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# ESTIMATION OF PHENOTYPIC DIVERGENCE IN LINSEED (*LINUM USITATISSIMUM* L.) FOR YIELD-RELATED TRAITS UNDER CHANGED CLIMATE IN MID-HILLS OF NORTH-WEST HIMALAYAS

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*Key words*: *Linum usitatissimum*, Genetic diversity, Mahalanobis $D^2$-statistics

**Abstract**

Thirty two genotypes were analysed for nine morphological traits in RCBD replicated two times in two consecutive years (E-I, E-II) to investigate the genetic diversity pattern. Field data of two consecutive years were initially subjected to analysis of variance. There were highly significant ($p \leq 0.01$) differences among the genotypes for all the traits at both environments except for seeds per capsule, indicating the presence of adequate variability among the genotypes and the possibility to undertake cluster analysis. Moreover, genotypes responded differently to change in the environmental conditions at the two environments, as genotype × environment interaction mean squares were highly significant ($p \leq 0.01$) for all the traits. The phenotypic divergence and relative importance were estimated by multivariate analysis. The cluster analysis based on Tocher's method classified the genotypes into eight (E-I) and six (E-II) major groups of different sizes during both the years. The maximum distance was found between clusters V and VII (E-I) and between clusters IV and V (E-II). The genotypes from these clusters can be utilized for the improvement of linseed yield and obtaining good segregants in linseed breeding programs. In both the years, 1000-seed weight contribute maximum in E-I (93.55%) and E-II (91.33%) total genetic divergence between genotypes.

## Introduction

Flax *(Linum usitatissimum* L., 2n = *2x* = 30), is an annual self-pollinated crop which is commercially grown as a source of stem fibre and seed oil. The species is believed to have originated in either the Middle East or Indian regions (Vavilov 1951) and spread throughout Asia and Europe, prior to its introduction into the New World (Soto-Cerda *et al*. 2013). Fibre flax cultivars are taller and less branched and are grown in the cool-temperate regions of China, the Russian Federation and Western Europe (Soto-Cerda *et al*. 2013). Oilseed type flax plants (linseed) are more branched and shorter than the fibre type and are grown over a wider area in continental climate regions of Canada, India, China, the United States and Argentina (Soto-Cerda *et al*. 2013). Flax seed oil is utilized for the fabrication of various biodegradable products such as high quality drying oil, paints, varnishes and linoleum flooring. In addition, interest in flax oil and seeds as food products has increased due to their health benefits. Flax seeds contain relatively large amounts of α-linolenic acid, an omega-3 fatty acid, which is considered essential for human health. Despite huge benefits of linseed, it is grown only in 2.5 M ha of area in the world with annual production and productivity of 2.1 M tonnes and 827 kg/ha, respectively. India ranks second in terms of area (0.3 M ha) after Canada, but third in terms of production (0.2 M tonnes) after Canada and China, contributing about 14.89 per cent to world acreage and about 6.56 per cent to world production (Anon. 2013-14). In Himachal Pradesh total area under linseed is 0.0012 M ha with a total production of 0.00032 M tonnes with 270.0 kg/ha average productivity (Anon. 2013-14).

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Linseed being an important oilseed crop has a very low average productivity in India as well as in Himachal Pradesh because of many reasons such as, narrow genetic base of the available varieties, cultivation in marginal lands and due to biotic and abiotic stresses. Low yield of this crop is attributed to non availability of improved varieties to suit the diverse agro-climatic conditions. To overcome the poor yield levels, development of high yielding varieties becomes the top priority. Improvement in any crop depends on the availability of wide genetic diversity. Identification of promising genotypes is very useful during breeding from initial parent lines to the final variety release. Therefore, it is essential not only to conserve the genotypes but also to explore the gene-pool of linseed for breeding purposes of well adapted, better quality and high yielding varieties.

