oil seed plants.

1

Due to quick drying properties, it's oil has huge manufacturing applications including preparation of paints, varnish, soap, putty and polymers.Through mutation breeding approach altered fatty acid profiles flaxseed lines, such as low linolenic acid and high linolenic acid, have been developed for linolenic acid, have been developed for food purposes (Green *et.al,* 2008). Fibre industries developed high value products from linseed for applications in automobile, biofuel industries and construction industries a pulp in last decade (Diederichsen and Ulrich, 2009). A single domestication event for L. bienne oil has been proposed as the ancestor of the cultivated flax (Allaby *et.al,* 2005). Flax is thought to have a complex population structure and limited gene flow due to its complicated domestication process and divergent breeding history. Since defining the population stratification within the associations, population structure analysis is also crucial for association mapping (Flint-Garcia *et.al,* 2005). Linssed's health-related qualities and current global prospects have made it necessary to assess its genetic diversity using molecular markers and use marker-assisted breeding (Pali *et.al,* 2015, 2014., Chan-drawati *et.al,* 2014., Rajwade *et.al*, 2010 and Kale *et.al*, 2012). Linseed continues to be extremely valuable for gene diversity research despite attempts to create mungbean cultivars through systematic breeding (Joshi *et.al,* 2022). It was emphasized that this study helps from diverse lines and identify genotype variation. For hybridization to be successful, it is essential to choose genotypes with a variety of genetic backgrounds. This increases the possibility of incorporating desirable genes and creating variability in subsequent generations (Joshi *et.al,* 2022). In order to address concerns like its low input nature, vulnerability to fungal diseases, and lack of genetic diversity in current cultivars, linseed's genetic potential is required to meet growing demands for its health benefits (Sood *et.al,* 2007; Guha Roy *et.al,* 2012). Crop diversity gives plant breeders a starting point for choosing appropriate parents and assessing genetic variation

in germplasm (Govindaraj *et.al,* 2015). Finding superior germplasm accessions for upcoming linseed breeding and selection initiatives requires evaluating agro-morphological traits.

Materials and Methods

The investigation was done in C.S.A. University of agricultural Kanpur, Department of Linseed, Kanpur. The soil was alluvial characterized by a uniform distribution of calcium carbonate, varying between 10% and 40% throughout the soil profile. During the crop-growing season, the weather was favorable for the best possible plant development. The study assessed 26 linseed cultivars (see table 1) that were purchased from the linseed CSA University, Kanpur, genetics and plant breeding department. A randomized block design methodology was used to carry out the experimental design, and Fisher and Yates (1963) statistical techniques were used to analyze the data. To elevated the linseed genetic divergence. After applying D^2 statistics as outline by Mahalanobis (1936), clustering analysis based on Tocher's (1952) methodology is used.

2

Table 1. Genotypes details of species

No.	Genotypes	No.	Genotypes
No.	Genotype		
1	RLC197	10	OL-2013-14-2022-6
19	LCK2209		
2	SLS143	11	SL-5
20	NL505		
3	SHEKHAR(ZC)	12	LCK2220
21	NL408		
4	LMS-2020-R-5	13	SLS144
22	RL18122		
5	RLC198	14	BAU-2021-23
23	RCRLV-22-1		
6	T397(NC)	15	OL-2013-14-2022-6
24	RL18116		
7	NL506	16	DLV-115
25	BRLS119-1		
8	SLS145	17	NL407
26	SABOUR TISI2		
9	LMS-2020-R-7	18	BRLS106-1

Result and Discussion

Variance Analysis

The result of the variance analysis on the different attributes are summarized in Table 2. Therefore, their diversity was measured by all genotypes in this study. Significant differences between genotypes were observed in a number of traits, including plant height and seed germination. The number of primary branches, secondary branches, capsules and seeds per capsule and seed yield were additional agronomic characteristics taken into account in the study (Kumar *et.al,* 2019; Kasanaetal., 2018a). These findings imply a great deal of variability in the investigated material.

Genetic Diversity

Table 3. shows that 26 linseed genotypes were categorized using Tocher's method into eleven distinct clusters. Eight of the 26 genotypes were included in cluster II, which was the largest cluster, while four were included cluster I. Significant genetic variation among these 26 genotypes was also shown by D^2 statistics over fifteen characters. Eleven clusters are formed by the distribution of the D^2 based metrics. There were only three genotypes in cluster III, compared to eight in cluster II and four in cluster I. Cluster IV, V and VI each had two genotypes, while clusters VII, VIII, IX, X and XI had only one member. The results of the study show that the genomes of all the different kinds of linseed samples that were examined exhibit a great deal of genetic variability.

