Genetic variabilitycharacter association and path analysis for yield attributing traits in linseed

Abstract

This study was conducted to assess the induced genetic variability, interrelationship among yield attributing traits and their direct and indirect effect on yield. Ninety-twogenotypes along with four varieties taken in the study and were planted during two seasons *i.e*.,*Rabi* 2022-23 and *Rabi* 2023-24 atResearch Farm, Department of Genetics & Plant Breeding, College of Agriculture, RVSKVV, Gwalior. These genotypes were evaluated for analysis of genetic variability, phenotypic and genotypic coefficient of variation, correlation and path analysis for seed yield and its related traits. Higher estimates of GCV and PCV were observed for traits like seed yield per plant, harvest index, thousand seed weight, numbers of seeds per capsule, numbers of capsules per plant, numbers of secondary and primary branches. Highly significant and positive correlation with seed yield was found for numbers of capsules per plant (0.82), numbers of secondary branches per plant (0.64) and thousand seed weight (0.31). In addition to the genetic variability, knowledge of heritability and expected genetic advance helps the breeder to employ the suitable breeding strategies for development of superior cultivar (s) in future.

Keywords: Correlation, Genetic advance, Genotypic coefficient of variation, Heritability, Path coefficient analysis, Phenotypic coefficient of variation

Introduction

Linseed (*Linum ustiatissimum* L.) is a significant rabi oilseed crop grown for its fibre, oil, and chemicals with potential medical uses [1]. Genetically, linseed has a tiny genome and is a self-pollinated diploid crop (2n=2x=30). The Indian subcontinent, which is known to have a large biological diversity of the species *Linum*, is where flax was domesticated, close to the Mediterranean Sea [2-3]. Since the biologically active components of linseed have health advantages, it has garnered considerable attention in the field of nutrition and disease investigation throughout the past 20 years. It has nutritional qualities that are a rich source of ω-3 fatty acids, α-linolenic acid (ALA), short chain polyunsaturated fatty acids (PUFA), soluble and insoluble fibres, phyto estrogenic lignans, proteins, and a variety of antioxidants [4-7].

Linseed crop has continued to move toward greater productivity, while the area under observation indicates a falling trend, which has led to stagnating production. Grown on marginal soil with inadequate management, linseed is the most ignored crop in developing nations dueto lack of better cultivars appropriate for the numerous agroclimatic situations owing to low yield of the crop. To overcome from such constraint, the creation of high yielding cultivars needsprecedence [8]. To full fill such goal, genetic diversity is a prerequisite for genetic improvement of any crop to break the yield plateau [9-12].Furthermore, agronomic, and genetic crop development depends heavily on the methodical research and assessment of germplasm lines in every crop improvement programme [8].A complicated feature, seed yield is greatly impacted by a variety of environmental and genetic variables. Thus, yield-based direct selection may be beneficial, so the knowledge of the relationship between morpho-agronomic characteristics and seed production is essential for a successful selection process [13].

The most accurate way to assess the link between significant yield components is to use correlation in conjunction with path coefficient analysis [14-16]. These methods were employed in the breeding effort to take advantage of the yield potential for raising the linseed's productivity and creating superior types with higher yields.The reciprocal link between the factors is known as correlation, and it helps to identify the best practices for selecting superior genotypes. Breeding techniques would be particularly effective when there is a positive connection between the primary yield components; on the other hand, selection becomes quite challenging [17]. The reciprocal cancellation of component features can sometimes lead to incorrect estimations of correlation coefficients alone. Accordingly, a more advantageous method for investigating the traits that contribute to yield is to combine the research of correlation with a route analysis [18]. A prerequisite for improving seed yields is the identification and selection of the main yield components. Considering these factors, an evaluation of the relationship between the yield components and their direct and indirect effects on seed yield was conducted in present study with 92 genotypes.

Materials and Method

Present investigation was carried out with eighty-eight linseed germplasm accessionsalong with four varieties *viz.*,LMS-2015-42, LMS-2045-81, SLS-135 and SLS-140 acquired from All India Coordinated Research Project on linseed, Crop Research Farm, Mauranipur, BUA & T, Banda U.P., India. Experiment was conducted at Research Farm, Department of Genetics & Plant Breeding, College of Agriculture, RVSKVV, Gwalior, M.P., India during two successive seasons *i.e*., *Rabi* 2022-23 and *Rabi* 2023-24 to generate quantitative data. An augmented design was adopted forexperimentation.Field was divided into four blocks. Each block consists of twenty-two germplasm lines along with four varieties were randomly replicated in four blocks. Spacing followed wasplant to plant distance of 10cm followed by 30cm row to row distance. To guarantee adequate germination, pre-sowing irrigation was given. The field trial plots were meticulously prepared before seeding, and Farm Yard Manure (FYM) was added. The recommended magnitude of fertilizers were applied during the growth and development of crop.

