IJCRT.ORG

ISSN: 2320-2882



INTERNATIONAL JOURNAL OF CREATIVE RESEARCH THOUGHTS (IJCRT)

An International Open Access, Peer-reviewed, Refereed Journal

Genetic Diversity Analysis Of Linseed And Industrial Edible Property

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Abstract

In the present investigation a total 30 linseed genotypes including released varieties were evaluated during Rabi 2022-2023 at C.S.A Agriculture Research Station, Kanpur, U.P for understanding genetic diversity for grain yield and its component traits using principal component analysis. Study of genetic diversity is the process by which physiological data, agronomic performance data, biochemical data, and variation among individuals or groups of individuals more recently molecular (DNA-base) data. Genetic analysis can be assessed using morphological characteristics and or molecular markers. The availability of several DNA marker has increased the efficiency of genetic diversity analysis as they are reliable and unaffected by environmental factors. Genetic diversity is important because it helps species adapt to environmental changes, which can help them survive. It also helps to prevent inbreeding and disease epidemics. Genetic diversity helps plant breeders to develop new improved cultivars with desirable characteristics. Genetic diversity helps to develop climatic – resilient varieties. Thirty genotypes were grouped into six cluster. Cluster I constituted maximum number of genotypes followed by cluster III, Cluster II, Cluster V, Cluster IV and Cluster VI. Suggested that the genotypes from these cluster may use hereafter be as a parent for future hybridization programme to obtain heterotic recombinants or even transgressive segregants.

Key words: Genetic diversity, linseed, cluster and transgressive segregants.

Introduction

Linseed is one of the chronic yields being ploughed since the beginning of decency. Every part of the linseed plant is and exploitage commercially, either directly through processing" (Qamar et.al 2019), Similitude with other oil yields, linseed containing about 36-40% oil is the richest drift of polyunsaturated fatty acids like alpha-linolenic acid, the majority copious drift of antioxidants (Andruzczak et.al 2015; Goyal et.al 2014) and lignin (Kajla et.al 2015), which has profitable impact on the stopover of the illness and human soundness. Due to its high 45-60% linolenic acid content, the marl is primarily employed in the industrial manufacture of varnishes, soaps and paints (Wakjira, 2007; Biradar et.al 2016). However, inferior linolenic acid content is expected for human expenditure. deferment in view, the increasing requirement for linseed due to diver health gain, there is a consistent importance to increase the genetic potential for seed crop (Anonymous, 2020-2021). Linseed is used for fiber and oil (Chauhan et al 2009). Linseed oil has many technical and medicinal availability (Kumar et.al 2018). Linseed oil cake also restrain very good feeder feeding value for animals (Bibi et.al 2015). The general causes behind its inferior produce can be due to marginal cultivation of linseed and prone to biotic and abiotic stress (Kumar et.al 2018). Linseed/flax seed propagate for two reasons, its fiber and its seed oil, the fiber gain from the stem is weave in to linen cloth for uses in the home and in the industries and for clothing (Zohary, 1999). These plants are raised in India, United Kingdom, Ethiopia primarily for its fibre, oil and medicative compounds. India holds the second position in the world in terms of linseed cultivated land after Canadanwhile fourth in terms of produce following China and United States of America (Yadav et.al 2012; Chandravathi et.al 2014).

Therefore, studies on genetic diversity prove to be a necessary criterion for the yield improvement since picking of convenient divergent parent for Hybridization offer great probability of obtaining desirable segregants in the segregating (Samantara *et.al* 2020). Mahalanobis D² statistic is usable for qualifying the degree of divergence among genotypes. In the current investigation, an attempt is made to understand the nature and magnitude of genetic divergence and to select divergent parents for hybridization programs. Asunder scientists have highlighted the value of parental diversity in optimum magnitude to get better genotypes in the segregating generations (Srivastava *et.al* 2009; Tyagi *et.al* 2015).

Material and Methods

Twenty genotypes of linseed were sown in a Randomized Complete Block Design with three replications during Rabi 2022-2023 at Research field, College of Agriculture, C.S.A, Agriculture University, Kanpur (U.P). Observations were recorded for 12 characters viz., days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of capsules per plant, number of seeds per capsule, test weight (g), biological yield per plant (g), harvest index (%), oil content (%), protein content (%) and seed yield per plant (g). The genetic divergence in 30 genotypes has been estimated by using MahalanobisD2 statistics (1936) with inter and intra cluster distances, as suggested by Rao (1952).

Result and Discussion

Thirty genotypes of linseed were grouped into six distinct non-overlapping clusters (Table 1). Cluster I constituted maximum numbers of 20genotypes (NL-93, KL-32, ACC NO442, Gaurav, NL-165, LBR-6, LC-2023, NL-165, BAU-06-17,NDL-2005-29, BAU-06-5, OLC-99-57, RRN-2, LCK9211, NDL-2005-24, RRN-1, NDL-2005-16, SLS-68, Garima and NL- 260) followed by cluster III with 4 genotypes (Shubhra-106, Shubhra-06, NL-93-34 and NL-93-26), cluster II with 2 genotypes (LC-2279-4 and LCK9211), cluster V with 2 genotypes (LCK-6028 and Kiran-112) and while rest of the cluster IV and VI contained single genotype each (LC-2023-4and

NL-93-17). Distribution pattern of all the genotypes in six clusters showed the presence of considerable genetic diversity among them for all the traits under considerable. Inter and intra-cluster distances were present in Table 2. The maximum intra-cluster distance was observed in cluster V (173.32) followed by cluster I (112.05), cluster III (85.66) and cluster II (69.72). While it was zero for cluster IV and cluster VI. Maximum inter- cluster distance was found between cluster IV and VI (1728.35) followed by cluster I and VI (1062.19) and cluster III and IV (947.45) while minimum inter cluster distance was recorded between cluster I and II (164.09). The greater the distance between two clusters, wider the expected genetic diversity. Similar studies done by Thakur et al. (2021); Kumar et al. (2017); Nizar and Mulani (2015); Begum et al. (2007).

