



Plant Archives

Journal homepage: <http://www.plantarchives.org>DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.no.2.191>

VARIABILITY STUDIES IN RADISH (*Raphanus sativus* L.)

Nikita Devenda¹, Dipayan Sarkar^{*1}, Usha Shukla¹, Manoj Kumar Bundela¹, Indra Raj Yadav²,
L.S. Dhayal³, Pooja Naruka⁴ and P.K. Yadav¹

¹Department of Horticulture, School of Agriculture, Suresh Gyan Vihar University, Jaipur, Rajasthan, India.

²Department of Soil Science, School of Agriculture, Suresh Gyan Vihar University, Jaipur, Rajasthan, India.

³Department of Genetics and Plant Breeding, School of Agriculture, Suresh Gyan Vihar University, Jaipur, Rajasthan, India.

⁴Department of Entomology, School of Agriculture, Suresh Gyan Vihar University, Jaipur, Rajasthan, India.

*Corresponding author E-mail: dipayan.flori@gmail.com

(Date of Receiving-30-06-2026; Date of Revision-06-09-2026; Date of Acceptance-11-09-2026)

ABSTRACT

The present investigation entitled “Variability Studies in Radish (*Raphanus sativus* L.)” was carried out during the *Rabi* season of 2025 at the Agricultural Research Farm, SGVU, Jaipur, to assess the genetic variability, trait associations and direct indirect effects governing yield in radish. Twelve diverse genotypes were evaluated in a Randomized Block Design with three replications for nine growth traits, three yield attributes and three quality parameters. Analysis of variance revealed significant differences among genotypes for all traits, indicating ample genetic variability. High heritability coupled with high genetic advance was recorded for root weight, total fresh weight, leaf area and yield per plot and per hectare, suggesting the predominance of additive gene action and the scope for improvement through direct selection. Correlation analysis showed that yield was strongly and positively associated with root weight ($r_p = 0.92$; $r_g \approx 1.00$), root length, root diameter and total fresh weight. Path coefficient analysis identified root weight as the most influential trait contributing directly to yield, followed by total fresh weight and yield per hectare, whereas shoot to root ratio exerted a strong negative direct effect. Multivariate analyses (PCA and UPGMA) grouped genotypes into distinct performance clusters and identified Pusa Mridula, IVR-1 and Arka Nishant as the most superior and genetically divergent high yielding types. Overall, the study highlights substantial exploitable genetic variability and identifies key selection criteria and promising genotypes for use in future radish improvement and hybrid development programmes.

Key words : Correlation, Genotypes, Path analysis, Principal component analysis, Radish, Variability.

Introduction

Radish (*Raphanus sativus* L.), a diploid ($2n=2x=18$) *Brassicaceae* member, originated in Central/Western China and India around 2700 B.C. This ancient cool-season root vegetable, grown worldwide on 204,000 hectares in India (3.236 million metric tonnes yield), features diverse root shapes (round to spindle), colors (white to black/red via anthocyanins) and uses (salad, garnish, pods as Moongra) (Anonymous, 2024). Nutritionally rich in vitamin C, fiber and minerals (leaves > roots; pink varieties higher in ascorbic acid), it aids piles, hepatic issues and jaundice; its pungency stems from isothiocyanates, with neutraceutical/antioxidant anthocyanins (Singh and Nath, 2012; Brar and Nandpuri,

1972; Horbowicz *et al.*, 2008; Jing *et al.*, 2014). Asian types tolerate heat better than European; key Indian states include West Bengal, Bihar, Uttar Pradesh, with Rajasthan at 520 hectares (10.31 metric tons) (Kaneko and Matsuzawa, 1993; Anonymous, 2024).

The genetic improvement of the crop depends on the amount of genetic variability present in the population and the germplasm serves as a valuable source of base population and provides the possibility for wide variability (Vavilov, 1951). The role of genetic variation in a crop is of paramount importance in selecting the best genotypes for rapidly improving yield and desirable horticultural characteristics, as well as in selecting the most suitable parents for further breeding programme. Genetic

variability study helps in understanding the nature of variation in different horticultural traits both quantitative and qualitative, respectively. Variations may be caused by environmental factors, genetic factors, mutations or by attacks by any biological agents. Genetic variation is important in a given germplasm and is a fundamental necessity for crop improvement, as it provides more opportunities for selection to implement an efficient and productive breeding programme. It is therefore essential to know the amount of genetic variability available and the efficacy of the selection depends on the magnitude of genetic variability present in the given set of germplasm collected from indigenous and exotic sources. Further the extent of heritability helps the breeder to identify the traits which can be easily selected. Genetic advance explains the degree of gain obtained in a given character under a particular selection pressure. Estimates of heritability with genetic advance are more reliable and meaningful. The correlation studies help the breeder to know about the type of association between the various traits in a given set of germplasm. The path coefficient analysis helps to work out the direct and indirect effect of the various horticultural traits on the dependent character like yield. In the light of the above, the present investigation was carried in radish to study the variability in Radish (*Raphanus sativus* L.) genotypes. This study will help to identify promising genotypes for use in breeding program for yield, yield attributes and quality traits improvement *i.e.* development of superior radish cultivars suited for diverse end use.

