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Variability and genetic divergence studies in red cabbage (*Brassica oleracea* var. *capitata* f. *rubra*) under North-Western Himalayas

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Abstract

This investigation was conducted at the Experimental Research Farm of the Department of Vegetable Science, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, to work out the variability and genetic divergence among twenty-eight genotypes of red cabbage. Analysis of variability revealed high phenotypic and genotypic coefficients of variation for the trait number of non-wrapper leaves, while these were moderate for net head weight, stalk length, core length, and vitamin C content. Based on genetic divergence, the genotypes were further grouped into four clusters (I-IV), among which the maximum number of genotypes were accommodated in cluster II (13 genotypes) and least in cluster IV (2 genotypes), respectively. The maximum inter-cluster distance was found between clusters I and IV (385.17), indicating the potential for hybridization between the genotypes of these clusters to produce better hybrids or recombinants in segregating populations for future breeding programs.

Keywords: Crop improvement, Genetic divergence, Heritability, Red cabbage, Variability.

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Introduction

Cultivars of *Brassica* species are well recognized as significant crops in both horticulture and agriculture globally. These plants are mostly utilized for their vegetables, oil production, fodder, green manure, and spice properties. Brassica crops include a diverse range of physiologically active substances such as enzymes, pigments, vitamins, and secondary metabolites, making them an essential part of the human diet (Manchali et al., 2012; Witzel et al., 2021). White cabbage (*Brassica oleracea* var. *capitata* f. *alba*) is majorly grown in most of countries around the world, but red cabbage (*Brassica oleracea* var. *capitata* f. *rubra*) due to its potential health benefits has become more and more significant in recent years (Wojciechowska et al., 2007; Singh, 2007; Tendaj and Sawicki, 2012). Red cabbage is an important, fancy and highly nutritive exotic vegetable crop, biennial in nature but grown as annual for its characteristic purple or red edible heads. In India, green and red cabbages are cultivated over an area of 423 thousand hectares producing around 9784 thousand tones (Anonymous, 2021a) while in Himachal Pradesh, both green and red cabbages are grown over an area of 4.66 thousand hectares with a production of 146.66 thousand tones (Anonymous, 2021b).

Cole crops exhibit significant variability, which complicates breeding operations compared to other vegetable crops. An essential aspect of improving breeding efficiency is conducting initial research on the variability and

inheritance of fundamental traits based on morphological and economic characteristics, which are influenced by genetic diversity and environmental factors (Cervenski et al., 2002; Autonova, 2009). Improvement of any crop depends on the level of genetic diversity and the transfer of traits from one generation to the next. Hence, it is necessary to separate the total variability into its inheritable and non-inheritable parts to enhance the consistency of selection. This is because phenotypic selection depends on the extent of genetic variability within the population. Estimates of variability factors such as heritability and genetic advance are crucial indications for enhancing traits in a certain genetic material through selection.

Diverse germplasm reflects genetic variability present in the crops, their landraces and wild relatives. These genetic resources are of tremendous value in order to achieve production supremacy in any crop. Furthermore, the variety in plant genetic resources offers plant breeders a wide range of possibilities to create new and enhanced cultivars that exhibit desirable qualities for both farmers and breeders (Bhandari et al., 2017). The Mahalanobis D^2 technique is a valid and often-used approach for studying genetic divergence in different genotypes. D^2 analysis is a valuable method for measuring the extent of variation between biological populations at the genotypic level and determining the proportionate impact of various factors on the overall variation within and between clusters. It is a possible method for assessing genetic differences within a population by utilizing statistical distance and multivariate measures. Genotypes are grouped into clusters using Tocher's approach as outlined by Rao (1952). Thus, the current study was undertaken to assess the extent of genetic variability and divergence to find or generate superior genotypes that can provide larger yields with desirable quality features in red cabbage.

