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Genetic diversity in carrot (*Daucus carota* L.) germplasm using mahalanobis D^2 statistics

ASIMA AMIN, T.S. DHILLON AND YOGESH VIKAL

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See end of the article for authors' affiliations

Correspondence to :

ASIMA AMIN
Department of Vetetable Crops, Punjab Agricultural University, LUDHIANA (PUNJAB) INDIA

ABSTRACT

Field experiment with 48 genotypes was carried out to assess the association between pairs of traits and their contribution towards root yield. The genetic divergence was estimated by utilizing Mahalanobis D^2 statistics. The range of D^2 values observed for the present material was 7.71 to 727.17. The lowest end of this D^2 range depicts between IPC-122 and CA-05-01, whereas the upper end is the D^2 between CCA-05-01 and Nantes. All the 48 genotypes were grouped into fourteen clusters and the pattern of clustering of genotypes is independent of their place of collection or development. The inter cluster distance ranged between 83 to 630.37, maximum inter cluster distance was recorded between cluster VI and I (D^2 value= 630.37) indicating wide diversity between these two clusters, while the minimum inter cluster distance wit D^2 value of 83 was observed between cluster XI and V. The intra cluster values ranged from 118.26 (10.87) for cluster II to zero for cluster IV, XII and XIII. Selection based on weight of marketable roots per plot, root weight, shoot weight per plant and per cent marketable roots would be more efficient for the improvement of better quality roots in carrot crop.

Key words : Carrot, Genetic diversity, Mahalanobis D^2 statistics

Carrot (*Daucus carota* L.) 2n=2x=18 belongs to family Umbelliferae and is the native of Afghanistan (Banga, 1976) is an important root crop grown in India. Carrot roots are used as vegetables for soups, stews, curries and pies; grated roots as salads, tender roots as pickles and for canning. Carrot jam is also popular and roots in the form of discs and slices can also be used after dehydration. Carrot juice is a rich source of carotene and is sometimes used for colouring butter and other food articles. Carrots are an important source of pro-vitamin A, fiber and other dietary nutrients (Simon, 2000). In India, carrot occupies an area of 24,000 ha with a production of 350 thousand MT and an average yield of 145.83 q/ha (Anonymous, 2003). Diversity exists in pigmentation of wild and cultivated carrot roots. White, yellow, orange, red, purple and pink types are known to exist. Yellow carrots contain xanthophylls, which help develop healthy eyes and may prevent lung and other cancers. Red carrots also contain lycopene which help to prevent heart diseases and some cancers including prostate cancer. Purple carrots contain pigments called anthocyanin that act as a powerful antioxidants, grabbing and holding on to harmful free radicals in the body. Anthocyanins also help prevent heart diseases by slowing blood clotting. White carrots lack pigment, but contain other health promoting substances generally called phytochemicals. Carrot is also an important source of calcium, magnesium and potassium. There is as much calcium in a carrot as there is in a glass (250 ml) of whole milk. For the improvement of yield, a dependant character, the knowledge about association of yield with its contributing traits is important pre-requisite for further breeding plan. The correlation study doesn't indicate the direct and indirect contribution of individual character towards yield. On the basis of these studies the importance of component characters are marked to facilitate the selection programme for better gains. Hence, present investigation was carried out to study diversity and correlation for fourteen characters.

MATERIALS AND METHODS

The present investigation was carried out during Oct 2007-08 and 2008-09 at Vegetable Experimental Area, Department of Vegetable Crops, Punjab Agricultural University, Ludhiana on sandy loamy soil in sub tropical climate. Forty eight diverse germplasm lines were grown on 20th October 2007-08 and 2008-09 in a randomized block design with three replications. All the genotypes were sown on ridges of 3m length in each replication with 45 cm spacing between rows and 7.5 cm between plants, respectively. All the recommended package of practices was followed during the course of investigation for raising a good carrot crop. The observations for fourteen traits were recorded on ten competitive plants of each genotype selected randomly in each replication after 120 days of sowing. Genetic diversity was carried out as per method of Rao (1952).

