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Characterization for Different Traits in Asiatic and European Type Carrot (*Daucus carota* var. sativa L.) Germplasm Lines

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Authors' contributions

This work was carried out in collaboration among all authors. Author DS designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors TSD and RS managed the analyses of the study. Author RS managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation was carried out to characterize the eighty one carrot genotypes through variability, heritability and genetic gain for different characters. Analysis of variance revealed highly significant differences among the genotypes for all the characters. Genetic variability, heritability and genetic advance were estimated for marketable and its component yield traits in 81 lines of carrot (*Daucus carota* var. sativa L.). The study showed high ranges for total yield (4.9-9.3 kg plot^{-1}), marketable yield (4.6-9.2 kg plot^{-1}), root length (13.8-30.8 cm) and root weight (101.4-127.2 g). Genotypes PC-161, PC-15, PC-173 (red), PCO-30, PCO-5, PCO-7 (Orange) PCP-2, PCP-1 and PCP-17B (Purple) were superior with respect to total and marketable yield per plot along with various horticultural traits. Magnitude of phenotypic coefficient of variation (PCV) was higher than corresponding genotypic coefficient of variation (GCV) for all the characters which indicated the role of environment on the character expression. Quantitative traits like Anthocyanin content (mg 100 g^{-1}), Total sugar content (%), Carotene content (mg 100g^{-1}) and Dry matter content (%) have higher values of GCV, heritability, genetic advance and genetic gain hence these were the most important traits for applying selection in carrot for crop improvement.

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Keywords: Carrot genotypes; PCV; GCV; heritability; genetic advance.

1. INTRODUCTION

Carrot (*Daucus carota* var. *sativa* L.), a member of family *Apiaceae*, is one of the most important vegetables in the world. Most cultivated carrots are diploid with average chromosome length of 2.34 µm [1,2]. It occupies the pride place due to its delicious taste, flavour and nutritive value. Eastern carrots are thought to originate from Afghanistan, while the origin of western carrots is still uncertain [3,4]. At present it is grown throughout the world and also has a pride place in Indian market [3]. The colour of the cultivated carrot flowers are usually white, and have compound leaves [5,6]. The carrot root is a good source of carotenoids, vitamins and is also rich source of minerals and antioxidants [7,8]. With increasing health awareness, carrot as raw and its products are becoming more popular due to the presence of nutrients and antioxidants. Carrot is an important root vegetable used for salad, cooking, processed product like canned pickles, preserves, gajar halwa, powders and kanji (an appetizing drink) etc. Carotenoid and other biochemical composition determines the white, yellow, orange or red root colour in the carrot [9,10]. Major carrot growing countries in the world are China, Russia, India and United State of America [11]. During 2016-17 in India, area under carrot crop was 86 thousand hectares and production was 1.35 MT [12]. Major carrot growing states in India are Haryana, Tamil Nadu, Punjab, Karnataka, Uttar Pradesh and Assam [13]. One of the limiting factors for low productivity of any crop is lack of superior genotypes or improved cultivars. So, there is need for development of new varieties and hybrids with high productivity. The critical assessment of nature and magnitude of variability in the germplasm stock is one of the important pre-requisites for formulating effective breeding programme [14]. With the development of molecular techniques, huge amount of information has been produced in research on carrot crop. The greater the variability in a population, the greater the chances for effective selection for desirable types [15]. Phenotypic and genotypic coefficients of variation are useful in detecting the amount of variability present in germplasm. High heritability in broad sense indicated that large proportion of phenotypic variance was attributable to the genotypic variance and that these character differences among the genotypes were real and these traits were less influenced by the environment. Hence, heritability studies are of foremost importance to judge whether the observed variation for a particular character is due to genotype or due to environment. Improvement in the mean genotypic value of the selected families over base population is known as genetic advance. Johnson et al. [16] stressed that for estimating the real effects of selection, heritability alone is not sufficient, genetic advance along with heritability is more useful as high heritability coupled with high genetic advance indicates the role of additive gene action and consequently a high genetic gain (GG) is expected from selection under such situation [17]. As genetic coefficient of variability, phenotypic coefficient of variability and heritability estimates determine the component of heritable variation and genetic advance measures the extent of its suitability under selection, all these parameters should be considered simultaneously so as to bring effective improvement in yield and other characters. The information on carrots in India is very scanty because tropical and temperate types have not received sufficient attention for its genetic improvement. Therefore in the present study 81 germplasm lines representing both tropical and temperate types were evaluated in order to compare their genotypes for variability, heritability and genetic advance for various economic characters.

