Indian Journal of Ecology (2025) 52(2): 364-368
DOI: https://doi.org/10.55362/IJE/2025/4503

Manuscript Number: 4503
NAAS Rating: 5.38

Genetic Diversity Based on Principal Component Analysis for yield and its Contributing Character in Linseed (*Linum usitatissimum* L.)

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Abstract: A field experiment was carried out to determine the principal component among eleven traits of linseed using 36 genotypes along with three checks. The data of eleven traits were recorded and analyzed to find out principal component to reveal the diversity among the linseed genotypes. the first five principal components exhibited more than one eigen values and consider for 70.60% of the total variation that consist of 20.56% (PC 1), 16.75% (PC 2), 11.87% (PC 3), 11.42% (PC 4) and 10.10% (PC 5) for eleven traits. PC I contributed maximum towards the variability (20.57%) followed by PC II (16.75%) and PC III (11.87%). The genotypes 180513 along PCA I axis and RL-15580 along PCA II axis identified on extreme positive side on both the axis were ponder to be the superior genotypes PC1 contributed the maximum towards the total variability (20.56%). The characters *viz.,* days to maturity, number of primary branches per plant, number of capsules per plant, number of seeds per capsule clarify the maximum variance in PC1. This study helps to the characterization, reduction of overlap in the data collection and evaluation of genetic diversity in linseed.

Keywords: Diversity, Eigen values, Linseed, Principal component analysis, Scatter plot

Linseed (*Linum usitatissimum* L.) is the most important *Rabi* oilseed crop after rape-seed and mustard, originates from Mediterranean and the south-west Asian regions Linseed is an annual herbaceous self-pollinated crop and belongs to the order Malpighiales, genus Linum and family *Linaceae*. The important linseed growing countries are India, Canada, China, USA, Russia, Egypt and Ethiopia. In India the area of linseed is (181 thousand ha) with production (41 thousand tones) and productivity (227 kg/ha), (Anonymous, 2020-2021). In terms of Rajasthan total area of growing linseed is nearby 5.7 thousand ha with production 6.1 thousand tones and productivity 1066 kg/ha. (Anonymous, 2019-20). The development of improved plant cultivars is restricted mainly due to narrow genetic pool, which results into limited possibility to restructure the linseed crop. Therefore, a technique is required for systematic reduction and summarization of data sets (Tanwar and Bisen 2017). The principal component analysis (PCA) was performed, which resulted to an effective contribution of different traits on the basis of respective variation. Evaluation of germplasm is helpful for both choosing a core collection and using it in breeding initiatives. PCA is superior over cluster analysis because it permits each genotype to be assigned into a single group (Mohammadi, 2002). The main objective of this research was to determine the potential genetic diversity and correlation by selecting parents for a hybridization programme based on PCA techniques in order to produce desirable segregants in the advanced generation.

MATERIAL AND METHODS

Thirty-six linseed genotype and three commercial checks (Pratap Alsi-1, Kota Barani-3, and Kota Barani-4) were obtained from the Agricultural Research Station, Kota and the Indian Institute of Pulse Research, Kanpur. These genotypes were grown randomized block design with three replications at College of Agriculture, Kota, during the *Rabi* season of 2019-20 situated at 234 meters above mean sea level on latitude 24º7' N and 76º62' E. Each genotype of linseed was sown in a 3 m long plot. The row to row and plant to plant distance was kept 20 cm and 10 cm, respectively. All required plant protection measures were taken to combat pests and diseases, and the suggested packages of practices were adhered to in order to raise a healthy crop (Sharma and Gupta, 2020). Observations were recorded on ten randomly selected plants per replication for eleven traits *(*Table 2*)* The scatter plot, correlation plot was performed using the package version 4.0.2 and principle component analysis by STAR (IRRI, 2014), XLSTAT (Addinsoft 2020).

