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Genetic diversity estimates of exotic and indigenous cauliflower (*Brassica oleracea* var. *botrytis*) genotypes

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Abstract

Exotic cauliflower genotypes are widely cultivated in Pakistan due to their excellent curd quality. Exotic and indigenous genotypes are important source for valuable genes and required to broaden the genetic base of a crop. A comprehensive knowledge regarding genetic variation and genetic diversity is required to select parents for future breeding program. In the present study, one indigenous and eighteen exotic genotypes were evaluated for the presence of genetic diversity through principal component and cluster analyses. Experiment was designed in randomized complete block design with two replications at the experimental area of Vegetable Research Institute, Faisalabad, Pakistan. In principal component analysis, five principal components extracted had eigen value >1 and contributed 82.23% of variation among the genotypes. Traits i.e. maturity days, plant weight, curd weight, curd yield, plant height to extreme, plant width, D9L, plant height to apex, D1L, D9L, leaf attitude contributed significant positive component loading to these PCs. Biplot analysis among these PCs found the genotypes FDIII, Pelican, TCF603, Tabinda, C002F1, Giewont, CF-16049, SV-3630 AC, CF-370 and Whistler as diverse ones. Cluster analysis based on Euclidian distance grouped the genotypes in to 5 distinct clusters. Some of the exotic genotypes were grouped into similar cluster and tend to have narrow genetic base. Based on these results, it may conclude that accessions from distinct cluster may be used for obtaining diverse recombinants in segregating generations, exploiting heterosis and broaden the genetic base of the exciting cauliflower germplasm.

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Introduction

Cauliflower (*Brassica oleracea* L. var. *botrytis*) is acool season vegetable andmostly cultivated for its white curd. It evolved from wild cabbage (*Brassica oleracea* L. 2n=18, CC)known as coleworts through mutation, selection and adaptation(Purugganan *et al.*, 2000). Cauliflower was firstly originated in Cyprus after this it was moved to other regions such as Syria, Turkey, Egypt, Italy, Spain, North Western Europe, America and USA. Through domestication in these areas, different forms of cauliflower such as italin, cornish, notherns, roscoff, angers, indian, erfurt and snow ball were evolved in 18th and 19th century(Swarup and Chatterjee, 1972).Now, cauliflower is mostly cultivated in China, India, USA, Spain and Italy. In Pakistan, mean yield of cauliflower is 17.0 t/ha that is 2.7 t/ha less compared to largest producing country China (FAO, 2017).To boost the yield of cauliflower, exploitation of genetically diverse plants with desirable traits is required in breeding program.

Genetic diversity is the baseline of any breeding programme as it provides a great array of diverse genotypes that could be used for the development and evaluation of breeding material and new varieties with desirable characteristics (Vanlalneihi *et al.*, 2019). Knowledge about genetic diversity helps the breeders to identify diverse parents for creating segregating population with maximum variability and for introgressing desirable genes such as biotic and abiotic stresses resistance and wider adaptability from diverse material to available genetic material (Evgenidis *et al.*, 2011; Tuhina-Khatun *et al.*, 2015; Javed *et al.*, 2017; Dangi *et al.*, 2018;). Comprehensive information regarding genetic diversity also helps in developing superior genotypes to be used in hybrid breeding as parents (Singh *et al.*, 2014). For the estimation of genetic diversity morphological traits are considered as a powerful tool in cauliflower genotypes. The extent of genetic diversity could either be estimated through univariate and multivariate analyses. In recent times, multivariate analyses such as cluster, principal component analysis(PCA) and principal coordinate analysis (PCoA) has become popular to check similarities and differences among genotypes regarding multiple traits. Recently, in many crops such as cotton, rice, tomato, maize, wheat, sugar cane, ginger, bittergourd, garlic and onion PCA and cluster analyses have been widely used for estimation of genetic diversity(Evgenidis *et al.*, 2011;Chakma *et al.*, 2012;Baranwal *et al.*, 2013;Ravishanker *et al.*, 2013;Tahir *et al.*, 2013; Singh *et al.*, 2014;Pahadi *et al.*, 2017;Dangi *et al.*, 2018; Sharma *et al.*, 2018;Jarwar *et al.*, 2019;). Limited studies are also available in cauliflower (Chatterjee *et al.*, 2018; Yousef *et al.*, 2018; Zhu *et al.*, 2018b).

