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RESEARCH ARTICLE

Genetic Analysis of Polygenic Traits for Seed, Fibre and Dual Purpose Linseed (*Linum usitatissimum* L.) Genotypes Grown under Sub Temperate Conditions of Western Himalayas

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Genetic analysis of linseed plant genetic resources is very important to understand gene action and combining ability for crop improvement. Eight genetically diverse lines of linseed namely Surbhi, Bhagsu, Nagarkot, T-397, Himani, Baner, JRF-1 and JRF-4 were evaluated through half diallel cross analysis under sub temperate conditions of Western Himalayas. These eight parental lines identified for seed, fibre and dual purpose trait and 28 F_1 progenieswere grown in CRBD to identify potential parents and their cross combinations for yield and associated traits under variable environments. Significant level of genetic variability was observed among studied genotypes for the yield, fibre and their contributing traits. Genotype×environment (G×E) interaction was also significant except for plant height and technical height indicating a definite role of environment in the performance of genotypes. Non-additive gene action was recorded for maximum traits. Based on GCA, three genotypes *viz*., Baner, Nagarkot and Surbhi were recorded to be good general combiner for seed yield whereas genotypes, JRF-1 and JRF-4 were good for early maturity and fibre yield. These promising genotype harbor the genes for various traits like high seed and fibre yield, early maturity, rust and powdery mildew tolerance. On the basis of high SCA effect, four cross combinations *viz*., Himani×JRF-4, T-397×JRF-4, Bhagsu×Nagarkot and Surbhi×Baner were found best for seed yield while four other *viz*., Surbhi×T-397, Nagarkot×Himani, Surbhi×Baner and Surbhi×Bhagsu were found best for fibre yield in pooled over environments. These genotypes and cross combinations can be used in further hybridization and selection can be done for early maturity, disease tolerance, seed, fibre and dual purpose trait as per the need of linseed breeding programmes in the country.

Key Words: Combining ability, G×E interaction, Gene action, *Linum usitatissimum*

Introduction

Linseed (*Linum usitatissimum* L.) is an annual, self-pollinated, diploid (2x=2n=30) oilseed belonging to the family Linaceae (Singh *et al*., 2021). The species is believed to have originated in regions of the east Mediterranean Sea (Vavilov, 1951). Linseed occupies an important place among oilseed as it is highly nutritive and every portion of it is used commercially (Sran *et al*., 2021). Higher availability of an essential polyunsaturated Omega-3 and Omega-6 fatty acids makes linseed oil unique (Gill, 1987; Reddy *et al*., 2013; You *et al*., 2018; Walkowiak *et al*., 2022). The fibre extracted from straw is utilized to make strong yarns, such as, linen fabrics, sewing strings,carpets and curtains while the coarser grades are used for making twines, canvas bags and quality papers (Jhala and Hall, 2010). In India, the linseed productivity is very low (567 kg/ha) as compared to that of the world (1005.90 kg/ha) (FAO Stat, 2017). The main encumbrances behind low production are the crop cultivation mainly on marginal or sub-marginal soils under rainfed and input-starved conditions. The lower productivity can also be attributed to non-availability of high yielding varieties for routine cultivation (Kiran *et al*., 2012). Development of high yielding varieties along with earliness is always prioritized by the breeders. In linseed, the major breeding goals for seed purpose involves improving seed yield, oil content and its quality and for flax purpose objectives mainly includes higher technical height and quality of fibre (Zare *et al*., 2021).

In order to amalgamate desirable attributes along with high yield, the pertinent approach is recombinant breeding. Thereby, choice of the parents having abundant potential for hybridization is one of the critical tasks. Selection of appropriate parents helps in production of superior recombinant genotypes (Bertan *et al*., 2007). Mostly parents are selected on the basis of *per se*

**Author for Correspondence: Email-jeetsran10@gmail.com* performance, adaptation and diversity, but such criteria do not give desired results because the ability of the parents to combine properly with each other dependson the complex interactions among genes (Allard, 1960). Therefore, the selection of best parents for hybridization must be based upon the knowledge of the combining ability of parents. Some genotypes have the ability to combine with number of other lines indicating good general combining ability (GCA) whereas some combine well only in few cross combinations suggesting specific general combining ability (SCA) (Zhang *et al*., 2015).

