

# EVALUATION OF GENETIC DIVERGENCE IN INDIAN FLAX (*LINUM USITATISSIMUM* L.)

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## ABSTRACT

An experiment with forty eight genotypes of flax carried out to study the nature and magnitude of divergence using Mahalanobis  $D^2$  statistics, in randomized block design with three replication. The data for ten important quantitative traits recorded from the genotypes raised. The variability study indicated high to moderate phenotypic and genotypic coefficient of variation accompanied by high heritability and genetic advance as per cent of mean for traits, days to 50 per cent flowering, plant height and number of capsules per plant. The major character seed yield per plant possesses high heritability with high genetic advance, indicating their importance in selection for yield improvement. The 48 genotypes of flax were grouped into five clusters using Tocher's method. Cluster IV comprising is the most divergent cluster. The genotypes in cluster III and cluster V, exhibited high degree of genetic diversity. Cluster III was suitable for seed yield per plant, number of capsules per plant, number of primary branches per plant and number of secondary branches per plant. Days to 50 per cent flowering and oil content contributed maximum towards genetic divergence.

## INTRODUCTION

Flax (*Linum usitatissimum* L.) belongs to the genus *Linum* of the family Linaceae commonly known as "Alsi" and has  $2n = 30$  chromosomes. Linseed is one of the important rabi oilseed crops of India, cultivated in light soil under one or two irrigation in Madhya Pradesh, Chhattisgarh, Uttar Pradesh, Maharashtra, Rajasthan, West Bengal, Karnataka, Orissa and Bihar (Pali and Mehta, 2014). Chhattisgarh is one of the important linseed growing states of India, which accounts for nearly 18.05% area and 15.21% production of country. In Chhattisgarh, linseed is grown on 81.54 thousand hectare area with a productivity of 409 kg/ha (Anonymous, 2014). Improvement in genetic architecture of any crop depends upon the nature and extent of genetic variability required to effect selection in any breeding material.

Yield components are the primary objectives under study for crop improvement as because Grafius (1978) suggested that there may not be genes for yield per se but rather for the various components, the multiplicative interactions of which result in the artifact of yield. In any program aimed at genetic amelioration of yield, genetic diversity is the basic requirement. Effective hybridization program between genetically diverse parents will lead to considerable amount of heterotic response in  $F_1$  hybrids and broad spectrum of variability in segregating generations (Parhe *et al.*, 2014). Mahalanobis's  $D^2$  statistics is a powerful tool in quantifying the degree of variability at the genotype level. The utility of multivariate analysis have greatly been emphasized (Murty and Arunachalam, 1966). Several workers studied the genetic diversity, clustering pattern, relative contribution of different characters toward divergence and effectiveness of selection (Venkateswarlu, 2001; Manivannan

*et al.*, 2002; Patil *et al.*, 2003; Bisht *et al.*, 2005). So, the present experiment was formulated to study the genetic divergence and clustering pattern of the flax genotypes for selection of suitable parents for utilizing in hybridization programme and to study the genetic parameters attributing to yield.

For realizing genetic diversity among the parents with their direct and indirect effects of different traits on seed yield and selection of best diverse parents for flax breeding programme at IGKV, Raipur present investigation was undertaken.

## MATERIALS AND METHODS

The experimental material comprising forty eight genotypes of flax (Table 1) was grown during Rabi 2012-13 in a Randomized Block Design with three replication at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, AICRP on Linseed, I.G.K.V., Raipur. Data were recorded on five randomly tagged plants for viz., days to 50 % flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, number of seeds per capsule, 1000-seed weight, oil content and seed yield per plant. Wilks (1932) criteria were used to test the significance differences in mean values of all the ten characters. Statistical analysis: Mahalanobis (1936) defined the distance between two populations as  $D^2$ , which was obtained by Tochers method, described by Rao (1952). Contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1985). Grouping of variety into various clusters was done and average intra and inter cluster distance were estimated.

