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Assessment of Genetic Variance, Heritability, Genetic Advance, Correlation and Cluster Analysis in Mutagens Induced Ten Variants of *Brassica Campestris* L. Toria

Research Article

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Abstract

The study was taken up to estimate genotypic and phenotypic variability, heritability with genetic advance, correlation and cluster analysis on growth and yield parameters in 10 variants of variety T-9 of *Brassica campestris* (toria). These variants were obtained through mutagenesis. Analysis of variance reveals that there are highly significant differences among all the traits studied. Comprehensively, phenotypic coefficients of variance were higher than their respective genotypic coefficients of variance for all the traits. High GCV was observed for pods plant^{-1}, beak length and seed yield plant^{-1} while highest PCV was exhibited for secondary branches plant^{-1}. Broad sense heritability ranged from lowest 16.41 for secondary branches per plant to highest 72.35 for plant height. Pods plant^{-1}, plant height, beak length, pod length and seed yield plant^{-1} showed high genetic advance over mean percent. The results of correlation revealed that seed yield plant^{-1} exhibited highly significant positive association with stem perimeter, secondary branches, pods on main raceme, pod plant^{-1} and 100 seed weight, although significant negative correlation with beak length. The traits which showed positive correlation with seed yield were the main contributor towards high seed yield plant^{-1}. All genotypes were grouped into two clusters at 3% linkage. The cluster I comprising variants with maximum mean value for plant height, raceme length, pod length whereas cluster II genotypes showed high mean value for pod plant^{-1}, 100 seed weight and seed yield plant^{-1}.The result of genetic divergence in variants shows that it is helpful in the selection of superior yield attributes in breeding program of oilseed *Brassicas*.

Keywords: *Brassica campestris*; Mutagenesis; Genetic variance; Heritability

Introduction

The oleiferous *Brassica* spp. commonly known as rapeseed/ mustard is one of the economically important agricultural commodities. Rapeseed/ mustard is being grown throughout the world as a source of oil and protein for human/animal consumption [1]. In India, rapeseed/mustard plays an important role in the economy by providing edible oil, vegetables, condiments and animal feed.

The three ecotypes of Indian rape, *B.*(2n=BB=20) viz.,toria, brown sarson (lotni and tora types) and yellow sarson [2]. *Brassica campestris* is relatively young species of Asiatic origin [3]. The primary centre of origin of *Brassica campestris* is near the Himalayan region and history suggested that rapeseed was cultivated as early as two centuries B.C. in India and introduced in China and Japan at the time of Christ [4]. The rapeseed oil contains lowest amount of saturated fatty acids as compared to other vegetable oils. It contains nutritionally desired oleic acid, which gives stability to the oil, along with two essential fatty acids, linoleic acid and linolenic acid, which are not present in many of the other edible oils. Many nutritionists suggested that this composition of fatty acids in oil is considered as ideal for human nutrition and superior than that of many other vegetable oils [5]. In present scenario, India has been importing

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edible oil to meet household requirements. The increasing population may affect the supply-demand gap which can eventually increase the importation of edible oils. Hence the oilseed production needs a substantial boost to meet the demands in our country. Therefore developing genotypes with diverse and desirable characteristics will be of great value. Such improvement program in oilseed *Brassica* will help in the enhancement of yield and nutritional qualities.

Mutagenesis has come up with a hope as an efficient tool for creating genetic variability in various crops. Plant breeders are also employing this method in rapeseed/ mustard. Development of desirable genotypes requires excellent knowledge of the existing genetic variation for yield and its components. The magnitude of heritable variation in the traits has immense value for designing the breeding programme for potential genotype. Thus assessment of genetic parameters such as PCV (Phenotypic coefficient of variation), GCV (Genotypic coefficient of variation), Heritability and Genetic advancement is prerequisite for devising effective selection [6]. The phenotypic values of different traits in the same individual are often found to be correlated and may be useful for indirect selection [7]. Cluster analysis reveals existence of genetic variability in different genotypes. With the consideration of above facts, the present study emphasizes the nature and extent of variability present in mutagens induced 10 variants (namely TV1,TV2,TV3,TV4,TV5,TV6,TV7,TV 8,TV9 and TV10) and control plant (TV0) of *Brassica campestris* .