Cluster analysis had traditionally been used to distinguish the accessions from each other, their relationships and to get useful information on estimates of genetic diversity. In order to get transgressive segregation, genetic distance between parents is necessary (Joshi *et al.* 2004). Through higher genetic distance between parents, the higher heterosis in progeny can be observed (Ahmed *et al*. 2014). Initial diversity assessments in flax were carried out using morphological parameters (Bibi *et al.* 2013). Flax germplasm collections contain thousands of accessions of *L. usitatissimum* and related species, of which, subsets were assessed for the extent of genetic diversity for morphological characteristics (Sivaraj *et al*. 2012, Tyagi *et al.* 2014, Dikshita and Sivarajb 2015).

The present studies were thus planned to estimate genetic diversity in linseed germplasm using cluster analysis on the basis of morphological traits and to identify the best parent lines for using in future breeding programme.

## Materials and Methods

A total of 32 genotypes of linseed were used in the present study (Table 1). All the 32 genotypes, including three check, *viz.,* Bhagsu, Binwa and Baner, of linseed were raised at the experimental farm of the Department of Crop Improvement, CSK HPKV Palampur (H.P.), India, during two consecutive years of *rabi* season, 2010-11 (E-I) and 2011-12 (E-II), for recording the morphological data. At two environments, experimental layout was a randomized complete block design with two replications. Plot size was 1.90 $m^2$ (3 rows, 2.5 m long and 25 cm row spacing). Data were recorded on nine different quantitative traits namely, days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, capsules per plant, seeds per capsule, 1000-seed weight (g) and seed yield per plot (g). Five competitive plants were tagged randomly from each genotype in each replication for recording field observations for all the traits except for days to 50 per cent flowering, days to maturity and seed yield per plot, which was observed on plot basis during both years. The data recorded for each genotype at each environment were subjected to statistical analysis. ANOVA was conducted in each environment to test significant differences among genotypes (Panse and Sukhatme 1985).

Homogeneity of error variance tests were conducted to determine if data from individual environments (E) could be pooled to evaluate G × E interaction using a combined ANOVA. The Homogeneity of error variances was tested with F–test or the 'variance ratio' test as described by Gomez and Gomez (1984). For the combined analysis, variation was partitioned into relevant sources of variation to test for differences among genotypes and for the presence of G × E interaction. The phenotypic divergence among the accessions was estimated by the multivariate techniques, as follow: Tocher's cluster analysis as described by Rao (1952), using Mahalanobis $D^2$-statistics (Mahalanobis 1936) to measure the genetic distance.

**Table 1. List of linseed genotypes (seed flax) and their parentage used in the study.**

| S.No. | Genotype | Parentage | S.N. | Genotype | Parentage |
|---|---|---|---|---|---|
| 1. | KL-240 | RLC-29 × NL-93 | 17. | KL-257 | LC-2323 ×KLS-1 |
| 2. | KL-241 | Giza-7 × KLS-1 | 18. | KL-258 | Janaki×Surbhi |
| 3. | KL-242 | Gaurav× KLS-1 | 19. | KL-259 | KL-187 × Flak-1 |
| 4. | KL-243 | RL-904 × Exotic-2 | 20. | KL-260 | KL-210 ×KLS-1 |
| 5. | KL-244 | (RLS-29 ×Jeewan) ×Jeewan | 21. | KL-261 | KL-233 × KLS-1 |
| 6. | KL-245 | Jeewan× KLS-1 | 22. | KL-262 | Himalini× Flak-1 |
| 7. | KL-246 | Him Alsi-2 × RLC-29 | 23. | KL-263 | KL-223 × KL-224 |
| 8. | KL-247 | Neelam×Nagarkot | 24. | KL-264 | LC-2232 × KLS-1 |
| 9. | KL-249 | Surbhi fawn seeded (selection) | 25. | KL-265 | KL-168 × KL-224 |
| 10. | KL-250 | DC-3 | 26. | KL-266 | LCK-9826 × KL-221 |
| 11. | KL-251 | DC-5 | 27. | KL-267 | KL-223 × Flak-1 |
| 12. | KL-252 | DC-7 | 28. | KL-268 | Early selection Him Alsi-2 |
| 13. | KL-253 | Chambal × KL-221 | 29. | KL-269 | Medium selection Him Alsi-2 |
| 14. | KL-254 | KL-223 ×KL-221 | 30. | Bhagsu | RL-50-3 ×Surbhi |
| 15. | KL-255 | KL-210 × KL-224 | 31. | Binwa | Flak-1 × SPS 47 / 7-10-3 |
| 16. | KL-256 | KL-210 × Flak-1 | 32. | Baner | EC-21741 × LC-216 |