The data was recorded on five randomly selected plants from each line for 11 quantitative traits including days to 50 % flowering, days to maturity, plant height at maturity, numbers of primary and secondary branches per plant, numbers of capsules per plant, numbers of seeds per capsules, 1000- seed weight, biological yield per plant, harvest index and seed yield per plant. The values of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (Hb) and genetic advance as percentage of mean (GCA % M) at 5 % selection intensity were estimated following standard biometrical methods. Phenotypic and genotypic correlation coefficients were estimated from the respective variances and covariation components as per methods described by Burton [19] andSearle [20]. While path coefficient analysis was analysed as described by Dewey and Lu [21].

Results and discussion

The analysis of variance for 92 linseed genotypes was carried out for eleven quantitative traits. The mean sum of squares due to treatments was found highly significant for every trait(Table 1), suggested that there is a considerable magnitude of genetic variability present in investigated genetic materials.

The analysis of variance revealed that treatment (eliminating blocks) and test effects were significant for all traits.Varieties mean sum of square was significant for all traits except numbers of seeds per capsule that suggested that there was not any significant difference between the varieties in terms of numbers of seeds per capsule. Likewise, the mean sum of square due to test v/s variety wasinvestigatedsignificant for all the traits except biological yield per plant and harvest index, indicating that the germplasm lines were meaningfullydiffered from varieties except for biological yield per plant and harvest index. However, the adjusted block effects were found non-significant for all investigated traits indicating homogeneity of evaluation blocks. Similar results were also reported by Gudmewad *et al*.[22], Semahegn *et al*. [23], Leelavathi and Mogali [8], Rajanna *et al*.[24], Kumar and Kumar [13], Saroha *et al*.[25]and Kaur *et al*. [26].

To predict genetic variability in the population, various parameters *viz.*, range, mean, genotypic and phenotypic coefficient of variance, heritability and genetic advance for yield attributing traits were estimated and are presented in Table 2 and Fig.1. Days to 50% flowering ranged between 47 to 62 days with a mean of 55 days while days to maturity exhibited an average value of 126 days and varied from 109 to 144 days. Plant height arrayed between 42.06 cm to 112.06 cm with a mean worth of 68.52 cm. Numbers of primary branches had a mean of 4.47 and ranged from 1.62 to 7.13, while numbers of secondary branches ranged between 6.81 to 22.06 with a mean performance of 14.60. Numbers of seeds per capsule had a mean value 9.75 and arrayed between 7.94 to 9.94. Whereas, thousand seed weight had a mean value of 6.88 g and varied between 4.44 to 9.44 g; biological yield per plant ranged from 8.97 g to 17.63with a meanvalue of 13.42 g. However, harvest

Index (%) showed a mean value of 48.91%, while it ranged from 22.88 % to 83.67 % and seed yield per plant arrayed between 3.42 to 8.90 g with an average value of 6.37 g.

In general, the phenotypic variance must be higher in magnitude than that of genotypic variance [27-30]. The same trend was experimented in the present investigation for all the studied traits. High estimates of GCV and PCV observed for traits like seed yield per plant, harvest index, thousand seed weight, numbers of seeds per capsule, numbers of capsules per plant, numbers of secondary and primary branches, while characters like plant height and biological yield per plant expressed a moderate levelof GCV and PCV. Low level of GCV and PCV observed for the traits like days to maturity and days to 50% flowering. These results agreed with the findings of Chauhan *et al*. [31], Manhar [18], Reddy *et al*. [32], Sathish *et al*.[33]and Hoque *et al*. [34].

The characters *viz*., plant height, numbers of primary and secondary branches, numbers of capsules per plant, numbers of seeds per capsule, thousand seed weight, biological yield, harvest index and seed yield per plant displayed high heritability coupled with higher genetic advance indicated additive type of gene action for these characters and can be exploited to produce better genotype (s) in linseed breeding as suggested by Kaur *et al.*[35], Upadhyay *et al.* [36], Rajanna *et al.*[37] and Kumar and Kumar [13]. The parameter days to 50% flowering and days to maturityexhibited high heritability coupled with medium genetic advance that indicated the significance of dominance and epistatic effects in the inheritance of these characters and selection for these traits would be less effective, so hybridization may be facilitate their improvement. Analogous research that supports this study include findings of Semahegn *et al*. [23], Leelavathi and Mogali [8], Rajanna *et al*. [37] and Kaur *et al*. [26].

Correlation provides the magnitude of linear association between pairs of characters and form the basis of selection index, thereby aiding the breeder in crop improvement programme through simultaneous manipulation of the paired traits [38-40].Paired wise correlation values and scatter plot is shown in Fig. 2. Highly significant and positive correlation with seed yield was found with numbers of capsules per plant (0.82), numbers of secondary branches (0.64) and thousand seed weight (0.31) as shown in heat map for Pearsons's correlation coefficient in Fig. 3. While biological yield per plant displayed high negative correlation with harvest index (-0.56) which interprets that decreasing biological yield would result higher harvest index. Numbers of capsules per plant showed positive correlation with two traits *i.e.*, numbers of secondary branches (0.76) and thousand seed weight (0.22) which led to the interpretation that by increasing these two traits, numbers of capsules will increase substantially increasing seed yield per plant. Numbers of secondary branches is positively correlated with thousand seed weight (0.28). Among other traits days to 50% flowering strongly correlated with days to maturity (0.68). These results are in conformation with those obtained by Gudmewad *et al.*[22], Shukla [41], Prasanna *et al*. [42], Rizvi *et al*. [43], Sathish *et al*.[33] and Hoque *et al*. [34].