Moreover, efficiency of the breeding programme will also depend on the genetic architecture of the traits which are under improvement (Cockerham, 1961). The understanding of gene action helps in the formulation of an efficient breeding programme since it provides exhaustive information about various gene interactions such as additive, dominance and non-allelic interactions. Overall, information like this is more authentic when attained over different environments and forms the foundation of any of the breeding programme. The present research was therefore undertaken on eight diverse germplasm lines to generate information on the nature and the magnitude of the gene action and combining ability effects for early maturity, seed yield, fibre yield and their component traits across environments so that the best parents and cross combinations can be used as apotential genetic resources for future crop improvement programmes in linseed.

Material and Methods

The experiment was conducted under sub temperate conditions of Western Himalayas during three successive *rabi* seasons, from 2015–16 to 2017–18 at the Experimental Farm of the Department of Crop Improvement, CSK HPKV, Palampur at an altitude of 1290.80 meters amsl at 32°80' N latitude and 76°33' E longitude. The experimental material comprised of eight linseed (*Linum usitatissimum* L.) genotypes and 28 cross combinations (F_1's) (Table 1). The cross combinations were attempted as per the 8 × 8 diallel mating design excluding reciprocals during *rabi* 2015-16.

Experimental design, data recording and statistical analysis

Eight linseed genotypes and 28 cross combinations (F_1's) were grown in a randomized complete block design (RCBD) with three replications at same location for two consecutive years i.e., *rabi* 2016-17 and *rabi* 2017-18. Each genotype and cross combinations were raised in a single row of 1.5 m with plant to plant and row to row spacing of 10 cm and 30 cm, respectively. The data were recorded from five random competitive plants in each line across replications on plant height, technical height, capsules per plant, seeds per capsule, primary branches per plant, secondary branches per plant, 1000-seed weight, seed yield per plant, aerial biomass per plant, harvest index, straw yield per plant, retted-straw yield per plant and fibre yield per plant, while phenological traits i.e., days to 50% flowering and days to 75% maturity were recorded on plot basis. To test the significance of differences among different genotypes/breeding material used in the study, the data on mean values for the different traits were analyzed as per Panse and Sukhatme (1985):

$$Y_{ij} - \mu_1 + g_1 + r_j + e_{ij}$$

where, Y_{ij} = phenotypic observation of i^{th} genotype grown in j^{th} replication, μ = general population mean, g_1 = effect of i^{th} genotype, r_j = effect of j^{th} replication, and e_{ij} = error component of i^{th} genotype in j^{th} replication.

Diallel Cross Analysis

The replication wise mean data obtained from F_1 population of twenty eight cross combinations for each trait were subjected to combining ability analysis of Griffing's (1956) Method 2 Model I.

When the F-test revealed significant differences among the genotypes, combining ability analysis was followed. A linear mathematical model for an observation made on ij^{th} genotype is expressed as:

$$Y_{ij} - \mu + g_i + g_j + s_{ij} + \frac{1}{bc}\sum_{K}\sum_{L} e_{ij}KL$$

where,

Y_{ij} = phenotype of the hybrid between i^{th} and j^{th} parents in k^{th} block

