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# Genetic diversity for curd yield and its attributes in late cauliflower

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## ABSTRACT

**Genetic diversity was studied in 26 genotypes of late group of cauliflower during winter 2018-19 and 2019-20. Based on mean performance, DPCaCMS-1 produced significantly high marketable curd weight, 27.38% better than the best check. D2 analysis clustered the genotypes in seven clusters, with the maximum in Cluster I. Genotypes from clusters V and VI with higher inter-cluster genetic divergence would be a valuable source of genes for improvement. Cluster IV represented maximum mean values for marketable curd weight. The maximum contribution towards genetic diversity was made by days to curd initiation followed by leaves/plant and curd diameter. Principal component analysis indicated the five most informative principal components with more than one eigen value, accounting for 83.59% of the total variance for all traits. The genotypes, namely, DPCafW3, DPCaf US, DPCaCMS-1, DPCaCMS-2, DPCaf-1, DPCaCMS-3, DPCaf30, DPCaf13, and DPCafS5-1 seem to be the promising potential genotypes that can be involved in hybridization programmes to identify transgressive segregants with desirable attributes.**

**Keywords:** *Brassica oleracea* L. var. *botrytis*, Genetic diversity, PCA, Variability, Transgressive segregants.

## INTRODUCTION

Cauliflower (*Brassica oleracea* L. var*. botrytis*), having chromosome number 2*n* = 2*x* = 18, is cultivated in many countries across the globe and is recognized as a potential vegetable crop based on its nutritive value along with its importance in the processing industry. Vegetable brassicas are rich in different phytochemicals and bioactive compounds. It is cultivated over 1417.80 thousand ha worldwide with a total production of 26504.00 thousand metric tonnes and an average productivity of 18.69 metric tonnes ha-1 (FAO, 1). India's global rank is second in area and production after China, with a share of 32 per cent in the area and 36 per cent in production (Sharma *et al.,* 10). The preliminary and economic input for enhanced crop productivity is the continuous availability of high-yielding varieties with wider adaptability, which can be evolved through a well-planned breeding programme. To achieve this goal, the maximization of genetic diversity is a significant and essential component that can be utilized to detect superior alleles regulating substantial yield and quality attributes (Sharma *et al.,* 7). A thorough understanding of levels and patterns of genetic variability would be a paying proposition in breeding to identify diverse genotypes as parental lines to be involved in hybridization to produce transgressives with a broad genetic base and introgression of target genes from diverse germplasm into the prevailing genetic pool (Thompson and Nelson, 12). The hybridization programme should be framed by selecting superior parents based on the complete genetic information of potential parents. Emphasis must be given to exploiting the genetically diverge parents in the breeding programme to increase the marketable curd yield in cauliflower. The present study was conducted to study multivariate analysis, using Mahalanobis's D2, to identify diverse parents involved in the breeding programme for obtaining desirable transgressive segregants.

## MATERIALS AND METHODS

The experiment was conducted for two consecutive years, during the winter season of 2018-19 and 2019-20, at the Vegetable Research Farm, Department of Vegetable Science and Floriculture, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, Himachal Pradesh. The farm is located at an elevation of 1290.8 m above mean sea level with 32º 6' N latitude and 76º 3' E longitude. The experimental material comprised 26 cauliflower genotypes (Table 1). The experiment was laid out in randomized complete block design (RBD), replicated thrice at a spacing of 45 cm × 45 cm on 12th October 2018 and 16th October 2019. The recommended cultural practices were applied to raise the crop. The farmyard manure was applied @ 20 tonnes/ha along with synthetic fertilisers at the recommended rates of 125:75:50 kg of N: P2O5: K2O /ha through urea, single super phosphate, and