It is important to understand the overall impact of the direct influence of particular trait as well as any indirect impacts through other characteristics, regardless of whether the connection between yield and its components is positive or negative. To separate the observed correlation into direct and indirect effects and to show the cause-and-effect relationship between yield and associated qualities, it is required to find the path coefficients. Results from path analysis (Table 3) showed that numbers of clusters per plant was the major contributor to the seed yield (0.7950) followed by harvest index (0.1762) and biological yield (0.1211) then numbers of seeds per capsule (0.1079). Rahimi *et al*. [44] and Reddy*et al*. [45] found a strong favourable direct impact of each plant's capsule on its seed output. The strong positive direct influence of seeds per capsule on seed output was observed by Rajanna*et al*. [37]. Direct effects of 1000- seed weight on seed yield were documented by Leelavathi and Mogali [8]. Therefore, choosing genotypes with greater numbers of capsules per plant, major branches per plant, seeds per capsule, and 1000- seed weight might result in desired improvement.

Conclusion

The investigation of diverse linseed germplasm across different genetic parameter suggested that seed yield is influenced by many traits including numbers of capsules per plant, numbers of seeds per capsule and numbers of secondary branches that will ultimately lead to significant increase in seed yield. By increasing the capsule numbers subsequently numbers of seed per plant increases, likewise by increasing numbers of secondary branches the numbers of capsule per plant also increases. Low productivity of linseed in India compared to other countries can be overcome by imploring these traits in the breeding programme and selecting the traits for next breeding cycle to bread higher yielding cultivar (s).

References

1. Paliwal S, Tripathi MK, Tiwari S, Tripathi N, Payasi DK, Tiwari PN, Singh K, Yadav RK, Asati R, Chauhan S. Molecular advances to combat different biotic and abiotic stresses in linseed (*Linum usitatissimum* L.): A comprehensive review. Genes, 2023; 14(7): 1461. https://doi.org/10.3390/genes14071461.
2. FuY B. Geographic patterns of RAPD variation in cultivated flax. Crop Science, 2005; 45(3): 1084-1091.
3. Kaur V, Yadav R, Wankhede D P. (). Linseed (*Linum usitatissimum* L.) genetic resources for climate change intervention and its future breeding. Journal of Applied and Natural Science, 2017; 9(2): 1112-1118.

4. Ivanov S, Rashevskaya T, Makhonina, M. (). Flaxseed additive application in dairy products production. Procedia Food Science, 2011; 1:275-280.
5. Singh KK, Mridula D, Rehal J, Barnwal P. Flaxseed: a potential source of food, feed and fiber. Critical Reviews in Food Science and Nutrition, 2011; 51(3): 210-222.
6. Touré A, XuemingX. (). Flaxseed lignans: source, biosynthesis, metabolism, antioxidant activity, bio- active components, and health benefits. Comprehensive Reviews in Food science and Food Safety, 2010; 9(3):261-269.
7. Paliwal S, Tripathi MK, Sikarwar RS, Yadav RK and Sonaniya P. Evaluation of biochemical parameters in linseed (*Linum usitatissimum*). International Journal of Advanced Biochemistry Research, 2024; 8(4):260-267DOI: 10.33545/26174693.2024.v8.i4d.947
8. Leelavathi T M, Mogali SC. Genetic variability, character association and path analysis for yield and yield components in mutant population of linseed. J. Farm Sci, 2018; 31(1): 17-20.
9. Barfa D, Tripathi MK, Kandalkar VS, Gupta JC, Kumar G. Heterosis and combining ability analysis for seed yield in Indian mustard [*Brassica Juncea* (L) Czern & Coss]. Ecology, Environment and Conservation, 2017; (23) Suppl 75-83.
10. Rajpoot P, Tripathi M. K, Solanki RS, Tiwari S, Tripathi N, Chauhan S, Pandya RK and Khandelwal V. Genetic variability and multivariate analysis in pearl millet (*Pennisetum glaucum* (L.) R. Br.) germplasm lines. The Pharma Innovation, 2023; 12(4): 216-226
11. Shrivastava A, Tripathi M. K., Solanki R. S., Tiwari S, Tripathi N, Singh J. and Yadav R. Genetic correlation and path coefficient analysis of yield attributing parameters in Indian mustard. Current Journal of Applied Science and Technology.202342 (7): 42-58. DOI: 10.9734/CJAST/2023/v42i74079
12. Ningwal R, Tripathi MK, Tiwari S, Yadav RK, Tripathi N, Solanki RS, Asati R, Yasin M. Assessment of genetic variability, correlation and path coefficient analysis for yield and its attributing traits in chickpea (*Cicer arietinum* L.) The Pharma Innovation, 2023;12(3): 4851-4859
13. Kumar N, Kumar V. Assessment of genetic diversity in linseed germplasm using morphological traits. Electronic Journal of Plant Breeding, 2021; 12(1) : 66-73.
14. Shyam C, Tripathi MK, Tiwari S, Tripathi N. Genetic components, and diversity analysis in Indian mustard [*Brassica juncea* (Linn.) Czern & Coss] based on different morpho-

physiological traits. Current Journal of Applied Science and Technology. 2021;40 (20):34-57. DOI: 10.9734/CJAST/2021/v40i2031462