## Results and Discussion

Homogeneity of variance tests were conducted to determine if data from individual environments could be pooled to evaluate G × E interaction using a combined ANOVA. For the combined analysis, variation was partitioned into relevant sources of variation to test for differences among genotypes and for the presence of G × E interaction. Pooling is valid only when the variances are homogenous. The equality of two variances may be tested by using F test or the 'variance ratio' test. Homogeneity of variances tests indicated heterogeneous error variance for each trait in each of the two environments and does not allow for a combined, across environment analysis (Table 2). Highly significant genotypic differences were found for all the characters studied in both the environments except for the seeds per capsule. Significant variation for all the characters was also observed by earlier workers (Diederichsen and Fu 2008, Sivaraj *et al*. 2012, Bibi *et al*. 2013, Tyagi *et al*. 2014). The genotype × environment interaction was highly significant ($p \leq 0.01$) for all traits except for seeds per capsule, suggesting the relative genotypic values for these traits changed significantly over the years. Therefore, no pooled analysis was possible for these traits. Moreover, genotypes responded differently to change in the environmental conditions at the two environments, as genotype × environment interaction mean squares were highly significant ($p \leq 0.01$) for all the traits (Table 2). This indicates that experiments at several environments are required for evaluating the diversity in linseed germplasm.

The cluster formation (Tocher's analysis) distinguished the genotypes into eight (E-I) and six (E-II) diversity classes of different sizes during both the years (Tables 4, 5 and Figs 1, 2), different members within a cluster being assumed to be more closely related in terms of traits under consideration with each other than those members in different clusters. During first year, distribution of different groups revealed that there were six genotypes in clusters I, III and VI, four in cluster II, five in cluster IV, two in clusters V and VIII and only one in cluster VIII. On the other hand, in second year, cluster I was the largest with eleven genotypes followed by cluster II with ten genotypes and cluster III with genotypes.

Clusters IV, V and VI had one genotype each. Different clustering pattern were also reported on linseed by some earlier workers (Srivastava *et al*. 2009, Kant *et al*. 2011, Khan *et al*. 2013).

The pairwise generalized squared distances ($D^2$) among the eight clusters is presented in Table 3. The average intra-cluster distance ranged from 0.00 (cluster VIII) to 21.40 (cluster VI), while inter-cluster distance ranged from 19.32 (between clusters I and VIII) to 248.64 (between clusters V and VII). The maximum distance was found between clusters V and VII ($D^2$ = 248.64). The second most divergent clusters were II and V ($D^2$ = 212.20) followed by clusters VI and VII ($D^2$ = 188.60). Fulkar *et al.* (2007) reported maximum inter cluster distance between cluster II and X, Tadesse *et al.* (2009) reported between cluster I and IV, cluster I and III and minimum for cluster VIII and IX and IX and X. Maximum segregation and genetic recombination is expected from crosses that involve parents from the clusters characterized by maximum distances. It is assumed that genotypes in clusters with minimum distances are closely related among themselves.

Sinha and Wagh (2013) grouped linseed genotypes into 3 clusters and suggested that intercrossing of genotypes from different clusters may help in obtaining new lines with higher yield. Genotypes tended to group together in separate clusters on the basis of low, moderate or high mean values for different traits (Table 5). Cluster means revealed considerable differences among the clusters. Cluster I comprised genotypes with greater plant height and low seeds per capsule. Cluster II consisted mainly of early maturing genotypes with less number of primary branches per plant. Cluster III comprised mainly of late flowering genotypes with shortest plant height and low yield potential. Cluster V mainly comprised genotypes with late maturity, high 1000-seed weight, low number of secondary branches per plant and capsules per plant. Cluster VII mainly comprised genotypes with maximum seeds per capsule and small in seed size.