Exotic germplasm is a good source of wider availability, good quality and yield contributing genes and also has the ability to broaden the genetic base of theexciting genetic material. In Pakistan, exotic genotypes are widely used for their good curd quality. Limited studies are available regarding their genetic diversity. Therefore, the present study was conducted to estimate genetic variation among indigenous and exotic cultivars using different quantitative and qualitative traits. This studywould provide usefulinformation regarding genetic diversity and characterization of genotypes for desirable traits that would be usefulfor future cauliflower breeding.

Materials and methods

Experimental design and measurement of traits

This experiment was conducted at the experimental area of Vegetable Research Institute, Faisalabad, Pakistan (73–74° E and 30–31.5° N). Sowing of nursery was done on September 4, 2018. The trial was laid out according to RCB design with two replications keeping plot size of 7 × 1.5 m. Seedlings of all the genotypes were transplanted in the field on October 10, 2018 keeping planting geometry of P×P=45 cm and R×R=75 cm. Standard cultural practices and plant protection measures were carried out regularly. Data regarding nineteen traits were recorded and used for further analyses. Five plants of each replication were tagged and used for data collection of all morphological parameters. Data of the following characters was measured plant weight

(PWt) kg (average plant weight including curd and vegetative part), Stem length (SL) cm (length from soil surface to base where curd start), Number of leaves (NL) (number of leaves at maturity), Leaf length (LL) cm (from the base of the leaf to tip at maturity), Leaf width (LW) (blade width of leaf at maturity), D1L (distance from center of curd to 1st leaf), D5L (distance from center of curd to 5th leaf), D9L (distance between center of curd to 9th leaf), Plant height to extreme (PHE) (length from the base of soil surface to tip of the maximum leaf), Plant height to apex (PHA) (length from the base of soil surface to tip of curd), Plant width (PW) cm (Breadth at the time of maturity), Curd height (CH) cm (from the base of the curd to tip of the curd), Curd diameter (CD) cm (average width of the curd) and curd weight (CWt) cm (average weight of mature curd). Curd color, curd compactness and leaf attitude was characterized according to (Zhu *et al.*, 2018b). Leaf length, stem length, Leaf width, D1L, D5L, D9L, plant height to extreme, plant height to apex, plant width, curd height and curd diameter were measured by ruler. The curd weight was measured by electronic balance. Curds of all the plants of experimental unit area were harvested at maturity and then curd yield (CY) was calculated in tonnes per hectare.

Experimental materials

Nineteen cauliflower genotypes including one indigenous and eighteen exotic genotypes were used to assess the extent of phenotypic variation and genetic diversity. The exotic genotypes were obtained from different private seed companies and indigenous one was received from vegetable research institute. The detailed information of all genotypes is presented in the Table 1.

Statistical analyses

The analysis of variance and variety means comparisons were performed by statistix 8.1 software to check either any difference exist between means of genotypes. Genetic diversity among the genotypes was carried out by PCA. Before performing PCA, redundancy between traits was checked through correlation coefficient analysis. For better understanding the patterns of variation among genotypes, Euclidean distance matrices developed through morphological data was used for cluster analysis Unweighted pair group method with arithmetic mean (UPGMA). PCA and Cluster analyses were performed by using Addinsoft (2019) XLSTAT statistical and data analysis solution.

Results

Principal component analysis

To check the redundancy among the studied traits correlation coefficient analysis was performed. Bold values of correlation coefficient in the Table 2 indicating that correlation/redundancy was exist between the variables so; it could be possible to reduce the observed variables into smaller number of principal components.