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**Table 1.** List of cauliflower genotypes

| S. No. | Genotypes | Source | S. No. | Genotypes | Source |
|---|---|---|---|---|---|
| 1. | DPCa CMS 1 | Department of Vegetable Science & Floriculture, COA, CSKHPKV, Palampur | 14. | DPCaf 12 | Department of Vegetable Science & Floriculture, COA, CSKHPKV, Palampur |
| 2. | DPCa CMS 2 | -do- | 15. | DPCaf 13 | -do- |
| 3. | DPCa CMS 3 | -do- | 16. | DPCaf 18 | -do- |
| 4. | DPCaf 8 | -do- | 17. | DPCaf 24 | -do- |
| 5. | DPCaf 10 | -do- | 18. | DPCaf 29 | -do- |
| 6. | DPCaf 1 | -do- | 19. | DPCaf 30 | -do- |
| 7. | DPCaf 2 | -do- | 20. | DPCaf 35 | -do- |
| 8. | DPCaf W3 | -do- | 21. | Pusa Paushja | IARI, New Delhi |
| 9. | DPCaf US | -do- | 22. | Pusa Himjyoti | IARI Regional Station, Katrain, Kullu, HP |
| 10. | DPCaf S5-1 | -do- | 23. | Pusa Snowball KT-25 | -do- |
| 11. | DPCaY 1 | -do- | 24. | Pusa Snowball-1 | -do- |
| 12. | DPCaY 7 | -do- | 25. | Pusa Snowball K-1 (Check) | -do- |
| 13. | DPCaf 9 | -do- | 26. | Palam Uphar (Check) | Department of Vegetable Science & Floriculture, COA, CSKHPKV, Palampur |

muriate of potash, respectively. The full dose of P, ⅓N, and ½K was applied at planting time, ⅓N after one month as a split application, and the remaining ⅓N and ½K at the curd initiation stage. Observations were recorded for marketable curd weight (g) along with 18 related traits, *viz*., days to curd initiation, days to marketable curd maturity, stalk length (cm), leaves/plant, leaf length (cm), leaf width (cm), plant height (cm), plant frame (cm), curd depth (cm), curd diameter (cm), curd angle (°), curd size index ($cm^2$), curd solidity (g/cm), gross plant weight (g), net curd weight (g), marketable curds (%), total soluble solids (°Brix) and harvest index (%).

Statistical analysis of pooled data was subjected to Mahalanobis's generalized distance (D2) to determine the extent of divergence, and the grouping of genotypes was generated using Tocher's method described by Rao (5). In addition, Wilk's criterion was followed to test the significance of the difference in mean values for 19 traits. Finally, XLSTAT software was used for principal component analysis (PCA) to determine the appropriate associations among different attributes.

## RESULTS AND DISCUSSION

The success of any breeding programme depends upon the final product, *i.e.,* marketable yield, and therefore, is the primary objective taken into consideration by the breeders. The detailed evaluation of twenty-six genotypes (Fig. 1) revealed a wide range of variation for marketable curd weight ranging from 480.75 g (DPCaf 9) to 865.90 g (DPCaCMS 1). DPCaCMS 1 produced the highest marketable curd weight, with an increase of 27.38% over best check Palam Uphar. Shree *et al.* (11) have also observed variable mean performance of different genotypes for marketable curd weight.

Twenty-six genotypes were categorized into seven clusters (Table 2) using Tocher's method (Rao, 5), which is also represented through a dendrogram (Fig. 2). Cluster I contained the maximum number of genotypes (20), while the remaining clusters were mono genotypic and thus more diverged than Cluster I. The genotypes of identical geographical distribution were clustered into different groups, indicating that genetic and geographical diversity are not always associated (Dey *et al.,* 3; Santonsha *et al.,* 6; Kumar *et al.,* 4; Chauhan and Sharma*,* 2). Cluster I observed an intra-cluster distance of 1.85, whereas the rest were mono-genotypic with zero intra-cluster values (Table 3). Other authors also observed similar intra-cluster variations in their respective materials (Dey *et al.,* 3; Santhosha *et al.,* 6 Chauhan and Sharma*,* 2). Hybridization between the genotypes within a cluster would not provide variable populations. Hence, the involvement of genotypes based on their