RESULTS AND DISCUSSION

The first five PCs (PC1, PC2, PC3, PC4 and PC5) were responsible for 70.60 of the total variation. The first PC has the highest eigen value (2.27), explaining 20.56 percent of the variation (Table 1, Fig. 1). PCs with eigen values less than one were declared non-significant and so discarded since they are unlikely to have any practical significance (Mustafa et al., 2015). The majority of the variability in the set of all PCs

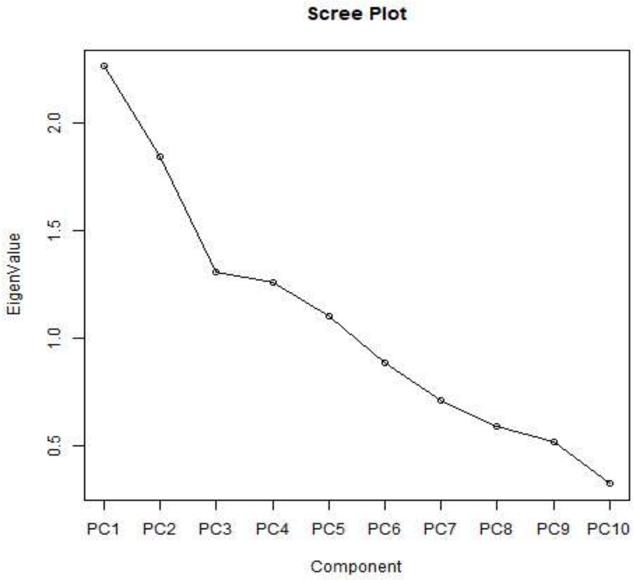

Fig. 1. Scree plot of 36 Linseed genotypes

was provided by PC1, while the remaining PCs tended to exhibit less variance.

Factor loading of various characters: The factor loadings of various variables computed *via* PCA. In the first PC, plant height, number of primary branches per plant, harvest index, 1000-seed weight and protein content had contributed greatest of the variation with positive significant coefficients of 0.61, 0.66, 0.51, 0.43 and 0.08 respectively. Seed yield per plant also showed positive coefficient which had contributed to the principal axis one and all remaining traits has negatively contributed to the principal axis one. High positive coefficients were for the number of primary branches per plant, capsules per plant and days 50% flowering in the second principal axis. Number of seed per capsule, harvest index and 1000-seed weight exhibited a negative impact on the second principal axis. In the third principal axis, days to maturity (0.45) , number of primary branches per plant (0.38) and plant height (0.32) had the highest co-efficient values,

Table 1. Eigen values and percent variation accounted for the 11 principle components of linseed genotypes

Statistics	Eigen values	Expression of proportion of variance	Expression of cumulative proportion
PC1	2.27	20.56%	20.56%
PC2	1.84	16.75%	37.31%
PC3	1.31	11.87%	49.18%
PC4	1.26	11.42%	60.60%
PC5	1.10	10.10%	70.60%
PC6	0.89	8.06%	78.67%
PC7	0.71	6.44%	85.10%
PC8	0.59	5.38%	90.48%
PC9	0.52	4.72%	95.20%
PC10	0.32	2.94%	98.14%
PC11	0.21	1.87%	100.00%

Table 2. Factor loading of eleven traits with respect to the significant principle component of linseed genotypes

Statistics	PC1	PC2	PC3	PC4	PC5
Days to 50% flowering	-0.37	0.42	-0.03	0.42	0.41
Days to maturity	-0.58	-0.06	0.45	0.43	-0.14
Plant height (cm)	0.61	-0.14	0.32	0.38	-0.05
Number of primary branches per plant	-0.01	0.73	0.38	-0.08	0.15
Number of capsules per plant	0.66	0.47	0.10	0.11	0.23
Number of seeds per capsule	-0.21	-0.72	0.10	-0.04	0.18
Harvest index (%)	0.51	-0.50	0.25	0.42	-0.07
1000 seed weight (g)	0.43	-0.18	0.20	-0.65	0.31
Protein content (%)	0.08	0.23	-0.44	0.01	-0.66
Oil content (%)	-0.15	-0.18	-0.63	0.23	0.52
Seed yield plant (g)	0.68	0.06	-0.38	0.28	0.04

whereas traits like oil content (-0.63), protein content (-0.44) and seed yield per plant (-0.38) shown highly negative contribution. In fourth principal axis, days to maturity (0.43), days to 50% flowering (0.42) and harvest index (0.42) had the highest co-efficient values, whereas traits 1000-seed weight shown highly negative contribution. In fifth principal axis, oil content, days to 50% flowering (0.41) and 1000-seed weight (0.31) had the highest co-efficient values, whereas traits

