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ESTIMATION OF GENETIC VARIABILITY AND CORRELATION IN F_2 SEGREGATING GENERATION IN LINSEED ((*LINUM USITATISIMUM* L.)

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Abstract

Twenty hybrids of linseed generated by crossing of 5 lines and 4 testers in line × tester mating design were sown along with their nine parental lines to assess the genetic variability and correlation for seed yield and its component traits during *Rabi,* 2014-2015 and 2015-2016. This experiment was carried out at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, AICRP on Linseed, I.G.K.V., Raipur, Chhattisgarh. The phenotypic coefficient of variation and genotypic coefficient of variation for days to flowering and days to maturity showed less difference indicating the greater role of genetic factors in expression of these traits. Differences between genotypic coefficient of variation and phenotypic coefficient of variation were observed for plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, seed yield plant^{-1}(g), 1000 seed weight (g), total number of branches plant^{-1}, indicating higher environmental influences. The days to maturity recorded high heritability and coupled with low genetic advance of mean. Highly significant and positive correlation was shown by plant height with number of secondary branches plant^{-1} and number of capsules plant^{-1} at genotypic and phenotypic level. It also showed significant positive correlation with number of capsules plant^{-1} at only genotypic level.

Key words : Linseed, GCV, PCV, heritability, correlation.

Introduction

Linseed (*Linum usitatissimum* L.) 2n = 30, is an important oilseed crop that belongs to the genus *Linum* of the family Linaceae. It is also called flax or flaxseed. The name *Linum* originated from *lin* or "thread" and the species name *usitatissimum* is a Latin word meaning "most useful". Around the globe linseed crop occupies an area of 22.70 lakh ha yielding out 22.39 lakh tones having an average productivity of 986 kg/ha. In India, it is grown in an area of 29210 ha with production and productivity being 141200 tones and 484 kg/ha, respectively. India ranks second in area after Canada which is almost equivalent to China which so far occupied the second slot in world area by the crop. Our national production slides to third place after Canada and China. In India, the crop is mainly cultivated in the states like Madhya Pradesh, Chhattisgarh, Uttar Pradesh, Maharashtra, Bihar, Odisha, Jharkhand, Karnataka and Assam accounting for more than 97 per cent of the total area. Chhattisgarh is one of the important linseed growing states of India, which account 26200 hectares area and 1100 tonnes production with productivity of 424 kg/ha (Annual Report, Linseed 2014-15). Linseed is one of the important *Rabi* oilseed crops of India, cultivated in light soil under one or two irrigation in Madhya Pradesh, Chhattisgarh, Uttar Pradesh, Maharashtra, Rajasthan, West Bengal, Karnataka, Orissa and Bihar. In Chhattisgarh, linseed is grown mostly rainfed as "utera" as well as in crop fields whereas in overseas countries it is widely grown in cool temperate regions of Argentina, Northern Europe, China, Russia, USA and Canada (Gauraha *et al*., 2011). It has been grown from ancient times for fiber (flax) and for its seed which is rich in oil. The genus *Linum* comprises about 290 species (Gill, 1987) of which only *Linum usitatissimum* L. is of economic importance *Linum usitatissimum* L. is one of the oldest

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plant species cultivated for oil and fiber (Lay and Dybing, 1989). Flax is the third largest natural fiber crop and one of the five major oilseed crops in the world. The crop is predominantly self pollinated, but out crossing (less than 2%) occasionally results from insect activity (Dilman, 1928). The two important products of the seed are linseed oil and linseed-meal. The oil content of seed generally varies from 33 to 45 per cent (Gill, 1987). Linseed oil has been used for centuries as a drying oil. Most part of the linseed plant are used in the paints and varnish industry.

Materials and Methods

The biological experimental materials comprised of five lines RLC-92, Sagar Local, Sabour Yellow, Sakoor, and Neela were crossed as per Line × Tester design with four tester T-397, Chambal, Neelam and Shekhar genotypes, which was taken from AICRP on Linseed, Department of Genetics and Plant Breeding IGKV, Raipur (C.G.) during *Rabi* 2014-15 and 2015-16. The parentage of genotypes presented in Table 1.1.