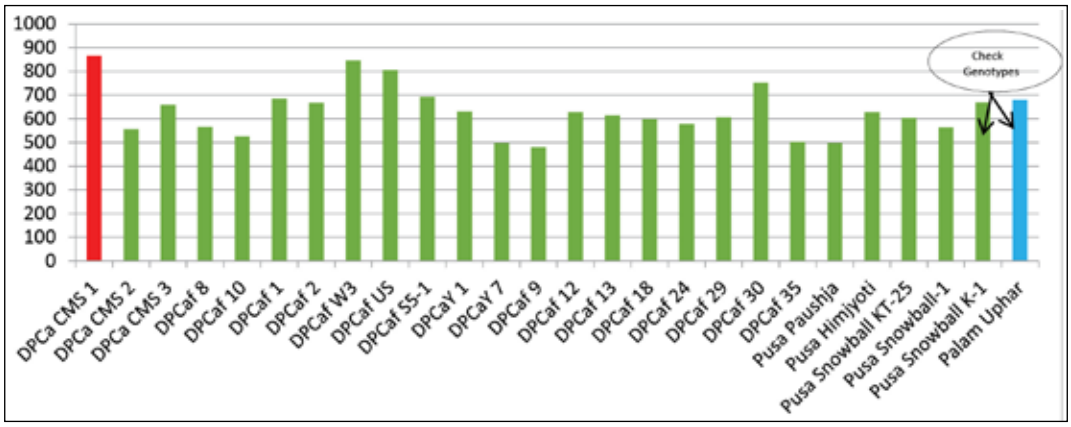


**Fig. 1.** Genotypes and mean of marketable curd weight (g) studied with the check cultivars.

**Table 2.** Cluster compositions in cauliflower following multivariate analysis.

| Cluster number | No. of genotypes | Genotypes |
|---|---|---|
| I | 20 | DPCaf 13, DPCaf 18, Palam Uphar, DPCa CMS 3, DPCa CMS 2, DPCaf 8, DPCaf 30, DPCaY 7, DPCaf 10, DPCaf 2, DPCaf 24, DPCaf 1, DPCaf 12, DPCaf 35, DPCaf 29, PusaPaushja, Pusa Snowball KT-25, Pusa Snowball-1, Pusa Snowball K-1, Pusa Himjyoti |
| II | 1 | DPCaf 9 |
| III | 1 | DPCaf S5-1 |
| IV | 1 | DPCa CMS 1 |
| V | 1 | DPCaY 1 |
| VI | 1 | DPCaf W3 |
| VII | 1 | DPCaf US |

**Table 3.** Average intra and inter-cluster distances in cauliflower.

| Clusters | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|
| I | 1.85 | 2.61 | 2.69 | 3.06 | 3.29 | 3.23 | 3.09 |
| | (1.36) | (1.62) | (1.64) | (1.75) | (1.81) | (1.80) | (1.76) |
| II | | 0.00 | 2.84 | 4.35 | 4.07 | 4.23 | 3.60 |
| | | (0.00) | (1.69) | (2.09) | (2.02) | (2.06) | (1.90) |
| III | | | 0.00 | 2.83 | 3.72 | 3.63 | 4.44 |
| | | | (0.00) | (1.68) | (1.93) | (1.91) | (2.11) |
| IV | | | | 0.00 | 4.37 | 4.29 | 3.33 |
| | | | | (0.00) | (2.09) | (2.07) | (1.82) |
| V | | | | | 0.00 | 5.11 | 3.21 |
| | | | | | (0.00) | (2.26) | (1.79) |
| VI | | | | | | 0.00 | 3.06 |
| | | | | | | (0.00) | (1.75) |
| VII | | | | | | | 0.00 |
| | | | | | | | (0.00) |

Values in parenthesis are intra-cluster distances

inter-cluster distances from various clusters would lead to obtaining target segregants with desirable attributes. The highest inter-cluster distance was achieved between clusters V and VI (5.11), followed by clusters III and VII (4.44). Since the genotypes in the same Cluster diverged very little from one another and thus desirable transgressive segregants could not be obtained by involving them in the crossing programme. Selecting genotypes from different clusters rather than the selection of genotypes within the clusters would be beneficial for the hybridization programme. Varalekshmi *et al.* (13) and Kumar *et al.* (4) have also suggested the selection of genotypes from diverse clusters to be involved in a hybridization programme.

