Vol.67: e24230627, 2024
https://doi.org/10.1590/1678-4324-2024230627
ISSN 1678-4324 Online Edition

BABT
Brazilian Archives of Biology and Technology

Article - Agriculture, Agribusiness and Biotechnology

Morphological Characterization and Analysis of Genetic Variability in Radish (*Raphanus sativus*) Genotypes for Important Qualitative and Quantitative Traits

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Editor-in-Chief: Bill Jorge Costa
Associate Editor: Bill Jorge Costa

Received: 16-Jun-2023; Accepted: 12-Apr-2024

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HIGHLIGHTS

- First detailed characterization of radish gene pool in Pakistan.
- Germplasm variability was evaluated the basis of morphological and genetic parameters.
- Maximum variability was studied in various quantitative and qualitative traits.
- Provides a basis for new radish breeding programs.

Abstract: Genetic diversity plays a critical role in crop improvement. Radish is one of the important vegetable crops of Rabi season, however, there is a lack of information about radish germplasm resources available in Pakistan. The present research was carried out to characterize radish gene pool on the basis of qualitative and quantitative traits. Twelve genotypes of radish comprised of local and exotic sources were evaluated for genetic variability through morphological, quality, and quantitative traits. Analysis of variance depicted maximum variation among genotypes for all studied straits. High genotypic co-efficient of variance (GCV) value (>20%) in all traits indicates that these traits can be improved through selection. The estimate of genotypic co-efficient of variance (GCV) in present research was closer to phenotypic co-efficient of variance

(PCV), suggesting the key role of genotype as compared to the environment. However, high heritability along with genetic advance (as % of mean) among studied genotypes suggests that the selection of studied traits simply on phenotypic basis can also be effective for the breeding program. Cluster analysis based on morphological traits, grouped genotypes into three clusters and cluster I, contained the maximum number of genotypes. In correlation analysis, significant positive correlation among plant fresh weight, root length, root weight, number of leaves and yield can be directly used a selection criteria. Studying of variability in qualitative traits through frequency distribution exhibited maximum variation for root shape and root base. This study showed considerable variability exists in studied genotypes that can further be used for the improvement of radish breeding.

Keywords: Agro-morphological traits, Characterization, Cluster analysis, Genotypic diversity, Germplasm, Radish

INTRODUCTION

Radish (*Raphanus sativus*), is a specie belongs to genus *Raphanus* in Brassica family. It is classified as root due to its specialized structure (hypocotyl) and shape which represents true root and it can store starch and other compounds [1]. It is an annual herbaceous vegetable having diploid ploidy level with two sets of chromosomes (2x=2n= 18) [2]. It is cultivated in temperate and tropical regions of world due to its wide adaptability, high nutritional value and yield [3,4]. Radish is usually consumed as root vegetable, leafy vegetable, seeds, pods and used as cover, forage crop. While seeds are also used for oil extraction [5]. It is a good source of vitamin B_6, vitamin C, potassium, calcium, folate, magnesium, copper and manganese and is low in calories [1].

It is an annual or biennial multi-polymorphic crop and high level of genetic variation is observed in radish due to cross pollination and self-incompatibility [6]. A diverse range of cultivars are present within species while various wild species are included in genus Raphanus [7]. Radish was originally classified into five morphotypes according to morphology of edible parts (root, siliqua, and seed). These group includes East Asian long radish (*R. sativus convar.* hortensis), European small radish (*R. sativus convar*. sativus), rat tailed radish (*R. sativus convar.* caudatus), oil radish (*R. sativus convar.* Oleifer) and black radish (*R. sativus* var. niger) [5,7]. Surface color of taproot can varies from white to green, red to purple, to pink, to bicolor due to accumulation of anthocyanin [8]. In addition to this, it is also classified according to its cropping pattern (summer, spring, autumn) in some regions which correlate with temperature, bolting and stress resistance. Consumer preference varies with the region and leads to morphological diversity in accordance to adaptation to environmental conditions [5]. In Asian countries, long season and large rooted varieties are grown whereas in Europe and America, short season and small roots are preferably cultivated [9].

In radish, breeding occurs through mass or pedigree selection [10]. Breeders always emphasis on developing high quality radish varieties suitable of sub-tropical and tropical temperatures [2]. Its breeding objectives are based on size, shape, root color [5], early maturity, heat tolerance, drought resistance, cold hardiness, high yield, late bolting with pungency [2]. Further, breeding goals includes uniform plant growth and root development with high quality roots free from pithiness, forking and cracking [11]. However, collection of various genotypes and mutants' population seeds is difficult due to self-incompatibility and high out-crossing traits [7]. Radish is important vegetable being consumed in Asian countries, but there is little or no information is available on phenotypic and genetic variation. Variation in establishment of uniform seedling, vegetative growth, yield and quality are major constraints in fresh root production and seed yield [12]. Thus, lack of publicly available data on genetic diversity is a main bottleneck in breeding of radish [7]. Hence, an extensive study of local and exotic genepool is necessary for radish breeding as method of evaluating the breeding material for economically important traits in radish is not sufficiently developed [10].

For development of any breeding program, detail characterization of diverse genepool is a pre-requisite [13]. As in any crop improvement study, the success of breeding program depends upon the variability present in calculated germplasm [14]. While extent of variability in population along with heritability, phenotypic and genotypic correlation among traits and genetic gain are important steps for efficient selection in breeding program [4]. Large scale evaluation and characterization of germplasm will help in identifying variation as new breeding material [9] and to avoid duplication [15]. Moreover, morphological analysis is considered as a first process for analysis of genetic diversity, for preservation and conservation of genetic resources [13] and help breeders to developed new combinations on the basis of studied traits [16]. Furthermore, genetic divergence studies help to identify diverse parents which can be further used in heterosis or cross combination [17].