In the present study, PCA analysis was used to find the traits that were major contributors to variation and to explain the genetic diversity among the exotic and indigenous cultivars. Selected 19 genotypes were characterized according to 19 phenotypic traits. Total variation was divided in to 19 principal components, but all these components did not have equal worth. The first five PCs that have eigen values >1 were selected as these selected PCs explained the 82.37% variation cumulatively, indicating that these attributes contribute more to variation than remaining ones (Table 3). Eigen values, variability % and cumulative contribution of each component to variation along with contribution of each character to respective PCs are presented in Table 3. PC1 explained the 34.36% of the total variability and majorly influenced by maturity days, plant weight, curd weight and curd yield. PC2 with 18.84% contribution was highly associated with four traits: plant height to extreme, plant width, D9L and plant height to apex. In PC3 (15.28%), D1L, D9L, leaf attitude had a major impact. The remaining components PC4 and PC5 explained 13.89% collectively of total morphological variability. Traits such as number of leaves, plant weight, curd length, curd compactness and stem length contributed positively to these PCs.

Table 1. List of exotic and indigenous genotypes along with their supplier.

Sr. No.	Genotypes name	Origin	Seed supplier
1	Whistler	Exotic	Monsanto Pakistan private limited
2	TCF-603	Exotic	Tara crop science private limited
3	Tabinda	Exotic	NTL seed company
4	SV 5777-AC	Exotic	Monsanto Pakistan private limited
5	SV 3630-AC	Exotic	Monsanto Pakistan private limited
6	Pelican	Exotic	Ch Ahmed din and sons
7	Moon light	Exotic	Ch Ahmed din and sons
8	Giewont	Exotic	Monsanto Pakistan private limited
9	FD-III	Indigenous	Vegetable research institute
10	Cielo Blanco	Exotic	Monsanto Pakistan private limited
11	CF-497	Exotic	NTL seed company
12	CF-4180	Exotic	Ch. Ahmed Din and Sons
13	CF-385	Exotic	NTL seed company
14	CF-370	Exotic	NTL seed company
15	CF-325	Exotic	NTL seed company
16	CF-16049	Exotic	NTL seed company
17	CF 4175	Exotic	Ch. Ahmed Din and Sons
18	C-002F1	Exotic	NTL seed company
19	BENAZIR	Exotic	Green gold Agri seed private limited

Table 2. Correlation matrix among studied phenotypic traits.

	MD	PWt	CWt	CY	SL	NL	LL	LW	D1L	D5L	D9L	PHE	PHA	PW	CH	CL	CC	CCmp	LA
MD	1	0.67	0.82	0.78	0.34	-0.14	0.04	0.36	-0.33	-0.39	-0.51	0.26	0.40	0.39	0.23	0.66	-0.39	0.49	-0.55
	PWt	1	0.82	0.83	0.44	-0.30	0.25	0.29	-0.22	-0.14	-0.30	0.46	0.61	0.50	0.43	0.37	-0.36	0.31	-0.29
		CWt	1	0.99	0.19	-0.25	-0.11	0.31	-0.19	-0.12	-0.36	0.11	0.41	0.22	0.39	0.72	-0.42	0.55	-0.36
			CY	1	0.17	-0.28	-0.14	0.28	-0.17	-0.08	-0.33	0.09	0.42	0.20	0.42	0.70	-0.39	0.55	-0.33
				SL	1	-0.26	0.52	0.51	-0.47	-0.19	-0.33	0.75	0.59	0.62	0.17	-0.09	-0.61	0.15	-0.22
					NL	1	-0.05	-0.42	0.23	0.00	0.31	-0.20	-0.21	0.04	-0.18	-0.07	-0.04	0.00	0.18
						LL	1	0.43	0.01	-0.17	0.08	0.84	0.46	0.73	0.16	-0.19	-0.22	-0.36	0.13
							LW	1	-0.07	-0.01	-0.03	0.43	0.48	0.24	0.38	0.08	-0.39	0.17	0.13
								D1L	1	0.37	0.82	-0.22	-0.08	-0.18	0.40	0.11	0.25	-0.07	0.66
									D5L	1	0.51	-0.19	-0.03	-0.35	-0.02	-0.20	0.17	0.22	0.52
										D9L	1	-0.06	0.03	-0.12	0.35	-0.16	0.23	-0.20	0.93
											PHE	1	0.70	0.89	0.33	-0.05	-0.31	-0.14	-0.04
												PHA	1	0.56	0.55	0.08	-0.47	0.25	0.05
													PW	1	0.40	0.15	-0.29	-0.07	-0.19
														CH	1	0.29	-0.11	0.18	0.25
															CL	1	-0.32	0.35	-0.28
																CC	1	-0.27	0.19
																	CCmp	1	-0.22
																		LA	1