Materials and Methods

The current study was conducted at the Agriculture Research farm SGVU, Jaipur during the *Rabi* season of 2025. The experimental material is consisted of 12 genotypes of radish are as follows Pusa Chetki, Pusa Himani, Pusa Desi, Pusa Mridula, Japanese White, Japanese Pink, Early Radish, Sonar Bangla, IVR-1, IVR-11 Radish, Japanese Red and Arka Nishant, which were raised in Randomised Block Design (RBD) with three replications. There was sowing of each genotype in 4 rows of 2×1.2 m plot by row to row spacing of 30cm and plant to plant spacing of 10cm. In this study implemented all standard agricultural practices and plant protection methods for this radish crop. Agro climatic conditions needed observations of 9 growth parameters including Plant height (20, 40 DAS and at harvest), Number of leaves per plant (at 20, 40 DAS and at harvest), Leaf length (cm), Leaf width (cm), Root length (cm), Root diameter (cm), Shoot to root ratio, Leaf area (cm²) and Total fresh weight of plant (g), 3 yield parameters including Root weight, Yield per plant and

Yield per plot and 3 quality traits like Vitamin C (mg/100g), Total soluble solids (Brix) and Total chlorophyll content. Five competitive plants were selected at random from each genotype and the plants were appropriately tagged and labelled to record the observations. In accordance with (Fisher, 1936), the statistical analysis such as analysis of variance (ANOVA) was calculated. Coefficients of variation for genotype and phenotype were computed using (Burton 1952) recommended methodology. The formula provided by (Johnson *et al.*, 1955) was used to estimate the coefficient of variation, heritability and genetic advancement as a percentage of mean. The degree of a character's association with yield and the variables that influenced yield were used to calculate the correlation coefficients. The coefficient of correlation between genotype and phenotype was computed by Searle (1961). Path coefficient analysis was performed using the idea first proposed by Wright (1921) and then refined by Dewey and Lu (1959) to determine the direct and indirect effects of the different characters on yield. PCA was performed using standardized data to determine major contributing traits and genotype grouping patterns. A two-dimensional biplot was generated to visualize trait-genotype relationships. Hierarchical clustering using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) was conducted based on Euclidean distances to determine genetic divergence among genotypes. Trait-trait association networks were constructed to depict correlation strength and interaction pathways. These observations were collected in a data book as raw data and analyzed through windostat software version 9.50.

Results

Morphological characterization based on selected traits

Among the 12 radish varieties, plant height at 20 days after sowing varied from 10.1 cm in T₁ (Pusa Chetki) to 14.5 cm in T₄ (Pusa Mridula), at 40 days after sowing from 21.5 cm (T₁) (Pusa Chetki) to 32.8 cm (T₄) (Pusa Mridula) and at harvest from 42.5 cm (T₁) (Pusa Chetki) to 62.5 cm (T₄) (Pusa Mridula) (Table 1). Number of leaves per plant at 20 days after sowing ranged from 5.2 (T₁) (Pusa Chetki) to 7.5 (T₄) (Pusa Mridula), at 40 days after sowing 11.5 (T₁) (Pusa Chetki) to 17.8 (T₄) (Pusa Mridula), and at harvest 14.0 (T₁) (Pusa Chetki) to 22.4 (T₁₂) (Arka Nishant). Among the 12 radish varieties leaf length varied from 22.5 cm in T₁ (Pusa Chetki) to 34.5 cm in T₄ (Pusa Mridula) while similarly leaf width varied from 8.5 cm (T₁) (Pusa Chetki) to 11.5 cm (T₄) (Pusa Mridula). Root length ranged from 18.2 cm (T₃) (Pusa

Table 1 : Characterization of 12 Radish varieties on the basis of quantitative morphological parameters.

Treatment	PH20	PH40	PH	NL20	NL40	NL	LL	LW	RL	RD	SRR	LA	TFW	RW	YPlot	YHa	VitC	TSS	TC
T ₁	10.1	21.5	42.5	5.2	11.5	14	22.5	8.5	24.5	4.8	0.6	210.4	340.5	212.4	12.7	53.1	14.5	3.2	2.6
T ₂	11.8	26.5	52.1	5.8	13.8	17.5	27.2	9.8	22.8	4.5	1.0	250.2	340.2	175.5	10.5	43.9	15.8	3.6	2.8
T ₃	11.2	24.1	48.5	6.1	13.2	16.2	26.5	9.5	18.2	3.2	1.9	245.5	290.5	102.3	6.1	25.6	16.2	3.5	2.6
T ₄	14.5	32.8	62.5	7.5	17.8	22.5	34.5	11.5	21.5	4.1	1.6	320.8	395.6	154.2	9.3	38.5	13.1	2.9	3.0
T ₅	12.2	27.7	54.1	5.9	14.1	17.9	28.1	10.0	23.9	4.7	0.8	260.1	375.2	202.8	12.2	50.7	14.2	3.1	2.8
T ₆	13.8	30.1	58.8	7.1	16.4	20	30.8	10.5	22.1	4.3	1.4	295.5	390.4	165.8	10.0	41.5	14.9	3.3	2.8
T ₇	11.2	25.5	49.2	5.6	13	16.2	26.1	9.1	21.2	4.0	1.1	238.2	305.8	148.5	8.9	37.1	14.5	3.4	2.6
T ₈	12.6	28.3	53.5	5.8	13.6	17.2	29.0	10.1	22.5	4.4	1.0	258.5	335.5	170.2	10.2	42.6	15.6	3.6	2.7
T ₉	10.8	24.4	45.5	5.4	12.5	15.8	25.5	8.9	20.5	3.8	1.2	230.5	290.5	135.2	8.1	33.8	21.1	4.5	2.6
T ₁₀	12	27.1	51.2	5.9	13.9	17.6	26.8	9.5	23.2	4.6	0.8	245.8	342.5	192.5	11.6	48.1	16.0	3.7	2.8
T ₁₁	11.9	26.7	52.7	5.9	13.7	17.4	27.5	9.8	22.9	4.5	0.9	252.5	350.2	182.5	11.0	45.6	15.9	3.6	2.8
T ₁₂	13.2	29.5	58.4	6.5	15.2	19.5	30.5	10.8	26.2	5.2	0.8	280.5	420.2	240.5	14.4	60.1	18.4	4.0	3.1
Mean	12.1	27.0	52.4	6.1	14.1	17.6	27.9	9.8	22.5	4.3	1.1	257.4	348.1	173.5	10.4	43.4	15.8	3.6	2.8
Min	10.1	21.5	42.5	5.2	11.5	14	22.5	8.5	18.2	3.2	0.6	210.4	290.5	102.3	6.1	25.6	13.1	2.9	2.6
Max	14.5	32.8	62.5	7.5	17.8	22.4	34.5	11.5	26.2	5.2	1.9	320.8	420.2	240.5	14.4	60.1	21.1	4.5	3.1
CV(%)	9.8	7.3	6.5	6.8	7.2	10.4	5.7	7.3	6.9	7.6	6.3	6.5	5.6	8.3	6.5	6.2	8.3	8.5	7.3
SEm	0.6	1.1	1.9	0.2	0.5	1.1	0.9	0.4	0.9	0.2	0.0	9.7	11.3	8.3	0.4	1.5	0.7	0.2	0.1
CD@5%	2.0	3.3	5.8	0.7	1.7	3.13	2.7	1.2	2.6	0.6	0.1	28.3	33.2	24.3	1.1	4.5	2.2	0.5	0.3
CD@1%	2.7	4.5	7.9	0.9	2.4	4.2	3.6	1.7	3.6	0.8	0.2	38.5	45.1	33.0	1.5	6.2	3.0	0.7	0.5

