The Pharma Innovation Journal 2022; 11(7): 1014-1016

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(7): 1014-1016

www.thepharmajournal.com
Received: 01-03-2022
Accepted: 07-06-2022

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Genetic diversity in golden flax (*Linum usitatissimum* L.) for irrigated situation

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Abstract
Collection and evaluation of divergence among genotypes are fundamental for know the spectrum of diversity. An experiment was conducted During the Rabi season 2019-20 and 2020-21, 40 accessions of golden flax (37) and brown flax (3) (checks RLC-143, RLC-148, RLC-153, and Surabhi) were shown in an irrigated situation at the Research cum Instructional Farm of AICRP on Linseed, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. Maximum % contribution towards the divergence noted for days to maturity followed by days to 50% flowering, capsule size (mm), number of seeds per capsules & oil content %. On the basis of D^2 values 40 golden flax were grouped into 9 clusters, the maximum lines were grouped in cluster II (12 genotypes) followed by cluster I (9 genotypes), cluster III and VI (5 genotypes), cluster IV and V (3 genotypes) and cluster VII, VIII and IX had only one genotype in each. Highest intra-cluster distance was recorded for cluster VI followed by cluster IV, cluster II, cluster I, cluster V & cluster III whereas Cluster VII, VIII & IX were mono-genotypic. The highest inter cluster divergence was observed between genotypes of cluster VI & cluster V followed by cluster V & cluster VI, cluster V & cluster VIII, cluster III & cluster IX & cluster II & cluster V. Divergence golden flax *viz.,* YLS-8, YLS-28, YLS-3, YLS-5, YLS-6, YLS-21, YLS-30, YLS-33 & RC-153 (c) grouped in different clusters.

Keywords: Genetic diversity, cluster, quantitative traits

1. Introduction
Linseed (*Linum usitatissimum* L.) is an important oilseed crop having 2n = 30 chromosome number belongs to the genus *Linum* of the family *Linaceae* and order *Geraniale* having genome size of ~370 Mb and is the species in the family, which is of economic significance. The cultivated flax is supposed to have originated from *The Central Asiatic Centre, The Near-Eastern Centre, The Mediterranean Centre and The Abyssinian Centre* (Vavilov 1926).
Information on genetic divergence in available genotypes is extremely useful and timely in determining which guardians should be used in a hybridization programme to obtain beneficial hereditary recombination. It is difficult for the breeder to select the most suitable genetically diverse parents for a successful hybridization programme unless the accessible genetic material contains the required information on genetic variation and genetic divergence. The more different the parents, the more likely there are to be substantial heterotic effects and a wide range of diversity in the segregating generations. The Mahalanobis D2 statistic is a useful tool for determining the degree of genetic divergence across genotypes and connecting clustering patterns to geographic origin. The hereditary distance had a significant role in the successful selection of guardians for the hybridization programme. As a result, including prominent genotypes from distant clusters into breeding programmes may result in the generation of new genotypes with a broader genetic base.

2. Material and Methods
During the *Rabi* seasons 2019-20 and 2020-21, the investigation was conducted on 40 golden flax at the AICRP Linseed Research and Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. Forty (40) accessions including checks *viz;* golden flax (37) & brown flax (3) (checks RLC-143, RLC-148, RLC-153 and Surabhi) were collected from All India Coordinated Research Project on Linseed, Department of Genetics & Plant Breeding, College of Agriculture, IGKV, Raipur, these lines were grown on two situations in randomized complete block design with three replication during *rabi* 2019-20 and *rabi* 2020-21 under

irrigated situations. Genetic diversity for seed yield and its attributing traits was done by help of observations taken on traits, *viz.;* days to 50% flowering, days to maturity, plant height (cm), number of capsule per plant, number of seeds per capsule, 1000 seed weight (g), oil content, seed yield per plant(g). The mean data were subjected to standard statistical techniques to estimate genetic divergence through Mahalanobis D^2 analysis (1928).

