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# Assessment of genetic analysis and correlation studies in released varieties of linseed (*Linum usitatissimum* L.) from IGKV

**Jhanendra Kumar Patel, Karabi Biswas and Nandan Mehta**

**Abstract**
The field experiments were conducted in Randomized complete block design with three replications during *rabi* season 2019-20 in twenty-seven IGKV released linseed genotypes including three checks (RLC-92, RLC-133 and RLC-143). Analysis of variance for all the traits showed the existence of sufficient amount of variability present among twenty-seven linseed genotypes. The maximum genotypic coefficient of variation and phenotypic coefficient of variation was found to be the highest in number of secondary branches per plant followed by number of capsules per plant, number of primary branches per plant, harvest index (%) and seed yield per hectare (qt.) implying the existence of appreciable amount of variability for those traits among the genotypes. Number of secondary branches per plant recorded high broad sense heritability coupled with high genetic advance as percent of mean followed by number of capsules per plant, harvest index (%), seed yield per hectare (qt.), number of primary branches per plant, 1000 seed weight (g), plant height (cm), seed size (mm) and oil content (%). Highest significantly positive correlation was observed for harvest index (%) and number of capsules per plant" subsequently, positive correlation with number of primary branches per plant, days to 50% flowering and oil content (%) at both genotypic and phenotypic level. Presence of Positive association among the desirable characters is favorable because it encourages simultaneous improvement in both the characters. Hence, these characters can be considered as yield determinants.

**Keywords:** Variance, genotypic, seed yield, oil content

## Introduction
Linseed (*Linum usitatissimum* L.) 2n=30, is a versatile crop grown in diverse regions mainly for the purpose of food, oil, fodder, fibre and pharmaceuticals. The presence of diverse range of genotypes for the characterization as well as the assessment of data is of immense importance to realize the prospects of linseed in agriculture. Large numbers of linseed varieties have been released from IGKV, AICRP on Linseed since 1967. In general, all varieties of linseed have greater uniformity for their plant morphology additionally for blue flower that holds important place for DUS testing and variety identification.

Area & production of linseed is being declined year by year due to non-availability of identifiable variations for different varieties. As per the Food and Agriculture Organization statistical data (FAOSTAT, 2021) [11], currently, the overall world production of linseed is around 3.34 million tonnes, with Canada (34%), Russia (15%), and China (13%) being the major producers. In the world, India is the 6$^{th}$ largest producer adding 13% and 5.5% to global linseed area and production respectively. In the world, India is the foremost growing country of linseed ranking 4$^{th}$ in area 19.65 mha and production of 12.96 mt followed by Russia, Kazakhstan, and Canada, with annual area whereas, in terms of productivity India (543.8 Kg/ha) is far behind to other country (FAOSTAT, 2021) [11].

In India, linseed is mostly occupied under rainfed (63%), utera (25%) and irrigated (17%) conditions and in famished conditions in the major linseed producing states of India are Madhya Pradesh, Chhattisgarh, Maharashtra, Jharkhand, Uttar Pradesh and Odisha. Currently, linseed is grown in Chhattisgarh in 29900 ha with 1030 tonnes production and average productivity 344 Kg/ha (INDIASTAT, 2018). Production and area wise, Chhattisgarh is one of the significant linseed producing states of India. In Chhattisgarh, Durg, Rajnandgaon, Bilaspur, Raigarh, Raipur, Dhamtari, Sarguja, Raipur and Kabirdham are the prime growing districts of linseed. In Chhattisgarh, linseed is grown as a rabi crop under rainfed (63%) and in utera (25%) under sub-marginal lands.

For the genetic enhancement of linseed crop either through direct enhancement of traits in which plant breeder is interested or indirect enhancement through component traits can be successfully achieved using ample genetic information on linseed crop. In order to touch the eventual goal of getting high quality seed yield, study of presence of genetic variability for seed yield and its improvement, and the nature of correlation among themselves is a crucial prerequisite. Plant height and seed yield in linseed will provide an additional assistance in deciding the selection criteria for selecting dual purpose linseed genotypes and would provide enough opportunities to enhance its cultivation in the state of Chhattisgarh. Correlation coefficient provides degree of association between two variables or characters helps us in understanding the nature and magnitude of association among seed yield and yield components, on which selection can be done for genetic improvement of crops for yield. At genetic level, coupling phase of linkage is reason for positive correlation.

