



## Evaluation of genetic variability, heritability and genetic advance for seed yield in oilseed camelina [*Camelina sativa* (L.) Crantz.]

Om Prakash, Ankur Agarwal\* and Madhu Bala

Defence Institute of Bio-Energy Research, DRDO, Goraparao, Haldwani, Nainital 263139 (Uttarakhand), India

\*Corresponding author: [ankurdr@rediffmail.com](mailto:ankurdr@rediffmail.com)

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### Abstract

Camelina, a short gestation biofuel crop, has proved its potential as source of renewable biofuel worldwide. Introduction of this crop to India is very recent. Twenty genotypes/lines including selective F1 crosses were evaluated in the present study for genetic variability, heritability and genetic advance. High amount of inherent variability (genotypic coefficient of variation) was exhibited by seed yield per plant (36.54), number of seeds per pod (21.00) and number of pods per plant (12.17). Variability observed among the genotypes pointed out that there is large scope for selection of promising material for the economically important traits such as plant height, number of branches per plant. The characters studied in the present investigation expressed low to high heritability estimates ranging from 31.12% (number of branches per plant) to 85.21% (Days to 50% flowering). Genetic advance was recorded high (>20%) for seed yield per plant (46.57) and number of seeds per pod (28.43) whereas low genetic advance (<20%) was recorded for all other characters. High heritability coupled with high genetic advance was recorded for number of seed yield per plant, and number of seeds/pod indicating that these characters seems to be more heritable and can be improved by selection.

**Keywords:** *Camelina*, *Cruciferae*, *genetic variability*, *genetic advance*, *heritability*

### Introduction

Camelina [*Camelina sativa* (L.) Crantz.] is a member of the family Cruciferae (Brassicaceae). Camelina has originated in the Mediterranean to Central Asia. It is an under-exploited oilseed, low input crop and was the favourite one used in oil lamps and edible purpose from the Roman Empire to the discovery of gas and electricity. It is reported that camelina with high content of unsaturated fatty acids (approx. 90%) was more difficult and expensive to hydrogenate than rapeseed oil and this led to its decline. In recent times, camelina with its high content of Omega-3 fatty acids (38% of the total fatty acid content) offers an opportunity to meet the growing demands for high quality fatty acids (Abramovic and Abram, 2005) as well as a good raw material for biofuel (Shonnard *et al.*, 2010; Moore *et al.*, 2017). In India, camelina has been successfully introduced and being in the category of non-edible oils possesses a good potential for its commercialization as biofuel crop. In India, efforts have been made by DIBER, (DRDO) Haldwani to introduce germplasm from International centres (Agarwal *et al.*, 2010; Agarwal *et al.*, 2013; Agarwal *et al.*, 2014).

The genetic improvement of any crop is expected through breeding which requires precise information on the nature and degree of genetic variability present in any germplasm. Success of any breeding programme is dependent on

variability available or created. The large spectrum of genetic variability in segregating population depends on the amount of the genetic variability among genotypes and offer better scope for selection. The magnitude of heritable variation in the traits studied has immense value in understanding the potential of the genotype for further breeding programme. Assessment of variability for yield and its component characters becomes absolutely essential before planning for an appropriate breeding strategy for genetic improvement. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm. Heritability coupled with high genetic advance would be more useful tool in predicting the resultant effect in selection of the best genotypes for yield and its attributing traits. It helps in determining the influence of environment on the expression of the genotypic and reliability of characters. The more diverse parents within all limits of fitness, the greater are the chances of heterotic responses in F<sub>1</sub>s and broad spectrum of variability on segregation (Anand and Murthy, 1968). Considering the fact that very scanty information is available on crop improvement in this crop for Indian conditions, the present investigation was undertaken to study the genetic parameters i.e. genetic variability, heritability and genetic advance among the twenty camelina germplasm lines.

