J. Hortl. Sci.
Vol. 6(1):21-24, 2011

Genetic diversity in early cauliflower (*Brassica oleracea* var. *botrytis* L.) germplasm

H.M. Santhosha[1], B. Varalakshmi[2] and N.C. Narase Gowda[1]
Department of Horticulture, University of Agricultural Sciences
GKVK Campus, Bangalore-560 065, India
E-mail: san3070@gmail.com

ABSTRACT

An experiment was conducted to study genetic divergence in 51 genotypes of cauliflower. Data was recorded for 16 quantitative characters. The genotypes were grouped into 14 clusters. A majority of the genotypes grouped together in Cluster 14 (with 14 genotypes), followed by Cluster 12 (with 8 genotypes). Intra-cluster value was maximum in Cluster 8 and minimum in Cluster 2. Maximum inter-cluster distance was observed between Clusters 8 and 10, followed by that between Clusters 10 and 13 and between Clusters 8 and 12. Hence, genotypes IIHR-323-13, IIHR-214-5 and IIHR-277-14 of Cluster 8, and genotypes IIHR-263 and IIHR-272 of cluster 10 present the best choice for hybridization. Highest mean value for plant weight, leaf number, curd diameter, curd size, net curd-weight , net plot yield, yield per hectare and marketable curd-weight was also observed in Cluster 10, which indicates that genotypes included in this cluster are potential parents for hybridization programmes aimed at increasing cauliflower yields.

Key words: Cauliflower, genetic diversity, hybridization

INTRODUCTION

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is one of the important cole crops grown for its curd in India. Information on genetic divergence of plant material is vital to a plant breeder for efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregants. More diverse the parents greater the chances of obtaining high heterotic F_1s and broad-spectrum variability in segregating generations (Murthy, 1965; Murthy and Arunachalam, 1966; Moll *et al*, 1974). Improvement in yield and quality can be normally achieved by selecting genotypes with desired character-combinations existing in nature or inducing through hybridization. Parents identified on the basis of divergence analysis are expected be more promising in hybridization for both cross-and self-pollinated crops.

Mahalanobis's D^2 statistic has been proved to be a powerful tool in quantifying genetic divergence in germplasm and has successfully used in various crops (Mahalanobis, 1936). Very little information is available on genetic divergence. In cauliflower, the present study was carried out to ascertain nature and magnitude of genetic diversity among 51 germplasm lines of early cauliflower, using D^2 statistic. This shall be eventually helpful in planning appropriate breeding programmes for developing of superior varieties/hybrids.

MATERIAL AND METHODS

The experiment was conducted at Indian Institute of Horticultural Research (IIHR), Hessaraghatta, Bengaluru. Twenty three days old seedlings of 51 genotypes of early cauliflower (*Brassica oleracea* var. *botrytis* L.) were transplanted from the nursery to the field and were grown during kharif 2008-09. Sixty plants represented each genotype per replication. Standard package of practices was followed to raise a good crop, in Randomized Complete Block Design (RCBD) at spacing of 50cm between rows and 40cm between plants, with two replications. Observations were recorded on 10 randomly selected plants in each replication, for 16 quantitative parameters, namely, days to 50% curd initiation, days to 50% curd maturity, plant weight, leaf number, leaf length, leaf breadth, leaf weight, stalk length, stalk weight, curd depth, curd diameter, curd size, net curd-weight, net plot-yield, yield per hectare and marketable curd weight.

To assess genetic diversity among the 51 genotypes of early cauliflower, Mahalanobis D^2 statistic (Mahalanobis, 1936) was used, following the procedure given by Rao

[1] Unniversity of Horticultural Sciences, Bagalkot
[2] Division of Vegetable Crops, IIHR, Hessaraghatta, Bangalore-89

(1952). Grouping of genotypes into clusters was done using Tocher's method, as described by Rao (1952). Statistical analysis of data was carried out using the statistical program GENRES at IIHR, Bangalore.

