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EVALUATION OF GENETIC DIVERGENCE IN RADISH (*RAPHANUS SATIVUS* L.) GERMPLASM USING MULTIVARIATE APPROACHES IN NORTH-WESTERN HIMALAYAS

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Abstract

The present study was conducted to evaluate genetic divergence among 18 radish (*Raphanus sativus* L.**)** genotypes. High heritability was recorded for ascorbic acid, days to 50% germination, and root diameter. Correlation analysis revealed a positive association between root yield and traits such as root weight, root length, and plant height, while path analysis identified root weight, root diameter, and leaf traits as key yield contributors. Principal Component Analysis (PCA) revealed that the first two principal components explained a major portion of total variability, with PC1 strongly associated with yield traits and the first five principal components (PCs) explain 80.9% of the total variance, and PC1 contributing the most (31.3%). Hierarchical clustering grouped genotypes into distinct clusters, indicating diverse genetic backgrounds and potential for targeted breeding. These findings provide valuable insights for selecting superior genotypes to enhance radish breeding and production across diverse agro-climatic conditions.

Introduction

Radish (*Raphanus sativus* L.) belongs to the family Brassicaceae (Cruciferae), originating from Central and Western China and India. It is one of the oldest cultivated vegetables, which is grown primarily for its tuberous roots and hypocotyls. It is low-calorie crop rich in vitamin C, protein, minerals, fiber, and carbohydrates (Singh and Nath 2012). Radish has medicinal properties, benefiting individuals with piles, hepatic disorders, and jaundice.

The success of genetic improvement in radish relies on the extent of genetic variability present in the germplasm, which serves as the foundation for crop improvement (Vavilov 1951). Genetic variability is crucial for selecting superior genotypes and identifying suitable parents for breeding programs. A diverse genetic base enhances selection efficiency, allowing breeders to implement effective breeding strategies (Jing *et al.* 2014). PCA simplifies complex datasets by identifying the most influential traits contributing to genetic variation, while cluster analysis groups genetically similar genotypes, aiding in the selection of diverse parents for hybridization (Thakur *et al.* 2024). These techniques provide a comprehensive understanding of genetic relationships among radish genotypes, enhancing breeding strategies for yield improvement, stress tolerance, and overall crop performance. The study was aimed to evaluate genetic divergence among 18 radish (*R. sativus*) genotypes to identify key traits contributing to root yield. It sought to assess heritability, correlations, and trait contributions using statistical tools like path analysis and PCA. The ultimate goal was to identify genetically diverse and high-yielding genotypes for targeted breeding and improved radish production.

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Materials and Methods

The study was conducted in the Department of Vegetable Science, College of Horticulture and Forestry, Neri, Hamirpur, Himachal Pradesh, India, using 18 genotypes of Asiatic radish, including a check cultivar. The experiment was laid out in a randomized complete block design (RCBD) with three replications, having a plot size of 1.2 m x 1 m and spacing was 30 cm x 7.5 cm. Standard agronomic practices were followed (Anonymous 2022), and observations were recorded on days to 50% germination, plant height (cm), number of leaves per plant, leaf length (cm), leaf width (cm), crown diameter (mm), root length (cm), root diameter (mm), days taken to marketable maturity, average root weight with leaves (g), average root weight without leaves (g), total soluble solids (^{0}B), root yield per plot (kg), root shape and ascorbic acid (mg/100g). Data were analyzed using SPSS (v20) to perform correlation and hierarchical clustering analyses were conducted using PAST (v4.11), and PCA was performed to reduce data dimensions and understand trait relationships. Results were visualized through scatter plots, and PCA biplots to provide insights into variability and associations among traits.

Results and Discussion

The study highlighted significant phenotypic variability among traits, with the phenotypic coefficient of variation (PCV) ranging from 7.65 to 27.60% (Fig. 1). High PCV was observed for root yield per plot, root diameter, average root weight, ascorbic acid, and the number of leaves per plant, indicating substantial diversity. Moderate PCV was recorded for root length, crown diameter, leaf length, days to 50% germination, total soluble solids (TSS), and plant height, while days to marketable maturity had the lowest PCV. The genotypic coefficient of variation (GCV) ranged from 7.23 to 26.07%, with high GCV in root diameter, ascorbic acid, and root weight, suggesting strong genetic influence (Fig. 1). These findings align with Kaur *et al.* (2017) and Singh (2020).