Desi) to 26.2 cm (T₁₂) (Arka Nishant), and root diameter 3.2 cm (T₃) (Pusa Desi) to 5.2 cm (T₁₂) (Arka Nishant). Shoot to root ratio varied from 0.6 in T₁ (Pusa Chetki) to 1.9 in T₃ (Pusa Desi). Leaf area ranged 210.4 cm² (T₁) (Pusa Chetki) to 320.8 cm² (T₄) (Pusa Mridula) while total fresh weight varied from 290.5 g (T₃, T₉) to 420.2 g (T₁₂) (Arka Nishant) and root weight from 102.3 g (T₃) (Pusa Desi) to 240.5 g (T₁₂) (Arka Nishant). Yield per plot ranged from 6.1 kg (T₃) (Pusa Desi) to 14.4 kg (T₁₂) (Arka Nishant) similarly total yield varied from 25.6 t/ha (T₃) to 60.1 t/ha (T₁₃) (Arka Nishant). Vitamin C content varied from 13.1 mg/100g (T₄) (Pusa Mridula) to 21.1 mg/100g (T₉), TSS 2.9 °Brix (T₄) (Pusa Mridula) to 4.5 °Brix (T₉) while total chlorophyll ranged from 2.55 mg/g (T₁) (Pusa Chetki) to 3.1 mg/g (T₁₂).

Variability, Heritability and Genetic advance

Genotypic coefficient of variation (GCV) ranged from 3.757% (TC) to 33.586% (SRR), while phenotypic coefficient of variation (PCV) spanned 8.238% (TC) to 34.177% (SRR), indicating low environmental influence where GCV approached PCV (e.g., SRR). Heritability (h²) was high (>70%) for PH (70.592%), NL40 (71.674%), LL (77.178%), LA (73.698%), TFW (80.356%), RW (86.197%), YPlot (91.277%), and YHa (91.984%), signaling strong additive gene action suitable for selection. Genetic advance as mean (GAM) exceeded 20% for NL40 (20.246%), PH40/PH (17.159–17.621%), LL (18.832%), RD (18.961%), LA (19.255%), TFW (21.043%), RW (39.535%), YPlot/YHa (41.097–41.285%) and VitC (21.193%), confirming high improvement potential via selection. Moderate GAM (10–20%) occurred in PH20 (12.083%), NL20 (17.625%), NL (16.34%), LW (10.737%), RL (12.781%), and TSS (16.465%); low values (<10%) for TC (3.528%) suggest non-additive control. Traits like RW, YHa, YPlot, TFW, and SRR showed superior GCV (>20%), PCV (>20%), h² (>85%) and GAM (>35–67%), ideal for direct selection in radish breeding. Yield-related parameters (YHa, YPlot) exhibited highest responsiveness, aligning with vegetative vigor (TFW, LA) for hybrid development targeting subtropical conditions.