Materials and Methods

The present work focused on mutation induction followed by selection of genetic variability in *Brassica campestris* cultivar T-9 . The seeds were obtained from U.P. State Seed Corporation, Lucknow, India. In order to induce genetic variability artificial mutagenesis has been carried out by using physical mutagen (Gamma rays) and chemical mutagen (Ethyl Methane Sulphonate). For physical mutagenesis, three lots of seeds were subjected to 25, 35 and 45 Krad doses of gamma irradiation at room temperature at National Botanical Research Institute, Lucknow. The source of gamma rays was ^{60}CO.

In chemical mutagenesis, the seeds of cultivar T-9 (four lots of each) were pre-soaked for 4 hrs in distilled water and then treated with different concentrations(0.3%, 0.6 % and 0.9%) of EMS solution prepared in phosphate buffer at pH 7.0 for 6 hrs at 30±1°C reaction temperature. The treated seeds of both the varieties along with their respective control were sown at the Lucknow University experimental field in Randomized Block Design (RBD) to rise the M_1 generation in three replicates. Seeds were hand dibbled approximately an inch deep with the spacing of 10- 12 cm between them in a well loosened and watered soil. The rows were kept at a distance of about 30 cm with plants at a spacing of 15 cm in each row. Based on visual observations, few morpho-variants were isolated from M_1 and M_2 generation. Progeny row of the isolated variants were raised in M_3 generation to confirm the stability of altered characters. Five competitive plants from each row of all the variants were selected randomly for recording the data on 12 characters viz. plant height (cm), stem perimeter, number of primary branches per plant, number of secondary branches per plant, length of main raceme (cm), number of pods on main raceme, pod length (cm), beak length (cm), pods per plant, number of seeds per pod, 100-seed weight (g) and seed yield per plant (g). Data obtained from M_3 generation were statistically analyzed by using SPSS software. The mean data was subjected to analysis of variance. The Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV) and heritability in broad sense were calculated using the formula suggested by Burten and Devane [7]. Genetic advance was calculated by the method suggested by Johansson [8].

Results

To assess the extent of genetic variability and divergence in the variants of T-9, the statistical analysis was done on 12 quantitative phenotypic traits. To compare the variation among the variants, mean value, analysis of variance, Genotypic and Phenotypic coefficient of variability, heritability, genetic advance and genetic advance over percent mean are given in Tables 1 and 2.

Plant height is an important yield contributing character. The mean value reveals that variants TV3 (52.50±3.35, 3.22±0.16), TV9

Table 1: Growth and Yield trait summary (Mean ± SE, n=6) of different variants and control of var. T9 at M_3 Generation.

Parameters	TV0	TV1	TV2	TV3	TV4	TV5	TV6	TV7	TV8	TV9	TV10
Plant height	79.17 ± 3.06	69.67 ± 3.21	105.50 ± 1.95	52.50 ± 3.35	78.17 ± 2.83	68.50 ± 2.40	88.83 ± 2.29	105.50 ± 2.67	79.83 ± 3.11	62.67 ± 0.88	57.17 ± 3.67
Stem perimeter	0.46 ± 0.04	0.46 ± 0.01	0.59 ± 0.02	0.50 ± 0.04	0.49 ± 0.03	0.53 ± 0.02	0.75 ± 0.05	0.69 ± 0.06	0.41 ± 0.06	0.54 ± 0.02	0.40 ± 0.03
No. of primary branches	4.00 ± 0.63	3.33 ± 0.76	5.00 ± 0.45	4.50 ± 0.43	4.17 ± 0.54	2.33 ± 0.21	7.00 ± 0.58	6.00 ± 0.52	5.00 ± 0.52	5.83 ± 0.60	5.50 ± 0.72
No. of secondary branches	3.33 ± 0.67	5.67 ± 0.92	8.83 ± 0.65	5.67 ± 0.56	4.83 ± 0.40	4.50 ± 0.34	8.50 ± 0.96	6.17 ± 0.83	4.67 ± 0.92	6.50 ± 1.02	7.00 ± 1.44
Main raceme length	40.33 ± 3.23	29.17 ± 1.97	36.33 ± 2.64	22.83 ± 2.15	33.33 ± 3.54	33.83 ± 2.43	44.83 ± 2.09	47.00 ± 3.70	33.00 ± 2.24	29.83 ± 1.45	22.33 ± 2.11
Pods on main raceme	28.00 ± 1.29	20.17 ± 2.06	20.00 ± 1.71	14.00 ± 1.44	21.00 ± 3.15	20.67 ± 2.44	36.17 ± 2.56	24.17 ± 2.29	16.00 ± 0.89	19.00 ± 2.48	14.83 ± 1.68
Pods plant^{-1}	103.33 ± 5.88	154.00 ± 15.37	155.50 ± 5.38	90.33 ± 4.92	195.50 ± 5.71	122.00 ± 6.02	270.17 ± 18.60	179.50 ± 19.50	107.50 ± 10.06	163.67 ± 12.28	127.67 ± 11.87
Pod length	5.05 ± 0.12	5.08 ± 0.21	3.77 ± 0.11	7.68 ± 0.28	5.30 ± 0.11	4.05 ± 0.10	4.92 ± 0.08	6.37 ± 0.28	4.92 ± 0.18	5.47 ± 0.13	5.62 ± 0.06
Beak length	1.30 ± 0.13	1.22 ± 0.07	0.70 ± 0.04	1.92 ± 0.16	1.07 ± 0.05	1.00 ± 0.06	1.28 ± 0.07	1.32 ± 0.04	2.00 ± 0.11	1.23 ± 0.04	1.52 ± 0.11
Seeds pod^{-1}	13.00 ± 1.13	14.67 ± 1.71	9.67 ± 0.67	19.67 ± 1.20	13.17 ± 0.79	12.33 ± 0.49	12.17 ± 0.83	15.67 ± 0.92	9.50 ± 0.62	12.00 ± 0.86	12.83 ± 0.25
100 seed weight	0.29 ± 0.00	0.45 ± 0.03	0.25 ± 0.01	0.22 ± 0.01	0.31 ± 0.01	0.36 ± 0.02	0.33 ± 0.01	0.38 ± 0.02	0.19 ± 0.01	0.30 ± 0.02	0.35 ± 0.02
Seed yield plant^{-1}	2.87 ± 0.16	4.82 ± 0.49	3.66 ± 0.14	3.22 ± 0.16	4.87 ± 0.24	4.23 ± 0.16	6.28 ± 0.72	5.45 ± 0.78	2.09 ± 0.12	4.00 ± 0.53	3.45 ± 0.41