## Material and Methods

### Experimental area and materials

The field experiments were conducted in Randomized complete block design with three replications during *rabi* season 2019-20 in twenty-seven IGKV released linseed genotypes including three checks (RLC-92, RLC-133 and RLC-143). The genotypes were collected from All India Coordinated Research Project (AICRP) on Linseed, functioning at the Research Cum Instructional Farm, Department of Genetics & Plant Breeding Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. All the recommended package of practices was carried out to raise the good crops. All the genotypes were sown on 28th November, 2019 in plots of three rows each of 4 m length with row to row spacing of 30 cm and plant to plant spacing approximately 10 cm. five competitive plants have been randomly selected from each plot for taking observations.

### Trait measured

In this study, observations on characters related to seed yield and its components along with morphological traits based on linseed descriptor, Kanpur (2010) [6] "National guidelines for the conduct of tests for Distinctness, Uniformity and Stability in linseed, India" published as per Catalogue on linseed germplasm, Project Coordinating Unit (Linseed), Kanpur, (2010) [6] have to record. Following traits were evaluated plant height (cm), days to 50 percent flowering, number of capsules per plant, days to maturity, number of primary branches/plant, number of secondary branches/plant, 1000 seed weight (g), seed size (mm), oil content (%), harvest index (%), seed yield/ plant (g). Climatic variations were monitored using a meteorological station set up close to the experimental area.

**Table 1:** Experimental material used in the present study

| S. No. | Genotypes | S. No. | Genotypes | Source |
|---|---|---|---|---|
| 1. | R-7 | 15. | RLC-165 | AICRP on Linseed, Department of Genetics and Plant Breeding, IGKV, Raipur (C.G.) |
| 2. | R-17 | 16. | RLC-167 | |
| 3. | KIRAN | 17. | RLC-171 | |
| 4. | R-552 | 18. | RLC-172 | |
| 5. | KARTIKA | 19. | RLC-173 | |
| 6. | DEEPIKA | 20. | RLC-175 | |
| 7. | IA-32 | 21. | RLC-176 | |
| 8. | RLC-92 | 22. | RLC-177 | |
| 9. | RLC-133 | 23. | RLC-178 | |
| 10. | RLC-143 | 24. | RLC-179 | |
| 11. | RLC-148 | 25. | RLC-180 | |
| 12. | RLC-153 | 26. | RFC-2019-1 | |
| 13. | RLC-161 | 27. | RFC-2019-2 | |
| 14. | RLC-164 | | | |

### Genetic-statistical analysis

All the statistical analysis has to be done with the aid of windostat version 9.2 from indostat service, Hyderabad." The data were processed with the aid of different standard statistical procedures as mentioned below.

Analysis of Variance was carried out as per the method suggested by Panse and Sukhatme (1967) [30].

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Whereas,

$Y_{ij}$ = Yield of $j^{th}$ genotype in $i^{ts}$ replication. $\mu$ = General mean $g_i$ = Effect of $i^{th}$ genotype $r_j$ = Effect if $j^{th}$ replication $e_{ij}$= Error component

### Assessment of variability parameters

All the observed traits were analyzed for each of the test genotypes taken under study and were evaluated with the help of various variability parameters as mentioned below:

$$X = \frac{\Sigma Xi}{n}$$

Where,

X = Mean,

$\Sigma X_i$ = Sum of all observations,

N = Total number of all observations

$$SD = \sqrt{\frac{\Sigma d2}{N}}$$

SD =Standard deviation

X = Mean

Heritability in terms of broad sense (bs) was evaluated by using the formula given by Allard (1960) [2]. It is expressed as%.

$$\text{Heritability } (h^2_{bs}) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,
$\sigma^2$g= genotypic variances,
$\sigma^2$p = phenotypic variances.

Genetic advance (GA) = $h^2_{(bs)} \times K \times \sigma_p$

Where,
$h^2_{(bs)}$ = Heritability in terms of broad sense
$\sigma_p$ = Phenotypic standard deviation of the original population
K = Selection intensity at 5% = 2.06 suggested by "Allard (1960) [2]"

Genetic advance as a percentage of $\bar{x} = \frac{GA}{\bar{x}} \times 100$

Whereas,
GA = Genetic advance
$\bar{x}$ = Population mean

The genotypic coefficient of variation and phenotypic coefficient of variation was computed as per Burton (1952) [5], heritability (broad sense), and genetic advance as a percent of the mean as per Allard (1960) [2]. The genotypic and phenotypic coefficient of correlation was calculated using the method given by Johnson *et al.* (1955a) [17].

