



ISSN (E): 2277- 7695

ISSN (P): 2349-8242

NAAS Rating: 5.03

TPI 2021; 10(2): 636-638

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Received: 18-12-2020

Accepted: 23-01-2021

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## Genetic variability for quantitative and qualitative traits of radish (*Raphanus sativus* L.)

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### Abstract

The present investigation entitled Genetic Variability for Quantitative and Qualitative traits of Radish which was carried out during 2019-2020 at the Horticultural Research Farm, of Department of Horticulture, AKS University, Sherganj, Satna (M.P.). Seeds were sown directly in the field on of 15<sup>th</sup> October, 2019 at a spacing of 30.0 x 10.0 cm in a plot of 1.80 x 1.20 m<sup>2</sup> size. There were five rows in each plot. Each genotype was sown in a Random Block Design (RBD) with three replications. Twelve radish genotype were evaluated to estimate, Genetic Variability, Genetic Heritability and Genetic Advance to six Quantitative and two Qualitative traits. The overall values of GCV lower then the PCV for all the traits. The mean sum of square due to treatment was found significant for all the characters on the basis of analysis of variance which suggested the presence of sufficient variability in radish genotypes. The phenotypic coefficient of variance (PCV) was slightly higher in magnitude than genotypic coefficient of variance (GCV) for all the characters studied which suggests that the phenotypic expression of characters is largely influenced by the prevailing environmental conditions. The estimates of heritability were recorded high for the characters namely, number of leaves per plant, length of root, fresh weight of leaves per plant, plant spread and root yield indicating that these characters are governed by additive gene effect and are less influenced by environment and hence, selection for these characters, if found positively associated with yield will be beneficial in improvement of radish.

**Keywords:** Radish, heritability, genetic variability, genetic advance, yield

### Introduction

Radish is an important root vegetable which is grown from world-wide both in tropical and temperate regions. It is one of the important root vegetables and cultivated in India since time immemorial. Inscriptions on the inner walls of pyramids show that radish was an important vegetable in Egypt about 2000 B C. It is cultivated under glass house for early production but large scale production in field which is more common. Being a quick growing crop, it is easily planted as a companion crop or intercrop between the rows of other vegetables Anonymous (1970) [1]. It is a favourite crop of the kitchen garden as it can be easily cultivated ready for use within 3 to 6 weeks from the time of seed sowing. Genetic variability plays an important role in a crop is of paramount importance in selecting the best genotypes for making rapid improvement in yield and desirable characters as well as to select most potential parents for further breeding programme. Study of genetic variability reveals variation in different quantitative and quality traits. Variation may be due to environmental factor, mutation agents or may be due to attack of any biological agents. Also, genetic variability is essential and basic requirement for crop improvement as it provides wider scope for selection for initiating an effective and successful breeding program. The phenotypic expression of the plant characters is mainly controlled by the genetic makeup of the plant and the environment, in which it is growing. Further, the genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance and include dominance and epistasis (non-allelic interaction). Hence, the present study was undertaken to analyse the extent of variability present in seventy five germplasm lines of chilli in respect of traits contributing to yield and quality of radish.

### Materials and Method

The present investigation entitled “Genetic Variability for Quantitative and Qualitative traits of Radish (*Raphanus sativus* L.)” which was carried out during 2019-2020 at the Horticultural Research Farm, of Department of Horticulture, AKS University, Sherganj, Satna (M.P.). Seeds were sown directly in the field on of 15<sup>th</sup> October, 2019 at a spacing of 30.0 x 10.0 cm in a plot