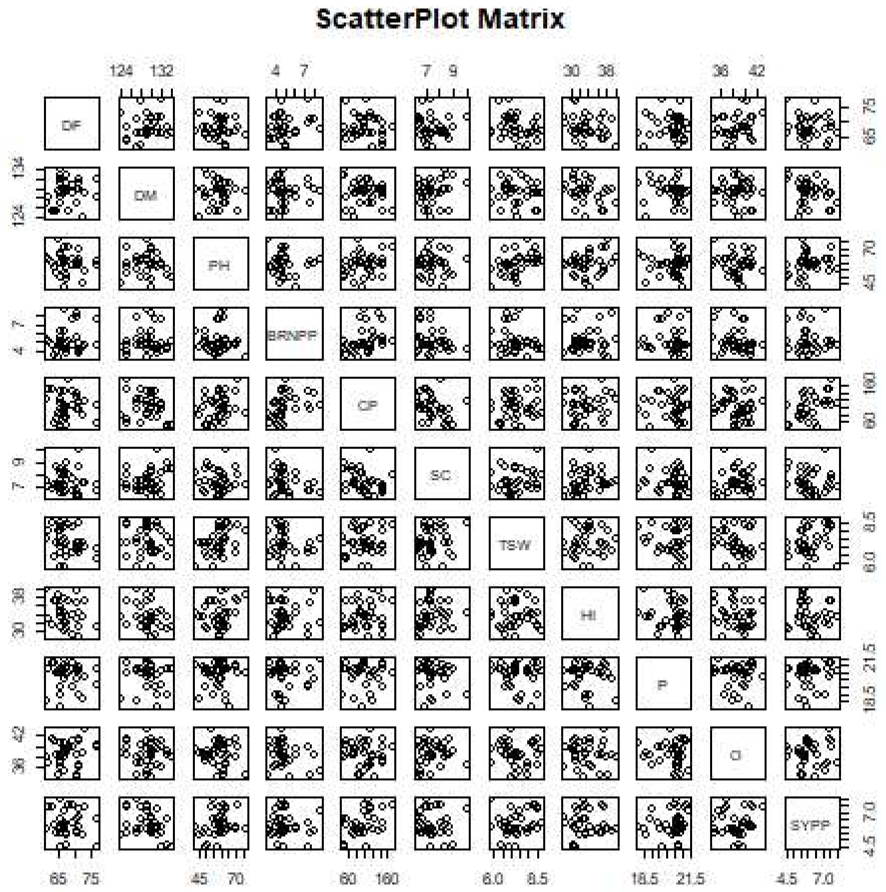

Fig. 2. Scatter plot with correlation value for eleven traits of 36 Linseed genotypes

