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Genetic diversity assessment in European carrot genotypes

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ABSTRACT

To assess the nature and magnitude of genetic diversity in carrot germplasm using the multivariate analysis, the experiment was carried out with 40 European carrot genotypes. The genotypes were classified for four principal components having the eigen values more than one. The first principal component largely accounted for total variation among the genotypes followed by second principal component. Component PC-I, had a high positive loading for root weight (0.420), root diameter (0.378), crown diameter (0.404), root weight and yield (q/ha), PC-II had the high positive loading for root: top ratio, PC-III for top length and PC-IV for flesh thickness. Plotting of PC-I against PC-II differentiated SH-C-12, SH-C-27, SH-C-136, SH-C-101, SHC-7-3-2, CITH-C-1 and SH-C-54 as the most divergent genotype. On the basis of single-linkage cluster analysis means, cluster-IV was the most important for number of leaf /plant, root weight, root length, crown diameter, flesh thickness and yield, whereas, cluster-I was important for minimum core thickness. Highest inter-cluster distance was observed between clusters II and IV (282.50). Most divergent accessions with high inter-cluster distance could be most appropriate parent for crop improvement.

Key words: Carrot, genetic diversity, principal component analysis, single linkage cluster analysis.

INTRODUCTION

Carrot (*Daucus carrota* L.) is one of the important root vegetable crop grown all over the world and praised for a rich pro-vitamin A and other dietary nutrients. There are two groups of carrot, *i.e*. Asiatic and European types. Asiatic types are high yielding and produce the root and seeds under tropical conditions but are comparatively poor in β-carotene and other quality traits (Ramesh *et al*., 9). European types forms root under tropical and temperate conditions but form seed only under temperate regions because they need thermal induction for flowering. The uniform shape, size and colour of root with thicker phloem (cortex) and thinner xylem (core**)** are unique characteristics of European carrot referred in market and fetch higher return. There is need to initiate the crop improvement programme to develop varieties on such lines. The level of genetic diversity in carrot germplasm is a critical component in breeding of new cultivars. The presence of genetic diversity play a vital role to meet the diversified goals of plant breeding such as breeding for higher yield, uniformity, desired quality and resistance to biotic and abiotic stresses. A sound understanding of genetic diversity of different targeted traits is an effective tool for targeted breeding programme). Breeding for particular set of growing conditions, it is pertinent to know the use of local populations, since in them the relationship in yield components are balanced and in harmony with effect of the specific climatic and edaphic factors. The numerical taxonomic techniques are reliable tool to classify the variation pattern at inter- and intra-specific level (Ario and Odulaja, 2). The multivariate analysis is useful technique for characterization, evaluation and classification of plant genetic resources, when a number of accessions are to be evaluated for several characters of agronomic importance (Peter and Martinelli, 8). Different types of analysis such as principal component analysis (PCA) and single linkage cluster analysis (SLCA) are used to identify groups of accessions that have desirable traits for breeding and assessing the patterns of variation in germplasm collection. However, PCA alone would not give an adequate character representation in terms of relative importance, when numerous characters are considered simultaneously (Shalini *et al.*, 11). Thus, this study is aimed at identifying the major characters responsible for variation among European carrot genotypes with a view to group accessions and for identifying the potential parental stocks within groups of local germplasm by employing the multivariate analysis.

MATERIALS AND METHODS

The present investigation was carried out at the Experimental Farm of the ICAR-CITH, Srinagar during 2013 and 2014. The material consisted of 40 variable genotypes collected from different carrot growing hot spots in temperate regions of Kashmir