Radish has short life cycle (30-50 days) and possess male sterility and multi allelic self-incompatibility which make it an ideal model for studying molecular genetics [18]. In Pakistan, indigenous cultivars i.e., Desi white, Narrow leave, Minnow local are normally white having cylindrical or triangular root shape with pungent taste, while introduced ones are less pungent with circular root shape. Therefore, keeping in view radish importance as vegetable crop, present study was conducted to identify different traits in available genotypes from different backgrounds with an aim to assess diversity among genotypes for selection of parents to develop best performing hybrids.

MATERIAL AND METHODS

Experimental site

Evaluation of radish germplasm for different qualitative and quantitative traits were conducted in Rabi season 2021-22 at vegetable research area of Barani Agricultural Research Institute, Chakwal. It is located at 72°51′20″E longitude and 32°55′49″N latitude at an elevation of 575m. The climate of an area is arid to semi-arid having annual mean temperature of 22.3^{o}C with average annual rainfall up to 519 mm [19].

Plant Material

Plant Material consisted of 11 radish genotypes varying in shape, size and color were collected from different resources. Among them, 9 genotypes were of Pakistan origin whereas 2 were of exotic origin (Table 1).

Table 1. List of radish genotype, their coding, name and source

Genotype Code	Genotype Name	Source
RGP-1	BARI Red	Local Selection
RGP-2	BARI Purple	Local Selection
RGP-3	Green Neck	VRI-FSD
RGP-4	Desi White	Local Selection
RGP-5	Lalpari	VRI-FSD
RGP-6	Minnow Local	VRI-FSD
RGP-7	Purple Neck	VRI-FSD
RGP-8	Narrow Leave	VRI-FSD
RGP-9	Minnow Selection	VRI-FSD
RGP-10	Belly Red	USA
RGP-11	Black Radish	Spain

Experimental design

Seeds of radish accession were sown on raised beds at 5 cm plant to plant and 75 cm row to row distance in mid-October. After 1 week of emergence, seedlings were thinned to avoid competition, and to provide space for radish roots to grow. Different agronomic practices such as irrigation, weeding, earthing up and fertilization were carried out as per crop requirement. The experiment was laid out in Randomized Complete Block Design (RCBD) having 3 replications using plot size 7×1.5 m^2. Twelve plants of each accession were randomly selected from replicates for data collection.

Trait characterization

Various agro-morphological and biochemical traits were recorded after harvest of radish roots

Qualitative parameters

For characterization of qualitative parameters, data were obtained for plant fresh weight (g), root weight (g), root length (cm), root width (cm), no of leaves, leaf length (cm), leaf width (cm) and yield (kg/plot).

For color analysis, Chroma meter (Konica Minolta, CR-400) is used to assess skin, flesh and leaf color. Three parameters: L*, a* and b* were studied to identify surface color of any object. L* depicts

lightness/brightness or darkness of a surface and it ranges from 0-100 (lower values represents darker surface color while as the value goes higher, surface color of object becomes lighter. 0= black color, 100= white color). Parameter a* is used to find out redness and greenness index (negative value shows green color: a*< 0 and positive value is for red color: a*> 0). Color parameter b* is used for blueness and yellowness index (negative value describes blue color: b*< 0 and positive value shows yellow color: b*> 0) [20,21]

Firmness was measured in Newton (N) though penetrometer (FR-5120 digital) by inserting a probe perpendicular to the equilateral surface of radish. For biochemical traits: Total soluble solids-TSS was measured through hand held refractometer (REF101/111) and reading were expressed in terms of ^{o}Brix. Titratable acidity % (TA) expressed as percentage of malic acid is measured through titration method using phenolphthalein as indicator using following formula:

$$\% \text{ acid} = \frac{[\text{mls NaOH used}] \times [0.1 \text{ N NaOH}] \times [\text{milliequivalent factor}^{*}] \times [100]}{\text{grams of sample}}$$

*Milliequivalent factor of malic acid: 0.067

Maturity index was calculated as relation between total soluble solids and titratable acidity: TSS/TA [22].

Quantitative parameters

Quantitative parameters such as leaf shape, leaf hairiness, anthocyanin coloration in leaves, root shape and root base were recorded analyzed as frequency percentage.

Statistical analysis

Morphological data was analyzed by analysis of variance (ANOVA) using STATISITX 10.1 software. Different among means were computed through least significant difference (LSD) at 5% probability level. Further, descriptive studies i.e, mean, range, cv etc were calculated to estimate agro-morphological variation among radish germplasm. While statistical software R package (Version 1.2.1335) was used to compute correlation analysis. Absolute values of correlation co-efficient “r” are considered as very week at values of 0.00-0.19, weak: 0.20-0.39, moderate: 0.40-0.59, strong: 0.60-0.79 and very strong: 0.80-1.00 [23].

Genetic parameters

Genetic parameters were calculated using ANOVA through formulas proposed by [24-26].