Table 4 shows all the eleven cluster pairs found in intra and inter-clusters distances (D^2). What was seen is that, while genotypes from different places were clustered together, those with similar geographical locations were split into different clusters. Therefore, this picture means that genotype of members has little connection to their geographic origin. The largest distance was found between cluster IX and III (D^2 =274.24) followed by cluster VI and III (D^2 =233.79), or cluster IV and III (D^2 =215.63). Conversely, the smallest between-cluster distances were observed in the pair of clusters IV and I (D^2 =35.08), II and I (D^2 =35.11), V and I (D^2 36.64).

3

With a D^2 of 23.17, cluster II has the largest distance within a single cluster, whereas cluster III has a slightly smaller value at D^2=22.24. With a value of 21.79, cluster I has the lowest values. However, each cluster had a single genotype, such as cluster VII, VIII, IX and XI, which all had the lowest intra-cluster distance (D^2=0). Thus, overall, it can be concluded that intercluster distances are greater than intracluster distances are greater than intracluster ones, indicating a high level of genetic diversity among the genotypes under consideration. In order to maximize heterotic effects with regard to the yield attributes discussed here and the Quality traits associated with these features in general traits, parents should be selected for breeding from a variety of groups.

Table 2. The analysis of variance (ANOVA) for characters in linseed species

Characters Mean sum of squares		
Replication	**Genotype**	**Error**
df = 2	df = 25	df = 50
Seed	germination	(%)
2.62	39.01**	3.81
Harvest	index	(%)
0.05	4.26**	0.95

Test weight (g)		
0.15	1.32 **	0.11
Seedling shoot length (cm)		
0.24	1.10 **	0.17
Seedling root length (cm)		
0.15	1.22 **	0.2
Vigour index I		
118.99	3089.44**	120.72
Vigour index II		
23.25	3093.22 **	76.49
Days to 50% flowering		
1.24	9.49 **	1.37
Days to maturity		
0.66	11.70**	1.94
Number of primary branches per plant		
0.24	1.02 **	0.18
Number of secondary branches per plant		
1.16	1.52 **	0.71
Plant height (cm)		
4.51	141.88 **	3.73
Number of capsules per plant		
36.82	65.29 **	5.68
Number of seeds per capsule		
0.58	0.69 **	0.34
Seed yield (q/ha)		
0.0074	0.017 **	0.008

Table 3. Distribution of 26 genotypes of linseed samples to different clusters based on D2 statistics

Sr. No.	cluster	No. of genotypes	Name of genotypes
1	I	4	DLV-115, LCK2209, BRLS106-1, BAU-2021-23
2	II	8	SL-5, LCK2220, T397 (NC), RLC197, SLS145, LMS-2020-R-7, NL505, NL407
3	III	3	LMS-2020-R-5, OL-2013-14-2022-6, SABOUR TISI2
4	IV	2	SLS143, NL408
5	V	2	SLS144, OL-2013-14-2022-6
6	VI	2	NL506, RL18122
7	VII	1	SHEKHAR (ZC)
8	VIII	1	RLC198
9	IX	1	RCRLV-22-1
10	X	1	RL18116
11	XI	1	BRLS 119-1

4

Table 4. Average Intra-cluster and Inter-cluster distance of twenty-six genotypes of linseed species

Cluster	**I**	**II**	**III**	**IV**	**V**
VI	**VII**	**VIII**	**IX**	**X**	**XI**
I	**21.79**	35.11	114.90	35.08	36.64
48.06	166.93	53.72	93.07	58.56	47.10
II		**23.17**	76.64	75.81	53.75
135.94	150.51	73.24	155.01	78.62	54.51
III			**22.24**	215.63	170.72
233.79	140.64	169.58	274.24	139.27	71.07
IV				**18.64**	55.06
35.85	36.27	152.60	48.40	54.33	172.13
V					**20.05**
41.29	103.42	99.78	71.34	51.18	170.17
VI					**20.18**
159.49	60.09	180.28	77.28	172.24	
VII					
0.00	132.91	80.56	72.70	186.74	
VIII					
0.00	171.60	109.03	176.35		
IX					
0.00	141.03	133.24			
X					
0.00	164.54				
XI					
0.00					

