Study of Genetic Variability and Path Analysis for Yield Attributing Traits in Linseed (*Linum usitatissimum* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

This study was conducted to assess genetic variability, interrelationship among yield attributing traits and their direct and indirect effect on yield. Ninety-two genotypes including four checks was taken in the study and were planted during two seasons i.e., Rabi 2022-23 and Rabi 2023-24 at Research 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 documented for numbers of capsules per plant (0.82), numbers of secondary branches per plant

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(0.64) and thousand seed weight (0.31). Path coefficient analysis revealed that numbers of capsules per plant was the major contributor to the seed yield (0.7950) followed by harvest index (0.1762) and biological yield (0.1211).

1. 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. In the world, linseed takes up 32.23 lakh ha and yields 30.68 lakh tones with an average productivity of 952 kgha^{-1}; in India, on the other hand, it takes up 1.7 lakh ha and yields approximately 1 lakh tones and 574 kgha^{-1}, respectively [8]. Grown on marginal soil with inadequate management, linseed is the most ignored crop in developing nations due to 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 needs precedence [9]. To full fill such goal, genetic diversity is a prerequisite for genetic improvement of any crop to break the yield plateau [10]. Furthermore, agronomic, and genetic crop development depends heavily on the methodical research and assessment of germplasm lines in every crop improvement programme [9]. 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 [11].

The most accurate way to assess the link between significant yield components is to use correlation in conjunction with path coefficient analysis [12]. 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 [13]. 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 [14]. A prerequisite for improving seed yields is the identification and selection of the main yield components. Considering these facts, an evaluation of the relationship between the yield components and their direct and indirect effects on seed yield was undertaken in present investigation with 92 genotypes.

2. MATERIALS AND METHODS

Present investigation was carried out with a total of ninety-two linseed genotypes along 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 *viz.,* days to 50% flowering, days to maturity, plant height, numbers of primary branches, numbers of secondary branches, numbers of capsules per plant, numbers of seeds per capsule, thousand seed weight, biological yield per plant, harvest index and seed yield. An augmented design was adopted for experimentation. Field was divided into four blocks. Spacing followed was plant to

plant distance of 10 cm followed by 30 cm 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 was applied during the growth and development of crop.

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 covariance components as per methods described by Burton [15] and Searle [16]. While the direct and indirect effect were estimated using path coefficient analysis as described by Dewey and Lu [17].

3. RESULTS AND DISCUSSION

The analysis of variance for 92 linseed genotype 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. Genotypes 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 genotypes in terms of numbers of seeds per capsule. Likewise, the mean sum of square due to test v/s genotype was found significant for all the traits except biological yield per plant and harvest index, indicating that the germplasm lines were meaningfully differed from genotypes 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. [18], Semahegn et al. [19], Leelavathi and Mogali [9], Rajanna et al. [20], Kumar and Kumar [11], Saroha et al. [21] and Kaur et al. [22].

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 17.63 with a mean value 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. 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 level of 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. [23], Manhar [14], Reddy et al. [24], Sathish et al. [25] and Hoque et al. [26].

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.[27], Upadhyay et al. [28], Rajanna et al.[29] and Kumar and Kumar [11]. The parameter days to 50% flowering and days to maturity exhibited high heritability coupled with medium genetic advance that indicated the significance of dominance and epistatic effects in the inheritance of these