The experimental data was analyzed statistically by the method of analysis of variance for single factor (Gomez and Gomez, 1984) and lastly to find out the significance mean difference between varieties of different genetic parameters were estimated. Analysis of variance was performed to test the significance of difference among the genotypes for the characters studied, as suggested by Panse and Sukhatme (1957). Genetic variability parameters were estimated by the method proposed by Johnson *et al.* (1955).

## RESULTS AND DISCUSSION

In the present investigation, 48 diverse genotypes of flax (Table 1) were studied to assess their yield and yield related attributing characters. The analysis of variance clearly indicated that there was highly significant variation among the genotypes for all the traits studied. This in turn indicated that there was sufficient variability in the material studied, which could be utilized in further breeding programme. Similarly, Many earlier workers Bhatia *et al.* (2001), Varshney *et al.* (1995), Gupta *et al.* (1999), Mishra and Yadav (1999) and Verma (1999) reported

high variability for different traits in flax. Thus, it is implied that there was reasonably sufficient variability in material used for their study, which provides ample scope for selecting superior and desire genotypes by the plant breeder for further improvement.

The phenotypic variances (Table 2) for all the traits under studied were higher than the genotypic variances (Payasi *et al.*, 2000). This may be due to the non-genetic factor which played an important role in the manifestation of these characters. Wide ranges of variance (phenotypic and genotypic) were observed in the experimental material for all the characters under investigation. Comparison of relative magnitude of genotypic coefficient of variation for parental population revealed that maximum amount of genetic variability was present for seed yield plant per plant. High amount of genotypic coefficient of variation was possessed by seed yield per plant, number of primary branches per plant, number of capsules per plant and number of secondary branches per plant. These findings were in accordance of Bhatia *et al.* (2001) and Varshney *et al.* (1995) reported seed

**Table 1: List of 48 genotypes and their source of collection**

S. No	Genotypes	Source	S. No.	Genotypes	Source
1.	Kiran	Raipur, India	25.	GS-64	Gurdaspur, India
2.	Deepika	Raipur, India	26.	GS-129	Gurdaspur, India
3.	Kartika	Raipur, India	27.	RLC-92	Raipur, India
4.	Indira Alsi-32	Raipur, India	28.	RLC-94	Raipur, India
5.	Shekhar	Kanpur, India	29.	RLC-122	Raipur, India
6.	Neela	Berhampore, India	30.	RLC-123	Raipur, India
7.	Rashmi	Kanpur, India	31.	RLC-128	Raipur, India
8.	Sharda	Jhansi, India	32.	RLC-129	Raipur, India
9.	Meera	Kota, India	33.	RLC-132	Raipur, India
10.	PKDL-43	Pawarkheda, India	34.	RLC-133	Raipur, India
11.	PKDL-58	Pawarkheda, India	35.	RLC-134	Raipur, India
12.	PKDL-62	Pawarkheda, India	36.	RLC-135	Raipur, India
13.	JRF-5	Kanpur, India	37.	RLC-137	Raipur, India
14.	JLS-9	Jabalpur, India	38.	R-552	Raipur, India
15.	KL-1	Palampur, India	39.	CI-229	Ludhiana, India
16.	KL-168	Palampur, India	40.	NL-97	Nagpur, India
17.	GS-27	Gurdaspur, India	41.	Polf-22	Poland, Europe
18.	GS-61	Gurdaspur, India	42.	T-397	Kanpur, India
19.	LC-54	Ludhiana, India	43.	R-4140	Raipur, India
20.	LCK-88068	Kanpur, India	44.	R-4141	Raipur, India
21.	FRW-12	France, Europe	45.	R-4152	Raipur, India
22.	Gcwargi 1-2	Kanpur, India	46.	R-4154	Raipur, India
23.	R-2678	Raipur, India	47.	R-4158	Raipur, India
24.	R-4129	Raipur, India	48.	R-4168	Raipur, India