3. Result and Discussion

The contribution (%) of characters days to maturity showed most toward genetic divergence followed by days to 50% flowering, capsule size, number of seeds per capsules & oil content % showed low percentage of contribution, whereas remaining characters exhibited very low contribution towards divergence Table 1.

Forty genotypes of golden flax were grouped into nine (9) clusters based on divergence analysis. Distributions of genotypes into different clusters were presented in table 2. Cluster II was the largest number genotypes comprising 12 genotypes, followed by cluster I had 9 genotypes, cluster III & VI consist of five genotypes, cluster IV & V consist three genotypes. Cluster VII, VIII & IX comprising only one genotype. On the basis of clusters similar findings were recorded from Gulla *et al.* (2021) [6], Ankit *et al.* (2019) [2], Tyagi *et al.* (2015) [12], Abdul & Mulani (2015) [1], Dikshit & Sivaraj (2015) [4]; Kumar *et al.* (2015). The high diversity of the material is indicated by the D^2 values of the genotypes and the clustering pattern.

Distributions of genotypes into different clusters were presented in Table 3. Inter cluster distance ranged from 0.0 to 282.6. The highest intra cluster value were recorded for cluster VI followed by cluster IV, cluster II, cluster I, cluster V & cluster III, whereas cluster VII, VIII & IX were mono-genotypic, resulting in a value of zero for intra cluster distance. The largest inter-cluster divergence was found between genotypes of cluster VI & cluster V followed by cluster V & cluster VI, cluster V & cluster VIII, cluster III & cluster IX & cluster II & cluster V, indicating that the genetic make-up of genotypes remembered for these groups has a significant level of inconstancy. The highest inter cluster divergence was recorded between genotypes of cluster VI & cluster V. Crossing the genotypes of these most distinct clusters could result in the highest levels of recombinant in the material. When the genotypes of these distinctively positioned clusters are crossed, high heterosis/heterotic sergeants result. Cluster I and cluster III had the lowest inter-cluster distance, indicating that they were in close proximity. Divergence genotypes *viz*., YLS-8, RLC-143(C), YLS-28, RLC-148 (c), YLS-3, YLS-6, YLS-11, YLS-21, YLS-30, YLS-33, RLC-153 (C) grouped in different clusters, there is no association between geographical distribution and genetic divergence of genotypes. Genotypes from a similar source appropriated various clusters. Genotypes select from various clusters intercrossed for inciting changeability in the particular characters for abuse in future breeding programs.

The cluster mean for different characters are presented in Table 4. Wide series of variation were found for all the traits under experiment. In case of cluster IX observed maximum value for days to 50% flowering & cluster III was recorded minimum. Cluster V observed maximum value for days to maturity & cluster II showed minimum days to maturity.

Plant height had maximum value in cluster IX. Number of capsules per plant was recorded maximum in cluster VI. Number of seeds per capsule found maximum in cluster VI & minimum in cluster V, 1000 seed weight noted in cluster VII had maximum & cluster I minimum. Seed yield per plant had maximum value in cluster VII & minimum in cluster IX.

P.C. Mahalanobis was the first to propose D^2 statistics in 1928. This is one of the most effective methods for determining genetic divergence. Genetic diversity is essential in plant breeding because hybrids between lines of diverse sources have more heterosis than those between closely related parents. Geographical separation or genetic barriers to crossability produce genetic diversity. These findings confirm in earlier studies of Gulla *et al.* (2021) [6], Samantara *et al.* (2021) Thakur *et al.* (2020), Ankit *et al.* (2019) [2], Patil *et al.* (2019), Kasana *et al.* (2018) [7], Pali & Mehta (2016), Tyagi *et al.* (2015) [12].

