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Singh, Davinder

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2022-08-15

Singh, D.; Dhillon, T.S.; Javed, T.; Singh, R.; Dobaria, J.; Dhankhar, S.K.; Kianersi, F.; Ali, B.; Poczai, P.; Kumar, U. Exploring the Genetic Diversity of Carrot Genotypes through Phenotypically and Genetically Detailed Germplasm Collection. Agronomy 2022, 12, 1921.

http://hdl.handle.net/10138/347426

agronomy

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Exploring the Genetic Diversity of Carrot Genotypes through Phenotypically and Genetically Detailed Germplasm Collection

Davinder Singh [1], Tarsem Singh Dhillon [2], Talha Javed [3], Rajinder Singh [2], Jalpa Dobaria [4], Surender Kumar Dhankhar [1], Farzad Kianersi [5], Baber Ali [6], Peter Poczai [7,*] and Uttam Kumar [8]

1 Department of Vegetable Science, CCS Haryana Agricultural University, Hisar 125004, India
2 Department of Vegetable Science, Punjab Agricultural University, Ludhiana 141004, India
3 College of Agriculture, Fujian Agriculture and Forestry University, Fuzhou 350002, China
4 Department of Biochemistry, Anand Agricultural University, Anand 388110, India
5 School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada
6 Department of Plant Sciences, Quaid-i-Azam University, Islamabad 45320, Pakistan
7 Botany Unit, Finnish Museum of Natural History, University of Helsinki, FI-00014 Helsinki, Finland
8 College of Plant Protection, Fujian Agriculture and Forestry University, Fuzhou 350002, China
* Correspondence: peter.poczai@helsinki.fi

Abstract: Germplasm evaluation, classification, characterization, and preservation are the initial requirements for any crop genetic improvement programs meant to promote economically important traits. Mean performance and range of different expressible traits through ANOVA showed highly significant differences within the various genotypes and helped to evaluate several promising carrot genotypes. The multivariate analysis method was used in this study, which was helpful in resolving different phenotypic and genotypic parameters/measurements of big collections into easy interpretable dimensions.The research work was carried out with eighty-one genotypes to evaluate genetic diversity in a germplasm collection through multivariate analysis.The divergence analysis grouped all eighty-one genotypes into ten clusters and cluster VI was found to be the biggest, comprised of 30 genotypes, followed by IV, which was comprised of 16 genotypes. Cluster X exhibited a high mean value for root weight and anthocyanin content; cluster III showed high value for days to 1st root harvest and root girth, and cluster V for dry matter content, total sugar content, and carotene content; respectively. The maximum distance between clusters was recorded among II and X cluster (43,678.5) follow by I and X (43,199.7), and it indicated that genotypes from these far away clusters could be used efficiently in breeding programs to obtain superior hybrids. Total sugar content (36.14%) contributed most to genetic divergence, followed by anthocyanin content (35.74%). Out of four principal components, PC1 largely contributed towards total variation, followed by PC2. The partial variances (%) from the first to fourth PC-axes were 36.77, 25.50, 12.67, and 10.17, respectively. Genotypes like PC-161, PC-173, PAU-J-15, PC-103, and PC-43 were considered superior with respect to marketable yield and its associated traits such as root length and root weight, and hence can be released directly as a variety.

Keywords: carrot; genetic diversity; characterization; cluster analysis; principal component analysis

Citation: Singh, D.; Dhillon, T.S.; Javed, T.; Singh, R.; Dobaria, J.; Dhankhar, S.K.; Kianersi, F.; Ali, B.; Poczai, P.; Kumar, U. Exploring the Genetic Diversity of Carrot Genotypes through Phenotypically and Genetically Detailed Germplasm Collection. *Agronomy* **2022**, *12*, 1921. https://doi.org/10.3390/agronomy12081921

Academic Editors: Antonio M. De Ron and A. Paula Rodiño

Received: 7 July 2022
Accepted: 12 August 2022
Published: 15 August 2022

1. Introduction

The Apiaceae family includes many vegetables, among which carrot is a leading economical root crop, and is a major contributor of pro-vitamin A and dietary fibers [1,2]. It is a phenotypically diverse crop found mostly in both undomesticated and domesticated forms within Asia, Africa, the Mediterranean, and Australia [3,4]. Carrots have a diploid (2n = 2x = 18) genome sized 480 Mb [5] and the average chromosome is found to be 2.34 µm in length [6]. A total of 32,113 genes are predicted from the carrot's genome and around 10,530 genes are found to be unique [5]. Around 5000 years ago, carrots were first found to be cultivated in Afghanistan, Pakistan, and Iran (i.e., Iranian Plateau), and from there,

they were domesticated in other parts of the world [7]. The initial evidence of the use of carrots as a food crop was found fromAfghanistan, Iran, and Persia during the 10th century AD [7,8]. The first-used roots were yellow and purple in color, and there is excellent genetic evidence that wild or undomesticated carrots are the ancestors of the cultivated or domesticated carrot [9]. According to the history of the cultivated modern carrot, root color was found to be the most important structural factor of carrot germplasm [10]. Carrots are classified as Eastern/Asiatic/black-purple/red colored, and as Western/European/orange-yellow/white tap root types, based on pigmentation [11]. The Western type was possibly derived from the Eastern types by natural mutation, hybridization, and artificial selection during the 17th century [12,13].

Carrotis a cool season crop, which grow suitably in a deep, well-drained and light loam soil [14]. In India, carrot crops are grown on an area of 0.109 million ha with a production of 1.893 million metric tons. Based on different phenotypic characters, carrots can be classified into several classes [9]. Phenotypic and genotypic assessment of diversity within carrot cultivars depicted orange, purple, red-yellow, and white-roots that accumulate different types of secondary compounds, particularly anthocyanins, carotenoids, and lutein, which play important roles as antioxidants and anticancer protectants [15–17]. They contain moisture (86–89%), fat (0.2%), protein (0.9%), carbohydrates (10.6%), calcium (80 mg/100 g), and iron (2.2 mg/100 g) [18]. Dietary carrot intake may improve immune-system activity, provide protection against heart stroke, high and low blood pressure, eye-related disorders, osteoporosis, and urinary tract infection [19]. Carrot processed products, such as beverages, candy, chops, and powder, provide various health benefits, which are attributed to the carotenoids preserved, biscuits, and halwa [20,21]. Carrot juice also offers health benefits when blended with other types of fruit juices [22].

Exploring the genetic diversity of carrots might also be helpful in identifying the genetic material [23,24] tolerant/resistant to biotic [25,26] and abiotic [27,28] stressors under the current climate change scenario. Germplasm collection is an important source of natural variants found in nature, and is further found valuable for the analysis of phenotypic and genotypic diversity and for achieving breeding goals [29]. The accessibility of genetically diverse germplasm of carrot requires exploration, collection, assessment, and proper characterization to exploit in crop breeding [30]. The genetic variations of collected germplasm have been evaluated in carrot breeding programs to develop new varieties [29]. The available germplasm can be characterized by evaluating different qualitative and quantitative traits by exploring them in different field experiments [31]. Breeders primarily focus on the detection of genomic variation present in germplasm collections and its utilization for improvement of crops. Carrot breeding played an important role in improving dietary balance through a 50% increase of carotenoids as compared to the last forty years in the United States [32].