**Table 2: Genetic parameters of variation for yield and its components in flax**

Characters	Mean	Range	PCV (%)	GCV (%)	Heritability bs (%)	Genetic advance (GA)	GA as % of mean
Days to 50% flowering	50.25	82 – 25	14.09	12.89	83.70	39.42	78.44
Days to maturity	116.36	135 – 108	3.51	3.33	89.89	7.57	6.50
Plant height (cm)	51.00	79 – 34	13.50	13.40	98.16	35.20	69.01
Number of primary branches plant <sup>-1</sup>	5.77	18 – 1	53.58	33.69	39.54	2.51	43.64
Number of secondary branches plant <sup>-1</sup>	17.5	46 – 4	48.08	29.10	36.64	6.35	36.30
Number of capsules plant <sup>-1</sup>	30.20	110 – 40	32.20	30.40	89.13	22.30	73.84
Number of seeds capsule <sup>-1</sup>	5.65	9.9 – 5.7	10.00	6.30	39.29	1.68	29.73
1000 seed weight	6.50	9.1 – 3.6	14.00	12.30	77.14	1.47	22.61
Seed yield plant <sup>-1</sup> (g)	6.55	13.34 – 6.11	38.00	36.30	91.05	4.28	65.34
Oil content %	38.41	42.68 – 33	4.56	4.42	94.14	16.40	42.69

**Table 3: Distribution of 48 flax genotypes into different clusters**

Clusters No.	No. of genotypes	Name of the genotypes
I	7	Deepika, Kartika, Indira Alsi-32, Shekhar, T-397, RLC-122, Polf-22
II	8	Rashmi, Sharda, JLS-9, GS-27, GS-61, GS-64, R-2678, LCK-88068
III	9	PKDL-62, GS-129, RLC-134, R-552, CI-229, NL-97, FRW-12, Gcwargi 1-2, R-4129
IV	15	Neela, PKDL-58, PKDL-43, JRF-5, KL-1, KL-168, RLC-123, RLC-128, RLC-129, RLC-135, RLC-137, LC-54, R-4152, R-4158, R-4168
V	9	Kiran, RLC-92, Meera, RLC-94, RLC-132, RLC-133, R-4140, R-4141, R-4154,

**Table 4: Average intra and inter-cluster D<sup>2</sup> value of 48 flax genotypes**

Clusters	I	II	III	IV	V
I	2.476	3.654	3.848	3.289	3.280
II		2.432	5.720	3.429	2.977
III			3.021	3.964	5.847
IV				3.039	3.401
V					2.314

yield per plant exhibiting the highest range and days to maturity showed the lowest range. In the present investigation, the genotypic and phenotypic coefficient of variation for seed yield per plant was found high. This result is in agreement with Gupta *et al.* (1999). The results showed that, seed yield per plant, number of primary branches per plant, number of secondary branches per plant and plant height exhibited very high GCV and PCV indicating the importance of this trait in evaluation and selection of the genotypes. In this study, the phenotypic and genotypic coefficient of variance was found moderate for plant height, days to 50 per cent flowering and 1000 seed weight. Similar results were also reported by Mishra and Yadav (1999) and Verma (1999). They found high GCV and PCV for respective traits. The genotypic and phenotypic coefficient of variation for days to maturity, oil content and number of seeds per capsule was found lowest. Bhatia *et al.* (2001) and Varshney *et al.* (1995) reported days to maturity exhibit the lowest GCV as well as PCV. These findings were clearly indicated that selecting genotypes through these traits will be effective. It is interesting to note that the differences between GCV and PCV values were minimum implying least influence of environment and additive gene effects indicating genotypes can be improved and selected for these characters for improvement of yield. The coefficient of variation indicated the extent of variability present in these characters and does not indicate the heritable portion. This could be ascertained from the heritability estimates, which in broad sense include both additive and non-additive gene effects and in narrow sense include the portion of heritable variation which is due to additive component (Lush, 1940). The knowledge of heritability is helpful in assessing merits and demerits of a particular trait as it enables the plant breeder to decide the course of selection procedure to be followed under a given situation.