Materials and Methods

Experimental Details

This experiment was conducted during *Rabi* 2018-19 to work out the variability and genetic divergence among twenty-eight genotypes of red cabbage, of which twenty-seven genotypes were procured from Horticultural Research International, Wellesbourne, United Kingdom and check variety (Kinner Red) from Department of Vegetable Science, Dr YS Parmar University of Horticulture and Forestry, Nauni Solan, Himachal Pradesh, India. The list of genotypes, along with their sources of availability, has been presented in Table 1. The experiment was conducted using a randomized block design with three replications in plots of 1.8 × 1.8 m in size. Seedlings that were one month old were transplanted with a spacing of 45 × 45 cm between and within rows, allowing 16 plants per plot. The suggested cultural practices from

the Package of Practices for Vegetable Crops published by the Directorate of Extension Education, UHF Nauni, Solan (Anonymous, 2014) were adhered to for promoting a healthy crop stand.

Analysis of Genetic Variability

Observations were recorded with respect to number of non-wrapper leaves, head compactness, head shape, head color, gross plant weight (kg), net head weight (kg), polar diameter (cm), equatorial diameter (cm), stalk length (cm), core length (cm) and ascorbic acid content (mg/100 g) from five randomly selected plants for each genotype and replication. The head compactness was calculated following Pearson's (1931) method, while the head shape was determined using the head shape index provided by Selvakumar (2014). Data on days to 50% marketable maturity was, however, taken on the whole plot basis, while for yield, the mean net head weight was transformed to work out yield potential at plot basis in kilograms, which was further converted to estimate yield per hectare in quintals. Ascorbic acid was quantified using a direct volumetric approach described by Sadasivam and Manickam in 1996. Analysis of variance (ANOVA) was calculated according to (Gomez and Gomez, 1984). The genotypic and phenotypic coefficients of variation were computed using the formulae provided by Burton and De-Vane in 1953. Heritability in a broad sense (h^2_{bs}) and genetic advance as a percent of the mean was calculated by the formula suggested by (Allard, 1960). Traits that differed significantly were further utilized for the estimation of the genetic parameters.

Analysis of Genetic Divergence

Genetic divergence was estimated by statistically analyzing the data on head and quality characters using Mahalanobis D^2 statistics (1936) following the method proposed by Rao in 1952. Genotypes were grouped into a number of clusters. D^2 is treated as the square of the generalized distance, according to the method described by Tocher (Rao, 1952). Finally, the statistical analysis for each observed character was conducted using MS Excel, OPSTAT (Sheoran et al., 1998), and IBM SPSS 20 software.

Results and Discussion

The analysis of variance showed considerable variation among genotypes for all horticultural parameters, thus indicating the presence of adequate amount of variability in the germplasm. The extent of variability and inheritance pattern present in the germplasm was assessed in terms of phenotypic and genotypic coefficient of variation (PCV and GCV) and heritability in a broad sense (h^2_{bs}) along with genetic advance as a percentage of the mean. According to the mean performance of genotypes (Table 2), genotype EC 890002 exhibited the earliest maturation at 124.33 days, while 24 genotypes matured earlier than the standard check,