Table 1. Classification of 51 early-cauliflower genotypes into 14 different clusters

Cluster No.	No. of accessions	Genotype
1	4	IIHR-73
		IIHR-78-7
		IIHR-385
		IIHR-391
2	2	IIHR-375
		IIHR-384
3	2	IIHR-381
		IIHR-386
4	2	IIHR-249
		IIHR-264-3
5	2	IIHR-380
		IIHR-389
6	2	IIHR-223-10
		NS-60
7	2	IIHR-266
		IIHR-324-1-5
8	3	IIHR-214-5
		IIHR-277-14
		IIHR-323-13
9	3	IIHR-217-1-4
		IIHR-371
		IIHR-392
10	2	IIHR-263
		IIHR-272
11	3	IIHR-231-4
		IIHR-318-2
		IIHR-345
12	8	IIHR-249-5
		IIHR-250
		IIHR-265-2
		IIHR-305
		IIHR-311-3
		IIHR-316
		IIHR-343-1
		IIHR-387
13	2	IIHR-376
		IIHR-377
14	14	IIHR-352
		IIHR-368
		IIHR-369
		IIHR-370
		IIHR-372
		IIHR-373
		IIHR-374
		IIHR-378
		IIHR-379
		IIHR-382
		IIHR383
		IIHR-388
		IIHR-390
		Early Kunwari

RESULTS AND DISCUSSION

Analysis of variance revealed significant variation among genotypes in early-cauliflower for all 16 quantitative characters studied (Table 1). D^2 values ranged from 6.83 to

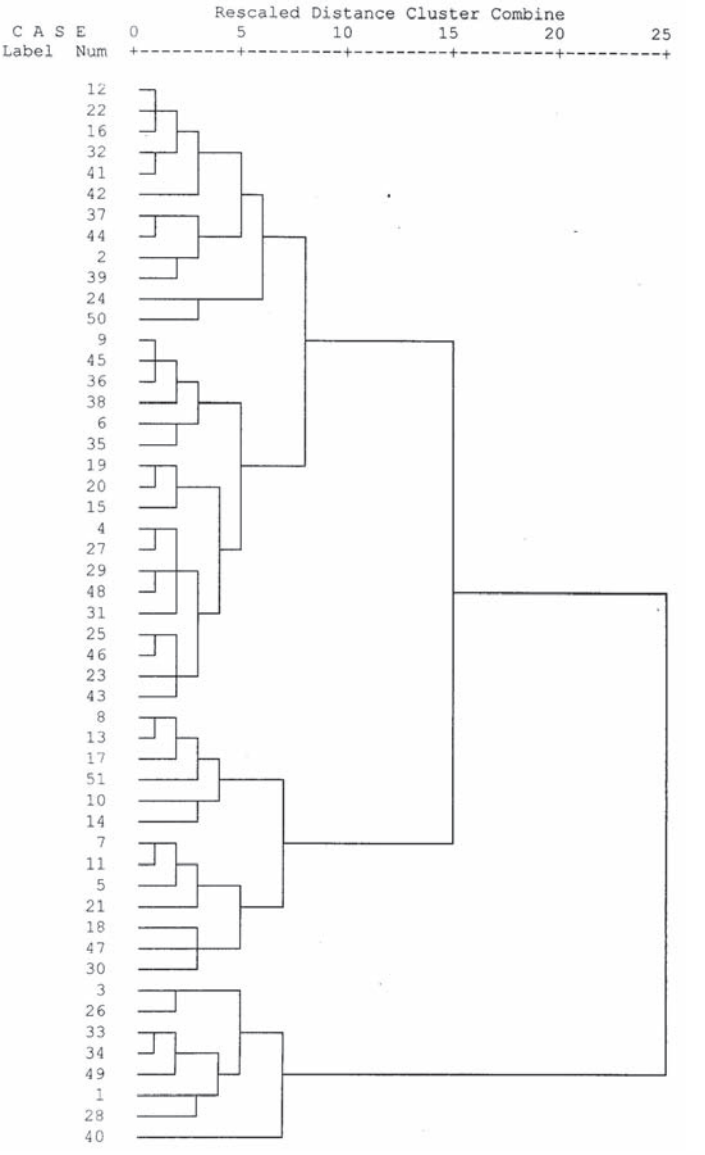

Fig 1. Dendrogram of early-cauliflower genotypes for quantitative traits, using average degree of linkage (between groups)