In this study, heritability in broad sense for all the characters namely, seed yield per plant, days to 50 per cent flowering, plant height and number of capsules per plant were found high. High heritability value for these traits indicated that the variation observed was mainly under genetic control and was less influence by environment. So, these traits may be used as a selection criteria for yield improvement in confirmation with

the result of earlier workers viz. Mirza *et al.* (1996) and Mishra and Yadav (1999) and Lush (1940). In the present investigation, the characters, namely seed yield per plant, days to 50 per cent flowering, plant height, number of capsules per plant, number of primary branches per plant and number of secondary branches per plant have high heritability and genetic advance as per cent of mean. Hence, direct selection can be done through these characters for future improvement of genotypes for higher seed yield. Similar results were also reported by earlier workers Mirza *et al.* (1996), Mishra and Yadav (1999), Singh (2001). The high heritability associated with high genetic advance indicated, the variation was mostly due to additive gene effects. It indicates that if these characters are subjected to any selection scheme for exploiting fixable genetic variance, a wide adopted genotype can be developed. Plant height and days to maturity exhibited high heritability and moderate genetic advance as per cent of mean. These traits indicated that their manifestation is governed by both additive and non-additive genetic effects and therefore, selection should be practiced in later segregating generations i.e. by hybridization programme to exploit heritability. These findings were in accordance with Nandani *et al.* (2010).

Success of any crop improvement programmes mainly depends on amount of diversity available in the crop. The genotypes belonging to diverse ecological regions clustered together, while those of same region entered separate groups. In the present investigation, 48 genotypes were grouped into five clusters on the basis of D<sup>2</sup> statistics (Table 3). On the basis of inter or intra-cluster distances (Table 4) of 48 flax genotypes were obtained. Cluster IV was the biggest with 15 genotypes followed by cluster III and V with 9 genotypes each, cluster II contains 8 genotypes, while the lowest entries was found in the cluster I contains 7 genotypes (Table 3). The average D<sup>2</sup> values ranged from 2.314 to 5.847. Intra cluster distances exhibited a range of 2.314 to 3.039 and inter cluster distance ranged from 2.977 to 5.847 (Table 4). From the present investigation, it was clear that cluster IV comprising is the most divergent cluster. Cluster III showed maximum inter cluster distance with cluster V. Therefore, it can be concluded that the genotypes present in these clusters can be utilized for successful hybridization programme.

Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the first rank (Table 5). It has been observed that 50 per cent flowering was highest contributor towards divergence followed by oil content, plant height, days to maturity, seed yield per plant and plant height. While, number of secondary branches per plant was the least contributor towards total divergence. Therefore, these characters should be given importance during hybridization

**Table 5: Cluster means and percent contribution for yield and its components in 48 flax genotypes**

Clusters	I	II	III	IV	V	Contribution (%)
Days to 50 % flowering	52.14	51.08	58.89	61.13	49.04	41.22
Days to maturity	113.83	114.17	115.89	117.22	119.37	13.21
Plant height	63.38	49.42	61.48	59.11	60.0	2.48
Number of primary branches plant <sup>1</sup>	5.71	4.83	8.56	6.20	3.30	1.24
Number of secondary branches plant <sup>1</sup>	16.19	13.54	27.22	17.67	12.04	0.09
Number of capsules plant <sup>1</sup>	92.33	64.88	168.96	86.64	70.81	0.00
Number of seeds capsule <sup>1</sup>	8.36	6.85	8.07	7.80	8.23	0.71
1000 seed weight	6.10	6.50	5.91	5.80	7.06	1.6
Oil content	40.22	38.55	37.76	37.66	38.71	36.7
Seed yield plant <sup>1</sup>	11.10	6.03	13.82	7.13	5.91	2.75

