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Short communication

Genetic diversity in early cauliflower

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Cauliflower (*Brassica oleraceae* var. *botrytis*) is a member of the Cruciferae family. It is one of the most important and popular vegetables of cole group, widely cultivated in the country. Since very little information on genetic divergence in early cauliflower is available, the present study was carried out to ascertain nature and magnitude of genetic diversity among 77 germplasm lines of early cauliflower using the D^2 statistic. Such a measure will eventually help in planning appropriate breeding programmes and the development of superior varieties/hybrids.

The present investigation was carried out at the Vegetable Farm in the Division of Vegetable Crops, IIHR, Bangalore during *kharif* season of 2005-06. The experimental material comprised 77 germplasm and advanced breeding lines of early cauliflower including some of the commercially released varieties from different institutes of India. The seeds were sown in the seedbed on 1st June 2005. Twenty-one days old seedlings were transplanted in the main field. The trial was laid out in randomized block design with three replications. Each entry was represented by 20 plants per replication with a spacing of 60 cm x 45 cm. Data was recorded on five randomly selected plants in each replication for seven quantitative parameters at the time of harvest, namely total plant weight (g), leaf number, leaf weight (g), curd diameter (cm), curd depth (cm), curd size (sq. cm) and curd weight (g). Genetic diversity was estimated following Mahalanobis's (4) generalized distance (D^2) extended by Rao (9). Tocher's method (Rao, 9) was followed for determining the group constellations.

The analysis of variance revealed significant variations among the genotypes of early cauliflower for all the seven characters studied. The D^2 values ranged from 2.32 to 385.18, showing high divergence among the germplasm and advanced breeding lines. On the basis of relative magnitude of D^2 values, the 77 germplasm / advanced breeding lines of early cauliflower were grouped into 13 clusters with the assumption that those within the cluster have smaller differences in D^2 values among themselves than those belonging to different clusters. Cluster I was the largest comprising 30 genotypes, followed by cluster IV with 22 genotypes. Rest of the clusters had either two or three genotypes. The distribution pattern of genotypes into different clusters, along with their origin, is given in Table 1.

In general, the pattern of distribution of genotypes from different regions into different clusters was random indicating that there is no association between geographical distance and genetic divergence (Table 1). Similar observations were also reported by Varalakshmi *et al.* (10) in ridge gourd. One of the possible reasons may be the fact that it is very difficult to establish the actual location of origin of a genotype. The free and frequent exchange of genetic material among farmers and breeders in the country makes it very difficult to maintain the real identity of the genotype. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin such as genetic drift, exchange of genetic stock, spontaneous variation, natural or artificial selection are responsible for genetic diversity. Therefore, selection of genotypes for hybridization should be based on genetic diversity rather than geographic divergence (Arurachalam, 1; Bhatt, 2; Murthy and Arunachalam, 7; Varalakshmi *et al*., 10).

Intra-cluster distances ranged from 1.58 in cluster II to 8.99 in cluster XI. Maximum inter-cluster distance was observed between clusters VII and XI followed by cluster XI and XII, and cluster VIII and XI. Genotypes belonging to the cluster with maximum inter-cluster distance are genetically more diverged. Selection of parents for hybridization should be done from two clusters having wider inter-cluster distance to get more variability. The genotypes IIHR-73 and IIHR-263 from cluster VII and genotypes IIHR-260-1, IIHR-311 and IIHR-293-3 from cluster XI are the best choice for hybridization. On the other hand, minimum inter-cluster distance (2.97) occurred between cluster VI and cluster IX indicating the close relationship of the genotypes included in these clusters (Table 2).

Differences in cluster means existed for almost all the characters (Table 3). The highest mean value for total plant weight, curd diameter, curd size and curd weight was observed in cluster XI, for leaf number and leaf weight in cluster XII and for curd depth in cluster XIII. Cluster VII ranked lowest in total plant weight; leaf number, leaf weight and curd weight, which might be

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Table 1. Distribution of 77 early cauliflower genotypes into different clusters.