**Evaluation of correlation coefficients**

For evaluating coefficient of phenotypic and genotypic correlation, make all possible combination pair. Correlation coefficient analysis have been carried out with the aid of following formula given by Miller *et al.* (1958) [23], Hanson *et al.*, (1956) [15] and Johnson *et al.*, (1955b) [18] was taken.

The component of genotypic co-variance among two characters and the component of phenotypic co-variance were obtained in the same way like for the component of variance. This co-variance was utilized to evaluate phenotypic and genotypic association among the pair of traits are as follows:

**Genotypic correlation coefficient between character x and y**

$$r_{xy\ (g)} = \frac{Cov(g)X.Y}{\sqrt{\sigma^2(g)X \times \sigma^2(g)Y}}$$

Where,
$r_{xy\ (g)}$ = Genotypic correlation coefficient between x and y
Cov $_{(g)}$ xy = Genotypic covariance between x and y
$\sigma^2_{x\ (g)}$ = Genotypic variance of character x
$\sigma^2_{y\ (g)}$ = Genotypic variance of character y

**Phenotypic correlation coefficient between character x and y**

$$r_{xy\ (p)} = \frac{Cov(p)X.Y}{\sqrt{\sigma^2(p)X \times \sigma^2(p)Y}}$$

Where,
$r_{xy\ (p)}$ = Phenotypic correlation coefficient between x and y
Cov $_{(p)}$ xy = Phenotypic covariance between x and y
$\sigma^2$x $_{(p)}$ = Phenotypic variance of character x
$\sigma^2$y $_{(p)}$ = Phenotypic variance of character y

**Testing for significance of correlation coefficients-**'t' test was applied to test the significance of correlation coefficients. 't' values were estimated by using the following formula:

$$T = \frac{r}{\sqrt{1-r^2}} \times \sqrt{n-2}$$

Comparing the 't' values at (n-2) degree of freedom, we test the significance of correlation coefficient (r). If calculated value of t is higher than the tabular value of't' at (n-2) degree of freedom at given probability level, the coefficient of correlation is considered significant.

**Result and Discussion**

**Genetic variability**

For the genetic enhancement of linseed crop either through direct enhancement of traits in which plant breeder is interested or indirect enhancement through component traits can be successfully achieved using ample genetic information on linseed crop. In order to touch the eventual goal of getting high quality seed yield, study of presence of genetic variability for seed yield and its improvement, and the nature of correlation among themselves is a crucial prerequisite.

Analysis of variance indicated that the linseed genotypes were highly significant for all the traits taken under study such as plant height (cm), days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per pant, 1000 seed weight (g), seed size (mm), number of capsules per plant, oil content, harvest index (%) and seed yield per hectare (qt). This shows there is presence of sufficient amount of variation between the genotypes of linseed for seed yield and its attributing traits are given in Table 2.

Earlier finding of Tadesse *et al.* (2010) [40], Reddy *et al.* (2013) [35], Tyagi *et al.* (2014) [41], Kanwar *et al.* (2015) [20], Patial *et al.* (2018) [32] and Dhirhi and Mehta (2019) [10] reported that analysis of variance clearly indicated that there was highly significant variation amongst the genotypes for all the traits studied.

**Genotypic coefficient of variation and phenotypic coefficient of variation**

Results regarding genetic variation under present investigation revealed that generally, phenotypic coefficient of variation for all the traits under investigation was found to be higher than their corresponding genotypic coefficient of variation, indicating masking effect of environment in the expression of traits represented in Table 3.