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Table 2: Genetic variations in growth and yield traits of different variants.

Parameters	Mean	Tmss	Emss	ANOVA F value	Variability			Coefficient of variability (%)			Heritability (%)	Genetic advance	Genetic advance over mean (%)
					Genotypic	Phenotypic	Environmental	Genotypic	Phenotypic	Environmental			
Plant height	77.05	1862.20	46.27	40.25**	121.06	167.33	46.27	14.28	16.79	8.83	72.35	19.28	25.02
Stem perimeter	0.53	0.07	0.01	9.49**	0.00	0.01	0.01	12.13	20.78	16.88	34.07	0.08	14.58
No. of primary branches	4.79	10.37	1.88	5.52**	0.57	2.45	1.88	15.71	32.65	28.62	23.14	0.75	15.56
No. of secondary branches	5.97	16.96	4.30	3.95**	0.84	5.14	4.30	15.39	37.99	34.73	16.41	0.77	12.84
Main raceme length	33.89	380.88	40.32	9.45**	22.70	63.02	40.32	14.06	23.43	18.74	36.02	5.89	17.38
Pods on main inflorescence	21.27	243.64	26.38	9.24**	14.48	40.86	26.38	17.89	30.05	24.15	35.44	4.67	21.94
Pods plant^{-1}	151.74	15844.25	824.88	19.21**	1001.29	1826.17	824.88	20.85	28.16	18.93	54.83	48.27	31.81
Pod length	5.29	6.76	0.17	40.61**	0.44	0.61	0.17	12.53	14.76	7.79	72.10	1.16	21.92
Beak length	1.32	0.86	0.05	18.21**	0.05	0.10	0.05	17.60	24.43	16.94	51.92	0.34	26.13
Seeds pod^{-1}	13.15	47.78	6.08	7.85**	2.78	8.86	6.08	12.68	22.64	18.75	31.38	1.92	14.63
100 seed weight	0.31	0.03	0.00	18.52**	0.00	0.00	0.00	13.94	20.06	14.43	48.28	0.06	19.95
Seed yield plant^{-1}	4.08	8.80	1.09	8.11**	0.51	1.60	1.09	17.57	31.04	25.59	32.04	0.84	20.49

** - b<0.00↓

Table 3: Inter-correlation (n=66) among growth and yield traits of variants (ns p>0.05 or *p<0.05 or **p<0.001- as compared to Control (TV0))