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valley and heterotic selection from carrot lines bred at CITH (Table 1). Seed was sown at 30 cm × 10 cm inter- and intra-row spacing in mid of August in plot size of 3 m × 2 m in randomized block design with three replications. Geographic position of the experimental site lies between latitude of 34°05 N and longitude of 74°50 E at an altitude of 1,640 m above mean sea level. The average maximum 19.63°C and minimum 6.52°C temperature, amount of rainfall 160.72 mm and relative humidity 58.35%, evaporation 2.45 and soil characteristics, *viz.* pH = 6.81, EC = 0.36 dSm^{-1} recorded during the cropping season August to November. Recommended agronomic and cultural practices were adopted to obtain better phenotypic expression of the traits. Observations were recorded for top length, petiole length, number of leaves/ plant, leaf weight/ plant, root weight, leaf: root ratio, root length, root diameter, core thickness, crown diameter, flesh thickness and root yield (q/ha). The pooled data over two years was analyzed as per the method suggested by Gomez and Gomez (4). Genetic diversity was studied following Mahalanobis's (7) generalized distance (D^2 analysis) extended by Rao (10). Clustering of genotypes was done according to Tocher's method (Rao, 10). Average intra-cluster distance was calculated by the following formula as suggested by Singh and Choudhry (12). Trait variability analysis was performed by the PCA method, with the number of principal components being chosen based on the screen test (Kovacic, 6). Agglomerative Hierarchical cluster analysis was used to determine differences and similarities among the genotypes and as the Euclidean's distance measure used to reflect the differences existing among the genotypes (Kendall, 5). All statistical analysis was carried out based on 12 traits using statistical XL STAT-2011 and SAS 9.3 standard software.

RESULTS AND DISCUSSION

The analysis on 40 genotypes over traits variability expressed on range, standard deviation and coefficient of variation. The highest coefficient of variation was observed for flesh thickness (39.14%), number of leaves/ plant (37.58%), root: top ratio (34.17%), average root weight and root yield (25.89%). The mean root yield /ha was 394.70 q, ranging from 180 to 732 q/ha, average root weight range from 45 to 183 g, root length ranged from 119 to 179 mm and core thickness from 6.54 to 16.93 mm (Table 2). The

Table 1. Carrot genotypes evaluated.

S.No.	Genotype	Area of collection/ source	S.No.	Genotype	Area of collection/ source
1	SH-C-136	Srinagar	21	SH-C-25	Srinagar
2	SH-C-7-5-1	Srinagar	22	Kashmiry Black	Budgam
3	SH-C-2007	Srinagar	23	Pink Carrot	Srinagar
4	SH-C-9005B	Budgam	24	SH-C-20	Budgam
5	Yellow Root	Budgam	25	SH-C-121-1	Srinagar
6	SH-C-75	Srinagar	26	SH-C-120	Srinagar
7	SH-C-33	Srinagar	27	NANTES TYPE	Budgam
8	SH-C-42	Srinagar	28	SH-C-101	Srinagar
9	SH-C-12	Srinagar	29	SH-C-51	Srinagar
10	SH-C-58	Srinagar	30	SH-C-7-3-2	Srinagar
11	SH-C-39	Srinagar	31	SH-C-27	Srinagar
12	SH-C-95	Budgam	32	SH-C-150	Srinagar
13	SH-C-11	Budgam	33	SH-C-52-05B	Srinagar
14	SH-C-54	Budgam	34	SH-C-124	Srinagar
15	CITH-C-1	CITH*	35	SH-C-134	Srinagar
16	CITH-C-5	CITH	36	SH-C-152	Srinagar
17	SH-C-141	CITH	37	SH-C-38	Srinagar
18	SH-C-151	Budgam	38	SH-C-59{LT}	Srinagar
19	American	CITH	39	SH-C-22	Srinagar
20	SH-C-19	Srinagar	40	SH-C-52-1	Srinagar

Table 2. Variation in quantitative traits of carrot accessions.

Trait	Range		Mean	Std. deviation	CV (%)
	Min.	Max.			
Top length (cm)	21.50	58.80	40.15	7.99	19.90
Petiole length (cm)	11.10	31.50	21.30	5.32	24.98
No. of leaves/ plant	5.00	14.00	9.50	1.98	20.84
Top wt./ plant (g)	6.00	42.00	24.00	9.02	37.58
Root wt. (g)	45.00	183.00	114.00	29.51	25.89
Root: top ratio	2.31	16.71	9.51	3.25	34.17
Root dia. (mm)	18.38	42.72	30.55	6.02	19.71
Root length (mm)	119.00	179.00	149.00	12.15	8.15
Core thickness (mm)	6.54	16.93	11.74	2.84	24.20
Crown dia. (mm)	11.16	29.92	20.54	4.37	21.28
Flesh thickness (mm)	0.56	17.15	8.85	3.466	39.14
Yield (q/ha)	180.00	732.00	456.00	118.04	25.89

high coefficient variation and range indicated that a large genetic variability among the all the traits in delineated genotypes. Similar, results on variability in horticultural traits of carrot were also reported by Ramesh *et al.* (9).