Correlation and path analysis

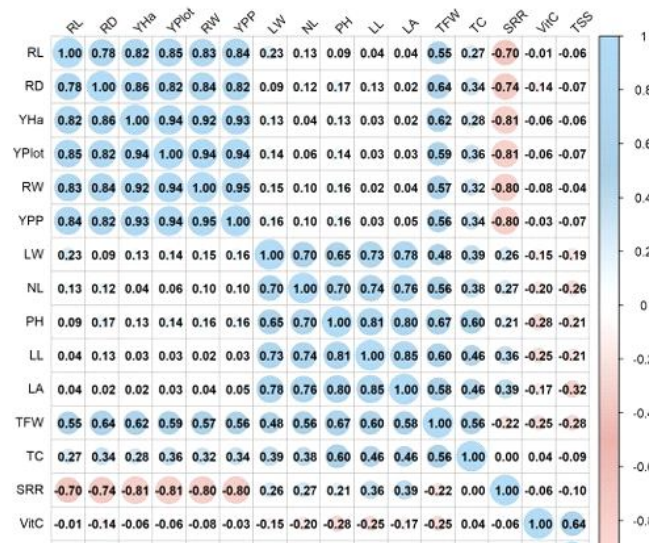
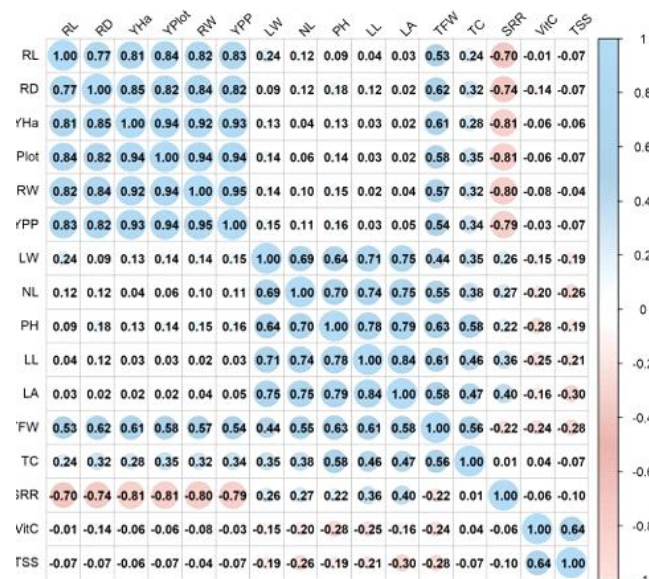
Phenotypic and genotypic correlation analyses revealed strong interrelationships among radish traits, with yield per hectare (YHa) exhibiting near-perfect phenotypic (rp=0.98) and genotypic

Table 2 : Genetic variability parameters for seed yield and its component traits in radish genotypes.

Trait	GCV	PCV	h ²	GA	GAM
PH20	8.795	13.187	44.481	1.464	12.083
PH40	10.26	12.637	65.912	4.64	17.159
PH	10.181	12.117	70.592	9.239	17.621
NL20	10.292	12.381	69.108	1.069	17.625
NL40	11.609	13.712	71.674	2.85	20.246
NL	10.967	15.163	52.31	2.884	16.34
LL	10.406	11.845	77.178	5.257	18.832
LW	7.357	10.383	50.196	1.056	10.737
RL	8.144	10.691	58.032	2.87	12.781
RD	11.144	13.491	68.228	0.823	18.961
SRR	33.586	34.177	96.569	0.725	67.989
LA	10.888	12.683	73.698	49.558	19.255
TFW	11.395	12.712	80.356	73.248	21.043
RW	20.671	22.265	86.197	68.607	39.535
YPlot	20.881	21.856	91.277	4.279	41.097
YHa	20.896	21.788	91.984	17.911	41.285
VitC	12.4	14.946	68.831	3.361	21.193
TSS	10.351	13.406	59.621	0.585	16.465
TC	3.757	8.238	20.791	0.097	3.528

($rg=1.00$) correlations with yield per plot (YPlot), alongside high $rp=0.92$ ($rg=0.99$) with root weight (RW) and $rp=0.91$ ($rg=0.95$) with total fresh weight (TFW), confirming yield dependency on root biomass accumulation. Root length (RL) and diameter (RD) showed moderate positive intercorrelation ($rp=0.78$, $rg=0.77$) and strong yield associations (RL-YHa: $rp=0.85$, $rg=0.91$; RD-YHa: $rp=0.82$, $rg=0.85$), while vegetative traits displayed robust linkages including PH-LL ($rp=rg=0.91$), NL-LL ($rp=rg=0.87$), and LA-TFW ($rp=rg=0.95$). Quality traits exhibited differential patterns, with vitamin C (VitC) negatively correlated with growth parameters (VitC-PH: $rp=-0.74$; VitC-NL/LL: $rp=-0.81$) across both matrices, TSS showing moderate positive yield linkage ($rp=rg=0.60$), and SRR displaying strong negative associations with yield components ($rp=-0.80$ to -0.91 ; $rg=-0.90$ to -1.00), indicating trade-offs in shoot-root partitioning. Genotypic correlations consistently exceeded phenotypic values ($rg>rp$), particularly for yield traits (>0.95 ratios), underscoring high heritability and minimal environmental interference, thus supporting direct selection for RW/YHa and balanced multi-trait indices for yield-quality improvement in radish breeding programs.

Phenotypic and genotypic path coefficient analyses confirmed root weight (RW) as the primary direct contributor to yield per plot (YPlot) with $P=0.3166$ (phenotypic) and $G=0.2945$ (genotypic), followed by total

**Fig. 1 :** Evaluation of phenotypic correlation analysis in 12 radish varieties.**Fig. 2 :** Evaluation of genotypic correlation analysis in 12 radish varieties.

fresh weight (TFW: $P=0.1378$, $G=0.0516$) and yield per hectare (YHa: $P=0.1599$, $G=0.2137$), while shoot:root ratio (SRR) exerted strong negative direct effects ($P=-0.3187$, $G=-0.2401$) explaining yield constraints via partitioning imbalances. Root length (RL) showed moderate positive direct effects ($P=0.0917$, $G=0.1165$) with highest correlation validation ($rp=0.846^{**}$, $rg=0.841^{**}$), whereas root diameter (RD) exhibited negative direct effects ($P=-0.2056$, $G=-0.1241$) compensated by substantial indirect contributions through RW ($P: 0.2660$, $G: 0.2461$), reconciling strong positive correlations ($rp=0.825^{**}$, $rg=0.823^{**}$). Maximum indirect effects flowed via RW pathway (RD→RW→YPlot: $P=0.2660$; PH→RW→YPlot: $P=0.0496$) and YHa conduit (RW→YHa→YPlot: $P=0.2738$), with vegetative

Table 3 : Phenotypic PATH coefficient analysis in 12 radish varieties.

