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STUDY ON GENETIC DIVERGENCE IN LINSEED (*LINUM USITATISSIMUM* L.) GERMPLASM BASED ON MORPHOLOGICAL AND QUALITY TRAITS

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ABSTRACT

One hundred sixty Linseed accessions were evaluated for phenotypic variability, heritability, genetic advance and diversity. Analysis of variance revealed significant difference among genotypes for all the twelve characters studied. High heritability combined with high genetic advance was recorded for capsule/plant indicating that this character is controlled by additive gene effect and phenotypic selection of this character would be effective for further breeding purpose. Non-hierarchical Euclidean cluster analysis grouped germplasm into thirteen different clusters. Maximum inter cluster distance was observed between cluster XI and cluster IX (913.221) followed by clusters IX and IV (869.117) while, lowest divergence was noticed between cluster II and I (103.402). Among the twelve characters studied, Capsules/plant contributed highest towards genetic divergence (35.76%), followed by plant height (26.84%). Cluster XI exhibited highest means for days to 50% flowering (90.97), plant height (65.778), test weight (8.686) and biological yield (16.123). Cluster IX exhibited lowest means for plant height (35.592), harvest index (17.256), and test weight (6.680). Greater genetic divergence was found between XI and IX followed by clusters IX and IV indicating superior and novel recombinants and explore the fullest range of variability for the characters and to realize good recombinant can be released by mating between the lines of these clusters in a definite fashion.

INTRODUCTION

Linseed or flax (*Linum usitatissimum*) is a diploid (2n = 30), self pollinated annual plant (Ragupathy *et al.*, 2011). It has been under cultivation for its seed oil (linseed) or stem fibers (flax) or both (dual purpose) for 1000 years (Dillman, 1953; Zohary, 1999). Globally, the important flaxseed–linseed cultivating and producing countries include Canada, India, China, the United Kingdom, Ethiopia, and the United States of America. In India, it is mainly grown as an industrial oil seed crop in marginal soils and rainfed conditions. Linseed is an important industrial crop plant as its oil with high linolenic acid content (45-65%) is used for manufacturing rapidly drying paints, stains, inks, varnishes and the polymer linoleum (Rowland, 1998). Besides its oil, the linseed fibers (phloem fiber) are used by industries for producing high quality linen fabrics, pulp, biofuel (Diederichsen and Ulrich, 2009), raw materials of thermal insulations (Kymalainen and Sjoberg, 2008) and bioplastics (Kwiatkowska *et al.*, 2009). However, the high level of linolenic acid in the oil causes it to be unsuitable for use in edible products because of undesirable odour and flavour that result from the auto-oxidation of this unsaturated fatty acid (Green, 1986). Efforts have been made to develop edible purpose linseed by reducing the level of linolenic acid content to <5%. Before embarking any plant breeding programme a plant breeder must survey and assess the variability with respect to yield and its components. Information on genetic variability and heritability is useful to formulate selection criteria for improvement of seed yield. Burton (1952) and Johnson *et al.* (1955) found that it is more useful to estimate heritability value along with genetic advance value in predicting the expected progress to be achieved through selection.

The importance of genetic diversity of parents in a hybridization programme has been emphasized as the crosses involving genetically diverse parents are likely to produce not only high heterotic effects but also desirable transgressive segregants in the later segregating generations. Several workers emphasized the need of parental diversity in optimum magnitude to obtain superior genotypes in the segregating generations (Ramakant *et al.,* 2011; Srivastava *et al.,* 2009 and Tyagi *et al.,* 2015). Genetic diversity arises due to either geographical separation, crossability barriers or due to different patterns of evolution. The present study was conducted with an objective to select the diverse parents for further use in linseed breeding programme.