2. MATERIALS AND METHODS

2.1 Plant Material and Traits Studied

The present investigation was carried out at Vegetable farm, Department of Vegetable Science, College of Agriculture, Punjab Agricultural University, Ludhiana during rabi season. Experimental material consisted of eighty one genotypes procured from different carrot growing areas. These genotypes were analysed in Simple Lattice Design (LD). Each genotype was replicated twice and every genotype was planted on 67.5 cm raised beds (37.5 cm bed and 30 cm furrow) in 4 rows with spacing of 10 cm between rows and 8 cm between plants and the data were recorded on ten plants randomly taken in each plot. Observations were recorded on nineteen economic characters *viz.*, plant height (cm), number of leaves, shoot weight (g), root length (cm), root weight (g), root girth (cm), core girth (cm), flesh thickness (cm), root shoot ratio, total root yield (kg $plot^{-1}$), marketable root yield (kg $plot^{-1}$) and days to first root harvest. The biochemical traits evaluated included sugar

content (%) [18], lycopene content (mg $100g^{-1}$) [19], total soluble solids (TSS %) (using hand refractometer), dry matter content (%), β-carotene (mg $100g^{-1}$) [20,21], juice yield (ml kg^{-1}) and anthocyanin content (mg $100g^{-1}$) [22].

2.2 Analysis

For quantitative parameters, mean values of ten plants from each replication were used for statistical analysis. Data were subjected to analysis of variance (ANOVA) accessed as per standard procedure of Simple Lattice design. Different quantitative traits from the first and second year were combined for Analysis of Variance procedures of SAS [23]. Effects were considered significant at P values ≤0.05 in the F-test. The phenotypic and genotypic coefficients of variation (PCV and GCV) were estimated as per Burton and DeVane [24]. Heritability in the broad sense and genetic advance (in terms of percentage of mean) were computed according to Allard [25] and Johnson et al. [16], respectively.

$$\text{Dry matter content (\%)} = \frac{\text{Final dry wt.of sample}}{\text{Initial fresh wt.of sample}} \times 100$$

3. RESULTS AND DISCUSSION

Analysis of variance revealed significantly high differences among the genotypes for all the characters which indicated that experimental material possessed good deal of variability for improvement (Table 1). The extent of variability present in the carrot genotypes was measured in terms of range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and expected genetic advance as per cent of mean. Magnitude of phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation for all the characters (Fig. 1). The estimates of PCV and GCV for root length (GCV = 12.05%, PCV = 14.98%), shoot weight (GCV = 10.51%, PCV = 14.71%), carotene content (GCV = 19.03%, PCV = 19.28%), sugar content (GCV = 20.47%, PCV = 20.67%), anthocyanin (GCV = 172.27%, PCV = 172.36%) and lycopene (GCV =43.36%, PCV = 47.74%) respectively were presented in Fig. 1. This was similar with the results obtained by Yadav et al. [26,27]. Priya and Santhi [28] observed high GCV and PCV for carotene content in carrot.