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of 1.80 x 1.20 m<sup>2</sup> size. There were five rows in each plot. Each genotype was sown in a Random Block Design (RBD) with three replications. Five randomly selected plants in each replication were tagged for recording observations and the mean values were used for statistical analysis. Observations on plant and root characters were recorded in ten fresh roots selected at random from each plant and mean worked out. Observations were recorded for different quantitative traits viz., plant height, plant spread, number of leaves per plant, fresh weight of leaves per plant, leaf area and qualitative traits viz., moisture content of root, TSS and Ascorbic acid content. The statistical analysis was carried out for each observed character under the study using MS-Excel, OPSTAT and SPAR 1.0 packages. The mean values of data were subjected to analysis of variance as described by Gomez and Gomez (1983) for Randomized Block Design (RBD). All genotypes (Kashi Sweta, Fiber white, Sparkle white, Long chetki, White Princes, Menu early, Maya- 22, Green Radish, Red Round Radish, Hill Queen, Radish Marwari and Palak Patta) of radish were collected from I.I.V.R. Varanasi (U.P.). The ascorbic acid content was analyzed at fresh root with mature stage as per the standard procedure (Anon., 1970) while the TSS was estimated as per the procedure given by Miller (1972) [2]. The genotypic and phenotypic coefficients of variation were computed as per Burton and De Vane (1953) [3] while the genetic advance was calculated as per Johnson *et al.* (1955) [7].

## Results

The present investigation reported significant variations in the characters among all the genotypes due to effect of genotype and environment both. Phenotypic and genotypic coefficient of variations provides information about the magnitude of genotypic and phenotypic variability. A perusal of data for all the characters studied indicated that phenotypic and genotypic coefficients of variation have difference but very less for most of characters. The magnitude of coefficients of variation varied from character to character from moderate to high which indicates about varying amount of variability present for different traits. The phenotypic (PCV) and genotypic coefficients of variability (GCV) were high (i. e. >20 per cent) for total root yield per plot (36.91 % and 33.48 %), diameter of root (25.48 % and 20.31 %), fresh weight of leaves per plant (24.32 % and 22.56%) and length of root (22.03 % and 20.78 %). Whereas, the moderate magnitude of PCV and GCV (10- 20 per cent) were observed for fresh weight of root (21.57 % and 19.26 %). The low magnitude of GCV and PCV were recorded for plant height (15.87% and 14.11%), number of leaves per plant (15.78% and 15.18%), leaf area (14.72% and 13.06%), TSS °Brix (12.18% and 12.00%), Ascorbic acid in root (mg / 100 g) (13.18% and 11.52%) and plant spread (13.02% and 11.92%). The phenotypic coefficient of variance (PCV) was slightly higher in magnitude than genotypic coefficient of variance (GCV) for all the characters studied which suggests that the phenotypic expression of characters is largely influenced by the prevailing environmental conditions. A highly significant positive genotypic and phenotypic correlation of yield was found with root weight, diameter of root, length of root, number of leaves per plant, fresh weight of root, plant height, leaf area, fresh weight of leaves per plant and plant spread. Therefore, main emphasis should be given on these characters, while making selection in radish genotypes. The highest heritability in broad sense was recorded for TSS °Brix (97.18%) followed by number of

leaves per plant (92.46 %), length of root (88.92 %), fresh weight of leaves per plant (86.07 %), plant spread (83.81 %) and root yield per plot (82.29 %). While the fresh weight of root (79.75 %) followed by plant height (79.05 %), leaf area (78.71 %), Ascorbic acid in root (mg/100 g) (76.40%) exhibited the moderate heritability. However, low heritability was observed for diameter of root (63.54 %). The estimates of heritability were recorded high for the characters namely, number of leaves per plant, length of root, fresh weight of leaves per plant, plant spread and root yield indicating that these characters are governed by additive gene effect and are less influenced by environment and hence, selection for these characters, if found positively associated with yield will be beneficial in improvement of radish. Genetic gain was measured as genetic advance under selection of per cent of population mean was low to high for various characters studied in the present experiment. Genetic gain (genetic advance expressed as per cent of population mean) was low to high in nature and ranged from 22.48- 62.56 per cent for different characters under the study. In the present study highest estimates of genetic gain as percentage of mean were obtained for characters namely total root yield per plot (62.56 %), fresh weight of leaves per plant (43.12 %), length of root (40.36 %) and moderate for fresh weight of root (35.44 %), diameter of root (33.35 %) and number of leaves per plant (30.06 %). These findings are in accordance with the findings by Rajput and Pal (2014) [9], Chen *et al.* (2015) [5] and Mallikarjunarao *et al.* (2015) [8].