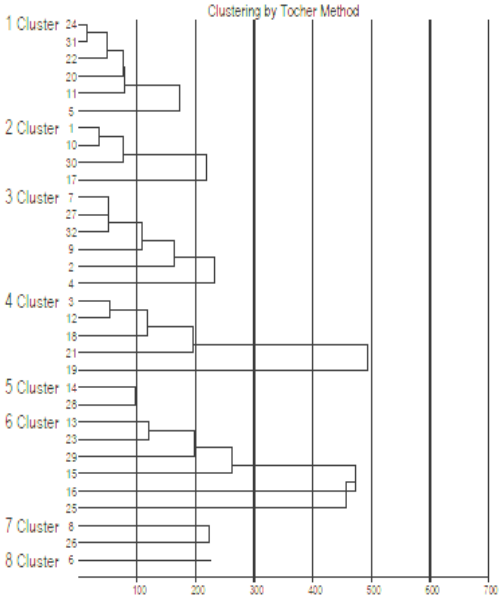


Fig. 1

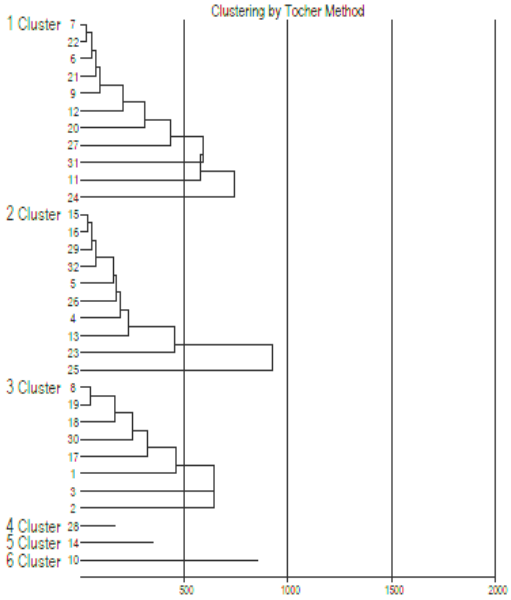


Fig. 2

Figs 1-2. Dendrograms showing grouping of 32 Linseed genotypes generated using $D^2$ cluster analysis (Tocher's method) in E-I and E-II.

Cluster VIII constituted superior genotypes for most of the traits *viz.*, high yield potential with early in flowering and high number of primary branches per plant, secondary branches per plant and capsules per plant.

**Table 2. Univariate analysis of variance (ANOVA) for tests of significance of differences among genotypes, environments and their interaction, for nine traits in a collection of 32 linseed genotypes evaluated in two environments during 2010 - 2012.**

| Characters | E-I | | E-II | | Combined | | | |
|---|---|---|---|---|---|---|---|---|
| | Mean squares | | | | | | | |
| Source | Genotypes | Error | Genotypes | Error | Genotypes | Environments | G × E | Pooled error |
| df | 31 | 31 | 31 | 31 | 31 | 1 | 31 | 62 |
| Days to 50% flowering | 46.29** | 0.43 | 40.94** | 1.61 | 59.11** | 37709.45 | 28.13** | 1.02 |
| Days to maturity | 6.32** | 0.51 | 13.30** | 0.13 | 11.18 | 2476.32 | 8.45** | 0.32 |
| Plant height (cm) | 37.50** | 15.96 | 75.38** | 1.78 | 87.98** | 2083.35 | 24.91** | 8.87 |
| Primary branches/plant | 0.49* | 0.26 | 0.39** | 0.10 | 0.44 | 2.59 | 0.44** | 0.19 |
| Secondary branches/plant | 3.21** | 1.15 | 1.04** | 0.20 | 2.9** | 0.19 | 1.363** | 0.68 |
| Capsules/plant | 64.29** | 15.59 | 14.83** | 1.09 | 47.29 | 689.13 | 31.83** | 8.34 |
| Seeds/capsule | 0.64 | 0.58 | 0.12 | 0.10 | 0.29 | 0.95 | 0.46 | 0.34 |
| 1000-seed weight (g) | 3.28** | 0.001 | 1.90** | 0.001 | 4.56** | 17.08 | 0.63** | 0.001 |
| Seed yield/plot (g) | 25307.86** | 612.90 | 5509.68** | 179.38 | 18952.32 | 200028.13 | 11865.23** | 396.14 |

* and ** indicate significant at p value of 0.05 and 0.01 levels, respectively, G × E - genotype × environment.