- Genotypic variance (σ^2_G) $= \frac{MS_G - MS_E}{r}$

MS_G is mean square of genotype, MS_E is mean square of error and *r* attributes to replication

- Phenotypic variation (σ^2_P) = (σ^2_G) + (σ^2_E)

Environmental variance (σ^2_E) = error mean square = MS_E

- Genotypic co-efficient of variance % (GCV)= $\frac{\sqrt{\sigma^2_G}}{\bar{X}} \times 100$

- Phenotypic co-efficient of variance % (PCV)= $\frac{\sqrt{\sigma^2_P}}{\bar{X}} \times 100$

$\bar{X}$ refers to grand mean of a trait

Both GCV and PCV are categorized as low (<10%), moderate (>10-20%) and high (>20%)

- Broad sense Heritability % (H^2_b)= $\frac{\sigma^2_G}{\sigma^2_P} \times 100$

It was classified as low (0-30%), moderate (30-60%) and high (above 60%)

- Genetic Advance (GA)= $\mathrm{K\,x}\sqrt{\sigma_P^2} \times \mathrm{H}_B^2$
- Genetic Advance (as % of mean) = $\frac{\mathbf{GA\ x\ 100}}{\bar{X}}$

Where K is a constant value and it is 2.06 at selection intensity of 5%. It is categorized as percent of mean as low (<10%), moderate (10-20%) and high (>20%).

RESULTS

Agro-morphological characterization of qualitative traits

Level of variability present in radish genotypes were analyzed by ANOVA and studied through grand mean, ranges, sum of squares and co-efficient of variance. Considerable variation was observed in all studied traits among genotypes (Table 2, Figure 1). All fifteen traits exhibited highly significant sum of squares due to genotypes at 5% probability level. Highest variable means were studied in plant fresh weight (PFW) with mean square value of 20222.4, whereas lowest variable mean with sum of square 0.26 were recorded for titratable acidity (TA). Moreover, performance of genotypes generated wide range of variability for different quantitative traits. Maximum variation was observed in characters i.e., plant fresh weight (PFW) (71.43-392.43g), root weight (RWT) (50.47-330.10g), skin color L* (20.94-85.01), flesh color L* (44.04-81.01) and maturity index (MI) (5.41-63.17). While minimum range of variation were examined in traits like root width (1.23-2.35 cm), yield (2.16-6.21 kg/plot), leaf width (LW) (2.50-4.86 cm), total soluble solids (TSS) (5.76-11.70 ^{o}Brix) and titratable acidity (TA) (0.12-0.93%) respectively.

Table 2. Mean square for different quantitative traits, grand mean, range and coefficient of variation (CV%) among different lines of genepool

Traits		MS_g	$MS_{g\times r}$	MS_e	Grand Mean	Range	CV%
PFW		20222.4	134.9	328.9	173.67 ± 80.88	71.43-392.43	10.44
RL		12.75	1.66	1.16	9.12 ± 2.19	5.67-13.56	11.87
RW		0.41	0.04	0.07	1.77 ± 0.41	1.23-2.35	15.37
RWT		16476.9	52.1	142.4	130.25 ± 72.39	50.47-330.10	9.16
Yield		3.95	0.01	0.01	4.34 ± 1.11	2.16-6.21	1.63
Skin color	L*	1632.06	24.67	10.39	62.76 ± 22.76	20.94-85.01	5.14
	a*	719.09	17.30	6.45	12.77 ± 15.16	0.86-37.83	19.88
	b*	110.46	1.75	3.21	10.60 ± 6.05	-4.72-18.65	16.92
Flesh color	L*	333.70	47.62	24.85	70.55 ± 11.08	44.04-81.01	7.07
	a*	217.48	0.15	0.37	3.84 ± 8.25	-0.12-28.12	16.01
	b*	31.13	1.21	3.37	8.66 ± 3.45	1.19-14.22	17.22
LL		25.55	0.14	0.83	13.12 ± 2.92	6.46-16.13	6.97
LW		2.10	0.21	0.15	3.76 ± 0.87	2.50-4.86	10.34
NL		13.61	0.63	1.23	10.54 ± 2.25	6.67-15.33	10.54
Leaf color	L*	44.63	9.86	12.06	45.19 ± 4.70	39.03-51.13	7.69
	a*	47.48	2.66	2.08	-11.27 ± 4.03	-16.42- -0.59	-12.82
	b*	49.51	3.46	9.67	26.46 ± 4.66	20.07-29.32	11.75
Firmness		92.05	7.09	4.27	22.07 ± 5.64	15.91-34.80	9.36
TSS		11.83	0.10	0.13	7.06 ± 1.94	5.76-11.70	5.19
TA		0.26	0.00	0.00	0.34 ± 0.28	0.12-0.93	7.79
MI		1349.84	15.75	21.18	34.29 ± 20.88	5.41-63.17	13.14

MSg: Mean square due to genotypes; $MS_{g\times r}$: Mean square due to genotype and replication interaction; MS_e: Mean square due to error; CV: Coefficient of variation

PFW: Plant fresh weight (g); RL: Root length (in); RW: Root width (in); RWT: Root weight (g), LL: Leaf length (in), LW: Leaf width (in); NL: Number of leaves; TSS: Total soluble solids (Brix^{o}), TA: Titratable acidity (%); MI: Maturity index