The highest genotypic coefficient of variation observed for number of secondary branches per plant (39.1%) which was followed by number of capsules per plant (37.9%), harvest index (%) (26.5%), number of primary branches per plant (25.1%) and seed yield per hectare (qt.) (22.6%) whereas, phenotypic coefficient of variation was highest in number of secondary branches per plant (39.3%) which was followed by number of capsules per plant (38.5%), number of primary branches per plant (29.5%), harvest index (%) (26.7%) and seed yield per hectare (qt.) (23.3%). In variability studies the PCV and GCV showed a smaller amount of difference for number of secondary branches per plant, seed size (mm), oil content (%), days to maturity and harvest index (%) which signifying influence of genetic causes in the expression of these traits. The traits such as number of secondary branches per plant, number of capsules per plant, number of primary branches per plant and harvest index (%) exhibits higher GCV and PCV indicates the presence of sufficient amount of

variation for these traits among the linseed genotypes. Thus, there is possibility of improvement through selection of these traits. In the present study genotypic coefficient of variation was observed to be moderate in plant height (cm) (12.9%), 1000 seed weight (g) (15.3%), seed size (mm) (10.8%) and oil content (%) (10.5%) and similarly phenotypic coefficient of variation was observed to be moderate in plant height (cm) (13.6%), 1000 seed weight (g) (16.8%), seed size (mm) (10.9%) and oil content (%) (10.6%). The lowest genotypic coefficient of variation was found in days to 50% flowering (7.8%) and days to maturity (8.9%) similarly, the lowest phenotypic coefficient of variation was found in days to 50% flowering (8.2%) and days to maturity (9.0%).

Similarly, the reports made by earlier workers in linseed *viz*., Mahto and Rehman (1998) [22], Payasi *et al*. (2000) [33], Jain and Rao (2003) [16], Awasthi and Rao (2005) [5], Reddy *et al*. (2013) [35] and Kanwar *et al*. (2015) [20], who reported "higher phenotypic and genotypic coefficient of variations for these traits. However, moderate values of PCV and GCV were noticed for days to 50 percent flowering, number of primary branches per plant, number of secondary per plant and seed yield per hectare. Similar findings were in agreement with Payasi *et al*. (2000) [33] the result indicated that the PCV values were greater than the corresponding GCV values for the traits studied like number of primary branches per plant, number of secondary per plant and number of capsules per plant indicating that the apparent variation is not only due to genotypes but, also due to the influence of environment. Therefore, one has to give emphasis on phenotypes for making successful selection of these traits, as environment exhibits unpredictable variations in nature.

**Heritability and genetic advance**

Heritability estimates the degree of resemblance between phenotypic and breeding value. It is the heritable portion of phenotypic variance. Heritability plays an important role in selection of superior genotypes from genetically diverse populations. Heritability is valid for the population from which they are originated. Broad sense heritability is useful in understanding the relative influence of genotypes and environment in determining the phenotypic variation. The estimation of heritability has been broadly grouped into three classes *viz*., low (0-50%), medium (50-70%) and high (>70%) according to Robbinson (1966). Broad sense heritability was evaluated for each of the yield attributing trait under study. (Table 3)

Genetic advance gives an estimation of reliable gain at a specified intensity of selection which is a chief implement in plant breeding. Therefore, heritability coupled with genetic advance is helpful in laying emphasis in selection for seed yield and its component. However, the proportion of enhancement in trait would be more reliable on the amount of variability in the population where selection has to be done. According to Johnson *et al.*, (1955) estimate genetic advance as mean percent was broadly categories into low (<10%), medium (10-20%) and high (>20%) classes.

The highest heritability was recorded for seed size (mm) (99.4%) which was followed by number of secondary branches per plant (98.7%) and harvest index (%) (98.2%) whereas, the lowest value for heritability was calculated for number of primary branches per plant (72.5%) given in Table 3.

The high amount of genetic advance as mean percent was observed for number of secondary branches per plant (79.9%) followed by number of capsules per plant (77.2%), harvest index (54.1%), seed yield per hectare (qt.) (45.3%), number of primary branches per plant (44.1%), 1000 seed weight (g) (28.5%), plant height (cm) (25.4%), seed size (mm) (22.2%) and oil content (%) (21.5%). The moderate amount of genetic advance was recorded for days to 50% flowering (15.2%) followed by days to maturity (18.2%) given in Table 3.

These results are in agreement with the findings of Satpathi *et al.* (1989) [37], Mirza *et al*. (1996) [24], Payasi *et al*. (2000) [30], Akbar *et al.* (2003) [1], Kant *et al.* (2005) [19], Gauraha *et al.* (2011) [13], Pali and Mehta (2013) [28], and Dash *et al.* (2016) [9] reported high heritability for seed yield per hectare and number of capsules per plant. Similarly, this result is in agreement with Mirza *et al*. (1996) [24], Naik and Satapathy (2002) [26], Pali and Mehta (2014) [29] revealed that "broad sense heritability for all the characters *viz*., days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, 1000 seed weight and harvest index were found high".