Characteristic features of parent

The characteristic features of parents included in present study are presented in table 1.

Methods

The crosses were attempted as per Line × Tester design. An F_1 population from a cross between line and tester was generated, for advancement of F_1 population, seeds were grown in pots in a greenhouse and sufficient F_2 seeds were produced. In the next *Rabi* season 2015-2016 parents, F_1 and F_2 was grown and genetic studies was done.

The observation was recorded for ten quantitative characters *viz*. Days to 50% flowering, Days to maturity, Plant height (cm), number of primary branches plant^{-1}, Number of secondary branches plant^{-1}, Total number of branches plant^{-1} , Number of capsules plant^{-1}, Number of seeds capsule^{-1} Seed weight (1000 seeds), Seed yield plant^{-1} (g). The experimental data was recorded on five randomly selected plants from the entire population of F_2 population. All the observations taken at flowering; except capsule size, capsule dehiscence, shape of tip, seed colour, seed size, seed weight are taken at maturity.

Results and Discussion

In present investigation parents and twenty F_2 segregating population is used to study the genetic variability and correlation study.

Analysis of variance

Analysis of variance (ANOVA) is a collection of statistical models used to analyze the differences between group means and their associated procedures (such as variation among and between groups), developed by R. A. Fisher. Analysis of variance for 10 yield and yield attributing traits in linseed have been given in table 2. For replication mean sum of square found significant for character namely days to 50% flowering, days to maturity, plant height, number of primary branches plant^{-1} and seed

Table 1 : Characteristic features of parents.

S.N.	Line/ Tester	Origin	Parentage	Special features
	Lines			
1	RLC-92	IGKV, Raipur	Jeevan× LCK 9209	Resistant to powdery mildew, tall, violet flower, brown seeded, oil content- 39%.
2	Sagar Local	Sagar, M.P.	Local selection	Resistant to powdery mildew, Red violet flower
3	Sabour Yellow	RAU, Bihar	Local selection	Resistant to powdery mildew, Red violet flower
4	Sakoor	GMU, Kanpur	Local selection	Resistant to powdery mildew, violet flower
5	Neela	W.B.	Local selection of W.B.	Resistant to powdery mildew Brown, medium seeded, Oil content - 40%.
	Testers			
1	T-397	Kanpur	T491 x T1193-1	Susceptible to powdery mildew, brown seeded, Oil content - 44%.
2	Chambal	Rajasthan	Local x RR45	Susceptible to powdery mildew, brown, large seeded, Oil content - 44%.
3	Neelam	Kanpur	T1 x NP(RR)9	Susceptible to powdery mildew, brown seeded, Oil content - 43%.
4	Shekher	Kanpur	Laxmi 27 x EC1387	Susceptible to powdery mildew, Shiny brown seed, Oil content - 43%. bv

Table 2 : Analysis of Variance for genetic parameters for seed yield and its components in linseed during 2015-16 at Raipur, C.G.

S. no.	Source of variation	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of capsules plant^{-1}	Number of seeds capsule^{-1}	Total number of branches plant^{-1}	1000 seed weight	Seed yield plant^{-1}
1.	Replication	32.42**	16.21**	10.89**	23.27**	1.52	2.71	0.24	1.52	0.38	252.08**
2.	Treatment	242.0**	3.24	24.96**	1762.21**	3.40*	3.94*	15.17**	21.86**	0.95	16.45**
3.	Error	44.75	1.18	11.07	664.9	1.44	2.66	4.05	1.77	0.38	11.95

yield plant^{-1}.

Mean and range parameters of parents and crosses

Genetic parameters of mean and range for seed yield and its components are given in table 3.

Days to 50% flowering ranged from 52.3 to 60 with an overall mean of 55.7. The minimum value was found in Sakoor x Neelam and the highest range found in RLC-92 × Neelam.

Days to maturity ranged from 111 to 120.6 with an overall mean of 116.7. The minimum value was found in Sakoor × Shekhar and the highest range found in Sabour Yellow × T-397.