Cluster means showed considerable differences among the clusters for each trait (Table 4). The present study revealed that the genotypes in Cluster II took a minimum of days to curd initiation (62.83) and days to curd maturity (95.40). The maximum curd depth (9.71), curd diameter (13.89), curd size index (135.18), and per cent marketable curds (93.05) were observed in Cluster VII, along with minimum stalk length (3.15). The genotypes in Cluster I showed maximum mean values for leaves/plant (15.97) and leaf length (40.91), but leaf width (17.48) was the highest in Cluster III. Cluster IV represents maximum mean values for plant height (47.60), plant frame (47.37), gross plant weight (1342.99), and marketable curd weight (865.90).

On the other hand, maximum curd solidity (66.90), net curd weight (579.87), total soluble solids (9.86),

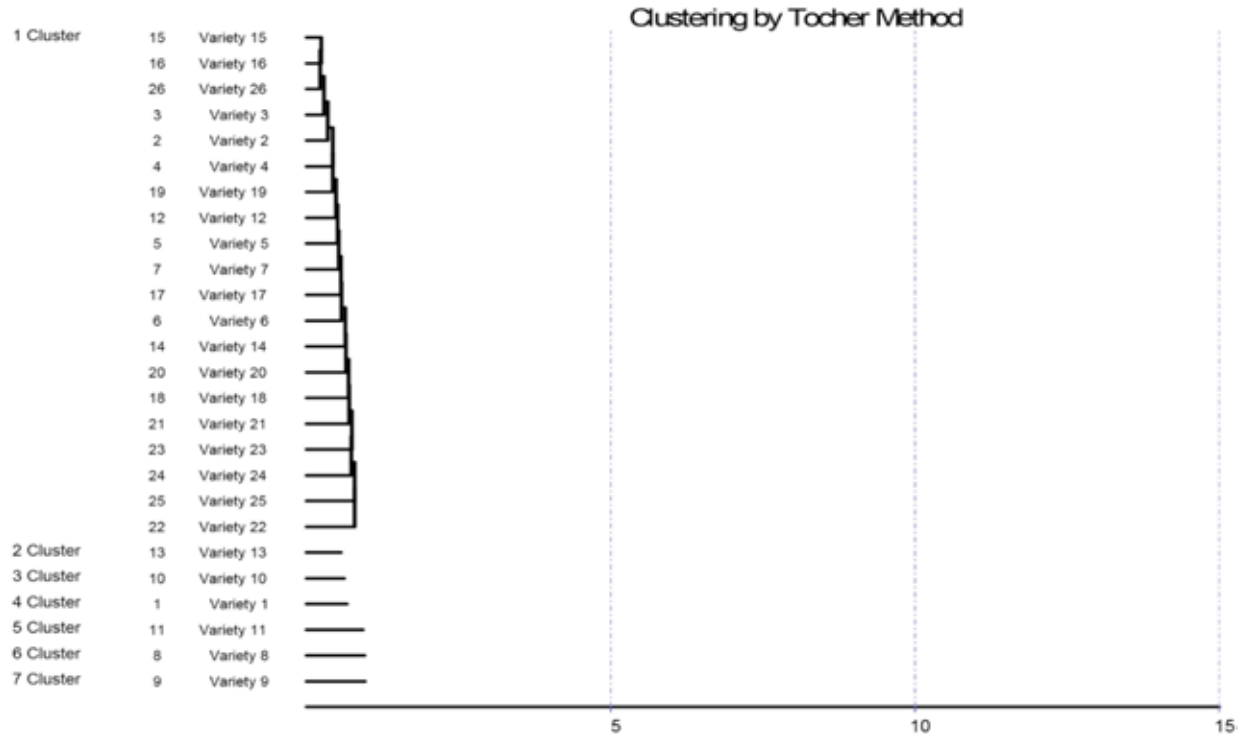


**Fig. 2.** Dendrogram showing grouping of 26 genotypes of cauliflower generated using D2 cluster analysis (Tocher's method).

**Table 4.** Cluster means for different characters in cauliflower.

| Traits Clusters | I | II | III | IV | V | VI | VII | Mean | Max. | Min. |
|---|---|---|---|---|---|---|---|---|---|---|
| Days to curd initiation | 66.54 | 62.83 | 63.50 | 67.67 | 79.83 | 65.00 | 83.83 | 69.89 | 83.83 | 62.83 |
| Days to marketable curd maturity | 101.59 | 95.40 | 100.91 | 103.98 | 121.33 | 105.53 | 112.33 | 105.87 | 121.33 | 95.40 |
| Stalk length (cm) | 3.53 | 3.70 | 4.08 | 4.00 | 3.46 | 3.73 | 3.15 | 3.66 | 4.08 | 3.15 |
| Leaves/plant | 15.97 | 15.86 | 15.23 | 15.72 | 14.61 | 15.51 | 15.78 | 15.53 | 15.97 | 14.61 |