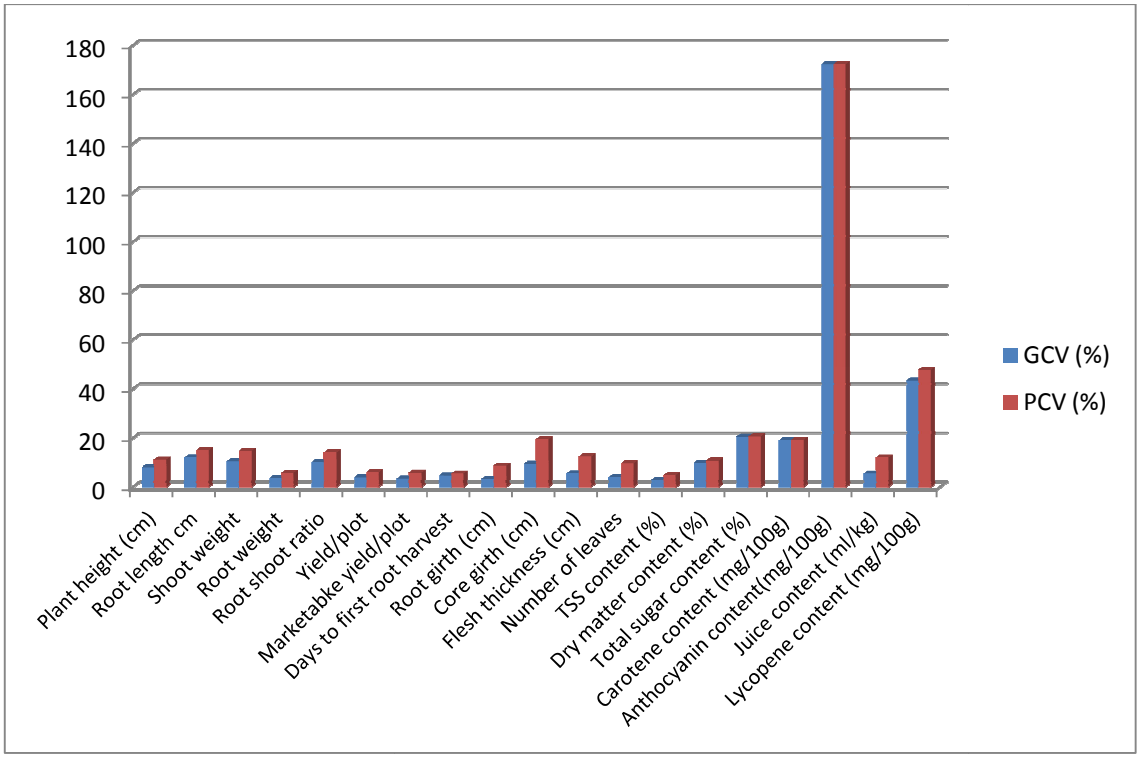

Fig. 1. Genetic coefficient of variation and phenotypic coefficient of variation analysed for different traits in carrot germplasm

Table 1. Pooled analysis of variance (ANOVA) for different traits of carrot genotypes

Characters	Mean square					Error mean square
	Year	Replication (year)	Block (year x replication)	Treatment	Year x treatment	
Plant height	10.09	6.43	14.43	114.01*	46.52*	14.40
Number of leaves	0.85*	0.19	0.1523	1.22*	0.897*	0.15
Shoot weight	613.66*	14.06	12.84	99.98*	40.31*	12.08
Root length	77.63*	2.39	6.26	32.11*	8.86	7.26
Root weight	809.09*	44.85	17.82	103.71*	53.66*	20.51
Root girth	0.61*	0.09	0.07	0.15*	0.1002	0.07
Core girth	0.013*	0.000051	0.0013	0.061*	0.039*	0.0014
Flesh thickness	0.83*	0.00081	0.0047	0.14*	0.09*	0.006
Root shoot ratio	1.12*	0.01	0.014	0.36*	0.12*	0.023
Total root yield	3.22*	0.04	0.13	0.61*	0.27*	0.12
Marketable root yield	6.08*	0.20	0.11	0.49*	0.27*	0.12
Days to first root harvest	30.07	3.45	9.59	63.17*	14.24	11.53
Dry matter cont.	0.007	0.101	0.085	2.89*	0.25*	0.15
TSS	0.11	0.005	0.074	0.43*	0.198*	0.09
Total sugar cont.	0.0044	0.009	0.084	2.33*	0.037	0.10
Juice content	5145.67*	77.08	235.09	8241.40*	5426.85*	218.85
Anthocyanin	0.021	0.78	0.66	1502.06*	1.102	1.13
Carotene	0.03	0.074	0.13	5.39*	0.108	0.10
Lycopene	0.00000031	0.00213	0.0011	0.632*	0.06083*	0.00156072

** 5% level of significance, DF- Year (1), Replication x year (2), Block [year x replication] (32), Treatment (80), Year x treatment (80)*

Table 2. Heritability (h^2), genetic advance (GA) and genetic gain (GG) for different characters studied in carrot