Foot note:

1. IIHR-73 2. IIHR-78-7 3. IIHR-214-5 4. IIHR-217-1-4 5. IIHR-223-10 6. IIHR-231-4 7. IIHR-249 8. IIHR-249-5 9. IIHR-250 10. IIHR-263 11. IIHR-264-3 12. IIHR-265-2 13. IIHR-266 14. IIHR-272 15. IIHR277-14. 16. IIHR-305 17. IIHR-311-3 18. IIHR-316 19. IIHR-318-2 20. IIHR-323-13 21. IIHR-324-1-5 22. IIHR-343-1 23. IIHR-345 24. IIHR-352 25. IIHR-368 26. IIHR-369 27. IIHR-370 28. IIHR-371 29. IIHR-372 30. IIHR-373 31. IIHR-374 32. IIHR-375 33. IIHR-376 34. IIHR-377 35. IIHR-378 36. IIHR-379 37. IIHR-380 38. IIHR-381 39. IIHR-382 40. IIHR-383 41. IIHR-384 42. IIHR-385 43. IIHR-386 44. IIHR-387 45. IIHR-388 46. IIHR-389 47. IIHR-390 48. IIHR-391 49. IIHR-392 50. Early Kunwari 51. NS-60

469.19, showing a high divergence among germplasm lines. Similar observations were also reported by Varalakshmi *et al* (2010) in cauliflower. On the basis of relative magnitude of D^2 values, the 51 germplasm lines of early-cauliflower were grouped into 14 clusters (Fig. 1) with an assumption that those within a cluster had smaller differences in D^2 values among themselves than those of other clusters.

Depending on their genetic divergence, Cluster 14 had the highest number of genotypes (14), indicating that less variation existed among the genotypes for these quantitative traits, followed by Cluster 12 and 1 (each with 8 and 4 genotypes), respectively. Clusters 8, 9, 11 had 3 genotypes each, while, Cluster 2 to 7, 10 and 13 had two genotypes each. Distribution of genotypes in different clusters is shown in Table 1. Inter-cluster distances were higher than intra-cluster distances, indicating presence of a wider genetic diversity among genotypes included in these clusters (Table 2). These results are in conformity with finding of Quamruzzaman *et al* (2007) in cauliflower. Occurrence of such diversity contributes to heterosis and is, therefore, useful in identifying transgressive segregation.

Intra-cluster distance varied from 2.84 to 10.13, with Cluster 8 showing the maximum distance. Maximum inter-cluster distance (Table 2) was observed between Cluster 8 and 10 (14.1). Genotypes of clusters with maximum inter-cluster distance are expected to be genetically more

Table 2. Inter-cluster and intra-cluster (in bold type-face) distances among 14 clusters in early-cauliflower, based on D^2 analysis

Cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	**8.09**	7.29	6.13	8.56	6.03	8.75	8.11	9.72	9.16	9.82	7.85	9.04	8.16	8.21
2		**2.84**	5.55	6.11	4.57	7.91	8.31	11.88	9.31	6.31	9.27	6.01	9.58	7.73
3			**2.98**	7.22	3.64	9.44	8.85	9.89	6.85	9.35	8.32	8.14	5.61	6.95
4				**3.09**	5.97	7.62	7.76	12.55	10.01	6.05	10.83	7.24	10.61	8.72
5					**3.21**	8.29	7.53	9.84	7.47	8.14	8.03	7.32	6.91	6.71
6						**3.31**	5.48	11.27	12.20	6.46	8.28	8.37	12.67	9.71
7							**3.42**	9.80	12.28	7.93	7.50	9.24	12.09	9.46
8								**10.13**	11.63	14.10	8.26	13.21	10.40	10.90
9									**9.30**	12.61	10.77	10.94	6.73	9.37
10										**3.74**	11.57	6.92	13.40	10.25
11											**6.73**	10.55	10.03	9.39
12												**7.33**	11.33	9.60
13													**4.02**	8.88
14														**9.08**