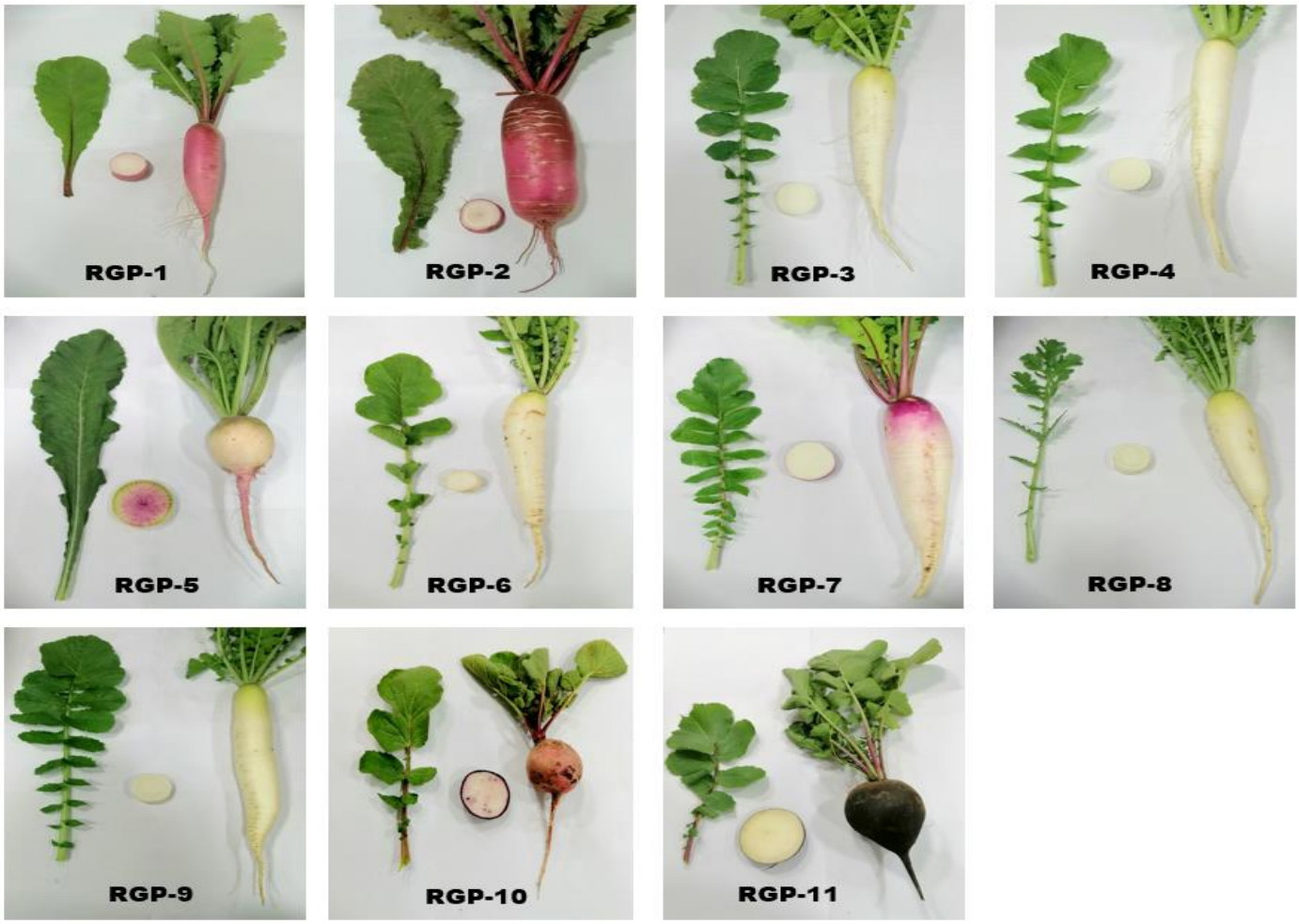

Figure 1. Morphological diversity of some genotypes for foliage and root characteristics

Genetic Parameters

Degree of variability among genotypes estimated through genotypic variance (δ^2_G), phenotypic variance (δ^2_P), genotypic co-efficient of variance (GCV), phenotypic co-efficient of variance (PCV), broad sense heritability (h^2_b), genetic advance (GA) and genetic advance as per of mean (GAM) were presented in Table 3. From the results it was evident that both phenotypic variance (δ^2_P) and phenotypic co-efficient of variance (PCV) were slightly higher in magnitude than genotypic variance (δ^2_G) and genotypic co-efficient of variance (GCV). This indicates that environment has some effect on expression of measured traits except titratable acidity, no difference is observed between phenotypic and genotypic variance. Higher estimates of PCV and GCV (>20%) were recorded for approximately all traits that ranges from 23.29%, 27.68% (GCV, PCV) in root width to 271.33%, 271.79% (GCV, PCV) in flesh color a*. Whereas moderate (>10-20%) estimate of both co-efficient of variance were recorded for color parameters that includes flesh color L* (17.61%=GCV, 18.98%=PCV) and leaf color b* (16.87%=GCV, 20.56%=PCV). However, for leaf color L* GCV was low (8.93%) less than 10% but PCV was in moderate range (11.78%) respectively.

In present research, heritability in broad sense (h^2_b), ranged from 57.45% (leaf color L*) to 100% (titratable acidity). Estimate for heritability was high (above 60%) for all traits except leaf color L* where it falls in moderate range (30-60%) and calculated to be 57.45%. High genetic advance as % of mean (>20%) in related to high heritability were recorded for all traits and ranges from 28.51% (leaf color b*) to skin color a*(301.79). Similarly for leaf color L* trait, GAM recorded to be 13.94% that sits in moderate range (10-20%). But the trait leaf color a*, exhibited low GAM (-83.35%) at high heritability (91.61%).