RESULTS AND DISCUSSION

Pooled analysis of variance for the characters under study presented in Table 1 reveals that the mean squares due to genotypes were significant for all the characters studied for two years as well as in pooled analysis. This indicates the presence of genetic variability in the experimental material. The pooled analysis indicated that the genotypes x years interaction were highly significant for top height, root weight, root girth, core girth, flesh thickness, root to top ratio, total yield, marketable yield, dry matter, carotene content and juice yield. The two environments (years) were diverse for top height, plant height, flesh thickness, total yield, marketable yield, root-top ratio, dry matter and juice content *i.e.* the environments exhibited a greater influence on the variation in these characters. The pooled data were also represented in the form of a dendrogram. Software package NTSYS PC version 2.02e Rohlf (1998) was used for estimation of genetic similarities among the lines using SIMQUAL mode of NYTSYS.

The similarity matrix value based on Jaccard (1990) coefficient of similarity was used to generate dendrogram. Clustering was done by UPGMA using SHAN module of NTSYS PC version 2.02e.

Knowledge of genetic diversity present among population and its quantitative assessment usually helps a plant breeder in choosing desirable parents for breeding programme. Genotypic diversity which has been generally considered as a criterion for the measure of genetic diversity in crop plants, very often fails to convey information about the genetic divergence. Therefore, it is worthwhile to use suitable tools like Mahalanobis D^2 statistics as described by Rao (1952).

The range of D^2 values observed for the present material was 7.71 to 727.17. The lowest end of this D^2 range depicts between IPC-122 and CCA-05-01, whereas the upper end is the D^2 between CCA-05-01 and Nantes. On the basis of relative magnitude of D^2 values the forty eight genotypes were grouped into fourteen different clusters. The cluster composition is given in Table 2. Cluster XI was the largest one comprising seven genotypes, while cluster IV, XII and XIII comprised only single genotype each. The constellation of genotypes into clusters was done by following Tocher's Method Rao (1952).

In the present study, the genotypes collected from same places have not been found to be grouped together in the same cluster like Amity's carrot and JKC (from Jammu and Kashmir) were grouped into cluster VI and X, respectively. The genotype hybrid-501 (from Kashmir), PC-83, PC-84 and HCP-2 (from HAU, Hisar) were grouped in IX cluster, genotypes Nantes, IPC-122. IPC-25 and IPC-126 all from IARI but grouped into different clusters. Genotypes which were collected from Punjab were scattered from III to XIII clusters. These findings suggested that the pattern of clustering was independent to their geographical origin. The same findings of distribution of genotypes into different groups are independent to place of collection. This implied that genetic material from same geographical region may provide substantial diversity. It also indicated that forces other than ecogeographical differentiation such as natural and human selection pressure would exert considerable influence on the genetic divergence.

Table1: Pooled analysis of variance for different characters in carrot

Character	Mean	Squares			
	Years (1)	Replications (2)	Genotypes (47)	Genotypes x Years (47)	Error (188)
Top height	2488**	228.625**	154.698**	34.886**	12.220
Plant weight	3342**	37.000**	21104.000**	306.425	133.968
Root length	9.641	92.476**	8.379**	4.168	4.669
Root weight	100.000	72.500	5153.649**	149.389**	116.434
Root girth	0.000	0.439**	0.134**	0.139**	0.074
Core girth	0.018	0.014	0.071**	0.059**	0.051
Flesh thickness	1.053**	0.168**	0.160**	0.116**	0.047
Root to top ratio	52.420**	0.066	0.183**	0.217**	0.047
Total yield	0.796*	0.634**	14.070**	0.267**	0.184
Marketable yield	6.684**	0.650	11.624**	0.643**	0.275
Total soluble solids	0.346	0.338	2.524**	0.105	0.179
Dry matter	2.885**	0.219	1.354**	0.366**	0.096
Beta carotene content	0.202	0.111	3.484**	2.427**	0.104
Juice yield	16296**	188.000**	9203.404**	6820.368**	55.801

* and ** indicate significance of values at P=0.05 and 0.01, respectively

Table 2 : Clustering pattern of 48 genotypes of carrot on the basis of genetic divergence

