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## Genetic variability for seed yield and its component characters in taramira (*Eruca sativa* Mill.)

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### Abstract

The present research was carried out to estimate the genetic variability for 11 characters among 30 different genotypes of Taramira (*Eruca sativa* Mill.) at Research farm of SKN College of Agriculture, Jobner (SKNAU, Jobner) during the *rabi* 2018-19. The phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the characters. Wide range was observed for the number of siliquae per plant, seed yield per plant and secondary branches per plant. The high heritability coupled with high genetic advance as percentage of mean indicated presence of additive gene action in these traits *viz.*, Number of siliquae per plant, oil content and seeds per siliquae, additive gene action is pronounced in the expression of these character early generation selection would be effective in breeding programmed. High heritability is found with low genetic advance as percentage of mean for plant height and secondary branches per plant, which is indicative of aforesaid characters, are governed under non additive gene action.

**Keywords:** Genetics advance, genotypic coefficient of variation, heritability and phenotypic coefficient of variation

### Introduction

Taramira (*Eruca sativa* Mill.) is an important winter season oil seed crop of the family Brassicaceae. South Europe and North Africa are believed to be the native place of taramira (Bailey, 1949 and Prakash, 1980) [2, 11] and it is introduced to India. It has diploid number of chromosomes  $2n = 22$ . Taramira has desirable traits particularly resistance to powdery mildew that can be transferred to *Brassica campestris* and *Brassica juncea* (Sastry, 2003) [13]. In India, it is known by many names such as tara, trara, schwan, duan, turra, tirwa, merha, merkai, chara, ushan and sondha (Singh, 1958) [15]. In Europe it is known as rocket salad, rocket, roquette or arrugula, where it is generally grown for young leaves that are eaten as green salad. The seed yield is complex trait and its combined effect of many contributing characters. The direct selection of yield is not effective due to low heritability. The efficiency of selection depends on the identification of genetic variability from the phenotypic expression of the character. Variability means differences among the individuals of a single species or different species. The variability may be due to environment or genotypes or interaction of both. Assessment of genetic variability in the original population is the first step in any breeding. Study of variability, heritability and genetic advance in the germplasm will help to ascertain the real potential value of the genotype. Hence, this present study was planned to assess the variability, heritability and genetic advance for yield and other characters in a set of genotypes.

### Material and Methods

**Genetic material:** The material for the present investigation were consist of a set of 30 germplasm lines including two checks i.e. RTM-314 and RTM- 1351 which were obtained from the collection being maintained at the AICRP Oilseeds (Taramira Unit), Department of Plant Breeding and Genetics, S.K.N. College of Agriculture, Jobner (Table 1). This investigation was conducted at Research Farm, SKN College of Agriculture, Jobner (Rajasthan). Jobner is located at 26.97°N and 75.38°E. It has an average elevation of 400 metres above mean sea level (1312 feet). These entries were evaluated in randomized block design with 3 replications. In each replication each entry was sown in a plot of two rows, each row consisting with 4-meter length and plant to plant distance were maintained at 10 cm by thinning after 15 days of sowing.

**Statistical analysis:** The genotypic coefficient of variation (GCV) and phenotypic coefficient Variation (PCV) computed by the formula suggested by Burton (1952) [4]. The PCV and GCV values were ranked as low (0-10%), medium (10-20%) and high (>20%). The heritability in percent in broad sense was calculated by the procedure suggested by Singh and Choudhary (1985) [6]. Heritability values are categorized on

the basis of range of percentage as low (<50%), moderate (50-70%) and high (>70%). Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al.*, (1955) [7]. Genetic advance as percent of mean was classified as low (0-10%), moderate (10- 20%) and high (>20%).

**Table 1:** List of germplasm lines

Sr. No.	Genotypes	Sr. No	Genotype
1	RTM-314	16	RTM-1805
2	RTM-1791	17	RTM-1806
3	RTM-1792	18	RTM-1807
4	RTM-1793	19	RTM-1808
5	RTM-1794	20	RTM-1809
6	RTM-1795	21	RTM-1810
7	RTM-1796	22	RTM-1811
8	RTM-1797	23	RTM-1812
9	RTM-1798	24	RTM-1813
10	RTM-1799	25	RTM-1814
11	RTM-1800	26	RTM-1815
12	RTM-1801	27	RTM-1816
13	RTM-1802	28	RTM-1817
14	RTM-1803	29	RTM-1818
15	RTM-1804	30	RTM-1351

**Table 2:** Observations recorded for seed yield and its components characters.

S. No.	Characters
1	Days to 50 percent flowering
2	Days to maturity
3	Plant height (cm)
4	Primary branches per plant
5	Secondary branches per plant
6	Number of siliquae per plant
7	Length of siliqua (cm)
8	Seeds per siliqua
9	Test weight (g)
10	Oil content (percent)
11	Seed yield per plant (g)

