GENETIC VARIABILITY AND CHARACTER ASSOCIATION ANALYSIS IN TARAMIRA (ERUCA SATIVA MILL.)

THESIS

Submitted to the
Swami Keshwanand Rajasthan Agricultural University,
Bikaner

In partial fulfillment of the requirements for
the degree of

Master of Science
in the

Faculty of Agriculture
(Plant Breeding & Genetics)

By

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2013
1. INTRODUCTION

Oilseed crops have been recognized as a major source of fats and protein in human diet. More than 85 per cent of country's vegetable oil supply depends on seven edible oil (groundnut, rapeseed mustard, soybean, sesame, sunflower, safflower and niger) and non-edible oil (linseed and castor). Oilseed occupy a significant place in national economy next only to food grains. The bulk of the country's edible oils are derived from major oil seed namely; soybean, rapeseed-mustard and groundnut which account for about 87.5 per cent of the total oil seed production (Anonymous, 2009-10).

Rapeseed mustard crops in India comprise traditionally grown indigenous species namely toria (Brassica campestris L. var. toria), brown sarson (Brassica campestris L. var. brown sarson), yellow sarson (Brassica campestris L. var yellow sarson), Indian mustard [Brassica juncea (L.) Czern and Coss], black mustard (Brassica nigra) and taramira (Eruca sativa Mill), which have been grown since about 3500 BC along with non-traditional species like gobhi sarson (Brassica napus L.), and Ethiopian mustard or Karan rai (Brassica carinata A. Braun). The rapeseed-mustard group is comprised of two distinct type (i) self pollinated – Indian mustard, raya and yellow sarson of which Indian mustard is the most important member of the group accounting 75-80 per cent of the area under rapeseed and mustard and (ii) cross pollinated – brown sarson, toria and taramira.

Taramira (Eruca sativa Mill.) is an important winter season oilseed crop of the family Brassicaceae. It is an introduced crop in India. South Europe and North Africa are believed to be the native place of it. It has diploid number of chromosomes 2n = 22 and the chromosomes are very small. Taramira has desirable traits particularly resistance to powdery mildew that can be transferred to Brassica campestris and Brassica juncea both of which are important crops (Sastry, 2003). In India, it is known by many names such as tara, schwan, seoha, duan, turra, tirwa, merha, merkai, chara, ushan and sondha (Singh,
In Europe it is known as rocket salad, rocket, roquuette or arrugula, where it is generally grown for young leaves that are eaten as green salad.

Taramira is a herbaceous annual, 2 to 4 feet tall and is a common cold weather oilseed crop of the drier areas of north-west India where it is commonly grown mixed with gram and barley. It does not require much preparatory tillage due to efficient and fast penetrating root system permitting extrusion of soil water from deep soil layers. It is a hardy crop that can be successfully grown in dry land areas and poor sandy soils with conserved moisture during the years of severe drought coupled with late Rabi rains, it is the only alternative available for sowing on soils having limited moisture supply (Gupta et al., 1998).

The oil content in taramira ranges from 31.6 - 41.31% (Yadav et al., 1980) which is affected by manuring, irrigation and disease management. Analysis of the oil profile has indicated that taramira oil has about 46.3 per cent erucic acid which is comparable to other rape seed mustard crops, while oleic acid (28.7 per cent), linolic acid (12.4 per cent) and linolenic acid (2.1 per cent) are considerably lower as compared to mustard oil. Saturated fatty acid are around 10.5 per cent. In general low erucic acid is preferred for human consumption while high erucic acid is desired for industrial purposes namely in the manufacture of grease, soap, plastics, lubricants, paints and chemicals etc. Taramira oil is mainly used in adulteration of mustard oil to increase pungency. The cake of taramira is used as manure for improving the soil physical condition and soil fertility and it can also be used as nutritional feed for animals.

It is cultivated to an extent in Sweden, Germany, France, India, Poland, Canada and China. In India, taramira is mainly grown in the states like Rajasthan, Haryana, Punjab, Gujarat, Madhya Pradesh and Uttar Pradesh. In Rajasthan major taramira growing districts are Jaipur, Sawai Madhopur, Sri Ganganagar, Bhilwara, Bikaner, Jalore, Nagaur and Pali. In Rajasthan it is grown on area of 118870 hectares with an annual production of 48635 tonnes and productivity of 409 kg per hectare (Anonymous, 2011-12). The farmers use locally available seed and do not follow improved package of practices resulting in poor yield.
The average productivity of taramira is very low and unstable. The low productivity of the crop can mainly be attributed to the growing of the crop on marginal and sub marginal lands of poor fertility with very low level of input application, lack of improved package of practices, use of locally available varieties and lack of varieties having diversified characteristics. The lack of variability for different morpho-physiological traits, seed yield and oil content and a limited knowledge on genetics of these traits in this crop has restricted the development of high yielding varieties (Sharma et al. 1991).

The success in any breeding programme depends on the amount of variability present for different characters in the population and its efficient management and utilization. Further, the association analysis which generates information on the relationship between the characters and possibility of indirect selection, is also necessary. Path coefficient analysis may be carried out to obtain the information on the direct and indirect effects of particular character on other characters and finally on yield. Therefore, keeping in view the above outlined necessities the present investigation was carried out to determine relationship between different morphological characters in taramira besides assessing the extent of genetic variation for various traits.

The material for study consisted of a large collection of germplasm of taramira have been maintained in All India Coordinated Research Project on Oilseed (Taramira unit), Department of Plant Breeding and Genetics, S.K.N. College of Agriculture, Jobner. The present study was undertaken with following objectives.

(i) To estimate the variability for seed yield and related characters in the germplasm.
(ii) To assess the degree of association among various characters and 
to measure their direct and indirect effect on yield.

(iii) To identify the superior genotypes for seed yield and oil content.

2. REVIEW OF LITERATURE

Taramira is one of the most drought tolerant crop. The 
crop is specially suitable to the dryland areas as it has efficient 
root system to extract moisture from deeper soil layers. It is a 
highly cross- pollinated crop due to sporophytic type of 
incompatibility (Sharma et al. 1985). Verma et al. (1977) have 
shown that the self- incompatibility is controlled by two genes s 
and z.

The crop suffers from the disadvantage of low yield 
potential as compared to the other crops of group. Thus, 
concerted breeding work is required to bring about favourable 
changes in yielding ability and agronomic characteristics of this 
crop. The present research work was carried out to estimate 
the variability for different characters in the set of germplasm
lines for its efficient management and utilization in breeding programmes. The literature available on the topics related to the present investigation is briefly reviewed under the following headings:

2.1 Studies on variability, heritability and genetic advance.
2.2 Studies on correlation and path coefficient.

### 2.1 Studies on variability, heritability and genetic advance

The information on the nature and magnitude of variability in germplasm collection for yield and yield contributing characters is the primary requirement for planning of any crop improvement programme. Estimation of heritability is important to determine the extent to which a character is heritable and the role of environmental factors on the expression of the character. Heritability indicates the possibility and extent to which improvement can be brought through selection.

Lush (1949) defined the heritability in broad and narrow sense. The ratio of genetic variance to the total phenotypic variance expressed in per cent determine the heritability in
broad sense. Whereas, in narrow sense it is the ratio of genetic variance due to additivity of genes (additive genetic variance) to phenotypic variance.

Estimation of genetic advance or gain is an important parameter to evaluate effectiveness of the selection. The genetic advance is the product of heritability, selection differential and phenotypic standard deviation of a character. Comstock and Robinson (1952) reported that the genetic gain depends on the amount of genetic variability, the magnitude of making effect on the genetic diversity and the intensity of selection.

Yadav and Kumar (1984) and Kumar and Yadav (1986) estimated variability in taramira and reported higher estimates of genetic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance for secondary branches per plant, siliqua length, seeds per siliqua and test weight and also reported moderate variability, genetic advance with high heritability for seed yield per plant.

Sodani et al. (1990) indicated that in taramira siliquae per plant, seed yield per plant and test weight have the greatest contributions to genetic divergence.
Sharma *et al.* (1991) worked on taramira and reported a wide range of variability for siliquae per plant, plant height, primary and secondary branches per plant, and seed yield. The variation for days to 50 per cent flowering and maturity and oil content was very much limited. High genetic advance was also reported for secondary branches per plant (34.29%), siliquae per plant (32.86%) and seed yield per plant (34.25%).