Based on degree of divergence of 40 genotypes were grouped for four principal components having the eigen values more than one contributed significantly in total variation (Table 3). The other factors having the eigen value <1.0 were ignored considering the Guttmann's lower bound principal. The first four principal components accounted for maximum estimated variation (81.77%) of total multivariate variations. The first principal component (PC-I) explains for 40.82% of total variation was positively loaded with yield (q/ha), root diameter, crown diameter, root weight and number of leaves /plants, whereas negatively loaded with root: top ratio. The second principal component (PC-II) explained 19.27% of total variability was positively loaded with root: top ratio.

Table 3. The Principal component latent vector for Eigen values and proportion of variance accounted for different components with respect of studied traits.

Trait	PC-I	PC-II	PC-III	PC-IV
Top length (cm)	0.169	0.306	0.590	0.081
Petiole length (cm)	0.125	0.328	0.574	0.257
No. of leaves/ plant	0.198	-0.429	0.041	0.043
Top wt./ plant (g)	0.286	-0.409	0.218	-0.102
Root wt. (g)	0.420	0.080	-0.102	-0.180
Root: top ratio	-0.008	0.544	-0.327	0.083
Root dia. (mm)	0.378	0.122	-0.141	0.113
Root length (mm)	0.132	-0.260	0.234	-0.118
Core thickness (mm)	0.294	0.198	-0.045	-0.551
Crown dia. (mm)	0.404	0.027	-0.180	0.189
Flesh thickness (mm)	0.268	-0.129	-0.190	0.691
Yield (q/ha)	0.420	0.080	-0.102	-0.180
Eigen value	4.89	2.31	1.52	1.08
Variability (%)	40.82	19.27	12.65	9.01
Cumulative %	40.82	60.10	72.75	81.76

The third principal component (PC-III) contributed 12.65% of total variation was loaded with top length, petiole length, and root length followed fourth principal component (PC-IV), which explained 9.01% of total variability was loaded with high flesh thickness and low core thickness, suggesting that these principal component score might be used to summarize the 12 variables in any further analysis of data. The traits with largest absolute value closer to unity within the first component influence the clustering than those to lower absolute value closer to zero. Thus, in present study differentiation of genotypes into different components was because of high contribution of few traits rather than small contribution of each trait. The positive and negative loadings show positive and negative correlation trends between the component and variable. Thus, above mentioned characters which load high positively or negatively contributed to more diversity. The similar results have been reported by Ramesh *et al*. (9). The principal component analysis has also been used for studying the genetic variability in germplasm collection of other crop species (Ahmed *et al.*, 1; Singh *et al.*, 13), The traits contributing in first four principal component could be in consideration in selecting the genotypes with appropriate trait and yield potential. The graph of PC- I verses PC-II indicates some groups of isolated genotypes clearly define the diversity, *viz.*, SH-C-12,SH-C-27, SH-C-136, SH-C-101, SHC-7-3-2, CITH-C-1 and SH-C-54 were most divergent. Usually, it is customary to use one important variable from theses identified groups. Hence, for PC-I root weight is first choice, which has largest positive loading, root: top ratio for second principal component, top length for third and flesh thickness for fourth component. The results of study are useful as it furnish the information about the groups, where certain traits are more important allowing the breeder to execute the specific breeding programme with higher yield and better flesh core ratios.

The biological implication of principal component analysis can be quantified from the contribution of different variables to each principal component as revealed by eigen vector. The clustering score among the principal component axes suggest that some relationship exists among the individuals within a cluster but it does not provides a clear position of genotypes. Single linkage cluster analysis is better

Table 4. Cluster means for 12 traits in 40 carrot genotypes with their distribution in various clusters based on agglomerative hierarchical clustering analysis.