15. Sharma S, Tripathi MK, Tiwari S, Solanki RS, Chauhan S, Tripathi N, Dwivedi N, TiwariPN. Discriminant function analysis for yield improvement in bread wheat (*Triticum aestivum* L.) The Pharma Innovation, 2023;12(5):224-232
16. Sharma S, Tripathi MK, Tiwari S, Solanki RS, Chauhan S, Tripathi N, Dwivedi N, Kandalkar VS. The exploitation of genetic variability and trait association analysis for diverse quantitative traits in bread wheat (*Triticum aestivum* L.)Curr. J. Appl. Sci. Technol, 2023;42(8):19-33.
17. Kanwar RR, Saxena RR, Ekka RE. Correlation and path co-efficient analysis of some quantitative traits in linseed (*Linum usitatissimum* L.).International Journal of Plant Sciences. 2013; 8 (2): 395-397
18. Manhar P. Genetic diversity analysis of linseed (*Linum usitatissimum* L.) at Bilaspur plain region of Chhattisgarh. Acta Scientific Agriculture, 2021; 5: 59-63.
19. Burton GW. Quantitative inheritance in grasses. Proc. 6th Int. Grassld. Cong. 1952; 1: 277
20. Searle SR. Phenotypic, genetic and environmental correlations. Biometrics,1961**; 17**: 474-480.
21. Dewey DR, Lu KI. (). A correlation and path coefficients analysis of components of crested wheat grass seed production. Agron. J.,1959; 1: 515-518
22. Gudmewad R, Misal A, Dhutmal, R, Pole S. Variability studies in linseed. Annals of Plant and Soil Research, 2016; 18(1): 88-90
23. SemahegnY, Tesfaye M. Genetic variability and correlation analysis of Ethiopian linseed (*Linum usitatissimum* L.) accessions. Molecular Plant Breeding, 2016; 7 (22) doi: 10.5376/mpb.2016.07.0022
24. RajannaB, Biradar S A, Ajithkumar K. Correlation and path coefficient analysis in linseed (*Linum usitatissimum* L.). The Bioscan,2014; 9 (4): 1599-1602
25. Saroha A, Pal D, KaurV, Kumar S, BartwalA, Aravind J, ... Wankhede, DP. (2022). Agro-morphological variability and genetic diversity in linseed (*Linum usitatissimum* L.) germplasm accessions with emphasis on flowering and maturity time. Genetic Resources and Crop Evolution, 69(1): 315-333
26. Kaur V, Gomashe SS, AravindJ, Yadav SK, Singh D, Chauhan SS, ... Singh GP. (). Multi-environment phenotyping of linseed (*Linum usitatissimum* L.) germplasm for

morphological and seed quality traits to assemble a core collection. Industrial Crops and Products, 2023; 206: 117657

27. Mihoariya M, Tiwari S, Yadav R K, Asati R, Solanki RS, Tiwari PN, Chauhan S, Tripathi N, Tripathi MK.Genetic variability and diversity analysis for yield and its associated traits in chickpea (*Cicer arietinum* L.) Current Journal of Applied Science and Technology, 2023; 42(16):17-33
28. Yadav P K, Tripathi MK, Tiwari S, Chauhan S, Tripathi N, Sikarwar RS, Solanki RS, Yadav S, SinghAK.Genetic components and variability assessment for grain yield and its accrediting traits in maize (*Zea mays* L.). International Journal of Environment and Climate Change,2023; 13(9):772-784.
29. Makwana K, Tiwari S, Tripathi MK, Patel V. Morphological diversity analysis of foxtail millet (*Sateria italica* (L.) Beauv.) using qualitative and quantitative traits. Scientist.2(2); 2023; 319-326.DOI: https://doi.org/10.5281/zenodo.7654168
30. Yadav R K, Tripathi M K, Tiwari S, Asati R, Chauhan S, Sikarwar RS, Yasin M.Evaluation of genetic diversity through D^2 statistic in chickpea (*Cicer arietinum* L.).2023; International Journal of Environment and Climate Change, 13(10):1598-1611.
31. Chauhan MP, Singh HK, Yadav JK, Maurya MK. Extent and pattern of genetic diversity in linseed (Linum usitatissimum L) under irrigated ecology: Genetic diversity in linseed. Journal of AgriSearch, 2018; *5*(1): 1-4
32. Reddy BC, Nair BM., Rananaware S, Prajapati SS, Gujar M, Mate A, Shinde J. Genetic diversity in exotic linseed germplasm for yield and yield contributing traits.The Pharma Innovation, 2022; 11(11): 1205-1209
33. Sathish K, Parte D, Rohit MVSK, Roy S, Sahu J, Mehta N. Genetic-morphological characterization and diversity analysis of linseed (*Linum usitattissimum* L.) germplasm.International Journal of Plant & Soil Science, 2022; 34(22): 1655-1663
34. Hoque A, Anderson JV, Rahman M. Genomic prediction for agronomic traits in a diverse Flax (*Linum usitatissimum* L.) germplasm collection. Scientific Reports, 2024; 14(1): 3196
35. Kaur V, Kumar S, Yadav R, Wankhede DP, Aravind J, Radhamani J, Rana JC. Kumar A.. Analysis of genetic diversity in Indian and exotic linseed germplasm and identification of trait specific superior accessions. J. Environ. Biol.2018; 39:702-709
36. Upadhyay S, Mehta N, Tiwari AK. Assessment of variability among flax type linseed genotypes (*Linum usitatissimum* L.) of Chhattisgarh plains. Int. J. Curr. Microbiol. Appl. Sci. 2019; 8(06): 2633-2637.

