



Studies on Genetic Divergence in Cabbage Genotypes in the Mid Hills of Solan District, Himachal Pradesh, India

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Cabbage (*Brassica oleracea* var. *capitata* L.) is one of the most important vegetables of the family Brassicaceae and is grown under temperate to tropical climatic conditions for its head in more than ninety countries throughout the world. The diversity in cabbage is immense due to the presence of variation in shape, size, weight and maturity of heads. The greater the variability in the available germplasm, more would be the chances for selecting superior genotypes for use in breeding programmes or direct use as cultivars. Twenty three genotypes of cabbage including check variety, Golden Acre were evaluated in a Randomized Complete Block Design (RCBD) with three replications. The results concluded that twenty-three diverse genotypes of cabbage were grouped into four clusters. The resultant four clusters showed genetic diversity and maximum number of genotypes were accommodated in cluster I (12) followed by II (7), IV (3) and III (1). The maximum inter cluster distance was recorded between cluster II and III, therefore, the hybridization between

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the genotypes of cluster II and III can be performed to get superior hybrids or recombinants in segregating populations for further breeding programmes. Based on the mean performance, genetic distance and clustering pattern, inter-varietal crosses can be made which may be advantageous in creating wider variability for better heterotic combinations and transgressive segregants in cabbage.

Keywords: Cabbage genotypes; genetic divergence; genetic diversity; hybrids.

1. INTRODUCTION

Cabbage (*Brassica oleracea* var. *capitata* L.) is one of the most important vegetables of the family Brassicaceae and is grown under temperate to tropical climatic conditions for its head in more than ninety countries throughout the world. Modern compact-head cabbage cultivars have descended from wild, non-heading cabbage types, originating in the eastern Mediterranean region and Asia Minor [1]. The vegetable Brassicas are consumed for its nutritional values, minerals, carotenoids, and vitamins. Cabbage is a rich source of Vitamin A, B1, B2 and C, besides being fairly rich in protein, carbohydrates and minerals, viz., phosphorus, potassium, sodium and sulphur. In addition to being nutrient-dense, cabbage provides medicinal benefits like anti-inflammatory and anticarcinogenic characteristics, since it contains chemical substances like glucosinolates, glutathione and isothiocyanates [2-4].

The diversity in cabbage is immense due to the presence of variation in shape, size, weight and maturity of heads. The greater the variability in the available germplasm, more would be the chances for selecting superior genotypes for use in breeding programmes or direct use as cultivars. Due to the high market demand for the crop, it has become necessary to develop new and promising hybrids of cabbage. Plant breeders must assess genetic diversity among germplasms while selecting possible parental lines for two reasons:

- (i) In the hybridization programme, genetically diverse parents are likely to provide a significant heterotic effect, and
- (ii) Genetically distant parents may produce a wide range of variability in the segregating generation.

2. MATERIALS AND METHODS

Twenty three genotypes of cabbage including check variety, Golden Acre were evaluated in a Randomized Complete Block Design (RCBD) with three replications. Ten plants were selected for recording the data on different observations.

The observations were recorded on plant height (cm), days to fifty per cent marketable maturity, number of non wrapper leaves, stalk length (cm), head colour, leaf margin, shape of blade, attitude of outer leaves, polar diameter of head (cm), equatorial diameter of head (cm), head shape index, head compactness (g/cm^3), core length (cm), gross head weight (g), net head weight (g), yield per plot (kg) & per hectare (q), TSS ($^{\circ}\text{B}$), ascorbic acid content (mg/100g) and anthocyanin content (mg/100g). The standard growing practices of cabbage recommended in the Package of Practices for Vegetable Crops-2020 by Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan (HP) were followed to raise a healthy crop. Many cabbage researchers (Singh, 2011) [5] have emphasised the use of Mahalanobis D^2 statistics [6] for evaluating genetic divergence since it allows accurate comparison of all potential pairs of populations in any given group effecting actual crosses. TNUSTAT software was used to process the data. List of cabbage genotypes along with their sources have been presented in Table 1.