MATERIALS AND METHODS

One hundred sixty seeded germplasm accessions planted in Augmented Block Design with three checks were studied during winter (rabi) 2010 at Genetics and plant Breeding Research farm of N.D. University of Agriculture and Technology, Faizabad, India. The entire experimental field was divided into 8 blocks of equal size and each block had 23 plots. The checks were distributed in each block. Each plot consisted of single row of 5 meter length spaced 30 cm apart with plant to plant distance of 10 cm. All the recommended cultural practices were followed to raise a good crop. Observations were recorded on five random selected plants from each line for 12 quantitative characters. Differences between genotypes for different characters were tested for significance using analysis of variance. Genotypic coefficient of variation, phenotypic coefficient of variation, heritability (broad sense) and genetic advance was measured by Burton (1968) and Hanson *et al.*, 1956 method. Genetic divergence among diverse genotypes was studied through Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) and genotypes were grouped into different clusters by Toucher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance pertaining to twelve quantitative traits of linseed showed significant differences for all the quantitative traits studied, indicating the considerable amount of variation among the genotypes. The variation of different traits under study revealed the measure of free variability in the population of different genotypes, which would reflect the unforeseen impact of potential variability on yield. The traits seed yield per plant followed by number of secondary branches, and harvest index showed high PCV and GCV estimates. High coefficient of variation for seed yield per plant and number of secondary branches per plant (Kanwar *et al.,* 2014) and seed yield(Tewari *et al.,* 2012, Chauhan *et al.*, 2012 and Nagaraja *et al.*, 2009**)** has also been reported. Hence, these characters can be relied upon and simple selection can be practiced for further improvement. The estimates of genotypic and phenotypic coefficient of variations were moderate for plant height, number of primary branches, capsules/plant, seed/ capsule, biological yield and test weight (Nagaraja *et al.*, 2009) has also reported more or less similar results. Variations for days to 50% flowering, days to maturity and oil content indicated low estimates of genotypic and phenotypic coefficient of variations (Table 1).

Heritability in broad sense estimates were highest for days to maturity, days to 50% flowering, plant height and capsules/ plant. The estimates were moderate for number of secondary branches, biological yield/ plant, harvest index and oil content. Estimates were low for seed yield/plant, 1000 seed weight, seed/ capsule, number of primary branches (Table 1). Genetic advance as per cent of mean (GA) is more reliable index for understanding the effectiveness of selection in improving the traits because the estimates are derived by involvement of heritability, phenotypic standard deviation and intensity of selection. Thus, genetic advance along with heritability provides clear picture regarding the effectiveness of selection for improving the plant characters. As presented in Table 1, the estimate of genetic advance were recorded highest for seed yield per plant (73.89) followed by number of secondary branches (61.73) and harvest index (58.20); moderate for capsule/plant (39.88), seed/capsule (32.06), 1000 seed weight

Table 1: Parameters of genetic variability for morphological and quality traits of linseed

S.no.	Character	Range minimum	Maximum	Mean	GCV(%)	PCV (%)	h2 (bs)(%)	GA as %of mean
1	50 % F	69.08	94.42	82.32	4.376	5.120	82.29	9.873
2	DM	123.5	139.83	132.24	2.101	2.340	132.19	5.36
3	PH	31.17	69.24	53.08	11.07	13.87	53.03	23.31
4	No. of Primary Branches	2.40	4.608	3.45	12.457	14.22	3.44	28.79
5	No. of Secondary Branches	9.64	28.77	19.98	24.03	24.69	19.89	61.73
6	Capsule/Plant	29.59	68.79	50.31	15.56	16.03	50.21	39.88
7	Seed/Capsule	5.23	9.97	7.85	12.191	12.235	7.83	32.069
8	Biological yield/plant	8.86	16.74	13.42	11.64	12.55	13.40	28.52
9	Harvest Index	1.42	5.72	3.04	22.86	23.71	22.47	58.20
10	1000 seed wt.	10.58	39.53	22.57	11.50	11.56	7.61	30.18
11	Oil Content %	4.79	10.25	7.62	5.47	5.61	35.60	14.08
12	Seed yield/ plant	32.06	40.56	35.64	28.36	28.74	3.02	73.89

Table 2: Estimates of average intra and inter- cluster distances for the 13 clusters in linseed

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	60.368	103.402	258.086	176.082	310.689	373.214	155.541	179.246	446.139	169.061	395.879	334.133	376.545
II		72.218	164.157	157.916	379.353	452.021	163.569	272.068	449.118	196.096	396.412	309.937	364.080
III			51.738	111.608	707.554	696.295	388.343	618.807	843.817	280.904	297.602	482.579	444.586
IV				78.088	693.379	702.723	392.261	504.693	869.117	291.112	348.937	554.251	544.355
V					70.334	113.332	128.159	171.674	176.352	235.576	591.971	180.174	243.739
VI						42.616	183.377	276.721	327.320	168.939	378.398	143.288	135.171
VII							61.935	152.988	198.332	140.579	423.612	154.319	204.625
VIII								103.127	271.622	276.965	647.548	300.565	428.526
IX									83.270	440.599	913.221	325.655	430.618
X										66.682	168.175	167.280	127.819
XI											65.743	338.878	219.775
XII												52.273	129.200
XIII													73.973