Plant height (cm) ranged from 44.3 to 78 with an overall mean of 61.18. The minimum value was found in Sabour Yellow × Shekhar and the highest range found in Sabour Yellow × T-397.

Number of primary branches plant^{-1} ranged from 1 to 4.6 with an overall mean of 2.87. The minimum value was found in Neela, T-397 and the highest range found in Sabour Yellow × Chambal.

Number of secondary branches plant^{-1} ranged from 4 to 19.3 with an overall mean of 8.41. The minimum value was found in Neela and the highest range found in Sabour Yellow × Chambal.

Number of capsules plant^{-1} ranged from 10.6 to 135.6 with an overall mean of 35.24. The minimum value was found in Shekhar and the highest range found in Sabour Yellow × Chambal.

Number of seeds capsule^{-1} ranged from 6 to 10 with an overall mean of 8.56. The minimum value was found in Chambal and the highest range found in T-397.

Total number of branches plant^{-1} ranged from1.33 to 9.33 with an overall mean of 4.97. The minimum value was found in Shekhar and the highest range found in Sabour Yellow × Chambal.

1000 seed weight (g) ranged from 4.02 to 6.58 with an overall mean of 5.34.The minimum value was found in T-397 and the highest range found in Chambal.

Seed yield plant^{-1}(g) ranged from 2.78 to 7.09 with an overall mean of 4.51. The minimum value was found in Neela × Chambal and the highest range found in RLC-92.

Variability, heritability and genetic advance

In present investigation twenty F_2 segregating population is used to study the genetic variability and correlation study. The analysis of variance showed significant differences among the genotypes for all the

characters under study. Genetic parameters of variation, heritability and expected genetic advance as percentage over mean for seed yield and its components are given in table 4.

Variability

The genotypic coefficient of variation ranged from days to maturity (2.2) to number of capsules plant^{-1} (54.2). The phenotypic coefficient of variation and genotypic coefficient of variation for days to flowering and days to maturity showed less difference indicating the greater role of genetic factors in expression of these traits. Differences between genotypic coefficient of variation and phenotypic coefficient of variation were observed for plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1}, seed yield plant^{-1}(g), 1000 seed weight (g), total number of branches plant^{-1}, indicating higher environmental influences.

The existence of high magnitude of genetic variability observed for all the character under study revealed by high genetic coefficient of variation. The genotypic variance was smaller than phenotypic variance, it showed that environment, did exert masking influence on the expression of genetic variability.

Comparison of relative magnitude of genotypic coefficient of variation for parental population revealed that maximum amount of genetic variability was present for number of capsules plant^{-1}. High amount of genotypic coefficient of variation was possessed by number of capsules plant^{-1}, number of primary branches plant^{-1}, number of secondary branches plant^{-1} and total number of branches plant^{-1}. The moderate genotypic coefficient of variation was recorded for seed yield plant^{-1} (g), plant height (cm), number of seeds capsule^{-1}, 1000 seed weight (g) (table 4). Breeder has to select superior individual from their phenotypic expression for any crop improvement. Selection based on the phenotypic expression is sometime misleading, as the development of character is the result of the heritable and non-heritable factors. This highlights the imperative need for partitioning the overall variability in to its heritable and non-heritable components. Thus, the components of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed. The GCV was higher than the PCV; it indicates that there is little influence of environment on the expression of character. The PCV was higher than the GCV; it means that the apparent variation is not only due to genotypes but also due to the influence of environment. Earlier findings of Varshney *et al.* (1995), Gupta *et al*. (1999), Mishra and Yadav (1999), Verma (1999), Bhateria *et al*. (2001), Saidi *et al.* (2003), Jain and Rao (2003), Akbar *et al.* (2003), Vardhan and Rao (2012), Pali and Mehta (2013 a), Reddy *et al.* (2013a), Kanwar *et al.* (2014), Kumar *et al.* (2014), Rajanna *et al.* (2014), Kumar *et al*. (2015), Singh *et al.* (2015), Patel *et al.* (2015) and Dash *et al*. (2016b) were in agreement with present study.

