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Genetic divergence in off-season cabbage (*Brassica oleracea* var. *capitata* L.) under sub- humid conditions of Himachal Pradesh

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Abstract

Twenty five diverse genotypes of cabbage were evaluated for genetic divergence for yield and its important traits under mid hill sub-humid conditions of Himachal Pradesh. Based on D^2 values, 25 genotypes were grouped into four clusters. The intra- and inter-cluster distances among genotypes under study revealed that cluster IV had the maximum intra-cluster distance (8.02), indicating the diverse nature of the genotypes included in the cluster. At inter-cluster level, the cluster I and II displayed the lowest degree of divergence suggesting close genetic relationship among the genotypes included in these clusters. The maximum inter-cluster distance was found between the cluster II and IV (8.58) followed by the cluster I and III (8.06), which indicated greater degree of genetic divergence among the genotypes included in these clusters. Therefore, intermating between the genotypes included in these clusters is expected to give transgressive segregants in succeeding generations. The present study further revealed the highest contribution of gross weight per plant towards divergence followed by marketable heads (%), days to maturity and number of non-wrapped leaves, thereby indicating the possibility of selection for these characters. Therefore, these characters need to be given utmost importance in the selection programme aimed at breeding high yielding early varieties of cabbage.

Key words: Cabbage, genetic divergence, homogeneous, heterogeneous, hybridization.

Introduction

Cabbage (*Brassica oleracea* var. capitata L.) is one of the most important vegetables in the world. It occupies the pride place among cole crops due to its delicious taste, flavour, nutritive and medicinal value. In Himachal Pradesh, cabbage is a major off-season vegetable crop covering an area of about 2195 hectare with the production of 66,311 tonnes (Anonymous, 2006). It is commonly grown as an off-season vegetable in mid and high hills of Himachal Pradesh during summer months and brings lucrative returns to the farmers. The major constraints in increasing and stabilizing cabbage production and prices are the lack of high yielding and compact headed varieties. At present only four cultivars of cabbage, *viz.* Golden Acre, Pusa Mukta, Pride of India and Pusa Drum Head are on the recommended list for cultivation not only in Himachal Pradesh but also throughout the country since long and these have a tendency to produce loose and unmarketable heads in large proportion during summer months in the hills. In spite of its economic importance, only a limited research on varietal development has been carried out in India because of limitations of crossing work and seed production, which is possible only in the high hills. The knowledge of nature and degree of divergence in existing germplasm is prerequisite in breeding programme of any crop including cabbage for effective varietal improvement. For a successful breeding programme, selection of suitable and genetically diverse parents is crucial. To achieve this, multivariate analysis using Mahalanobis's D^2-statistics has been extensively used as a quantitative measure of genotypic divergence among the parents. Therefore, an attempt was made to study the genetic variability and divergence among 25 genotypes of cabbage under mid hill sub-humid conditions of Himachal Pradesh.

Material and Methods

The experiment was conducted at Experimental Farm of the Himachal Pradesh Krishi Vishvavidyalaya, Hill Agricultural Research and Extension Centre, Bajaura, Kullu (32.2° N, 77° E and 1090 m a.m.s.l.) during summer season of 2003 and 2004. The experimental area represents typical mid hill sub-humid conditions of Himachal Pradesh. Twenty five genetically diverse genotypes of exotic cabbage, *viz.* EC 481002, EC 481006, EC 481007, EC 481015, EC 481016, EC 481019, EC 481022, EC 481030, EC 481031, EC 481033, EC 481034, EC 481035, EC 481038, EC 481039, EC 481040, EC 481045, EC 481055, EC 481056, EC 481058, EC 481059, EC 481060, EC 481067 (Horticultural Research International, Wellsborne, U.K.), KGAT-III (CSK HPKV, Palampur), Golden Acre and Pusa Mukta (IARI, Katrain) were grown in randomized block design with three replications. Each genotype was planted in a plot of 2.25x1.8 m at a spacing of 45 cm both between and within

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rows. The observations were recorded on ten competitive plants for important characters, *viz.* days to maturity, gross weight per plant (g), marketable head yield per plant (g), marketable head (%) and number of non-wrapped leaves per plant. The mean values pooled over years were used for standard statistical analysis. Mahalanobis's generalized distance (D^2) was used to determine the degree of divergence and the group constellations were arrived by Tocher's method as described by Rao (1952). The percentage contribution of a character towards genetic divergence was calculated as the percentage of combinations in which the character has ranked first (Singh and Chaudhary, 1985).