Yield is a complex quantitative trait, hence, a complete insight into the association of different qualitative and quantitative traits related to yield is required. Principle components analysis (PCA) was found to be helpful for identifying the most relevant traits from total variation of an original set of variables. Literature is available on phenotypic variability and characterization of carrot crops [33,34]. Modern day carrot research projects have been focused on improving yield and other quality traits, such as color, firmness, texture, and resistance to biotic and abiotic factors [35]. The blend of phenotypic and genetic information converts the evaluated collection of genotypes into a powerful tool for further use in breeding [29]. Hence, the present genetic diversity study aimed to identify potential parental stocks from germplasm available through multivariate analysis [36].

2. Materials and Methods

2.1. Plant Material under Study

The present study was carried out at the experimental area of the Department of Vegetable Science, Punjab Agricultural University, Ludhiana, and Punjab, India. Different biochemical parameters were analyzed at the Biochemistry Laboratory of the same

department. It is located at 30°54′ and 75°48′ North and East latitude, respectively, at a height of 248 m above sea level, with a soil texture of predominantly sandy loam [36]. The plant material consisted of eighty-one (81) genotypes (Table S1) collected from various carrot-growing regions. All the genotypes were evaluated in a Simple Lattice Design in three replications for two years. Spacing was maintained at 67.5 cm row-to-row and 8 cm plant-to-plant. Plot size was 1.35 m^2. Thinning was performed to maintain the proper spacing between plants, after fifteen days of seedling emergence. From mid January onwards, the roots were ready for harvesting. Ten roots (plants) were taken randomly from each genotype, and were replicated for recording observations. The average data of these plants were used for further statistical analysis.

2.2. Traits under Study

Data were collected for different quantitative and qualitative characters pertaining to the study. For qualitative analysis, observations were recorded for root color, shape and core color. Quantitative data observations were recorded for plant height at harvesting stage (measured through meter scale; unit: cm), number of leaves (only the fully grown leaves were taken into consideration), shoot weight (measured with electrical balance; unit: g), root length (tip to the bottom of roots; unit: cm), root weight (leaves and the tip of the roots were removed; unit: g), root girth (measured from one cm below the top of the root with Vernier-Caliper; unit: cm), core girth (as measured root girth; unit: cm), flesh thickness (difference b/w root girth and core girth; unit: cm), root shoot ratio (comparing the weight of root and shoot), total root yield (yield of roots/plot (1.35 m^2); unit: kg), marketable root yield (unmarketable roots were sorted out from the total roots; unit: kg), and days to 1st root harvest (days from sowing to first root harvest). Genotypes were characterized on the basis of biochemical traits also viz., total sugar content (%), lycopene content (mg/100 g), total soluble solids (TSS %) [37], dry matter content (%), carotene content (mg/100 g), juice content (mL/kg), and anthocyanin content (mg/100 g) [38].

2.3. Statistical Analysis

For quantitative parameters, mean values of ten plants from each replication were used for statistical analysis. Data of different traits for both years were combined and subjected to analysis of variance (ANOVA), accessed as per standard procedure of Simple Lattice designthrough SAS software (version 9.0). Effects were considered significant at *p*-values 0.05 in the F-test. The feature of balanced square lattices is that the number of treatments, t, is equal to the square of the number of units per block, k or $t = k^2$. Assume there are t treatments labeled as 1, 2, . . . , k^2 with treatment numbers arranged in a k × k square. For a 3 × 3 square, the treatment numbers arranged in a specific order, such that each row of the square array is considered as a block containing three treatments. To construct Replication II, each column of the array for Replication I is taken to form the three blocks in Replication II. For statistical analysis, adopt the following notation. Let t denote the total number of treatments, k denote the number of units per block or block size, s denote the number of blocks per replication which is equal to k, and r denote the number of replications (for balanced designs, r = k + 1). Let $y_{ij}(l)$ denote the response value of the jth treatment in the lth block within ith replication, i = 1, 2, . . . , k + 1, j = 1, 2, . . . , k^2, l = 1, 2, . . . , rk.

The model is:

$$y_{ij}(l) = \mu + \pi_i + \beta_i(l) + \tau_j + \varepsilon_{ij}(l)$$

where μ, π_i, $\beta_i(l)$, andτj represent the effect of the mean, the replicate, the incomplete block, and the treatment, respectively. $\varepsilon_{ij}(l)$ is the intra-block residual, assumed to be normally and independently distributed with mean 0 and variance σ^2_e. Various ANOVA sums of squares are now presented:

1. Total Sum of Squares:

$$SSTot = \sum y^2_{ij}(l) - CF$$

where, CF = $(\sum y_{ij}(l))^2/(rk^2)$, $\sum y_{ij}(l)$ is the grand total.

2. Unadjusted treatment sum of squares:

$$SSTrtU = \sum T^2_j - CF_r$$

where, T_j is the sum of observations for treatment j.

3. Replication sum of squares:

$$SSR = \frac{\sum R^2_i}{k^2} - CF$$

where, R_i is the sum of observations in replication i.

4. For computing the adjusted block sum of squares, SSB_{Adj}, several quantities are required to be computed. Let B_j denote the sum of block totals for the blocks with treatment j, j = 1, 2, . . . , t, T_j denote the total of the jth treatment total from all replications, and W_j denote the weight for the jth treatment, which is used for adjustment for block,

$$W_j = kT_j - (k + 1)B_j + G$$

where $G = \sum y_{ij}(l)$, or the grand total. Note that $\sum W_j = 0$. The sum of squares for blocks within replication, adjusted for treatment effects, SSB_{Adj}, is defined as:

$$SSB_{Adj} = \frac{\sum W^2_j}{k^3(k + 1)}$$

5. Intra-block error sum of squares:

$$SSE = SST - SSR - SSTrtu - SSB_{Adj}$$

Principal Components Analysis [39,40] is a technique used to restructure data in a way to minimize a bulky set of variables into 'principal components'. PCA was done by analyzing similarity between the genotypes by PC1 and PC2 analysis. Multivariate analysis was done as recommended by Mahalanobis D^2 [41,42] statistic through means of statistical software WINDOSTAT [43]. During initial multivariate analysis, there were nineteen traits, but those contributed less in genetic divergence were excluded from the final analysis of data.

3. Results

3.1. Assessment of Quantitative and Biochemical Traits

Analysis of variance (ANOVA) indicated the huge amount of variability present in experimental material for further improvement (Table 1). The range of variation and mean value for different yield-contributing quantitative traits i.e., root length (range 13.8–30.8 and mean value 23.6 cm), root weight (range 101.4–127.2 and mean value 117.5 g), root shoot ratio (range 2.07–3.56 and mean value 2.66), root girth (range 2.5–3.5 and mean value 3.0 cm), flesh thickness (1.65–2.64 and mean value 2.06 cm), and marketable yield (range 4.6–9.2 and mean value 7.4 kg) showed ample variability for all the studied traits. Furthermore, an adequate amount of variability for biochemical traits was also found in the germplasm evaluated. The range and mean value for biochemical traits were: total soluble solids 7.8–9.5 and 8.7; °Brix, dry matter content 5.8–11.8 and 8.5%; total sugar content 5.1–8.3 and 7.2%; carotene content 2.3–9.5 and 6.9 (mg/100 g); anthocyanin content 2.8–252.1 and 18.2 (mg/100 g); juice content 379.5–597.9 and 510.2 (mL/kg); and lycopene content 0.20–1.67 and 0.90 (mg/100 g), respectively (Table 2).