The high value of genetic advance for these traits showed that these characters are governed by additive genes and selection will be rewarding for the further improvement of such traits. However, low genetic gain was recorded for plant height (25.84 %), TSS °Brix (24.37%), leaf area (23.86 %), plant spread (22.48 %) and Ascorbic acid in root (mg/100 g) (20.76%). Similar findings were observed by Zhao *et al.* (2008) [10], Jabal *et al.* (2015) [6] and Chaitra *et al.* (2019) [4].

This indicates the presence of non-additive gene effects. In the present investigation, high heritability coupled with high genetic advance was recorded for the traits viz., root yield per plot, fresh weight of leaves per plant and length of root. Thus, it can be concluded that the selection of these traits may accumulate more additive genes leading to further improvement of these characters. Correlation refers to degree and direction of association between two or more than two variables. Correlation coefficient among different traits was worked out at phenotypic and genotypic levels are presented. To estimate the association between two variables, correlation coefficient at phenotypic and genotypic levels, was worked out in all possible combination. In general, genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients. The information on nature and magnitude of correlation coefficients helps breeders to determine the selection criteria for concurrent progress of various characters along with economic yield. The genotypic correlation coefficients among different characters showed that total root yield per plot (kg) had positive and significant association with diameter of root (0.999), length of root (0.998), number of leaves per plant (0.998), fresh weight of root (0.995), plant height (0.975), leaf area (0.962), fresh weight of leaves per plant (0.950), TSS °Brix (0.904) and plant spread (0.897). The phenotypic correlation coefficients among different characters showed that total root yield per plot (kg) had positive and significant association with leaf area (0.869), number of leaves per plant (0.866), length of

root (0.859), fresh weight of root (0.838), TSS °Brix (0.790), plant spread (0.780), plant height (0.775), fresh weight of leaves per plant (0.767) and diameter of root (0.728). The

current results are confirmed with the finding of Johnson *et al.* (1955) [7] and Chen *et al.* (2015) [5].

**Table 1:** Estimates of components of, PCV, GCV and genetic advance for 11 characters in Radish.

S. No.	Parameters	GCV	PCV	Heritability (H <sup>2</sup> b) %	Genetic Advance K=20.6	Genetic Advance as % of mean
1.	Plant height (cm)	14.11	15.87	79.05	7.10	25.84
2.	Plant spread (cm)	11.92	13.02	83.81	428.14	22.48
3.	Number of leaves per plant	15.18	15.78	92.46	5.15	30.06
4.	Fresh weight of leaves per plant	22.56	24.32	86.07	46.1	43.12
5.	Leaf area (cm <sup>2</sup> )	13.06	14.72	78.71	77.52	23.86
6.	Fresh weight of root (g)	19.26	21.57	79.75	25.84	35.44
7.	Length of root (cm)	20.78	22.03	88.92	5.33	40.36
8.	Diameter of root (cm)	20.31	25.48	63.54	1.22	33.35
9.	Total yield per kg	33.48	36.91	82.29	2.52	62.56
10.	TSS °Brix	12.00	12.18	97.18	1.36	24.37
11.	Ascorbic acid in root (mg /100g)	11.52	13.18	76.40	3.27	20.76