Results and Discussion

Selection is the basis of every breeding programme and it operates only on variation, which is of genetic nature. Wide range of variability present in any crop always gives better chances of selection for desired types. In present study, the analysis of variance for 25 genotypes of cabbage revealed highly significant differences for all the characters indicating existence of genotypic variability and validated further genetic analysis. The D^2 values reflected wide diversity amongst the genotypes. Based on D^2 values, 25 genotypes were grouped into four clusters (Table 1). Among four clusters, the cluster I had the maximum number of genotypes (13) followed by cluster II (7) and cluster III (3). The cluster IV comprised of only two genotypes. The composition of clusters revealed that clusters were comprised of the genotypes of heterogeneous geographic origin indicating that the genotypes were distributed amongst different clusters randomly irrespective of their geographical origin. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. These results are in agreement with the findings of Sharma and Verma (2001) in cauliflower.

The intra- and inter-cluster distances among 25 genotypes (Table 2) revealed that cluster IV had the maximum intra-cluster distance (8.02) indicating that genotypes included in this cluster are diverse. At inter-cluster level, the cluster II and I (4.74) displayed the lowest degree of divergence suggesting close genetic makeup of the included genotypes. The maximum inter-cluster distance was found between the cluster II and IV (8.58) followed by cluster I and III (8.06), which indicated that the genotypes included in these clusters had maximum divergence. Hence, intermating between the genotypes included in these clusters is expected to give transgressive segregates in the advanced generations. Kalloo *et al.* (1980) and Sureja and Sharma (2001) also suggested that the crosses between selected varieties from widely separated clusters are most likely to give desirable recombinants. The magnitude of intra-cluster distance was lesser than the inter-cluster ones, thereby indicating homogenous and heterogeneous nature of the strains within and between the clusters, respectively.

Table 1. Clustering pattern based on D^2 – statistics in cabbage

Clusters	No. of genotypes	Populations
I	13	EC-481002, EC-481006, EC-481030, EC-481031, EC-481033, EC-481034, EC-481039, EC-481045, EC-481056, EC-481058, EC-481060, KGAT-III and Pusa Mukta
II	7	EC-481007, EC-481015, EC-481016, EC-481019, EC-481022, EC-481038 and EC-481055.
III	3	EC-481067, EC-481040 and Golden Acre
IV	2	EC-481059 and EC-481035

Table 2. Average intra and inter cluster distance in cabbage

Clusters	I	II	III	IV
I	3.03	4.74	5.66	7.23
II		3.34	8.06	8.58
III			4.21	6.27
IV				8.02

Underlined values indicate intra-cluster distance

The success of breeding programme depends largely upon the degree of genetic divergence. The cluster mean values (Table 3) indicated that genotypes in cluster I had the lowest days to marketable maturity, which could be exploited for breeding early varieties of cabbage. Genotypes in cluster III exhibited the highest mean values for gross weight per plant (1.523 kg) and marketable yield per plant (0.943 kg) and marketable heads (21.60%). Amongst five important characters studied, the maximum contribution towards divergence was made by gross weight per plant (48.40%)

followed by marketable heads (23.08%), days to maturity (18.16%) and number of non-wrapped leaves (10.45%), thereby indicating the possibility of selection for these characters. Sharma and Verma (2001) also reported similar findings in cauliflower.

Based on D^2 statistics, it is suggested that high yielding early varieties of cabbage with higher gross weight per plant and higher percentage of marketable heads could be bred by utilizing the genotypes from cluster I and III in the hybridization programme. The present study further suggests that gross weight per plant and percentage marketable heads should be given utmost importance in selection programme aimed at breeding high yielding cabbage varieties.

Table 3. Cluster means and percent contribution of different characters towards divergence in cabbage

Characters/ Clusters	Days to maturity	Gross weightper plant (kg)	Marketable head yield per plant (kg)	Marketable head (%)	Number of non-wrapped leaves per plant
I	85.10	1.000	0.607	84.83	12.97
II	91.76	0.668	0.484	82.95	11.64
III	87.05	1.523	0.943	89.61	14.50
IV	98.00	1.425	0.695	82.08	17.58
Percent contribution of each character towards divergence	18.16	48.40	1.39	21.60	10.45

References

Anonymous 2006. *Annual Progress Report.* Directorate of Agriculture, Himachal Pradesh, Shimla-5.

Kalloo G, Singh VP Dudi BS and Pratap PS 1980. Analysis of variation and genetic diversity in garden pea (*Pisum sativum* L.). J. Res. H.A.U. **10**: 540-46.

Rao CR 1952. *Advanced Statistical Methods in Biometric Research.* John Wiley and Sons, New York, p 357.

Sharma KC and Verma S 2001. Genetic divergence in cauliflower (*Brassica oleracea* var. *botrytis*). Indian J. Agric. Sci. **71**: 529-30.

Singh RK and Chaudhary BD 1985. *Biometrical Methods in Quantitative Genetics Analysis.* Kalyani Publishers, Ludhiana, p 54.

Sureja AK and Sharma RR 2001. Genetic divergence in garden pea (*Pisum sativum* L.). Veg. Sci. **28**: 63-64.