μ = population mean,

g_i = GCA effect of the i^{th} parent,

g_j = GCA effect of the j^{th} parent,

s_{ij} = SCA effect of the hybrid between i^{th} and j^{th} parents such that $s_{ij} = s_{ji}$

bc = block effect,

$e_{ij}kL$ = environment effect linked with $ijkL^{th}$ observation

$\frac{1}{bc}\sum_{k}\sum_{L} e_{ij}kL$ = is the mean error effect

Table 1. Linseed genotypes and their parentage/source used in the study

Sl. No.	Genotypes	Parentage/Source	Type	Seed colour	Maturity	Year of release	Reaction to Major diseases	
							Rust	Powdery mildew
1.	Surbhi	LC-216 × LC-185	Seed type	Yellow	Medium	1994	Resistant	Susceptible
2.	Bhagsu	RL-50-3 × Surbhi	Seed type	Brown	Late	2008	Moderately resistant	Susceptible
3.	Nagarkot	New River × LC-216	Dual purpose	Light brown	Medium	1995	Resistant	Resistant
4.	T-397	T491 × T1193-2	Seed type	Brown	Early	1984	Highly susceptible	Highly susceptible
5.	Himani	DPL-20 × KLS-1	Seed type	Brown	Late	2008	Moderately resistant	Moderately resistant
6.	Baner	EC-21741 × LC-214	Seed type	Light brown	Late	2005	Resistant	Moderately resistant
7.	JRF-4	CRIJAF, Barrackpore*	Fibre type	Brown	Early	-	Moderately resistant	Moderately resistant
8.	JRF-1	CRIJAF, Barrackpore*	Fibre type	Brown	Early	-	Moderately resistant	Moderately resistant

*[CRIJAF: Central Research Institue for Jute and Allied Fibre]

Combining ability analysis for pooled over environments

The combining ability analysis for pooled over environments for experimental Method 2 Model I was done by using method of Singh (1973). The notations used were: p (number of parents), b (number of blocks), c (number of observations) and L (number of environments).

The model used was:

$$Xijk = \mu + gi + gj + gj + Sij + LK + (gL)\ ik + (gL)\ jk + (SL)\ ijk + H + \frac{1}{bc}\sum_{m}\sum_{ijkmr} e$$

where, μ = population mean, gi (gi) = GCA effect of i^{th} (j^{th}) parent, Sij = SCA effect of the crosses between the i^{th} and j^{th} parents, LK = effect of k^{th} environment, (gL)ik or (gL)jk interaction between GCA effects of the i^{th} and j^{th} parents with k^{th} environment, (SL)ijK = the interaction between SCA effects of the ij^{th} cross and the k^{th} environment, and H = 0 for fixed effect model.

Results and Discussion

The analysis of the variance revealed significant differences among the genotypes for all traits (Table 2). Variance due to environments in pooled analysis also indicated significant differences for the all traits studied except seeds per capsule suggesting considerable variation present amongst all the environments. The genotype×environment (G×E) interaction was also significant for all the traits except plant height and technical height. This indicates that genotypes behaved in a different way as the environmental conditions got changed and the variation in the stability of their performance over the environments was mainly due to G×E interaction. Yadav *et al*. (2014) observed significant G × E interaction for primary branches per plant, secondary branches per plant, days to maturity, number of seeds per capsule, 1000-seed weight, harvest index and seed yield per plant. Significant G × E interaction for different traits has been reported by Alem and Dessalegn (2014) and Temesgen *et al*. (2014). Parents vs. hybrids also expressed significant differences for all the traits studied indicating the existence of substantial amount of genetic variability.

The analysis of variance forthe combining ability affirmed mean squares due to GCA and SCA were significant for all the traits studied in pooled over environments (Table 2). Significant variation due to GCA and SCA indicates the importance of additive as well as non-additive types of gene action for the expression of the traits under study. These results are similar to the findings of Abdel-Moneam (2014), Abd Al-Sadek (2015), Singh *et al* (2016) and Kumar *et al* (2017).