Trait	PC-I No. of genotype-7	PC-II No. of genotype -19	PC-III No. of genotype -12	PC-IV No. of genotype -1	PC-V No. of genotype-1
	SH-C-136, SH-C-7-5-1, SH-C-25, Pink Carrot, SH-C-27, SH-C-124, SH-C-52-1	SH-C-2007, Yellow Root, SH-C-75, SH-C-58, SH-C-95, SH-C-11, SH-C-54 ,SH-C-151, American, SH-C-19, Kashmiry Black, SH-C-120, SH-C-101, SH-C-51, SH-C-52-05B, SH-C-134, SH-C-152, SH-C-38, SH-C-22	SH-C-9005B, SH-C-33, SH-C-42, SH-C-39, CITH-C-1, CITH-C-5, SH-C-141, SH-C-20, SH-C-121-1, SH-C-7-3-2, SH-C-150, SH-C-59 {LT}	SH-C-12	Nantes Type
% of total genotypes	17.50	47.50	(30.00	2.50%	2.50%
Top length (cm)	37.77	39.62	41.49	42.10	29.30
Petiole length (cm)	21.31	21.09	22.78	14.40	11.90
No. of leaves/ plant	7.43	9.26	9.17	9.00	7.00
Top wt./ plant (g)	12.00	18.00	21.83	30.00	10.00
Root wt. (g)	57.29	92.84	128.00	183.00	63.00
Root: top ratio	5.54	6.36	7.34	6.10	6.30
Root dia. (mm)	24.15	33.46	38.28	35.31	18.38
Root length (mm)	151.00	150.11	150.75	179.00	119.00
Core thickness (mm)	8.30	11.09	13.84	15.59	16.60
Crown dia. (mm)	17.59	22.73	27.04	29.75	19.35
Flesh thickness (mm)	9.29	11.64	13.20	14.16	2.75
Yield (q/ ha)	229.14	371.37	512.00	732.00	252.00