Cluster No.	Genotypes	Frequency
I	CCA-05-01, CT-2, IPC-122	3
II	PC-94, KTCTH-7, IPC-106, IPC-7, PC-61	5
III	PC-43, PC-44, PC-41, PC-16	4
IV	HC-1	1
V	PC-87, PC-76, IPC-40, IPC-4, IPC-118, IPC-109	6
VI	Amity's carrot, Nantes	2
VII	HC-199-1, IPC-37	2
VIII	PC-81, HC-100	2
IX	PC-83, PC-84, HC-22-2, Hybrid-501	4
X	PC-82, PC-42, HC-4-2, Early Nantes, JKC, PC-15	6
XI	PC-79, HCP-2, PC-99, PC-34, IPC-25, PC-101, IPC-34	7
XII	PC-5	1
XIII	PC-35-A	1
XIV	HCY-183-1, PC-50, PC-96, KTCTH-8	4

The maximum intercluster distance was recorded between cluster VI and I (D^2 value= 630.37) indicating wide diversity between these two clusters, while the minimum intercluster distance with D^2 value of 83 was observed between cluster XI and V indicating their close relationship. So the clusters VI and I were generally the most divergent from the other clusters. The inter and intra cluster average D^2 values and distances (vD^2) values among 48 genotypes of *Daucus carota* were shown in the Table 3.

The intra cluster values ranged from 118.26 (10.87) for cluster II to zero for cluster IV, XII and XIII. Out of