Success of improvement in any character is based on phenotypic selection, which depends upon the correspondence between phenotype and genotype. Hence, the selection intensity in a population relies upon the amount of heritable variation present in the population. Therefore, heritability estimates along with genetic advance considered useful in understanding the pattern of inheritance of quantitative traits (Johnson *et al*., 1955).

Heritability and genetic advance

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.

Narrow sense heritability is important for breeding programmes as it estimates the relative importance of the additive portion of the genetic variance that can be transmitted to the next generation. The narrow sense heritability estimates were classified as high (>50%), medium (30-50%) and low (<30%) according to Bhateria *et al.,* (2006). On the basis of present study, all the characters revealed low narrow sense heritability, indicating the non-fixable component of variation are governing by these characters. This indicate that heterosis breeding may be useful. Similar result also found by Kant *et al.* (2005) and Kumari (2015).

The days to maturity recorded high heritability (79.01%) and coupled with low genetic advance of mean (4.0). Moderate heritability coupled with low genetic advance was observed for plant height (cm) (59.50%, 21.06%) and moderate heritability coupled with moderate genetic advance observed for number of primary branches plant^{-1} (36.72%, 36.02%), number of capsulesplant^{-1} (35.48%, 66.59%) and low heritability was observed for number of secondary branches plant^{-1} (29.49%, 28.6%), total number of branches plant^{-1} (11.15%, 16.93%) and seed yield plant^{-1}(g) (13.73%, 11.02%). The traits possessing low heritability are difficult to improve through phenotypic selection due to masking influence of environment on the genotypic effect. The character which exhibited high heritability indicates the presence of additive gene action and such characters could be fixed by resorting to selection. These results fall in line with those of Mirza *et al.* (1996) and Mishra and Yadav (1999),

Table 3 : Mean performance of parents and crosses for seed yield and its components in linseed during 2015-16 at Raipur, C.G.

S. no.	Genotypes	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of capsule plant^{-1}	Number of seeds capsule^{-1}	Total number of branches plant^{-1}	1000 seed weight(g)	Seed yield plant^{-1}(g)
1	RLC-92	56.3	118.3	60.6	2.6	8.6	40.6	9	2.6	4.5	7.0
2	Sagar Local	58	119.3	50	4	8.6	27.3	7.6	4	5.3	6.6
3	Sabour Yellow	57.6	119.3	55	3.6	6.3	23.6	9	6.3	5.0	5.4
4	Sakoor	55.3	118.3	51	2.3	7	23	9.6	2.3	4.9	5.2
5	Neela	58.3	120.6	66.3	1	4	12.6	9.3	4	6.2	4.6
6	T-397	59	118.6	54	1	6.6	16.3	10	6.6	4.0	4.4
7	Neelam	53	116.6	64.3	2.3	6.6	21.3	9.6	2.3	6.2	4.6
8	Shekhar	56.6	118.6	44.6	1.3	4	10.6	8.3	1.3	5.5	4.2
9	Chambal	57.6	119.3	52.6	3.3	8.3	28.3	6	3.3	6.5	5.6
10	RLC-92 x T-397	55	113.3	69.6	2.6	12	51.6	9.3	2.3	4.4	6.0
11	RLC-92 x Neelam	60.3	119.3	75.3	1.6	7.6	48.3	8.6	1.6	5.1	5.1
12	RLC-92 x Shekhar	54.3	115	58.3	3	10.3	54.6	9.6	3.3	5.2	4.9
13	RLC-92 x Chambal	53.3	113	71.6	3	8	21.3	9.6	3.6	5.0	3.3
14	Sagar Local x T-397	59.3	119	67.3	4	6.3	26.6	9.3	7	5.8	5.1
15	Sagar Local x Neelam	53	113	52.6	3.6	6.3	19.6	8.3	7.3	5.8	3.0
16	Sagar Local x shekhar	58	118.3	63	4	9	32.6	9.3	8.6	5.3	5.0
17	Sagar Local x Chambal	56.6	116.6	60.3	2	9	55.3	7	6.3	6.1	3.5
18	Sabour Yellow x T-397	57.6	120.6	78	4	10	67.6	8	7.6	5.0	4.4
19	Sabour Yellow x Neelam	57	118	57	4.3	11	56.6	8.3	8.6	4.7	3.9
20	Sabour Yellow x Shekhar	54.6	113.6	44.3	3.3	5.6	20.6	8.3	9	5.2	2.8
21	Sabour Yellow x Chambal	56.6	119	74.6	4.6	19.3	135.6	7.3	9.3	4.9	2.9
22	Sakoor x T-397	52.6	116.6	59	2.3	8.6	19.3	6.3	3.3	5.7	3.2
23	Sakoor x Neelam	52.3	113	60	2.6	10.3	32	9.6	4.3	5.1	3.8
24	Sakoor x Shekhar	54	111	62.3	4	7.6	32.3	9	5.3	5.3	4.5
25	Sakoor x Chambal	54.6	115.6	63	2	8.3	41.3	9.3	3.3	5.4	4.8
26	Neela x T-397	53	113	72	2.6	11.3	33.3	8	4	5.3	3.6
27	Neela x Neelam	53.3	115.3	64.3	4	8	26.3	8	6	5.2	5.9
28	Neela x Shekhar	55.3	115	70	2	8.6	24.6	9	5.3	5.7	3.3
29	Neela x Chambal	54.6	117.3	52.6	1.6	6	17.6	7	4.6	5.6	2.7