**Table 2:** Genotypic Correlations Matrix for 11 characters in Radish.

	Character 1	Character 2	Character 3	Character 4	Character 5	Character 6	Character 7	Character 8	Character 9	Character 10	Character 11
Character 1	1	0.891**	0.889**	0.798**	0.952**	0.986**	0.912**	0.836**	0.975**	0.802**	0.870**
Character 2		1	0.994**	0.728**	0.996**	0.988**	0.870**	0.792**	0.897**	0.757**	0.788**
Character 3			1	0.891**	0.897**	0.895**	0.962**	0.929**	0.998**	0.873**	0.938**
Character 4				1	0.893**	0.878**	0.972**	0.995**	0.950**	0.996**	0.954**
Character 5					1	0.987**	0.978**	0.992**	0.962**	0.917**	0.942**
Character 6						1	0.999**	0.989**	0.995**	0.902**	0.906**
Character 7							1	1.077**	0.998**	0.969**	0.904**
Character 8								1	0.999**	1.053**	0.927**
Character 9									1	0.961**	0.934**
Character 10										1	0.904**
Character 11											1

**Table 3:** Phenotypic Correlations Matrix for 11 characters in Radish.

	Character 1	Character 2	Character 3	Character 4	Character 5	Character 6	Character 7	Character 8	Character 9	Character 10	Character 11
Character 1	1	0.851**	0.889**	0.648**	0.820**	0.826**	0.800**	0.639**	0.775**	0.716**	0.696**
Character 2		1	0.870**	0.632**	0.783**	0.869**	0.786**	0.604**	0.780**	0.659**	0.690**
Character 3			1	0.796**	0.886**	0.872**	0.860**	0.743**	0.866**	0.838**	0.777**
Character 4				1	0.760**	0.697**	0.820**	0.844**	0.767**	0.897**	0.775**
Character 5					1	0.812**	0.809**	0.603**	0.869**	0.812**	0.733**
Character 6						1	0.864**	0.656**	0.838**	0.786**	0.744**
Character 7							1	0.798**	0.859**	0.902**	0.795**
Character 8								1	0.728**	0.826**	0.723**
Character 9									1	0.895**	0.860**
Character 10										1	0.790**
Character 11											1

## References

- Anonymous. Official Methods of Analysis. Ninth edition. AOAC, Washington, D. C. 1970.
- Miller GL. Estimation of reducing sugars by nitrosalicylic acid method. *Annals of Chemistry* 1972;31:426.
- Burton GW, De Vane EM. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal* 1953;45:478-441.
- Chaitra Kulkarni C, Manikanta DS, Chaitra Poleshi A, Sarvamangala Cholin S, Raghavendra G, Ambika DS, *et al.* Genetic Variability, Heritability and Genetic Advance for Economic Root Traits in Asiatic and European Type Carrot Germplasm Lines (*Daucus carota* L.). *International Journal of Current Microbiology and Applied Sciences* 2019;8(7):2553-2563.
- Chen F, Liu H, Yao Q, Fang P, Lv F. Genetic variations and evolutionary relationships among radishes (*Raphanus sativus* L.) with different flesh colours based on red pigment content, karyotype and simple sequence repeat analysis. *African Journal of Biotechnology* 2015;14(50):3270-3281.
- Jabal S, Al Sadi Y, Abbas G. Variability and phenotypic correlation among yield and some yield components in different genotypes of local radish (*Raphanus sativus* L.). *Journal of Agricultural Sciences* 2015;31(1):121-130.
- Johnson HW, Robinson HE, Comstock RS. Estimates of genetic and environmental variability in soybean. *Agronomy Journal* 1955;47:314-318.
- Mallikarjunarao K, Singh PK, Vaidya A, Das RK, Pradhan R. Genotypic correlation and path coefficient analysis of yield and its components in radish (*Raphanus sativus* L.) under Kashmir valley. *Ecology, Environment and Conservation* 2015;21:73-77.
- Rajput RN, Pal AK. Correlation and path analysis studies in radish grown under partial shade. *Annals of Plant and Soil Research* 2014;16(2):131-134.
- Zhao L, Li-wang L, Xiao-yan L, Yi-qin G, Xi-lin H, Xian-wen Z, *et al.* Analysis and evaluation of nutritional quality in Chinese radish (*Raphanus sativus* L.). *Agricultural Sciences in China* 2008;7(7):823-830.