The main factors influencing genetic diversity are shown in table.5 above. Other distinguishing factors included test weight (10.85%), harvest index (6.99%), seeds per capsule (6.04%), and seed germination (5.17%). The number of capsules per plant leads with approximately 26.05% and days to flowering at (23.06%). Days to maturity (4,20), vigour index I (2, 54), number of secondary branches per plant I (4.53%), days to flower in percentages (4:05) and vigour index II (4.79%). In order to improve germplasm based on genetic potential maximization- a step that should not be disregarded for its vitality- three traits- number of capsules, plant height and days to flowering- must be prioritized during the selection process. The results also shoe the importance of these traits in determining genetic diversity levels within a population.

In breeding programs, both genetic divergence and variability are crucial. This particular study made use of D^2analysis, a technique devised by Mahalanobis, to evaluate genetic divergence. This evaluation is very importance due to the main reasons that genetically diverse parents may produce significant heterotic effects leading to an increase in vigor and performance of their progenies. Also, crossing genetically distant or unrelated parents within the same species brings about a wider range of variability in the oofspring. Statistical techniques like Mahalanobi's D^2 analysis and Rao's Tocher method are suitable in the given context. The degree of variation between the clusters is indicated by the distance between them. Long distance indicate greater divergence between them, while short distances suggest less genetic variation between them. Significant genetic diversity was found among the clusters in this study, with cluster IX and cluster III showing the greatest distance from one another. Opportunities for genetic improvement in linseed are presented by this significant diversity. Cluster IV and I, on the other hand, showed the smallest inter-cluster distance, indicating comparatively small

genetic differences between them. In a similar vein, there were stronger genetic between cluster II and I and V and I. The multi-genotypic cluster for various traits showed a wide range of variation.

5

The number of capsules per plant was found to have the greatest impact on genetic divergence. 26.05% was contributes. Plant height (25.73%), 1000-seed weight (10.85%), days to 50% flowering (23.06%), seed yield per plant (5.65%), harvest index (6.99%), and days to maturity (4.20%) were additional significant traits that accounted for (98.87%) of the genetic diversity in the sample. These traits are essential for linseed breeding efforts that select advantageous genotypes. Vigor indices I and II (2.55% and 2,98%), as well as the genetic difference in plant's primary branches (1.54%), secondary branches (1.0%), and capsule number (0.95%), were the least significant variations (below 3%). These findings demonstrate how important it is to evaluate diversity in breeding initiatives to maximize the use of a range of characteristics to improve linseed cultivars. Similar result regarding plant height and the length of seedlings roots and shoots have been documented by (Kasanaet *et.al*, 2018., Rizvi *et.al*, 2018., Kumar *et.al*, 2019 and Chaudhary *et.al*, 2016).

Table 5. Linseed Genotypes' Genetic Diversity in Terms of Various Characters' Contribution species

Sr. No	Characters	Contribution to divergence (%)
1	Seed germination	5.17
2	Harvest index	6.99
3	Test weight	10.85
4	Seedling shoot length	3.63
5	Seedling root length	4.81
6	Vigour index I	2.55
7	Vigour index II	2.98
8	Days to 50% flowering	23.06
9	Days to maturity	4.20
10	Number of primary branches per plant	1.54
11	Number of secondary branches per plant	1.80
12	Plant height	25.73
13	Number of capsules per plant	26.05
14	Number of seeds per capsule	0.95
15	Seed yield	5.65

Conclusion

After evaluating 26 linseed genotypes, a significant amount of genetic heterogeneity was discovered, and these genotypes were grouped into fifteen different groups. Because there is less genetic distance between these is less genetic distance between these clusters than within them, the genotypes variety within them is highlighted. Clusters IX and III had the longest inter-cluster length, indicating a high degree of genetic dissimilarity between these populations. Genetic improvement applications of linseed breeding are possible because of this marked variation. A closer genetic link among genotypes in these clusters is illustrated by clusters IV and I, for which they had the least inter-cluster separation.

6

The most important trait causing genetic differentiation among the individuals was the number of capsules per plant. Days to 50% flowering, plant height, seed yield, 1000-seed weight, days to maturity, and harvest index were the second most significant characteristics for population segregation.