Table 1: Details of red cabbage genotypes procured and their sources

S. No.	Genotypes	Source(s)	Head Shape	Head Color
1.	EC 889989	Horticulture Research International, Wellesbourne, UK	Round	Purple
2.	EC 889990	Horticulture Research International, Wellesbourne, UK	Round	Purple
3.	EC 889991	Horticulture Research International, Wellesbourne, UK	Conical	Purple
4.	EC 889992	Horticulture Research International, Wellesbourne, UK	Round	Dark red
5.	EC 889993	Horticulture Research International, Wellesbourne, UK	Round	Purple
6.	EC 889994	Horticulture Research International, Wellesbourne, UK	Round	Greenish purple
7.	EC 889995	Horticulture Research International, Wellesbourne, UK	Round	Dark red
8.	EC 889996	Horticulture Research International, Wellesbourne, UK	Round	Purple
9.	EC 889997	Horticulture Research International, Wellesbourne, UK	Conical	Greenish purple
10.	EC 889998	Horticulture Research International, Wellesbourne, UK	Conical	Purple
11.	EC 889999	Horticulture Research International, Wellesbourne, UK	Conical	Purple
12.	EC 890000	Horticulture Research International, Wellesbourne, UK	Round	Purple
13.	EC 890001	Horticulture Research International, Wellesbourne, UK	Conical	Purple
14.	EC 890002	Horticulture Research International, Wellesbourne, UK	Round	Dark red
15.	EC 890003	Horticulture Research International, Wellesbourne, UK	Round	Greenish purple
16.	EC 890004	Horticulture Research International, Wellesbourne, UK	Round	Purple
17.	EC 890005	Horticulture Research International, Wellesbourne, UK	Round	Greenish purple
18.	EC 890006	Horticulture Research International, Wellesbourne, UK	Round	Purple
19.	EC 890007	Horticulture Research International, Wellesbourne, UK	Round	Greenish purple
20.	EC 890008	Horticulture Research International, Wellesbourne, UK	Conical	Purple
21.	EC 890009	Horticulture Research International, Wellesbourne, UK	Conical	Purple
22.	EC 890010	Horticulture Research International, Wellesbourne, UK	Conical	Dark red
23.	EC 890011	Horticulture Research International, Wellesbourne, UK	Conical	Purple
24.	EC 890012	Horticulture Research International, Wellesbourne, UK	Conical	Greenish purple
25.	EC 890013	Horticulture Research International, Wellesbourne, UK	Conical	Purple
26.	EC 890014	Horticulture Research International, Wellesbourne, UK	Conical	Purple
27.	EC 890015	Horticulture Research International, Wellesbourne, UK	Round	Purple
28.	Kinner Red (C)	Department of Vegetable Science, UHF, Solan HP, India	Round	Purple

Kinner Red, which matured at 138.33 days. The cultivar EC 890012 took the longest time to mature (143.33 days). The yield per plot and yield per hectare were found to be higher for 13 genotypes than the check variety (10.60 kg and 261.66 q). Among all the genotypes, EC 890012 exhibited maximum yield (13.98 kg and 345.15 q), followed by EC 890011 (13.37 kg and 330.00 q) and EC 890013 (13.06 kg and 322.37 q) on per plot and per hectare basis respectively. Balkaya et al. (2005) and Cervenski et al. (2011) observed similar variations in cabbage head yields in their respective investigations. Genotype EC 890012 had superior gross and net head weights of 1092.00 and 873.67 g, respectively. In contrast, genotype EC 890013 demonstrated the highest head compactness at 52.83 g/cm³. The genotype EC 890012 had

the highest vitamin C concentration at 42.61 mg/100 g, with fifteen other genotypes showing greater vitamin C content than the check cultivar at 31.05 mg/100g. Dominguez et al. (2014) found significant variation in ascorbic acid levels within white and red cabbage in their investigation. The variability, heritability, and genetic progress were assessed and quantified as shown in Table 3. A wide range of horticultural parameters varied significantly, including gross head weight, net head weight, number of non-wrapper leaves, head compactness, yield per plot, and vitamin C content.

The coefficients of variability (phenotypic and genotypic) provided a clear indication of the level of variation present in the germplasm under study. Phenotypic coefficients

Table 2: Mean performance of red cabbage genotypes for different traits under study