Similarly, results were in agreement with Gauraha *et al*., (2011) [13], Rajanna *et al.* (2014) [34] and Dash *et al.* (2016) [9] reported that "high heritability coupled with high genetic advance as percent of mean was obtained for number of primary branches per plant, number of secondary branches per plant, number of capsule per plant and seed yield per hectare (qt.) which indicated that most likely the heritability might be due to additive gene effect and selection may be effective in segregating generations.

**Correlation analysis**

The seed yield mostly in all the crops is referred to as main trait of interest which results from interaction of several component characters that are termed as yield components. Therefore, identification of important yield component and information about their association with seed yield per hectare (qt.) is very important to understand efficient breeding strategy for evolving high yielding varieties.

Correlation coefficient provides degree of association between two variables or characters helps us in understanding the nature and magnitude of association among seed yield and yield components, on which selection can be done for genetic improvement of crops for yield. At genetic level, coupling phase of linkage is reason for positive correlation. While, negative correlation arises due to repulsion phase of linkage of genes controlling two different traits. Both types of correlation may result of pleiotropy, *i.e.* developmental correlation. No correlation indicates that genes concerned are located far apart on the same chromosome or they are located on the different chromosomes. Nature of correlation can often be altered by selection and hybridization.

In above experiment genotypic and phenotypic correlation coefficients of seed yield and its component traits are shown in Table 4.Correlation analysis in IGKV released linseed genotypes revealed that seed yield per hectare (qt.) positively and significantly correlated with harvest index (%) ($r_g$= 0.871, $r_p$= 0.849) and number of capsules per plant ($r_g$=0.285, $r_p$=0.283) whereas, positive correlation with number of primary branches per plant ($r_g$=0.068, $r_p$=0.056), days to 50% flowering ($r_g$=0.058, $r_p$=0.048) and oil content (%) ($r_g$=0.144, $r_p$=0.141) at both genotypic and phenotypic level.

Correlation analysis in IGKV released linseed genotypes revealed that seed yield per hectare (qt.) negatively correlated

with "plant height (cm) ($r_g$= -0.184, $r_p$= -0.167), number of secondary branches per plant ($r_g$= -0.014, $r_p$= -0.012), days to maturity ($r_g$= -0.023, $r_p$= -0.018), 1000 seed weight ($r_g$= -0.106, $r_p$= -0.084) and seed size (mm) ($r_g$= -0.065, $r_p$= -0.057)" at both genotypic and phenotypic level. The negative correlation suggested that higher value for negatively correlated traits might show lower seed yield.

The high significant and positive correlation of seed yield per hectare (qt.) with harvest index (%) suggested that high harvest index (%) might show higher seed yield. Therefore, selection based on harvest index (%) could be depending on rich seed yield for the development of varieties. Similar finding have also been reported by Patel and Rao (2009) [31], Gauraha *et al.* (2011) [13], Savita *et al.* (2011) [38], Chandarwati *et al.* (2016) [7] and Sharma *et al.* (2016) [7].

Similar result has been reported earlier by Muduli and Patnaik (1994) [25] observed that 1000-seed weight was negatively correlated with seed yield" whereas, Foster *et al.* (1998) [12], Gauraha *et al.* (2011) [13], Tadesse *et al.* (2010) [40] and Choudhary *et al.* (2017) [8] contradicts this result as they noticed positive correlation of 1000-seed weight with seed yield.

Similarly, Foster *et al.* (1998) [12], Payasi *et al.* (1999) [43], Pal *et al.* (2000) [27], Akbar *et al.* (2003) [1], Gauraha *et al.* (2011) [13], Kumar *et al.* (2015) [21], Tadesse *et al.* (2010) [40], Choudhary *et al.* (2017) [8] and Ankit *et al.* (2019) [3] reported that number of capsules per plant and harvest index (%) had significant positive correlation with seed yield.