## Results and Discussion

The result on analysis of any breeding program lies upon the thorough knowledge of genetic variability, heritability and type of gene action involved in the inheritance of importance of improvement of desirable characters thus, and success of genetic enhancement is attributed to the magnitude and nature of variability present for a specific character. The wide range was observed for the number of siliquae per plant, seed yield per plant and secondary branches per plant. The phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the characters, indicating positive effect of environment on the expression of a character. Genotypic and phenotypic coefficient of variation was high in case of number of siliquae per plant (23.55, 24.17) and seeds per siliquae (20.65, 22.67) which indicates the presence of high amount of variation among the genotypes. Lowest genotype and phenotype coefficient of variation estimate was found for days to 50 percent flowering (6.42, 7.98), days to maturity (3.46, 4.71), plant height (5.26, 6.14), primary branches per plant (6.87, 9.21), secondary branches per plant (7.97, 9.26), test weight (7.68, 8.77), oil

content (8.46, 9.43) and seed yield per plant (7.56, 9.75) (Table 3). The other character which recorded moderate GCV and PCV has in length of siliqua (10.12, 12.90). The similar results are finding by Jajoria, (2001) [5], Bind *et al.* (2015) [3], Kumar *et al.* (2019) and Amsalu *et al.* (2020) [1].

Heritability estimate ranged from 65.67% (primary branches per plant) to 96.84% (number of siliquae per plant) (Table 3). High heritability coupled with high genetic advance as percentage of mean indicated presence of additive gene action in these traits *viz.*, Number of siliquae per plant (96.84, 29.35), oil content (87.86, 25.65), seeds per siliquae (78.56, 41.70). High heritability with low genetic advance as percentage of mean it is indicated non-additive gene action in these traits *viz.*, Plant height (80.40, 9.32) and secondary branches per plant (80.71, 8.14). Respectively, the high heritability is being exhibited due to favorable influence of environment rather than genotype and selection for such traits may not be rewarding. Lyngdoh *et al.* (2017) [9], Shekhawat *et al.* (2018) [14], Jat *et al.* (2019) [6], Pal *et al.* (2019) [10] and Rout *et al.* (2019) [12].

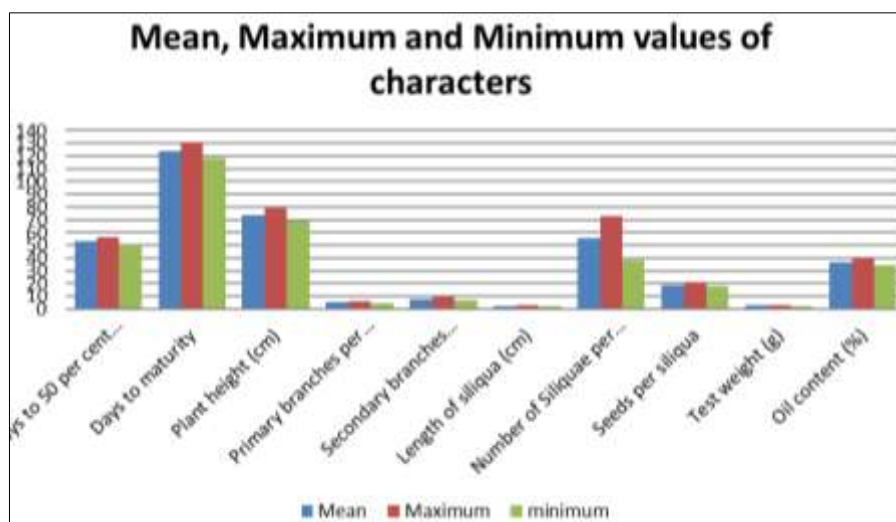


Fig 1: Maximum, minimum and mean values of all characters

Table 3: Genetic parameters of variation for seed yield and its component characters in Taramira

S. No.	Character	Mean	Min	Max	GCV (%)	PCV (%)	Heritability	GA% mean
1	Days to 50 percent flowering	52.95	56.44	49.78	6.42	7.98	70.66	10.65
2	Days to maturity	123.97	130.67	118.34	3.46	4.71	74.67	7.39
3	Plant height (cm)	73.48	79.18	68.68	5.26	6.14	80.40	9.32
4	Primary branches per plant	5.71	6.52	4.87	6.87	9.21	65.89	17.30
5	Secondary branches per plant	7.89	9.44	6.77	7.97	9.26	80.71	8.14
6	Length of siliqua (cm)	2.49	2.75	2.25	10.12	12.90	65.67	23.57
7	Number of siliquae per plant	55.78	72.60	38.55	23.55	24.17	96.84	29.35
8	Seeds per siliquae	18.99	20.80	17.75	20.65	22.67	78.56	41.70
9	Test weights (g)	2.87	3.25	2.43	7.68	8.77	83.75	13.89
10	Oil content (%)	36.76	39.92	34.47	8.46	9.43	87.86	25.65
11	Seed yield per plant (g)	3.18	3.99	2.73	7.56	9.75	81.45	16.46

### Conclusion

High heritability coupled with high genetic advance as percentage of mean indicated presence of additive gene action in these traits viz., Number of siliquae per plant, oil content and seeds per siliquae, additive gene action is pronounced in the expression of these character early generation selection would be effective in breeding programmed. High heritability is found with low genetic advance as percentage of mean for traits like plant height and secondary branches per plant, which is indicative of aforesaid characters, are governed under non additive gene action.

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