Variables	Plant Height	Stem perimeter	No. of primary branches	No. of secondary branches	Main racemelength	Pods on main raceme	Pods plant^{-1}	Pod length	Beak length	Seeds pod^{-1}	100 seed weight	Seed yield plant^{-1}
Plant Height	1.00											
Stem perimeter	0.49**	1.00										
No. of primary branches	0.29*	0.52**	1.00									
No. of secondary branches	0.22ns	0.48**	0.49**	1.00								
Main raceme length	0.72**	0.56**	0.26*	0.10ns	1.00							
Pods on main inflorescence	0.46**	0.52**	0.20ns	0.09ns	0.68**	1.00						
Pods plant^{-1}	0.41**	0.68**	0.50**	0.50**	0.39**	0.51**	1.00					
Pod length	-0.34**	-0.02ns	0.20ns	-0.06ns	-0.22ns	-0.21ns	-0.16ns	1.00				
Beak length	-0.37**	-0.22ns	0.12ns	-0.21ns	-0.21ns	-0.25*	-0.33**	0.63**	1.00			
Seeds pod^{-1}	-0.32**	0.03ns	-0.03ns	-0.18ns	-0.21ns	-0.17ns	-0.14ns	0.70**	0.37**	1.00		
100 seed weight	-0.01ns	0.12ns	-0.10ns	0.06ns	0.14ns	0.18ns	0.27*	-0.09ns	-0.38**	0.08ns	1.00	
Seed yield plant^{-1}	0.28*	0.62**	0.26*	0.32**	0.30*	0.41**	0.74**	-0.06ns	-0.36**	0.08ns	0.48**	1.00

(62.67±0.88, 4.00±0.53) and TV10 (57.17±3.67, 3.45±0.41) were not only dwarf in stature but also had higher yield as compared with their control (79.17±3.06,3.45±0.41). The variant TV6 showed increase in the number of branches, pods on main raceme and also had maximum pods plant^{-1}. Variants TV3, TV7 showed significant increase in pod length and also seeds pod^{-1}. Most of the variants viz., TV1, TV3, TV7 exhibited higher 100 seed weight than their parent. Barring TV8, all the variants produced higher seed yield plant^{-1}. However, TV6 (6.28±0.72), TV7 (5.45±0.78) were superior to the parent variety in terms of seed yield plant^{-1}. The analysis of variance among the genotypes (parent and variants) showed highly significant ($p< 0.001$) difference for all the traits (Table 2). Genotypic and phenotypic variances were highest for pods plant^{-1} (1001.29 and 1826.17) and lowest for beak length. The highest Phenotypic coefficient of variation was recorded for secondary branches(37.99%) followed by primary branches (32.65%) and seed yield plant^{-1}(31.04 %) whereas maximum Genotypic coefficient of variation were observed for pods plant^{-1} (20.85%) followed by pods on main raceme (17.89%) and beak length (17.60%). The lowest PCV for pod length (14.76%) and stem perimeter (12.13%) were observed. The result indicates that phenotypic coefficient of variance was higher than their respective genotypic coefficient of variation for all the traits studied. The GCV was higher than their respective environmental coefficient of variability for all traits except for plant height, pods plant^{-1}, pod length and beak length. The heritability (%) estimates revealed highest value for plant height (72.35%) followed by pods length (72.10 %), pods plant^{-1} (54.83 %), beak length (51.92%), moderate for 100 seed weight (48.28%), main raceme length, pods on main raceme, pods plant^{-1}, seeds pod^{-1}, number of primary branches plant^{-1} and seed yield plant^{-1} whereas lowest heritability (%) was recorded for secondary branches plant^{-1} (16.41%).

The genetic advance over control mean (%) was ranged from 12.84% for secondary branches to 31.81% for pods plant^{-1}. Among the traits, plant height, pods on main raceme, pod length, beak length, seed yield plant^{-1} and 100 seed weight showed high percentage of genetic advance over mean. Relatively high heritability and genetic advance were observed for plant height. Secondary branches plant^{-1} showed low heritability and genetic advancement.