Rathore (1995) studied taramira germplasm for yield and its contributing traits in 90 genotypes and observed that phenotypic coefficient of variation is higher than genotypic of variation for all the characters and heritability (broad sense) estimates high for biological yield (90%), test weight (80.20%), siliquae per plant (77.80%), secondary branches per plant (76.70%) and primary branches per plant (75.83%). Most of above traits also had high genetic advance whereas heritability and genetic advance estimates were low for plant height (3.82%) and seeds per siliqua (5.39%).

Palsania (1995) reported high heritability values for plant height (88.34%), days to 50% flowering (84.40%), biological yield (84.32%) and seed yield per plot (80.22%) and moderate values of heritability for seed yield per plant (77.78%), oil
content (77.00%), siliquae per plant (73.96%), seeds per siliqua (76.53%) and test weight (73.68%) in taramira. Genetic advance estimates were high for plant height (61.15%), seed yield per plant (59.62%) and seed yield per plot (58.55%). While the estimates were low for days to maturity (1.37%), days to 50 per cent flowering (9.37%) and oil content (9.84%).

Yadav et al. (1998) evaluated twenty five diverse genotypes of taramira for eleven yield components. They revealed that secondary branches per plant had highest coefficient of variation followed by test weight and primary branches per plant. Heritability was high for test weight, siliqua length, seeds per siliqua and seed yield per plant.

Kaushik (1998) observed high variability for days to flowering, branches per plant, siliquae per plant, siliqua length, seeds per siliqua, seed yield per plant and biological yield per plant similarly high heritability (broad sense) values were also observed for biological yield per plant, siliquae per plant and number of branches per plant and moderate heritability values was observed for number of seeds per siliqua and seed yield per plant and genetic advance was higher for biological yield
per plant, it was moderate for siliquae per plant and seed yield per plant and minimum for siliqua length.

Shalini et al. (2000) assessed the magnitude of genetic variation in 81 diverse Indian mustard genotypes. The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all 10 characters studied. Genetic coefficient of variation, heritability values and genetic gain were moderate to high for test weight, number of siliquae per plant and number of secondary branches per plant. Thus response to selection would be very high for these traits.

Jajoria (2001) working on genetic divergence for seed yield and its components in 150 genotypes of taramira reported high values of phenotypic coefficient of variation and genotypic coefficient of variation along with high heritability and higher genetic advance as percentage of mean for siliquae per plant and seed yield per plant.

Mahla et al. (2003) reported high heritability coupled with higher genetic advance for seed yield per plant, test weight, siliquae on main branch and branches per plant and suggested selection for these traits would be effective. High heritability accompanied with moderate to low genetic advance for plant
height, main branches length, days to flowering indicated role of non additive gene action in the expression of these traits.

Singh (2003) observed the variability, heritability and genetic advance of 40 Indian mustard cultivars. The cultivars differed significantly for plant height, days to 50% flowering, siliquae per plant, seeds per siliqua, days to maturity, test weight and seed yield per plot. The genotypic and phenotypic coefficient of variation were highest for test weight and minimum for days to maturity. The highest genetic advance was observed for test weight followed by seed yield per plant, days to 50% flowering and siliquae per plant.

Manohar and Sharma (2005) reported high PCV for some traits in taramira which indicated that these traits were highly influenced by the environment. The estimates of GCV were high for primary branches per plant, seed yield per plant and siliquae per plant. Similarly, high heritability (>70%) coupled with high genetic advance (> 40 %) was observed for primary branches per plant, seed yield per plant and siliquae per plant.

Patel et al. (2006) reported high heritability ranging from 67.9 to 97.8 % for days to 50% flowering, 1000- seed weight, oil content, seed yield per plant, plant height and days to
maturity and suggested that these characters could be improved through selection. The higher estimates of heritability (72%) coupled with high genetic advance (41.4%) for plant height indicated that the trait was mainly under the control of additive gene effects. Seed yield per plant, days to 50% flowering and 1000-seed weight had heritability (71-99%) with moderate genetic advance (2.1-16.0%).

Brar et al. (2007) observed that the heritability was high (>75%) with moderate genetic advance (13.1%) for siliquae on main raceme in Indian mustard. Primary branches and 1000-seed weight had high heritability (>75%) with low genetic advance (1.3-2.1%). Moderate heritability (65.5%) and genetic advance (14.9%) was recorded for main raceme length. Low heritability (<50%) was associated with moderate genetic advance (17.4%) for plant height.

Kumhar et al. (2007) observed that the crosses shown significant desirable heterosis for primary branches per plant fruiting branches per plant and siliquae per plant. Thus, the characters primary branches per plant, fruiting branches per plant and siliquae per plant appear to be important seed yield components.
Upadhyay and Kumar (2008) studied the heritability and genetic advance for 11 metric traits (days to 50 % flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, number of siliquae per plant, number of siliquae on main raceme, length of main raceme, seeds per silique, 1000- seed weight, seed yield per plant and oil content) using 7 Indian mustard cultivars (NFDR-190, NDR-8208, NDYR-8, NDRE-4, Uravashi, Vardan and PHR-1). 8F\textsubscript{1} hybrid and 8F\textsubscript{2} hybrids using generation mean analysis. High heritability coupled with high genetic advance was recorded for secondary branches per plant in cross V and VIII under normal sown condition. Under late sown condition seed yield per plant in cross VIII high heritability and high genetic advance. High heritability is due to additive gene effects and suggested that selection for these traits would be more effective for improvement.

Manohar and Sharma (2008) observed higher estimates of genotypic coefficient of variation, phenotypic coefficient of variation, heritability (bs) and genetic advance expressed as percentage of mean for seed yield per plant, secondary
branches per plant, seeds per siliqua and siliquae per plant in taramira.

Dar et al. (2010) worked on brown sarson and observed high GCV and PCV for 1000 - seed weight, seed yield per plant, number of siliquae per plant, days to 50% flowering and high heritability was observed for days to 50% flowering, 1000 - seed weight, oil content, seed yield per plant, plant height and days to maturity and suggested that these characters can be improve through visual selection based on their phenotypes.

Doddadhimappa et al. (2010) worked on Indian mustard and reported that genetic diversity for secondary branches per plant attributed maximum per cent towards divergence followed by biological yield per plant, days to maturity and seed yield per plant under protected and unprotected conditions.

Singh et al. (2010) reported that seed yield, 1000 - seed weight, number of secondary branches, number of seeds per siliqua, siliqua length, number of primary branches, plant height and number of siliquae on main raceme were the maximum contributors to genetic diversity among all the genotypes.

Keer and Jakhar (2012) observed high heritability along with high genetic advance for number of siliquae per plant,
number of secondary branches per plant and seed yield per plant. High heritability and moderate to low genetic advance for siliqua length, 1000-seed weight, days 50 per cent flowering, plant height, number of primary branches per plant and oil content.

### 2.2 Correlation and path coefficients analysis

When change in one variable causes the change in other variable, the two variables are said to be correlated. This association between the attributes is quantified by the statistic called correlation coefficient.

Path coefficient is a standardized partial regression coefficient. It measures the direct and indirect effect of one variable on the other and allows the partition of the total correlation coefficient between two variable into direct and indirect components. The concept of path analysis was initially suggested by Wright (1921) and was applied for first time in plant breeding by Dewey and Lu (1959).

Correlation and path coefficient studies in *B. juncea* indicated that plant height, secondary branches per plant, seed yield and seeds per siliqua should be considered in breeding
for increasing seed yield (Singh and Choudhary, 1979). Similarly genotypic, phonotypic, partial and multiple correlations were also studied among seed yield and days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, plant height and days to maturity in *B. juncea* by Katiyar and Singh (1984). They also reported that the seed yield was positively associated with days to 50% flowering, number of primary branches per plant, number of secondary branches per plant and plant height. Plant height, number of primary branches per plant, primary and secondary branches were positively associated with each other. However, days to flowering showed negative association with days to maturity.