S. No.	Genotypes	Days to 50% marketable maturity	Number of non-wrapper leaves	Head Compactness (g/cm³)	Gross Head Weight (g)	Net Head weight (g)	Equatorial Diameter (cm)	Polar Diameter (cm)	Stalk Length (cm)	Core Length (cm)	Yield Per Plot (kg)	Yield Per hectare (q)	Vitamin C Content (mg/100 g)
1.	EC 889989	131.33	7.80	43.73	812.33	603.00	10.49	9.73	6.64	7.96	9.65	238.22	31.81
2.	EC 889990	126.00	7.40	42.34	883.67	586.67	10.49	9.67	5.81	8.60	9.39	231.77	30.88
3.	EC 889991	132.66	8.07	31.88	866.00	571.00	8.15	9.25	5.65	6.87	9.14	225.58	28.05
4.	EC 889992	133.33	12.17	43.72	919.00	661.33	10.83	9.48	6.65	7.43	10.58	261.26	34.76
5.	EC 889993	136.66	8.00	39.49	1014.00	701.67	9.75	9.73	5.69	7.08	11.23	277.20	31.87
6.	EC 889994	130.66	8.80	42.80	913.00	610.00	9.22	9.81	4.84	8.26	9.76	240.98	28.17
7.	EC 889995	132.33	8.40	39.96	896.00	653.00	9.97	9.27	6.81	5.93	10.45	257.97	27.83
8.	EC 889996	130.00	11.30	40.42	969.33	765.33	10.86	9.10	6.81	7.51	12.25	302.35	31.93
9.	EC 889997	131.33	9.00	34.80	1074.00	731.67	8.67	9.91	5.66	8.05	11.71	289.05	31.93
10.	EC 889998	134.66	7.00	40.42	985.67	638.67	10.51	12.51	5.03	9.04	10.22	252.31	27.65
11.	EC 889999	126.33	7.07	39.35	901.00	591.33	10.11	12.43	6.97	5.73	9.46	233.61	25.62
12.	EC 890000	133.33	10.13	35.55	952.67	659.67	11.04	9.50	5.01	7.43	10.55	260.61	33.15
13.	EC 890001	131.66	7.33	40.38	838.33	606.33	10.26	12.24	5.03	8.15	9.70	239.54	29.64
14.	EC 890002	124.33	6.87	40.71	737.67	556.33	8.14	8.39	4.27	5.42	8.90	219.78	27.47
15.	EC 890003	134.66	10.77	38.38	1046.33	761.00	9.95	9.95	5.48	7.35	12.18	300.64	29.24
16.	EC 890004	133.00	9.00	45.25	917.00	600.33	11.66	9.86	8.19	6.35	9.61	237.17	31.62
17.	EC 890005	134.33	8.53	47.81	898.33	656.33	10.05	9.17	8.25	6.40	10.50	259.29	26.68
18.	EC 890006	126.66	7.80	47.03	973.67	720.00	10.64	11.43	5.19	7.89	11.52	284.44	27.10
19.	EC 890007	137.33	13.00	49.19	1020.67	751.00	10.65	9.67	5.49	6.72	12.02	296.69	34.22
20.	EC 890008	139.33	7.80	41.81	920.67	752.67	8.56	10.93	7.07	7.36	12.04	297.35	32.20
21.	EC 890009	127.66	7.80	45.97	871.33	591.67	8.27	10.61	5.50	6.31	9.47	233.74	26.60
22.	EC 890010	134.33	10.53	40.26	1011.00	794.33	8.21	9.20	4.35	8.00	12.71	313.81	33.00
23.	EC 890011	136.33	8.40	47.79	1056.67	835.33	8.61	10.86	5.11	8.57	13.37	330.00	32.65
24.	EC 890012	143.33	13.83	43.14	1092.00	873.67	11.83	12.60	8.38	9.40	13.98	345.15	42.61
25.	EC 890013	128.66	10.50	52.83	953.67	816.00	8.43	10.90	5.03	7.77	13.06	322.37	33.41
26.	EC 890014	139.33	7.73	44.21	854.67	691.00	8.71	10.27	4.91	9.00	11.06	272.98	33.55
27.	EC 890015	135.00	8.07	44.49	998.33	777.67	10.15	9.05	5.34	8.37	12.44	307.22	32.24
28.	Kinner Red (Check)	138.33	8.47	47.65	880.00	662.33	10.84	11.10	6.45	8.02	10.60	261.66	31.05
	CD (0.05)	1.64	1.08	6.44	142.37	155.11	1.85	1.74	0.21	0.60	2.48	61.27	2.49
	CV (%)	8.75	8.37	9.29	9.24	13.76	11.48	10.40	7.25	7.48	13.76	13.76	6.90

Table 3: Estimates of phenotypic and genotypic coefficients of variability, heritability and genetic advance as per cent of mean for various characters