## Materials and Methods

The experimental materials for the present investigation consisted of 20 genotypes/ lines, namely, EC-751491, EC-751492, EC-751494, Iwan, Calina, PI 650151, PI 650147, PI 650141, PI 650165, PI 650146, PI 650885, PI 650145, EC-751494 × EC-643910, EC-751491 × EC-643909, EC-751494 × EC-751492, EC-643909 × EC-643910, EC-643910 × EC-751491, EC-751492 × EC-751494, EC-751491 × EC-751492, and EC-643910 × EC-751492. These genotypes were taken on the basis of morphological differences with respect to various traits. Source of these parents are appended in Table 1. All genotypes/ varieties were sown on 24 November 2018 in a randomized block design with three replications at field experimental facility, Defence Institute of Bio- Energy Research, DRDO, Haldwani. Each treatment

was sown in a 20 m<sup>2</sup> plot with 30 cm spacing between the rows and 5 cm within the rows. All recommended agronomic package of practices were followed during the crop growth period for raising good crop. The data were recorded on five randomly selected plants from each plot for quantitative traits viz., seed yield per plant (g), plant height (cm), days to 50% flowering, days to pod formation, number of branches per plant, number of pods per plant, number of seeds per pod and days to maturity. The mean data was compiled after computing for each character was subjected to standard method of analysis of variance following Panse and Sukhatme (1961), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance were estimated by the formula as suggested by Burton and De Vane (1953) and Johanson *et al.* (1955).

Table 1: Source of origin and pedigree of Germplasm/varieties of Camelina

Germplasm	Pedigree	Source of origin
EC-751491	-	Plant Introduction Station, Iowa State University, USA through NBPGR
EC-751492	-	Plant Introduction Station, Iowa State University, USA through NBPGR
EC-751494	-	Plant Introduction Station, Iowa State University, USA through NBPGR
Iwan	EC-643909	BOKU University, Vienna, Austria through NBPGR
Calina	EC-643910	BOKU University, Vienna, Austria through NBPGR
PI 650151	-	Plant Introduction Station, Iowa State University, USA through NBPGR
PI 650147	-	Plant Introduction Station, Iowa State University, USA through NBPGR
PI 650141	-	Plant Introduction Station, Iowa State University, USA through NBPGR
PI 650165	-	Plant Introduction Station, Iowa State University, USA through NBPGR
PI 650146	-	Plant Introduction Station, Iowa State University, USA through NBPGR
PI 650885	-	Plant Introduction Station, Iowa State University, USA through NBPGR
PI 650145	-	Plant Introduction Station, Iowa State University, USA through NBPGR
C X E	EC-751494 X EC-643910	DIBER, DRDO, Haldwani
A X D	EC-751491 X EC-643909	DIBER, DRDO, Haldwani
C X B	EC-751494 X EC-751492	DIBER, DRDO, Haldwani
D X E	EC-643909 X EC-643910	DIBER, DRDO, Haldwani
E X A	EC-643910 X EC-751491	DIBER, DRDO, Haldwani
B X C	EC-751492 X EC-751494	DIBER, DRDO, Haldwani
A X B	EC-751491 X EC-751492	DIBER, DRDO, Haldwani
E X B	EC-643910 X EC-751492	DIBER, DRDO, Haldwani

## Results and Discussion

Analysis of variance revealed highly significant variation among the germplasm lines for all the traits under study (Table 2). Mean values and range of germplasm are presented in Table 3. The results revealed that plant height ranged from 72.17-98.67 cm at maturity. Days to 50% flowering varied from 44.33 to 59.33 days. Days to pod formation ranged from 58.0 to 78.0 days and days to maturity ranged from 90.33 to 107.67. Number of pods per plant varied from 141.0 to 203.67 and number of seeds per pod from 8.67 to 14.0. Seed yield per plant ranged from

0.81 to 2.17 g. Vollmann *et al.* (2007) has also reported significant variation for various yield and oil attributing traits in germplasm of Camelina in Austria. Agarwal *et al.* (2010) also reported similar findings in camelina material imported to India.

It is well known that the genotypic co-efficient of variation is more important than the phenotypic co-efficient of variation, because high amount of genetic variation help in the formation of effective breeding programme for crop improvement. Genetic variation as compared to phenotypic variation gets fixed in subsequent generations

Table 2: Analysis of variation for seed yield and yield attributing traits in camelina

Source of variation	df	Plant Height (cm)	Days to 50% flowering	Days to pod formation	Branches / plant	Pods / plant	Seeds / pod	Days to maturity	Seed yield/ plant (g)
Replication	2	0.816	0.216	8.067	22.074	34.067	0.014	0.161	0.447
Genotype	19	42.232**	100.431**	30.438**	276.909**	3551.455**	0.664**	11.073**	17.442**
Error	38	1.676	5.620	3.382	7.290	94.768	0.012	0.659	0.405