Table 3. Cluster means for 16 quantitative characters and relative contribution of individual characters to total divergence in early-cauliflower, based on D^2 analysis

Cluster No.	Characters															
	DCI	DCM	PW	LN	LL	LB	LW	SL	SW	CD	C Dia.	CS	NCW	NPY	Y/ha	MCW
1	40.00	56.30	507.50	14.80	30.00	14.50	189.50	3.30	26.60	4.20	7.70	34.20	157.50	9.00	11.10	294.00
2	38.80	54.00	617.90	15.30	32.70	16.10	227.70	3.20	24.10	5.00	9.70	49.30	199.80	11.00	13.50	365.00
3	37.50	54.50	500.40	14.40	28.40	14.30	170.60	3.20	23.10	4.20	8.40	35.70	145.00	9.10	11.30	303.80
4	37.00	52.50	681.40	17.40	31.30	14.60	299.50	3.30	19.30	4.80	8.90	41.40	198.90	10.70	13.30	366.40
5	38.50	53.00	539.60	15.40	31.40	15.30	190.40	3.10	23.10	4.30	9.00	38.90	182.30	9.60	11.80	324.30
6	43.00	57.00	741.10	18.10	34.60	17.60	327.40	2.90	27.00	4.60	8.90	42.50	195.80	10.30	12.70	386.80
7	41.30	54.50	738.80	17.90	37.40	17.40	306.50	3.10	27.50	4.40	8.50	39.10	205.30	12.00	14.90	408.50
8	40.80	58.00	453.80	15.20	35.30	16.30	184.40	3.20	22.70	4.10	6.30	27.80	126.10	7.90	9.10	271.80
9	37.30	54.00	370.20	13.50	24.20	12.20	130.20	3.10	20.50	4.10	7.00	30.50	121.20	5.80	7.20	221.20
10	38.30	56.00	802.30	18.70	33.80	17.30	314.50	3.30	28.30	4.80	10.00	50.70	235.60	12.50	15.40	462.10
11	43.70	56.30	515.80	15.60	33.20	14.90	196.20	3.20	28.40	4.50	7.40	35.10	143.80	8.50	10.50	291.40
12	39.00	54.10	640.70	16.00	31.50	14.10	242.20	3.70	30.70	4.80	9.40	46.80	197.30	10.00	12.40	370.60
13	37.50	55.00	294.10	11.50	23.50	12.10	95.30	3.70	24.60	3.40	6.50	22.40	104.30	5.30	6.60	177.70
14	39.00	54.60	523.00	14.90	30.70	15.70	198.00	3.10	23.10	4.60	8.20	37.40	168.40	9.00	11.10	309.20
Percentage contribution	4.16	0.08	16.94	0.16	0.24	0.47	1.73	2.75	3.22	1.10	7.29	9.02	6.51	13.49	5.88	26.98

DCI = Days to 50% curd initiation
DCM = Days to 50% curd maturity
PW = Plant weight (g)
LN = Leaf number
LL = Leaf length (cm)
LB = Leaf breadth (cm)
LW = Leaf weight (g)
SL = Stalk length (cm)
SW = Stalk weight (g)
CD = Curd depth (cm)
C Dia. = Curd diameter (cm)
CS = Curd size (cm^2)
NCW = Net curd-weight (g)
NPY = Net plot-yield ($kg/6m^2$)
Y/ha = Yield/hectare (tons)
MCW=Marketable curd-weight (g)

divergent. Selection of parents for hybridization should be done from two clusters having higher inter-cluster distance, to aim for higher variability. Therefore, genotypes IIHR-323-13, IIHR-214-5 and IIHR-277-14 from Cluster 8, and genotypes IIHR-263 and IIHR-272 from Cluster 10 are the best choice to be parents for hybridization.