Table 1. Analysis of Variance (ANOVA) for different traits of carrot genotypes.

Characters	Mean Square					Error Mean Square
	Year	Replication (Year)	Block (Year × Replication)	Treatment	Year × Treatment	
Plant height (cm)	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 (g)	613.66 *	14.06	12.84	99.98 *	40.31 *	12.08
Root length (cm)	77.63 *	2.39	6.26	32.11 *	8.86	7.26
Root weight (g)	809.09 *	44.85	17.82	103.71 *	53.66 *	20.51
Root girth (cm)	0.61 *	0.09	0.07	0.15 *	0.1002	0.07
Core girth (cm)	0.013 *	0.000051	0.0013	0.061 *	0.039 *	0.0014
Flesh thickness (cm)	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 (kg)	3.22 *	0.04	0.13	0.61 *	0.27 *	0.12
Marketable root yield (kg)	6.08 *	0.20	0.11	0.49 *	0.27 *	0.12
Days to 1st root harvest	30.07	3.45	9.59	63.17 *	14.24	11.53
Dry matter content (%)	0.007	0.101	0.085	2.89 *	0.25 *	0.15
Total soluble solids content (°Brix)	0.11	0.005	0.074	0.43 *	0.198*	0.09
Total sugar content (%)	0.0044	0.009	0.084	2.33 *	0.037	0.10
Juice content (mL/kg)	5145.67 *	77.08	235.09	8241.40 *	5426.85 *	218.85
Anthocyanin content (mg/100 g)	0.021	0.78	0.66	1502.06 *	1.102	1.13
Carotene content (mg/100 g)	0.03	0.074	0.13	5.39 *	0.108	0.10
Lycopene content (mg/100 g)	0.00000031	0.00213	0.0011	0.632*	0.06083 *	0.00156072

* 5% level of significance.

3.2. Phenotypic Variability

The present set of genotypes was categorized based on qualitative characteristics like root length (Plate S1), color, core, cortex, and shape (IPGRI, 1998). Root shape, color, flavor, and other morphological traits were conjectured as selection criteria for the improvement of carrot crops [44]. Genotypes were shown to code for orange, white, red, purple, yellow, and black root color with different intensity (Plate S2). The self-color and light-yellow-colored core was present in most of the genotypes (Plate S3). Great variability was observed in root shape within genotypes (Plate S4). Out of 81 genotypes, 18 have conical, 40 tapering, and 23 cylindrical shapes. The promising genotypes like PAU-J-15, PC-43, PC-161, and PC-173 have good length, contrasting color, and self-colored core roots (Plate S5).

Table 2. Mean performance of all the 81 genotypes for different characters studied in carrot.