Yadav and Kumar (1984) reported that in the early sown as well as late sown taramira, the association of seed yield with siliquae on main shoot and siliquae per plant was significant and positive in both the sowing dates on the contrary, seed yield had a significant positive association with secondary branches per plant, siliqua length and 1000-seed weight in the early sowing and with main shoot in late sowing.
Nehra et al. (1989) reported significant and positive correlation of seed yield with days to maturity, plant height, primary branches per plant, secondary branches per plant and siliquae per plant. These characters also showed significant positive association among themselves.

Sharma et al. (1991) observed in taramira that the seed yield per plant and seed yield per plot were significantly and positively correlated at phenotypic level with siliquae per plant (0.861), plant height (0.346), primary branches per plant (0.255), secondary branches per plant (0.249) and days to maturity (0.196). These characters have also shown significant positive association among themselves.

Palsania (1995) in taramira reported that seed yield per plot had positive and significant correlation at phenotypic level with seed yield per plant (0.499), biological yield (0.187), siliquae per plant (0.184), plant height (0.180), test weight (0.162) and days to 50 per cent flowering (0.141).

Rathore (1995) in taramira reported that seed yield per plant was positively associated with number of primary branches per plant, number of secondary branches per plant siliquae per plant and biological yield. Path analysis revealed
that number of secondary branches per plant, number of primary branches per plant, siliquae per plant and biological yield were the most important characters for selection of high yielding genotypes as they exerted positive direct as well as positive significant association with seed yield per plant.

Meena (1996) worked on taramira and reported that the seed yield per plant was significantly and positively associated with days to maturity primary branches per plant, number of siliquae per plant, biological yield and harvest index. The number of siliquae per plant and harvest index has high significant positive correlation with seed yield. The path analysis revealed high and positive direct effect of number of siliquae per plant on seed yield. He concluded that number of siliquae per plant is the most important yield component trait in taramira.

Yadav (1996) has shown positive associations for plant height, primary branches per plant, secondary branches per plant, siliquae per plant with seed yield per plant in the parent (RTM-314) as well as in half-sib families.

Kaushik (1998) worked on taramira and revealed that path coefficient analysis for the number of siliquae per plant
was the important character for the selection of high yielding genotypes as it exerted positive direct effect as well as had positive significant association with seed yield per plant.

Yadav *et al.* (1998) in a study on twenty five diverse genotypes of taramira for eleven yield components observed that seed yield was positively correlated with length of main raceme, siliqua on main raceme, siliquae per plant, seeds per siliqua and plant height.

Patel *et al.* (2000) reported that seed yield, days to 50% flowering, days to maturity, plant height, length of main branches per plant, number of siliquae per plant, length of siliqua, seeds per siliqua and 1000-seed weight were the most important character for selection of high yielding genotypes.

Singh *et al.* (2000) reported significant and positive correlation of seed yield with secondary branches, main shoot height and siliquae on the main shoot, while plant height, primary branches and 1000-seed weight showed a positive but non-significant association with seed yield. These characters also showed significant positive association among themselves.
Shah et al. (2000) while working on taramira reported significant and positive correlation between yield and yield component traits (days to 50% flowering, days to maturity, number of primary branches per plant, plant height, number of siliquae per plant, number of seeds per siliqua, siliqua length and test weight). The genetic correlation was higher than the phenotypic correlation for majority of the characters.

Kumar and Srivastava (2003) reported that phenotypic correlation for character seed yield was highly significant and positive with oil yield and both were positively and significantly correlated with plant height, primary branches, days to flowering, seed oil content.

Khan and Khan (2003) worked on Brassica germplasm collections and reported that seed yield per plant was positively correlated with plant height number of primary branches, number of secondary branches, number of pods per plant and seed index.

Sastry (2003) worked on taramira and reported that seed yield per plant and per plot were significantly and positively correlated with days to maturity, plant height, primary branches per plant, secondary branches per plant and siliquae per plant.
These characters have also shown significant positive association among themselves.

Akbar et al. (2003) studied variability, correlation and path coefficient analysis in summer mustard (*Brassica juncea* L.) and reported that number of siliqua per plant was found strong parameter followed by number of branches and plant height for seed yield improvement.

Mahla et al. (2003) worked on Indian mustard and reported that seed yield per plant exhibited highest positive association with branches per plant (0.813), followed by siliqua on main branches (0.463), plant height (0.413), seeds per siliqua (0.392) and length of main branch (0.296). The negative correlation were observed for oil content with test weight (-0.050).

Naazar Ali et al. (2003) reported positive and significant correlation between seed yield and harvest index, seed weight and flower duration in winter rape seed (*Brassica napus* L.). Significant and positive correlation of seed weight with harvest index, flower duration and seed yield indicated that improvement in seed weight will give higher harvest index ultimately resulting high seed yield.
Pandey and Singh (2005) worked on Indian mustard (*Brassica juncea* L.) and reported seed yield per plant showed significant and positive correlation with number of secondary branches, length of main shoot, length of silique and silique on main shoot while 1000 - seed weight and oil content had negative correlation with seed yield.

Tuncturk and Ciftic (2007) noted positive correlation of seed yield with number of branches, number of pods per plant, number of seeds per pod and 1000 - seed weight in *Brassica napus.*

Akbar *et al.* (2007) found that genotypic mean square for each trait was highly significant except 1000- seed weight which is only significant and highest GCV for seed yield was found followed by pod per plant, plant height, 1000- seed weight while lowest GCV for primary branches per plant. They also found that pod per plant have strong positive correlation with seed yield followed by plant height.

Ivanovasca *et al.* (2007) found that seed yield had highest correlation with number of pods per plant followed by seed weight per pod and 1000-seed weight in *Brassica napus.*
Dilek Basalma (2008) observed positive and statistically significant correlation between branches per plant, number of pods on the main stem and plant height. Plant height was negatively correlated with seed yield, 1000-seed weight and oil content.

Manohar and Sharma (2008) reported that seed yield was positively and significantly correlated in taramira with plant height, primary and secondary branches per plant, siliqua length, seeds per siliqua, siliquae per plant, test weight. They further, reported that siliquae per plant had maximum direct positive effects on the seed yield per plant followed by siliqua length, secondary branches per plant, seeds per siliqua and primary branches per plant.

Aytac and Kinaci (2009) found that seed yield was positively and significantly correlated with number of branches per plant, plant height, number of pod per plant.

Doddabhimappa et al. (2009) studied correlation and path analysis in India mustard (*Brassica juncea* L. Czern and Coss) and reported that yield was highly and significantly correlated with, number of siliquae per plant, number of primary and secondary branches per plant, biological yield per plant,
1000-seed weight, number of seeds per siliqua in protected and unprotected conditions.

Sabaghnia et al. (2010) found that all morphological traits have positive correlation with seed yield except stem diameter, days to flowering, lateral branch height and number of pods per plant.

Sadet et al. (2010) found number of branches, number of pods per plant, number of seeds per pod and 1000 - seed weight directly and positively correlated with seed yield.

Keer and Jakhar (2012) worked on taramira and revealed that path coefficient analysis for seed yield per plant, 1000-seed weight and number of primary branches per plant were the traits for the selection of high yielding genotype as it exerted positive direct effect as well as had positive significant association with seed yield per plant.
3. MATERIAL AND METHODS

The present investigation entitled “Genetic Variability and Character Association Analysis in Taramira (Eruca sativa Mill.)” was conducted during Rabi season of 2012-2013 at research farm of S.K.N. College of Agriculture, Jobner. Jobner is situated at a latitude of 26° 05’ N longitude 75° 20’ E and at an altitude of 425 meters above the mean sea level. The details of material and methods used in the present investigation are given below under separate heading.

3.1 Experimental material:

A set of 100 accessions lines of taramira were obtained from the germplasm collection of “All India Coordinated Research Project on Oilseeds (Taramira Unit)” located at Jobner. The list of accessions used in the study are presented in Annexure-1.

3.2 Experimental method:

The experimental material was evaluated in Augmented Randomized Block Design (Federer, 1956). The experiment material was divided into 5 groups each of 25 accessions. Each group of accession was assigned to a separate block. Five check varieties i.e. RTM-2002, RTM-314, T-27, RTM-1212 and RTM-1359 were also assigned to each block. In each block, accessions and check varieties were sown in a plot size of 5 x 0.60m² accommodating 2 rows spaced 30 cm apart, after randomization the plant to
plant distance was maintained at 10 cm by thinning. Recommended cultivation practices was followed to raise a good crop.