| Leaf length (cm) | 40.91 | 30.09 | 30.96 | 35.81 | 31.92 | 27.37 | 30.21 | 32.47 | 40.91 | 27.37 |
| Leaf width (cm) | 14.95 | 15.64 | 17.48 | 16.97 | 16.11 | 13.50 | 15.07 | 15.67 | 17.48 | 13.50 |
| Plant height (cm) | 40.96 | 39.29 | 39.65 | 47.60 | 40.56 | 36.80 | 40.49 | 40.76 | 47.60 | 36.80 |
| Plant frame (cm) | 43.68 | 43.67 | 46.48 | 47.37 | 42.37 | 42.46 | 42.88 | 44.13 | 47.37 | 42.37 |
| Curd depth (cm) | 8.63 | 8.36 | 8.22 | 9.67 | 8.90 | 8.68 | 9.71 | 8.88 | 9.71 | 8.22 |
| Curd diameter (cm) | 12.72 | 11.92 | 12.10 | 13.85 | 11.80 | 12.89 | 13.89 | 12.74 | 13.89 | 11.80 |
| Curd angle (°) | 100.24 | 98.64 | 102.73 | 105.34 | 99.84 | 106.45 | 106.45 | 102.81 | 106.45 | 98.64 |
| Curd size index ($cm^2$) | 109.87 | 99.80 | 99.84 | 134.02 | 105.12 | 112.02 | 135.18 | 113.69 | 135.18 | 99.80 |
| Curd solidity (g/cm) | 40.85 | 28.92 | 48.08 | 49.02 | 33.85 | 66.90 | 52.66 | 45.75 | 66.90 | 28.92 |
| Gross plant weight (g) | 902.38 | 700.44 | 1045.48 | 1342.99 | 963.14 | 1149.72 | 1104.20 | 1029.76 | 1342.99 | 700.44 |
| Net curd weight (g) | 352.94 | 242.80 | 396.17 | 474.71 | 298.94 | 579.87 | 511.15 | 408.08 | 579.87 | 242.80 |
| Marketable curd weight (g) | 603.91 | 480.75 | 692.96 | 865.90 | 630.01 | 844.96 | 805.70 | 703.46 | 865.90 | 480.75 |
| Marketable curds (%) | 88.46 | 85.00 | 87.50 | 89.72 | 74.44 | 93.05 | 93.05 | 87.32 | 93.05 | 74.44 |
| Total soluble solids (°Brix) | 9.26 | 9.16 | 9.22 | 9.71 | 9.54 | 9.86 | 9.73 | 9.50 | 9.86 | 9.16 |
| Harvest index (%) | 66.96 | 68.14 | 66.22 | 64.51 | 65.40 | 73.52 | 72.99 | 68.25 | 73.52 | 64.51 |