Table 3. Genetic parameters study of different quantitative traits among genepool

Traits		δ^2_G	δ^2_P	PCV (%)	GCV (%)	h^2_b	GA	GAM (%)
PFW		9946.75	10275.65	58.37	57.43	96.80	202.14	116.39
RL		5.80	6.96	28.92	26.40	83.32	4.53	49.63
RW		0.17	0.24	27.68	23.29	70.83	0.71	40.39
RWT		8167.25	8309.65	69.99	69.38	98.29	184.57	141.70
Yield		1.97	1.98	32.42	32.34	99.49	2.88	66.45
Skin color	L*	810.84	821.23	45.66	45.37	98.73	58.29	92.87
	a*	356.32	362.77	149.15	147.82	98.22	38.54	301.79
	b*	53.63	56.84	71.12	69.08	94.35	14.65	138.24
Flesh color	L*	154.43	179.28	18.98	17.61	86.14	23.76	33.68
	a*	108.56	108.93	271.79	271.33	99.66	21.43	557.98
	b*	13.88	17.25	47.96	43.02	80.46	6.88	79.50
LL		12.36	13.19	27.68	26.80	93.71	7.01	53.44
LW		0.98	1.13	28.21	26.26	86.67	1.89	50.36
NL		6.19	7.42	25.84	23.61	83.42	4.68	44.41
Leaf color	L*	16.29	28.35	11.78	8.93	57.45	6.30	13.94
	a*	22.70	24.78	-44.17	-42.28	91.61	9.39	-83.35
	b*	19.92	29.59	20.56	16.87	67.32	7.54	28.51
Firmness		43.89	48.16	31.44	30.02	91.31	13.03	59.03
TSS		5.85	5.98	34.64	34.26	97.83	4.93	69.80
TA		0.13	0.13	106.05	106.05	100	0.74	218.45
MI		664.33	685.51	76.36	75.17	96.91	52.27	152.43

σ^2_G = Genotypic variance, σ^2_P= Phenotypic variation (σ^2_P), σ^2_E= Environmental variance, GCV= Genotypic co-efficient of variance %, PCV= Phenotypic co-efficient of variance %, H^2_b = Broad sense Heritability %, GA= Genetic Advance, GAM= Genetic Advance (as % of mean)

Qualitative traits

Frequency distribution of five quantitative traits were presented in Figure 2. Significant variation were observed for leaf shape, leaf hairiness, anthocyanin coloration in leaves, root shape type and root base type. Leaf shape of radish germplasm was divided into three types with 63.6% genotypes had lyrate type, 27.2% had entire and only 9% had lacerate leaf shape. For analysis of root shape types, narrow obtriangular shape was abundant with 54.5% frequency, followed by rectangular (27.2%), circular (18.2%). While both iciclical and obovate shapes had same frequency (9%). Root base also varied into five different types with maximum genepool of narrow acute shape (54.5%) and (18.2%) where rest of them were acute, obtuse and flat. Maximum genepool had hairs present on leaves (72.7%) while for remaining genotypes, hairs were absent (27.2%). Anthocyanin coloration in leaves were present in 54.5% and absent in 45.5%.