3.3 Observation recorded:

Ten plants were randomly selected and tagged before flowering from each plot to record the data on the following attributes. Data on days to 50% flowering was, however, recorded on whole plot basis. The method used for recording observations are described below:

3.3.1 Days to 50 per cent flowering:

It was recorded as the number of days taken from sowing to anthesis in 50 per cent of the plants in each plot.

3.3.2 Days to maturity

It were recorded as the days taken for completion of physiological maturity in 90 per cent plant in a plot.

3.3.3 Plant height (cm):

The plant height was measured from ground level to the tip of the main stem of each randomly selected plant in cm from each plot and averaged.

3.3.4 Number of primary branches per plant:

The number of primary branches arising from the main shoot were counted in ten randomly selected plants in a plot and averaged.

3.3.5 Number of secondary branches per plant:

The number of secondary branches arising from the main primary branches bearing the siliquae was counted at the time of harvest on ten randomly selected plants per plot and mean over ten plants were recorded.
3.3.6 Siliquae per plant:

The number of siliquae bearing seeds per plant were recorded by counting total number of siliquae on ten randomly selected plants of each plot and then averaged.

3.3.7 Seeds per siliqua:

The ten siliquae per plant were selected randomly from each of the ten randomly selected plants and total number of seeds counted and averaged to obtain the number of seeds per siliqua.

3.3.8 Siliqua length (cm):

The siliqua length of the same ten siliqua selected for counting the number of seeds per siliqua were used to measures the siliqua length in cm from the base of the siliqua to the tip of it.

3.3.9 1000-seed weight (g):

A random sample of one thousand seeds were drawn from the harvest of each genotype and weighed on sensitive electronic balance to recorded test weight in gm.

3.3.10 Seed yield per plant (g):

Total seeds obtain from the ten randomly selected plants were weighted and divided by ten and express as yield per plant in gm.

3.3.11 Oil content (%):
The oil content was recorded on per cent basis using “Nuclear magnetic Resonance method by Nuclear Magnetic Resonance spectrometer apparatus at DRMR, Sewar, Bharatpur.

STATISTICAL ANALYSIS

Analysis of variance:

The mean data were subjected to analysis of variance as per the method suggested by Federer (1956). The ANOVA table with appropriate sources of variation and degrees of freedom along with expectations of mean sum of squares are given below.

The analysis of variance table and expected of mean square:

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>MSS</th>
<th>Expected M.S.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Block (eliminating check + var.)</td>
<td>b-1</td>
<td>MS_b</td>
<td></td>
</tr>
<tr>
<td>Entries (ignoring blocks)</td>
<td>(c+g)-1</td>
<td>MS_{c+g}</td>
<td></td>
</tr>
<tr>
<td>Check</td>
<td>c-1</td>
<td>MS_c</td>
<td></td>
</tr>
<tr>
<td>Accessions</td>
<td>g-1</td>
<td>MS_g</td>
<td></td>
</tr>
<tr>
<td>Checks vs. accessions</td>
<td>1</td>
<td>MS_g</td>
<td>σ^2_g + σ^2_e</td>
</tr>
<tr>
<td>Error</td>
<td>(c-1) (b-1)</td>
<td>MS_e</td>
<td>σ^2_e</td>
</tr>
<tr>
<td>Total</td>
<td>N-1</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Whereas,

- \( b = \) Number of block
- \( c = \) Number of check varieties in each block.
- \( g = \) Number of accessions in all blocks.
- \( σ^2_g = \) Genotypic variance (MS_g-MS_e)
- \( σ^2_p = \) Phenotypic variance (σ^2_g + σ^2_e)
- \( σ^2_e = \) Error variance (MS_e)
The critical difference (C.D.) at 5 per cent was calculated by the following formulae:

1. Between check varieties = \( \sqrt{\frac{2 \times \text{MSe}}{b}} \) \( \times t \)

2. Between accessions within a block = \( \sqrt{2 \times \text{MSe}} \) \( \times t \)

3. Between accessions between block = \( \sqrt{\frac{2 \times \text{MSe} \times (c+1)}{c}} \) \( \times t \)

4. Between check varieties and accessions = \( \sqrt{\frac{\text{MSe} \times (b+1) \times (c+1)}{b \times c}} \) \( \times t \)

Where,

\( \text{MSe} \) = Error variance

\( b \) = Number of blocks

\( c \) = Number of checks

\( t \) = \( t \) value at 0.05 at error d.f. (c-1) (b-1) = 12

1. Genetic Analysis

Various parameter of genetic variability that is mean, range, components of variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability (in broad sense), genetic advance expressed as percentage of mean were computed as given below.

(i) Mean: Mean was calculated using the following formula

\[
\bar{X} = \frac{\sum_{i=1}^{N} X_i}{N}
\]

Where,

\( \bar{X} \) = Character mean

\( X_i \) = Value of \( i^{th} \) observations.

\( N \) = Total number of observations
(ii) **Range:**

The range of characters represented the lowest and highest means values among the accessions.

(iii) **Coefficient of variation**

Genotypic coefficient and phenotypic coefficient of variation were calculated by the standard procedures using adjusted and unadjusted accession values respectively.

\[
\text{G.C.V.} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100
\]

\[
\text{P.C.V.} = \frac{\sqrt{\sigma_p^2}}{\bar{X}_a} \times 100
\]

Where,

- G.C.V. = Genotypic coefficient of variation
- P.C.V. = Phenotypic coefficient of variation
- \( \sigma_g^2 \) = Genotypic variance
- \( \sigma_p^2 \) = Phenotypic variance
- \( \bar{X} \) = Over all mean of the characters based on adjusted values
- \( \bar{X}_a \) = Over all mean of characters based on unadjusted values

These formulae have been earlier used by Burton (1952) and Johnson *et al.* (1955).

(iv) **Genetic advance:**
The genetic advance for each character was calculated as suggested by Lush (1949) and Johnson et al. (1955) using following formula :-

\[
\text{Genetic Advance} = k \cdot \sigma_p \cdot h^2
\]

\[
\text{Genetic advance as percentage of mean} = \frac{k \cdot \sigma_p \cdot h^2 \times 100}{\bar{x}}
\]

Where,

- \(k\) = intensity of selection (constant 2.06 at 5 per cent selection intensity).
- \(\sigma_p\) = phenotypic standard deviation
- \(h^2\) = broad sense heritability in fraction.
- \(\bar{x}\) = overall mean of the character

(v) Heritability

Heritability in broad sense was estimated by the formula proposed by Hanson et al., (1955) i.e.

\[
\text{Heritability in broad sense} (h^2) = \frac{\sigma^2_g}{\sigma^2_e + \sigma^2_g} \times 100
\]

\[
h^2 = \frac{\text{Total genotypic variance}}{\text{Total phenotypic variance}} \times 100
\]

2. Association analysis

The association analysis were carried out using the adjusted means of the characters.

\[
\text{Adjusted mean} = \text{raw mean value} - \text{rj factor}
\]
rj factor = \frac{\text{Block total checks – total of mean checks}}{\text{Number of checks}}

The correlation coefficients for the ten characters combinations were calculated using the formula given by Johnson et al., (1955).

Which is

\[ r_{xy} = \frac{\text{Cov}_{xy}}{\sqrt{\text{Var}_x \cdot \text{Var}_y}} \]

Where,

- \( r_{xy} \) = Correlation coefficients between trait x and y
- \( \text{Cov}_{xy} \) = Covariance between trait x and y
- \( \text{Var}_x \) = Variance of trait x.
- \( \text{Var}_y \) = Variance of trait y.

The adjusted values of x and y were used for estimation of correlation coefficient.

The significance of correlation coefficient was tested comparing the calculated value with table value of r [Gomez and Gomez, 1980] at 106 d.f.

3. Path coefficient analysis

A path coefficient is a standardized partial regression coefficient. It measure the direct and indirect effect of one variable on the other and allows to partitioning the total correlation coefficient between two variables into direct and indirect components. The correlation coefficient provides information about the degree of association between two characters. However it is now known that almost all the characters are polygenic and
almost all genes are pleiotropic in action such that each gene apart from its direct contribution to a particular characters, contributes to several other characters.