Cluster	No. of genotypes	Genotypes
I	30	IIHR-73-4-2, IIHR-73-24, IIHR-73-24-1, IIHR-73 –56, IIHR-311-3 & IIHR-318-2 (Pune); IIHR-87-4 (Israel); IIHR-217-1-4-6-12, (Uttar Pradesh); IIHR-249-5, IIHR-250-4, IIHR-250-4-1-11-28, IIHR-266, IIHR-266-1-14, IIHR-266-15, IIHR-371, IIHR-372, IIHR-376 & IIHR-324-1-5 (Hazipur, Bihar); IIHR-263-4, (Rajasthan); IIHR-272, (New Delhi); IIHR-306-1, IIHR-316, IIHR-316-1, IIHR-316-2, IIHR-316-4, IIHR-316-10, IIHR-316-11 & IIHR-316-5 (Taiwan); IIHR-345 (Ranchi, Jharkhand); IIHR-Sel-11 (Bangalore)
II	2	IIHR-73-3-20 (Pune), IIHR-382 (Bihar)
III	2	IIHR-250-4-4-2-8-11, IIHR-266 (Hazipur, Bihar)
IV	22	IIHR-305, IIHR-316-8 (Taiwan); IIHR-265-5, IIHR-265-2, IIHR-377, IIHR- 391, IIHR-386, IIHR-375, IIHR-388, IIHR-379, IIHR-390, IIHR-368, IIHR-392, IIHR-370, IIHR-387, IIHR-250-4-1-11-1& IIHR-250-4-1-11-2, (Hazipur, Bihar); IIHR-263-4-1 (Rajasthan); IIHR-342-4, (Ranchi, Bihar); IIHR-73-24-10, IIHR-73-3 (Pune); IIHR-Sel-15 (Bangalore)
V	2	IIHR-231-4 (Uttar Pradesh), IIHR-385 (Hazipur, Bihar)
VI	2	IIHR-250-4-4-16-27, IIHR-250-4-4-16 (Hazipur, Bihar)
VII	2	IIHR-73, (Pune), IIHR-263 (Rajasthan),
VIII	2	IIHR-243-1 (West Bengal), Pusa Meghna (New Delhi)
IX	2	IIHR-217-1-6-5, (Uttar Pradesh) IIHR-378 (Hazipur, Bihar)
X	2	IIHR-264-3 (Rajasthan), IIHR-374 (Hazipur, Bihar)
XI	3	IIHR-260-1 IIHR-311 (Pune), IIHR-293-3 (New Delhi)
XII	3	IIHR-Sel-10 (Bangalore), IIHR-316-3 (Taiwan), IIHR-73-5 (Pune)
XIII	3	IIHR-384 (Hazipur, Bihar), IIHR-73-24-14 & IIHR-318-1 (Pune)

Table 2. Mean intra- (bold) and inter-cluster distances (D^2 values) in early cauliflower.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	**8.30**	6.68	8.25	8.60	7.32	6.64	10.23	6.98	7.31	7.80	12.65	9.93	9.03
II		**1.58**	3.37	6.95	4.68	3.41	7.16	4.74	5.00	4.63	12.13	9.40	7.91
III			**1.59**	7.98	6.99	4.77	8.40	7.53	6.16	5.97	11.82	10.88	9.18
IV				**7.76**	9.10	5.77	12.16	7.83	6.41	9.15	11.56	9.77	10.05
V					**2.01**	6.69	5.25	5.21	7.90	4.18	13.26	11.13	7.88
VI						**2.13**	9.76	5.80	2.97	6.16	10.52	8.58	8.14
VII							**2.86**	8.51	10.51	5.89	16.08	14.19	9.40
VIII								**3.59**	6.96	6.98	14.25	8.24	8.59
IX									**3.76**	7.00	10.67	8.74	8.07
X										**4.73**	12.69	11.43	8.20
XI											**8.99**	15.48	12.60
XII												**8.90**	11.50
XIII													**8.94**

due to small size of the marketable curds and small stature of the plants of the genotypes, IIHR-73 and IIHR-263 which are included in this cluster. It is observed from Table 3 that crossing between genotypes of cluster VII and cluster VIII with genotypes of cluster XI are likely to be exploited for high heterosis for curd weight in turn curd yield/ha in early cauliflower.