S. No.	Characters	Range	Mean	PCV (%)	GCV (%)	h^2_{bs} (%)	GA
1.	Days to 50% marketable maturity	124.33-143.33	133.66	3.57	3.50	95.64	37.04
2.	Number of non-wrapper leaves	6.87-13.83	8.98	21.48	20.18	88.23	39.04
3.	Head compactness	31.88-52.83	42.55	13.16	9.39	50.84	23.79
4.	Gross head weight	737.67-1092.00	937.75	11.71	7.17	47.54	29.06
5.	Net head weight	556.33-873.67	686.40	17.11	10.05	44.77	22.21
6.	Equatorial diameter	8.14-11.83	9.82	14.76	9.27	39.45	
7.	Polar diameter	8.39-12.60	10.24	14.15	9.58	45.88	13.37
8.	Stalk length	4.27-8.38	5.91	19.28	19.15	98.64	39.18
9.	Core length	5.42-9.40	7.54	13.82	13.59	96.77	27.55
10.	Yield per plot	8.90-13.98	10.98	17.92	12.76	50.73	22.83
11.	Vitamin C content	25.62-42.61	30.96	11.93	10.88	83.11	20.43

PCV: Phenotypic coefficient of variability; GCV: Genotypic coefficient of variability
h^2_{bs}: Heritability in broad sense; GA: Genetic advance as percentage of mean

of variability were greater in magnitude than genotypic coefficients of variability for all the traits examined. Small discrepancies between PCV and GCV were seen for most traits except for gross and net head weights, head compactness, polar and equatorial diameters, and yield per plot, suggesting that these features were less affected by environmental factors. The PCV and GCV were high for the number of non-wrapper leaves (21.48 and 20.18), moderate for stalk length (19.28 and 19.15), net head weight (17.11 and 10.05), core length (13.82 and 13.59), yield per plot (17.92 and 12.76), and vitamin C content (11.93 and 10.88). They were found to be low for days to 50% marketable maturity (3.57 and 3.50). All the traits that exhibited high to moderate genetic coefficient of variation (GCV) had significant variability and, thus, offered a good possibility for improvement in red cabbage via diverse breeding methods.

Calculating the heritability and genetic advance as a percentage of the mean allows one to infer the heritable portion of the variance. When heritability is high (>60%), it means that a significant amount of the variation in attributes is due to genetic differences, allowing for accurate selection based on observable characteristics. The heritability in a broad sense (h^2_{bs}) for all the studied traits varied from 39.45 to 98.64 percent. Stalk length had the highest heritability estimate at 98.64%, followed by core length at 96.77%, days to 50% marketable maturity at 95.64%, number of non-wrappers leaves at 88.23%, and vitamin C content at 83.11%. These results are in consonance with the findings of Singh et al. (2011), who revealed high heritability in a broad sense for the core size and stalk length, Sharma (2010) and Soni et al. (2013) for days to 50% marketable maturity, and Singh et al. (2013) for the number of non-wrappers

leaves in cabbage in their corresponding studies. Moderate heritability (30–60%) was observed for head compactness at 50.84%, yield per plot at 50.73%, gross head weight at 47.54%, a polar diameter of the head at 45.88%, net head weight at 44.77%, and equatorial diameter of the head at 39.45%. These results are in agreement with the findings of Atter et al. (2009) and Thakur and Vidyasagar (2016) in cabbage, who reported high estimates of heritability for net head weight, gross head weight and marketable yield per plot in their respective studies; however, in the present study, it ranged from medium to high.

Genetic advance provides a decent approximation of the actual gain that will occur in the population being assessed. For the purpose of estimating the actual effects of selection, heritability on its own is not adequate; rather, genetic advance in conjunction with heritability is more informative (Johnson et al., 1955). The genetic advance as a percentage of the mean ranged from 11.99 to 39.18%. High estimates of genetic advance, over >30% of the average value, were observed for stalk length (39.18%), a number of non-wrapper leaves (39.04%) and days to 50% marketable maturity (37.04%). Moderate estimates for genetic advance (10-30%) were found in gross head weight (29.06%), core length (27.55%), head compactness (23.79%), yield per plot (22.83%), net head weight (22.21%), vitamin C content (20.43%), polar and (13.37%) and equatorial diameter of heads (11.99%), respectively. These results were in consonance with the findings of Chura et al. (2016) who also recorded high genetic advance for stalk length and number of non-wrapper leaves in cabbage.