The estimates of direct and indirect effects were calculated by path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The following set of simultaneous equations were formed and solved for estimating the various direct and indirect effects.

\[
\begin{align*}
    r_{1y} &= P_{1y} + P_{2y}r_{1.2} + P_{3y}r_{1.3} + \ldots \ldots \ldots \ldots P_{9y}r_{1.9} \\
    r_{2y} &= P_{1y}r_{2.1} + P_{2y} + P_{3y}r_{2.3} + \ldots \ldots \ldots \ldots P_{9y}r_{2.9} \\
    r_{9y} &= P_{1y}r_{9.1} + P_{2y}r_{9.2} + P_{3y}r_{9.3} + \ldots \ldots \ldots \ldots P_{9y} \\
\end{align*}
\]

Where,

- \( r_{1y} \) to \( r_{9y} \) = correlation between 1 to 9 (independent characters) and y (dependent character).
- \( P_{1y} \) to \( P_{9y} \) = direct effect of characters 1 to 9 (independent) on character y.
- \( P_{1y}r_{1.2} \) to \( P_{9y}r_{8.9} \) = indirect effects of characters 1 to 9 on the dependent character 1 to 9

represent the independent characters namely:

1. Days to 50 per cent flowering
2. Days to maturity
3. Plant height (cm)
4. Number of primary branches per plant
5. Number of secondary branches per plant
6. Siliquae per plant
7. Seeds per siliqua
8. Siliqua length (cm)
9. 1000- seed weight (g)
10. Oil content

\[ Y = \text{Seed yield per plant (dependent character)} \]

The above equation can be written in a matrix form shown as:

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td>r_{1y}</td>
<td>1</td>
<td>r_{12}</td>
</tr>
<tr>
<td>r_{2y}</td>
<td>1</td>
<td>r_{23}</td>
</tr>
<tr>
<td>r_{3y}</td>
<td>1</td>
<td>r_{34}</td>
</tr>
<tr>
<td>r_{4y}</td>
<td>1</td>
<td>r_{45}</td>
</tr>
<tr>
<td>r_{5y}</td>
<td>1</td>
<td>r_{56}</td>
</tr>
<tr>
<td>r_{6y}</td>
<td>1</td>
<td>r_{67}</td>
</tr>
<tr>
<td>r_{7y}</td>
<td>1</td>
<td>r_{78}</td>
</tr>
<tr>
<td>r_{8y}</td>
<td>1</td>
<td>r_{89}</td>
</tr>
<tr>
<td>r_{9y}</td>
<td>1</td>
<td>P_{9y}</td>
</tr>
</tbody>
</table>

Replacing the corresponding elements in A and B matrix obtained the genotypic and phenotypic path coefficients by genotypic correlation coefficients or phenotypic coefficients. B matrix was inverted and the inverted B matrix was multiplied by A matrix to obtain path coefficients.

Residual effects:

Residual factor which measures the contribution of rest of the characters of the cancel scheme, was obtained by using the following formula –

\[ \text{Residual factor (X), } P_{xy} = \sqrt{(1-R^2)} \]

Where,

\[ R^2 = \sum p_{1y}^2 + 2 \sum_{j} p_{iy} \cdot P_{3y} \cdot R_{ij} \text{ and } 1 > j \]
4. EXPERIMENTAL RESULTS

The present investigation in taramira was carried out to estimate the genetic variability, heritability, genetic advance and association among different morphological characters with each other and with seed yield in a germplasm set of 100 taramira accessions along with five checks namely, RTM-314, RTM-2002, RTM-1359, T-27 and RTM-1212, which were evaluated in an augmented randomized block design. Path coefficient were also worked out to determine the magnitude of direct and indirect effects of different morphological characters on seed yield.

4.1 GENETIC VARIABILITY

The analysis of variance showed significant variability for days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, siliquae per plant, siliqua length, seeds per siliqua, seed yield per plant and oil content while 1000-seed weight showed non-significant differences among all the genotypes. The mean value squares due to accessions showed significant variability for all the traits except plant height and 1000-seed weight while checks varieties exhibited non significant variability for all the traits except seeds per siliqua. The blocks exhibited significant variability for all traits except days to maturity (Table 4.1)

The range, general mean, genotypic and phenotypic coefficient of variation, heritability in board sense and genetic advance expressed as percentage of mean value for different characters are given in (Table
4.2). The adjusted mean values of accessions along with their CD for different characters are given in (Annexure – II). Heritability, genetic advance expressed as percentage of mean, correlation coefficient and path analysis were worked out for all the eleven characters are presented characterize here as under:

4.1.1 Days to 50 per cent flowering

The overall mean value of days to 50 per cent flowering was 57.59. The adjusted mean values of accessions showed a range of 50.57(RTM-1423) to 67.35(RTM-1479) days. The genotypic (GCV) and phenotypic (PCV) coefficient of variations were 4.00 and 4.67 per cent, respectively. The heritability in broad sense was 68.71 per cent and the genetic advance expressed as percentage mean value was 6.56 (Table 4.2). The accessions RTM-1423 was the earliest to flower followed by RTM-1513, RTM-1417, RTM-1515, RTM-1506, RTM-1418, RTM-1422, RTM-1416, RTM-1437, RTM-1433, RTM-1421, RTM-1500.(Annexure II)

4.1.2 Days to maturity

The overall mean value of days to maturity was 138.06 The adjusted mean values of accessions showed a range of 131.46 (RTM-1509) to 146.24 (RTM-1438) days. The genotypic (GCV) and phenotypic (PCV) coefficient of variations were 2.04and 2.35 per cent, respectively. The heritability in broad sense was 74.24 per cent and the genetic advance expressed as percentage mean value was 3.58 (Table 4.2). The accessions RTM-1509 was the earliest to mature followed by RTM-1510, RTM-1483, RTM-1500, RTM-1506, RTM-1474, RTM-1491, RTM-1490,
4.1.3 Plant height

The mean value of plant height was 94.54 cm with a range of 77.79 cm (RTM-1465) to 123.97 cm (RTM-1455). The genotypic and phenotypic coefficient of variations were 9.33 and 11.34 per cent, respectively. The heritability in broad sense was 71.45 per cent. The estimated genetic advance expressed as percentage of mean value was 16.73 (Table 4.2). The tallest accessions was RTM-1455 followed by RTM-1481, RTM-1483, RTM-1464, RTM-1485, RTM-1461, RTM-1458, RTM-1470, RTM-1444, RTM-1497 and RTM-1509. (Annexure-II).

4.1.4 Number of primary branches per plant

The primary branches per plant ranged from 4.07 (RTM-1512) to 11.59 (RTM-1464) with mean value of 6.93. The genotypic and phenotypic coefficient of variation were 21.69 and 25.40 per cent, respectively. The broad sense heritability was 74.41 per cent. The estimated genetic advance expressed as percentage of mean value was 39.36 (Table 4.2). The highest primary branches per plant were observed in RTM-1464, RTM-1451, RTM-1455, RTM-1461, RTM-1452, RTM-1438 RTM-1468, RTM-1499, RTM-1491, RTM-1456 and RTM-1465 (Annexure - II).
4.1.5 Number of secondary branches per plant

The mean value of secondary branches per plant was 17.59. The accessions showed a ranged from 8.56 (RTM-1511) to 32.48 (RTM-1479). The genotypic and phenotypic coefficient of variations were 25.39 and 27.14 per cent, respectively.

The broad sense heritability and genetic advance expressed as percentage of mean for this character were 85.10 and 47.31 per cent, respectively (Table 4.2). The highest number of secondary branches per plant were observed in RTM-1479, RTM-1438, RTM-1454, RTM-1487, RTM-1466, RTM-1492, RTM-1475, RTM-1480, RTM-1457, RTM-1437 and RTM-1429 (Annexure - II).