Serial Number	Genotypes	Plant Height (cm)	Shoot Weight (g)	Root Length (cm)	Root Weight (g)	Root Shoot Ratio	Root Girth (cm)	Core Girth (cm)	Flesh Thickness (cm)	Total Yield (kg)	Marketable Yield (kg)	Days to 1st Root Harvest	Number of Leaves	Total Solube Solids; (°Brix)	Dry Matter (%)	Total Sugar (%)	Carotene (mg/100 g)	Anthocyanin (mg/100 g)	Juice (mL/kg)	Lycopene (mg/100 g)
1.	PC-5	70.8	39.6	26.3	114.3	2.95	2.6	0.78	1.83	8.4	8.2	95.4	8.2	8.3	7.7	7.9	7.0	9.7	533.8	0.88
2.	PC-5-1	69.4	52.5	26.4	107.4	2.07	2.7	0.96	1.65	7.8	7.6	99.3	7.8	8.6	6.8	6.5	6.6	5.4	534.5	1.03
3.	PC-6	69.8	47.8	26.1	117.1	2.47	2.5	0.77	1.71	8.6	8.2	90.5	7.7	8.8	6.6	7.8	6.5	8.7	426.1	1.11
4.	PC-17	68.6	46.5	30.8	120.2	2.57	3.0	0.83	2.16	8.8	8.5	96.4	7.8	9.0	7.0	6.1	6.4	3.9	591.1	1.20
5.	PC-34	66.8	42.9	26.9	116.7	2.76	3.1	0.95	2.07	8.5	8.4	91.3	6.7	8.7	10.9	8.1	7.8	8.7	495.7	0.86
6.	PC-43	70.9	43.2	23.6	124.4	2.94	2.8	0.83	1.93	9.2	8.7	92.5	7.6	8.8	7.2	7.7	6.4	3.8	572.9	0.95
7.	PC-69	66.5	46.0	24.9	122.4	2.64	3.0	0.94	2.01	8.9	8.8	89.6	7.8	8.7	6.6	7.7	7.2	3.3	468.8	0.95
8.	PC-79A	68.9	49.3	29.0	123.6	2.56	2.9	0.75	2.05	9.1	8.6	91.6	8.3	9.4	7.3	8.2	6.3	8.1	492.8	1.65
9.	PC-79B	71.8	48.9	23.7	116.0	2.42	3.0	0.99	1.98	8.5	8.3	96.7	8.6	9.0	6.8	6.4	6.6	8.3	481.0	1.25
10.	PC-80	71.7	50.7	28.0	122.0	2.46	3.0	0.98	1.94	9.1	8.6	90.5	8.1	8.8	6.7	6.1	6.1	7.8	503.0	0.26
11.	PC-100	60.3	44.9	22.9	121.5	2.73	3.1	0.93	2.11	8.9	8.5	89.2	7.3	8.5	6.2	7.9	7.6	3.2	529.0	1.09
12.	PC-103	74.6	45.1	25.4	124.1	2.75	3.2	0.84	2.40	9.2	8.8	90.5	8.9	9.0	6.9	7.5	6.9	8.5	444.1	1.12
13.	PC-105	67.9	44.7	24.2	117.3	2.62	3.3	1.35	1.88	8.7	8.4	99.9	8.4	8.9	5.9	7.8	7.4	7.8	543.8	0.79
14.	PC-112	71.7	52.5	28.3	119.3	2.24	3.3	1.03	2.20	8.7	8.3	97.2	7.8	8.6	7.3	7.9	7.2	12.5	571.0	0.30
15.	PC-14-1	65.7	44.8	24.0	122.9	2.77	2.9	1.10	1.80	9.0	8.7	88.4	8.1	8.9	7.0	6.1	5.2	11.0	531.9	0.87
16.	PC-142	71.5	54.5	22.7	119.8	2.20	2.8	1.14	1.67	8.7	8.5	94.8	8.7	8.8	7.3	7.5	6.5	8.7	423.5	1.35
17.	PC-143	75.8	50.6	22.2	114.2	2.26	3.0	1.00	1.94	8.5	8.4	87.6	8.2	8.1	7.0	7.8	7.0	4.8	446.2	0.92
18.	PC-144	60.2	45.0	24.7	122.5	2.74	3.2	1.03	2.09	9.0	8.6	94.5	8.2	8.8	6.7	7.4	6.6	6.5	472.5	0.34
19.	PC-160	68.9	48.3	26.3	122.8	2.59	3.1	0.78	2.13	9.1	8.6	91.4	8.2	8.6	6.8	7.9	6.6	7.4	514.7	1.13
20.	PC-161	73.5	48.5	30.0	127.2	2.62	3.0	0.69	2.23	9.3	9.2	90.5	8.2	9.5	9.7	8.3	8.7	8.4	583.5	1.67
21.	PAU-J-1	69.6	49.8	23.6	121.2	2.51	3.0	1.03	1.92	8.9	8.6	86.4	6.7	8.5	7.6	6.2	5.8	7.9	503.1	1.21
22.	PAU-J-2	69.5	43.9	26.1	118.7	2.67	2.9	0.87	2.02	8.8	8.4	86.9	7.3	8.5	7.6	6.9	6.8	3.8	470.8	0.99
23.	PAU-J-3	66.8	42.0	27.3	118.3	2.83	3.0	1.02	1.91	8.7	8.7	95.8	7.6	8.9	5.8	6.6	7.0	3.1	508.9	1.04
24.	PAU-J-4	61.3	44.2	23.8	116.0	2.67	3.1	0.91	2.18	8.5	8.2	95.3	8.2	8.4	7.7	7.2	7.3	8.3	507.4	0.70
25.	PAU-J-5	62.7	57.5	24.5	121.2	2.10	3.0	0.86	2.10	8.9	8.5	94.7	7.8	9.0	6.8	7.9	7.1	8.3	530.4	0.31
26.	PAU-J-6	71.0	55.2	23.7	122.2	2.16	3.1	0.87	2.24	8.9	8.5	95.4	7.7	8.6	6.8	5.2	7.4	9.2	561.8	0.29
27.	PAU-J-7	72.2	44.7	22.2	120.6	2.80	3.0	1.15	1.85	9.0	8.5	92.7	7.8	8.9	9.2	5.1	6.4	9.6	496.7	0.79
28.	PAU-J-8	73.4	51.5	27.1	121.5	2.38	2.7	0.79	1.90	8.9	8.5	89.2	8.0	9.0	8.9	6.4	6.9	5.3	560.1	1.17
29.	PAU-J-9	68.3	47.9	26.6	121.6	2.54	2.9	0.86	2.05	8.8	8.4	94.4	8.9	8.6	7.0	7.0	7.7	3.8	528.4	0.97
30.	PAU-J-10	67.2	50.0	25.8	121.3	2.43	3.1	1.01	2.10	8.8	8.7	95.5	8.7	8.4	7.2	5.2	7.9	6.7	506.3	1.02
31.	PAU-J-11	75.4	49.7	21.5	109.3	2.27	3.3	0.85	2.46	8.2	7.7	92.6	8.2	8.4	9.2	7.6	7.1	8.0	414.2	1.38
32.	PAU-J-12	70.2	51.0	28.8	118.1	2.35	3.0	0.84	2.12	8.8	8.4	90.4	8.8	8.7	7.0	8.2	6.8	9.4	474.9	1.28
33.	PAU-J-13	57.1	52.8	26.0	123.2	2.39	2.8	1.02	1.84	9.0	8.7	91.0	7.3	8.7	7.0	6.3	7.6	6.8	454.9	0.33
34.	PAU-J-14	62.9	44.5	23.6	118.6	2.67	3.0	1.24	1.81	8.8	8.4	94.0	8.5	8.5	6.8	6.9	5.7	12.2	499.6	0.24
35.	PAU-J-15	66.3	48.5	26.7	124.4	2.85	3.0	0.95	2.05	9.2	8.8	91.3	9.3	9.4	7.2	7.3	7.7	3.4	544.9	1.07
36.	PAU-KPT-1	67.7	47.2	29.0	116.2	2.53	2.7	0.80	1.92	8.4	8.2	93.6	8.8	8.5	7.0	5.8	7.5	8.3	554.8	1.60
37.	Karnana-1	63.9	45.0	26.6	123.1	2.77	3.1	0.93	2.18	9.0	8.5	90.3	8.5	8.6	7.0	7.7	7.5	3.1	520.7	0.92
38.	Pusa Vrishti	55.0	47.5	24.3	124.0	2.65	3.4	0.84	2.56	8.9	8.7	94.0	6.5	8.6	6.2	7.7	6.8	3.8	556.9	1.06
39.	Pusa Rudira	73.0	46.4	25.8	112.6	2.44	2.6	0.85	1.79	8.3	8.0	89.3	8.4	8.7	6.4	8.0	7.0	9.6	552.0	1.13
40.	Pusa Vasuda	74.5	47.8	26.1	118.8	2.45	2.8	0.84	1.96	8.7	8.4	95.3	8.5	8.6	7.3	8.3	7.6	5.3	437.2	1.11
41.	Hisar Gairic	69.6	48.1	24.9	111.8	2.36	2.8	0.81	1.97	8.2	8.1	94.7	7.4	8.4	6.2	7.6	7.2	3.2	464.9	1.04
42.	PC-171	68.9	54.5	29.3	123.6	2.29	2.7	0.67	2.00	8.9	8.9	92.9	8.2	8.3	6.8	8.0	6.6	11.3	550.0	1.06
43.	PC-172	67.0	52.1	26.0	120.2	2.32	2.8	0.94	1.93	8.8	8.4	90.0	9.4	8.8	6.5	8.3	7.9	12.3	597.9	0.98
44.	PC-173	70.2	49.0	26.2	126.0	2.57	3.4	1.05	2.31	9.1	9.0	92.4	8.6	9.4	8.7	8.3	7.8	5.5	582.3	1.03