Genetic diversity is crucial for the success of any breeding program. It is crucial for assessing the overall genetic

distance between the chosen genotypes acting as parents. Evaluating genetic diversity in germplasms is essential for plant breeders to select potential parental lines due to two main reasons: (i) Genetically diverse parents in hybridization programs are more likely to yield a high heterotic effect, and (ii) Parents that are genetically distant can lead to a broad range of variability in the segregating generations. Table 4 displays the clustering pattern of twenty-eight red cabbage genotypes based on their performance in several parameters. The genotypes were categorized into four groups labeled I-IV. Cluster II accommodated the highest number of genotypes (13), followed by cluster III (10), with cluster I and IV containing 3 and 2 genotypes, respectively. Genetic homogeneity between genotypes caused them to appear in the same cluster. Group constellation through genetic divergence has also been reported by Meena et al. (2013) in cabbage, Khan et al. (2009) in kale, Sharma and Verma (2001), Quamuruzzaman et al. (2007), Dey et al. (2010) and Santhosha et al. (2011) in cauliflower.

Average intra and inter-cluster divergence (D^2) values have been presented in Table 5. The diagonal figures in the table indicate the intra-cluster distances. The intra-cluster distance was maximum in cluster III (50.05) while it was minimum in cluster IV (27.12). The high intra-cluster distance

Table 4: Clustering pattern of 28 genotypes of red cabbage on the basis of genetic divergence

Cluster	Number of genotypes	Names of genotypes
I	3	EC 889989, EC 890001, EC 890002
II	13	EC 889990, EC 889991, EC 889992, EC 889994, EC 889995, EC 889998, EC 889999, EC 890000, EC 890004, EC 890005, EC 890009, EC 890014, Kinner Red
III	10	EC 889993, EC 889996, EC 889997, EC 890003, EC 890006, EC 890007, EC 890008, EC 890010, EC 890013, EC 890015
IV	2	EC 890011, EC 890012

Table 5: Average intra (diagonal) and inter cluster distance (D^2) among 28 genotypes of red cabbage

Cluster	I	II	III	IV
I	45.01	114.22	263.21	385.17
II		47.12	159.88	283.70
III			50.05	123.98
IV				27.12

Table 6: Cluster means for different characters among 28 genotypes of red cabbage

S. No.	Characters	Clusters			
		I	II	III	IV
1.	Days to 50 per cent marketable maturity	128.86	132.84	133.61	139.95
2.	Number of non-wrapper leaves	7.33	8.50	9.67	11.12
3	Head compactness (g/cm^3)	41.14	42.17	42.86	45.47
4.	Gross head weight (g)	796.11	902.94	998.16	1074.33
5.	Net head weight (g)	588.55	628.71	757.13	854.50
6.	Equatorial diameter of head (cm)	9.63	9.99	9.58	10.22
7.	Polar diameter of head (cm)	10.12	10.22	9.98	11.73
8.	Stalk length (cm)	5.31	6.15	5.61	6.74
9.	Core length (cm)	7.17	7.33	7.61	8.98
10.	Vitamin C content (mg/100g)	29.64	29.66	31.71	37.63

suggested that the genotypes in Cluster III are genetically diverse to a significant degree. The maximum inter-cluster distance was recorded between clusters I and IV (385.17), which indicated wide diversity between these two clusters, while the lowest (114.22) was observed between clusters I and II, indicating their close association. Different inter and intra-cluster distances have also been reported by Meena et al. (2013) in cabbage and Sharma and Singh (2018) in cauliflower using diverse genotypes in their concerned experiments.