and selection of segregating populations. Similar results were also obtained by Begum *et al.* (2007), Mahto (1999), Tadesse *et al.* (2009). Further, analysis of cluster means indicates diversity demonstrated by different clusters for a character. Based on the means, it is possible to know the character influencing divergence. The variation observed in cluster mean also points to the degree of variability (Verma, 1996, Golakia and Makna, 1992 and Verma, 1999). The cluster means from various characters are presented in (Table 5). The cluster III had the highest mean values for number of primary branches per plant (8.56), number of secondary branches per plant (27.22), number of capsules per plant (168.96), seed yield per plant (13.82), and genotypes in cluster I highest mean values for plant height (63.38), number of seeds per capsule (8.36), oil content (40.22) similarly, genotypes included in cluster V highest mean values for days to maturity (119.37), 1000 seed weight (7.06), whereas the cluster IV recorded highest mean values for days to 50 per cent flowering was (61.13). The genotypes included in these clusters may be utilized in future breeding programme to enhance the yield and its components.

Multivariate analysis based on D<sup>2</sup> analysis and canonical variational analysis has been considered as an important tool for quantifying genetic divergence in different crops (Rao, 1952). These analysis also provide a measurement of relative contribution of different components on diversity both at intra and inter-cluster level (Murthy and Quadri, 1996 and Somayajulu *et al.*, 1970). 48 genotypes of flax subjected to D<sup>2</sup> analysis for ten quantitative characters. Based on D<sup>2</sup> values five clusters were formed. Most of the genotypes derived from different crosses were grouped in single cluster (cluster V), indicating the similarity for the character studied in parental material. On contrary, the genotypes having similar pedigree were grouped in different clusters. It clearly demonstrated the impact of selection in increasing the genetic diversity. These results in conformity with the findings of Laxminarayana *et al.* (2004). The intra-cluster distance ranged from 3.039 to 2.314. It indicated wide range of diversity in terms of genetic distance (D<sup>2</sup> value). Thus it was evident that considerable amount of genetic divergence was present in material under study. Maximum inter-cluster distance was observed between cluster III and V (5.847) followed by cluster II and III (5.720) indicating maximum diversity between the genotypes of these clusters with respect to the traits considered. However, the lowest interaction distance was observed between cluster II and V (2.977) inferring the similarity for most of the characters among the genotypes of the respective clusters. Based on inter-cluster

distance and cluster means, it can be revealed that genotypes of the cluster III and V could be selected for hybridization programmes as they are expected to produce high heterotic crosses. The most diverse clusters among all clusters were cluster IV. Results indicated that inter crossing of genotypes from different clusters showing superior mean performance may help in obtaining high yield. The genotypes from above different cluster may be utilized as parents in crossing programme to isolate desirable segregants for yield traits. Selection of parents need not be necessary based on geographical diversity, the genetic diversity may prove more sound base for the purpose. Similar results were also observed by Chawala and Singh (1984), Mahto and Singh (1996) and Mahto and Verma (1998).

Based on the results obtained in present study, the major character seed yield per plant possesses high heritability with high genetic advance, indicating their importance in selection for yield improvement. From the diversity evaluation, it is advocated that the genotypes namely Neela, R-4158 followed by PKDL-43, RLC-137, KL-168 and R-4152 were identified as the most divergent genotypes for seed yield per plant. The cluster III (PKDL-62, GS-129, RLC-134, R-552, CI-229, NL-97, FRW-12, Gcwargi 1-2, R-4129) and cluster V (Kiran, RLC-92, Meera, RLC-94, RLC-132, RLC-133, R-4140, R-4141, R-4154) was most diverse to each other. Hence, crossing between these clusters would help to accumulate favorable and desirable alleles for further improvement in seed yield and its component in flax.