**Table 2:** Analysis of variance of IGKV released linseed genotypes

| | | | Mean sum of squares | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **S. N.** | **Source of variance** | **DF** | **Plant height (cm)** | **Days to 50% flowering** | **Days to maturity** | **Number of primary branches/plant** | **Number of secondary branches/plant** | **1000-Seed weight** | **Seed Size (mm)** | **Number of capsules/plant** | **Oil content (%)** | **Harvest Index (%)** | **Seed yield/ ha (Qt.)** |
| 1. | Replication | 2 | 4.4 | 1.2 | 4.1 | 0.1 | 0.9 | 2.1 | 0.004 | 128.1 | 0.1 | 2.01 | 1.7 |
| 2. | Genotype | 26 | 187.6** | 70.5** | 336.1** | 1.2** | 125.2** | 2.8** | 0.7** | 1177.6** | 46.9** | 123.4** | 19.03** |
| 3. | Error | 52 | 6.0 | 2.5 | 2.3 | 0.1 | 0.5 | 0.2 | 0.001 | 10.4 | 0.3 | 0.7 | 0.4 |

* Significant at 5% level, ** Significant at 1% level

**Table 3:** Genetic Parameter of variation for seed yield and its contributing traits in IGKV released linseed genotypes

| **S. N.** | **Characters** | **Range** | | **Mean** | **Critical Differences (5%)** | **Coefficient of Variations (%)** | | **$h^2$ (Broad Sense)** | **GA as% of Mean** |
|---|---|---|---|---|---|---|---|---|---|
| | | **Max.** | **Min.** | | | **GCV (%)** | **PCV (%)** | | |
| 1. | Plant Height (cm) | 72.8 | 44.2 | 60.1 | 4.0 | 12.9 | 13.6 | 91.0 | 25.4 |
| 2. | Number of Primary Branches/Plant | 3.8 | 1.4 | 2.4 | 0.6 | 25.1 | 29.5 | 72.5 | 44.1 |
| 3. | Number of Secondary Branches/Plant | 35.5 | 9.1 | 16.5 | 1.2 | 39.1 | 39.3 | 98.7 | 79.9 |
| 4. | Days to 50% Flowering | 69 | 50.3 | 61.4 | 2.6 | 7.8 | 8.2 | 90.0 | 15.2 |
| 5. | Days to Maturity | 134.6 | 95.6 | 117.9 | 2.5 | 8.9 | 9.0 | 98.0 | 18.2 |
| 6. | 1000 Seed Weight (g) | 7.8 | 4.4 | 6.1 | 0.7 | 15.3 | 16.8 | 82.4 | 28.5 |
| 7. | Seed size (mm) | 5.4 | 4.0 | 4.6 | 0.1 | 10.8 | 10.9 | 99.4 | 22.2 |
| 8. | Oil Content (%) | 44 | 30.9 | 37.4 | 0.9 | 10.5 | 10.6 | 98.1 | 21.5 |
| 9. | Number of capsules/Plant | 95.3 | 18.2 | 51.9 | 5.3 | 37.9 | 38.5 | 97.4 | 77.2 |
| 10. | Harvest Index (%) | 40.3 | 15.4 | 24.2 | 1.4 | 26.5 | 26.7 | 98.2 | 54.1 |
| 11. | Seed Yield/ha (qt.) | 18.77 | 6.76 | 11.0 | 0.9 | 22.6 | 23.3 | 94.4 | 45.3 |

**Table 4:** Genotypic and Phenotypic correlation coefficient for seed yield and contributing traits in IGKV released linseed genotypes