Table 1. Analysis 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 (eliminating 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		h²(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, h²(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
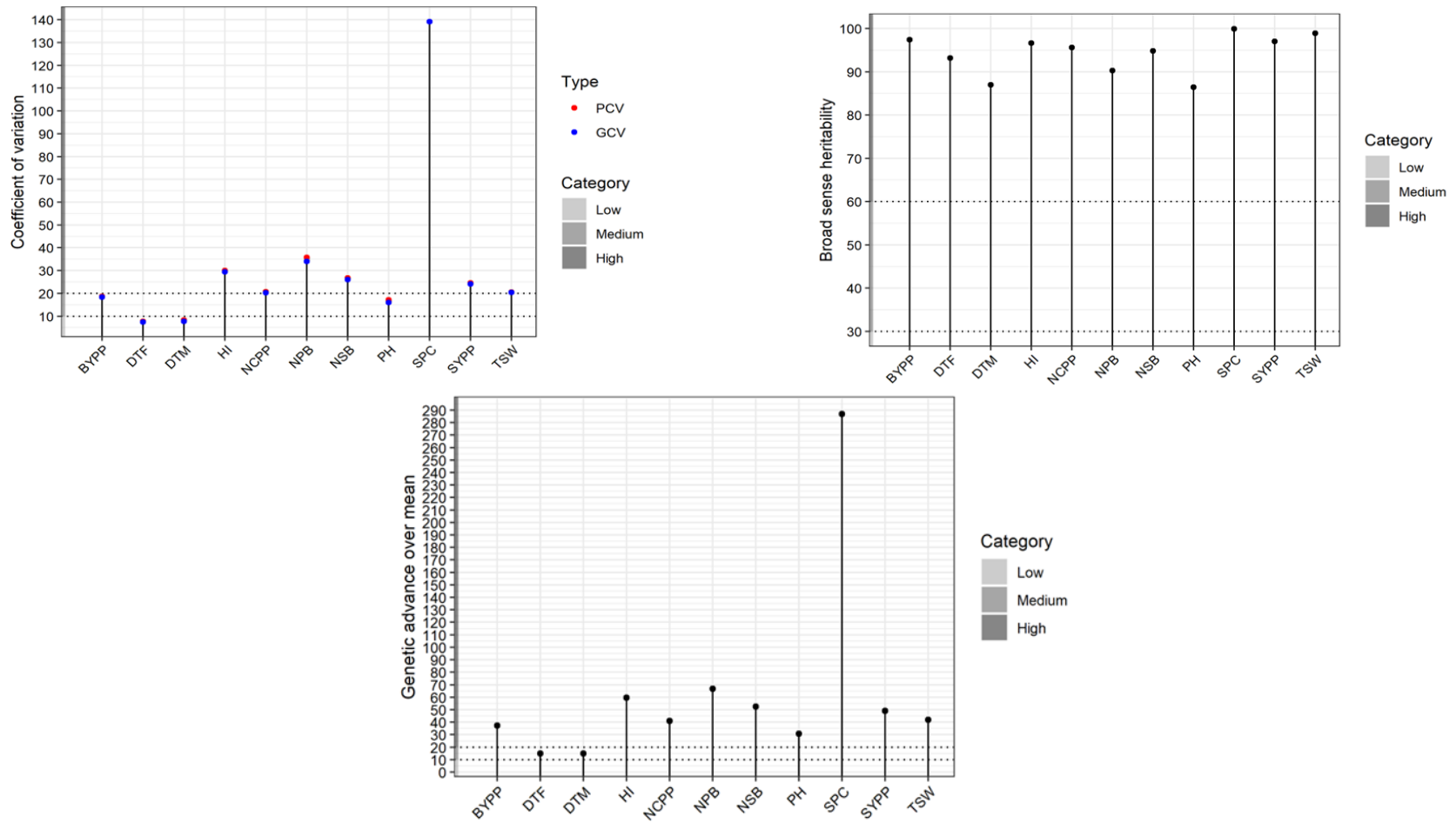
Fig. 1. (a) Coefficient of variation for eleven traits showing high, medium, and low categories (b) Heritability in broad sense for eleven traits of 92 linseed genotypes (c) Genetic advance over mean showing three different categories
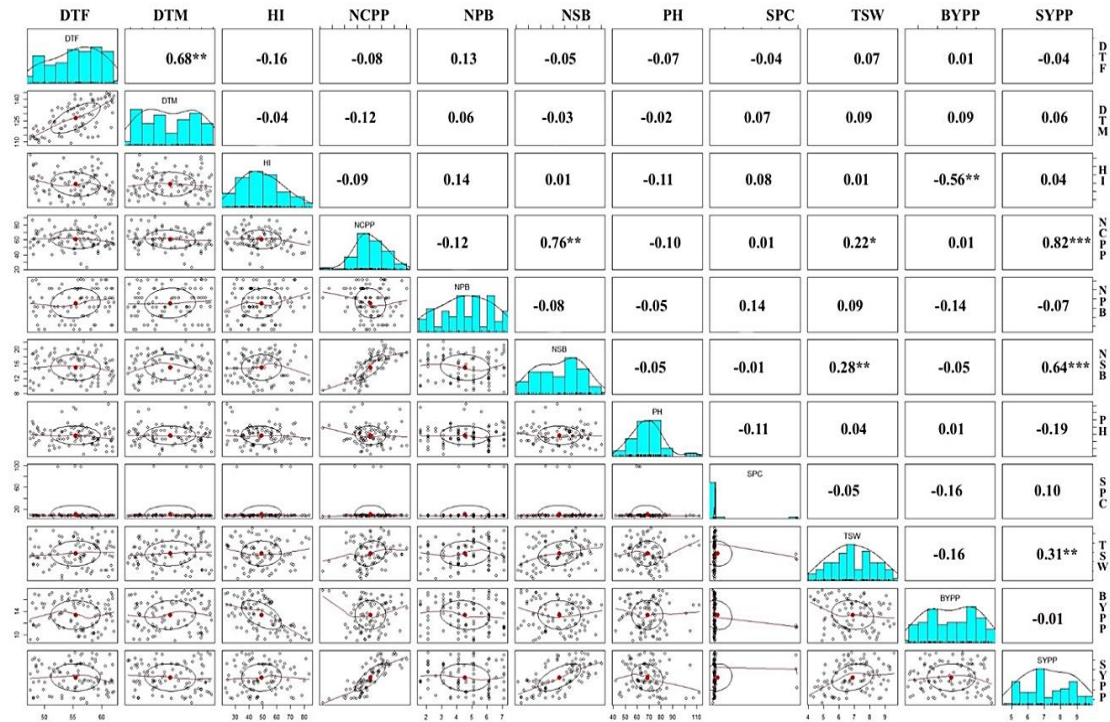
Fig. 2. Pairwise correlations of different quantitative traits of linseed genotypes
The upper panel showing the numerical values of the correlation
The *, **, and *** star indicate correlation significance at 0.05, 0.01 and 0.001 level of probability, respectively
The lower panel showing the scatter plots