Additionally, reliable conformity based on cluster means was estimated for numerous horticultural parameters and is displayed in Table 6. The number of days required to reach 50% marketable maturity was lowest in cluster I (128.86), followed by cluster II (132.84), cluster III (133.61), and cluster IV (139.95). The number of non-wrapper leaves sequentially increased through cluster I (7.33), cluster II (8.50) cluster III (9.67) and cluster IV (11.12). Cluster IV had the highest head compactness at 45.47, followed by cluster III at 42.86, cluster II at 42.17, and cluster I at 41.14. Cluster IV exhibited the highest gross head weight of 1074.33 g, followed by cluster III with 998.16 g, cluster II with 902.94 g, and cluster I with the lowest weight of 796.11 g. Cluster IV had the highest net head weight value of 854.50, followed by cluster III with 757.13, cluster II with 628.71, and the lowest value was in cluster I with 588.55. In cluster IV, red cabbage heads had the maximum equatorial diameter value of 10.22, followed by cluster II with 9.99 and cluster II with 9.63. The lowest value was found in cluster III at 9.58. The polar diameter of the head was ranked from highest to lowest in the following

order: cluster IV (11.73), cluster II (10.22), cluster I (10.12), and cluster III (9.98).

A comparable pattern of stalk length increase was observed between clusters: cluster I (5.31), cluster III (5.61), cluster II (6.15), and cluster IV (6.74). The longest core length was found in cluster IV (8.98 cm), followed by cluster III (7.61 cm), cluster II (7.33 cm), and cluster I (7.17 cm). Cluster IV had the highest vitamin C concentration at 37.63 mg/100 g, followed by cluster III at 31.71 mg/100 g, cluster II at 29.66 mg/100 g, and cluster I at 29.64 mg/100 g. Meena et al. (2013) recorded variable cluster means for several plant development and yield features in cabbage, whereas Sharma and Verma (2001) and Quamuruzzaman et al. (2007) reported similar findings in cauliflower.

Conclusion

This study revealed a significant amount of variability and diversity in the aforementioned genotypes of red cabbage. High phenotypic and genotypic coefficients of variability were observed in the number of non-wrapper leaves, suggesting a broad range of variations and potential for improvement by selection. High heritability and significant genetic advance were found in days to 50% marketable maturity, stalk length, and core length in red cabbage. This indicates that these traits were influenced by additive gene action, and selection for these traits directly may lead to substantial improvement in identifying superior genotypes. High heritability, along with moderate genetic advance, were reported for head compactness, net head weight, gross head weight, polar diameter, equatorial diameter of the head, and vitamin C content. Genetic divergence studies revealed that cluster II accommodated maximum genotypes (13) and cluster I and IV being more diverse, hybridization between genotypes would be more rewarding for getting superior hybrids and transgressive segregants.

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सारांश

यह अध्ययन डॉ. यशवंत सिंह परमार औद्यानिकी एवं वानिकी विश्वविद्यालय, नौणी, सोलन, हिमाचल प्रदेश के सब्ज़ी विज्ञान विभाग के अनुसंधान फार्म में लाल पत्तागोभी के अट्ठाईस (28) जीवद्रव्यों के मुल्यांकन व विविधता के बारे में किया गया था। परिवर्तनशीलता के मुल्यांकन के विश्लेषण से पता चला कि गैर-रैपर पत्तियों के फेनोटाइपिक और जीनोटाइपिक गुणांक उच्च थे लेकिन, यह शुद्ध बन्द के वजन, डंठल की लंबाई, कोर की लंबाई और विटामिन सी की मात्रा में मध्यम थे। आनुवंशिक विचलन के आधार पर अलग अलग जीवद्रव्यों को चार समूहों (I-IV) में वर्गीकृत किया गया था, जिनमें से अधिकतम जीवद्रव्य क्लस्टर II (13 जीवद्रव्य) और सबसे कम क्लस्टर IV (2 जीवद्रव्य) में पाये गये थे। क्लस्टर I और IV के बीच अधिकतम इंटरक्लस्टर दूरी (385.17) पाई गई, जो भविष्य की प्रजनन परियोजनाओं के लिए आबादी को अलग करने में बेहतर संकर किस्मों का उत्पादन करने हेतु या पुनः संयोजक उत्पन्न करने के लिए इन समूहों के जीवद्रव्यों के बीच संकरण की क्षमता को दर्शाता है।