| **Trait** | | **PH** | **PB** | **SB** | **D50%** | **DM** | **SW** | **SS** | **Oil** | **C** | **HI** | **SY** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PH | $r_g$ | 1.000 | | | | | | | | | | |
| | $r_p$ | 1.000 | | | | | | | | | | |
| PB | $r_g$ | -0.397** | 1.000 | | | | | | | | | |
| | $r_p$ | -0.311** | 1.000 | | | | | | | | | |
| SB | $r_g$ | -0.395** | 0.790** | 1.000 | | | | | | | | |
| | $r_p$ | -0.371 | 0.665 | 1.000 | | | | | | | | |
| D50% | $r_g$ | 0.537** | -0.085 | -0.039 | 1.000 | | | | | | | |
| | $r_p$ | 0.463 | -0.047 | -0.043 | 1.000 | | | | | | | |
| DM | $r_g$ | 0.559** | 0.051 | 0.106 | 0.927** | 1.000 | | | | | | |
| | $r_p$ | 0.524 | 0.039 | 0.105 | 0.876** | 1.000 | | | | | | |
| SW | $r_g$ | 0.013 | 0.153 | 0.101 | -0.185 | -0.0819 | 1.000 | | | | | |
| | $r_p$ | 0.007 | 0.113 | 0.095 | -0.137 | -0.079 | 1.000 | | | | | |
| SS | $r_g$ | -0.034 | 0.097 | 0.109 | -0.182 | -0.142 | 0.970** | 1.000 | | | | |
| | $r_p$ | -0.035 | 0.092 | 0.107 | -0.172 | -0.141 | 0.880 | 1.000 | | | | |
| Oil | $r_g$ | -0.600** | 0.171 | 0.033 | -0.61** | -0.55** | 0.329** | 0.284* | 1.000 | | | |
| | $r_p$ | -0.569 | 0.138 | 0.031 | -0.581 | -0.546 | 0.303** | 0.282* | 1.000 | | | |
| C | $r_g$ | -0.267* | 0.390** | 0.310** | -0.37** | -0.19 | -0.205 | -0.273* | 0.370** | 1.000 | | |
| | $r_p$ | -0.256* | 0.322** | 0.299** | -0.356** | -0.182 | -0.192 | -0.268* | 0.364 | 1.000 | | |
| HI | $r_g$ | -0.499** | 0.201 | 0.093 | -0.039 | -0.093 | -0.155 | -0.135 | 0.293** | 0.319** | 1.000 | |
| | $r_p$ | -0.480 | 0.156 | 0.093 | -0.037 | -0.090 | -0.142 | -0.131 | 0.291** | 0.315** | 1.000 | |
| SY | $r_g$ | -0.184 | 0.068 | -0.014 | 0.058 | -0.023 | -0.106 | -0.065 | 0.144 | 0.285** | 0.871** | 1.000 |
| | $r_p$ | -0.167 | 0.056 | -0.012 | 0.048 | -0.018 | -0.084 | -0.057 | 0.141 | 0.283 | 0.849 | 1.000 |

* Significant at 5% level, ** Significant at 1% level

| | |
|---|---|
| PH- Plant height (cm) | SS- Seed size (mm) |
| PB- Number of primary branches per plant | OIL- Oil content (%) |
| SB- Number of secondary branches per plant | C- Number of capsules per plant |
| D50%- Days to 50% flowering | HI- Harvest index (%) |
| DM- Days to maturity | SY- Seed yield per hectare (qt.) |
| SW- 1000 Seed weight (g) | |

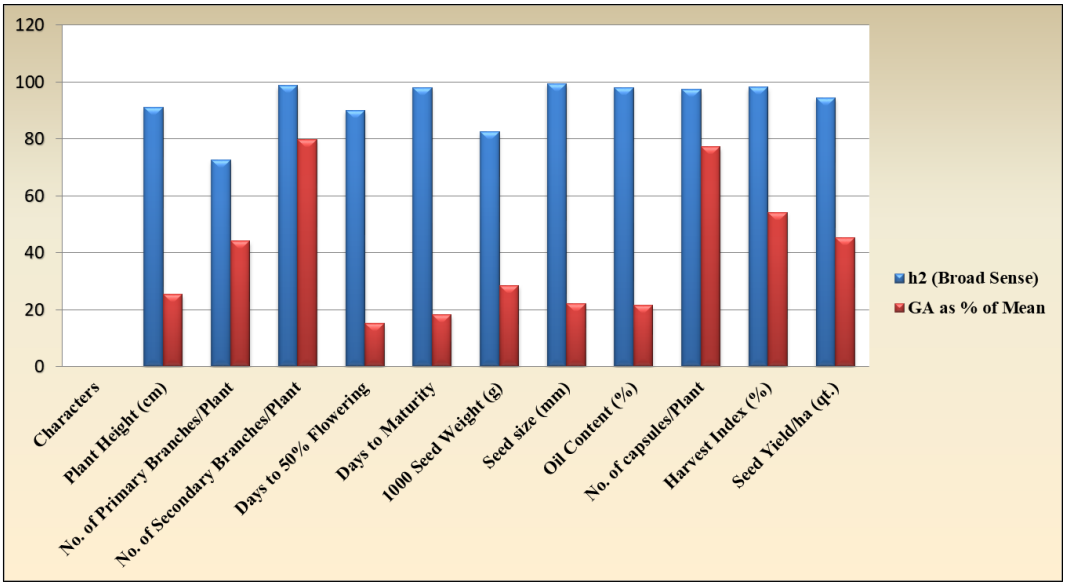


**Fig 1:** Heritability and genetic advance as mean percent for seed yield and its contributing characters in IGKV released linseed genotypes

