Frontiers in Crop Improvement 1(2) : 185-187 (2013)

ASSESSMENT OF GENETIC DIVERGENCE IN LINSEED (*Linum usitatissimum* L.)

D.D. Patel, S.P. Mishra, Y.S. Chauhan, S. Chaudhari, S.S. Porte and A. Tiwari
Department of Crop Sciences, Mahatma Gandhi Chitrakoot Gramodaya Vishwa Vidyalaya, Chitrakoot, Satna-485780
Email-devidaspatelp24@gmail.com

ABSTRACT

A set of 40 linseed accessions were evaluated under irrigated conditions during *Rabi* season 2008-09 at Research Farm of Mahatma Gandhi Chitrakoot Gramodaya Vishwa Vidyalaya, Chitrakoot, Satna (M.P.). The study on genetic divergence revealed that there was wide range of divergence among genotypes for all the nine traits *viz.* plant height (cm), number of primary/plant, number of secondary branches/plant, number of capsules/plant, number of seeds/capsule, days to maturity, 1000-seed weight, seed yield plant^{-1} and oil content (%). D^2 analysis grouped 40 genotypes into six clusters. The Cluster I had highest number of genotypes (22) followed by the cluster II and III which had 7and 6 genotypes respectively. The inter cluster D^2 values indicated that most diverse clusters were V and VI (2502.75) followed by cluster III and V (2502.27). The highest intra cluster distance was observed in cluster III (212.95) which indicates maximum variability within the cluster. The cluster IV consisted 3 genotypes, which had highest mean values for number of secondary branches/plant (29.85) and seed yield/plant (6.33 g). However, the cluster VI had single genotype (EC-3990-83) with highest mean values for plant height (109.47 cm), number of seeds/capsule (8.53), and seed yield/plant (6.33 g). The characters such as plant height (cm), number of secondary branches/plant and number of seeds/capsule had potential variability which can be used as parameters while selecting diverse parents in the hybridization programme for further yield improvement of linseed.

Key words : *Genetic divergence, cluster analysis, linseed.*

Linseed (*Linum usitatissimum* L.) (2n= 30) is an annual self-pollinated crop that is commercially grown as a source of fiber and oil of industrial use (1). The fiber is used in textile as well as automobile and construction industries, while seeds are used in animal feed (2). The linseed contain 30-45 % oil which is mainly used for manufacturing of high quality paints, printing ink, varnishes, resins and several innumerable byproducts. It imparts numerous health benefits, including anti-hypercholesterolemia and anti-carcinogenic effects and is also beneficial in the development of brain and retinal tissues of infants (3). In India, linseed is cultivated in 0.5 m ha with production of 0.13 mt and productivity of 260 kg/ha (4) which is very low as compared to its potential yields 20-24 q/ha due to lack of high yielding, biotic and abiotic resistance varieties. In view of low productivity, there is an urgent need to improve the seed yield potential of linseed varieties through systematic breeding programme.

Genetic diversity plays an important role in choosing parental materials to get maximum recombination in hybridization programme (5). Diversity in the germplasm is essential to meet different purpose of the crop such as increased yield and its contributing traits (6). Earlier workers considered genetic distance in the place of origin as index of genetic diversity and used in selection of parents for hybridization. However the genetic diversity of selected parents is not always based on factors such as geographical diversity/place of release (7). Hence, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures, such as D^2 statistic and cluster analysis. These procedures characterize genetic divergence using the criterion of similarly or dissimilarly based on the aggregate effect of a number of agronomically important characters. In view of this fact, 40 linseed germplasm were evaluated to assess extent of genetic divergence with following objectives. (i) To determine the grouping pattern of genotypes in different clusters and (ii) to identify genetically diverse and agronomically desirable genotypes for exploitation in breeding programme aimed for increasing seed yield of linseed.

MATERIALS AND METHODS

The material for the study comprised 40 diverse genotypes of linseed (*Linum usitatissimum* L.) received from the ICAR, Project Coordinating Unit (Linseed), C. S. Azad University of Agriculture and Technology, Kanpur (U. P.). The experiment was conducted at Research Farm, Rajoula, Mahatma Gandhi Chitrakoot Gramodaya, Vishwa Vidyalaya, Chitrakoot, Satna (Madhya Pradesh) during *Rabi* season of 2008-09. The experiment was conducted in Randomized Complete Block Design (RCBD) with three replications. Single row trail was planted of 3 m length for each entry with inter and intra row spacing of 30 cm and 10 cm respectively. In each accession, five competitive plants were randomly selected for collection of data on yield and its component traits such as plant height (cm), number of primary branches/plant, number of secondary branches/plant, number of capsules/plant, number of seeds/capsule, days of maturity, 1000-seed weight (g), seed yield/plant (g) and oil content (%). The analysed as per Mahalanobis D^2 statistics (8) and clustering was done as per method, (9) used for cluster formation. Average intra and inter cluster distances were estimated as per the procedure outlined by (10).