References

1. Allaby, R.G., Peterson, G.W., Merriwether, D.A and Fu, Y.B. (2005). Evidence of the domestication history of flax (Linum usitatissimum L.) from genetic diversity of the sad2 locus. Theor Appl Genet 112:58-65.
2. Chandrawati., Maurya, R., Singh, P.K., Ranade, S.A and Yadav, H.K. (2014). Diversity analysis in Indian genotypes of linseed (Linum usitatissimum L.) using AFLP marker. Gene 549:171-178.
3. Chaudhary, M., Rahul, V.P., Singh, V and Chauhan, M.P (2016). Study on genetic divergence in linseed) Linum usitatissimum L.) germplasm based on morphological and quality traits. International Quarterly Journal of Life Sciences, 11(2):953-957.
4. Diederichsen, A and Ulrich, A. (2009). Variability in stem fibre content and its association with other characteristic in 1177 flax (Linum usitatissimum L.) genebank accessions. Ind Crop Prod 30:33-39.
5. Flint-Garcia, S.A., Thuillet, A.C., Yu, J., Pressoir, G., Romero, S.M., Mitchell, S.E., Doebley, J., Kresovich, S., Goodman, M and Buckler, E. (2005). Maize association population: a high-resolution platform for quantitative trait locus dissection. Plant J 44:1054-1064.
6. Fisher, R.A and Yates, F. (1963). Statistical tables for biological, agricultural and

medical research. Oliver and Boyd, London, p143.
7. Green, A., Chem, Y., Singh, S and Dribnenki, P (2008). Flax. In: Kole, C, Hall TC (eds). A compendium of transgenic crop plants. Blackwell, Oxford, 199-206.
8. Govindaraj, M., Vetriventhan, M and Srinivasan, M. (2015). Importance of genetic diversity assessment in crop plants and its recent advances: as overview of its analytical perspectives. Genetic Research International, 1-14.
9. Joshi, D.P., Parmar, L.D., Meena, R.K and Chaudhary, G.K. (2022). Estimation of genetic diversity in mungbean (Vigna radiata (L.) Wilczek) genotypes grown in Gujrat. Legume Research – An International Journal, 45(7):828-833.
10. Kumar, S., Ran, S., Chakraborty, M., Ahmad, E., Verma, N., Lal, H.C and Choudhary, A.K. (2019). Role of genetic variability for seed yield and its attributes in linseed (Linum usitatissimum L.) improvement. Journal of Pharmacognosy. Phytochemistry, 8(2S):266-268.
11. Kale, S.M., Pardeshi, C.C., Kadoo, N.Y., Ghorpade, P.B., Jana, M.M and Gupta, V.S (2012). Development of genomic simple sequence repeat markers for linseed using next-generation sequencing technology. Mol Breed 30:597-606.

7

12. Kasana, R.K., Singh, P.K., Tolar, A., Mohan, S and Kumar, S. (2018). Genetic variability (Mean, range, general mean, standard error, coefficient of variability (PCV and GCV) in linseed (Linum usitatissimum L.). Journal of Pharmacognosy and Phytochemistry, 7(3):2279-2285.
13. Mahalanobis, P.C. (1936). On the generalized distance in statistics. Proceeding of the National Institute if Scienceof India, 2:49-55.
14. Pali, V., Mehta, N., Verulkar, S.B., Xalxo, M.S and Saxena, R.R. (2015). Molecular diversity in flax (Linum usitatissimum L.) as revealed by DNA based markers. Int J Plant Res 28:157-165.
15. Rizvi, A., Marker, S and Choudhary, A. (2018). Multivariate analysis in linseed (Linum usitatissimum L.). Journal of Pharmacognosy and Phytochemistry, 7(2):628-531.
16. Soods, S., Kalia, N.R., Bhateria, S and Kumar, S. (2007). Detection of genetic components of variation for some biometrical traits in Linum usitatissimum L. in sub-mountain Himalayan region. Euphytica, 155:107-115.
17. Vavilov, N. (1926). Studies on the origin of cultivated plants. Bull Appl Bot Plant Breed, Leningrad, USSR, 16:139-248.
18. Westcott, N.A and Muir, A.D. (2003). Flax seed lignan in disease prevention and health promotion. Phytochem Rev, 2:401-417.
19. Zeist, W.V and Bakker-Heeres, J.A.H. (1975). Evidence for linseed cultivation before 6000 BC. J Archeol Sci 2(3): 215-219.
20. Zohary, D and Hopf, M. (2000). Domestication of plants in the old world: the origin and spread of cultivated plants in West Asia, Europe and the Nile Valley. Oxford University Press, Oxford, P 316.

8