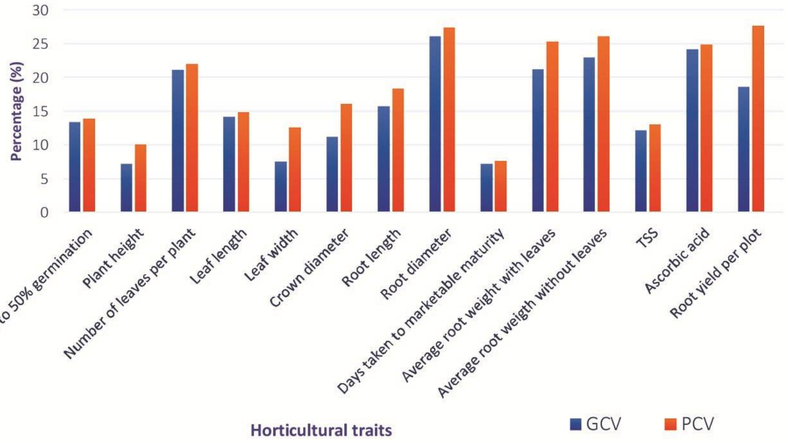

Fig. 1. Genotypic and phenotypic coefficient variation of the radish genotypes for different traits.

Heritability estimates for radish traits ranged from 35.76 to 94.74%, with the highest recorded for ascorbic acid (94.74%), followed by days to 50% germination (93.11%), number of leaves per plant (92.57%), leaf length (91.25%), and root diameter (90.4%) (Fig. 2). Other traits, including total soluble solids (87.17%) and average root weight, also exhibited high heritability. Genetic advance ranged from 9.30 to 51.06%, with the highest value for root diameter (51.06%), ascorbic acid (48.49%), and number of leaves per plant (41.86%) (Fig. 2). Similar trends were reported by Roopa *et al.* (2018) in radish genotypes. The presented results follow the findings of Singh (2020). The combination of high heritability and genetic advance for traits such as leaf length, root length and ascorbic acid indicates strong additive gene effects, suggesting that direct selection could be an effective for improving these traits.

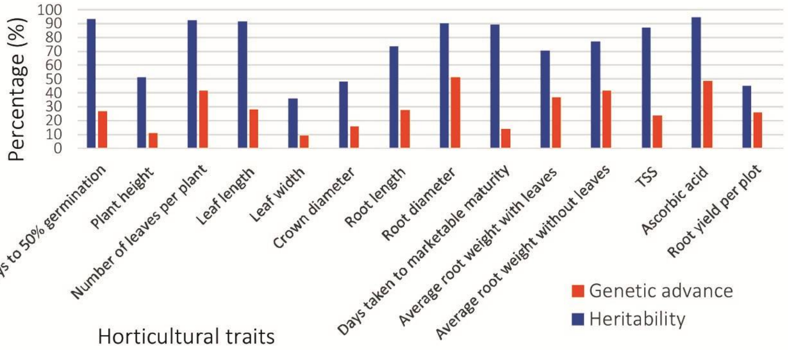

Fig. 2. Heritability and genetic advance (%) of the radish genotypes for different traits.

The correlation analysis revealed significant associations among key traits influencing root yield per plot in radish. Days to 50% germination exhibited a strong positive correlation with days to marketable maturity, root diameter, crown diameter, and leaf width at both genotypic and phenotypic levels (Fig. 3). Plant height showed highly significant correlations with root length, average root weight, root yield per plot, and the number of leaves per plant. Similarly root diameter showed significant correlations with root yield and ascorbic acid, while days to marketable maturity had a positive association with total soluble solids. Average root weight (with leaves) exhibited strong correlations with root yield and root weight (without leaves), emphasizing their role in yield improvement. Additionally, root yield per plot had significant positive associations with root length, plant height, root diameter, leaf length, and leaf width, highlighting the complex interrelationship among yield-contributing traits. These results were similar with the findings of Kaur *et al.* (2017) and Thakur *et al.* (2022).