The significant differences due to GCA, SCA and environments indicate the presence of sufficient genetic variability in the material. Furthermore, mean squares due to GCA×environment interaction were significant for all the traits studied except plant height, capsules per plant, seeds per capsule, harvest index, straw yield per plant, retted-straw yield per plant and fibre yield per plant, whereas mean square due to SCA×environment interaction were significant for all the traits studied except plant height, technical height and aerial biomass per plant. Significant mean squares due to GCA×environment and SCA×environment interaction effects indicated that the performance of the cross combinations and parents were affected by the environment and with the change in the environment combining abilities for traits did not remain same. Therefore, there is further need to test cross combinations as well as parents across the environments

Table 2. Variance and combining ability analysis for different traits in pooled over environments in linseed

	Variance over environments						Variance for combining ability					
Source of variation Traits	Replication	Genotypes	Environments	Genotypes × Environment (g × e)	Parents vs. Hybrids	Error	GCA	SCA	Environments	GCA × Environment	SCA × Environment	**Pooled error**
df	2	35	1	35	1	140	7	28	1	7	28	**140**
Days to 50% flowering	20.14	67.92*	1166.69*	20.90*	95.72*	1.28	74.41*	9.70*	583.34*	5.89*	7.24*	0.43
Days to 75% maturity	4.68	105.13*	3978.38*	12.38*	13.76*	2.32	142.94*	8.07*	1989.19*	3.59*	4.26*	0.78
Plant height	74.95	275.85*	481.27*	23.63	732.60*	19.39	308.14*	37.90*	240.64*	6.71	8.17	6.46
Technical height	2.34	137.01*	610.31*	13.28	79.53*	8.91	185.89*	10.62*	305.16*	6.67*	3.87	2.97
Primary branches per plant	5.16	23.30*	17.39*	4.11*	433.34*	0.84	9.56*	7.32*	8.69*	1.55*	1.33*	0.28
Secondary branches per plant	4.67	13.57*	34.08*	3.96*	176.18*	0.46	6.56*	4.01*	17.04*	1.17*	1.36*	0.15
Capsules per plant	145.58	1041.22*	5054.03*	163.31*	21714.86*	40.74	356.08*	344.82*	2527.01*	17.70	63.62*	13.58
Seeds per capsule	0.67	1.65*	0.71	0.67*	1.82*	0.26	0.83*	0.48*	0.36*	0.13	0.25*	0.09
1000-seed weight	0.22	3.36*	18.82*	0.83*	36.51*	0.21	1.48*	1.03*	9.41*	0.18*	0.30*	0.07
Aerial biomassper plant	2.34	8.49*	211.38*	1.57*	96.58*	1.04	3.39*	2.69*	105.70*	1.06*	0.39	0.35
Seed yield per plant	0.15	1.59*	7.16*	0.23*	32.88*	0.04	0.49*	0.54*	3.58*	0.10*	0.07*	0.01
Harvest index	2.01	120.69*	39.42*	23.29*	1790.42*	9.81	55.43*	36.43*	19.71*	3.44	8.85*	3.27
Straw yield per plant	0.31	197.95*	789.67*	45.81*	3144.37*	28.55	77.61*	63.07*	394.84*	14.96	15.35*	9.52
Retted-straw yield per plant	0.33	1.40*	10.05*	0.21*	18.00*	0.11	0.77*	0.39*	5.03*	0.04	0.08*	0.04
Fibre yield per plant	0.10	29.93*	98.28*	3.89*	388.22*	2.50	18.23*	7.91*	49.14*	1.04	1.36*	0.83

* Significance at $P \leq 0.05$

mainly for traits showing significant interaction with the environment. Further, non-significant GCA×environment interaction and significant SCA×environment interaction for capsules per plant, seeds per capsule, harvest index, straw yield per plant, retted-straw yield per plant and fibre yield per plant indicated that the non-additive effects were more influenced by environment than the additive effects controlling these traits.