Biplot analysis

In first two PCs some of the traits such as number of leaves and curd compactness that contributing more to variability were ignored. To check the diversity among selected genotypes they were plotted on biplot regarding all the PCs that had Eigen value greater than one and contributing 82.36% variability. Genotypes that are closely located on biplot, perceived as alike when rated on given attributes. More the distance between the point of origin and genotype, more diverse will be the genotype. Regarding all the selected PCs, genotypes were differentiated into to 5 to 6 diverse group (Fig. 1). On biplot between PC1 & PC2, PC1 & PC3, PC1 & PC4, PC1 & PC5, and PC3 & PC4 genotypes such as FDIII, Pelican, TCF603, Tabinda, C002F1, and Giewont clogged far away from the origin and considered as diverse ones from rest of the genotypes (Fig. 1).

Table 3. Principal component analysis for 19 morphological traits (Characters with high coefficients in PC axes considered more important, thus eigen values above 0.20 are shown in bold letter.

??	PC1	PC2	PC3	PC4	PC5
Eigenvalue	6.53	3.58	2.90	1.45	1.19
Variability (%)	34.36	18.84	15.28	7.63	6.26
Cumulative %	34.36	53.20	68.48	76.11	82.37
Traits			Eigen vectors		
Maturity days (days)	0.327	-0.180	0.037	0.137	0.018
Plant weight (kg)	0.328	-0.008	0.112	0.025	-0.118
Curd weight (kg)	0.314	-0.216	0.218	0.022	-0.047
Curd yield (t/ha)	0.305	-0.215	0.239	0.004	-0.080
Stem length (cm)	0.262	0.226	-0.192	-0.231	0.229
Number of leaves (pieces)	-0.131	0.007	0.026	0.480	0.620
Leaf length (cm)	0.129	0.425	-0.137	0.128	-0.049
Leaf width (cm)	0.202	0.192	0.092	-0.371	-0.082
Distance from center of curd to 1st leaf (cm)	-0.163	0.140	0.430	0.219	-0.066
Distance from center of curd to 5th leaf (cm)	-0.137	0.058	0.298	-0.420	0.196
Distance from center of curd to 9th leaf (cm)	-0.196	0.271	0.389	0.089	0.070
Plant height to extreme (cm)	0.236	0.380	-0.128	0.062	-0.032
Plant height to apex (cm)	0.269	0.246	0.123	-0.103	0.094
Plant width (cm)	0.247	0.284	-0.108	0.342	0.017
Curd height (cm)	0.161	0.175	0.362	0.115	-0.235
Curd length (cm)	0.194	-0.236	0.234	0.316	-0.051
Curd colour (code)	-0.235	-0.035	0.011	0.065	-0.517
Curd compactness (code)	0.157	-0.227	0.220	-0.232	0.383
Leaf attitude (code)	-0.186	0.291	0.337	-0.089	0.054

Table 4. Clustering of genotypes according to given morphological traits.

Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Whistler, SV 5777-AC, SV 3630-AC, Moon light, Cielo Blanco, CF-497, CF-4180, CF-385, CF-325, CF 4175, BENAZIR	TCF-603, Tabinda, Pelican, CF-370, C-002F1	Giewont	FD-III	CF-16049

While rest of the genotypes Whistler, SV-3630 AC, SV5777, Cielo blanco, MOONLIGHT, CF-4180, CF-4175, CF-385, CF-325, CF-370, CF-497, BENAZIR, and CF-16049 clogged near to each other and as well as to origin. Hence, these genotypes are less diverse and have less breeding value. Biplot between PC2 & PC3 differentiated the genotype such as CF-16049, SV-3630 AC and CF-370 along with Pelican, Tabinda, FD-III and C002 F1 from rest of the genotypes. When PC3 & PC4 and PC2 & PC5 used as coordinate for biplot then again CF-16049, SV 3630-AC, Tabinda, FD III, TCF-603 identified as diverse ones. PC3 and PC5 biplot found the genotype Whistler, CF-370, TCF-603, Tabinda, Pelican, FD-III and C002F1 dissimilar from rest of the genotypes (Fig. 1).