**Table 3. Intra- (bold) and intercluster divergence ($D^2$ values) among eight clusters of linseed during 2010 - 2011 (E-I).**

| Clusters | I | II | III | IV | V | VI | VII | VIII | Genotypes included in clusters |
|---|---|---|---|---|---|---|---|---|---|
| I (6) | **11.29** | 114.58 | 31.67 | 63.94 | 98.35 | 40.74 | 150.91 | 19.32 | KL-264, Binwa, KL-262, KL-260, KL-251, KL-244 |
| II (4) | | **13.78** | 85.79 | 54.53 | 212.20 | 152.46 | 38.68 | 122.85 | KL-240, KL-250, Bhagsu, KL-257 |
| III (6) | | | **13.78** | 37.55 | 127.58 | 68.99 | 122.16 | 42.67 | KL-246, KL-267, Baner, KL-249, KL-241, KL-243 |
| IV (5) | | | | **19.14** | 160.71 | 101.36 | 89.56 | 71.15 | KL-242, KL-252, KL-258, KL-261, KL-259 |
| V (2) | | | | | **9.83** | 62.30 | 248.64 | 92.52 | KL-254, KL-268 |
| VI (6) | | | | | | **21.40** | 188.66 | 36.32 | KL-253, KL-263, KL-269, KL-255, KL-256, KL-265 |
| VII (2) | | | | | | | **14.92** | 158.37 | KL-247, KL-266 |
| VIII (1) | | | | | | | | **0.00** | KL-245 |

**Table 4. Intra- (bold) and intercluster divergence ($D^2$ values) among eight clusters of linseed during 2011 - 2012 (E-II).**

| Clusters | I | II | III | IV | V | VI | Genotypes included in clusters |
|---|---|---|---|---|---|---|---|
| I (11) | **22.24** | 44.49 | 50.63 | 76.87 | 87.50 | 94.67 | KL-246, KL-262, KL-245, KL-261, KL-249, KL-252, KL-260, KL-267, Binwa, KL-251, KL-264 |
| II (10) | | **20.50** | 87.32 | 39.76 | 49.01 | 133.31 | KL-255, KL-256, KL-269, Baner, KL-244, KL-266, KL-243,KL-253, KL-263, KL-265 |
| III (8) | | | **23.60** | 121.86 | 132.49 | 50.44 | KL-247, KL-259, KL-258, Bhagsu, KL-257, KL-240, KL-242, KL-241 |
| IV (1) | | | | **0.00** | 18.67 | 168.29 | KL-268 |
| V (1) | | | | | **0.00** | 179.44 | KL-254 |
| VI (1) | | | | | | **0.00** | KL-250 |