3. RESULTS AND DISCUSSION

3.1 Composition of Clusters

The practical significance of grouping cucumber genotypes into clusters and estimating intra and inter-cluster distances among them, lies in providing an index of genetic diversity among the clusters. The grouping pattern of twenty-three cabbage genotypes has been provided in Table 2 based on the performance of various attributes. All genotypes were divided into four (I-IV) groups. Cluster I had the most genotypes (12), followed by Cluster II (7), Cluster IV (3) and Cluster III (1). The genotypes that appeared in the same cluster did so because they shared genetic homogeneity. Group constellation through genetic divergence has also been reported by Khan et al. [7] in kale, Meena et al. [5], Deep [8] and Kumari [9] in cabbage, Quamuruzzaman et al. [10], Dey et al. [11], Santhosha et al. [12] and Kumar et al. [13] in cauliflower.

Table 1. List of cabbage genotypes and their sources

Sr. No.	Genotypes	Source
1.	CB – 1	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
2.	CB – 3	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
3.	CB – 4	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
4.	CB – 5	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
5.	CB – 6	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
6.	CB – 7	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
7.	CB – 8	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
8.	CB – 9	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
9.	CB – 10	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
10.	CB – 11	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
11.	CB – 12	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
12.	CB – 13	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
13.	CB – 14	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
14.	CB – 15	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
15.	CB – 16	ICAR-IARI Regional Research Station, Katrain, Kullu, HP
16.	UHF–M–1	Dept of Vegetable Science, Dr YSPUHF – Nauni, Solan, HP
17.	UHF–M–2	Dept of Vegetable Science, Dr YSPUHF – Nauni, Solan, HP
18.	UHF–M–3	Dept of Vegetable Science, Dr YSPUHF – Nauni, Solan, HP
19.	UHF–M–4	Dept of Vegetable Science, Dr YSPUHF – Nauni, Solan, HP
20.	UHF–M–7	Dept of Vegetable Science, Dr YSPUHF – Nauni, Solan, HP
21.	UHF–M–9	Dept of Vegetable Science, Dr YSPUHF – Nauni, Solan, HP
22.	UHF-2	Dept of Vegetable Science, Dr YSPUHF – Nauni, Solan, HP
23.	Golden Acre (Check)	ICAR-IARI Regional Research Station, Katrain, Kullu, HP

Table 2. Clustering pattern of genotypes of cabbage on the basis of genetic divergence

Cluster	Number of genotypes	Name of genotypes
I	12	CB-1, CB-3, CB-4, CB-6, CB-7, CB-9, CB-10, CB-11, CB-12, CB-15, CB-16, UHF-2
II	7	CB-5, CB-9, CB-12, UHF-M-1, UHF-M-3, UHF-M-4, Golden Acre
III	1	CB-8
IV	3	CB-13, CB-14, UHF-M-2

Table 3. Average intra and inter-cluster distance among 23 genotypes of cabbage

Cluster	I	II	III	IV
I	14.16			
II	22.97	12.99		
III	23.45	36.24	0	
V	22.07	21.05	24.01	12.50

3.2 Intra and Inter-Cluster Genetic Divergence (D^2)

Table 3 displays the average intra and inter-cluster divergence (D^2) values. The intra-cluster distances are depicted by the diagonal figures in the table. Intracluster distance indicates the distance within a cluster. Cluster I had the greatest intra-cluster distance (14.16) while

Cluster IV had the lowest (12.50). The high intra-cluster distance suggested that the genotypes in cluster I were genetically diverse to a large extent. The maximum inter-cluster distance (36.24) was recorded between Cluster II and III, showing significant variability between these two clusters, while the least distance (21.05) was reported between Cluster II and IV, indicating a close association.