Cluster analysis

Principal component analysis clearly explained that some of the studied genotypes were highly divers from others. But clear-cut grouping of these genotypes not occurred by PCA.So to do grouping of genotypes, they were subjected to cluster analysis based on Euclidean distances among the phenotypic characters and grouped by UPGMA. Cluster analysis grouped the 19 genotypes in to 5 distinct clusters (Table 4).

Cluster 1 is the largest cluster and contains eleven genotypes. The genotypes Whistler, SV 5777-AC, SV 3630-AC, and Cielo Blanco belongs to Monsanto Moon light, CF-4180, and CF-4175 belongs to Ch.

Table 5. Phenotypic characterization of five clusters.

Characters	Unit	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Maturity days	D	97.12	78.50	115.00	82.50	92.50
Plant weight	Kg	2.66	2.06	4.06	3.05	2.77
Curd weight	Kg	1.40	1.00	2.00	1.00	1.30
Curd yield	t/ha	37.21	27.14	54.10	26.42	35.26
Stem length	Cm	17.18	12.67	20.67	26.67	17.00
Number of leaves	Piece	20.48	21.47	20.00	19.67	21.00
Leaf length	Cm	53.94	51.17	55.67	79.67	68.00
Leaf width	Cm	28.09	23.53	27.00	30.00	28.67
Distance from center of curd to 1st leaf	Cm	11.09	11.60	9.67	10.67	12.33
Distance from center of curd to 5th leaf	Cm	14.64	16.60	13.67	14.00	16.33
Distance from center of curd to 9th leaf	Cm	19.67	22.53	17.00	21.67	23.67
Plant height to extreme	Cm	68.33	61.73	78.33	100.67	85.67
Plant height to apex	Cm	30.67	24.13	33.00	39.67	36.00
Plant width	Cm	99.15	91.53	111.67	124.67	120.33
Curd height	Cm	17.30	14.80	18.67	19.00	19.33
Curd length	Cm	22.06	19.80	23.00	18.00	21.67
Curd colour	Code	1.00	1.40	1.00	1.00	1.00
Curd compactness	Code	2.64	2.20	3.00	1.00	3.00
Leaf attitude	Code	1.45	2.00	1.00	2.00	2.00

Ahmad din and sons, CF-497, CF-385, CF-325 belongs to NTL and BENAZIR belongs to Agri gold seed company. Cluster 2 contained 5 genotypes, out of which three genotypes CF-370, C-002F1 and Tabinda seed was provided by NTL seed company, 1(TCF-603) by Tara and 1(Pelican) by Ch. Ahmad din and sons seed company. Cluster 3 (Giewont), cluster 4(FD III) and cluster 5 (CF-16049) contained only single genotype that was provided by Monsanto, vegetable research institute and NTL seed company respectively.

Characterizations of clusters

Cluster means also showed significant differences for all the studied traits as shown in Table 5. Highest mean value for maturity days (115.0), plant weight (4.06 kg), curd weight (2.0 kg), curd yield (54.0t/ha), curd length (23.00 cm) and curd compactness (3) was seen in cluster 3. Cluster 4 contains the highest value for stem length (26.66 cm), leaf length (79.67 cm), leaf width (30.00 cm), plant height to extreme (100.67 cm), plant height to apex (39.67 cm) and plant width (124.67 cm). In cluster 2, highest mean values were recorded for number of leaves (21.47), D5L (16.60 cm), curd colour (2.20) and leaf attitude (2.0). Cluster 5 showed highest mean value for curd height (19.33 cm), D1L (12.33) and D5L (23.67 cm).

Cluster 4 showed lowest value for number of leaves (19.67) curd weight (1.00 kg), curd length (18.00 cm), and curd yield (26.42 t/ha) while cluster 3 ranked lowest for D1L (9.67 cm), D5L (13.67 cm), D9L (17.00 cm), curd compactness (1.00), and leaf attitude (1.00). Cluster 2 ranked lowest for maturity days (78.50), plant weight (2.06 kg), curd weight (1.00 kg), stem length (12.67 cm), leaf length (51.17 cm), leaf width (23.53 cm), plant height to extreme (61.73 cm), plant height to apex (24.13 cm), plant width (91.53 cm) and curd height (14.80).