4. Conclusion

Maximum % contribution towards the divergence noted for days to maturity followed by days to 50% flowering, capsule size, number of seeds per capsules & oil content %. On the basis of D^2 values 40 golden flax were divided into 9 clusters, with Cluster II containing the most lines (12 genotypes) followed by cluster I (9 genotypes), cluster III and VI (5 genotypes), cluster IV and V (3 genotypes) and cluster VII, VIII and IX had only one genotype in each. Cluster VI had the greatest intra-cluster distance, followed by cluster IV, cluster II, cluster I, cluster V and cluster III, while Cluster VII, VIII and IX were mono-genotypic. Cluster VI & cluster V genotypes had the highest inter cluster divergence, followed by cluster V & cluster VI, cluster V & cluster VIII, cluster III & cluster IX, and cluster II & cluster V. Crossing the genotypes of these most divergent clusters may result in the highest number of recombinant / sergeants in the material. Divergence golden flax *viz*., YLS-8, YLS-28, YLS-3, YLS-5, YLS-6, YLS-21, YLS-30, YLS-33 & RC-153 (c) grouped in different clusters.

Table 1: Contribution (%) of characters towards divergence for irrigated situation

S. No.	Source	Contribution %	Times ranked 1st
1.	Days to maturity	38.05%	367
2.	Days to 50% flowering	23.39%	354
3.	Capsule size (mm)	14.26%	216
4.	Number of seeds per capsules	8.52%	161
5.	Oil content %	6.30%	67
6.	Seed yield per plant (g)	4.10%	32
7.	1000 seed weight (g)	1.69%	25
8.	Number of capsules per plant	1.30%	21
9.	Seed size (mm)	1.24%	18
10.	Plant height (cm)	1.15%	9

Table 2: Distribution of genotype in different clusters using Mahanlobis D^2

Cluster. No.	No. of genotypes	Genotypes include in cluster
Cluster I	9	YLS-8, RLC-143(C), YLS-17, YLS-2, YLS-13, YLS-16, YLS-4, YLS- 9 & YLS-12.
Cluster II	12	YLS-28, RLC-148 (c), YLS-22, YLS-24, YLS-23, YLS-29, Surabhi (C), YLS-15, YLS-20, YLS-34, YLS-32 & YLS-35.
Cluster III	5	YLS-3, YLS-18, YLS-7, YLS-1 & YLS-10.
Cluster IV	3	YLS-5, YLS-31 & RLC-148 (C).
Cluster V	3	YLS-6, YLS-11 & YLS-14.
Cluster VI	5	YLS-21, YLS-26, YLS-27, YLS-25 & YLS-19.
Cluster VII	1	YLS-30
Cluster VIII	1	YLS-33
Cluster IX	1	RLC-153 (C)

Table 3: Inter and intra cluster D^2 values for different clusters

Table 4.7.11 Cluster Distances for irrigated situation									
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	22.7	88.1	42.6	122.1	65.2	111.7	65.0	114.3	135.9
Cluster II		26.9	121.1	56.2	236.2	48.9	110.3	75.6	130.2
Cluster III			18.4	141.5	73.8	108.3	156.9	194.8	235.9
Cluster IV				28.7	282.6	92.1	153.2	57.6	159.0
Cluster V					19.3	253.2	132.4	252.6	226.5
Cluster VI						39.6	181.4	161.7	232.5
Cluster VII							0	62.7	66.4
Cluster VIII								0	46.1
Cluster IX									0

Table 4: Cluster mean for yield and its component characters

Cluster Means for irrigated situation							
	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of capsules per plant	Number of seeds per plant	1000 seed weight (g)	Seed yield per plant (g)
Cluster I	59.9	121.5	52.9	35.9	6.9	5.4	4.0
Cluster II	60.3	113.0	54.5	46.3	7.6	5.4	3.4
Cluster III	55.1	122.7	53.4	33.6	6.9	5.4	3.4
Cluster IV	59.4	112.4	53.6	32.4	6.6	5.7	3.3
Cluster V	59.8	128.3	52.8	36.3	6.3	5.5	3.7
Cluster VI	55.9	113.5	52.8	63.8	8.0	5.5	3.2
Cluster VII	66.3	119.7	48.1	44.9	7.0	5.8	4.9
Cluster VIII	66.7	114.3	54.4	28.1	6.7	5.6	3.7
Cluster IX	71.0	118.0	59.9	11.0	7.7	5.6	2.8

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