4.1.6 Siliquae per plant

The mean value of siliquae per plant was 120.13. The accessions showed a range of siliquae per plant from 75.5 (RTM-1512) to 225.54 (RTM-1476). The genotypic and phenotypic coefficients of variations were 29.65 and 30.60 per cent, respectively. The broad sense heritability and genetic advance expressed as percentage of mean for this character were 80.20 and 53.11 per cent, respectively (Table 4.2). The highest number of siliquae per plant were observed in RTM-1476, RTM-1461, RTM-1464, RTM-1479, RTM-1492, RTM-1455, RTM-1454, RTM-1491, RTM-1506, RTM-1496 RTM-1498 and RTM-1504. (Annexure - II).
4.1.7 Seeds per siliqua

The number of seeds per siliqua ranged from 14.71 (RTM-1458) to 23.33 (RTM-1454) with a mean value of 18.45. The genotypic and phenotypic coefficient of variations were 8.52 and 10.98 per cent, respectively. The broad sense heritability of this character was 65.37, whereas the genetic advance expressed as percentage of mean value was 14.87 (Table 4.2). The highest number of seeds per siliqua were observed in RTM-1454, RTM-1494, RTM-1477, RTM-1455, RTM-1495, RTM-1479, RTM-1492, RTM-1496, RTM-1436, RTM-1445 and RTM-1440. (Annexure - II).

4.1.8 Siliqua length (cm)

The mean value of siliqua length was 2.25cm with a range of 1.78 cm (RTM-1436) to 3.29 cm (RTM-1450). The genotypic and phenotypic coefficient of variations were 8.54 and 11.39 per cent respectively. The broad sense heritability and genetic advance expressed as percentage of mean for this character were 59.68 and 14.58 per cent, respectively (Table 4.2). The longest siliqua length accessions were RTM-1450, RTM-1449, RTM-1447, RTM-1505, RTM-1426, RTM-1459, RTM-1451, RTM-1479, RTM-1501, RTM-1509 and RTM-1452. (Annexure - II).

4.1.9 1000- seed weight (g)
The test weight ranged from 1.82 (RTM-1468,1470) to 3.60 g (RTM-1436) with corresponding mean value of 2.45 g. The genotypic and phenotypic coefficient of variations were 11.89 and 14.20 per cent, respectively. The broad sense heritability and genetic advance expressed as percentage of mean were 71.87 and 20.69, respectively (Table 4.2). The highest test weight were observed in RTM-1436, RTM-1450, RTM-1453, RTM-1449, RTM-1417, RTM-1447, RTM-1448, RTM-1474 RTM-1467, RTM-1426, RTM-1479 and RTM-1451. (Annexure - II).

4.1.10 Seed yield per plant (g)

The mean value of seed yield per plant was 7.38 g. The accessions showed a ranged of seed yield per plant from 3.29 g. (RTM-1423) to 11.60 g (RTM-1455). The genotypic and phenotypic coefficient of variations were 25.66 and 25.84 per cent, respectively. The broad sense heritability and genetic advance expressed as percentage of mean value were 95.85 and 50.84, respectively (Table 4.2). The highest seed yield per plant were observed in RTM-1455, RTM-1476, RTM-1447, RTM-1505, RTM-1494 RTM-1492, RTM-1461, RTM-1429, RTM-1493, RTM-1463 and RTM-1451. (Annexure - II).

4.1.11 Oil content (%)

The mean value of oil content was 37.54%. The accessions showed a ranged of oil content from 33.5 % (RTM-1464) to 40.35% (RTM-1440). The genotypic and phenotypic coefficient of variations were 4.28 and 4.48 per cent, respectively. The broad sense heritability and
genetic advance expressed as percentage of mean value were 91.33 and 8.44, respectively (Table 4.2). The highest per cent of oil content were observed in RTM-1440, RTM-1460, RTM-1428, RTM-1432, RTM-1443, RTM-1449, RTM-1475, RTM-1513, RTM-1416, RTM-1444, RTM-1490 and RTM-1449. (Annexure –II).

4.2 ASSOCIATION ANALYSIS

The genotypic (based on adjusted values) correlation coefficient of variation were calculated on seed yield with other characters namely days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, siliquae per plant, seeds per siliqua, siliqua length, 1000-seed weight, and oil content in all possible combination (Table 4.3). Seed yield per plant had positive and significant correlation with days to 50 per cent flowering, plant height, siliquae per plant, 1000-seed weight, oil content and siliqua length while non- significant correlation with days to maturity, number of primary branches per plant, number of secondary branches per plant and seeds per siliqua. Days to 50 per cent flowering exhibited positive and significant correlation with days to maturity, plant height, number of primary branches per plant, siliquae per plant, oil content and seed yield per Plant while non significant association with number of secondary branches per plant, siliqua length, 1000-seed weight and seeds per siliqua.
Days to maturity exhibited positive and non-significant correlation with all the other traits except number of secondary branches per plant while negative but non-significant association with plant height.

Plant height exhibited positive and significant correlation with siliquae per plant and seed yield per plant but non-significant association with number of primary branches per plant, siliqua length, 1000-seed weight and oil content while negative but non-significant correlation number of secondary branches per plant and seeds per siliqua.

Number of primary branches per plant had positive and significant association with siliquae per plant and oil content while non-significant with number of secondary branches per plant, 1000-seeds weight and seed yield per plant but negative and non-significant association with siliqua length and seeds per siliqua.

Number of secondary branches per plant had positive and significant association with siliquae per plant, seeds per siliqua and oil content but non-significant association with siliqua length, 1000-seed weight and seed yield per plant.

Siliquae per plant had positive and significant correlation with 1000-seed weight, oil content and seed yield per plant but non-significant association with siliqua length while negative but non-significant association with seeds per siliqua.
Siliqua length had positive significant association with seeds per siliqua and seed yield per plant while non-significant association with 1000-seed weight but negative and non-significant association with oil content. 1000-seed weight had positive and significant correlation with oil content and seed per yield but non-significant association with seeds per siliqua. Seeds per siliqua had positive and non-significant correlation with oil content and seed yield per plant. Oil content had positive and significant correlation with seed yield per plant.

4.3 PATH ANALYSIS

In a breeding programme, we are often concerned with the improvement in yield as a overall product dependent on a number of morpho-physiological attributes, such characters are often interrelated, hence their effect on yield is also modified by others. Path coefficient analysis helps in separating the direct effect of a component character on yield from indirect effects via other traits. The genotypic correlation coefficient of seed yield with its contributing characters were partitioned into direct and indirect effects through path coefficient analysis and are presented in Table 4.4. At genotypic level siliquae per plant exerted the highest direct effect on seed yield. Their indirect effect via other characters was low. This was followed by siliqua length, days to 50 per cent flowering, seeds per siliquae and days to maturity. Siliquae per Plant and siliqua length exhibited positive correlation with seed yield per plant. The indirect effect of days to 50 per cent flowering was positive with days
to maturity, siliquae per plant, siliqua length and seeds per siliqua while siliqua length is the other character which shows positive indirect effect through days to 50 per cent flowering, days to maturity, siliquae per plant, seeds per siliqua and oil content.

The association of siliquae per plant, siliqua length, days to 50 per cent flowering, days to maturity and seeds per siliqua. Hence direct selection based on these characters should be beneficial in increasing the seed yield.
5. DISCUSSION

Taramira (*Eruca sativa* Mill.) is an important member of group rapeseed and mustard and grown, widely in the arid region of Rajasthan during *Rabi* season. It is a highly cross pollinated crop due to sporophytic type of self-incompatibility (Sharma *et al.* 1985). The crop is specially suited to the dry land areas as it has efficient root system to extract moisture from deeper soil layers. Owing to its drought tolerance and adaptability to adverse environmental conditions it is preferred over *Brassica* species. Despite its merit as a drought tolerant oilseed crop, it was always given minor importance and thus concerted efforts for improvement the yielding ability are also very much limited in this crop.

The concerted efforts in taramira for improvement were started with the establishment All India Coordinated Research Project on Oilseeds (Taramira unit) in 1987 at S.K.N. College of Agriculture, Jobner. The major objectives of the project were to make extensive collection of germplasm and its evaluation. As a result, extensive germplasm collections were made from various parts of Rajasthan. Besides this, studies on genetics of yield and its related characters are very much limited in taramira. Moreover, even the basic studies involving evaluation of accessions in order to identify the superior parents for hybridization programme are very much limited.

Thus in the present investigation an attempt was made to evaluate 100 accessions along with 5 check varieties for assessing genetic
variability present in the germplasm as well as to estimate the associations of seed yield with other morphological yield traits and to identify superior accessions.