37. Rajanna B, Gangaprasad S, ShankerGI, Dushyantha KBM, Girjesh GK, Sathish KM. (). Genetic variability, heritability and genetic advance of yield components and oil quality parameters in linseed (*Linum usitatissimum* L.). International Journal of Chemical Studies, 2020; *8*(1) :1768-1771
38. Jain N, Sikarwar RS, Tripathi MK, Tiwari S, Rahangdale S, Barela A.Assessment of genetic variability, heritability and genetic advance for seed yield and its contributing traits in greengram [*Vigna radiata* (L.) Wilczek]., International Journal of Environment and Climate Change, 2024;14(3): 250-256.
39. Jain N, Sikarwar RS, Tripathi MK, Tiwari S.Evaluation of genetic parameters for yield and its attributing traits in green gram [*Vigna radiata* (L.) Wilczek]. International Journal of Environment and Climate Change, 2024;14(2):482-487.
40. Tomar YS, Tiwari S, Tripathi MK, Solanki RS. Genetic diversity assessment and cluster analysis of morphological yield attributing traits of groundnut (*Arachis hypogaea* L.). The Pharma Innovation, 2022; 11(6): 1444-1450.
41. Shukla R. Combining ability, heterosis for yield and quality improvement of linseed (*Linum usitatissimum* L.) under utera cultivation. Doctoral dissertation, Indira Gandhi Krishi Vishwavidyalaya, Raipur, 2016
42. PrasannaNS, Mogali SC. (). Association analysis for morphological and nutraceutical traits in linseed (*Linum usitatissimum* L.) using microsatellite markers. J Farm Sci., 2017; 30:496-502
43. Rizvi A, Marker S, Choudhary A. (). Multivariate analysis in linseed (*Linum usitatissimum* L.). Journal of Pharmacognosy and Phytochemistry, 2018; *7*(2): 528-531
44. Rahimi MM, Zarei, MA, Arminian A, Selection criteria of flax (*Linum usitatissimum* L.) for seed yield, yield components and biochemical compositions under various planting dates and nitrogen. African Journal of Agricultural Research, 2011; 6(13) :3167-3175
45. Reddy MP, Reddy BN, Arsul BT, Maheshwari JJ, Genetic variability, heritability and genetic advance of growth and yield components of linseed (*Linum usitatissimum* L.). Int. J. Curr. Microbiol. Appl. Sci., 2013; 2 (9): 231-237

Table 1Analysis of variance for eleven characters

Source	**Mean sums of square**											
	Df	**DTF**	**DTM**	**PH**	**NPB**	**NSB**	**NCPP**	**SPC**	**TSW**	**BY**	**HI**	**SYPP**
Treatment (ignoring Blocks)	91	19.97^{**}	118.08^{*}	204.13^{**}	2.83^{**}	16.46^{**}	219.28^{*}	256.53^{**}	2.15^{**}	6.79^{**}	220.16^{*}	2.58^{**}
Varieties	3	61.75^{**}	228.83^{*}	1369.23^{**}	4.92^{**}	31.23^{**}	165.50^{*}	0.23^{ns}	3.14^{**}	25.09^{**}	442.31^{*}	7.45^{**}
Test	87	18.34^{**}	112.32^{*}	139.56^{**}	2.57^{**}	15.25^{**}	158.26^{*}	267.20^{**}	2.01^{**}	6.24^{**}	214.91^{*}	2.44^{**}
Test vs varieties	1	35.75^{**}	286.76^{*}	2326.16^{**}	19.64^{**}	77.47^{**}	568.54^{*}	96.96^{**}	11.41^{**}	0.06^{ns}	9.84^{ns}	0.41^{**}
Block (eliminatin treatments	3	0.42	7.33	17.06	0.25	0.23	1.50	0.06	0.01	0.11	1.95	0.05
Residuals	9	1.25	14.61	18.90	0.25	0.78	6.89	0.17	0.02	0.16	7.19	0.07

^{ns} $P > 0.05$; * $P <= 0.05$; ** $P <= 0.01$

DTF: days to 50% flowering, **DTM:** days to maturity, **PH:** plant height, **NPB:** numbers of primary branches, **NSB**: numbers of secondary branches, **NCPP**: numbers of capsules per plant, **SPC:** seeds per capsule, **TSW:** 1000 -seed weight, **BY:** biological yield**, HI:** harvest index, **SYPP:** seed yield per plant, **Test:**genotypes included in study