Table 4. Cluster means for different characters among 23 genotypes of cabbage

Sr. No.	Characters	Clusters			
		I	II	III	IV
1	Plant Height	15.86	16.42	17.50	16.83
2	Days to 50% marketable maturity	104.33	96.67	115.33	103.56
3	Number of non-wrapper leaves	16.75	15.81	26.00	18.78
4	Stalk length (cm)	7.12	8.28	6.50	7.80
5	Polar diameter (cm)	11.37	11.15	9.00	10.64
6	Equatorial diameter (cm)	10.30	10.97	8.43	10.48
7	Head Shape Index	1.11	1.02	1.07	1.02
8	Gross Head weight (g)	1031.33	1191.67	723.33	1214.44
9	Net Head weight (g)	555.60	684.29	366.67	685.56
10	Head Compactness (g/cm ³)	43.83	51.77	55.80	56.88
11	Core Length (cm)	5.74	5.35	4.33	5.62
12	TSS (°B)	6.34	6.26	7.50	6.50
13	Ascorbic Acid (mg/100 g)	15.36	28.64	12.37	27.63
14	Anthocyanin (mg/100 g)	5.47	5.05	8.29	7.49
15	Yield per plot (kg)	8.33	10.26	5.50	10.28

3.3 Mean Performance of Clusters

Furthermore, dependable conformity based on cluster means was determined for several horticultural traits and is shown in Table 4. Cluster III (17.50 cm) had the tallest plants, followed by cluster IV (16.83 cm), cluster II (16.42 cm) and cluster I (15.86 cm). Cluster II (96.67 days) had the earliest marketable maturity, followed by cluster IV (103.56 days), with a progressive delay in cluster I (104.33 days) and cluster III (115.33 days). The number of non-wrapper leaves orderly increased through cluster II (15.81), clusters I (16.75), cluster IV (18.78) and cluster III (26.00). Similarly, cluster-wise increment in stalk length was observed as; cluster III (6.50 cm), cluster I (7.12 cm), cluster IV (7.80 cm) and cluster II (8.28 cm). The highest value of polar diameter of head was recorded in cluster I (11.37 cm) followed by cluster II (11.15 cm), cluster IV (10.64 cm) and the lowest value was recorded in cluster III (9.00 cm). Highest to lowest values of equatorial diameter of head were scaled through cluster II (10.97 cm), cluster IV (10.48 cm), cluster I (10.30 cm) and cluster III (8.43 cm). Head shape index was recorded maximum in cluster I (1.11) followed by cluster III (1.07), cluster II (1.02) and cluster IV (1.02). The highest gross head weight was observed in cluster IV (1214.44 g) followed by cluster II (1191.67 g), and cluster I (1031.33 g), while lowest was observed in cluster III (723.33 g). The highest value of net head weight was depicted in Cluster IV (685.56 g) followed by Cluster II (684.29 g), cluster I (555.60 g) and cluster III (366.67). Maximum head compactness was observed in cluster IV (56.88 g/cm³) followed by

cluster III (55.80 g/cm³), cluster II (51.77 g/cm³) and cluster I (43.83 g/cm³). The smallest core length was observed in cluster III (4.33 cm) followed by cluster II (5.35 cm), cluster IV (5.62 cm) and cluster I (5.74 cm). The highest total soluble solids were estimated in the order viz., cluster III (7.50 °B), cluster IV (6.50 °B), cluster I (6.34°B) and cluster II (6.26 °B). Maximum ascorbic acid content was observed in cluster II (28.64 mg/100 g) followed by cluster IV (27.63 mg/100 g), cluster I (15.36 mg/100 g) and cluster III (12.37 mg/100 g). The maximum anthocyanin content was recorded in cluster III (8.29 mg/100g) followed by cluster IV (7.49 mg/100 g), cluster I (5.47 mg/100 g) and cluster II (5.05 mg/100 g). Cluster IV (10.28 kg) recorded the highest yield per plot, followed by cluster II (10.26 kg), cluster I (8.33 kg) and cluster III (5.50 kg).

4. CONCLUSION

In the present study, based on genetic divergence, twenty-three diverse genotypes of cabbage were grouped into four clusters. The resultant four clusters showed genetic diversity and maximum number of genotypes were accommodated in cluster I (12) followed by II (7), IV (3) and III (1). The maximum inter cluster distance was recorded between cluster II and III, therefore, the hybridization between the genotypes of cluster II and III can be performed to get superior hybrids or recombinants in segregating populations for further breeding programmes. Based on the mean performance, genetic distance and clustering pattern, inter-varietal crosses can be made which may be advantageous in creating wider variability for

better heterotic combinations and transgressive segregants in cabbage.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

We hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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