Discussion

PCA is a variable reduction procedure that reduced the observable variables into smaller number of artificially created variables that account for most of the variance in the observed variables as compared to large number of redundant variables. PCA reduced the variables on the basis of redundancy or correlation.

Those variables that were correlating and measuring a single construct could be collapsed into new artificial variables called principle components (PCs)

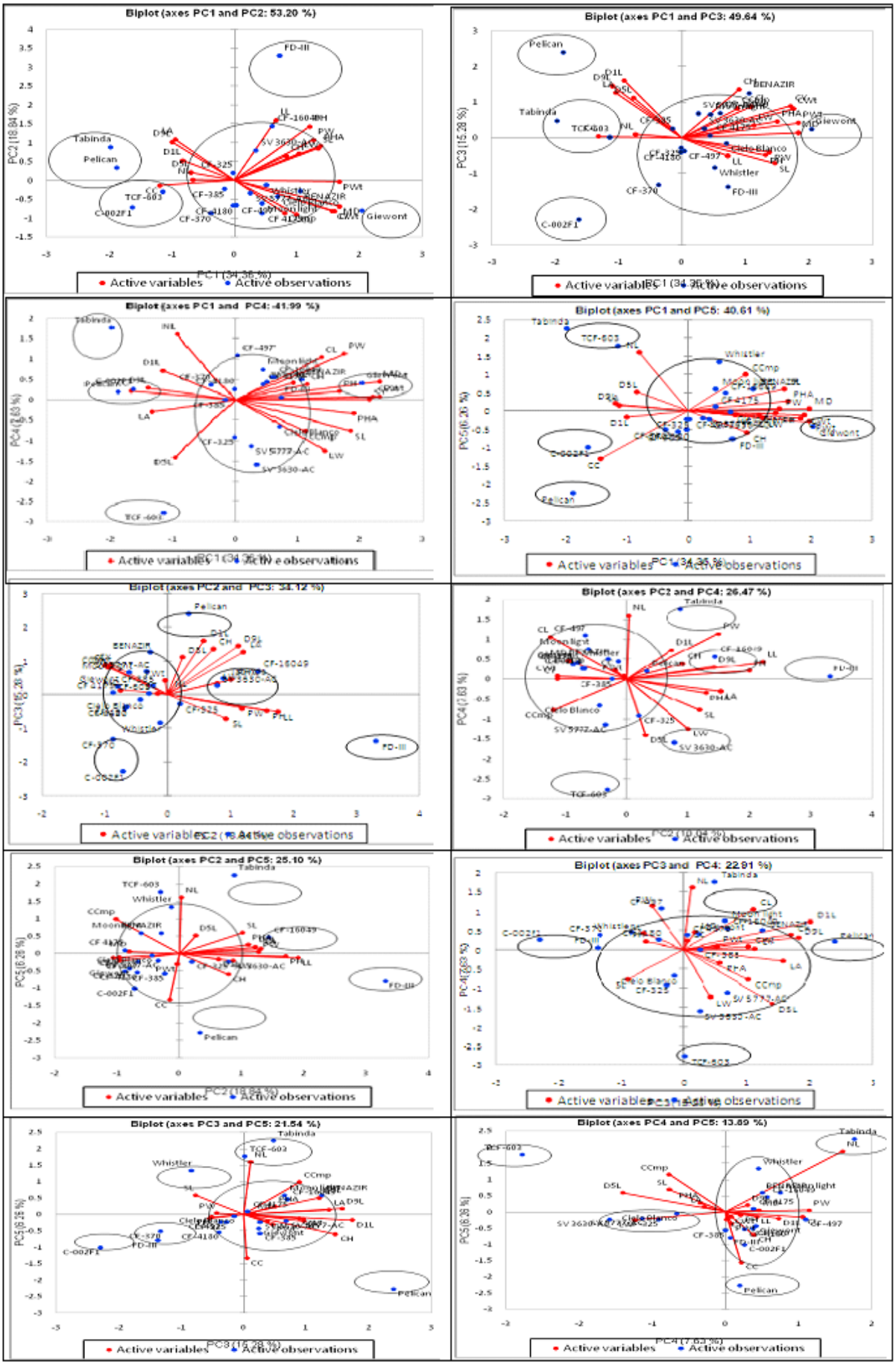

Fig. 1. Biplot among five selected PCs showing the genetic diversity among the genotypes.

