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Genetic diversity study in tropical carrot (*Daucus carota* L.)

Manisha*, Padmini K., Veere Gowda R. and Dhananjaya M.V.
Division of Vegetable Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru - 560089, Karnataka, India.
*Corresponding Author E-mail: mmanisha366@gmail.com

ABSTRACT

Genetic diversity study was conducted at ICAR- Indian institute of Horticultural Research, Bengaluru during 2018-19. In this study, 80 accessions were evaluated for 16 yield and yield attributing traits. The Mahalanobis' D^2 analysis grouped these accessions into seven clusters. Cluster I was the largest with 69 genotypes followed by cluster III comprising six genotypes while, the clusters II, IV, V, VI and VII contained one genotype each. Among the traits studied, yield contributed maximum (38.04 %) towards diversity, followed by root weight (26.58%), root color (9.18%) and plant height (6.7%). As far as root weight (g) [d1], leaf weight (g), root weight (g), number of leaves, TSS(°Brix), leaf weight (g), root diameter (mm), core diameter (mm), and root cracking are concerned, they contributed 3.45, 2.09, 1.77, 1.71, 1.55, 1.52, 1.46, 1.33, 1.01 and 0.82 percent respectively. Diversity analysis has given an indication about the genetic variation among the carrot accessions which will prove useful in selection of diverse parents in crop improvement programme.

Keywords: Carrot, cluster analysis, genetic diversity, root weight and yield

INTRODUCTION

Carrot (*Daucus carota* subsp. *sativus*), an important root tuber vegetable crop of Apiaceace family is a diploid species ($2n = 2x =18$) grown globally for its rich nutritional contents of vitamin A and carotenes. Other members of this family include celery, dill, parsley, fennel, cumin, coriander, cilantro and many other vegetables and spices. The objective of carrot breeding programmes is to evolve high yielding and well adapted cultivar with desirable economic traits. Edible carrots are thought to have originated in Afghanistan before the ninth century, according to historical evidence. Eastern carrots, as they were known to have yellow or purple roots. Their cultivation extended throughout Central and North Asia, as well as Japan (17th century). The Near East is often regarded as the second-largest source of variation for cultivated carrot variation. Western carrots differ from Eastern carrots in that they have fewer pubescent leaves and a reduced tendency to flower early. During the Middle Ages, yellow and purple carrots were widely grown in Europe, but they were gradually replaced by white and then orange-rooted varieties, which first appeared in the early seventeenth century, presumably as a result of selection from yellow carrot and hybridization of cultivated carrot and its wild relatives (Rubatzky *et al*. 1999). Carrots with orange roots expanded from Europe to other continents, eventually becoming the most common commercial crop in the world. Carrots with different root colours are more regularly grown in Asia, and they have just lately been reintroduced to specialist markets in Europe and America (Simon *et al*. 2008). A long history of carrot selection and the use of diverse parental materials in breeding programmes throughout the world have resulted in considerable variation in available cultivars. An understanding of the extent and nature of genetic variation within a crop species is required for efficient breeding effort. Better understanding of genetic diversity or genetic similarity might aid in the maintenance of long-term selection gain in plants (Chowdhury *et al*. 2002). Therefore, the present study was study in tropical carrot genotypes genetic diversity and cluster analysis.

MATERIALS AND METHODS

The present study was conducted at Vegetable Research Block of Division of Vegetable Crops, ICAR-Indian Institute of Horticultural Research, Hesaraghatta, Bengaluru (latitude 13°58' North and longitude 78°45' East and an altitude of 890 meters above mean sea level) during Rabi, 2018. Eighty accessions were used to study the genetic diversity. The experiment was laid out in a randomized block design with three replications and observations were recorded on a single plant basis for the following characters *viz.*, plant height (cm), number of leaves, leaf length (cm), root length (cm), root diameter (mm), root weight (g), core diameter (mm), root core color, TSS (°Brix), root cracking, root color, root fresh weight (g), root dry weight (g), leaf fresh weight (g), leaf dry weight (g) and yield (t ha^{-1}). Multivariate analysis was done utilising Mahalanobis D^2 statistic (Mahalanobis, 1936) and genotypes were grouped into different clusters following Tocher's method.