Table 3: Cluster mean of 13 Cluster for different characters in linseed

Cluster no.	Days to 50% flowering	Days to Maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Capsules / plant	Seeds / capsules	Biological yield / plant	Harvest index (%)	Test weight (g)	Oil content (%)	Seed yield / plant
I	77.176	130.130	55.598	3.516	23.929	55.429	8.016	14.032	23.638	7.657	35.444	3.265
II	80.599	134.008	53.131	3.293	24.765	56.313	8.295	13.717	27.594	8.112	35.043	3.773
III	86.052	137.109	59.443	4.073	26.041	63.749	8.573	15.483	29.791	8.473	36.686	4.615
IV	81.179	132.000	60.854	4.208	26.880	63.782	8.558	15.339	29.708	8.291	35.627	4.527
V	80.208	131.792	50.177	3.350	18.550	38.842	6.963	12.023	15.754	7.006	37.243	1.867
VI	84.131	130.333	55.377	3.170	13.308	40.782	6.844	12.885	16.458	7.393	35.733	2.113
VII	81.583	132.875	50.019	3.347	20.161	47.861	7.449	12.389	21.403	7.477	34.677	2.638
VIII	73.972	128.389	50.679	3.364	20.545	43.903	8.260	12.423	21.634	7.411	35.260	2.660
IX	81.506	132.100	35.592	3.275	17.273	44.467	7.637	12.893	17.256	6.680	35.283	2.230
X	85.053	131.379	58.357	3.590	18.545	51.913	7.777	14.247	21.528	7.590	35.571	3.065
XI	90.972	130.722	65.778	3.653	15.419	56.925	8.516	16.123	26.294	8.686	34.809	4.209
XII	86.125	133.750	53.479	3.092	13.967	43.033	8.927	10.752	27.399	7.742	37.601	2.951
XIII	90.083	134.189	56.050	3.271	14.677	47.996	7.540	13.750	19.905	7.567	36.274	2.734

Table 4: Contribution of different characters towards genetic divergence (D2) in linseed germplasm

Source	Times Ranked 1st	Contribution %
1 Days to 50% flowering	1928	14.60
2 Days to maturity	266	2.01
3 Plant height (cm)	3544	26.84
4 Primary branches/ plant	0	0.00
5 Secondary branches/ plant	1022	7.74
6 Capsules/ plant	4722	35.76
7 Seed/Capsule	0	0.00
8 Biological yield/ plant	16	0.12
9 Harvest index (%)	1635	12.38
10 Test weight (g)	0	0.00
11 Oil content (%)	70	0.53
12 Seed yield/ plant (g)	0	0.00

(30.18), number of primary branches (28.79), biological yield/ plant (28.52) and plant height (23.31); and low for oil content (14.08),days to 50% flowering (9.87) and days to maturity (5.36). Noor *et al.* (2004) had cautioned that high heritability per se is no index of high genetic gain hence should be accompanied by high genetic advance.High heritability accompanied with high genetic advance recorded for capsule/ plant indicated lesser influence of environment in expression of these characters and that these characters are controlled by additive gene effect, hence, amenable for simple selection.Similar results were reported by Kanwar *et al.* (2014), Chauhan *et al.* (2012)**.**High heritability accompanied with low genetic advance recorded for days to maturity and days to 50% flowering. It is indicative of non- additive gene action, the high heritability is being exhibited due to favourable influence of environment rather than genotype and selection for such traits may not be rewarding. Similar results were reported by Tahira *et al.* (2013). Low heritability and high genetic advance is recorded for seed yield/plant, harvest index and number of secondary branches. It reveals that characters are governed by additive gene affect. Low heritability is being exhibited due to high environmental effects. Selection may be effective in such case.Low heritability accompanied with low genetic advance was observed for oil content. Which may be due to non additive gene action, indicating characters is highly influenced by environment effects and selection would be ineffective.