The path coefficient analysis revealed the direct and indirect effects of 13 independent traits on root yield per plot in radish (Table 1). Days to 50% germination had a negative direct effect, while plant height showed a negative direct effect but contributed positively through total soluble solids, days to 50% germination, and ascorbic acid. Root length and root diameter had positive direct effects, while days to marketable maturity and average root weight with leaves also positively influenced root yield. In contrast, average root weight without leaves, total soluble solids, and ascorbic acid had negative direct effects, though ascorbic acid contributed positively through other traits, highlighting complex trait interactions influencing yield. These results were in line with Jamatia *et al.* (2015) and Roopa *et al.* (2018).

The hierarchical clustering dendrogram effectively grouped radish genotypes based on genetic and agronomic similarity. The first major cluster included R-COHF-NERI-11, R-COHF-NERI-1, R-COHF-NERI-4, and Japanese White, merging at a lower hierarchical distance, indicating high similarity (Fig. 4). A second distinct cluster comprised of R-COHF-NERI-5, R-COHF-NERI-15, and R-COHF-NERI-8, showing close genetic relationships with slight variation. The third cluster, including R-COHF-NERI-13, R-COHF-NERI-9, R-COHF-NERI-16, and R-COHF-NERI-17, exhibited moderate divergence. Another subgroup of R-COHF-NERI-6 and R-COHF-NERI-12

Table 1. Genotypic path coefficient analysis for effects of various traits on root yield per plot.

	DTFG	PH	NLPP	LL	LW	CD	RL	RD	DTMM	ARWWL	ARWWOL	TSS	AA	GCCRYPP
DTFG	**-0.708**	0.219	-0.010	0.062	-0.288	-0.105	-0.057	0.639	0.511	-0.518	0.221	-0.136	-0.012	-0.180
PH	0.138	**-1.125**	0.018	0.171	-0.017	0.016	0.452	0.085	-0.099	1.734	-1.277	0.285	0.085	0.465**
NLPP	0.126	-0.366	**0.055**	-0.028	-0.027	-0.007	0.151	-0.231	-0.062	1.149	-0.663	-0.062	0.183	0.217
LL	-0.104	-0.452	-0.004	**0.426**	-0.429	-0.026	0.014	-0.027	0.136	1.234	-0.473	0.002	0.028	0.326*
LW	-0.261	-0.025	0.002	0.233	**-0.783**	-0.063	-0.082	0.346	0.245	1.310	-0.792	0.111	0.178	0.420**
CD	-0.335	0.080	0.002	0.050	-0.221	**-0.221**	0.018	0.204	0.119	0.522	-0.560	-0.064	0.547	0.140
RL	0.070	-0.881	0.014	0.010	0.111	-0.007	**0.577**	0.282	0.123	1.720	-1.420	0.186	-0.057	0.731**
RD	-0.392	-0.083	-0.011	-0.010	-0.234	-0.039	0.141	**1.157**	0.146	0.611	-0.632	0.022	-0.290	0.385**
DTMM	-0.529	0.163	-0.005	0.085	-0.280	-0.039	0.104	0.246	**0.684**	0.028	-0.094	-0.249	-0.034	0.080
ARWWL	0.120	-0.636	0.020	0.171	-0.334	-0.038	0.224	0.130	0.006	**3.070**	-1.821	0.122	-0.095	0.939**
ARWWOL	0.083	-0.765	0.019	0.107	-0.330	-0.066	0.436	0.389	0.034	2.776	**-1.878**	0.146	-0.064	0.887**
TSS	-0.169	0.563	0.006	-0.002	0.153	-0.025	-0.188	-0.045	0.299	-0.659	0.480	**-0.570**	-0.035	-0.191
AA	-0.010	0.116	-0.012	-0.015	0.169	0.147	0.040	0.407	0.028	0.355	-0.145	-0.024	**-0.825**	0.231

*, ** : Significant at 5 and 1% , respectively.