The results of correlation analysis among the traits of var.T-9

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variants in M_3 generation were shown in Table 3. All the traits showed highly significant positive association with seed yield plant^{-1} except number of seeds pod^{-1}. Seed yield plant^{-1} exhibited significant negative correlation with beak length. Plant height had highly significant ($p<0.001$) positive correlation with main raceme length, pods on main raceme while significant ($p< 0.05$) with seed yield plant^{-1}. However, it showed highly significant ($p<0.001$) but negative association with pod length, beak length, seeds pod^{-1}. The stem perimeter had high significant and positive relation with all traits except pods length, beak length. The primary branches plant^{-1} exhibit highly significant association with pods plant^{-1}, the secondary branches with pods plant^{-1} and seed yield plant^{-1}, main raceme length with pods main raceme^{-1} and pod plant^{-1}, pods raceme^{-1}with pod plant^{-1}and seed yield plant^{-1}. The relationship of pods plant^{-1} was highly significant ($p<0.001$) and negative with beak length while positive with seed yield plant^{-1}. Pod length was correlated with beak length. Beak length showed significant and positive correlation with seeds pod^{-1} while significant negative association with 100 seed weight and seed yield plant^{-1}. 100 seed weight showed highly significant positive association with seed yield plant^{-1}. The positive correlation between pods plant^{-1} and seed yield plant^{-1} indicate the possibility of cumulative improvement in the yield attributes in rapeseed.

Cluster Analysis

Cluster analysis used to assess diversity among the genotypes. The ten variants (TV1- TV10) and one control (TV0) from cultivar T-9 were clustered on the basis of 12 quantitative traits recorded. The phylogenetic relationship among the variants and parent genotypes were presented in dendrogram (Figure 1). The genotypes grouped into two major clusters, cluster I possess six genotypes (parent and 5 variants) and cluster II confined five variant genotypes. The clustering pattern of genotypes in dendrogram revealed the dissimilarities between the clusters as well as within the cluster The genotypes with maximum mean values for various traits such as plant height, secondary branches, main raceme length, pod length, beak length, seeds pod^{-1} were placed together in cluster I whereas genotypes of cluster II, showed maximum mean value for number of primary branches, pod main raceme^{-1}, pods plant^{-1}, 100 seed weight and seed yield plant^{-1}. In cluster I, minimum linkage distance (0.2%) exists between TV5 and TV7, followed by TV2 and TV8 (0.3%). Variant named TV3 exists in separate sub cluster and showed maximum linkage distance (0.5%). In cluster II, minimum linkage distance (about 0.1%) present between TV4 and TV9, followed by TV1 and TV10 (0.2%). Variant TV6 which showed maximum seed yield plant^{-1} was found to be most mutated with respect to their parent and placed in separate sub cluster with linkage distance 0.3%. It was significant to note that parent variety formed an independent sub cluster which showed that the considerable genetic variations were created in the quantitative phenotypic traits of the cultivar due to mutagenic treatment.

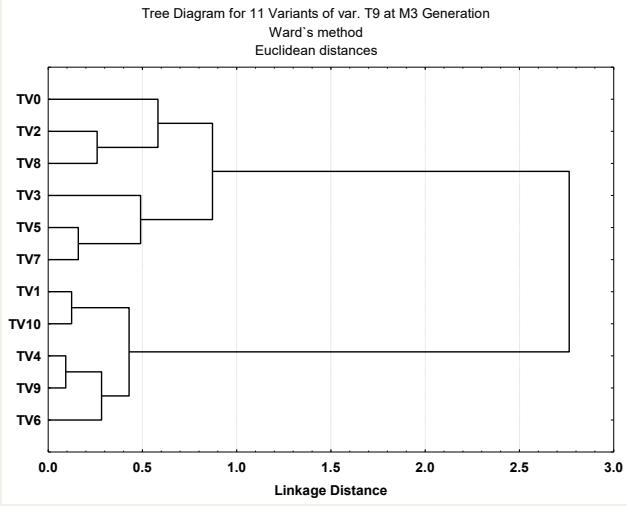

Figure 1: Tree diagram of control (TV0) and 10 variants on the basis of mean of traits of var. T9 at M3 Generation.