Differences in cluster-means (Table 3) existed for almost all characters. Highest mean value for plant weight (802.3g), leaf number (18.7), curd diameter (10.0cm), curd size (50.7cm^2), net curd-weight (235.6g), net plot yield (12.5kg/ 6m^2), yield per hectare (15.4t), and marketable curd-weight (462.1g) was observed in Cluster 10. Cluster 12 recorded maximum stalk-length (3.7cm) and stalk-weight (30.2g) while Cluster 6 recorded maximum leaf-breadth (17.6cm) and leaf-weight (327.3g). Clusters 7 and 2 showed highest mean value for leaf length (37.4cm) and curd depth (5.0cm), respectively.

Cluster 13 ranked lowest in plant weight (294.1g), leaf number (11.5), leaf breadth (12.1cm), leaf length (23.5cm), leaf weight (95.3g), curd depth (3.4cm), curd size (22.4cm^2), net curd-weight (104.2g), net plot-yield (5.3kg/ 6m^2), yield per hectare (6.6t) and marketable curd-weight (177.7g). Cluster 4 ranked lowest for days to 50% curd-initiation (37.0days), days to 50% curd-maturity (52.5days) and stalk-weight (19.3g). Cluster 6 showed the lowest mean for stalk-length (2.9cm) while Cluster 8 had the lowest curd-diameter (6.3cm), respectively. Lower yield in Cluster 13 may be due to smaller size of curd. Based on cluster-mean, cross between genotypes of Cluster 10, 12, 6, 7, 2, 8 & 11, with genotypes of Cluster 13 and 4 should result in production of highly transgressive segregants for yield-contributing characters. Also, this stands to increase variability and scope for selection of superior lines.

Important characters identified to be responsible for maximum divergence were marketable curd-weight (26.98%), followed by plant weight (16.94%), net plot-yield (13.49%) and curd size (9.02%) (Table 3). This confirms the existence of ample divergence among genotypes with respect to these traits, and hence, selection of best genotypes for these traits will help increase curd-yield in cauliflower.

From these studies, it is concluded that highest inter-cluster distance between Clusters, namely, 8 (IIHR-323-13, IIHR-214-5, IIHR-277-14 IIHR-263) and IIHR-272, IIHR 263 of Clusters 10 indicated the presence of large diversity among genotypes cluster segregants. Hence genotypes of Cluster 8 and 10 may be used as parents in hybridization for obtaining useful segregants.

REFERENCES

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proc. Nat'l. Instt. Sci*. (India), **2:**49-55

Moll, R.W., Salhauaonam, W.S. and Robinson, H.F. 1974. Quantitative genetics - empirical results relevant to plant breeding. *Adv. Agron*., **26**:277-313

Murthy, B.R. 1965. Heterosis and combining ability in relation to genetic divergence in flue-cured tobacco. *Ind. J. Genet*., **25**:46-56

Murthy, B.R. and Arunachalam, V. 1966. The nature of genetic divergence in relation to breeding system in crop plants. *Ind. J. Genet*., **26**:188-198

Quamruzzaman, A.K.M., Rahman, M.M., Nazim Uddin, M.N., Siddiky, M.A. and Prodhan, M.D.H. 2007. Genetic diversity in cauliflower (*Brassica oleracea* L. var. *botrytis*). *Ind. J. Hort.*, **64**:50-52

Rao, C.R. 1952. *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons Inc., New York

Varalakshmi, B., Pushpalatha, A. and Girigowda, J.R. 2010. Genetic diversity in early cauliflower (*Brassica oleracea* L. var. *botrytis*). *Ind. J. Hort.*, **67**:281-283

(MS Received 21 October 2010, Revised 15 April 2011)