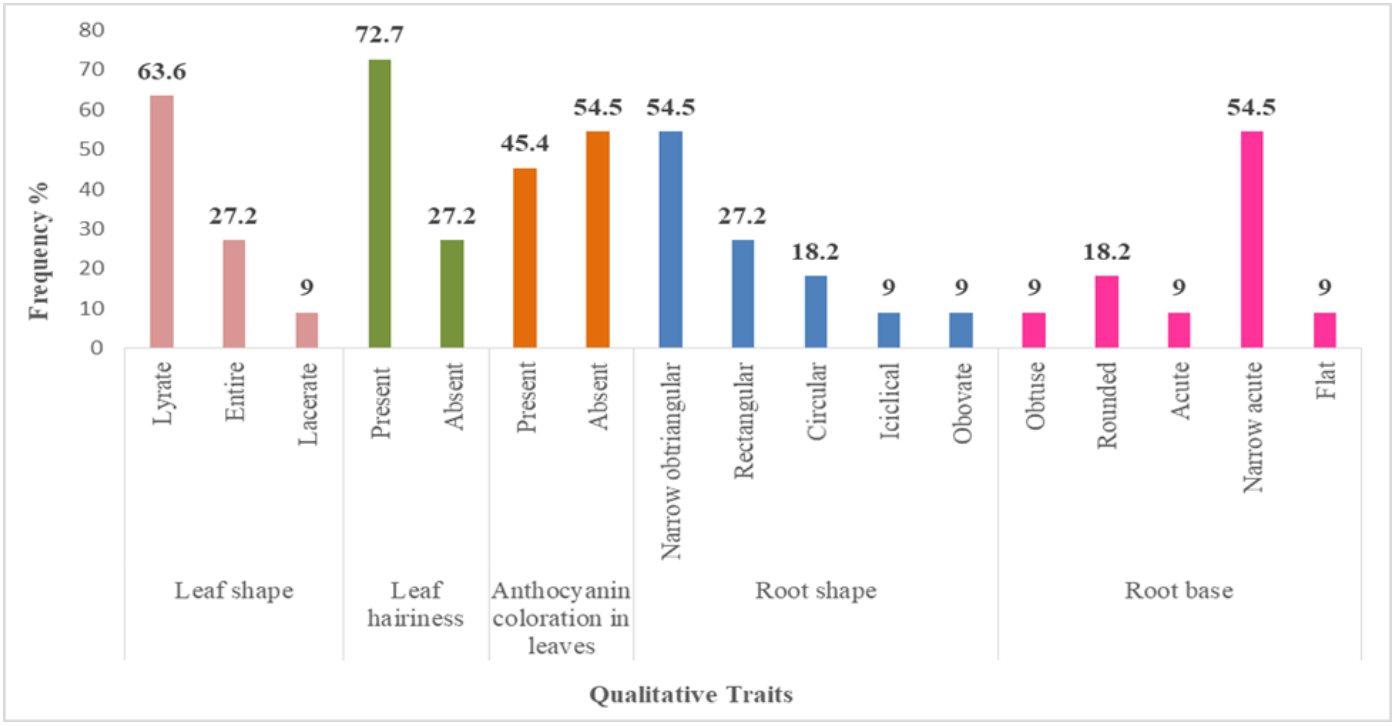

Figure 2. Frequency distribution study of radish genepool qualitative traits

Correlation

Correlation (positive and negative) among different morphological and biochemical traits were presented in Figure 3. The correlation co-efficient matrix represents positive correlation among variables in blue color while negative correlation is depicted by red color. According to analysis, number of leaves showed positive correlation with leaf length (0.82**), yield (0.59**) and root length (0.57**) while it was negatively correlated with leaf color L* (-0.57**) and a* (-0.53**). Plant fresh weight depicts significant positive association with root weight (1.00**) and root length (0.83**) and negative association with skin color b* (-0.7**). Yield an important variable trait, was positively associated with plant fresh weight (0.87**), root weight (0.85**), root length (0.72**), leaf length (0.66**) and leaf weight (0.44*). However, yield parameter was negatively correlated with maturity index and skin color b* (-0.39*). For biochemical traits, titratable acidity had strong positively association with root weight, length (0.7**), plant fresh weight (0.69**) and yield (0.55**) and negatively with skin color b* (-0.57**) respectively. Whereas maturity index positively correlated TSS (0.6**) and skin color b* (0.58**) and negatively correlated with titratable acidity (0.82**).