Max.- Maximum; Min.- Minimum

harvest index (73.52), and curd angle (106.45) were observed in Cluster VI. It is a well known fact in the breeding programme that the more genetically diverse parents, the better scope of gaining highly heterotic crosses and wider variability in segregating generations. Thus, for selecting diverse parents in a hybridization programme, different clusters can be used as indicators by considering their genotypic mean for the various traits (Dey *et al.,* 3, Sharma and Singh, 9). In calculating Cluster means, the dominance of a particular genotype for a specific trait could be weakened by the other genotypes grouped in the same Cluster due to their inferior/intermediate performance for the traits interest in question. Therefore, for the hybridization programme, apart from the selection of genotypes from clusters having high inter-cluster distance, the choice of parents may be made based on the degree of diversity concerning the target trait. The contribution of distinct characteristics to the divergence was based on the number of times the specific feature appeared first (Table 5). Days to curd initiation contributed the maximum, followed by the average contribution of leaves/plant, curd diameter, curd solidity, leaf width, stalk length, curd depth, total soluble solids, plant height, and harvest index.

**Table 5.** Percent contribution of various traits towards genetic divergence in cauliflower

| Traits | Times ranked Ist | Contribution (%) |
|---|---|---|
| Days to curd initiation | 86 | 26.46 |
| Days to marketable curd maturity | 5 | 1.54 |
| Stalk length (cm) | 18 | 5.54 |
| Leaves/plant | 32 | 9.85 |
| Leaf length (cm) | 6 | 1.85 |
| Leaf width (cm) | 20 | 6.15 |
| Plant height (cm) | 16 | 4.92 |
| Plant frame (cm) | 6 | 1.85 |
| Curd depth (cm) | 18 | 5.54 |
| Curd diameter (cm) | 31 | 9.54 |
| Curd angle (°) | 4 | 1.23 |
| Curd size index ($cm^2$) | 2 | 0.62 |
| Curd solidity (g/cm) | 29 | 8.92 |
| Gross plant weight (g) | 11 | 3.38 |
| Net curd weight (g) | 8 | 2.46 |
| Marketable curd weight (g) | 2 | 0.62 |
| Marketable curds (%) | 1 | 0.31 |
| Total soluble solids (°Brix) | 17 | 5.23 |
| Harvest index (%) | 13 | 4.00 |

In contrast, the other traits contribute moderately to very low toward the total divergence. Thus, these parameters can be effectively utilized for selecting diverged parents to create variability in the population based on the specific attribute. Varalakshmi *et al.* (13) also observed that the traits *viz.,* gross plant weight, leaves/plant, curd depth and curd diameter had a reasonable contribution towards the total genetic divergence in their breeding material.

Principal component analysis (PCA) imitates the significance of the major contributor to the total variation at each axis of differentiation (Sharma, 8). The criteria for selecting principal components are based on eigen values greater than one. The PCA (Table 6) for different traits revealed the five most informative principal components with eigenvalues 6.43, 3.53, 3.13, 1.628 and 1.12, respectively, accounting for 83.59 % of the total variance for all the characters. Keeping this in view, PCA 1 reflects