\*\*denote significance at  $P=0.01$

and carries the effect of environmental influence also. The results presented in Table 4 revealed that the genotypic co-efficient of variation (GCV) in general is less than phenotypic co-efficient of variation (PCV) suggesting the role of G x E interaction in the expression of these traits. Variation trends high amount of inherent variability (genotypic co-efficient of variation) was

exhibited by seed yield per plant (28.7) and number of seeds per pod (17.0). Variability observed among the genotypes pointed out that there is large scope for selection of promising individual for the potential traits like plant height (cm), days to 50 % flowering and number of pods per plant. Similar results were reported by Mahto and Mahto (1988) and Mishra and Yadav (1999) in linseed.

Table 3: Mean Value and Range of various traits in camelina germplasm

Characters	Mean	Range	
		Minimum	Maximum
Plant height (cm)	86.8	72.2	98.7
Days to 50 % flowering	49.8	44.3	59.3
Days to pod formation	63.4	58.0	78.0
Number of branches/plant	14.3	11.3	16.5
Number of pods/plant	166.1	141.0	203.7
Number of seeds/pod	12.9	8.7	14.0
Days to maturity	99.2	90.3	107.7
Seed yield per plant (g)	1.38	0.81	2.17

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Heritability is a good index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. Therefore, high heritability helps in effective selection for a particular character. Heritability is classified as low (below 30%), medium (30-60%) and high (above 60%). The characters studied in the present investigation expressed low to high heritability estimates ranging from 31.1% (number of branches per plant) to 85.2% (Days to 50% flowering) (Table-03). Except these extreme values high heritability was also recorded for number of Days to 50% flowering (85.21%), Seed yield per plant (g) (61.9%), Plant height (76.3%), Days to pod formation (78.0%), Number of seeds per pod (65.7%) and Number of pods per plant (62.6%) whereas Days to maturity (45.6 %) recorded medium heritability value and number of branches per plant (31.1%) recorded low heritability. High heritability values indicate that the characters under study are less influenced by environment in their expression. The plant

breeder, therefore, may make his selection safely on the basis of phenotypic expression of these characters in the individual plant by adopting simple selection methods. High heritability indicates the scope of genetic improvement of these characters through selection. Similar results have been reported by Rama Kant *et al.* (2005) in linseed crop.

The genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.*, 1955). Genetic advance was recorded high (>20%) for Seed yield per plant (46.6) and number of seeds/pod (28.4) whereas low genetic advance (<20%) was recorded for all other characters (Table 4). The information on genetic variation, heritability and genetic advance helps to predict the genetic gain that could be obtained in later generations, if selection is made for improving the particular trait under study. Similar findings were reported by Satapathi *et al.* (1987) and Patil and Chopde (1981). High heritability coupled with high

Table 4: Estimates of PCV, GCV, heritability, Genetic advance and genetic advance (percent of mean) among *Camelina* germplasm

Characters	Phenotypic co-efficient of variation (PCV)	Genotypic co-efficient of variation (GCV)	Heritability	Grand mean	Genetic advance	Genetic advance in per cent of mean
Seed yield per plant (g)	36.5	28.7	61.9	1.4	0.6	46.6
Plant height (cm)	10.1	8.8	76.3	86.8	13.7	15.8
Days to 50 % flowering	9.7	8.9	85.2	49.8	8.5	17.0
Days to pod formation	9.8	8.7	78.0	63.4	10.0	15.8
Number of branches/plant	10.7	6.0	31.1	14.3	1.0	6.9
Number of pods/plant	12.2	9.6	62.6	166.1	26.1	15.7
Number of seeds/pod	21.0	17.0	65.7	12.9	3.7	28.4
Days to maturity	7.3	4.9	45.6	99.2	6.8	6.9

genetic advance was recorded for number of seed yield per plant, and number of seeds/pod that these characters seems to be more heritable and can be improved by selection as evidenced by Singh and Dikshit (1988). Low heritability coupled with low genetic advance was recorded for number branches per plant indicating that these characters highly influence by environmental effect and selection would be ineffective as reported by Patil and Mehta (2013).

The success of any breeding programme largely depends upon the genetic variability present in the population under improvement. The present study revealed that a considerable amount of variability is present for agronomic traits. This shows that further improvement in the camelina through selection is very well possible for Indian conditions.

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