Genetic divergence

Genetic divergence among 160 linseed germplasm lines was determined for seed yield, its attributing characters and quality trait. The significant estimates of 'V' statistics during the analysis revealed significant differences among mean values of different correlated variables, thus analysis of genetic divergence among the tested linseed germplasm was considered to be relevant.

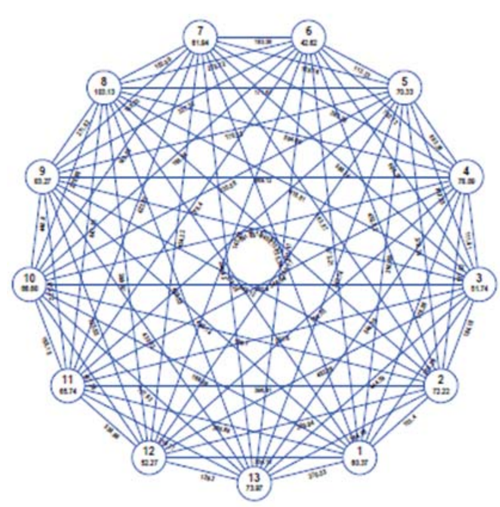
Non-hierarchical Euclidean cluster analysis based on agro morphological traits allocated the 160 linseed germplasm into thirteen clusters (Fig. 1). Critical assessment of clusters showed that clusters were heterogeneous within themselves and between each other based on major character relations. The composition of clusters and values of inter and intra clusters distances are given in tables 2 and 3, respectively. The results revealed that the inter cluster distance in most cases was larger than intra cluster distance suggesting wider diversity among the germplasm of different groups. Cluster VII possessed the maximum number of 24 genotypesfollowed by cluster I (18), cluster II (16), cluster IX and cluster XIII possessed (15) genotype each followed by cluster IV and VI having (14) genotypes, followed by cluster X (11) genotypes, cluster VIII (9) genotypes, cluster III, V and XII (8) genotypes, Cluster XI (3) possessed minimum number of genotypes in such a way that germplasm lines having minimum genetic distance were grouped in same cluster and *vice versa*. The range of inter and intra cluster distance was 103.40 to 913.22 and 42.61 to 103.12, respectively (Table 2). The maximum inter cluster distance

Table 5: Principal Component Analysis of linseed germplasm character

Characters	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector	6 Vector
Days to 50% flowering	0.007	0.659	0.334	0.148	0.098	0.175
Days to maturity	0.127	0.462	0.028	0.517	-0.108	-0.476
Plant height (cm)	0.252	0.149	0.323	-0.526	0.085	0.091
Primary branches/ plant	0.238	-0.169	0.395	0.049	-0.338	-0.080
Secondary branches/ plant	0.319	-0.382	0.018	0.124	-0.086	-0.384
Capsules/ plant	0.409	-0.144	0.192	0.137	-0.042	-0.047
Seed/Capsule	0.266	0.027	-0.434	0.304	0.007	0.562
Biological yield/ plant (g)	0.281	-0.088	0.413	0.099	0.025	0.397
Harvest index (%)	0.401	0.108	-0.391	-0.052	0.063	-0.076
Test weight (g)	0.269	0.250	-0.175	-0.470	0.253	-0.289
Oil content (%)	0.012	0.221	-0.176	-0.269	-0.881	0.089
Seed yield/ plant (g)	0.459	0.052	-0.131	0.000	0.053	0.094