Residual effect: 0.68804

DTFG : Days to 50% germination, PH : Plant height (cm), NLPP : Number of leaves per plant, LL: Leaf length (cm), LW: Leaf width (cm), CD: Crown diameter (cm), RL: Root length (cm), RD: Root diameter (mm), DTMM: Days taken to marketable maturity, ARWWL: Average root weight with leaves (g), ARWWOL: Average root weight without leaves (g), TSS: Total soluble solids (ºB), AA : Ascorbic acid (mg/100g) and GCCRYPP: Genotypic correlation coefficient of root yield per plot (kg).

showed strong similarity but remained distinct. Additionally, R-COHF-NERI-7 and R-COHF-NERI-14 clustered closely, while R-COHF-NERI-3, R-COHF-NERI-2, and R-COHF-NERI-10 formed the final major cluster. Long vertical branches in the dendrogram highlighted substantial genetic variability, suggesting diversity in traits. Similar results were found by Jamatia *et al.* (2015), and Thakur *et al.* (2025).

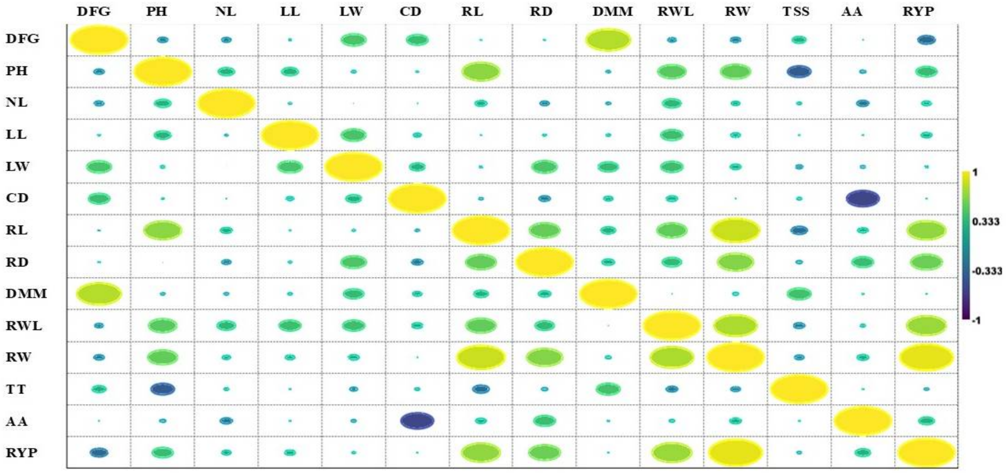

Fig. 3. Genotypic and phenotypic coefficients of correlation among different characters in radish. Abbreviations are similar as in Table 1.

Table 2. Principal component analysis of radish genotypes based on different qualitative and quantitative characters.

Variables	PC1	PC2	PC3	PC4	PC5
Eigen value	4.39	2.61	2.09	1.16	1.07
% Var. Exp.	31.30	18.70	15.00	8.30	7.60
Cum. Var. Exp	31.30	50.00	65.00	73.20	80.90
DTFG	-0.08	0.54	0.06	0.11	0.27
PH	0.31	-0.10	-0.31	0.13	0.28
NL	0.12	-0.13	-0.28	0.62	-0.14
LL	0.15	0.20	-0.20	-0.31	-0.49
LW	0.16	0.46	-0.12	-0.21	-0.13
CD	0.00	0.31	-0.44	-0.05	0.01
RL	0.41	-0.02	0.08	0.16	0.40
RD	0.30	0.14	0.36	-0.26	0.02
DMM	0.05	0.51	0.20	0.29	0.20
RWL	0.40	0.05	-0.17	0.05	-0.27
RW	0.46	-0.02	0.06	0.05	0.01
TSS	-0.15	0.20	0.20	0.52	-0.49
AA	0.10	-0.07	0.56	0.04	-0.15
RYP	0.42	-0.10	0.10	0.02	-0.20

Abbreviations are similar as in Table 1.