Table 2 Parameters of genetic variability

S. no.	**Traits**	**Mean**	**Range**		**CV**		**h^2(bs)**	**GAM%**
			Min.	**Max.**	**GCV%**	**PCV%**		
1.	**DTF**	55.43	47.62	62.12	7.46	7.73	93.19	14.85
2.	**DTM**	126.90	109.00	144.50	7.79	8.35	86.99	14.99
3.	**PH**	68.52	42.06	112.06	16.03	17.24	86.46	30.75
4.	**NPB**	4.47	1.62	7.13	34.04	35.83	90.27	66.72
5.	**NSB**	14.60	6.81	22.06	26.04	26.74	94.85	52.33
6.	**NCPP**	60.64	22.50	90.25	20.29	20.75	95.65	40.93
7.	**SPC**	9.75	7.94	9.94	39.10	39.15	99.94	86.88
8.	**TSW**	6.88	4.44	9.44	20.49	20.60	98.88	42.03
9.	**BY**	13.42	8.97	17.63	18.37	18.61	97.44	37.42
10.	**HI**	48.91	22.88	83.67	29.46	29.97	96.65	59.76
11.	**SYPP**	6.37	3.42	8.90	24.17	24.54	97.04	49.13

CV: coefficient of variation, **GCV:** genotypic coefficient of variation, **PCV:** phenotypic coefficient of variation, **h^2(bs):** heritability in broad sense, **GAM%:** genetic advance in percentage of mean

DTF: days to 50% flowering, **DTM:** days to maturity, **PH:** plant height, **NPB:** numbers of primary branches, **NSB**: numbers of secondary branches, **NCPP**: numbers of capsules per plant, **SPC:** seeds per capsule, **TSW:** 1000 -seed weight, **BY:** biological yield**, HI:** harvest index, **SYPP:** seed yield per plant

Table 3 Path coefficient analysis for yield and its attributing traits

Traits	**DTF**	**DTM**	**PH**	**NPB**	**NSB**	**NCPP**	**SPC**	**TSW**	**BY**	**HI**
DTF	**0.0612**	-0.0218	0.0056	-0.0035	0.0008	-0.0628	-0.0038	0.0115	0.0005	-0.0275
DTM	0.0413	**-0.0323**	0.0017	-0.0016	0.0005	-0.0980	0.0074	0.0147	0.0104	-0.0072
PH	-0.0043	0.0007	**-0.0791**	0.0012	0.0008	-0.0820	-0.0115	-0.0115	-0.0001	-0.0194
NPB	0.0077	-0.0018	0.0036	**-0.0270**	0.0014	-0.0928	0.015	0.0150	-0.0168	0.0239
NSB	-0.0029	0.0010	0.0038	0.0023	**-0.017**	0.6070	-0.015	-0.0015	-0.0066	0.0011
NCPP	-0.0048	0.0040	0.0089	0.0032	-0.0133	**0.7950**	0.00013	0.0381	0.00104	-0.0157
SPC	-0.0021	-0.0022	0.0085	-0.0038	0.0002	0.0009	**0.1079**	0.1070	-0.0188	0.0142
TSW	0.0041	-0.0027	-0.0030	-0.0025	-0.0049	0.176	-0.0056	**-0.0056**	-0.0192	-0.0003
BY	0.0002	-0.0028	0.0001	0.0039	0.0009	0.0068	-0.0167	-0.0167	**0.1211**	-0.0979
HI	-0.0095	0.0013	0.0088	-0.0038	-0.0001	-0.070	0.0087	-0.0003	-0.0673	**0.1762**