was found between clusters XI and IX (913.22), followed by clusters IX and IV (869.11), inter cluster distance between cluster IX and III (843.81) and cluster V and III (707.554) were also of high order. The minimum inter cluster distance was recorded between clusters II and I (103.40) followed by clusters III and IV (111.60) and clusters V and VI (113.33). The highest intra cluster distance was observed for cluster VIII (103.127). It indicates that the germplasm lines of cluster VIII were more diverged than any other cluster. This was also reflected in the scatter diagram. The germplasm lines belonging to the distant clusters could be used in hybridization programme for obtaining a wider range of variability. Similar observation made by Shekhawat*et.al*. (2014). Cluster means of germplasm for 12 characters in linseed (Table 3) revealed that cluster XI had maximum days to 50% flowering, plant height test weight and biological yield. Cluster IX reported to be early maturing average plant type, exhibited lowest means for plant height, harvest index, and 1000 seed weight. These clusters can be preferred in selecting germplasm lines for respective traits as they recorded good means. Clustering of germplasm was not associated with the geographical distribution and was mainly grouped due to their morphological differences. Thus, showing evidence that geographical isolation is not the only factor causing genetic diversity in linseed. Similarly, the forces other than geographical origin such as genetic drift, natural and artificial selection, exchange of breeding material might have played an important role in the fixation of diversity among the germplasm lines. A few ecological conditions could also direct the gene flow between populations from diverse geographical origins. The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times, each of the yield component character appeared first in rank and its respective per cent of contribution towards genetic divergence was presented in Table 4. The results showed that Capsules/plant (35.76 %) contributed highest towards genetic divergence by taking 4722 times first rank, followed by plant height (26.84 %) by 3544 times, days to 50 % flowering (14.60 %) by 1928 times, harvest index (12.38 %) by 1635 times, secondary branches/ plant (7.74 %) by 1022 times and days to maturity (2.01 %) by 226 times. These results are in agreement with those given by Solanki and Gupta (2003) for capsule/plant and plant height, Tripathi *et al*. (2013) for days to 50% flowering and secondary branches per plant. It indicates that these characters contribute towards the genetic divergence in the present germplasm lines. On the other hand, number of primary branches, seed/capsule, test weight and seed yield/ plant has negligible contribution of these characters towards the genetic divergence.

Principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998). The eigen values were often used to determine how many factors to retain. When the principal component analysis was run on correlations, one rule of thumb is to retain those factors whose eigenvalues are greater than one. Principle component analysis was also conducted and presented in Table 5. It showed association in PC1 with seed yield/plant, number of capsule/plant, harvest index and number of secondary branches, PC2 with days to 50% flowering, PC3 with biological yield/ plant, number of primary branches and plant height, PC4 with days to maturity, PC5 with test weight, PC6 with number of seed/ capsule. Thus, re-structuring plant type with more number of capsule/ plant, harvest index, more number of secondary branches, early flowering, biological yield/plant and more seed/capsule would



Euclidean^2 Distance (Not on Scale)

Figure 1: Diagram showing intra and inter cluster distances among XIII clusters

obviously generate plants with high seed yield.

The results indicated that the germplasm lines studied had a considerable level of variability that could be exploited in future breeding programs. Hybridization between genetically diverse genotypes in linseed to generate promising breeding material has been suggested by Ananda and Murty, (1968). Greater genetic divergence was found between clusters XI and IX followed by clusters IX and IV indicating that superior hybrids or recombinants can be realized by mating between the lines of these clusters in a definite fashion. Crossing between germplasms belonging to the same cluster might not be expected to yield desirable segregates. Further research on these selected germplasm will save a lot of time for the breeder in future. Morpho-agronomic traits have some shortcomings in evaluating genetic diversity as these are phenotypic markers and genetically distant germplasm may be morphologically similar. Further research should be done with molecular markers which can be used to determine genetic distance easily and successfully. DNA markers should provide more accurate measures of genetic similarity.

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AWARDS OF THE ASSOCIATION

The Association in its Seminars and Conferences provides the following category of awards on annual basis.

1. **The young scientists award** : It is given to the researchers below the age of 35 years.
2. **The senior scientists award** : It is awarded to the academicians above the age of 35 years.
3. **The best paper award**: It is awarded to the contributor of the Journal **The Bioscan** during the year.
4. **The best paper presentation award** : It is awarded to the scholar whose presentation is the best other than the young scientist category.
5. **The best oration award** : It is awarded to the scholar who delivered invited speech.
6. **The recognition award** : It is awarded to those senior scholars who have contributed to the subject through their continued research .
7. **The environmental awareness award** : It is awarded to those who, apart from their research contribution, have done commendable extension work for environmental betterment.

The number of recipients of award in each category will vary depending upon the recommendation of the panel of judges and the executive committee. The association has the provision to institute awards in the name of persons for whom a with desired sum is donated in consultation with the executive body.

PUBLICATION OF THE ASSOCIATION

In order to provide a platform to a vast group of researchers to express their views and finding of research as well as to promote the attitude of quality research among the scholars of younger generation the association publishes an international quarterly journal – **THE BIOSCAN (ISSN:0973-7049).** For the benefit of the potential contributors **instructions to authors** is given separately in this journal. However, the details regarding the journal and also the association can be seen on our website *www.thebioscan.in.*

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