The estimates of genetic components of variance along with related genetic parameters revealed that the magnitude of σ^2SCA was higher than σ^2GCA for days to 50% flowering, plant height, primary branches per plant, secondary branches per plant, capsules per plant, seeds per capsule, 1000-seed weight, aerial biomass per plant, seed yield per plant, harvest index, straw yield per plant, retted-straw yield per plant and fibre yield per plant in combined over environments. The estimates of σ^2GCA were higher than σ^2SCA for days to 75% maturity and technical height in all the environments. The preponderance of σ^2SCA indicated predominant role of non-additive gene action governing all the traits except days to 75% maturity and technical height. This was also confirmed by ratio of σ^2GCA: σ^2SCA which is less than the theoretical maximum of unity for all the characters except days to 75% maturity and technical height in pooled over environments. The preponderance of non-additive gene action for primary branches per plant, secondary branches per plant, plant height, capsules per plant, seeds per capsule, seed yield per plant, 1000-seed weight and harvest index is in agreement with the findings of Nirala *et al*. (2018) and Mahto *et al*. (2019).

Further, σ^2A with higher magnitude, was noticed for days to 50% flowering, days to 75% maturity, plant height and technical height which exhibited the involvement of additive gene action. However, for the remaining characters σ^2D was higher than those of σ^2A in pooled over environments, signifying predominance of non-additive gene action (Table 3). The predominance of non-additive gene action has also been stated by Bhateria *et al*. (2006); Kumar and Paul (2015) and Naik (2017). In case of days to 50% flowering and plant height, the σ^2SCA was higher than σ^2GCA but contrary to that σ^2A was higher than σ^2D. It can be so because statistically GCA variance is the additive part of variability, besides it involves additive × additive and higher order of epistatic interactions (Matzinger and Kempthorne, 1956).

Over dominance (> 1) observed for primary branches per plant, secondary branches per plant, capsules per plant, seeds per capsule, 1000-seed weight, aerial biomassper plant, seed yield per plant, harvest index, straw yield per plant, retted-straw yield per plant and fibre yield per plant indicates the non-additive genetic variance in controlling the characters except for days to 50% flowering, days to 75% maturity, plant height and technical height where partial dominance was

Table 3. Estimation of genetic components of variance and degree of dominance for different traits in pooled over environments in linseed

Traits	σ^2_{GCA}	σ^2_{SCA}	σ^2_{GCA}/ σ^2_{SCA}	σ^2A	σ^2D	Öσ^2D /σ^2A	Heritability (%) (h^2_{ns})
Days to 50% flowering	3.70	4.64	0.80	7.40	4.64	0.79	31.50
Days to 75% maturity	7.11	3.65	1.95	14.22	3.65	0.51	7.78
Plant height	15.08	15.72	0.96	30.17	15.72	0.72	28.77
Technical height	9.15	3.82	2.39	18.29	3.82	0.46	35.44
Primary branches per plant	0.46	3.52	0.13	0.93	3.52	1.95	11.14
Secondary branches per plant	0.32	1.93	0.17	0.64	1.93	1.74	13.27
Capsules per plant	17.12	165.62	0.10	34.25	165.62	2.20	9.15
Seeds per capsule	0.04	0.20	0.19	0.08	0.20	1.63	10.32
1000-seed weight	0.07	0.48	0.15	0.14	0.48	1.85	11.15
Aerial biomassper plant	0.15	1.17	0.13	0.30	1.17	1.96	8.62
Seed yield per plant	0.02	0.26	0.09	0.04	0.26	2.35	8.66
Harvest index	2.61	16.58	0.16	5.22	16.58	1.78	11.15
Straw yield per plant	3.40	26.78	0.13	6.81	26.78	1.98	8.01
Retted-straw yield per plant	0.04	0.18	0.21	0.08	0.18	1.56	13.60
Fibre yield per plant	0.87	3.54	0.25	1.74	3.54	1.43	14.94

* Significance at $P \leq 0.05$

observed indicating the predominance of additive gene action (degree of dominance being < 1) implying that selection may be effective in improving these characters (Table 3). The results are in confirmation with the findings of Kumar *et al*. (2016) and Singh *et al*. (2016).

