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Exploitation of Genetic Variability in Linseed

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ABSTRACT: The present experiment is undertaken to estimate the genetic variability in a set of 14 linseed genotypes. From ANOVA table it evidenced that significant variation for all the traits under study suggested existence of sufficient variability among themselves. PCV estimates were higher than GCV for all the character where as GCV estimates were higher than PCV for branch numbers and capsules numbers. For the traits, days to 50% flowering and days to maturity showed higher heritability due to major contribution of genotypic portion. Combined high heritability with high genetic advance was noticed for capsule number, branch number indicating these traits were under control of additive gene action. If selections were exercised based on phenotype would be effective for improvement of these traits.

Keywords: GCV, PCV, ANOVA.

INTRODUCTION

Linseed (*Linum usitatissimum* L.) is known for its oil and fibre content across the tropical and temperate regions of the world, most popularly referred to as Alsi in Hindi, Agase in Kannada. Predominantly a self-pollinated crop and its cultivation date back to 5000 years ago, belongs to the family *Linaceae.* Seeds are generally used in the preparation of chutney powder, rich in the protein, fat, dietary fiber and other micronutrient like magnesium, potassium and zinc. Industrially linseed oil is used for manufacturing of paints, varnish, oilcloth, linoleum and pad inks (Walsh, 1965). Oil cake is good for feeding of milch animals and can be as organic fertilizer to improve the soil fertility status and sometimes acts as germicide can be used to kill unwanted microbes. Higher portion of omega-3 fatty acid is found in linseed oil is an essential fatty acid where human body is not able to synthesize can be supplemented directly through the foods.

Globally crop occupies an area of 22.70 lakh ha with yield of 22.39 lakh tones and accounting an average production of 9.86 quintal/ha. At national level crop is cultivated on an area of 0.338 million ha with yield of 0.147 million tones. Madhya Pradesh, Chhattisgarh, Uttar Pradesh, Maharashtra, Bihar, Odisha, Jharkhand and Karnataka states were major contributing in terms of area constituting about 97 per cent of total cultivated area (Rajanna, 2020). Major constraints for lower productivity of the crop are due to its cultivation on marginal lands, moisture stress conditions, less input situations, narrow genetic base, lack of disease and insect resistant varieties. With necessities' there is an urgent need for development of high yielding varieties of linseed.

Varietal improvement progrmme mainly depends on the presence of variability for any trait in gene pool. Therefore, the first step in any crop breeding proramme is to estimation of genetic variability. Both genotypic and phenotypic variations were high for seed yield traits in linseed which triggers out potentiality of development of a new variety with higher yield.

Heritability is measure degree of transmission of desirable characters from parents to their offspring's. Estimation of genetic advance and heritability together were advantageous in predication of outcome of good selection. By considering above the facts, the present investigation is undertaken to estimate genetic variability in a set of 14 linseed genotypes.

MATERIAL AND METHODS

One hundred divergent linseed genotypes were obtained from Project Coordinating unit, AICRP on linseed, Indian Institute of Pulse Research, Kanpur. The experiment was taken up during *Rabi* 2017-18 at MARS, UAS, Raichur.

Each entry was sown in three meters length of single line with 30 cm × 5 cm spacing. All recommended package of practices and protection measures were taken to grow healthy crop. Out of one hundred, fourteen promising genotypes were selected based on field performance for yield traits and adoptability to local conditions.

During *rabi* 2018-19, identified fourteen genotypes (Table 1) were sown in RBD design with three replications by following above mention conditions. Phenotypic observations were recorded on days to 50% flowering, days to maturity and measurements were taken on five randomly selected plants in each entry for all the traits under study.

Average values were computed as genotype mean in each replication per entry per trait were analyzed in accordance with Sukhatme and Amble (1985) in Randomized block design (RBD) manner. Calculations on genotypic and phenotypic variances were made in accordance with Johnson *et al*., (1955). Genotypic and phenotypic coefficient of variance (GCV and PCV) were measured based on formulae given by Burton (1952). Heritability and genetic advance as percent mean were estimated according to Allard (1960).

Table 1: List of linseed genotypes used for study on variability parameters.

S.No.	Genotype name	Source of collection
1.	A-98	Project coordinating unit, IIPR, Kanpur
2.	A-116	Project coordinating unit, IIPR, Kanpur
3.	A-198	Project coordinating unit, IIPR, Kanpur
4.	GS-64	Project coordinating unit, IIPR, Kanpur
5.	BR-25	Project coordinating unit, IIPR, Kanpur
6.	A-429	Project coordinating unit, IIPR, Kanpur
7.	GS-54	Project coordinating unit, IIPR, Kanpur
8.	GS-203	Project coordinating unit, IIPR, Kanpur
9.	GS-205	Project coordinating unit, IIPR, Kanpur
10.	GS-220A	Project coordinating unit, IIPR, Kanpur
11.	GS-428	Project coordinating unit, IIPR, Kanpur
12.	KL-137	Project coordinating unit, IIPR, Kanpur
13.	R-5-6	Project coordinating unit, IIPR, Kanpur
14.	NP-RR-492	Project coordinating unit, IIPR, Kanpur

RESULT AND DISCUSSION

Variance analysis (Table 2) clearly suggested existence of sufficient variation for seed yield and other related traits. Among the genotypes mean sum of squares were significant for all the characters under study. Manifestation of larger variation gives a greater opportunity to choose desirable genotypes for efficient crop improvement programme. These findings were in parallel with Hussain *et al.*, (2016) who advocated the significant variability in linseed germplasm. Hence, it can be arrived at well planned crossing among selected genotypes establishes variability in subsequent generations.