Characters	h^2 (%)	GA	GG	General mean	Range
Plant height (cm)	52.0	9.87	15.22	64.85	50.8-75.8
Root length cm	65.0	6.13	25.57	23.99	13.8-30.8
Shoot weight	51.0	8.92	19.82	45.02	30.1-57.5
Root weight	39.0	7.02	5.97	117.66	101.4-127.2
Root shoot ratio	52.0	0.51	19.31	2.67	2.07-3.56
Yield/plot	43.0	0.59	6.91	8.59	4.9-9.3
Marketable yield/plot	35.0	0.44	5.36	8.29	4.6-9.2
Days to first root harvest	73.0	10.10	10.61	95.21	86.4-109.2
Root girth (cm)	15.0	0.10	3.38	2.96	2.5-3.5
Core girth (cm)	24.0	0.11	12.37	0.90	0.62-1.35
Flesh thickness (cm)	20.0	0.13	6.49	2.06	1.65-2.64
Number of leaves	18.0	0.36	4.50	7.96	6.5-9.4
TSS content (%)	39.0	0.42	4.86	8.74	7.8-9.5
Dry matter content (%)	84.0	2.07	23.88	8.67	5.8-11.8
Total sugar content (%)	98.0	2.26	53.53	4.22	5.1-8.3
Carotene (mg/100g)	97.0	3.70	49.56	7.47	2.3-9.5
Anthocyanin (mg/100g)	100.0	62.34	454.54	13.72	2.8-252.1
Juice content (ml/kg)	21.0	33.57	6.59	509.25	379.5-597.9
Lycopene (mg/100g)	83.0	0.94	103.99	0.90	0.20-1.67

Fig. 2. Variation in root colour of 18 carrot genotypes

Fig. 3. Variation in core colour of 16 carrot genotypes

Heritability is useful in predicting the expected progress to be achieved through selection [25, 16]. The highest broad sense heritability was noticed for anthocyanin content (100%) followed by total sugar content (98.0%), carotene content (97.0%), dry matter content (84.0%), lycopene (83.0%) and days to first root harvest (73.0%) (Table 2). High heritability in carrot was reported for TSS [26] and for root carotene content and root weight [28]. Jain et al. [29] for fresh weight per plant, root weight and root length, Kaur *et al*. [30] also observed high heritability for TSS and carotene content in carrot. High genetic advance was observed for Anthocyanin content (62.34%), juice content (33.57%) and days to first root harvest (10.10%). High genetic gain was observed for anthocyanin content (454.54%) followed by lycopene content (103.99%), sugar content (53.53%), carotene content (49.56%) and root length (25.57%) (Table 2). For carotene content, high genetic gain was noticed by Priya and Santhi [28]. Mean value for different traits were also presented in Table 2. Few important traits were discussed which have positive correlation with yield. Root length was ranged 13.8 to 30.8 cm with maximum value in PC-17 (30.8 cm) followed by PC-161 (30.0 cm). Tewatia et al. [31] observed root length varied 16.9 to 21.4 cm. Thakur and Jamwal [32] have also reported the existence of variability for root length. The highest root weight (127.2 g) was recorded in PC-161 with mean value 117.66 g while Flesh thickness had mean value 2.06 cm and varied 1.65 to 2.64 cm. Teli et al. [33] and Singh et al. [34] also observed large amount of variation in flesh thickness. Highest marketable yield was recorded in PC-161 (9.2 kg $plot^{-1}$) with mean value 7.4 (kg $plot^{-1}$). According to Amin and Singla [27] the marketable yield ranged from 2.6 to 6.9 kg $plot^{-1}$.

Present set of genotypes were also categorized on the basis of qualitative characteristics like root and core colour. The analysed genotypes corresponded to orange, white, red, purple or black root colour (Fig. 2). Self-coloured and light-yellow cores were observed in many genotypes (Fig. 3). The promising genotypes like PC-161, PC-15, PC-43 and PC-173 had self-coloured core.

4. CONCLUSION

In the present investigation, traits like anthocyanin content, lycopene content, total sugar content, dry matter content and carotene content have higher values of GCV, heritability, genetic advance and genetic gain. Selection for these characters would be effective in carrot improvement.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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