**Table 5. Cluster means for 32 genotypes studied for nine quantitative traits during 2010 -2011 (E-I).**

| Clusters / Characters | I | II | III | IV | V | VI | VII | VIII | Mean | Minimum | Maximum |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to50% flowering | 117.17 | 118.88 | 120.75** | 112.90 | 117.00 | 114.92 | 114.50 | 105.50* | 115.20 | 105.50 | 120.75 |
| Days to maturity | 206.42 | 204.75* | 206.25 | 206.50 | 207.75** | 206.42 | 206.25 | 206.00 | 206.29 | 204.75 | 207.75 |
| Plant height | 61.49** | 59.43 | 57.23* | 59.93 | 58.23 | 60.13 | 58.53 | 60.40 | 59.42 | 57.23 | 61.49 |
| Primary branches/plant | 3.87 | 3.50* | 4.23 | 3.86 | 3.55 | 4.07 | 4.10 | 4.70** | 3.99 | 3.50 | 4.70 |
| Secondary branches/plant | 4.83 | 5.18 | 6.08 | 5.13 | 3.50* | 4.58 | 5.15 | 6.10** | 5.07 | 3.50 | 6.10 |
| Capsules/plant | 19.58 | 21.63 | 24.58 | 23.40 | 16.25* | 19.50 | 25.50 | 27.00** | 22.18 | 16.25 | 27.00 |
| Seeds/ capsule | 7.00* | 7.00* | 7.25 | 7.00* | 7.25 | 7.42 | 7.75** | 7.50 | 7.27 | 7.00 | 7.75 |
| 1000-seed weight | 7.51 | 5.27 | 6.95 | 6.25 | 9.44** | 8.22 | 4.51* | 7.56 | 6.96 | 4.51 | 9.44 |
| Seed yield/plot | 380.83 | 387.50 | 324.17* | 439.00 | 330.00 | 338.33 | 402.50 | 580.00** | 397.79 | 324.17 | 580.00 |

**Table 6. Cluster means for 32 genotypes studied for nine quantitative traits during 2011 - 2012 (E-II).**

| Clusters / Characters | I | II | III | IV | V | VI | Mean | Minimum | Maximum |
|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | 132.50 | 132.17 | 131.25* | 136.93 | 140.75** | 136.75 | 135.06 | 131.25 | 140.75 |
| Days to maturity | 208.65* | 210.63 | 211.17 | 211.71 | 212.25** | 210.25 | 210.78 | 208.65 | 212.25 |
| Plant height | 60.62 | 63.64 | 63.18 | 65.16 | 74.05** | 56.00* | 63.78 | 56.00 | 74.05 |
| Primary branches/plant | 4.19 | 4.04 | 3.90* | 4.15 | 3.95 | 4.60** | 4.14 | 3.90 | 4.60 |
| Secondary branches/plant | 5.08 | 5.01 | 4.30* | 5.46 | 4.70 | 7.60** | 5.36 | 4.30 | 7.60 |
| Capsules/plant | 25.50 | 22.80 | 21.83* | 25.36 | 24.50 | 33.25** | 25.54 | 21.83 | 33.25 |
| Seeds/capsule | 7.29 | 7.35 | 7.35 | 7.12 | 7.00* | 7.70** | 7.30 | 7.00 | 7.70 |
| 1000-seed weight | 5.26* | 7.07 | 8.52** | 5.83 | 6.85 | 6.53 | 6.68 | 5.26 | 8.52 |
| Seed yield/plot | 317.00 | 326.33 | 298.33 | 427.5** | 225.00 | 192.50** | 297.78 | 192.50 | 427.50 |

* Min. value, ** Max. value.

The diversity in the present materials was also supported by the appreciable amount of variation among cluster means for different traits (Table 6). Cluster I mainly characterised genotypes with early in maturity and small in seed size. Cluster III comprised genotypes with early flowering, low in number of primary branches per plant, secondary branches per plant, capsules per plant and bold in seed size. Cluster IV consisted of genotypes with high yield potential. Cluster V comprised genotypes with late flowering/ maturity and low seeds per capsule. Cluster VI consisted mainly genotypes with short plant height, maximum number of primary, secondary branches per plant, capsules per plant, seeds per capsule and low in yield potential. Factor responsible for the differentiation of all genotypes in different clusters during both the years at genotypic level attributed to the percentage contribution of quantitative traits towards genetic distance. In both the years, 1000-seed weight contribute maximum in E-I (93.55%) and E-II (91.33%) total genetic divergence between genotypes. Srivastava *et al.* (2009) in their study on genetic divergence reported that seed yield per plant contributed maximum towards genetic divergence followed by number of capsules per plant and days to flowering. The wide range of genetic diversity was observed in the present tested genotypes. It is also suggested that said diversity could be utilized for improvement in linseed by crossing best performing lines of different clusters, followed by selection in segregating generations.