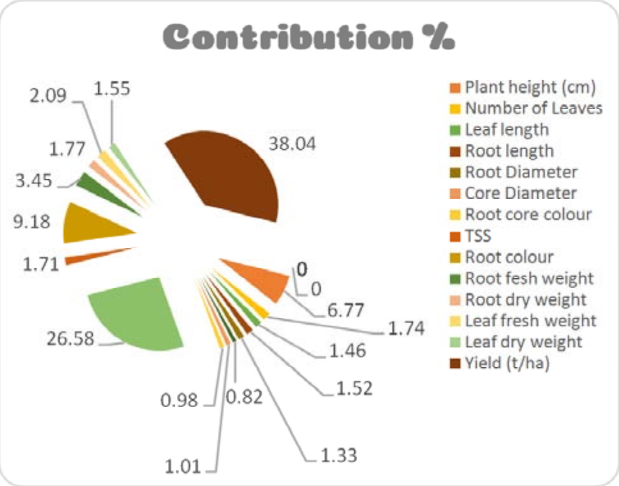

Fig 1. Per cent contribution of 16 characters towards diversity in carrot

RESULTS AND DISCUSSION

Using the pivotal condensation method, the mean values of genotypes were transformed into standardized uncorrelated mean values. The relative percent contribution of different characters included in the study towards diversity is presented in Table 1 and Figure 1. Yield contributed maximum (38.04 %) towards diversity, followed by root weight (26.58%), root colour (9.18%) and plant height (6.77%). Root fresh weight, leaf fresh weight, root dry weight, number of leaves, leaf dry weight, root length, leaf length, root diameter, core diameter and root cracking percent contribution showed 3.45,2.09,1.77,1.74,1.55, 1.52, 1.46,1.33, 1.01 and 0.82 respectively. Similar finding was reported by Jain *et al.,* (2010) Amin and Singla (2010), Nayak and Nagre (2013), Madavi *et al*., (2015), Reshmika *et al*., (2015) Tripathy *et al*., (2017) and Tirkey *et al*., (2018).

Table 1. Relative contribution of 16 characters to genetic diversity in 80 accessions of carrot

Sl. No.	Character	Contribution %	Times ranked first
1	Plant height(cm)	6.77	214
2	Number of leaves	1.74	55
3	Leaf length	1.46	46
4	Root length(cm)	1.52	48
5	Root diameter(mm)	1.33	42
6	Root weight(g)	26.82	840
7	Core diameter(mm)	1.01	32
8	Root core color	0.98	31
9	Root cracking	0.82	26
10	TSS(°Brix)	1.71	54
11	Root color	9.18	290
12	Root fresh weight(g)	3.45	109
13	Root dry weight(g)	1.77	56
14	Leaf fresh weight(g)	2.09	66
15	Leaf dry weight(g)	1.55	49
16	Yield (t/ha)	38.04	1202

Table 2. Clustering pattern of 80 accessions of carrot by D^2 analysis

Characters group	No.of Accessions	List of Accessions
1 Cluster	69	Acc-63, Acc -69, Acc -163B, Acc -52B, Acc -148, Acc -22B, Acc -52C, Acc -87, Acc -56B, Acc -77B, Acc -21A, Acc-72, Acc -76B, Acc -152B, Acc -76C, Acc -60A, Acc -155, Acc -50, Acc -22A, Acc -40, Acc -154A, Acc -140, Acc -77, Acc -777A, Acc -21C, Acc -54, Acc -113A, Acc -76A, Acc -72, Acc -76, Acc -70, Acc -84, Acc -22D, Acc -01, Acc -135, Acc -102, Acc -135, Acc -88, Acc -21, Acc -21B, Acc -60B, Acc -68, Acc -106A, Acc -153, Acc -02, Acc -77C, Acc -101, Acc -113B, Acc -144C, Acc -56, Acc -146, Acc -41, Acc -152A, Acc -145, Acc -06, Acc -105, Acc -54B, Acc -85, Acc -88, Acc -106B, Acc -144A, Acc -144B, Acc -54A, Acc -113B, Acc -105, Acc -20, Acc -80, Acc -164, Acc -156
2 Cluster	1	Acc -154B
3 Cluster	6	Acc -52A, Acc -163A, Acc -51, Acc -173, Acc -147, Acc -63
4 Cluster	1	Acc -75
5 Cluster	1	Acc -50
6 Cluster	1	Acc -150
7 Cluster	1	Acc -56A

The genetic diversity among 80 genotypes was measured by employing D^2 statistics and grouped into six clusters using Tocher's method given as by Rao (1952). Distribution of accessions in each cluster is presented in Table 2 and Figure 2. Cluster I was found largest with 69 accessions followed by cluster III comprising six accessions, cluster II and IV, V, VI and VII comprising one accessions in each cluster. Similar genetic diversity studies were carried out by many workers in this crop *viz.*, Amin *et al.*, 2010, Kumar *et al.*, 2021 and Meghashree *et al.*, 2018.

