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Effect of Mass Selection on Improving Chemical Quality Characters of The Land Race Cultivar "Balady Carrot", (*Daucus Carota*).

Aya A. Abd El-Baki, Ahmed R. Aggour, Mahran M. El Nagar, and Abdelhakeem S. Shams

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Department of Horticulture, Faculty of Agriculture, Moshtohor, Benha University.
Corresponding author: ahmedraggour@yahoo.com

Abstract

A study was conducted during the period 2023 to 2025, to evaluate the efficiency of two cycles of mass selection breeding method on improving some chemical quality characteristics of the land race cultivar " Balady Carrot". The base population P0-G, the population of the first cycle of mass selection MS-Cyc.1-G, and the population of the second cycle of mass selection MS-Cyc.2-G were evaluated in an experiment designed by randomized complete block method, with three replicates. The analysis of variance indicated significant differences for root total sugars, anthocyanin, and carotene contents between the different studied populations, while the differences concerning total soluble solids (TSS%), were not significant. The recorded means of total sugars content of the roots of the plants of the different studied populations, significantly increased with each cycle of mass selection, which were 3.545 %, 4.341 %, and 5.585 %, for the populations P0-G, MS-Cyc.1-G, and MS-Cyc.2-G, respectively. The significantly highest mean value of root anthocyanin content was that associated with the roots of the MS-Cyc.2-G plants (157.207 mg/100 g f.w.), while the lowest was associated with that of the PO-G population (134.423 mg/100 g f.w.). High PCV % and GCV %, were estimated for root total sugars and carotene contents. The broad sense heritability H^2_{bs} were 36.0%, 97.3%, 91.3%, and 86.3%, for root TSS, total sugars, anthocyanin, and carotene content, respectively. Genetic advance as percent of the mean GAM estimates were 6.3%, 46.3%, 15.9%, and 45.1%, for root TSS, total sugars, anthocyanin, and carotene content, respectively.

Key words: Carrot Breeding, Mass Selectin, Efficiency of Breeding Methods, Chemical Quality Characteristics, Genetic Parameters.

Review of Literature

It has been reported that mass selection is the most obvious method for the initial stage of a population improvement program, whereas the high additive genetic variance existing in a new population makes mass selection a relatively efficient method of selection (**Smith, 1936; Hazel, 1943; Kojima. 1961; Falconer, 1960 & 1981; Wolff, 1972**). The advantages of mass selection, in comparison to selection methods based on progenies are its relative simplicity, it takes only one generation per cycle, where most of the selection methods based on progenies take more than one generation per cycle, and it allows for the screening of large numbers of plants (**Wolff, 1972**). Open pollinated cultivars developed through mass selection are more widely adopted than pure lines. In addition, mass selection retains considerable variability and hence further improvement is possible in future by selection in mixed populations of open pollinated cultivars. Moreover, Mass selection method is a very suitable breeding method for preservation of land races cultivars **(Briggs and Knowles, 1977).** The relative efficiency of mass selection depends on the size of the heritability, whereas the higher the heritability the more favorable becomes the mass selection **(Falconer, 1960& 1981; Sprague, 1966)**. Mass selection affects many genes, both those that are directly selected and those that are linked to the selected genes **(Kojima. 1961).** However, mass selection can also lead to the loss of genetic diversity, as less desirable alleles are eliminated from the population **(Kojima. 1961; Briggs and Knowles, 1977; Hassan 2011 & 2012; Aggour, 2024)**. The mechanism of the genetic improvement of using mass selection with cross-pollinated vegetable crops is attributed to the predominance of cross pollination which result in new combinations of genes present in the genetic makeup of the base population with which the breeder started the

mass selection method (**Gardner, 1961; Aggour, 2024**). The importance of existing high genetic variance, high heritability, and high genetic advance, concerning characters of interest, in enhancing the expected improvement progress obtained from selection, has been reported **(Smith, 1936; Hazel, 1943; Falconer, 1960 & 1981; Kojima. 1961; Wolff, 1972).** It is worth mentioning that the genetic variance used in calculating the broad sense heritability "H2bs%" is the total genetic variance which includes both the additive and non-additive gene effects **(Briggs and Knowles, 1977; Hassan, 2012).** The negative effects of mass selection on some characters which are not included in a certain selection index, has been reported **(Falconer, 1960 & 1981; Hassan, 2011). Arscott and Tanumihardjo (2010),** reported that total anthocyanin concentration in the roots of purple carrots varied widely between cultivars and/or within a cultivar. **Lazcano et al. (2001), Kammerer et al. (2004), Arscott and Tanumihardjo (2010), Montilla et al. (2011), Iorizzo et al. (2020), Bhandari et al. (2022)**, and **Pérez et al. (2023),** evaluated carrot genotypes and found variability in root anthocyanin content between the evaluated carrot genotypes. **Yadav *et al.* (2009**), and **Kulkarni *et al.* (2019**), working on carrot genotypes, and found significant differences concerning root sugars content between the different genotypes; however, **Alasalvar et al. (2001), and Baranski et al. (2012)**, found no significant differences among carrot genotypes. **Yadav et al. (2009)**, evaluated different carrot genotypes and found that PCV% was higher than GCV%, for root total sugars. **Gajewski et al. (2007)**, found high environmental effects, i.e., low heritability, for root total sugars content of carrot genotypes. **Yadav *et al*. (2009), Kumar *et al.* (2010),** and **Baranski et al. (2012),** reported significant differences in root carotene content between carrot genotypes. In addition, variability among carrot genotypes concerning carotene contents of roots has been reported (**Amin et al., 2013; Yadav et al., 2009; Kumar et al., 2010; Ou et al. 2010; Kulkarni et al. 2019: Sitkey et al. 2024**). **Moreover, Yadav et al. (2009),** evaluated carrot genotypes and reported high H^2_{bs} for root carotene content. Furthermore, **Priya and Santhi (2015)**, found high values for each of heritability, PCV, GCV, and GAM for root carotene content in carrot genotypes. **Amin *et al* (2013), Moustafa and Abd El-Wahab (2016), Kumar *et al.* (2010)**, and **Yadav *et al.* (2009),** found significant genotype effect concerning root TSS% content of carrot genotypes. In addition, **Kulkarni *et al.* (2019)**, and **Hussain *et al.* (2005),** evaluated different carrot genotypes and found medium H^2_{bs} for root TSS% content.