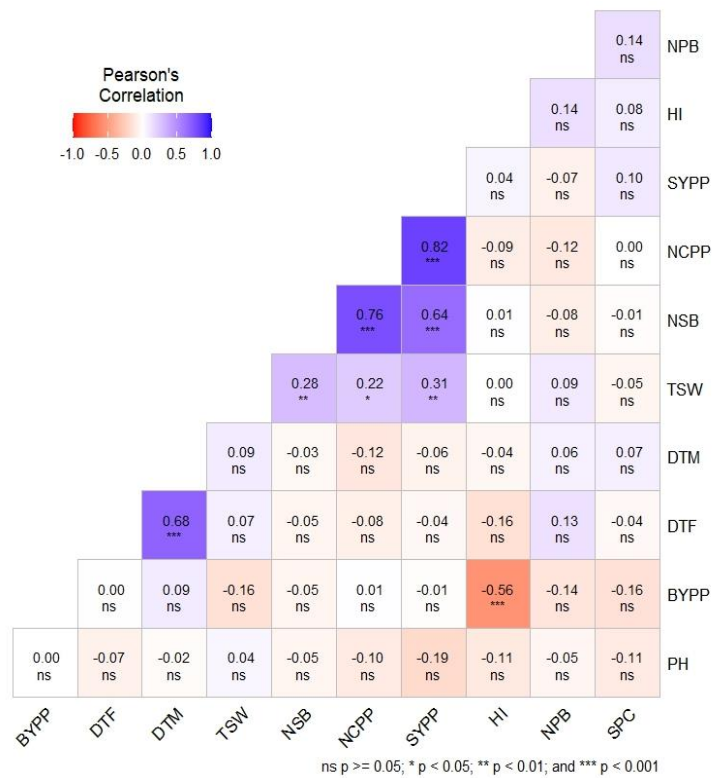ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001

Fig. 3. Heat map of pearson's correlation coefficient values

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. [19], Leelavathi and Mogali [9], Rajanna et al. [29] and Kaur et al. [27].

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 [31]. 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. [18], Shukla [30], Prasanna et al. [31], Rizvi et al. [32], Sathish et al. [25] and Hoque et al. [26].

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. [33] and Reddy et al. [34] 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. [29]. Direct effects of 1000- seed weight on seed yield were documented by Leelavathi and Mogali [9]. 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.

4. CONCLUSION

The investigation of diverse linseed germplasm across different genetic parameter concluded that seed yield is influenced by traits *viz.,* 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 capsules 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).

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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