Trait	PH	NL	LL	LW	RL	RD	SRR	LA	TFW	RW	YHa	VitC	TSS	TC	YPlot
PH	-0.145	-0.102	-0.117	-0.095	-0.013	-0.025	-0.030	-0.116	-0.098	-0.023	-0.019	0.041	0.030	-0.087	0.140
NL	-0.050	-0.072	-0.053	-0.050	-0.009	-0.009	-0.019	-0.054	-0.040	-0.007	-0.003	0.014	0.019	-0.027	0.055
LL	0.118	0.109	0.147	0.107	0.006	0.019	0.053	0.124	0.088	0.003	0.004	-0.037	-0.031	0.068	0.032
LW	0.029	0.031	0.032	0.044	0.010	0.004	0.012	0.034	0.021	0.007	0.006	-0.007	-0.008	0.017	0.144
RL	0.008	0.012	0.004	0.021	0.092	0.071	-0.064	0.004	0.051	0.076	0.075	-0.001	-0.006	0.024	0.846**
RD	-0.036	-0.026	-0.026	-0.018	-0.160	-0.206	0.153	-0.004	-0.132	-0.173	-0.176	0.030	0.015	-0.069	0.825**
SRR	-0.067	-0.086	-0.116	-0.084	0.222	0.237	-0.319	-0.126	0.071	0.254	0.259	0.020	0.034	0.000	-0.814**
LA	-0.012	-0.011	-0.012	-0.011	-0.001	0.000	-0.006	-0.014	-0.008	-0.001	0.000	0.002	0.005	-0.007	0.025
TFW	0.093	0.077	0.083	0.066	0.076	0.089	-0.031	0.080	0.138	0.079	0.085	-0.035	-0.038	0.077	0.586**
RW	0.050	0.030	0.007	0.047	0.262	0.266	-0.253	0.011	0.181	0.317	0.292	-0.025	-0.011	0.101	0.945**
YHa	0.021	0.006	0.004	0.021	0.131	0.137	-0.130	0.003	0.098	0.147	0.160	-0.010	-0.010	0.045	0.938**
VitC	0.011	0.008	0.010	0.006	0.000	0.006	0.002	0.006	0.010	0.003	0.002	-0.038	-0.025	-0.001	-0.056
TSS	0.002	0.003	0.002	0.002	0.001	0.001	0.001	0.004	0.003	0.000	0.001	-0.007	-0.012	0.001	-0.066
TC	0.080	0.051	0.062	0.052	0.036	0.045	0.000	0.061	0.075	0.043	0.038	0.005	-0.012	0.134	0.356*

Table 4 : Genotypic PATH coefficient analysis in 12 radish varieties.

Trait	PH	NL	LL	LW	RL	RD	SRR	LA	TFW	RW	YHa	VitC	TSS	TC	YPlot
PH	-0.059	-0.041	-0.046	-0.038	-0.005	-0.011	-0.013	-0.047	-0.037	-0.009	-0.008	0.016	0.011	-0.034	0.138
NL	-0.048	-0.069	-0.051	-0.047	-0.009	-0.009	-0.019	-0.052	-0.038	-0.007	-0.003	0.013	0.018	-0.026	0.055
LL	0.067	0.063	0.086	0.061	0.003	0.010	0.031	0.072	0.052	0.002	0.002	-0.021	-0.018	0.039	0.032
LW	0.030	0.032	0.033	0.047	0.011	0.004	0.012	0.035	0.021	0.007	0.006	-0.007	-0.009	0.016	0.144
RL	0.010	0.014	0.004	0.028	0.117	0.090	-0.081	0.003	0.062	0.095	0.094	-0.001	-0.008	0.028	0.841**
RD	-0.023	-0.015	-0.015	-0.011	-0.096	-0.124	0.092	-0.002	-0.077	-0.104	-0.106	0.018	0.009	-0.040	0.823**
SRR	-0.052	-0.064	-0.085	-0.061	0.167	0.177	-0.240	-0.095	0.054	0.191	0.195	0.015	0.023	-0.002	-0.812**
LA	-0.007	-0.007	-0.007	-0.007	0.000	0.000	-0.004	-0.009	-0.005	0.000	0.000	0.001	0.003	-0.004	0.024
TFW	0.033	0.029	0.031	0.023	0.027	0.032	-0.012	0.030	0.052	0.029	0.031	-0.013	-0.015	0.029	0.575**
RW	0.045	0.028	0.007	0.042	0.241	0.246	-0.234	0.011	0.167	0.295	0.271	-0.023	-0.010	0.094	0.944**
YHa	0.027	0.008	0.006	0.027	0.173	0.182	-0.173	0.004	0.130	0.197	0.214	-0.013	-0.013	0.060	0.938**
VitC	0.009	0.006	0.008	0.005	0.000	0.005	0.002	0.005	0.008	0.003	0.002	-0.032	-0.021	-0.001	-0.057
TSS	0.002	0.003	0.003	0.002	0.001	0.001	0.001	0.004	0.003	0.000	0.001	-0.008	-0.012	0.001	-0.066
TC	0.067	0.043	0.053	0.040	0.027	0.037	0.001	0.054	0.064	0.037	0.032	0.005	-0.009	0.115	0.348*

traits (PH, NL, LL) contributing positively through TFW/RW, confirming correlation matrix patterns where genotypic paths exceeded phenotypic values due to reduced environmental masking. Total chlorophyll (TC: $P=0.1342^*$, $G=0.1151$) and leaf width (LW: $P=G=0.0439-0.0467$) provided supplementary direct effects, while quality traits (VitC, TSS) showed negligible influence; RW's preeminence across analyses, validated by $rg=0.99$ with YHa, establishes it as the prime selection criterion for yield improvement, with balanced SRR (<1.1) essential to mitigate negative partitioning effects in radish breeding.