The percentage contribution of different characters towards total divergence is given in Table 4. The important characters responsible for maximum divergence were curd weight, curd diameter, total plant weight and leaf weight. Similar results were reported by Quamruzzaman *et al.* (8), Gaur *et al.* (3) and Murthy (6). Hence, considerable emphasis should be given

Table 3. Cluster means for seven characters in early cauliflower.

Cluster	Total plant weight (g)	Leaf number	Leaf weight (g)	Curd diameter (cm)	Curd depth (cm)	Curd size (sq.cm)	Curd weight (g)
I	675.85	16.39	287.31	10.77	5.56	60.49	374.66
II	577.05	14.77	229.16	9.25	4.91	45.92	340.62
III	550.00	14.50	186.25	8.00	4.25	34.25	350.00
IV	747.58	15.84	311.88	9.82	5.54	55.02	445.83
V	535.83	14.20	210.41	11.50	5.35	61.72	313.75
VI	700.00	16.50	281.25	9.62	5.25	50.68	425.00
VII	356.66	14.41	123.75	10.37	5.37	55.68	228.32
VIII	600.00	14.37	301.25	10.25	5.50	56.50	298.75
IX	725.00	18.75	301.25	9.75	5.62	54.62	446.25
X	552.91	16.41	190.83	10.83	4.87	52.78	340.83
XI	904.16	17.50	255.00	11.8	6.25	75.25	645.83
XII	746.66	19.16	414.16	9.66	5.00	49.66	344.16
XIII	620.00	19.08	260.83	11.08	6.66	74.62	362.50

Table 4. Relative contribution of seven characters to the total divergence in early cauliflower.

Character	% Contribution
Total plant weight	13.94
Leaf number	5.91
Leaf weight	11.44
Curd diameter	17.60
Curd depth	6.63
Curd size	4.92
Curd weight	39.54

these characters to increase curd yield in early cauliflower. Thus, this information, generated on genetic divergence will help to exploit the hybrid vigour in early cauliflower.

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REFERENCES

1. Arunachalam, V. 1981. Genetic distance in plant breeding. *Indian J.Genet*. **41**: 226-36.
2. Bhatt, G.M. 1970. Multivariate analysis approach to selection of parents of hybridization aiming at yield improvement in self-pollinated crops. *Australian. J. Agric. Res*. **21**: 1-7.
3. Gaur, P.C., Gupta, P.K. and Kishore, H. 1978. Studies on genetic divergence in potato. *Euphytica,* **27**: 361-68.
4. Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proc. Natl. Inst. Sci. India,* **2**: 49-55.
5. Moll, R.W., Salhuaonam W.S. and Robinson, H.F. 1974. Quantitative genetics-emperical results relevant to plant breeding. *Adv. Agron*. **26**: 277-313.
6. Murthy, B.R. 1965. Heterosis and combining ability in relation to genetic divergence in flue-cured tobacco. *Indian J. Genet*. **26 A**: 188-89.
7. Murthy, B.R. and Arunachalam, V. 1966.The nature of genetic divergence in relation to breeding system in crop plants. *Indian J. Genet*. **26**: 188-98.
8. Quamruzzaman, A.K.M. Rahman, MM., Nazim Uddin, M., Siddiky, M.A. and Prodhan, M.D.H. 2007. Genetic diversity in cauliflower (*Brassica oleraceae* var. *botrytis* L.). *Indian J. Hort.* **64**: 50-52.
9. Rao. C.R. 1952. *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons Inc. New York.
10. Varalakshmi, B., Narayana Reddy, Y. and Muralimohan Reddy, B. 1994. Genetic divergence in ridge gourd [*Luffa acutangula* (Roxb.) L.]. *J. Genet. Pl. Breed.* **48:** 131-34.

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