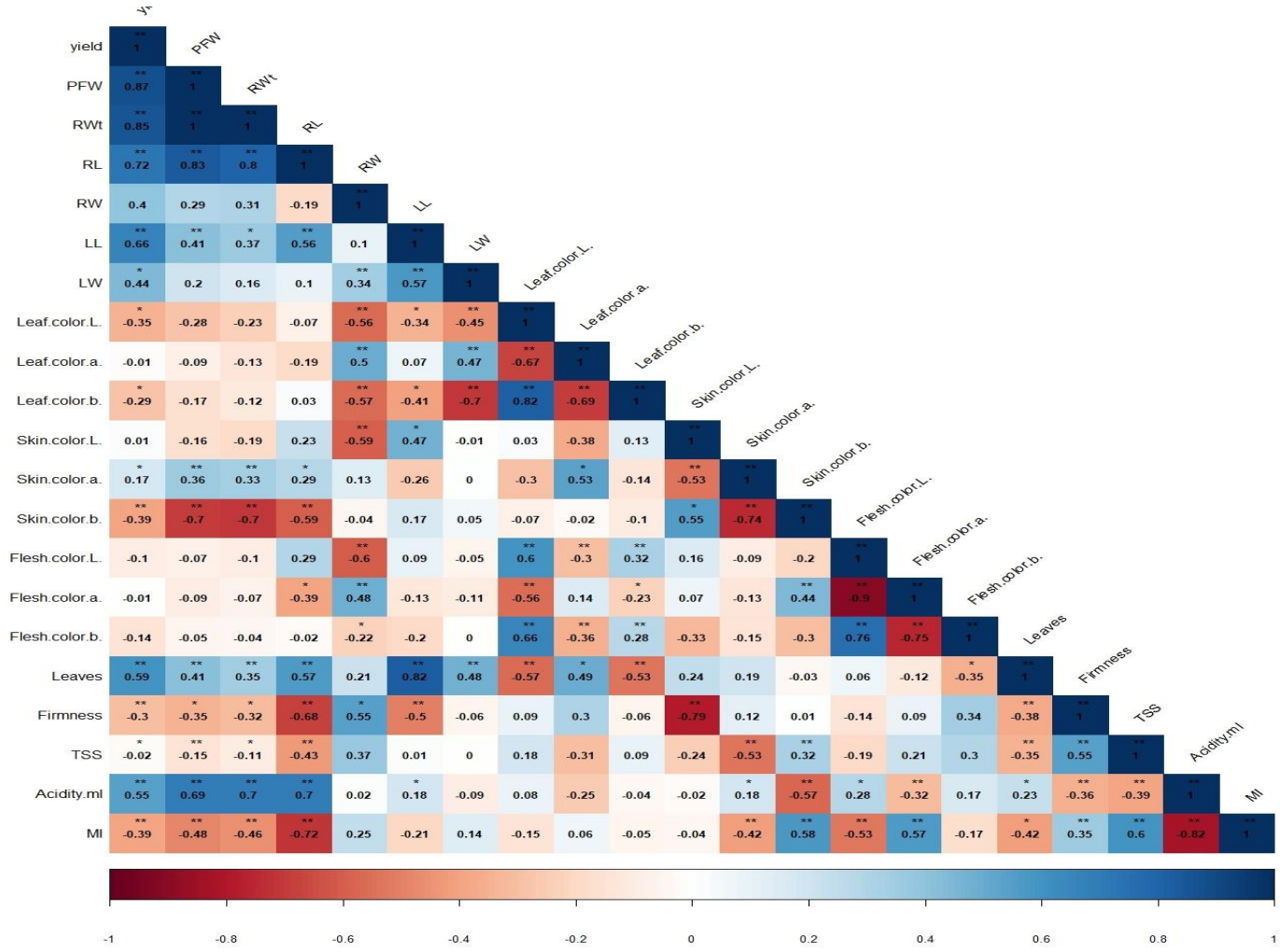

Figure 3. Correlation coefficient among different morphological traits

Cluster analysis

Eleven diverse radish genotypes were evaluated to study the structural relationship on the basis of different morphological traits. Hierarchical clustering was carried out by UPGMA cluster analysis (Figure 4). The genotypes were grouped into 3 different clusters. Maximum genotypes were found to be placed in cluster-I that were further divided into two sub clusters in first sub-cluster are two genotypes (RGB-10 and RGB-11), while in second sub-cluster there are six genotypes. In second major cluster, there were two genotypes, RGB-2 and RGB-5. While in third major cluster there was only one genotype that was RGB-7. The genotype found in different clusters means they are similar in one group but completely different from other clusters for morphological traits. It means that Genotype RGB-7 is totally different from other genotypes investigated in this study. While genotypes RGB-2 and RGB-5 are completely different from RGB-7 and genotypes in cluster-I for studied morphological traits.

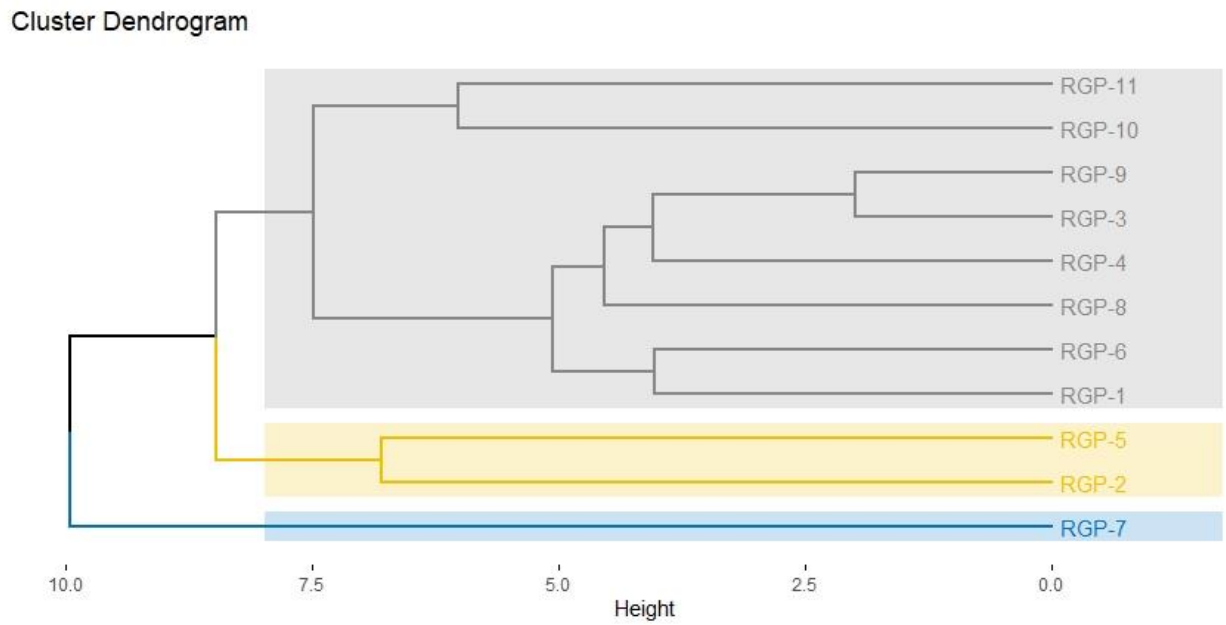

Figure 4. Dendogram depicting genotypes grouped into different clusters

DISCUSSION

For crop improvement, variability is important for genetic basis [15]. As genetic variability plays a significant role in selection of desirable parents from diverse sources for improvement in economically important (qualitative and quantitative) traits [10]. Usually, morphological studies have been carried out to study relationship between plant genotype and their environment and for estimation of variation. As morphological traits are easy to identify and measure moreover, they don't require expert knowledge [27]. In present research, radish genotypes were evaluated for different qualitative traits after harvesting to estimate variation through ANOVA. Analysis of variance were done to partition the total variation present in a trait into variation due to genotypes and other sources [28]. Significant amount of variation present in all studied traits showed that the maximum amount genetic variation or diversity present among different lines of radish genepool. CV is an important parameter that is used to indicate differences among morphological traits in germplasm screening and used as ideal marker for characterization showed that. Traits with low CV such as yield, leaf length, TSS indicates that they were similar (homogenous) and repeatable among lines while high CV for skin and flesh color (a* and b*) represent variation [29]. While variation studied through range showed maximum variation for plant fresh weight, root weight and maturity index. However, phenotypic variation studied through range doesn't yield reliable results as it is influence by different components such as genotype, environment, genotype*environment interaction. Furthermore, it does not indicate, which traits showed high level of variability [30]. High variation in plant biomass, root length, width and weight were also observed in exotic radish germplasm [18].