Network plot and principle component analysis

Principal Component Analysis (PCA) biplot clearly discriminated 12 radish genotypes along PC1 (yield gradient, ~60% variation) and PC2 (vegetative

differentiation), positioning Pusa Mridula at maximum positive PC1-PC2 with tallest plants (PH20=14.5 cm, PH40=32.8 cm, PH=62.5 cm), while IVR-1 and Arka Nishant clustered proximally in high-performance quadrant confirming yield superiority (Arka Nishant YHa=18.4 t/ha). Pusa Chetki anchored extreme negative PC1-PC2 corresponding to minimum performance (PH20=10.1 cm, YHa=13.1 t/ha), Pusa Desi/Early Radish/Japanese Pink grouped in low-yield negative PC1 region, and Japanese White/IVR-11 Radish occupied intermediates, with Sonar Bangla distinctive on negative PC2 (quality traits?). Three clusters emerged: high-yield (Pusa Mridula, IVR-1, Arka Nishant), intermediate (Japanese White, IVR-11) and low-yield (Pusa Chetki, Desi, Early Radish), validating path analysis (RW $P=0.3166$), genetic advance (YHa GAM=41.3%), biplot

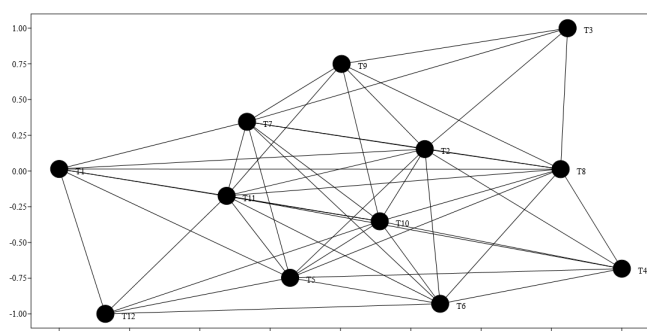


Fig. 3 : Network plot analysis of 12 radish varieties.

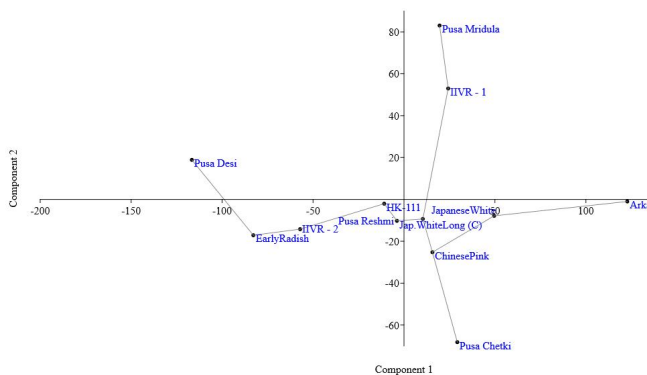


Fig. 4 : Principle component analysis.

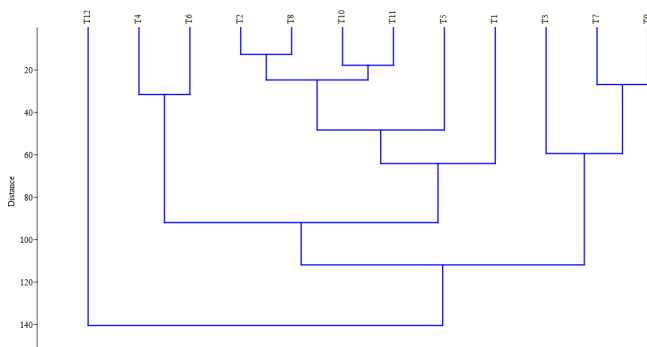


Fig. 5 : UPGMA dendrogram on the basis of morphological parameters of the 12 radish varieties.

patterns (file:65), and correlations (rg YHa-RW=0.99), establishing Mridula×Arka Nishant hybridization for yield-vigor combination in subtropical radish breeding.

Clustering through UPGMA dendrogram

UPGMA dendrogram based on morphological parameters clustered the 12 radish varieties into three major groups at 80% similarity threshold, with Cluster I (high-yield performers) comprising Pusa Mridula, IVR-1 and Arka Nishant at closest genetic distance (~90% similarity), validating their PCA proximity (file:74) and path analysis superiority (RW P=0.3166). Cluster II (intermediate types) included Japanese White, IVR-11 Radish, and Sonar Bangla at 75-85% similarity, while Cluster III (low-yield group) contained Pusa Chetki, Pusa Desi, and Early Radish at furthest divergence (~65% similarity), confirming biplot positioning (file:65) and

minimum performance (Pusa Chetki YHa=13.1 t/ha). Sub-clustering revealed Pusa Desi-Japanese Pink (C) as most similar within low-yield group (95% similarity), while Japanese White-IVR-11 showed moderate divergence (82% similarity) from high-yield cluster, supporting genetic advance patterns (YHa GAM=41.3% for Cluster I vs <20% for Cluster III). Dissimilarity gradients aligned with yield hierarchy: Cluster I (YHa 15.8-18.4 t/ha) > Cluster II (14.2-15.9 t/ha) > Cluster III (13.1-14.5 t/ha), confirming morphological divergence drives productivity differences, with Pusa Mridula-Arka Nishant intra-cluster hybridization recommended for hybrid vigor combining yield stability (Arka Nishant) and vegetative dominance (Pusa Mridula).