Table 2. *Cont.*

Serial Number	Genotypes	Plant Height (cm)	Shoot Weight (g)	Root Length (cm)	Root Weight (g)	Root Shoot Ratio	Root Girth (cm)	Core Girth (cm)	Flesh Thickness (cm)	Total Yield (kg)	Marketable Yield (kg)	Days to 1st Root Harvest	Number of Leaves	Total Solube Solids; (°Brix)	Dry Matter (%)	Total Sugar (%)	Carotene (mg/100 g)	Anthocyanin (mg/100 g)	Juice (mL/kg)	Lycopene (mg/100 g)
45.	PC-174	67.6	47.1	23.5	119.8	2.65	3.0	0.84	2.15	8.8	8.3	96.5	7.3	8.6	8.0	5.9	6.0	11.9	484.0	1.39
46.	PCR	65.6	50.4	27.4	114.7	2.27	2.9	0.79	2.08	8.2	8.1	88.9	7.9	9.2	10.0	8.0	7.4	10.4	515.3	1.30
47.	PCP-1	57.9	37.4	25.7	121.5	3.20	3.1	0.99	2.11	7.9	7.6	98.5	7.8	9.0	9.0	6.3	4.6	107.0	473.1	0.32
48.	PCP-2	67.5	46.6	26.3	123.1	2.64	3.2	1.06	2.09	8.1	7.7	101.0	7.3	8.6	8.5	6.1	5.0	85.3	513.2	0.20
49.	PCP-17A	57.4	40.0	22.8	110.9	2.77	3.0	1.07	1.86	7.6	7.2	89.4	8.4	8.6	8.6	6.0	3.5	92.0	474.4	0.66
50.	PCP-17B	61.8	39.7	27.0	120.0	3.02	3.0	0.90	1.93	7.8	7.3	92.7	7.8	8.7	8.5	5.8	3.4	83.9	538.6	0.24
51.	PCB-2	70.0	38.8	25.2	118.7	3.05	3.1	0.96	1.95	7.7	7.2	97.4	7.5	8.9	7.9	6.2	3.3	180.4	509.0	1.13
52.	Pusa Asita	66.1	43.1	24.3	115.1	2.66	2.9	1.18	1.97	4.9	4.6	91.7	7.8	8.9	9.3	6.0	2.8	135.5	379.5	1.57
53.	PBB	74.5	42.7	25.4	113.6	2.65	2.7	0.85	1.85	7.2	6.9	88.8	8.4	7.8	10.4	6.1	2.3	252.1	575.0	0.32
54.	PCW	71.5	42.8	22.0	116.0	2.70	3.1	1.11	1.98	6.9	6.4	90.4	8.4	8.4	9.0	6.0	5.4	3.7	467.3	0.87
55.	PCY-1	65.7	44.0	25.3	103.9	2.36	2.8	0.89	1.92	5.1	4.8	102.1	8.6	9.4	8.6	6.2	6.9	7.9	470.7	1.39
56.	Pusa Kulfi	64.1	41.3	23.4	119.5	2.89	3.5	1.11	2.33	5.3	5.1	94.8	8.6	9.2	7.7	6.2	6.7	9.4	448.8	1.29
57.	PCO-1	56.2	40.5	15.6	110.2	2.72	2.9	0.62	2.23	5.9	5.7	102.5	8.1	8.6	9.7	7.7	7.6	6.1	441.3	0.25
58.	PCO-3	64.9	40.6	21.3	111.8	2.75	2.9	0.78	2.10	6.3	6.0	97.6	6.9	9.5	10.9	7.8	7.3	8.7	546.8	0.34
59.	PCO-4	55.0	43.2	20.8	111.6	2.58	3.2	0.69	2.51	6.1	6.0	106.1	8.0	8.3	10.0	7.6	7.9	3.7	548.5	0.97
60.	PCO-5	58.6	43.4	24.0	123.7	2.85	3.2	0.92	2.21	6.8	6.5	97.9	7.8	9.3	10.6	8.0	9.5	3.1	568.9	0.96
61.	PCO-7	60.6	32.3	23.4	122.9	3.80	2.9	0.79	2.13	6.6	6.4	97.1	7.6	8.7	10.3	7.5	8.0	8.7	488.9	1.19
62.	PCO-7-1	56.9	37.7	18.0	112.2	2.97	2.9	0.96	1.97	6.2	6.0	98.4	8.5	8.5	10.7	7.7	7.5	6.8	466.0	1.00
63.	PCO-8	61.5	37.2	15.7	115.0	3.09	3.1	0.85	2.28	6.2	6.0	109.2	7.8	9.0	9.8	7.4	8.5	8.1	526.3	0.24
64.	PCO-13	56.2	39.0	20.7	113.5	2.91	3.1	0.79	2.33	6.3	6.0	99.1	8.1	9.0	10.4	7.7	8.0	9.4	514.9	0.21
65.	PCO-14	56.8	36.1	13.8	110.6	3.06	3.2	0.73	2.43	6.1	5.9	98.1	8.0	8.4	9.9	7.9	7.4	2.8	539.2	1.05
66.	PCO-15	57.1	36.5	16.7	112.7	3.08	2.8	0.84	2.01	6.1	5.9	100.0	7.2	9.0	10.6	7.7	8.6	4.8	568.9	0.91
67.	PCO-16	65.5	39.7	17.2	103.5	2.60	3.0	0.75	2.26	5.5	5.4	100.5	8.7	9.1	11.8	7.7	8.7	7.6	510.9	0.97
68.	PCO-17	60.6	33.7	22.0	119.5	3.55	3.2	0.87	2.40	6.5	6.2	99.4	8.3	9.3	10.7	8.1	7.8	8.9	567.9	1.22
69.	PCO-18	57.0	43.3	17.6	101.4	2.34	2.8	0.82	2.40	6.3	6.1	100.8	7.6	8.9	11.4	7.6	7.7	7.5	486.9	0.34
70.	PCO-19	61.3	40.6	19.3	118.2	2.91	2.8	0.76	1.99	6.4	6.1	97.5	8.0	9.3	10.8	7.6	7.9	3.2	425.5	0.97
71.	PCO-20	52.3	30.1	21.0	121.7	4.04	3.3	0.78	2.64	5.4	5.2	97.7	7.9	9.2	10.3	8.0	7.4	9.1	555.9	0.24
72.	PCO-24	54.5	43.8	14.8	109.8	2.51	3.0	0.99	2.04	6.0	5.8	96.1	7.5	8.4	10.7	8.0	7.7	3.6	541.6	1.11
73.	PCO-30	59.6	34.6	24.9	120.6	3.49	3.2	0.96	2.23	6.9	6.7	105.4	8.6	9.3	10.7	8.1	9.0	8.1	571.9	0.33
74.	Early Nantes Totum	62.6	46.9	18.0	114.7	2.45	2.8	0.90	1.87	5.5	5.3	97.9	8.6	8.3	10.6	7.7	7.1	5.1	481.1	0.93
75.	E N Kashmir	57.3	47.0	20.1	109.7	2.33	2.8	0.83	1.88	6.1	5.9	100.5	7.6	8.7	9.4	7.9	7.5	8.5	501.1	1.09
76.	E N Sona	57.5	42.5	23.8	119.0	2.80	3.2	0.87	2.20	5.5	5.4	104.2	7.2	8.3	10.7	8.2	7.4	7.6	577.6	1.66
77.	T1 103 (333)	58.5	43.3	18.4	111.9	2.58	3.1	0.66	2.38	5.9	5.8	99.4	7.5	8.8	10.6	7.5	7.1	8.3	543.6	0.24
78.	Samson-196	50.8	33.1	18.2	118.1	3.57	2.9	0.88	2.02	5.6	5.5	101.8	6.5	9.0	10.6	8.2	7.8	10.1	435.8	1.36
79.	Shin Kuroda	55.3	37.7	16.8	115.2	3.06	2.9	0.85	1.94	6.3	6.0	99.3	8.0	9.0	10.5	7.6	9.3	10.0	459.8	0.28
80.	Pusa Meghali	58.3	44.7	20.8	113.7	2.54	3.1	0.68	2.42	6.1	5.9	99.7	8.0	8.4	10.7	8.0	7.0	8.9	536.2	1.39
81.	Arka Suraj	59.7	47.5	20.0	112.9	2.38	2.9	1.05	1.86	6.1	6.0	100.5	7.4	9.0	10.2	7.5	7.5	10.2	528.8	0.87
	Overall Mean	**64.8**	**44.8**	**23.6**	**117.5**	**2.66**	**3.0**	**0.9**	**2.06**	**7.7**	**7.4**	**95.2**	**8.0**	**8.7**	**8.5**	**7.2**	**6.9**	**18.2**	**510.2**	**0.90**
	Range	**50.8–75.8**	**30.1–57.5**	**13.8–30.8**	**101.4–127.2**	**2.07–3.56**	**2.5–3.5**	**0.62–1.35**	**1.65–2.64**	**4.9–9.3**	**4.6–9.2**	**86.4–109.2**	**6.5–9.4**	**7.8–9.5**	**5.8–11.8**	**5.1–8.3**	**2.3–9.5**	**2.8–252.1**	**379.5–597.9**	**0.20–1.67**
	Critical difference (CD) at 5%	**5.3**	**4.9**	**3.8**	**6.3**	**0.21**	**0.4**	**0.05**	**0.11**	**0.5**	**0.47**	**4.75**	**0.5**	**0.4**	**0.5**	**0.44**	**0.44**	**1.49**	**20.7**	**0.06**