**Table 6.** Principal component analysis for 19 morphological traits

| | PC1 | PC2 | PC3 | PC4 | PC5 |
|---|---|---|---|---|---|
| Days to curd initiation | 0.15 | 0.43 | -0.16 | 0.01 | -0.15 |
| Days to marketable curd maturity | 0.12 | 0.46 | -0.16 | -0.07 | -0.09 |
| Stalk length (cm) | -0.01 | -0.14 | 0.26 | -0.26 | 0.60 |
| Leaves/plant | 0.01 | -0.30 | -0.21 | 0.37 | 0.38 |
| Leaf length (cm) | 0.14 | 0.16 | 0.37 | 0.33 | 0.15 |
| Leaf width (cm) | 0.07 | 0.15 | 0.40 | -0.19 | -0.12 |
| Plant height (cm) | 0.15 | 0.20 | 0.40 | 0.19 | 0.09 |
| Plant frame (cm) | 0.08 | -0.11 | 0.48 | -0.10 | -0.03 |
| Curd depth (cm) | 0.32 | 0.03 | -0.05 | 0.34 | 0.03 |
| Curd diameter (cm) | 0.30 | -0.17 | 0.03 | 0.27 | -0.24 |
| Curd angle (°) | 0.31 | 0.09 | -0.20 | -0.22 | 0.07 |
| Curd size index ($cm^2$) | 0.34 | -0.08 | -0.01 | 0.32 | -0.12 |
| Curd solidity (g/cm) | 0.32 | -0.06 | -0.07 | -0.36 | 0.04 |
| Gross plant weight (g) | 0.35 | -0.02 | 0.05 | -0.08 | 0.12 |
| Net curd weight (g) | 0.36 | -0.05 | -0.07 | -0.24 | 0.03 |
| Marketable curd weight (g) | 0.37 | -0.08 | -0.03 | -0.12 | 0.13 |
| Marketable curds (%) | 0.07 | -0.44 | 0.02 | 0.04 | -0.22 |
| Total soluble solids (°Brix) | 0.02 | -0.31 | 0.19 | -0.19 | -0.50 |
| Harvest index (%) | 0.12 | -0.22 | -0.23 | -0.11 | 0.10 |
| Eigenvalue | 6.48 | 3.53 | 3.13 | 1.62 | 1.12 |
| Variability (%) | 34.12 | 18.58 | 16.50 | 8.52 | 5.87 |
| Cumulative % | 34.12 | 52.70 | 69.20 | 77.72 | 83.59 |