Table 4 : Genetic parameters of variation for seed yield and its components in linseed during 2015-16 at Raipur, C.G.

S. no.	Characters	Mean	Range		GCV (%)	PCV (%)	Heritability ns (%)	Heritability bs (%)	Genetic Advance (GA)	GA as % of mean
			Max.	Min.						
1	Days to 50% flowering	55.7	60	52.3	3.4	4.9	0.38	47.7	2.7	4.9
2	Days to maturity	116.7	120.6	111	2.2	2.4	1.53	79.0	4.7	4.0
3	Plant height	61.1	78	44.3	13.2	17.1	2.71	59.5	12.8	21.0
4	Number of Primary branches plant^{-1}	2.8	4.6	1	28.8	47.6	2.67	36.7	1.0	36.0
5	Number of secondary branches plant^{-1}	8.4	19.3	4	25.5	47.1	3.24	29.4	2.4	28.6
6	Number of capsules plant^{-1}	35.2	135.6	10.6	54.2	91.1	3.53	35.4	23.4	66.5
7	Number of seeds capsule^{-1}	8.5	10	6	9.4	16.9	0.95	31.1	0.9	10.8
8	Total number of branches plant^{-1}	4.9	9.3	1.3	24.6	73.6	12.9	11.1	0.8	16.9
9	1000 seed weight	5.3	6.5	4.0	8.1	14.1	3.50	33.4	0.5	9.7
10	Seed yield plant^{-1} (g)	4.5	7.0	2.7	14.4	38.9	0.32	13.7	0.5	11.0

Adugna and Labuschagne (2004), Joshi (2004), Kumari and Rao (2007), Kant *et al.* (2005), Kandil *et al.* (2012), Bibi *et al.* (2013), Patel *et al.* (2015) and Dash *et al.* (2016b).

The number of capsules plant^{-1} recorded highest genetic advance as percent of mean (66.59) followed by number of primary branches plant^{-1} (36.02), number of secondary branches plant^{-1} (28.61), plant height(cm) (21.06), total number of branches plant^{-1} (16.93) and seed yield plant^{-1} (g) (11.02), number of seeds capsule^{-1} (10.86) showed moderate genetic advance. Characters days to 50% flowering, days to maturity, 1000 seed weight (g) showed low genetic advance as percentage of mean. Hence high heritability with high genetic advance indicates the preponderance of additive gene action and such characters should be improved through selection. The characters showed high genetic advance indicates that the character is governed by additive genes and selection will be rewarding for improvement of such trait. The traits having moderate to low genetic advance indicates that the character is governed by non-additive genes. Similar result also find by Satapathi *et al.* (1987), Satapathi *et al.* (1989), Payasi *et al.* (2000) and Dash *et al.* (2016b).