Genetic distance between the parents is hypothesized as origin of heterosis and highly correlated with diverse segregants in segregating generations (Dangi *et al.*, 2018; Kumar *et al.*, 2017; Rathinavel, 2019). Comprehensive knowledge regarding genetic diversity is required to decide breeding strategies. Here the genetic diversity among the cauliflower genotypes was studied by using morphological traits. Cauliflower morphological traits are complex and show redundancy as most of these traits were inter correlated (Zhu *et al.*, 2018b). Principal component analysis has the ability to reduce this redundancy by simplifying the phenotypic traits into several principal components and providing opportunity to select PCs with traits that are contributing greater to variation. From total of 19 PCs, only first 5 PCs were contributing more to total variation. Kumar *et al.*(2017) also found first 5 PCs as most informative when they evaluate 57 cauliflower genotypes through PCA. In the present study, PCA revealed that maturity days, plant weight, curd weight, curd yield, plant height to extreme, plant width, distance from centre of curd to 9th leaf, plant height to apex, distance from centre of curd to 1st leaf and leaf attitude were more prevalent traits than others in first 3 PCs and contributing cumulatively 68.83% to variation. As these traits contributing more to variation so, are the main traits for evaluating cauliflower genotypes for breeding program. The results of PCA are congruent with the (Kumar *et al.*, 2017), as plant weight, curd weight, and curd yield traits have highest variations and more prevalent in first five PCs variation. Similar observation was also found by (Zhu *et al.*, 2018b) while evaluating 165 cauliflower inbred lines.

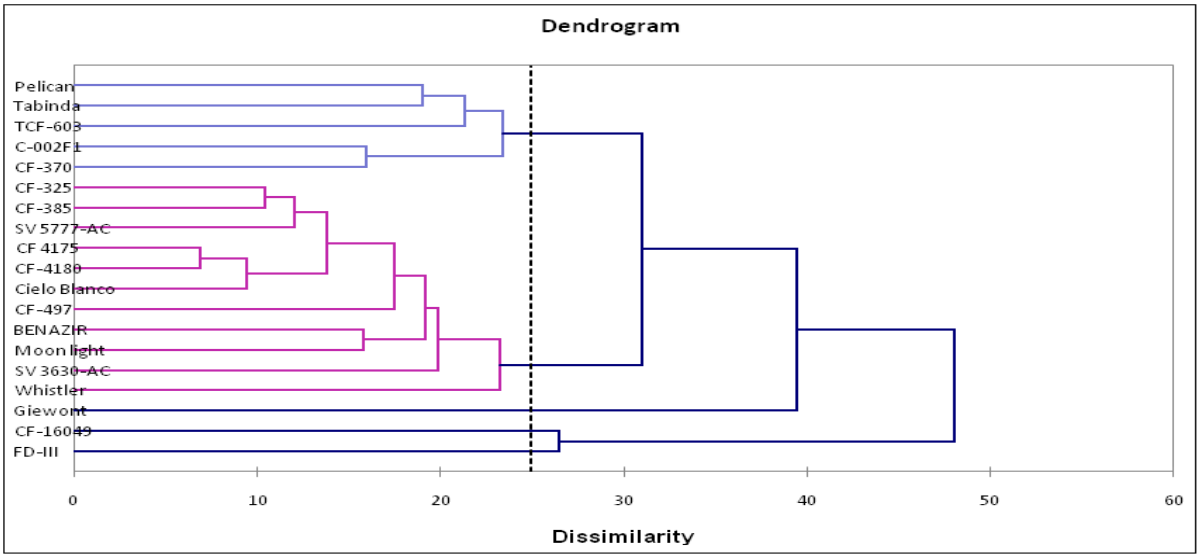

Fig. 2. UPGMA dendogram based on Euclidean distance matrix constructed from 19 phenotypic traits data of 19 cauliflower genotypes.