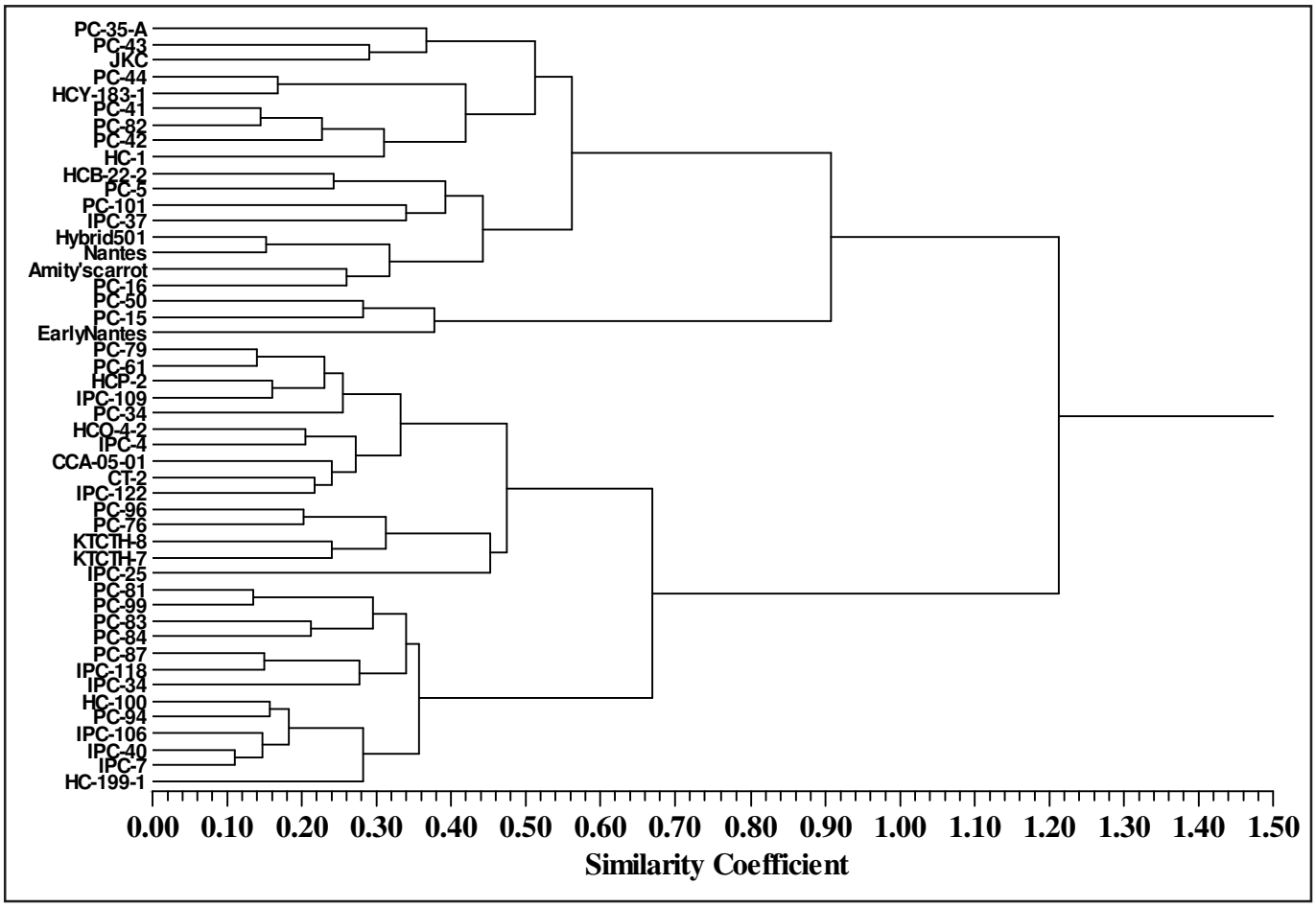

Table 3 : The inter and intra cluster (underlined) average D^2 values and distances ($\sqrt{D^2}$) among 48 genotypes of carrot germplasm

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	**10.02**													
	3.16													
II	241.15	**118.26**												
	15.53	**10.87**												
III	245.15	220.96	**62.85**											
	15.66	14.86	**7.93**											
IV	183.78	318.99	190.11	**0.00**										
	13.56	17.86	13.79											
V	185.41	83.72	212.72	236.95	**52.31**									
	13.62	9.15	14.58	15.39	**7.23**									
VI	630.37	307.60	260.88	567.09	295.75	**30.37**								
	25.11	17.54	16.15	23.81	17.20	**5.51**								
VII	133.68	215.00	255.64	173.49	160.51	410.14	**31.12**							
	11.56	14.66	15.99	13.17	12.67	20.25	**5.58**							
VIII	201.41	138.05	200.91	359.00	125.24	449.38	348.85	**54.05**						
	14.19	11.75	14.17	18.95	11.19	21.20	18.68	**7.35**						
IX	381.86	166.84	175.03	467.10	154.61	155.45	345.89	179.67	**101.77**					
	19.54	12.92	13.23	21.61	12.43	12.47	18.60	13.40	**10.09**					
X	412.72	309.41	98.55	315.83	251.48	177.82	321.13	345.38	191.36	**81.69**				
	20.31	17.59	9.93	17.77	15.86	13.33	17.92	18.58	13.83	**9.04**				
XI	185.83	137.14	148.68	142.11	83.00	384.58	158.85	175.72	240.99	248.68	**71.09**			
	13.63	11.71	12.19	11.92	9.11	19.61	12.60	13.25	15.52	15.77	**8.43**			
XII	427.41	574.8	160.70	315.63	472.97	543.55	542.54	464.61	441.31	215.81	416.38	**0.00**		
	20.67	23.97	12.68	17.76	21.75	23.31	23.29	21.55	21.00	14.69	20.40			
XIII	371.43	427.18	193.95	360.69	344.64	628.44	499.71	275.42	398.13	281.21	279.82	267.95	**0.00**	
	19.27	20.67	13.93	18.99	18.56	25.07	22.35	16.59	19.95	16.77	16.73	16.37		
XIV	281.8	114.72	174.88	405.63	100.21	219.16	286.10	115.77	84.72	236.79	186.16	461.91	390.23	**79.36**
	16.79	10.71	13.22	20.14	10.01	14.80	16.91	10.76	9.20	15.39	13.64	21.49	19.75	**8.91**

clusters comprising more than one genotype, the minimum intra cluster values for the cluster I, 10.02 (3.16) was recorded.

Authors' affiliations:
T.S. DHILLON, Department of Vetetable Crops, Punjab Agriculture University, LUDHIANA (PUNJAB) INDIA
YOGESH VIKAL, School of Agricultural Biotechnology, Punjab Agriculture University, LUDHIANA (PUNJAB) INDIA

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