Correlation studies

Correlation studies are of considerable importance in breeding programme. Galton (1888) was first to suggest the use of correlation index to describe the association for the effectiveness of indirect selection process. Estimation of genetic correlations along with phenotypic associations not only provides the idea about the extent of inherent association but also indicates how much of the phenotypically expressed correlation is influenced by the environment. The genotypic correlation reflects either the pleiotropic action of genes or linkage or both. Correlation coefficient measures the mutual relationship between various characters and determines the component characters on which selection can be based for genetic improvement of yield. From the results it was clear that the genotypic correlation was greater than the phenotypic correlation, indicating environmental influence on the association of characters correlation coefficients. Association analysis were estimated in all possible combination at phenotypic (P), genotypic (G) and environmental (E) level in F_2 generation and only significant correlations are described as under (table 5).

From the results, it was clear that the genotypic correlation was greater than the phenotypic correlation, indicating environmental influence on the association of characters correlation coefficients. Choudhary *et al.* (1984) also observed the environmental influence on the magnitude of correlation coefficients.

Highly significant and positive correlation was shown by plant height with number of secondary branches plant^{-1} and number of capsulesplant^{-1} at genotypic and phenotypic level. It also showed significant positive correlation with number of capsules plant^{-1} at only genotypic level.

Days to flowering exhibited highly significant and positive correlation with days to maturity at genotypic and phenotypic level respectively. It also showed significant positive correlation with number of capsulesplant^{-1} and 1000 seed weight (g) and highly significant with total number of branches plant^{-1} and seed

Table 5 : Phenotypic, genotypic and environmental coefficients of correlation for yield and its components in linseed during 2015-16 at Raipur, C.G.

Traits		Days to 50% flowering	Days to maturity	Plant height	Number of primary branches plant^{-1}	Number of secondary branches plant^{-1}	Number of capsules plant^{-1}	Number of seeds capsule^{-1}	Total number of branches plant^{-1}	1000 seed weight (g)	Seed yield plant^{-1} (g)
Days to 50% flowering	P		0.600**	0.082	-0.034	-0.078	0.109	0.065	0.074	0.025	0.185
	G	1	0.960**	0.044	-0.029	-0.130	0.210*	-0.079	0.403**	-0.232*	0.775**
	E		0.031	0.128	-0.038	-0.048	0.039	0.159	-0.028	0.2	-0.02
Days to maturity	P			-0.061	-0.087	-0.041	0.149	-0.07	0.002	0.051	0.191
	G		1	0.009	-0.079	-0.153	0.137	-0.319**	0.124	0.098	0.618**
	E			-0.232*	-0.121	0.086	0.207	0.231*	-0.081	0.003	-0.029
Plant height	P				0.106	0.295**	0.295**	0.06	0.037	0.01	-0.041
	G			1	0.134	0.742**	0.720**	0.241*	0.036	-0.201	0.026
	E				0.086	-0.030	-0.07	-0.083	0.046	0.192	-0.083
Number of primary branches plant^{-1}	P					0.199	0.159	-0.137	0.282**	-0.024	-0.051
	G				1	0.877**	0.824**	-0.236*	0.938**	-0.192	0.521**
	E					-0.134	-0.217*	-0.087	-0.012	0.067	-0.228*
Number of secondary branches plant^{-1}	P						0.756**	-0.214*	-0.017	-0.246*	-0.002
	G					1	0.986**	-0.173	0.917**	-0.444**	-0.287**
	E						0.600**	-0.232*	-0.278**	-0.156	0.071
Number of capsules plant^{-1}	P							-0.208	-0.027	-0.253*	0.007
	G						1	-0.176	0.948**	-0.270*	-0.260*
	E							-0.223*	-0.390**	-0.244*	0.087
Number of seeds capsule^{-1}	P								0.001	-0.168	0.117
	G							1	-0.475**	-0.790**	0.460**
	E								0.114	0.128	0.029
Total number of branches plant^{-1}	P									0.059	-0.239*
	G								1	-0.608**	-0.911**
	E									0.229*	-0.144
1000 seed weight (g)	P										-0.122
	G									1	-0.377**
	E										-0.055
Seed yield plant^{-1} (g)	P										1
	G										
	E										

