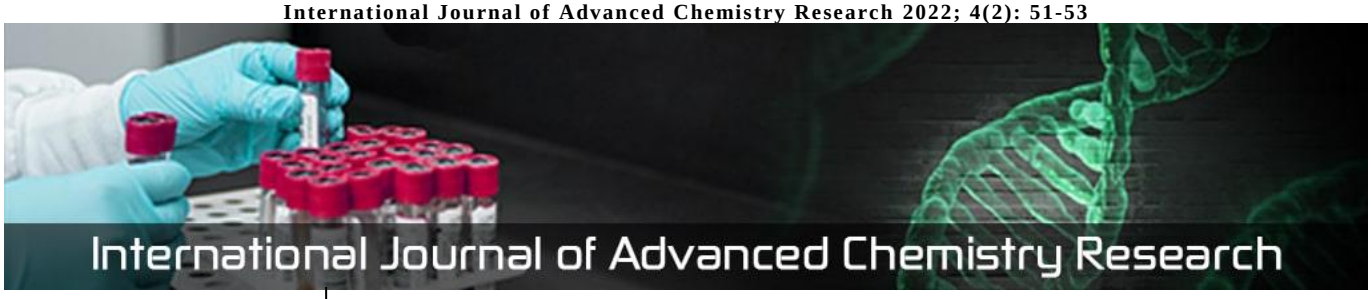

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Genetic diversity in golden flax (*Linum usitatisimum* L.) for Irrigated Situation

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Abstract
Collection and evaluation of divergence among genotypes are fundamental for know the spectrum of diversity. An experiment was conducted 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 during *Rabi* season 2019-20 and 2020-21 comprising 40 accessions including checks *viz;* golden flax (37) & brown flax (3) (checks RLC-143, RLC-148, RLC-153 and Surabhi) were shown in irrigated situation. 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 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 the accessible genotypes has an enormous significance and in line with quick need in the choice of guardians to be utilized in hybridization program for getting helpful hereditary recombination. It is difficult for the breeder to select most suitable genetically diverse parents for successful hybridization programme unless provides necessary information on genetic variation and genetic divergence present in the available genetic material. The more diverse the parents are more the chances of pronounced heterotic effects and increased spectrum of variability in the segregating generations. Mahalanobis D^2 statistic is a powerful tool used to quantify the degree of genetic divergence between the genotypes and relate clustering pattern with the geographic origin. The hereditary distance played an unmistakable part to play for productive selection of guardians for hybridization programme. Hence, utilization of prominent genotypes falling in distant clusters into breeding programme may lead to development of potential genotypes having broadened genetic base.

2. Material and Methods
The investigation was conducted on 40 golden flax 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 during *Rabi* season 2019-20 and 2020-21. 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), Ankit *et al.* (2019) [2], Tyagi *et al.* (2015) [13], Abdul & Mulani (2015) [1], Dikshit & Sivaraj (2015) [4]; Kumar *et al.* (2015) [13]. The D^2 values of the genotypes and clustering pattern indicates the material is highly diverse.

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 hence, showed zero value for intra cluster distance. 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, recommending the presence of high inconstancy in hereditary make-up of genotypes remembered for these groups. The highest inter cluster divergence was recorded between genotypes of cluster VI & cluster V. Crossing between the genotypes of these most unique clusters might prompt greatest recombinant/sergeants in the material. High heterotic combinations will get when genotypes of these distinctly placed clusters were crossed would give high heterosis/heterotic sergeants. Inter cluster distance was lowest between cluster I & cluster III, indicating existence of closer proximity between these clusters. 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 correlation 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.

D^2 statistics was originally developed by P.C. Mahalanobis in 1928. This is one of the potent techniques of measuring genetic divergence. In plant breeding, genetic diversity play an important role because hybrid between lines of diverse origin, display a greater heterosis than those between closely related parents. Genetic diversity arises due to geoghraphical separation or due to genetic barriers to crossability. These findings confirm in earlier studies of Gulla *et al.* (2021), 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) [13].

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 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. Crossing between the genotypes of these most divergent clusters may lead to maximum 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

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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