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## REFERENCES

- Anonymous.** 2014. Front line demonstration in oilseeds. *Annual Report Directorate of Oilseeds Research, Hyderabad.* pp.15-21.
- Arunachalam, V.** 1981. Genetic distance in plant breeding. *Indian J. Genet.* **4:** 226-236.
- Begum, H., Alam, A. K. M. M., Chowdhary, M. J. A. and Hossain, M. I.** 2007. Genetic divergence in linseed (*Linum usitatissimum* L.). *Int. J. Sustain. Crop Prod.* **2(1):** 04-06.
- Bhateria, S., Pathania, A., Sharma, J. K., Badiyala, D. and Bhandari,**

- J.C. 2001.** Combining ability for seed yield and its component in linseed (*Linum usitatissimum* L.) *J. Oilseeds Res.* **18(1)**: 44-47.
- Bisht, I. S., Bhat, K. V., Lakhanpaul, S., Latha, M., Jayan, P. K., Biswas, B. K. and Singh, A. K. 2005.** Diversity and genetic resources of wild vigna species in India. *Genet. Resource.Crop.Evol.* **52**: 53-68.
- Chawla, B.K. and Singh, P. 1984.** Genetic divergence in linseed. *J. Agric. Sci.* **54(4)**: 266-268.
- FAOSTAT data. 2006.** Food and Agriculture Organization of the United Nations, FAO Statistical Databases. <http://faostat.fao.org>.
- Flachowsky, G., Langbein, T., Bohme, H., Schneider, A. and Aulrich, K. 1997.** Effect of false flax expeller combined with short-term vitamin E supplementation in pigs feeding on the fatty acid pattern, vitamin E concentration and oxidative stability of various tissues. *J. Anim. Physiol. Anim. Nutr.* **78**: 187-195.
- Golakia, P. R. and Makne, V. G. 1992.** D<sup>2</sup> analysis in virginia runner groundnut genotypes. *Indian J. Genet.* **55(3)**: 252-256.
- Gomez, K. A. and Gomez, A. A. 1984.** Statistical Procedure for Agricultural Research. 2<sup>nd</sup> Edn. *J. Wiley and Sons, New York, ISBN-10*: 0471870927.
- Gupta, T. R., Pal, S. S. and Singh, I. 1999.** Parameters of genetic variability and correlation in linseed (*Linum usitatissimum* L.). *J. of Oilseeds Res.* **16(2)**: 213-215.
- Grafius, J. E. 1978.** Multiple characters and correlated response. *Crop. Sci.* **18**: 931-934.
- Johnson, H. W., Robinson, H. P. and Comstoc, R. E. 1955.** Estimation of genetic and environmental variability in soybeans. *Agron. J.* **47**: 314-318.
- Joshi, A. B. and Dhawan, N. L. 1986.** Genetic improvement of yield with special reference to self-fertilizing crops. *Indian J. Genet.* **26(A)**: 101-113.
- Khan, M. A., Mirza, M. Y., Amjad, M., Nawaz, N., Nawaz, M. S. and Baig, D. 2013.** Assessment of genetic diversity in germplasm of linseed (*Linum usitatissimum* L.). *Pakistan J. Agric. Res.* **26(3)**: 178-184.
- Laxminarayana, V. N., Sreedhar, N. and Prabhakaran, A. J. 2004.** Genetic divergence analysis in sunflower (*Helianthus annuus* L.). *J. Oilseeds Res.* **21(1)**: 162-164.
- Lush, J. L. 1940.** Intra sire correlation and regression of offspring on dam as a method of estimating heritability of characters. In: *Proc. American Animal Pro.* **33**: 292-301.
- Mahalanobis, P. C. 1936.** Study on the generalized distance in statistics. *Proc. Nat. Ins. Sci. India.* **2**: 49-55.
- Mahto, J. L. and Singh S. N. 1996.** Diversity studies in linseed. *J. Maharashtra Agric. Univ.* **21**: 341-344.
- Mahto, J. L. and Verma, A. K. 1998.** Genetic divergence in linseed. *J. Res. Birsa Agri. Univ.* **10**: 155-160.
- Mahto, J. L. 1999.** Correlation and genetic divergence in rainfed linseed. *Madras Agric. J.* **85(3/4)**: 154-157.