Narrow sense heritability predicts the importance of the additive portion of the genetic variance that can be transferred to the next generation. The perusal of data presented in Table 3 revealed that medium heritability was observed for days to 50% flowering and technical height whereas, rest of the traits studied showed low heritability. Medium heritability suggests that the traits may be improved by making selections among the recombinants obtained through segregating populations. On the other hand, low heritability implies non-fixable component of the variation. As genetic variation of all the traits is mainly affected by the non-additive gene effects with low and medium heritability, so direct selection for such traits will not be effective. Therefore, these cross combinations can be utilized in later generations for getting desirable segregants. These result are consistent with the findings of Naik (2017) who has reported that narrow sense heritability estimates were low for plant height, primary branches per plant, capsules per plant, seeds per capsule, 1000-seed weight and seed yield per plant. Similarly, low narrow sense heritability for seeds per capsule, 1000-seed weight and seed yield per plant were reported by Goral and Ejsmond (2008).

General combining ability effects contribute significantly for identification of the germplasm base for its inclusion in the hybridization program. Out of eight genotypes *viz*.,Baner, Nagarkot and Surbhi were good general combiners for seed yield and its related traits. For fibre yield, the genotypes *viz*., JRF-1, JRF-4 and Bhagsu were found as the best general combiners. For dual purpose trait, genotype Nagarkot was observed as the good general combiner in pooled over environments. For early maturity, T-397, JRF-1and JRF-4 were found as the good general combiners (Table 4). In the present study of general combining ability effects, significant values were observed for maximum number of traits over combined environments in four genotypes *viz*., Nagarkot, Surbhi, JRF-1 andJRF-4 on the basis of their magnitude of the GCA effect. It seems that the GCA rank for economic yield is linked to the GCA for the important component characters. It can be inferred that besides the economic yield, these genotypes also possessed significant desirable GCA values for its component characters and appeared to be worthy for exploitation in practical plant breeding for utilizing the fixable component of variation. Therefore, these parents can be used extensively in the hybridization followed by selection to hasten the pace of the genetic improvement of dual purpose trait, seed yield, fibre yield and their component characters.

The desirable SCA effects were not revealed by any of the cross combination for all studied traits. However, four cross combinationswere selected for economic traits in pooled over environments on the basis of higher and significant specific combining ability effects in relation to GCA effects and *per se* performance. Himani×JRF-4, T-397×JRF-4, Bhagsu×Nagarkotand Surbhi×Baner were the promising cross combinations with desirable SCA effects for seed yield. The promising cross combinations indicating desirable SCA effects for fibre yield were Surbhi× T-397, Nagarkot×Himani, Surbhi×Baner and Surbhi×Bhagsu. In case of dual purpose trait, single cross combination with fascinating SCA effects was Surbhi×Baner. The combinations which exhibited high SCA effects involved all types of parents possessing good, average as well as poor GCA effects. Bhateria *et al*. (2006) and Singh *et al*. (2009) reported similar kind of results that the cross combinations indicating desirable SCA effects for different characters involve good×good, good×poor and good×average general combiners. Furthermore, in case of seed yield, only one cross combination, Surbhi×Baner (good×good) indicated significant positive SCA effects along with parents possessing good general combining ability effects for the trait. Therefore, necessarily it is not that the cross combinations showing higher SCA effects must involve good general combiners like their parents as observed by Sood *et al*. (2011). This suggests that GCA had no bearing on the SCA effects of the cross combinations (Bhateria *et al*., 2006).