Residual effect=0.018

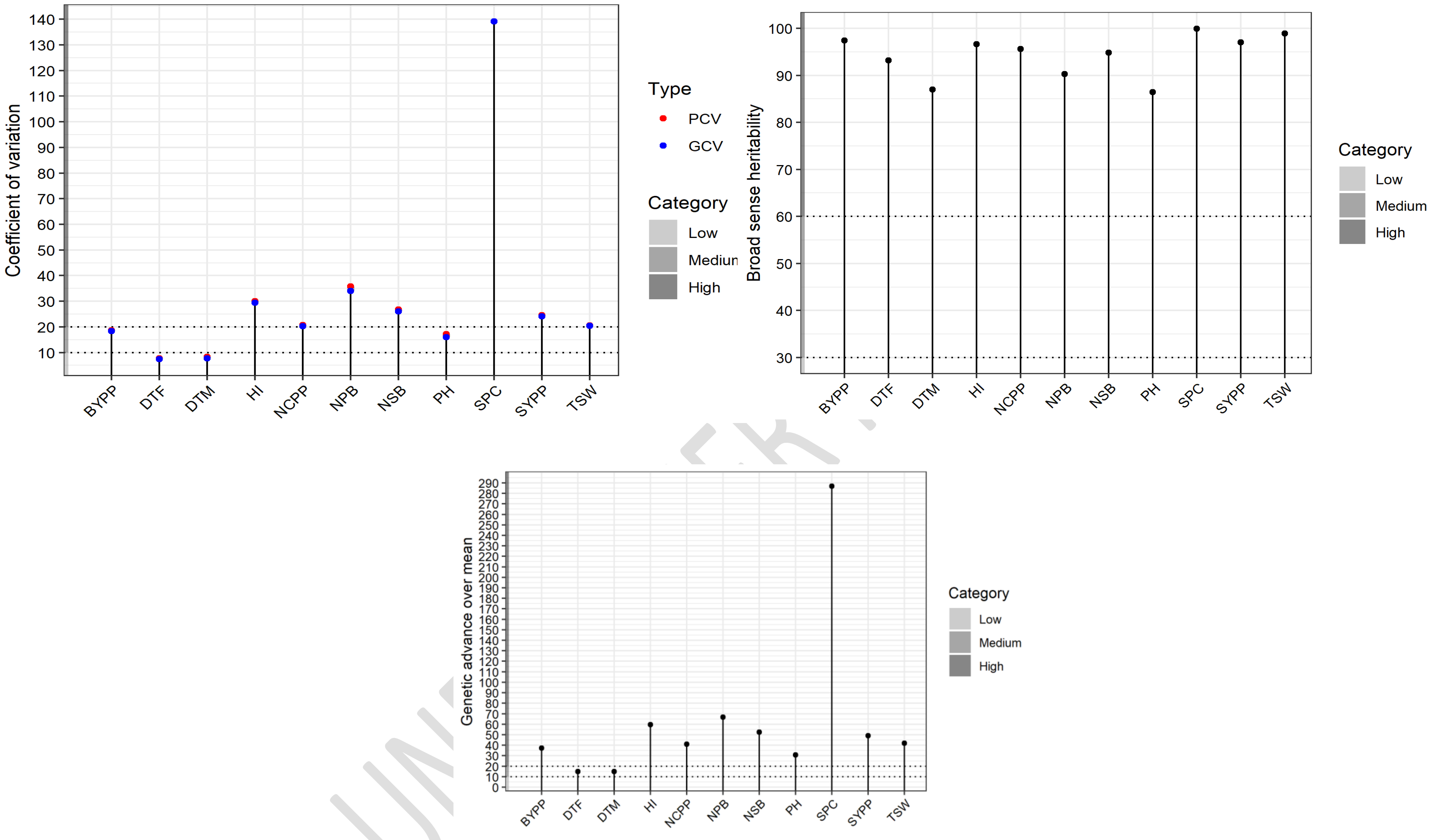


Fig.1 (a) Coefficient of variation for eleven traits showing high,medium, and low categories
(b) Heritability in broad sense for eleven traits of 92 linseed genotypes