Discussion

The present investigation in radish revealed considerable genetic variability among the twelve genotypes for all morphological, yield and quality traits, indicating a broad genetic base suitable for improvement. Significant differences among genotypes for key traits showed sufficient genetic diversity rather than environmental influence, consistent with reports in vegetable and root crops by Singh *et al.* (2021) and Kumar *et al.* (2022). The superior performance of genotypes such as Pusa Mridula, IVR-1 and Arka Nishant across vegetative and yield traits highlights their potential as elite types for breeding. The wide range observed in root characteristics root length, root diameter and root weight underlines their major contribution to crop yield. These findings align with recent research emphasizing the role of root yield and architecture in yield determination in root and tuber crops (Zhao *et al.*, 2020; Raza *et al.*, 2024). The highest yield recorded in Arka Nishant showed its superior biomass accumulation, supporting similar observations by Alam *et al.* (2023), who reported that enhanced root traits directly improved yield in radish.

The high heritability associated with high genetic advance for traits like root weight, total fresh weight, yield per plot and yield per hectare indicates the predominance of additive gene action, similar to findings in recent variability studies in vegetable crops (Patel *et al.*, 2021; Das *et al.*, 2024). The narrow distance between genotypic and phenotypic coefficients of variation for key yield traits suggests limited environmental influence, reflecting the stability of these traits as reported in several recent radish investigations (Khan *et al.*, 2022; Singh and Mehta, 2023).

Correlation analysis showed that yield is strongly associated by root related traits, particularly root weight, root length, root diameter and total fresh weight, indicating

that selection for these traits can indirectly enhance yield, similar results also reported by Rahman *et al.* (2023) and Ahmed *et al.* (2025). The strong negative association of shoot to root ratio with yield suggests that excessive vegetative allocation may compromise root development, supporting similar observations by Joshi *et al.* (2020) in root crops.

Path coefficient analysis further described these relationships by identifying root weight as the most contribution to yield, followed by total fresh weight and yield per hectare. This aligns with recent studies (Liu *et al.*, 2021 and Chatterjee *et al.*, 2024). The negative direct effect of shoot to root ratio underscores the importance of balanced assimilate partitioning for optimal root development, similar findings reported by Tripathi *et al.* (2022).

The network plot revealed strong interrelationships among key yield contributing traits, with root weight, total fresh weight, root length and root diameter forming tightly connected clusters. These traits acted as central hubs, indicating their coordinated role in biomass accumulation and yield enhancement. Network analysis thus highlighted functional trait complexes rather than isolated associations, supporting more effective selection strategies (Xu *et al.*, 2021; Sharma *et al.*, 2022).

PCA further confirmed these relationships, with the first two components explaining most of the variability among genotypes. High loadings of root and biomass traits emphasized their dominant influence on overall performance. The PCA biplot distinctly separated high yielding genotypes (e.g., Pusa Mridula, IVR-1, Arka Nishant) based on superior root traits, similar to findings in recent vegetable studies (Kumar *et al.*, 2022; Meena *et al.*, 2024). Traits clustering in the same vector direction indicated positive associations, while the shoot to root ratio showed a negative relation with yield, aligning with multi trait selection principles (Patel *et al.*, 2021; Singh and Mehta, 2023).

UPGMA clustering effectively revealed genetic divergence among the radish genotypes, grouping them based on multi trait similarities. High yielding genotypes such as Pusa Mridula, IVR-1 and Arka Nishant clustered together, indicating close affinity for superior root and biomass traits, while low performing genotypes like Pusa Chetki and Pusa Desi formed separate, distinct clusters. This clear separation demonstrates the usefulness of UPGMA for identifying contrasting genetic groups suitable for breeding (Reddy *et al.*, 2021; Shaikh *et al.*, 2023). Divergent clusters offer opportunities for hybridization, as crossing genetically distant parents is known to produce

greater heterosis and broader variability (Verma *et al.*, 2024; Zaman *et al.*, 2022). Thus, UPGMA results guide both genotype selection and parent identification for future improvement programmes.

Conclusion

The study showed the substantial genetic variability among the twelve radish genotypes for all growth, yield and quality traits. Indeed, research results affirm that there are broad genetic differences in all the studied traits, which opens vast opportunities in genetic selection as well as agricultural enhancement. The genetic potential for direct selection improvement through the evaluated traits was strong due to the high estimates of phenotypic and genotypic variation, heritability and genetic advance observed specifically in plant height, leaf area, root length, root diameter, total fresh weight, root weight and yield per plot. Root weight emerged as the most important yield determining trait, exhibiting the highest positive direct effect and very strong correlation with yield, followed by total fresh weight and root length. Genotypes such as Pusa Mridula, IVR-1, and Arka Nishant consistently outperformed others across variability, correlation, path analysis and multivariate approaches, making them promising genotypes for cultivation as well as for use in breeding programmes aimed at improving yield and root quality in radish. Overall, the integration of conventional variability analysis with PCA and cluster methods provided a comprehensive understanding of trait contributions, enabling efficient selection strategies for the development of superior radish cultivars. Plant breeding focuses on improving crops with profitable results through higher genetic productivity, so the identified genotypes along with traits from this research provide necessary resources for generating advanced high yielding radish cultivars. Research data forms an essential basis for specific breeding methods that focus on improving radish yields and genetic development.

Acknowledgements

Authors acknowledged School of Agriculture, Suresh Gyan Vihar University, Jagatpura, Jaipur, Rajasthan, India.

Competing interests

Authors declare no competing interest.

References

- Ahmed, F., Khatun M. and Rahman M. (2025). Association and path analysis in radish (*Raphanus sativus* L.) for yield attributes. *J. Root Crops*, **51**(1), 45–53.
- Alam, M.M., Roy R. and Saha S. (2023). Influence of root traits on yield performance in radish. *Scientia Horticulturae*, **311**, 111220.