Assessment of genetic variability is very important in order to know the possibility of improvement in characters under consideration. A complex character like seed yield is affected by several component characters thus assessment of genetic variability for these characters is also important. Moreover, response to selection is directly proportional to the variability present in the genetic material. Knowledge of estimates of heritability along with genetic advance as per cent of mean is important in order to know about the type of gene action governing the characters under consideration.

100 accessions of taramira were critically evaluated for days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, siliquae per plant, seeds per siliqua, siliqua length, 1000-seed weight, seed yield per plant and oil content. Analysis of variance showed that accessions had significant differences for all the traits except 1000-seed weight and plant height suggesting that material had adequate variability to support the breeding programme for improving the seed yield. The checks varieties exhibited non-significant differences for all the traits except seeds per siliqua, this indicated that check varieties had low variability among them. Partitioning of entries SS into entries SS, accessions and check v/s accessions indicated that the blocks had significant differences for all the
traits except days to maturity. Significant differences between accession were noted for all the traits excepting 1000-seed weight. Check vs accessions showed highly significant differences for all the characters except siliquae per plant. Genetic parameters of variation namely mean, range, phenotypic and genotypic variance and phenotypic and genotypic coefficient of variation were estimated. On the basis of estimates the accessions with higher mean values for various components were identified. Accession (RTM-1423) had lowest mean for day to 50 per cent flowering. Accession (RTM-1509) had lowest mean for days to maturity. Accession having highest mean values for plant height (RTM-1455), number of primary branches per plant (RTM-1464), number of secondary branches per plant (RTM-1479), siliquae per plant (RTM-1476), seeds per siliqua (RTM-1454), siliqua length (RTM-1450), 1000- seed weight (RTM-1436), seed yield per plant (RTM-1455), and oil content (RTM-1440) were also identified.

Wide range was observed for the character siliquae per plant, number of secondary branches per plant, plant height and seed yield per plant. Similar results of wider range were reported by Nehra et al. (1989) and Sharma et al. (1991). For number of secondary branches per plant, seed yield per plant, 1000- seed weight and seeds per siliqua by Rathore (1955) and Jajoria (2001), Singh et al. (2010) and for number of secondary branches per plant by Doddabhimappa et al. (2010).
Phenotypic, genotypic and environmental variances were estimated for various characters. The phenotypic variance was higher than the genotypic variance for each of the character studied, indicating positive effect of environment on the expression of a character. Rathore (1995), Kaushik (1998), Jajoria (2001) and Dar et al. (2010) had also observed same results in taramira indicating the role of environment in the expression of a character. The difference between the phenotypic and genotypic variances was less. This is expected in Augumanted design, as the error variance is based on the evaluation of checks. Due to less differences between the variances, the values of heritability are generally higher leading to higher GA estimates.

Coefficient of variance indicated that the variability was highest for siliquae per plant followed by seed yield per plant, number of secondary branches per plant and number of primary branches per plant. The lowest variability was observed for days to maturity, days to 50 per cent flowering, oil content, seeds per siliqua, siliqua length, plant height and 1000-seed weight. The variation observed in present study was in line with the variation reported in some of the earlier studies, for high genotypic coefficient of variance for seeds per siliqua and 1000-seed weight, number of primary branches per plant by Yadav and Kumar, 1984, for number of primary branches per plant, number of secondary branches per plant, siliquae per plant and seed yield per plant by Jajoria, 2001, for number of secondary branches per plant, and siliquae per plant by Khan.
and Khan, 2003, for siliquae per plant by Dar et al. 2010, for number of secondary branches per plant by Doddabhimappa et al., 2010. Lowest variability for seeds per siliqua and oil content was observed by Singh et al. (2010).

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicating the gain under selection than heritability estimate alone. However it is not necessary that a character showing high heritability will also exhibited high genetic advance (Johnson et al., 1955). Estimates of heritability give some idea about the gene action involved in the expression of various polygenic traits. The breeder is able to appropriate the variation that is due to genotypic (broad sense heritability) or additive (narrow sense heritability) effects, that is the heritable portion of variation of the first case, and the portion of genotypic variation that is fixable in pure lines is the later case. If the heritability of a character is very high eg. > 70%, selection for such a character should be fairly easy. This is because there would be close correspondence between genotypic and phenotypic variation due to a relatively small contribution of environment to the phenotype.

Because of the importance of heritability just enumerated, its was calculated for all the eleven characters and high heritability (broad sense value > 70%) was observed for days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, siliquae per plant, 1000-seed weight, oil content and seed yield per plant.
It indicates that the characters is least influenced by the environmental effects, the selection for improvement of such characters may not be useful, because broad sense heritability is based on total genetic variance which includes both fixable (additive) and non fixable (dominance and epistatic) variance. Days to 50 per cent flowering. Siliqua length and seeds per siliqua had moderate heritability less than 70%.

The similar pattern of high heritability was registered for plant height, seed yield per plant, number of secondary branches per plant, 1000- seed weight and siliquae per plant by Khan and Khan (2003); for days to 50 per cent flowering, 1000- seed weight, oil content, plant height and seed yield per plant by Dar et al., (2010), for number of secondary branches per plant by Rathore (1995), Palsania (1995), Meena (1996), Kaushik (1998) and Jajoria (2001), for days to 50 per cent flowering by Jajoria (2001) and Palsania (1995), for siliquae per plant, seeds per siliqua and seed yield per plant by Kaushik (1998), Palsania (1995) and Jajoria (2001).

High genetic advance is another parameter to assess the expected improvement in a character by hybridization and selection. Among the expected genetic advance of all the eleven characters calculated, high genetic advance value > 40% was recorded for number of secondary branches per plant, siliquae per plant and seeds yield per plant. Dar et al. (2010) in taramira reported high genetic advance for siliquae per plant and plant height, Rathore (1995), Palsania (1995), Meena (1996) and Jajoria (2001) for seed yield per plant, number of primary branches per
plant, siliquae per plant and number of secondary branches per plant. It show that these characters are governed by additive genes and selection will be rewarding for improvement of such traits.

Moderate to low genetic advance was observed for days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, siliqua length, 1000-seed weight, seeds per siliqua and oil content. This also confirms the earlier findings for days to 50 per cent flowering Palsania (1995), for siliqua length Meena (1996) and Kaushik (1998) and for 1000-seed weight and plant height Rathore (1995).for days to 50 per cent flowering, seed yield per plant, 1000-seed weight and seeds per siliqua, number of primary and number of secondary branches per plant Dar et al., (2010). It indicates that the characters are governed by non additive gene action.

High heritability coupled with high genetic advance was observed for seed yield per plant, number of secondary branches per plant and siliquae per plant. According to Lerner (1958), the estimates of broad sense heritability are reliable if combined with high genetic advance and indicate role of additive gene action which given better response to phenotypic selection than those characters having low values. Earlier Nehra et al., (1989), Rathore (1995) and Meena (1996) also reported high heritability with high genetic advance estimates for above traits. Thus the results of the present investigation are in line with the earlier reports. While Dar et al. (2010) reported high heritability with high genetic advance
for plant height whereas in present investigation high heritability coupled with low genetic advance indicating differences in germplasm lines.

When variability, heritability and genetic advance are considered together seed yield per plant, number of secondary branches per plant and siliquae per plant may be the best reliable traits that could be exploited for hybridization and selection for improvement since these characters recorded high variability, heritability and genetic advance.

CHARACTERS ASSOCIATION AND PATH ANALYSIS

Selection of yield as such may not be effective as it is a complex character and is a result of interaction among its various components (Grafius, 1964). A knowledge of relationship between yield and its components is essential as this may help in constructing suitable selection criteria for yield. Correlation coefficients, worked out among different characters including seed yield per plant based on adjusted values. The association analysis revealed that the seed yield per plant was positive and significant correlated with days to 50 per cent flowering, plant height, siliquae per plant, siliqua length, 1000-seed weigh and oil content while non-significant association of days to maturity, number of primary branches per plant, number of secondary branches per plant and seeds per siliqua.