(c) Genetic advance over mean showing three different categories

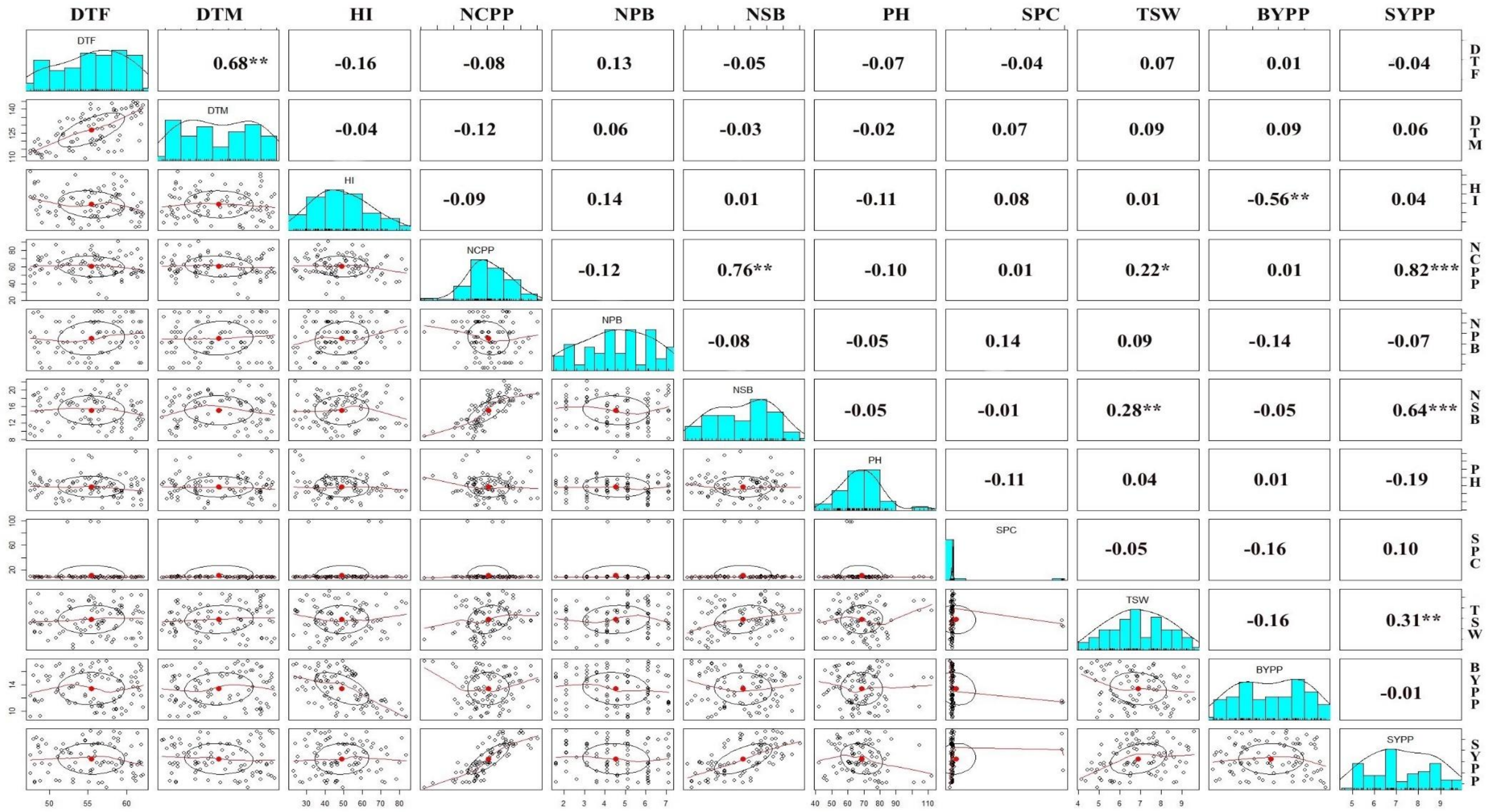
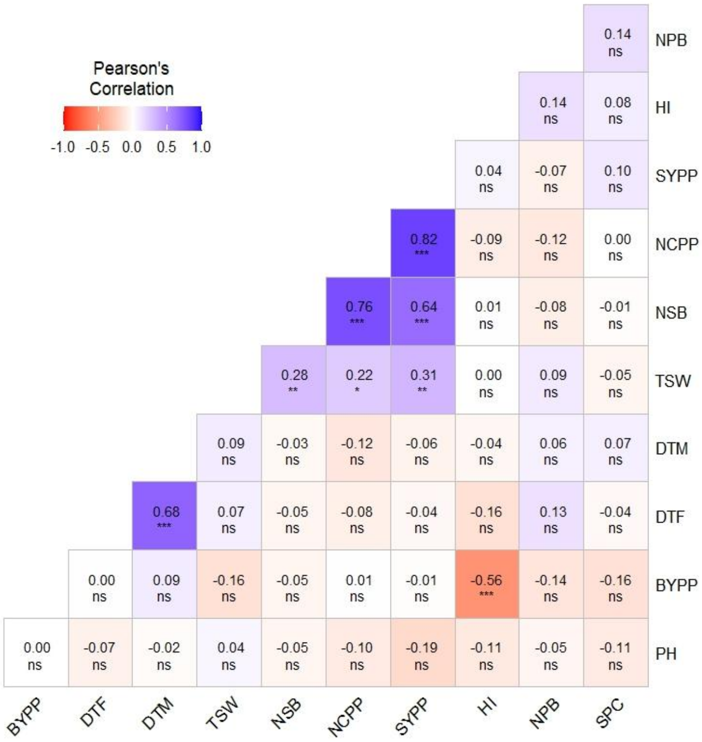


Fig. 2 Pairwise correlations of different quantitative traits of linseed genotypes

The upper panel showing the numerical values of the correlation

The *, **, and *** star indicate correlation significance at 0.05, 0.01 and 0.001 level of probability, respectively

The lower panel showing the scatter plots



	BYPP	DTF	DTM	TSW	NSB	NCPP	SYPP	HI	NPB	SPC
NPB										0.14 ns
HI									0.14 ns	0.08 ns
SYPP								0.04 ns	-0.07 ns	0.10 ns
NCPP							0.82 ***	-0.09 ns	-0.12 ns	0.00 ns
NSB						0.76 ***	0.64 ***	0.01 ns	-0.08 ns	-0.01 ns
TSW					0.28 **	0.22 *	0.31 **	0.00 ns	0.09 ns	-0.05 ns
DTM				0.09 ns	-0.03 ns	-0.12 ns	-0.06 ns	-0.04 ns	0.06 ns	0.07 ns
DTF			0.68 ***	0.07 ns	-0.05 ns	-0.08 ns	-0.04 ns	-0.16 ns	0.13 ns	-0.04 ns
BYPP		0.00 ns	0.09 ns	-0.16 ns	-0.05 ns	0.01 ns	-0.01 ns	-0.56 ***	-0.14 ns	-0.16 ns
PH	0.00 ns	-0.07 ns	-0.02 ns	0.04 ns	-0.05 ns	-0.10 ns	-0.19 ns	-0.11 ns	-0.05 ns	-0.11 ns

ns $p >= 0.05$; * $p < 0.05$; ** $p < 0.01$; and *** $p < 0.001$

Fig. 3 Heat map of Pearson’s correlation coefficient values