Conclusion

The results obtained in the present investigation suggested that dominance gene effects were predominant as compared to additive effects for most of the traits including seed yield and fibre yield. Under such genetic control in the expression of traits, heterosis breeding may be useful but chances of exploiting hybrid vigour through hybrid varieties in linseed due to its autogamous nature are bleak at present. Under such situations, diallel selective mating or biparental mating in early segregating

Table 4. Estimates of general combining ability effects of parents for various traits in pooled over environments in linseed

Traits: Parental lines:	Days to 50% flowering	Days to 75% maturity	Plant height	Technical height	Primary branches per plant	Secondary branches per plant	Capsules per plant	Seeds per capsule	1000-seed weight	Aerial biomass per plant	Seed yield per plant	Harvest index	Straw yield per plant	Retted-straw yield per plant	Fibre yield per plant
Surbhi	1.23*	0.63*	-6.62*	-5.00*	0.82*	0.83*	3.56*	-0.06	0.16*	-0.63*	0.09*	2.54*	-4.00*	-0.21*	-0.62*
Bhagsu	0.35*	1.05*	2.73*	-0.02	0.29*	0.38*	2.99*	0.19*	-0.16*	0.27*	0.01	-0.63	1.19	0.14*	0.67*
Nagarkot	2.53*	2.21*	2.67*	1.52*	0.52*	0.54*	6.39*	0.04	0.17*	0.09	0.14*	1.40*	0.31	0.06	0.44*
T-397	-2.03*	-1.39*	-3.94*	-3.21*	0.61*	0.17*	-0.54	-0.45*	0.41*	-0.60*	-0.18*	-0.52	-1.88*	-0.24*	-1.50*
Himani	0.63*	2.30*	-2.06*	-1.07*	-0.25*	-0.39*	-2.19*	0.01	-0.41*	0.21	0.02	-0.30	0.98	-0.10*	-0.76*
Baner	1.78*	2.78*	-0.43	0.57	-0.06	-0.24*	0.34	0.07	0.00	0.55*	0.24*	1.42*	2.03*	-0.14*	-0.41*
JRF-4	-1.98*	-3.65*	3.45*	3.72*	-0.85*	-0.43*	-4.44*	0.19*	0.12*	0.08	-0.09*	-1.45*	0.48	0.25*	1.05*
JRF-1	-2.52*	-3.92*	4.20*	3.49*	-1.08*	-0.86*	-6.10*	0.01	-0.29*	0.03	-0.21*	-2.46*	0.90	0.23*	1.13*
SE (gi) ±	0.14	0.18	0.53	0.36	0.11	0.08	0.78	0.06	0.06	0.12	0.02	0.38	0.65	0.04	0.19
SE (gi-gj) ±	0.21	0.28	0.80	0.55	0.17	0.12	1.17	0.09	0.08	0.19	0.03	0.57	0.98	0.06	0.29
CD (gi)	0.27	0.35	1.05	0.71	0.22	0.16	1.54	0.12	0.11	0.24	0.04	0.74	1.28	0.08	0.37
CD (gi-gj	0.41	0.55	1.59	1.08	0.33	0.24	2.30	0.18	0.17	0.37	0.07	1.13	1.93	0.12	0.57

generations followed by pedigree selection method might be appropriate approach toward genetic improvement of these traits for exploitation of both fixable and non-fixable gene effects.Based on GCA effect, three genotypes namely Baner, Nagarkot and Surbhi were identified good general combiner for seed yield whereas genotypes, JRF-1 and JRF-4 were good for early maturity and fibre yield. These genotypes are identified for different characters and their promising characters can be combined to develop high yielding varieties. On the basis of high SCA effect, four cross combinations *viz*., Himani×JRF-4, T-397×JRF-4, Bhagsu × Nagarkot and Surbhi×Baner were found best for seed yield while four other *viz*., Surbhi×T-397, Nagarkot×Himani, Surbhi×Baner and Surbhi×Bhagsu were found best for fibre yield in pooled over environments. These promising genotypes and cross combinations can be used in further hybridization and selection can be done for seed, fibre and dual purpose trait as per the need of linseed breeding programmes.

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