Discussion

The assessment of genetic diversity plays major role in creating a pool of variable germplasm, selection of superior genotypes from the pool and utilization of selected individuals to create desired variability [9]. The present study is carried out for the evaluation and selection of improved variant genotypes obtained through mutagenesis. Plant height is an important morpho- metric character. The variants of T-9 viz. TV3, TV9 and TV10 were dwarf in stature and had higher yield as compared with their respective parent. This confirms that induced mutation played a significant role in the alteration of plant architecture and effective selection of mutants will enhance yield potential in rapeseed and mustard [10]. The variant TV6 showed increase in the number of branches, pods on main raceme and highest number of pods plant^{-1}. Increase in pods plant^{-1} can be attributed to increased number of branches. Genotypes with more branches and pods plant^{-1} had been reported in oilseed *Brassica* as a consequence of mutagenesis [11]. It was found that the number of pods plant^{-1} majorly responsive for all yield contributing components in canola and was an important factor for yield compensation[12]. Variants TV3, TV7 showed significant increase in pod length and seeds pod^{-1}. Super long siliqua line also reported in *B. napus* [13]. However, Mendham have argued that canola breeders should aim to produce plant with fewer pods but with a higher number of seeds pod^{-1} to maximise the seed survival [14]. Long pods had more seeds resulting in a greater seed yield plant^{-1} [15]. All these results showed that longer pod could provide a better environment for a higher proportion of ovule surviving in mature seed. 100 seed weight of most of the variants was higher than their parent which indicates an increase in size of the seeds as a result of mutation. This is in conformity with [11] who have reported the bold seed mutants in *Brassica.* All the variants except TV8 produced higher seed yield plant $^{-1}$. This might be due to increase in yield contributing factors. The consistent performance of these variants in all three generations indicated an improvement in genetic constitution through gamma irradiation and EMS induced mutations. These results are in consonance with earlier reports [16,17].

The variance analysis showed that the genotypes differed significantly among themselves for all the traits. Genotypic and Phenotypic coefficient of variations had similar trend for all the traits.

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PCV although higher than GCV for all the traits indicating that had interaction with environment to some degree [18]. The GCV provides a mean to study the genetic variability generated in quantitative traits. Pods plant^{-1} recorded comparatively higher GCV followed by pods on main raceme and seed yield plant^{-1} which is in relation with the findings of [19]. The estimate of heritability with genetic gain was more useful than variability value along with predicting the resultant effect of best individual [8]. In this study, higher and moderate estimate of heritability observed for most of the traits whereas lowest heritability (16.41%) was recorded for secondary branches. High heritability for pods plant^{-1} is supported by the earlier findings in Mustard [20]. Akbar *et al.,* [21] also found high heritability for plant height, pods plant^{-1} and seed yield plant^{-1}. This suggested that the variation due to environment played a selectively limited role in influencing the inheritance of these characters. Among the traits, four traits namely pods plant^{-1}, plant height, pod length, seed pod^{-1} showed high heritability and genetic advance as mean percent. Our results are further strengthened by the earlier reports in *Brassica juncea* [22]. A trait with high heritability and genetic advance is to be considered under control of additive genes and selection is effective for such traits [23].

The correlation coefficient generally highlights the pattern of association among yield and growth attributes which characterize how yield, a complex character is expressed. Inter correlation among yield and growth parameters of all variants showed that the seed yield had highly significant and positive correlation with pods plant^{-1}, stem perimeter, pods on main raceme, secondary branches and plant height while negatively associated with pod length and beak length as compared with control. These results were in conformity with the earlier findings [24]. Positive contribution of plant height, stem perimeter, number of branches plant^{-1} and 100 seed weight for seed yield plant^{-1} noted in the present study was also mentioned by [25]. In this study negative correlation between beak length, pod length and seed yield plant^{-1} was found that also been reported [26]. The negative correlation of beak length with seed yield plant $^{-1}$ indicated that long beak length genotypes have less seed yield. The correlation study among the traits reveals that, these aforesaid attributes were main contributors towards the enhanced seed yield plant^{-1}.

Cluster analysis signifies the extent of genetic diversity and that is of much use in plant breeding [27]. Genetic similarity among different genotypes using Euclidean distance cluster analysis based on 12 traits grouped in to 2 clusters at 3% linkage (Figure 1). The cluster I consist of six genotypes (variants and parent variety) and others formed cluster II. On the basis of morphological traits, Kumar *et al.,*[16] reported the formation of 3 clusters of *Brassica rapa* mutants. The present study indicates that phenotypically similar variants need not have closer relationships. The variants TV1, TV4, TV9 and TV6 of T-9 differed significantly among them but fall in same cluster. However [28,29] reported the mutants with similar morphological traits fall in to the same cluster. The most distinct cluster with respect of parental cluster could be used for mutant selection in subsequent generations. Our study is favoured by the result of correlation and also represents that the traits showed positive association can be improved simultaneously and put together in a single genotype for yield enhancement.

Conclusion

From the above study, it can conclude that mutagenesis played a pivotal role in oilseed *Brassica* crop breeding. The genetic divergence study of the variant genotypes provides a clue that mutation in positive direction can successfully employ for the induction of variation. Assessment of genetic variability and inter-relationships among agronomic traits helps to select new genotypes with improved characters.

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