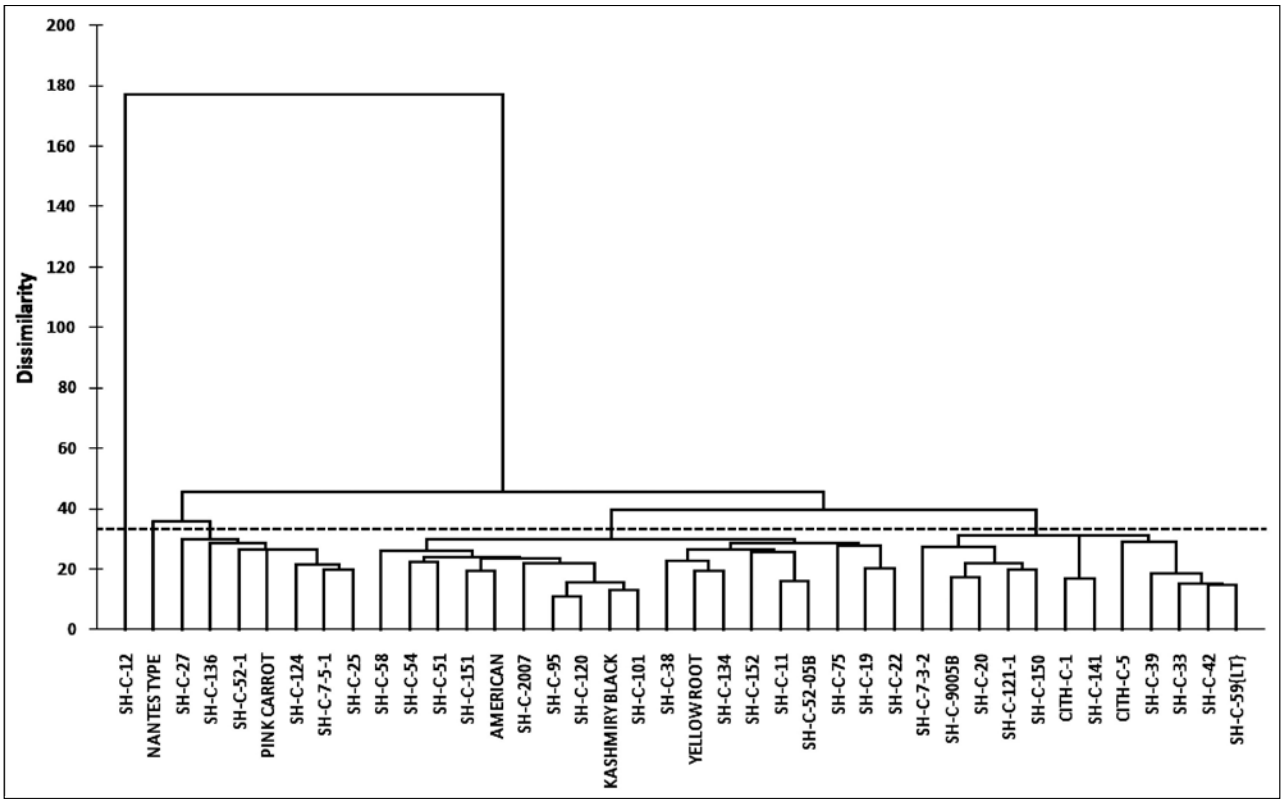

Fig. 1. Dendogram depicting genetic relationship among 40 carrot genotypes based on horticultural traits produced by complete linkage analysis (Scale-Euclidean distance).

technique to depict the clear position of a genotype. Based on the single linkage cluster analysis (SLCA), genotypes were grouped into five clusters identifying the share of genotypes cluster means of all traits (Table 4). The maximum number of genotypes were accommodated in cluster-II (19), followed by cluster-III (12), cluster-I (7), cluster-IV (1) and cluster-V (1) contributing 47.50, 30.00, 17.50, 2.50 and 2.50%, respectively. D^2 value estimates of genetic divergence suggests the resolution for carrot 40 genotypes in distinct five clusters with wide range of diversity in experimental material for majority of traits. The highest inter-cluster distance was observed between cluster-II and cluster-IV (283.50) followed by cluster-I and cluster-II (247.76). The use of wide distance parental lines implies a great number of contrasting alleles at desired loci and to the extent that these loci recombine in F_2 and F_3 generations. Following a cross of distant related parents, there will be a greater the opportunity for the effective selection of desired traits. Thus, crossing of genotypes for these clusters with others may produce higher amount of heterotic expression in first filial generations (F_1s) and wide range variability in subsequent segregating (F_2) populations. On the basis of cluster mean cluster-IV was most important for root weight, root length, crown diameter, flesh thickness and yield top length, number of leaf /plant. Cluster-I was important for minimum core thickness, cluster-III for petiole length, root top ratio and root diameter, whereas cluster-V for maximum core diameter. It can be concluded that for maximum yield, flesh thickness, root diameter, root weight, top weight cluste-IV and for better root top ratio, root diameter cluster-III should be selected for hybridization programme. Ahmed *et al*. (1) also suggested that clusters having high mean value may be used for hybridization programme to get better segregants. The dendogram drawn from single linkage cluster analysis shows variability among the genotypes. All the genotypes were distinct at 100% dissimilarity and formed 11 cluster at 89% dissimilarity and join hand with four cluster at 60% of dissimilarity and make one cluster at 55% of dissimilarity (Fig. 1). The dissimilarly range 55-100% among the genotypes is large enough to suggest the variability in the accessions for crop improvement (Denton and Nwangburuka, (5). The genotypes SH-C-12, SH-C-121-1, SH-C-52-1, SH-C150 and SH-C 136 are most divergent and may used for the specific hybridization programme. Furthermore, genotype

SH-C-12 have high potential for root length, top length, root weight, crown diameter, flesh thickness and high yield and CITH-C-1 for root diameter and root: top ratio can serve as parental line for improvement programme. However, morphological descriptors which environmentally influenced are not enough to indentify the genotypes because of differences among the them are ambiguous. The molecular markers are required to validate the study.

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