Cluster mean of 16 yield and yield contributing characters were assessed and presented in Table 3. along with supplementary data (Table S1 and Fig. S1). The mean comparison of the different characters indicated considerable differences among the clusters for all the characters. Maximum mean for plant height was observed in cluster III (85.9cm) followed by cluster II (85.1cm), while minimum cluster means of 53.8 cm were observed in cluster V. There were maximum number of leaves observed in cluster VII which recorded 18.3, followed by cluster IV which recorded 9.6, and cluster II recorded a minimum of 6.5. The maximum mean for leaf length (72.3 cm) was observed in cluster VII followed by cluster III (69.5cm) and minimum mean (47.0cm) was observed in cluster V.

The highest mean for the root length was recorded in cluster VII (19.3cm) followed by cluster V (16.3cm) while, lowest mean of 13.0 cm was shown by cluster VI. The highest mean for root diameter was observed in cluster VII (5.3mm) followed by cluster VI (4.7mm) while the lowest mean of 2.6 mm was shown by cluster IV. Root weight recorded a maximum mean in cluster III of 123.7g followed by cluster II of 116.8g while the minimum mean of 33.3g was observed in cluster IV. The core diameter recorded a maximum mean in cluster VII of 3.7mm followed by II of 2.7mm while, the minimum mean of 1.5mm was observed in cluster IV. The root core color that is self-core color was yellow (2) in cluster V followed by orange in other VI clusters. Root cracking was either obsent or rarely observed in cluster V, I and cluster III having mean 0, 0.1 and 0.6 percent respectively while other clusters was having root cracking having mean of 1.0 percent. The cluster mean observed in TSS (°Brix) was highest for cluster VI (14.2) followed by cluster II (13.8) and it was lowest for genotypes under cluster VII (11.17). Root color was very dark in cluster VII, III. IV and II having mean of 4.3, 4.0, 4.0 and 4.0 while dark orange color observed in cluster I having a mean of 3.6 and cluster VI was having orange root color with a mean of 2.0.

Root fresh weight recorded maximum cluster mean in cluster II (96.6g) followed by cluster III (95.0g) while cluster IV depicted minimum mean of 63.3g. Cluster IV recorded a maximum mean of 11.3g of root dry weight followed by 10.9 g observed in cluster III. Whereas, minimum mean of 8.0 g was observed in genotypes under cluster II. The maximum mean for leaf fresh weight (213.3g) was observed in cluster VII followed by cluster III (59.6g) while minimum mean of 18.5 g was observed in cluster V. with regard to leaf dry weight Cluster VII recorded a maximum mean of (leaf dry weight) 40.6g followed by 14.6g observed in cluster II while minimum mean of 2.2g was observed in genotypes under cluster V. The highest mean for yield was recorded in cluster IV (12.9t ha^{-1}) followed by cluster VI and VII (12.0 t ha^{-1}) while, the lowest mean of 9.0 t ha^{-1} was shown by cluster III. Similar reports were made by Amin *et al*., 2010, Kumar *et al*., 2021 and Meghashree *et al*., 2018.

Based on these results, Mahalanobis D^2 was found to be a useful tool in grouping genotypes phenotypically and geographically. Findings revealed that in carrot, there is a vast scope for developing new varieties with greater yield potential and to better other attributes of economic importance, using this elite germplasm. In crop improvement programmes, intercrossing among genotypes with outstanding mean performance for these characters would prove to be effective.

CONCLUSION

Genetic divergence has been considered as an important factor in selecting the genetically diverse parents for efficient and successful hybridization programme in order to get potential transgressive segregants and also provide new recombination of genes in the gene pool. It is desirable to select genotypes from clusters showing high inter-cluster distance cluster VI (Acc -150) and cluster VII (Acc -56A) for further crop improvement programme.

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