RESULTS AND DISCUSSION

The results of present study revealed that 40 linseed germplasm were grouped into 6 clusters by using Mahalanobis D^2 statistics in such a way that the genotypes within a cluster had a small or low D^2 values than those in between the clusters. The composition of each cluster is presented in Table-1. Cluster I had highest number of genotypes (22) followed by cluster II and cluster III which had seven and six genotypes respectively. Cluster IV had three genotypes (Palf-11, Acc. No. 534, & Palf-30) whereas two other genotypes EC-1424 and EC 3990-83 formed separate clusters V and VI respectively. Findings of (1) grouped 144 linseed lines into 6 clusters and suggested that best genotypes in cluster V, II and IV can be used for future breeding programme. (12) grouped 81 linseed genotypes into 10 distinctive clusters and reported that improvement in genotypes would be brought through crossing between accessions of different clusters followed by selection in segregating populations. (13) grouped 26 linseed genotypes into 3 clusters and suggested that intercrossing of genotypes from different clusters may help in obtaining new lines with higher yield.

The intra and inter- cluster distance among different clusters has been given in Table 2. The

Table-1: Distribution of 40 linseed germplasm in different clusters.

Cluster number	Number of germplasm	Germplasm
I	22	Belly, GS-280, Palf-15, NP-29, JRF-5, EC-3990-85, Palf-23, Acc-No. 135, EC-41472, EC-1427, H-12, Acc No. 113, EC-544, H-8, GS-401, EC-41494, Palf-14, NP-11, EC-41472, EC-89512, EC 3990-85, Palf-26
II	7	Palf-5, Kanpur local, EC-1667, EC 9825, Palf-13, H-40, Acc No. 442
III	6	H-10, H-34, Palf-34, EC 3990-83, H-18, Palf-31
IV	3	Palf-11, Acc No. 534, Palf-30
V	1	EC-1424
VI	1	EC-3990-83

Table-2: Intra and inter-cluster D^2 and D values among 6 clusters in linseed.

Cluster number	I	II	III	IV	V	VI
I	**199.40**	791.04	601.52	790.73	1049.11	625.13
II		**170.73**	1369.77	515.88	723.45	1309.71
III			**212.95**	608.90	2502.27	123.00
IV				**90.85**	1882.48	547.68
V					**0.00**	2502.75
VI						**0.00**

Bold figures represent intra-cluster distance.

Table-3: Cluster means for nine quantitative characters in linseed

Cluster numbers	Plant height (cm)	No. of Primary branches / pant	No. of Secondary branches/ plant	No. of capsules / plant	No. of Seeds/ per capsule	Days to maturity	1000-seed weight (g)	Seed yield/ plant (g)	Oil content (%)
I	80.91	5.08	24.59	32.70	7.79	146.12	35.61	5.24	2.04
II	76.68	5.65	24.52	80.79+	8.52	142.48	35.34	5.62	3.81+
III	106.66	5.06	23.62	24.65#	7.88	148.72+	36.17+	5.56	1.87#
IV	99.08	5.29	29.85+	65.88	7.76	147.89	35.90	6.33+	3.12
V	49.80#	5.93+	19.33#	70.47	7.13#	125.00#	34.20#	4.33#	3.70
VI	109.47+	4.53#	20.33	26.07	8.53+	145.00	35.20	6.33+	2.05

#, + indicates lowest and highest values, respectively.

inter-cluster distance was higher than intra-cluster, indicating wider genetic diversity among different genotypes of different clusters. The maximum inter cluster distance was observed between cluster V and VI (2502.75) followed by cluster III and V (2502.77). On the other hand minimum inter-cluster distance was observed between cluster III and VI (123.00) which indicating close relationship between genotypes of these clusters would not provide any significant diversity. The greater distance between clusters revealed wider genetic distance between genotypes. Highly divergent genotypes would produce a broad spectrum of variability in the subsequence generations enabling further selection and improvement due to better recombinations. The hybrid developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants or higher magnitude of heterosis. This would be useful in linseed breeding programme to develop genotypes with high yield potential. The maximum intra-cluster distance was reported for cluster III (212.95) (Table 02) whereas the minimum intra-cluster distance was observed in clusters V and VI (0.00) indicating homogenous nature of the genotypes with less deviation between genotypes, therefore selection will be ineffective. The similar findings were also reported by (14).