The estimates of GCV, PCV, broad sense heritability and genetic advance six characters under study are presented in Table 3. Clear observation on data manifested phenotypic co-efficient of variance (PCV) were higher than genotypic co-efficient of variance (GCV) showing influence of environmental variation within in the total variation. Genotypic coefficient of variation helps to measure the capacity of genetic variability present in a particular character.

Higher estimates of genotypic coefficient of variation and phenotypic co-efficient of variance were noticed for branches per plant followed by numbers of capsules and also for seed yield (Thakur *et al*., 2020)

Moderate values of genotypic co-efficient of variance and phenotypic co-efficient of variance were recorded on plant height. These findings were supported by Terfa and Gurmu (2020) in linseed. For the traits, days to 50 percent flowering and days to maturity recorded low values of genotypic co-efficient of variance and phenotypic co-efficient of variance respectively. Low to high estimates of heritability in broad sense was observed for days to 50% flowering followed by maturity days, plant height, capsule number, seed yield and branches per plant (Upadhyay *et al*., 2019; Rama *et al*., 2005). Higher board sense heritability values are indicators to identify the accurate character for selection and helping the breeder to choose promising genotypes based on phenotypic expressivity of quantitative character (Johnson *et al*., 1955).

Higher values of heritability estimates indicates the capability of character transfer from one generation to subsequent and not much affected by environmental effects. This also provides information on phenotypes where the real true paradigmatic transfer is successful if selections were practiced on visual observations will be effective.

Genetic advance was found maximum for capsule number followed by branch number per plant, plant height, seed yield, days to 50% per cent flowering and days to maturity.

Combined effect of Heritability and genetic advance together become a driven force to predict the perfection of selection for any character (Johnson *et al*., 1955). High heritability together with high genetic advance becomes most reliable parameter to achieve the significant progress in selection (Burton, 1952). High heritability estimates coupled with high genetic advance were noticed for number of capsule numbers, branches per plant, plant height and seed yield which may be due to presence of additive gene action and have selective advantage if selection is excised on these traits in targeted improvement (Terfa and Gurmu *et al*., 2020).

Table 2: ANOVA for six traits in a set of fourteen linseed genotypes.

Sr. No.	Source of variation	Mean squares		
		Replications	Genotypes	Error
	d.f.	02	13	26
1.	Plant height (PH)	16.09	162.83*	8.30
2.	Branches per plant	3.17	2.62*	0.50
3.	capsules per plant	30.31	232.83*	13.34
4.	Seed yield (kg/ha)	13884.07	29789.11*	4412.79
5.	Days to 50% flowering	0.21	12.64*	0.37
6.	Days to maturity	4.95	37.61*	1.88

Table 3: genetic variability parameters in Linseed.

Sr. No.	Character	Range	Mean	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Broad Sense Heritability (%)	Genetic advance
1.	Plant height (PH)	36- 64	50	14.46	15.58	86.12	27.64
2.	branches per plant	2- 6	4	19.38	25.33	58.51	30.53
3.	capsules per plant	32 -62	47	18.30	19.90	84.58	34.67
4.	Seed yield (kg/ha)	433-763	585	15.72	19.39	65.72	26.24
5.	Days to Fifty percent flowering	51- 59	55	3.71	3.87	91.74	7.31
6.	Days to maturity	103-113	107	3.22	3.46	86.40	6.16

FUTURE SCOPE

Dominance genetic variance with the predominance of additive type of gene action was noticed for seed yield, number of branches and number of capsules per plant. Hybridization and selections as per pedigree method would be beneficial for genetic improvement of these traits.

Conflict of interest. The authors declare that the research was conducted without any conflict of interest in terms of any commercial or financial matters.

REFERENCES

Allard, R. W. (1960). Principles of Plant Breeding. John Wiley and Sons, Inc., New York.

Burton, G. W. (1952). Quantitative inheritance in grasses. Proc. 6. *International Grassland Congress*, *1*: 227–283.

Hussain, M. E., Moitra, P. K., & Goyal, V. (2016). Genetic variability, correlation and path coefficient analysis in linseed (*Linum usitatissimum* L.). *The bioscan, 11*(4): 3111-3115,

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. *Journal of Agronomy*, *47*: 314–318.

Rajanna, B. (2020). Genetics analsysis and molecular diversity studies and Omega-3 fatty acid linseed (*Linum usitatissimum* L.). Ph.D., Thesis, submitted to university of agriculture and horticulture sciences, Shivamogga, Karnataka

Rama, K., Singh, P., Tiwari, S. K., & Sharma, R. M. (2005). Study of heritability and genetic advance for yield components and oil content in diallel cross of linseed (*Linum usitatissimum* L.). *Agriculture science digest, 25*: 290–292.

Sukhatme, P. V., & Ambe, V. N. (1985). Statistical methods for agricultural workers. 4th ed. ICAR, New Delhi.

Terfa, G. N., & Gurmu (2020). Genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L) genotypes for seed yield and other agronomic traits. *Oil Crop Science*, *5*: 156–160.

Thakur, R., Paul, S., & Satasiya, P. (2020). Genetic variability and path analysis for yield and its related traits in linseed (*Linum usitatissimum* L.). *International journal of current microbiology and applied sciences, 9*(10): 2579-2586.

Upadhyay, S., Nandan, M. & Ashish, K. T., (2019). Assessment of variability among flax type linseed genotypes (*Linum usitatissimum* L.) of Chhattisgarh plains. *International journal of current microbiology and applied sciences, 8*(6): 2633–2637.

Walsh, R. J. (1965). Linseed oil protection for New York State Thruway bridges. *Civil engineering, 15*(2): 39-41.

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