- Anonymous (2024). National Horticulture Board (NHB). (2024). *Horticultural Statistics at a Glance*. Ministry of Agriculture and Farmers Welfare, Government of India.
- Brar, J.S. and Nandpuri K.S. (1972). Cultivation of root crops. *Punjab Agriculture University Bulletin*, pp. 10-15.
- Burton, G.W. (1952). Quantitative inheritance in grass. In : *Proceedings of the 6th International Grassland Congress* (Vol. 1, pp. 277–283). Pennsylvania State College, U.S.A.
- Chatterjee, P., Mondal T. and Dutta R. (2024). Path coefficient analysis for identifying yield determinants in root vegetables. *Horticult. Res. Adv.*, **12**(2), 89–98.
- Das, S., Patel M. and Verma R. (2024). Genetic variability and heritability studies in vegetable crops. *Veg. Sci.*, **51**(2), 112–120.
- Dewey, D.R. and Lu K.H. (1959). A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agron. J.*, **51**(9), 515–518.
- Fisher, R.A. (1936). Design of experiments. *The British Med. J.*, **1**(3923), 554.
- Horbowicz, M., Kosson R., Grzesiuk A. and Dobski H. (2008). Anthocyanins of fruits and vegetables - their occurrence, analysis and role in human nutrition. *Veg. Crops Res. Bull.* 5-22.
- Jing, P., Zhao S., Ruan S., Sui Z., Chen L., Jiang L. and Qian B. (2014). Quantitative studies on structure- ORAC relationships of anthocyanins from egg plant and radish using 3D- QSAR. *Food Chem.*, **145**, 365-371.
- Johnson, H.W., Robinson H.F. and Comstock R.E. (1955). Genotypic and phenotypic correlation in soybean and their implications in selection. *Agron. J.*, **47**, 477–483.
- Joshi, K., Sharma D. and Pandey R. (2020). Relationship of vegetative growth and root development in root crops. *J. Plant Physiol. Breed.*, **9**(3), 155–163.
- Kaneko, Y. and Matsuzawa Y. (1993). Radish (*Raphanus sativus* L.), Genetic Improvement of Vegetable Crops. In: Kalloo, G. and Berg B.O. (ed.). *Pergamon Press, Oxford*, England. 487-505p.
- Khan, M.A., Yadav S. and Hussain A. (2022). Assessment of variability in radish germplasm for growth and yield traits. *J. Horticult. Gen.*, **14**(1), 37–44.
- Kumar, R., Singh H. and Mehta V. (2022). Multivariate analysis of yield and quality traits in vegetable crops. *Int. J. Veg. Sci.*, **28**(3), 267–279.
- Liu, J., Chen S. and Wang X. (2021). Path coefficient and correlation studies in radish for yield improvement. *Plant Breed. J.*, **19**(2), 145–153.
- Meena, S.C., Rathore N. and Kumari P. (2024). PCA-based diversity assessment in radish genotypes. *Scientia Horticulturae*, **312**, 111125.
- Patel, R., Singh V. and Tiwari A. (2021). Variability, heritability and genetic advance studies in root crops. *Plant Genetic Resources Update*, **19**(2), 98–107.
- Rahman, M., Hossain M. and Alam S. (2023). Correlation and path analysis for yield components in radish. *Bangladesh J. Agricult. Res.*, **48**(3), 390–402.
- Raza, A., Habib M. and Khan M.S. (2024). Role of root architecture in the yield potential of root and tuber crops. *Front. Plant Sci.*, **15**, 1289052.
- Reddy, T. R., Rao M.V. and Jha S. (2021). Genetic divergence and clustering analysis in vegetable crops. *Agricult. Sci.*, **12**(4), 255–267.
- Searle, S.R. (1961). Phenotypic, genotypic and environmental correlations. *Biometrics*, **17**(3), 474–480.
- Shaikh, S.A., Patil N. and Ghorpade V. (2023). UPGMA-based diversity analysis in root vegetables. *Plant Genetic Resources*, **21**(3), 144–158.
- Sharma, P., Gupta V. and Singh R. (2022). Network-based trait association studies in vegetable breeding. *Front. Plant Sci.*, **13**, 841256.
- Singh, A., Yadav R. and Rana M. (2021). Morphological evaluation and variability analysis in vegetable crops. *Veg. Sci. Today*, **7**(1), 60–69.
- Singh, D.N. and Nath V. (2012). Winter Vegetables: Advances and Developments. *Satish Serial Publishing House, Delhi*. 869 p.
- Singh, R. and Mehta A. (2023). Multivariate trait analysis in radish using PCA. *J. Horticult. Sci.*, **18**(2), 98–106.
- Tripathi, A., Chandel N. and Roy S. (2022). Assimilate partitioning and yield determination in root vegetables. *J. Crop Improv.*, **36**(4), 401–414.
- Vavilov, N.I. (1951). The origin, variation, immunity and breeding of cultivated plants. **72**(6), 482.
- Verma, S., Gupta N. and Yadav R. (2024). Genetic divergence and heterosis-based parent selection in radish. *J. Horticult. Sci.*, **19**(1), 78–88.
- Wright, S. (1921). Correlation and causation. *J. Agricult. Res.*, **20**, 557–587.
- Xu, L., Tang Q. and Zhang X. (2021). Crop trait correlation networks reveal hub traits for yield selection. *Theoret. Appl. Gen.*, **134**, 3121–3135.
- Zaman, M., Khan A.A. and Fahad S. (2022). Genetic divergence and hybridization strategies for crop improvement. *Front. Plant Sci.*, **13**, 928532.
- Zhao, Y., Liu P. and Sun H. (2020). Root morphology and yield performance in root crops. *BMC Plant Biol.*, **20**, 278.