3.3. Multivariate Analysis

3.3.1. Cluster Analysis

Mean data for quantitative traits were subjected to multivariate analysis as it helps to identify genetically diverse parents in germplasmcollections [42]. Divergence analysis based on quantitative traits grouped eighty-one genotypes into ten clusters (Figure S1). Wards' Minimum Variance Dendrogram showing similarity coefficient of all genotypes for 10 clusters and is presented in Figure 1. When a large collection of genotypes have to be classified, hierarchical classification was found to be equally effective to D^2 analysis [45] Cluster VI was found to be the biggest cluster, comprised of 30 genotypes, followed by cluster IV, which had 16 genotypes. Genotypes with black/purple color roots like PCP-2, PCB-2, PusaAsita, and PBB formed distinct clusters showing high genetic dissimilarity with other colored genotypes. Yellowand white-colored roots shared cluster I with red genotypes.

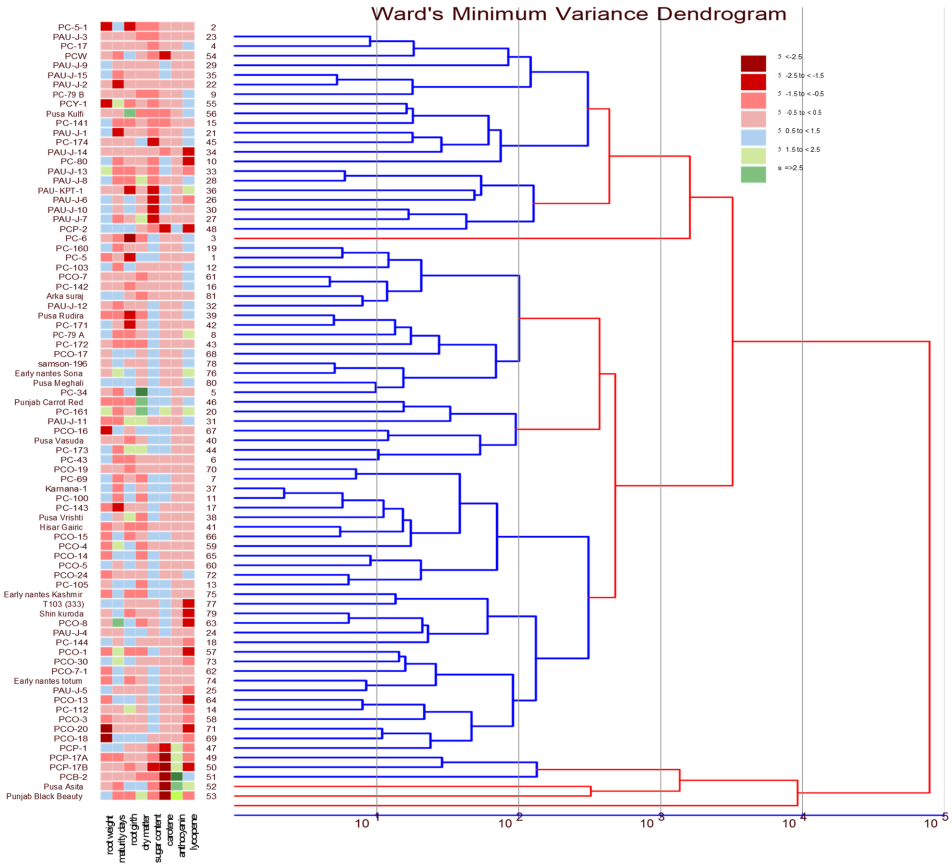

Figure 1. Wards' Minimum Variance Dendrogram (Euclidian's method) showing similarity coefficient and the genetic relationship between these 81 carrot genotypes forming ten clusters.

3.3.2. Estimation of Cluster Mean and Genetic Distance

Clusters with a high mean for yield-contributing traits, like root weight and root girth, with good horticultural traits were considered for the selection of superior genotypes for further hybridization programs. Based on desirable horticultural performance, Cluster X exhibited a high value for root weight and anthocyanin content; cluster III (genotype PBB) for days to 1st root harvest and root girth. Cluster V (PC-161, PC-173) possessed high value for dry matter content, total sugar content and carotene content; cluster IX (PusaAsita) had high value for lycopene content. Cluster means for different traits are shown in Table 3.

Table 3. Cluster means for different traits for 81 genotypes of carrot are shown in the table. Based on the average performance of the genotypes included in the cluster, cluster means for different characters were determined.

Clusters	Root Weight (g)	Days to 1st Root Harvest	Root Girth (cm)	Dry Matter Content (%)	Total Sugar Content (%)	Carotene Content (mg/100 g)	Anthocyanin Content (mg/100 g)	Lycopene Content (mg/100 g)
1	118.03	93.62	2.95	8.58	3.44	7.19	6.79	1.058
2	121.43	92.55	2.89	9.05	2.67	8.33	7.61	0.777
3	122.82	101.14	3.14	8.47	3.03	4.99	85.30	0.205
4	119.51	95.01	2.88	8.42	4.89	7.57	9.205	1.208
5	116.52	92.96	3.05	10.59	4.99	8.69	7.63	1.189
6	115.62	97.46	3.01	8.32	4.68	7.99	6.15	0.693
7	117.21	93.50	2.91	8.62	3.02	3.84	69.36	0.408
8	115.05	97.14	2.97	7.91	3.13	3.29	180.41	1.137
9	118.77	91.55	3.09	9.22	2.93	2.78	135.51	1.566
10	123.17	88.30	2.70	10.27	3.06	2.31	252.1	0.316

Average intra (within) and inter (between) distance between clusters demonstrated the nature of genetic divergence at both levels, respectively. In the current study, inter-cluster distance dominated the intra-cluster distance that represented the broad genetic diversity between the clusters. Similar results were reported by Samal and Jagadeb (1996) [46]. The greatest inter distance was estimated between clusters II and X (43,777.1) followed by I and X (43,199.7) (Table 4). Based on diversity, parents from groups with more inter-cluster distance yielded better recombinants and hybrids, and there may be a chance for the efficient selection of desirable characters [47]. Therefore, it is expected that crossing between the genotypes of cluster II (Superior genotypes PAU-J-10, J-6, J-7) and X (PBB), followed by cluster I (PAU-J-15, PC-174) and X (PBB), will result in F1s with high heterosis and better recombinants in further segregating generations.