- Manivannan, N. 2002.** Genetic diversity in cross derivatives of green gram. *Legume Res.* **25**: 50-52.
- Mishra, A. K. and Yadav, L. N. 1999.** Genetic parameters and association analysis in linseed. *Indian J. Agric. Res.* **33(2)**: 113-118.
- Mirza, S. H., Dauloton, N., Islam, S. and Nersa, D. 1996.** Genetic studies of inter-relationship between seed yield and its components in linseed (*Linum usitatissimum* L.). *Bangladesh J. Botany.* **25(2)**: 197-201.
- Murthy, B. R. and Arunachalam, V. 1966.** The nature of divergence in relation to breeding systems in some crop plants. *Indian J. Genet.* **26A**: 188-198.
- Murthy, V. R. and Quadri, M. L. 1996.** Analysis of divergence in some self-compatible forms of *Brassica campestris* var. Brown sarson. *Indian J. Genet.* **26**: 45-48.
- Nandini, B., Ravishankar, C. R., Mahesha, B., Shailaja, H., Kalyana, M. K. N. 2010.** Study of correlation and path analysis in F<sub>2</sub> population of finger millet. *International J. Plant Sciences.* **5(2)**: 602-605.
- Nevo, E., Golenberg, E., Beilies, A., Brown, A. H. D. and Zohary, D. 1982.** Genetic diversity and environmental associations of wild wheat *Triticum diococcoides* in Israel. *Theor. Appl. Genet.* **62**: 241-254.
- Pali, V. and Mehta, N. 2014.** Combining ability and heterosis for seed yield and its attributes in linseed (*Linum usitatissimum* L.). *The Bioscan.* **9(2)**: 801-806.
- Panse, V. G. and Sukhatme, P. V. 1957.** Statistical methods for agricultural workers, ICAR, New Delhi, pp. 100-108.
- Parhe, D. S., Harer, P. N. and Nagawade, D. R. 2014.** Investigation of genetic divergence in chickpea (*Cicer arietinum* L.) genotypes. *The Bioscan.* **9(2)**: 879-882.
- Patil, B. L., Hegde, V. S. and Salimath, P. M. 2003.** Studies on genetic divergence over stress and non-stress environment in mung bean. *Indian J. Genet.* **63**: 77-78.
- Payasi, S. K., Bose, U. S. and Singh, A. K. 2000.** Pooled analysis of genetic parameters in linseed (*Linum usitatissimum* L.). *Adv. Plant Sci.* **13(2)**: 559-562.
- Rao, C. R. 1952.** Advanced statistics methods in biometry, John Wiley, New York, pp.357-369.
- Schuster, A. and Friedt, W. 1998.** Glucosinolate content and composition as parameters of quality of *Camelina* seed. *Industrial Crops and Products.* **7**: 297-302.
- Somayajulu, P. L. N., Joshi, A. B. and Murthy, R. R. 1970.** Combining ability in wheat. *Indian J. Genet.* **30**: 134-141.
- Singh, D. N. 2001.** Heritability and genetic advance in linseed (*Linum usitatissimum* L.). *J. Res. Birsa Agril. Univ.* **13(1)**: 73-74.
- Singh, R. K. and Choudhary, B. D. 1985.** Biometrical methods of quantitative genetic analysis. Haryana. *J. Hort. Sci.* **12**: 151-158.
- Tadesse, T., Singh, H. and Weyessa, B. 2009.** Genetic divergence in linseed germplasm. *J. Innov. Dev. Strategy.* **3(2)**: 13-20.
- Varshney, S. K., Sah, J. N. and Singh, O. N. 1995.** Variability and correlation in linseed. *J. Oilseeds Res.* **12(1)**: 17-19.
- Venkateswarlu, O. 2001.** Genetic variability in green gram (*Vigna radiata* (L.) Wilczek). *Legume Res.* **24(1)**: 69-70.
- Verma, O. P. 1996.** Genetic divergence in linseed (*Linum usitatissimum* L.). *J. Oilseeds Res.* **13(2)**: 225-228.
- Verma, V. D. 1999.** Genetic diversity in linseed. *Indian J. Plant Genet. Resour.* **12(1)**: 16-19.
- Wilks, S. S. 1932.** Certain generalization in the analysis of variance biometrics. **24**: 471-494.