PCA also used to identify genetically diverse genotypes. For this all the PCs that have eigen value >1 were used for plotting biplots. Zhu *et al.*(2018b) also used this criterion for selecting PCs that are contributing more to variation. We found that although biplot between PC1 and PC2 have the ability to differentiate genotype but sometimes unable to identify genotypes that are also diverse ones. As genotype CF-16049, CF-370, Whistler, and SV-3630AC not differentiated by PC1and PC2 biplot. But these genotypes were characterized as diverse genotypes by PC2 & PC3, PC3& PC4, PC2 &PC5 and PC3&PC5 biplot. This means that information regarding genetic diversity of genotypes obtained by first two PCs biplot is not sufficient so, biplot between other PCs should be explored to get more precise picture of genetic diversity.

Cluster analysis is another important multivariate analysis that is useful for finding the phylogenetic relationship and choosing genetically diverse genotypes for getting desirable recombinants. In this

study, 19 cauliflower genotypes were grouped in to 5 clusters (Fig. 2, Table 3). Cluster 2 was far away from cluster 4 so these are the highly diverse cluster. Similarly, genotype FDIII was far away from pelican in dendogram, so both these genotypes considered as highly diverse. Indigenous genotype (FDIII) was more diverse from exotic genotypes and grouped into different cluster i.e. cluster 4.It was observed that the exotic genotypes (Whistler, SV 5777-AC, SV 3630-AC, Moon light, Cielo Blanco, CF-497, CF-4180, CF-385, CF-325, CF 4175, BENAZIR) imported by different seed companies were similar in nature. Similarly, the genotypes of the same seed company were also much similar and grouped into similar cluster such as Monsanto genotypes Whistler, SV 5777-AC, SV 3630-AC, and Cielo Blanco and Ch. Ahmad din and son's genotypes named Moon light, CF-4180, and CF 4175. These results showed the narrow genetic base of the exotic cauliflower genotypes. Narrow genetic base of cauliflower genotypes was also observed by (Zhao *et al.*, 2014;Yousef *et al.*, 2018; Zhu *et al.*, 2018a; Zhu *et al.*, 2018b).

Characterization of clusters regarding all the morphological traits showed that cluster 1 had medium to late maturity, medium curd weight, yield and vegetative growth.

This cluster showed semi erect type leaf attitude and had milky white curd. Cluster 2 genotypes were the type of early maturing, having lowest curd, plant weight, stem length leaf length, leaf width, plant height to extreme, plant height to apex, plant width and curd height. Cluster 3 showed late maturing habit and more yield than other clusters which was due to more curd weight. This cluster also showed erect type leaf attitude, compact and milky white curd. Less value for distance from centre of curd to 1st, 5th and 9th leaf was also seen in this cluster. It was observed that less the distance of leaves from the centre of curd, more properly curd covered by the leaves and whiter it would be. While studying inheritance of leaf geometry similar findings were also observed by (Werner and Honma, 1980). Cluster 4 exhibited mid late maturity, more vegetative growth and small curd size. This suggested that improvement in cauliflower yield and curd quality characters could be succeeded by selecting parents from diverse cluster. As an example, based on cluster mean data, it is predicted that cross between genotypes of cluster 3 and cluster 2 might results in transgressive segregants for curd weight, curd compactness, curd colour and short maturity contributing traits. Choosing genotypes from diverse clusters was expected to exploit maximum level heterosis in hybrid breeding and these genotypes might be used for creating variation in segregating conditions. Similarity among the exotic material might be creating a serious concern due to their narrow genetic base regarding their utilization in breeding programme.

Conclusion

Studied 19 cauliflower genotypes exhibited a wide range of genetic diversity for most of the phenotypic traits. The principal component analysis exhibited that some of the genotypes are highly diverse regarding the traits that have high proportion in variation. Cluster analysis grouped the genotypes in to 6 clusters based on phenotypic data. Different clusters displayed variation in traits such as maturity days, curd yield, curd weight, curd compactness, and curd colour. It indicated that both genetic variation and characteristics of the parents must be considered while choosing them for breeding programme.

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