Table 4. Intra-(diagonal) and inter-(off diagonal) cluster distance values of 81 carrot genotypes grown under potential environment of Punjab.

Clusters	1	2	3	4	5	6	7	8	9	10
1	**119.89**	191.19	1695.07	273.69	352.78	220.32	8166.87	18,279.17	12,310.03	43,199.74
2		**98.60**	1874.27	540.20	554.22	429.45	8494.65	18,777.75	12,750.21	43,777.10
3			**0.00**	1504.89	1950.35	1845.22	2555.98	9145.84	5090.16	28,310.94
4				**43.46**	127.99	100.15	7377.82	16,881.86	11,255.66	40,983.92
5					**73.18**	136.89	8192.63	18,037.99	12,229.84	42,592.09
6						**71.84**	8260.00	18,264.99	12,400.47	43,124.33
7							**162.93**	2159.81	542.02	14,067.31
8								**0.00**	644.11	5400.47
9									**0.00**	9595.32
10										**0.00**

3.3.3. Percent Contribution and Principal Component Analysis

The maximum percent contribution to genetic divergence was made by total sugar content (36.14%) followed by anthocyanin (35.74%) and carotene content (9.85%) (Table 5). Traits like total sugar content, anthocaynin content, and carotene content stood at 1171, 1158, and 319, respectively.When a trait is ranked first, it means that trait contributed more to divergence than other traits. By placing each character according to transformed uncorrelated values, the percent contribution of each character to the overall divergence was computed. Where n is the total number of characters, rank 1 was awarded for both the biggest mean difference and the lowest mean difference. In order to compute each character's percent contribution, the total ranks of all the characters were multiplied by 100. Percent contribution and times ranked first were estimated through statistical software WINDOSTAT. Breeding through less contributing traits, such as days to 1st root

harvest, lycopene content, and dry-matter content, provides little possibility for further improvement. There is immense scope for improvement of total sugar content, anthocyanin content, and carotene content exploiting those varieties. Different divergence studies have been evaluated previously by Dalsaniya et al. (2009) [48] and Gangadhara et al. (2014) [49].

Table 5. Percent contribution of different traits to genetic divergence.

Traits	Contribution %	Times Ranked 1st
Root weight (g)	0.19	6
Days to 1st root harvest	2.90	94
Root girth (cm)	3.80	123
Dry matter content (%)	6.02	195
Total sugar content (%)	36.14	1171
Carotene content (mg/100 g)	9.85	319
Anthocyanin content (mg/100 g)	35.74	1158
Lycopene content (mg/100 g)	5.37	174

Principal component analysis (PCA) provides expression of the maximum contributor towards the variability at every alignment of demarcation [50]. Traits with maximum fixed value near to one in the first principle component (PC1) control the grouping or clustering pattern more than those with a lesser value near to zero [51]. The cumulative proportion of variation explained by the four PC-axes was 85.12% (Table 6). The partial variance (%) from first to fourth PC-axes was 36.77, 25.50, 12.67, and 10.17, respectively. In the present research, differentiation of all the genotypes into different principle components were due a higher contribution from fewer traits rather than a lesser involvement from each and every trait. Hence, for first principal component (PC-I), anthocyanin is first preference, which has highest positive loading, followed by root girth for PC-II, dry matter for PC-III, and sugar content for PC-IV. Interpretations of PCA are valuable because they provide significant information about the various groups, where few traits are highly important in providing freedom to breeders to operate a particular research program to gain elevated yield benefits and better horticultural traits.

Table 6. Eigene Values, contribution of variance and factor loading for the Principal Component Analysis for different traits.

Traits	PC1	PC2	PC3	PC4
Root weight (g)	0.15	0.54	0.26	0.28
Days to 1st root harvest	−0.20	−0.42	0.24	0.16
Root girth (cm)	−0.20	−0.56	−0.21	−0.26
Dry matter content (%)	0.12	0.27	−0.78	−0.28
Total sugar content (%)	−0.29	−0.08	−0.42	0.81
Carotene content (mg/100 g)	−0.49	0.24	−0.13	−0.03
Anthocyanin content (mg/100 g)	0.54	−0.19	−0.05	0.10
Lycopene content (mg/100 g)	0.51	−0.22	−0.19	0.26
Eigene Value	**2.94**	**2.04**	**1.01**	**0.81**
Partial Variance (%)	**36.77**	**25.50**	**12.67**	**10.17**
Cumulative Variance (%)	**36.77**	**62.28**	**74.95**	**85.12**

Note: PC1, PC2, PC3, PC4-Principal Component 1, Principal Component 2, Principal Component 3, Principal Component 4.

4. Discussion

Characterization of germplasm based on morphological, horticultural, and genetic traits has great significance for plant breeders because these traits help in the commencement of specific crop improvement programs and in the judicious recognition and classification of better-quality genotypes [52]. The multivariate scrutiny study provides valuable knowledge about the preservation of different crop species and genotypes along with identification and genetic upgrading of the latest breeding lines [53].

In the current research, we studied the phenotypic diversity of eighty-one carrot genotypes collected from different regions through qualitative and quantitative traits.

According to previous studies, these traits were found to be useful in differentiating the carrot genotypes [33,54]. The majority-studied traits were of possible economic benefit, particularly the root weight and girth, dry matter, total sugar content, carotene content, anthocyanin content, and lycopene content. Hence, these economic characters present as a potential target for farmers to exploit high production and for breeders to obtain next-generation crop improvement. Thus, the present research study suggested that noteworthy phenotypic and genotypic variability is present among carrot genotypes collected from different regions.

This research work highlighted a broad range of variability in a set of carrot genotypes for all characteristics. Phenotypic and yield attributes have clear differences within the genotypes. The greatest root length was recorded for genotype PC-17 (30.8 cm), followed by PC-161 (30.0 cm), which differed significantly from all other genotypes. The greatest root weight was recorded for genotype PC-161 (127.2 g), followed by genotype PC-173 (126.0 g), and the highest root:shoot ratio (4.04) was recorded in PCO-20, followed by Samson-196 (3.57) and PCO-30 (3.49). Genotype Pusa Kulfi showed maximum root girth (3.5 cm), which was statistically on par with PC-173 (3.4 cm), PusaVrishti (3.4 cm). The greatest flesh thickness was recorded in genotypes PCO-20 (2.64 cm) and the least in PC-5-1 (1.65 cm), whilst the greatest marketable yield was achieved by PC-161 (9.2 kg/plot) followed by PC-173 (9.0 kg/plot). The root length of carrots varied from 16.9 to 21.4 cm [55]. Thakur and Jamwal (2015) [56] also documented the presence of variability for carrot root length. According to Tewatia et al. (2000) [55], root:shoot ratio was positively associated with root diameter, length, and weight, and negatively linked with shoot weight and leaf number. Teli et al. (2017) [57] calculated similar results for root girth. Teli et al. (2017) [57] also recorded a huge quantity of genetic variation in flesh thickness for thirty carrot genotypes ranging from 0.50 to 1.60 cm. It was significantly variable among varieties and correlated to total yield. The yield at marketable stage ranged 2.6 to 6.9 kg/plot In addition, the result is in agreement with Nayak and Nagre (2013) [58], Reshmika et al. (2015) [59], and Tirkey et al. (2018) [60].