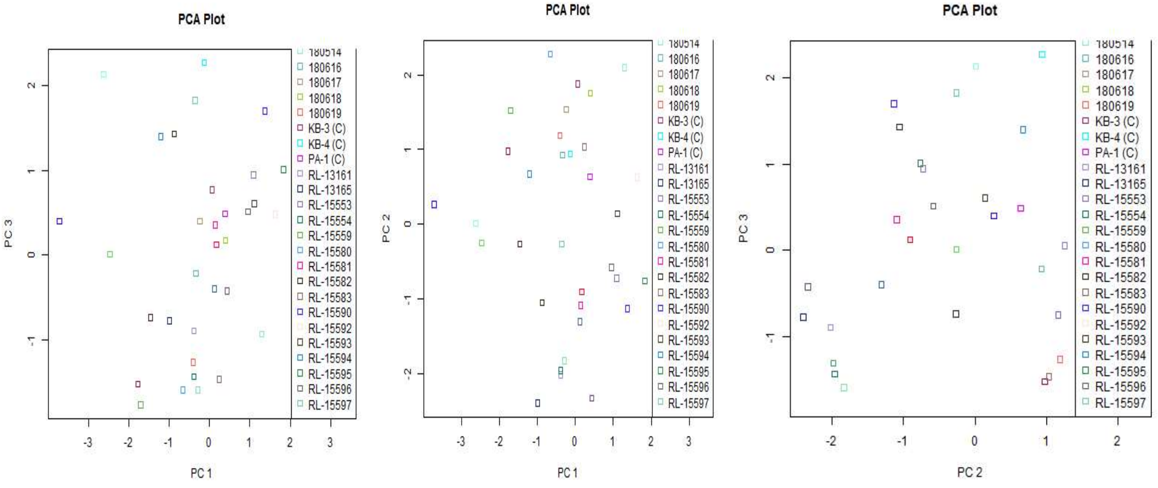

Fig. 3. Biplot of 36 genotypes of linseed on Principal Component axis I and II

protein content (-0.66) and days to maturity (-0.14) were shown highly negative contribution (Table 2, Fig. 2). The results on PCA indicated that these traits are important for trait manipulation and diversity in this population was present due to these traits. Similar trend was observed in earlier research (Singh et al., 2014, Kumar and Paul 2016, Rizvi et al., 2018 , Kumar and Kumar 2021.

Table 3. PCA scores of genotypes of linseed

Genotype	PC1 (X Vector)	PC2 (Y Vector)	PC3 (Z Vector)
180101	0.167	-0.905	0.120
180102	0.432	-2.337	-0.422
180103	0.117	-1.305	-0.397
180104	2.403	-1.978	-1.304
180107	-0.287	-1.830	-1.588
180203	-2.620	0.008	2.131
180204	-1.777	0.973	-1.521
180205	-2.464	-0.258	0.011
180512	3.349	1.249	0.054
180513	3.045	1.165	-0.750
180514	1.293	2.096	-0.928
180206	-3.715	0.264	0.398
180216	-1.456	-0.270	-0.738
180616	-0.337	0.928	-0.215
180617	-0.237	1.538	0.397
180618	0.395	1.751	0.172
180619	-0.409	1.184	-1.265
RL-15596	0.953	-0.583	0.514
RL-15597	-0.357	-0.264	1.821
RL-15595	1.831	-0.762	1.007
RL-15593	1.107	0.143	0.607
RL-15592	1.631	0.628	0.479
RL-15590	1.372	-1.133	1.697
RL-15553	1.085	-0.727	0.944
RL-15594	-1.205	0.672	1.395
RL-15581	0.143	-1.093	0.353
RL-15583	0.242	1.032	-1.466
RL-15580	-0.657	2.278	-1.590
RL-13161	-0.389	-2.019	-0.896
RL-13165	-0.994	-2.401	-0.777
RL-15554	-0.391	-1.960	-1.433
RL-15559	-1.707	1.521	-1.768
RL-15582	-0.877	-1.054	1.429
PA-1 (C)	0.382	0.637	0.489
KB-3 (C)	0.061	1.875	0.770
KB-4 (C)	-0.128	0.937	2.268

PC score of germplasm: The PCA scores for 36 linseed genotypes with three checks in the first three PCs were analyzed and considered three axes as X, Y and Z; and squared distance of each genotype from these three axes were computed (Table 3, Fig. 3). The genotypes identified on extreme positive side on both the axis were considered to be the best genotypes *i.e.* 180512 (3.349), 180513 (3.045), 180104 (2.403), RL-15595 (1.831), RL-15592 (1.631) and RL-15590 (1.372). These genotypes might be exploited in future breeding programs.

CONCLUSION

The study multivariate methodologies underscored the remarkable genetic diversity inherent in the utilized germplasm. Five out of the eleven principal components were significant (Eigen value >1) and accounted for 70.60 per cent of the variance, according to PCA. The yield and its contributing characteristics dominated in PC1 and PC2. Therefore, by utilizing heterosis, choosing germplasm with high PC1 and PC2 scores may lead to higher yield and yield characteristics. To develop superior high yielding lines, high performing material from each cluster can be used in a hybrid breeding program.

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Received 11 October, 2024; Accepted 10 March, 2025