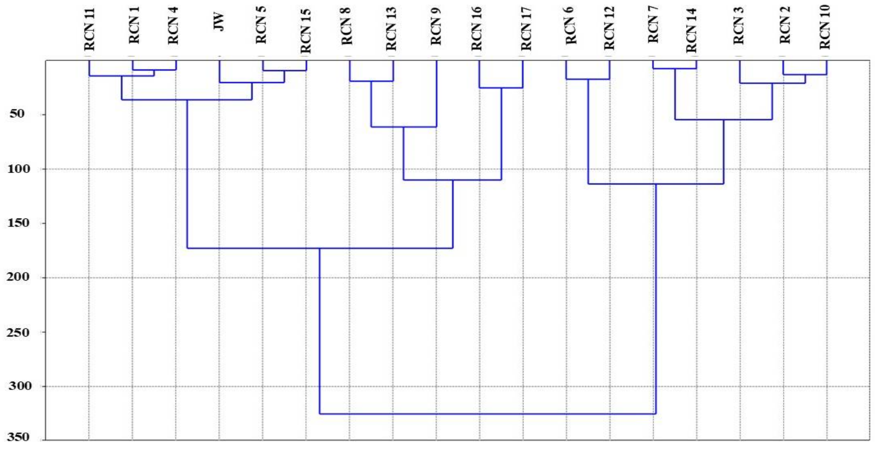

Fig. 4. Dendrogram visualization of radish genotypes based on different characters.

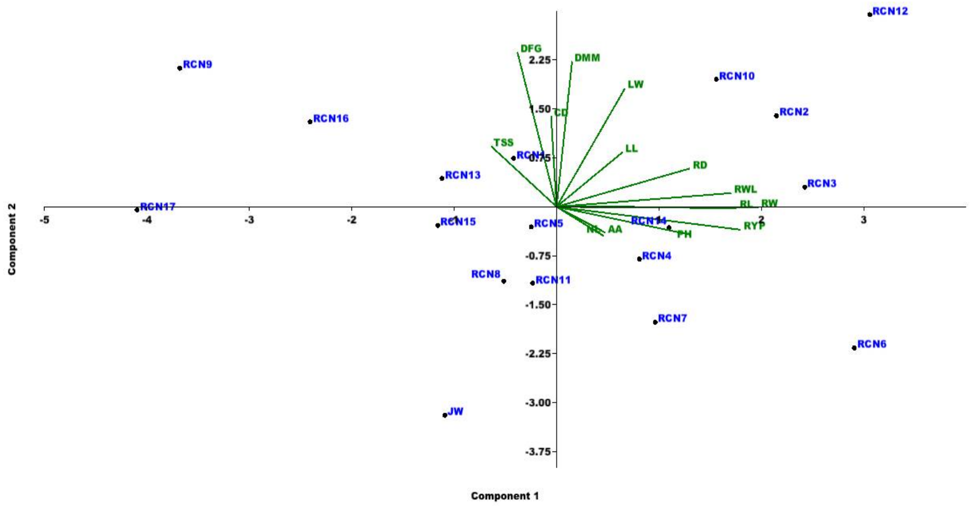

Fig. 5. PCA of the radish genotypes for different traits illustrated by bi-plot.

PCA showed that the first five principal components explained 80.9% of the total variance, with PC1 (31.3%) contributing the most, followed by PC2 (18.7%) and PC3 (15.0%) (Table 2). Root length, average root weight, and root yield per plant had high loadings in PC1, while PC2 was linked to days to first germination and days to marketable maturity, and PC3 emphasized antioxidant activity and collar diameter. The PCA biplot revealed genetic variability, clustering genotypes based on key traits (Fig. 5). High-performing genotypes (R-COHF-NERI-12, R-COHF-NERI-10, R-COHF-NERI-2) aligned with PC1, while lower-performing ones clustered negatively. These findings, corroborated with previous studies by Ali *et al.* (2017), Thakur *et al.* (2022) and Thakur *et al.* (2025) highlight the genetic diversity within radish populations.

Based on the performance of the genotypes it is concluded that the genotypes R-COHF-NERI-12, R-COHF-NERI-6, and R-COHF-NERI-3 exhibited superior root yield and key horticultural traits. Correlation analysis showed a positive association between root yield and traits like root weight, root length, and plant height, while path analysis identified root weight, root diameter, and leaf traits as major yield contributors. PCA revealed that the first five components explained 80.9% of total variance.Clustering grouped genotypes into distinct clusters, indicating diverse genetic backgrounds and potential for targeted breeding. So, selection based on these traits will be worthwhile for any breeding programme.

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