Color and flavor were the two most promising traits mentioned in several past studies about carrots [8,61], and these traits remain a focus of present day carrot-breeding programs that promote sweet flavor and self-core orange root for fresh market [3,16]. Carrot germplasm contains huge genetic variability for different carotenoids [62]; and flavor [11,63]. The highest carotene content is observed in PCO-5 (9.4 mg/100 g), followed by Shin Kuroda (9.3 mg/100 g), and PCO-30 (9.0 mg/100 g). According to Holden et al.(1999) [64], carrot roots typically contain 5.7 mg/100 g of beta carotene. Carrot germplasm presents wide genetic variation for carotenoid content [11,62]. Carotene, the bioavailable compound, is widely known as pro-vitamin A, which acts as an antioxidant and provides other benefits [65]. Orange-rooted European genotypes have more carotene content compared to Asian genotypes, while modern-day cultivars contained approximately 20% more carotenoids than older carrot germplasm material. Total sugar content varied between 5.1% to 13.6%, and European genotypes accounted for approximately 18% more total sugars than Asian ones [66].

PCO-16 genotypes offered the greatest amount of dry matter content (11.8%) and genotypes PC-161 and PCO-3 presented the most total soluble solids content (9.5 °Brix). Singh et al. (2004) [67] observed large variation for total soluble solids, which varied from 3.83–8.04%. PC-161 and PC-172 had the highest sugar content (8.3%). In earlier studies, sugar content ranged from 7.0% to 7.8% [54]. PBB had the highest anthocyanin content (252.1 mg/100 g) followed by PCB-2 (180.4 mg/100 g). Kirca et al.(2007) [68] found a high anthocyanin content (1750 mg/kg) in black carrots, with extraordinary quality. From a processing point of view, juice content is a vital trait for genotypic selection. Maximum juice yield was recorded for PC-172 (597.9 mL/kg). PC-161 showed the highest lycopene content of 1.67 mg/100 g, followed by Early Nantes Sona (1.66 mg/100 g) and PC-79A (1.65 mg/100 g).

Traits like color and shape of fruit/root linked with outer appearance of the horticultural crops are significant considerations for modern day consumers [69]. Root color is an important characteristic for the physical appearance of roots because the carotenoid and anthocyanin content are associated with the color of roots [2]. Core color and size of carrot are important traits from a processing point of view, as thinness and self-colored cores are preferred traits for commercial production. Root shape is an important characteristic, which increases the market value of the carrot root. Root shape is influenced by temperature, as long and cylindrical roots can be obtained at 13–20 °C, while temperatures above 20 °C result in shorter and thicker roots [70]. Carrots remain short in size and become conically sharp in shape at high soil density [71–73].

For carrot crop improvement, a simple classification method is required to group or cluster genotypes so that superior lines could be selected for future work. The cluster analysis divided eighty-one genotypes into ten clusters. There were two major clusters having seventy-five genotypes in major cluster I and six genotypes in cluster II (both major clusters were further sub divided). Most of the purple/black colored genotypes formed a distinct cluster (i.e., cluster VII, VIII, IX, and X). Cluster I contained a lowernumber of accessions (14), but it appears to have variability for qualitative traits as it had white- (PCW), yellow- (PCY-1 & Pusa Kulfi), and red- (rest 11 genotypes) colored genotypes (Figure S1). The vertical length of bars in Figure S1 denoted the mean value of traits in each genotype. High diversity in genotype population in this cluster may be due to high environmental variations.

Cluster II and X (43,777.1) showed an upper limit of inter-cluster distance, followed by cluster I and X (43,199.7). Based on diversity, genotypes or parents selected from highly distanced clusters provide superior hybrids on crossing and also provide better opportunities for the useful and efficient extraction of desired traits [36]. Therefore, based on cluster distance studies, a breeding block may promote crossing between genotypes of cluster II, X followed by cluster I, and X to result in better quality F^1 and segregants. Singh et al. 2017 [47] carried out principal components analysis on a group of forty genotypes under four components with Eigen values greater than one. Our study reported that PCA for the first four components considered a maximum estimated variation of 85.12 %. The traits, which load high positively or negatively, indicated that the possibility of positive and negative correlation within different components contributed more to diversity. For many crop species, genetic variability has been explored through PCA [74,75]. In one-way, morphological traits such as root color, shape, core, and cortex color, PCAwill help to use variation already present in carrot germplasm. In addition, a simple classification method for carrot genotypes into diverse clusters or groups is essential to promote their exploitation in crop breeding-improvement programs [76].

5. Conclusions

The selected carrot genotypes collected from various locations showed noteworthy variability with respect to all the traits examined in the research. All the selected carrot genotypes were differentiated on the basis of quantitative and qualitative traits. Genotypes were grouped into different clusters according to the major significant root traits including root weight, length, girth, flesh thickness, core girth, total and marketable yield, TSS, dry matter, total sugar, carotene, anthocyanin content, juice content, lycopene content apart from root color, root shape, core and cortex color in both the PCA and dendrogram.

There is plenty of room for varietal improvement through hybridization and selection, considering the wide genetic diversity present in carrot genotypes. Hence, the result of cluster analysis can contribute directly to the identification of diverse parents for hybrid development programs. It is necessary to take into account the scale of cluster distance cluster meanand the involvement of different traits headed for total divergencefor selection of genotypes. Based on cluster distance, the genotypes from cluster II particularly selected for dry matter, and the carotene content, while genotypes from cluster X are selected for root weight and anthocyanin content. Based on cluster mean, cluster III is selected for root

girth and genotypes from cluster V are selected for dry matter, total sugar, and carotene content. Finally, on the basis of cluster distance, cluster II and X, and on cluster mean, cluster III and V, should be selected as parents for further hybridization programs as well as for the introgression of useful traits in the commercial carrot cultivars.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy12081921/s1, Figure S1. Grouping of 81 carrot genotypes into different clusters by D2 analysis, where length of bars shows the contribution in the genetic variance and color shows the intensity of the variance. Plate S1. Diversity in root length. Plate S2. Diversity in root color. Plate S3. Diversity in core and cortex's color. Plate S4. Diversity in root shape. Plate S5. Few promising genotypes showing germplasm diversity. a. PC-161, b. PC-173, c. PAU-J-15, d. PC-160 e. PC-43, f. PCY-1, g. PCW, h. PCP-1, i. PBB. Table S1. Source of carrot genotypes used for characterization.

Author Contributions: Conceptualization, D.S. and T.S.D.; methodology, D.S.; software, T.J.; validation, T.S.D., R.S. and U.K.; formal analysis, D.S., J.D.; investigation, S.K.D.; resources, B.A.; data curation, F.K.; writing—original draft preparation, D.S., S.K.D. and U.K.; writing—review and editing, P.P., J.D.; visualization, U.K.; supervision, T.S.D.; project administration, R.S.; funding acquisition, P.P. All authors have read and agreed to the published version of the manuscript.

Funding: Open access funding provided by University of Helsinki.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not required.

Data Availability Statement: All the data was provided in the article.

Acknowledgments: Peter Poczai acknowledges the support of the Eötvös Research Fund.

Conflicts of Interest: The authors declare no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

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