The mean values of twelve different characters for six clusters are presented in Table 3. Higher mean value in cluster II was observed for characters like protein content (20.35 %). Whereas, clusters IV had high mean values for number of primary branches per plant (4.53), plant height (66.20 cm), and oil content (40.90 %) and also desirable for early flowering (67.00 days) and maturity (116.33 days). Cluster V for seed yield per plant (6.56 g), harvest index (41.71 %), test weight (8.88 g) and number of capsules per plant (95.23) Cluster VI for seed yield per plant (6.56 g), biological yield per plant (17.38 g), number of seeds per capsule (8.70). Therefore, hybridization between the selected genotypes form divergent clusters is essential to judiciously combine all the targeted characters. Earlier finding of Manhar et al. (2021); Thakur et al. (2021); Samantara et al. (2020); Tewari et al. (2020); Kasana et al. (2018); Kumar et al. (2018); Kumar et al. (2017); Tyagi et al. (2015); Nagaraja et al. (2010). The contributions of per cent toward genetic divergence by contributions of twelve characters of thirty genotypes of linseed are given in Table 4. The character showed maximum contribution oil content (47.12%) followed by test weight (36.32%), protein content (10.11%), days to 50 per cent flowering (3.90%), seed yield per plant (1.14%), days to maturity (0.22%), plant height (0.22%), number of primary branches per plant (0.22%), number of seeds per capsule (0.22%), biological yield per plant (0.22%) and harvest index (0.22%). Similar finding were also reported by Manhar et al. (2021); Tewari et al. (2020); Kumar et al. (2017); Pali and Mehta (2016); Chaudhary et al. (2016); Tyagi et al. (2015).

Table 1: Distribution of linseed genotypes in six clusters

Cluster	Number of	Genotypes				
	genotypes					
Cluster I	20	NL-93, KL-32, ACC NO442, Gaurav, LBR-6, LMS-3, LC-				
		2023, NL-165, NDL-2005-29, BAU-06-5, OLC-99-57,				
		RRN-2, LCK9211, NDL-2005-24, RRN-1, NDL-2005-1				
		SLS-68, BAU-06-17, NL-260, Garima, RRN-1, SLS-68				
Cluster II	02	LC-2279-4, LCK9211				
Cluster III	04	Shubhra-106, Shubhra-06, NL93-34, NL93-26				
Cluster IV	01 LC-2023-4					
Cluster V	02	LCK-6028, Kiran-112				
Cluster VI	01	NL93-17				

Table 2: Estimates of average intra and inter-cluster distances for six clusters

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	112.05	164.09	586.72	193.92	346.91	1062.19
Cluster II		69.72	278.55	288.77	376.75	751.69
Cluster III			85.66	947.45	488.04	237.65
Cluster IV				0.00	782.00	1728.35
Cluster V					173.32	521.63
Cluster VI						0.00

Table 3: Cluster mean of thirty genotypes of linseed for twelve characters

Cluster	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of primary branches per cent	Number of capsules per plant	Number of seeds per capsule	Test weight(g)	Biological yield per plant (g)	Harvest index (%)	Oil content (%)	Protein content (%)	Seed yield per plant (g)
Cluster I	73.35	120.83	61.07	3.97	84.35	7.83	6.31	14.99	36.82	40.41	19.73	5.51
Cluster II	76.66	120.00	62.10	3.86	78.90	7.30*	5.64	14.08*	34.37	37.50	20.35**	4.81
Cluster III	78.66	124.00	59.41	3.80*	82.91	7.85	6.32	16.01	33.73	32.75	19.15	5.39
Cluster IV	67.00*	116.33*	66.20**	4.53**	72.20*	7.73	4.52*	14.65	29.12*	40.90**	19.44	4.26*
Cluster V	74.33	120.66	63.03	4.15	95.23**	8.38	8.88**	15.72	41.71**	39.43	19.93	6.56
Cluster VI	79.00**	125.66**	57.93*	4.00	94.06	8.70**	8.66	17.38**	37.80	31.70*	18.52*	6.56**

Table 4: Contribution (%) of twelve characters towards genetic divergence in linseed

Sr. No.		Source		
1		Days to 50% per cent flowering	3.90%	
2		Days to maturity	0.22%	
3		Plant height (cm)	0.22%	
4	Nu	m <mark>ber of pri</mark> mary branches per plant	0.22%	
5		Number of capsules per plant	0.0%	
6		Number of seeds per capsule	0.22%	
7		Test weight(g)	36.32%	
8		Biological yield per plant(g)	0.22%	
9		Harvest index(%)	0.22%	
10		Oil content(%)	47.12%	
11		Protein content(%)	10.11%	
12		Seed yield per plant(g)	1.14%	

Conclusion

The application noticed that a considerable extent of genetic divergence was present among 30 genotypes of linseed. Cluster V has the highest intra cluster distance followed by cluster I, III and cluster II. The intracluster distance for cluster IV and VI was observed to Zero since these contains one genotypes. The highest inter-cluster distance was found between cluster IV and VI followed by cluster I and VI, cluster III and IV. Maximum mean value was observed in cluster II for characters like protein content. Cluster IV had high values for plant height, number of primary branches per plant, oil content and also desirable for early flowering and maturity. These characters should be taken under consideration for future breeding program.

Acknowledgement

The author is thankful to the Guide and committee members of the Department of Genetics and plant breeding, Agriculture University, Kanpur for their untiring help and assistance during the experiment and preparation of manuscript.

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