An exact assessment of genetic diversity, phenotypic and genotypic co-efficient of variance is used to assess variability exist in given genotypes and it is important in determining the success of any breeding program [31]. Presently in all traits, phenotypic co-efficient of variance was slightly higher than genotypic co-efficient of variance depicting minute to minimum influence of environment on expression of these traits [32]. Thus, selection only on phenotypic evaluation is effective [17]. Similar results were observed by Ullah and coauthors [33] during evaluation of twenty-one genotypes of radish, and Kumar and coauthors [17] in evaluation of temperate radish under local conditions of India.

Usually, it is difficult to estimate heritable and non-heritable variation present in a population on a basis of coefficients [28]. Therefore, in order to evaluate the contribution of both genotype and environment on the phenotypic variation, broad base heritability was studied [16]. Broad base heritability act as predictive estimate in evaluating reliability of phenotypic trait and high heritability value helps breeder in selection of particular trait [17]. Heritability of a respective trait enables breeder to decide level of selection applied under particular environment [30]. Heritability estimating genetic variation also includes both fixable (additive) and non-fixable (epistatic and dominance) variance [19]. But for achieving heritable variation with highest degree of accuracy, genetic advance as percentage of mean must be studied along [32-33]. High heritability coupled with high genetic advance (% of mean) in all quantitative traits was may be due to due to the action of additive

genes in expression of these traits and respond well in continuous selection [4, 34]. It means that pure line selection solely on phenotypic expressions followed by hybridization with subsequent selection in early generations are effective for these traits [32,35]. High heritability along with maximum genetic advance (%) was studied for root length, weight, diameter, leaf area and root yield/plot in radish [32]. But moderate level of heritability and genetic advance for leaf color L* and high heritability with low genetic advance for leaf color a* indicates non-additive gene effects that limited possibility in improvement of this trait through selection [33] and selection on the basis of phenotype is not effective for these traits [34]. High heritability with low genetic advance mean for TSS value in radish genotypes was observed by Mallikarjunaro and coauthors [14]. Generally, for heritable variation, selection is the first step in any breeding program, however it becomes difficult under low heritable variation because of environmental influence on the expression of traits [31].

Qualitative traits are usually studied to describe plant phenotype and to identify particular plant variety. They are influenced by natural selection, socio-economic factors and consumer preference [36] and are usually genetically controlled with minimum environmental effect [37]. Frequency distribution of qualitative traits during this study showed high level of variation for radish root shape and root base that could be used in future as an important source for development of new germplasm. While traits with low variability such as leaf shape suggested breeders to collect accession having distinct characteristics from diverse regions [18].

In any crop improvement program, selection is usually done on basis of yield related parameters. However, direct selection on the basis of yield parameters were complex and time consuming because traits such as yield are quantitatively inherited and mainly influenced by both genotype and environment. Moreover, it expressed at the end of growth stage [38]. Thus, Improvement in respective traits required indirect selection which is easier to select and heritable. But this technique requires deep understanding of interrelationship among different traits that can be achieved through correlation studies [39] Correlation is a mutual relationship between two traits without study cause and effect relationship and is computed at both phenotypic and genotypic level between two traits [40]. It is used to estimate the association strength between two parameters [39]. It is an important analysis in any breeding program because of selection of genotypes traits depends upon their association with yield and other related traits [41]. It is suitable to identify and select highly correlation (positive or negative) among traits to prevent depression of yield or other quality traits [42]. In present research, yield showed positive correlation with root length, weight, leaf length and width which may be due to presence of linked genes. Furthermore environment-gene interaction is also considered as influential effect on association among different traits. Usually, role of environment for correlated traits were direct or in same direction while in other cases, it is indirect and in opposite direction [43]. Positive correlation between no of leaves and root length were also observed by Jatoi and coauthors [18] in local as well exotic germplasm. Similarly, total weight of radish plant was in positive association with leaf width and root length [9]. Presently negative correlation was observed between maturity index (Sugar/acid ratio) and plant yield. As sugar (TSS) is nutritional or biochemical trait of a radish root, thus an increase in root yield may leads to decrease in TSS which results in decrease in maturity index value.

Plant traits with maximum correlation, high heritability and genetic advanced mean can leads to maximum genetic gain in successive generations and are ideal traits for selection in future breeding programs [41]. Grouping of genotypes in different cluster can be utilized for breeding radish to evolve new combinations similar studies were also conducted by Ahmad and coauthors [44]. Hierarchical clustering is an important approach to study genotypes and to use them into new cultivar development with desirable traits [45]. Different genotypes of radish from diverse backgrounds were investigated for morphological traits were significantly different from each other. It was observed that Genotype RGB-7 were different for most of the traits from other genotypes. Hence these genotypes grouped in different clusters and showed different traits can be used in future breeding program for improvement in radish and population development to acquire different combinations.

CONCLUSION

Knowledge about extent of variability and interrelationship among different traits is main criteria for designing any crop breeding program. Whereas, analysis of genetic diversity is one the key step in determining variation in an existing genepool. Thus, on the basis of variability estimation through ANOVA, coefficient of variability (PCV, GCV), heritability, genetic advance, correlation, cluster analysis and frequency distribution, significant variation were observed for all studied traits. Therefore, it was concluded that these diverse genotypes can offer a great potential to be used as parents in varietal development of radish for improvement of economically important traits. Furthermore, it is suggested that genetic base of existing germplasm should be widened by including more diverse germplasm from other source for the development of a successful and sustainable breeding program.

Funding: This research received no external funding.
Conflicts of Interest: The authors declare no conflict of interest.

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