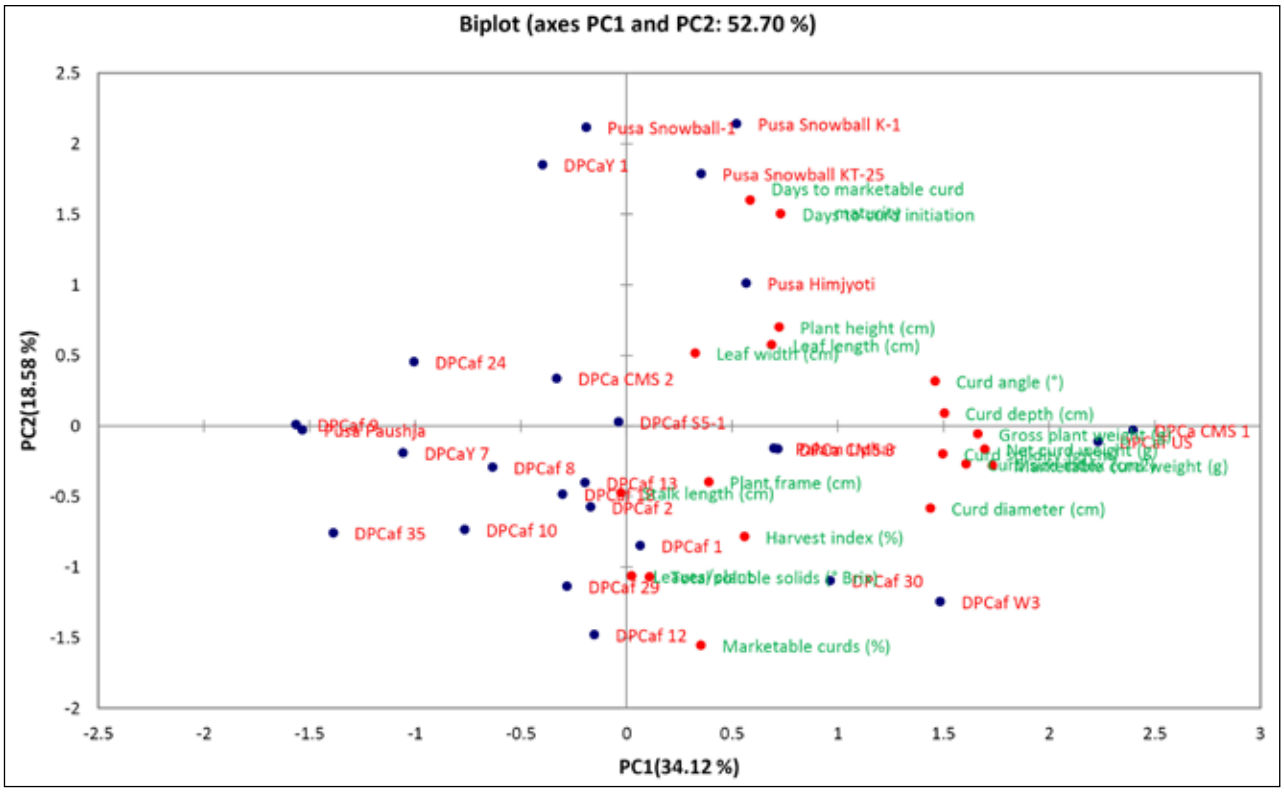


**Fig. 3.** Biplot among first two PCs representing genetic diversity

that marketable curd weight, net curd weight, and gross plant weight had comparatively more significant contributions to the total morphological variability. The results of PCA are like those of Kumar *et al.* (4), who found that curd weight and yield traits are more prevalent for variation. Zhu *et al.* (14) also reported similar findings while evaluating 165 cauliflower genotypes. The other traits are less important as per PC1. On the other hand, days to marketable curd maturity and days to curd initiation had maximum loading in PC2, whereas plant frame, leaves/plant and stalk length showed maximum loadings in PC3, PC4 and PC5, respectively.

Principal component analysis indicated the significance of PCA 1 and PCA 2, accounting for 52.70% of the total variance with respective loading of 34.12 and 18.58%. The biplot of the first two principal components, along with loadings of different traits and spread of genotypes, is shown in Fig. 3. Closely located genotypes on the biplot were supposed to be alike when rated on defined traits. However, genotypes with large distances from the point of origin are supposed to be highly diverse from other genotypes viz., DPCafW3, DPCaf35, DPCaCMS1, DPCafUS, DPCaf9, DPCaf12 and DPCafS5-1, and they should be utilized in the cauliflower improvement programme. PCA further pointed towards gross plant weight, marketable curd weight, net curd weight, curd solidity and curd diameter, and curd maturity as components of marketable curd yield.

The most desirable and diverse genotypes for the hybridization programme as potential parents should be selected from various clusters. Therefore, the hybridization programme should involve genotypes belonging to distance clusters. Accordingly, best-performing genotypes *viz.,* 'DPCaf W3', 'DPCaf US', 'DPCa CMS 1' 'DPCa CMS 2', 'DPCaf 1', 'DPCa CMS 3', 'DPCaf 30', 'DPCaf 13' and 'DPCaf S5-1' would have the more significant potential to be used as breeding stock for desirable traits or as parental lines in hybridization programmes to isolate transgressive segregants for further exploitation in cauliflower breeding programme.

## AUTHORS' CONTRIBUTION

Conceptualization of research (AS); Designing of the experiments (AS and JS); Execution of field/ lab experiments and data collection (AS, JS, HL and AT); Analysis of data (AS and NK); Preparation of the manuscript (AS, JS and NK).

## DECLARATION

The authors declare no conflict of interest

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