Similar association of seed yield per plant have been reported with plant height, number of primary branches per plant and number of secondary branches per plant, seeds per siliqua and 1000-seed weight by Sabaginia et al. (2010), Sadet et al. (2010), Tuncturk and Ciftic...

It is interesting to note that the characters which exhibited positive association with seed yield per plant have also exhibited positive association among themselves. Thus these characters may be simultaneously improved to increase the seed yield.

According to Falconer (1981), it is often assumed that association between two characters is an evidence of pleiotrophy rather than linkage hence under such complex situations, path coefficient analysis is a powerful tool for studying characters association. In other words the path coefficient analysis measures the direct and indirect contribution of various independent characters towards a dependent character such as seed yield per plant. There is good agreement between the values of direct and indirect effects obtained at genotypic level. Path coefficient analysis revealed that traits such as siliqua per plant, siliqua length and days to 50 per cent flowering for the selection of high yielding lines as they exhibited positive direct effect as well as showed positive correlation with seed yield. While days to 50 per cent flowering, number of secondary
branches per plant, seeds per siliqua, siliqua length and oil content showed negative and direct effects on seed yield per plant.

Earlier, positive direct effect on seed yield has been reported by Yadav and Kumar (1984), Nehra et al. (1989) and Rathore (1955); for secondary branches per plant, while for siliquae per plant reported by Nehra et al. (1989), Rathore (1995), Palsania (1995), Meena (1996), and Kaushik (1998). Thus most of these studies support the present study.

**PLANT BREEDING IMPLICATION**

Evaluation of germplasm is the first step in any plant breeding programme. In the present investigation 100 accession along with 5 check varieties were evaluated in Augmented complete Block Design with five blocks. The evaluation of accessions indicated existence for variability of all the characters studied including the seed yield. The association analysis revealed that the seed yield per plant was positive and significant correlated with days to 50 per cent flowering, plant height, siliquae per plant, siliqua length, 1000-seed weigh and oil content while non-significant association of days to maturity, number of primary branches per plant, number of secondary branches per plant and seeds per siliqua.

Path coefficient analysis revealed that traits such is siliqua per plant, siliqua length and says ti 50 per cent flowering for the selection of high yielding lines as they exhibited positive direct effect as well as showed positive correlation with seed yield. While days to 50 per cent flowering, number of secondary branches per plant, seeds per siliqua, siliqua length and oil content showed negative and direct effects on seed yield per plant.
The accessions were ranked based on performance for different characters and high seed yield per plant. Top ten accessions selected on the basis of performance are listed in Table 5.1.

Among the accessions tested ten accessions namely RTM-1455, RTM-1476, RTM-1447, RTM-1505, RTM-1494, RTM-1492, RTM-1461, RTM-1429, RTM-1493 and RTM-1463 were high for seed yield as well as for its component characters. The accessions namely RTM-1440, RTM-1460, RTM-1428, RTM-1432, RTM-1443, RTM-1449, RTM-1475, RTM-1513, RTM-1416 and RTM-1444 showed maximum oil content in their seeds. Hence, it is suggested that these accessions be tested in multilocation trail to confirm their superiority and may also be used as parents in hybridization programme to develop high yielding varieties along with high oil content.
The present investigation was carried out with a view to know the degree of genetic variability, association between seed yield and its component characters and their direct and indirect effects on seed yield in taramira (*Eruca sativa* Mill.). The experimental material consisted of 100 accessions which were, evaluated in an Augmented Randomized Block Design with five blocks during *Rabi* 2012-13 at Research Farm, S.K.N. College of Agriculture, Jobner.

The observations were recorded on days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, siliqua per plant, seeds per siliqua, siliqua length, 1000-seed weight, seed yield per plant and oil content.

The data were subjected to appropriate statistical analysis for estimation of mean, range, variance, heritability, genetic advance as percentage of mean correlation and path analysis. The result obtained have been summarized below.

1. Analysis of variance revealed highly significant differences among the accessions for all the characters namely, days to 50 per cent flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant,
siliquae per plant, siliqua length, seeds per siliqua, seed yield per plant, and oil content except plant height and 1000-seed weight.

2. The values of phenotypic coefficients of variation were higher than genotypic coefficients of variation for all the characters indicating a positive effect of environment on character expression. The genotypic and phenotypic coefficients of variation were higher for siliquae per plant followed by seed yield per plant, number of secondary branches per plant, number of primary branches per plant and 1000-seed weight. Whereas, low coefficients of variation were observed for days to maturity, days to 50 per cent flowering, oil content, seeds per siliqua, siliqua length and plant height.

3. High heritability coupled with high genetic advance were observed for seed yield per plant, siliquae per plant and number of secondary branches per plant. Whereas, high heritability and moderate to low genetic advance were observed for oil content, number of primary branches per plant, days to maturity, 1000-seed weight, plant height, days to 50 per cent flowering, seeds per siliqua and siliqua length.

4. The association analysis revealed that the seed yield per plant was positive and significant correlated with days to 50 per cent flowering, plant height, siliquae per plant, siliqua length, 1000-
seed weigh and oil content while non-significant association of days to maturity, number of primary branches per plant, number of secondary branches per plant and seeds per siliqua.

5. Path coefficient analysis revealed that traits such is siliqua per plant, siliqua length and says ti 50 per cent flowering for the selection of high yielding lines as they exhibited positive direct effect as well as showed positive correlation with seed yield. While days to 50 per cent flowering, number of secondary branches per plant, seeds per siliqua, siliqua length and oil content showed negative and direct effects on seed yield per plant.

6. Based on the mean performance the accessions RTM-1455, RTM-1476, RTM-1447, RTM-1505, RTM-1494, RTM-1492, RTM-1461, RTM-1429, RTM-1463 and RTM-1493 were found superior in seed yield and accessions namely RTM-831, RTM-869, RTM-808, RTN-845, RTM-884, RTM-868, RTM-830, RTM-852, RTM-870 and RTM-821 showed maximum oil content in their seeds. Hence, it is suggested that these accessions be tested in multilocation trial to confirm their superiority and may also be used as parents in hybridization programme to develop high yielding varieties along with high oil content.
Genetic Variability and Character Association Analysis in Taramira
(*Eruca sativa* Mill.)

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**ABSTRACT**

One hundred eight accessions along with five check varieties of taramira (*Eruca sativa* Mill.) were evaluated in an Augmented Randomized Block Design with four block during *Rabi*, 2010-11. The data were subjected to obtain estimates of variability, heritability and genetic advance for different characters. Correlation and path coefficient were also worked out to ascertain the nature and degree of association between different characters.

Results indicated significant variability among cheeks with respect to all the characters except for seeds per siliqua and siliqua length. The accessions were significant for days to 50 per cent flowering, plant height, number of primary branches per plant number of secondary branches per plant, siliquae per plant, siliqua length, 1000-seed weight, seed yield per plant and oil content.

High estimates of heritability along with high genetic advance were observed for siliquae per plant, number of secondary branches per plant and seed yield per plant. Whereas, high heritability and moderate to low genetic advance were observed for siliqua length, 1000-seed weight, days to 50 per cent flowering, plant height, number of primary branches per plant and oil content.

The seed yield per plant was positively correlated with number of primary branches per plant, plant height, 1000-seed weight and siliquae per plant. The path coefficient analysis revealed that on seed yield of plant height had highest direct effect followed by 1000-seed weight and number of primary branches per plant. Based upon correlation and path analysis it was concluded that plant height, 1000-seed weight and number of primary branches per plant are the most important yield component traits in taramira.

Based on the mean performance the accessions RTM-809, RTM-815, RTM-814, RTM-845, RTM-855, RTM-861, RTM-844, RTM-862, RTM-874 and RTM-848 were found superior in seed yield and accessions RTM-831, RTM-869, RTM-808, RTM-845, RTM-884, RTM-868, RTM-830, RTM-852, RTM-870 and RTM-821 showed maximum oil content in their seeds. These accessions may further be utilized in breeding programme aimed at improving high seed yield along with high oil content.

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**Thesis submitted in partial fulfillment of the requirement for the degree of M.Sc. (Ag.) in Plant Breeding & Genetics under the supervision of Dr. M.L. Jakhar, Associate Professor, Department of Plant Breeding & Genetics, S.K.N. College of Agriculture, Jobner – 303329 (Rajasthan).**


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