## References

Ahmad HM, Awan SI, Aziz O and Ali MA 2014. Multivariative analysis of some metric traits in bread wheat (*Triticum aestivum* L.). Eur. J. Biotec. Biosc. **1**(4): 22-26

Anonymous 2014. Annual report 2013-14 linseed. AICRP (All India Coordinated Research Project) on linseed. Kanpur, India.

Anonymous 2014. *Economic survey of Himachal Pradesh*. Economics and Statistical Department. Government of Himachal Pradesh, India. pp. 69-70.

Bibi T, Talat M, Yasin M, Tariq M and Hasan E 2013. Correlation studies of some yield related traits in linseed (*Linum usitatissimum* L.). J. Agr. Sci. **51**: 121-132.

Diederichsen A and Fu YB 2008. Flax genetic diversity as the raw material for future success. *In*: 2008 International Conference on flax and other plants. pp. 270-280.

Dikshita N and Sivarajb N 2015. Analysis of agromorphological diversity and oil content in Indian linseed germplasm. Fats and Oils **66**(1): 1-8.

Fulkar PL, Ghorpade PB, Maheshwari JJ, Patil SR, Reddy MN and Pavithran C 2007. Evaluation of linseed germplasm for genetic divergence and choice of parents. J. Soils and Crops **17**: 333-338.

Gomez KA and Gomez AA 1984. Statistical procedures for agricultural research, 2nd edn. Wiley, New York.

Joshi BK, Mudwari A, Bhatta MR and Ferrara GO 2004. Genetic diversity in Nepalese wheat cultivars based on agromorphological traits and coefficients of parentage. Nepal Agric. Res. J. **5**:7-17.

Kant R, Chauhan MP, Srivastava RK and Yadav R 2011. Genetic divergence analysis in linseed (*Linum usitatissimum* L.). Indian J. Agric. Res. **45**: 59-64.

Khan MA, Mirza MY, Amjad M, Nawaz N, Nawaz MS and Baig D 2013. Assessment of genetic diversity in germplasm of linseed (*Linum usitatissimum* L.). Pakistan J. Agric. Res. **26**(3): 178-184.

Mahalanobis PC 1936. On the generalized distance in statistics. *In*: Proceedings National Academy of Sciences, India. **2**: 49-55.

Panse VG and Sukhatme PV 1985. Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi. pp. 359.

Rao CR 1952. *Advance Statistical Methods in Biometrical Research*. John Wiley and Sons Inc. New York Edn.1.

Sinha S and P Wagh 2013. Genetic studies and divergence analysis for yield, physiological traits and oil content in linseed. Res. J. Agric. Sci. **4**(2): 168-175.

Sivaraj N, Sunil N, Pandravada SR, Kamal V, Babu A, Kumar V, Rao BVSK, Prasad RBN and Varaprasad KS 2012. Variability in linseed (*Linum usitatissimum* L.) germplasm collections from peninsular India with special reference to seed traits and fatty acid composition. Indian J. Agric. Sci. **82**: 102-105.

Soto-Cerda BJ, Diederichsen A, Ragupathy R and Cloutier S 2013. Genetic characterization of a core collection of flax (*Linum usitatissimum* L.) suitable for association mapping studies and evidence of divergent selection between fibre and linseed types. BMC Pl. Biol. **13**:78.

Srivastava RL, Singh HC, Karam H, Malik YP and Prakash O 2009. Genetic divergence in linseed, *Linum usitatissimum* L. under salt stress condition. J. Oilseeds Res. **26**: 159-161.

Tadesse T, Singh H and Weyessa B 2009. Genetic divergence in linseed germplasm. J. Inn. Dev. Stra. **3**: 13-20.

Tyagi AK, Sharma MK, Surya, Mishra SK, Kerkhi SA and Chand P 2014. Estimates of genetic variability, heritability and genetic advance in linseed (*Linum usitatissinum* L.) germplasm. Prog. Agric. **14**(1): 37-48.

Vavilov NI 1951. The origin, variation, immunity and breeding of cultivated plants. Chronica Botanica **13**: 1-366.

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