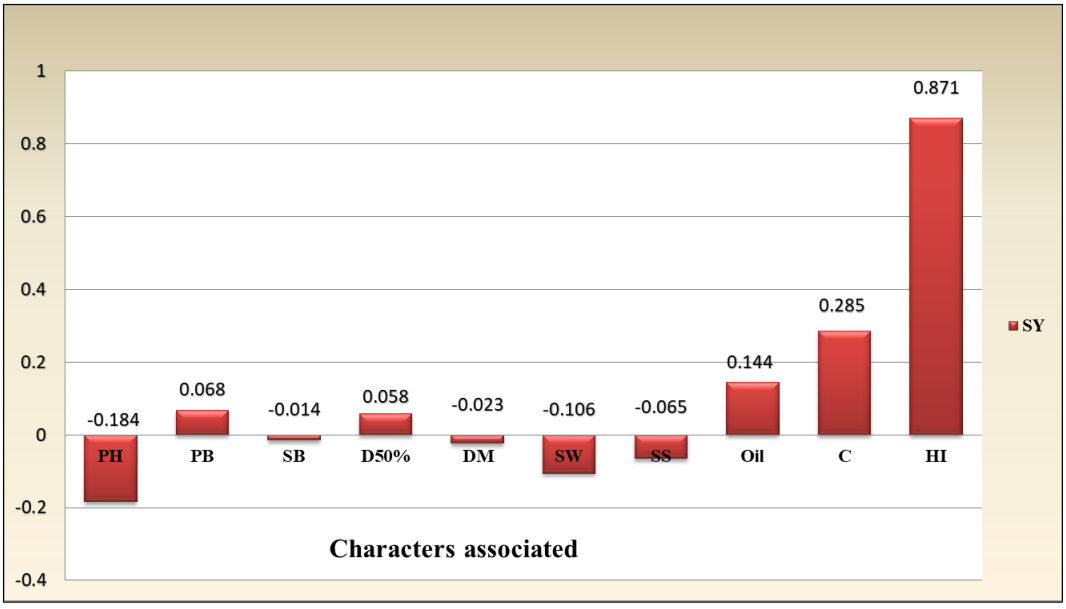


**Fig 2:** Genotypic Correlation among seed yield per hectare (qt.) and its contributing characters in linseed genotypes

## Conclusions

Analysis of variance clearly stated that significant amount of variability existed among all the linseed genotypes under study. The considerable amount of variability in any breeding material is essential not only for providing a foundation for selection but also for little useful information regarding selection of diverse parents that could be utilized in hybridization programmes. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) observed by the characters number of secondary branches per plant which is followed by number of capsules per plant indicating the presence of considerable amount of variability among genotypes for these characters whereas, days to 50% flowering and days to maturity showed low genotypic coefficient of variation and phenotypic coefficient of variation indicating less variability for these characters. The genotypic variances were smaller than phenotypic variances which imply that environmental conditions have concealing effect on the expression of genetic variability.

High heritability shown by the character seed size (mm) followed by number of secondary branches per plant and harvest index (%) whereas high genetic advance showed by the character number of secondary branches per plant followed by number of capsules per plant which indicates that these characters are governed by additive gene action. Hence,

selection based on these characters would be rewarding.

Studies on correlation analysis showed that characters *viz*., harvest index (%) and number of capsules per plant showed significantly positive association with seed yield per hectare (qt.) whereas, number of primary branches per plant, days to 50% flowering and oil content (%) showed positive but non-significant correlation with seed yield per hectare (qt.). Presence of positive association among the desirable characters is favorable because it encourages simultaneous improvement in both the characters. Hence, these characters can be considered as yield determinants. Characters *viz*., plant height, number of secondary branches per plant, days to maturity, 1000 seed weight and seed size showed negative correlation which indicates that increase in one variable will cause decrease in other and vice versa.

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