The mean performance of all the characters in different cluster is presented in Table 3. The Cluster I had medium mean value for 1000-seed weight (35.61 g). The cluster II had highest mean values for number of/ capsule (80.79) and oil contain (3.81 %). The cluster III had the highest mean values for days to maturity (148.72) and 1000-seed weight (36.17g). The cluster IV had highest mean values for number of secondary branches/plant (29.85) and seed yield/plant (6.33 g). The cluster V had highest mean value for number of primary branches/plant (5.93). It is also recorded the lowest mean values for plant height (49.80cm), number of secondary branches/plant (19.33), number of seeds/ capsule (7.13), days to maturity, 1000-seed weight (34.20g) and seed yield/plant (4.33g). The cluster VI had highest mean values for plant height (109.47cm), number of seeds/capsule (8.53), and seed yield/plant (6.33g). The similar findings were also reported by (14).

The results suggest that intercrossing between genotypes of different clusters indicating better mean performance may help in obtaining high yielding genotypes. The better genotypes can be selected for most of characters on the basis of their mean performance in the cluster.

REFERENCES

1. Cloutier S., Ragupathy R., Miranda E., Radovanovic N., Reimer E., Walichnowski, A., Ward K., Rowland G., Duguid S. and Banik M. (2012). Integrated consensus genetic and physical maps of Flex (*Linum usitatissimum* L.). *Theor. Appl. Genet. 125:* 1783-1795.
2. Smy'kal P., Bac^ova'-Kerteszorz N., Kalendar R., Corander J., Sculman A. H. and Pavelek M. (2012). Genetic diversity of cultivated flax (*Linum usitatissimum* L.). Germplasm assessed by retrotransposon based markers. *Theor. Appl. Genet*. 122: 1385-1397.
3. Payne T. J. (2000). Promoting better heath with flax seed in bread. *Cereal Foods World*. 45: 102-104.
4. FAOStat (2012) Online Agriculture Statistics *http/www.faostat.org.*
5. Arunachalam V. (1981). Genetic distance in plant breeding. *Indian J. Genet. 4 :* 226-236.
6. Joshi A. B. and Dhawan N. P. (1986). Genetic improvement of yield with special reference to self-fertilizing crops. *Indian J. Genet*. *26(A):* 101-113.
7. Bhatt, G.M., 1970. Multivariate analysis approach to selection of parents for hybridization aiming at yield improvement in self-pollinated crops. *Australian Agricultural Journal Research*, *21 :* 1-7.
7. Gauraha D. and Rao S. S. (2011). Association Analysis for Yield and its Characters in Linseed (*Linum usitatissimum* L.). *Research Journal of Agricultural Sciences*, *2(2):* 258-260.
8. Mahalanobis P. C. (1928). A statistic study Chinese head management. *Man in India 8 :* 32-64.
9. Rao, C.R. (1952). Advanced Statistical Methods in Biometric Research, *John Wiley and Sons, Inc ,* New York.
10. Singh, R.K. and Choudhary, B.D. (1977). Biometrical methods in quantitative genetic analysis, *Kalyani Publishers*, New Delhi.
11. Savita, S.G. (2006). Diversity of linseed germplasm for yield and yield components. *Unpubl. M. Sc. Thesis, University of Agricultural Sciences*, Dharwad.
12. Tadesse, T., Singh H. and Weyessa B. (2009). Genetic divergence in linseed germplasm. *J. Innov. Dev. Strategy, 3(2):* 13-20.
13. Sinha, S., and Wagh P. (2013). Genetic studies and divergence analysis for yield, physiological traits and oil content in linseed. *Res. J. Agric. Sci. 4(2):* 168-175.
14. Begum H., Alam A.K. M.M., Chowdhary M.J.A. and Hossain M.I. (2007). Genetic divergence in linseed. *Int.J. sustain. Crop prod. 2(1) :* 04-06

Received : April-2013; Revised : April-2013; Accepted : June-2013