1 Days to 50% flowering 2 Days to maturity 3 Plant height(cm) 4 Number of primary branche plant^{-1} 5 Number of secondary branches plant^{-1}
6 Number of capsules plant^{-1} 7 Number of seeds capsule^{-1} 8 Total Number of branches plant^{-1} 91000 seed weight (g) 10 Seed yield plant^{-1} (g)

yield plant^{-1}(g) at genotypic level only.

Days to maturity had highly significant negative correlation with number of seeds capsule^{-1} and highly significant positive correlation with seed yieldplant^{-1}(g) at genotypic level only. It also showed significant negative correlation with plant height (cm) and significant positive correlation with character number of seeds capsule^{-1}at environmental only.

Number of primary branches plant^{-1} was exhibited highly significant positive correlation with total number of branches plant^{-1} at the phenotypic level only and highly significant positive correlation with character number of secondary branches plant^{-1}, number of capsulesplant^{-1}, total number of branches plant^{-1}, seed yield plant^{-1}(g) and significant negative correlation with number of seeds capsule^{-1} at genotypic level. number of capsulesplant^{-1} and seed yield plant^{-1}(g) showed significant negative correlation at environmental level only.

Number of secondary branches plant^{-1} showed highly significant positive correlation with number of capsules plant^{-1} at phenotypic, genotypic and environmental level, number of seeds capsule^{-1} and 1000 seed weight (g) showed significant negative correlation at phenotypic level only. Total number of branches plant^{-1} showed highly negative correlation and number of seeds capsule^{-1} showed significant negative correlation at only environmental level.

Number of capsulesplant^{-1} showed significant negative correlation with 1000 seed weight (g) at phenotypic level, it shows highly significant positive correlation with total number of branches plant^{-1} and significant negative correlation with 1000 seed weight (g) and seed yield plant^{-1} (g) at genotypic level. Number of seeds capsule^{-1} and total number of branches plant^{-1} showed highly significant negative correlation and 1000 seed weight (g) showed significant negative correlation at environmental level.

Number of seeds capsule^{-1} recorded highly significant positive correlation with character seed yield plant^{-1} (g) and significant negative correlation with total number of branches plant^{-1} and 1000 seed weight (g) at genotypic level.

Total number of branches plant^{-1} recorded significant negative correlation with character seed yield plant^{-1} (g) at phenotypic level, 1000 seed weight (g) and seed yield plant^{-1} showed highly significant negative correlation at genotypic level and 1000 seed weight (g) showed significant positive correlation at environmental level.

Highly significant negative correlation was shown by seed yield plant^{-1} (g) with 1000 seed weight (g) at genotypic level only.

A positive correlation between desirable characters is favourable to the plant breeder because it helps in simultaneous improvement of both the character on the other hand negative correlation will hinder the simultaneous expression of both the characters with high value in such situations some economic compromise has to be made. Mass selection has been used to improve grain yield through indirect selection for highly heritable traits which are associated with yield. Hence the significant correlations may be used to improve the traits under selection. Similar findings have also been reported by Khaorgade *et al.* (1992), Agrawal *et al.* (1994), Kurt *et al.* (1996), Mahto and Mahto (1998), Gupta *et al*. (1999), Mishra and Yadav (1999), Payasi *et al.* (2000), Patel *et al.* (2001), Tiwari *et al*. (2001), Naik and Satapathy (2002), Sohan *et al*. (2004), Bhosle and Rao (2005), Dandigadasar *et al*. (2011), Gauraha *et al*. (2011), Dandigadasar *et al.* (2012), Iqbal *et al.* (2014), Rajanna *et al.* (2014), Tariq *et al*. (2014), Dash *et al*. (2016b) and Naik *et al.* (2016).

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