The objective of the present study was to evaluate the efficiency of mass selection breeding method in improving chemical characteristics of the carrot land race cultivar known by the name "Purple Balady Carrot", which was collected from Giza Governorate.

Materials and Methods

Carrot land race cultivar was used in this experiment, which is known in Egypt by the common name “Balady Carrot”, and is also known in some districts by the name “Red Balady Cultivar”, even though the outer color of the root surface is purple, (Figure, 1).

On January 23, 2023, about 1650 whole plants (plants with foliage and attached roots) of “Balady Carrot”, were collected randomly from a farm in Giza Governorate. Out of these plants, 350 plants were taken randomly from these plants, where its roots were separated from the foliage, about 3 cm above the root shoulder, and placed in paper bags, and then vernalized in the refrigerator at 8 ºC, for 10 days. After this period, these roots were taken out the refrigerator, and replanted in isolated piece of land, i.e., where no other carrot plants can be found within a circle with a diameter of at least 3 km, at private farm in an area called "Ezbet Moshtohor", following the recommendations of the Egyptian ministry of agriculture concerning carrot seed production. The plants grown from these replanted roots at flowering stage were left for open pollination in all directions, to obtain seeds of the base population, which was given the symbol P0-G. On the other hand, the rest of the plants (about 950 plants), were considered the source for the roots of the base population genotype (P0-G). The roots of these plants were visually evaluated, mainly, based on the outer and internal root color as well as accepted root shape and free from defects, where the relatively best 65 roots were selected, i.e., using 5% selection intensity (i). Before vernalization of these selected roots, i.e., roots of the P0-G population, the cut terminal portion of the selected roots were dipped in a dry mixture of the fungicide captan and talcum powder, at a rate of 2%. Then these selected roots of the population (P0-G), were placed in paper bags surrounded by dry wood dust. After that, the paper bags were inserted in plastic bags, which were carefully sealed, and then, kept in the refrigerator at 8 °C, for ten days.

Figure, 1: The Egyptian land race cultivar “Balady Carrot”, Collected from Giza governorate.

On February 2, 2023, the bags containing the best selected roots of the of P0-G plants, were taken out of the refrigerator. The selected roots were taken out of the bags, and replanted in a private farm located in an isolated area called "Ezbet Batata", where no carrot plants can be found within a circle with a diameter of at least 3 km, following the recommendations of the Egyptian Ministry of Agriculture. The plants grown from these replanted selected roots were left for open pollination in all directions, to obtain the seeds which represent the seeds of the first cycle of mass selection, which were given the symbol MS-Cyc.1-G. Collected seeds of the MS-Cyc.1-G. population were divided to two parts, where seeds of each part were kept in a separate paper bag with identification data written on it. Then each paper bag was inserted into well-sealed plastic bag and kept at the refrigerator at 8 °C, for the next planting time.

On October 4, 2023, the plastic bag, i.e., which contained half the seeds of the MS-Cyc.1-G population, was taken out of the refrigerator and the seeds were planted at isolated piece of land at private farm, in an area called “Ezbet Al-Asaria”, at Moshtohor, following the recommendations of the Egyptian Ministry of Agriculture.

On December 17, 2023, when the roots of the plants reached the full development stage, i.e. when the plants reached the end of the first growing season, the plants of the MS-Cyc.1-G population were uprooted from the soil. The roots of about 4000 plants were visually evaluated, mainly based on the outer and internal root color as well as accepted root shape and free from defects, where 250 best roots, were selected, i.e., using 5% selection intensity (i). Before vernalizing the best selected roots of the plants of MS-Cyc.1-D population, the cut terminal portion of the selected roots were dipped in a dry mixture of the fungicide captan and talcum powder, at a rate of 2%. Then, the selected roots were placed in paper bags surrounded by dry wood dust. After that, these paper bags were inserted in plastic bags, which were carefully sealed, and then, kept in the refrigerator at 8 °C, for two weeks.

On December 30, 2023, the bags containing the best selected roots of the plants of MS-Cyc.1-G population, were taken out of the refrigerator, to replant the roots, in an isolated piece of land, where no carrot plants can be found within a circle with a diameter of at least 3 km, at private farm located in an area called "Ezbet Moshtohor", following the recommendations of the Egyptian Ministry of Agriculture. The plants grown from the replanted roots, were left. at flowering stage, for open pollination in all directions, to obtain seeds of the second cycle of mass selection population, which was given the symbol "MS-Cyc.2–G". Collected seeds were divided to two parts, and seeds of each part were kept in a separate paper bag with identification data written on it. Then each paper bag was inserted into well-sealed plastic bag and kept at the refrigerator at 8 °C, for the next planting time.

On October 12, 2024, bags containing seeds of the different populations, i.e., P0-G, MS-Cyc.1-G, and MS-Cyc.2-G, were taken out of the refrigerator in order to plant the seeds of these populations, in a piece of land in private farm located in an area called "Ezbet Moshtohor", using randomized complete block design experiment with 3 replicates. The recommendations of the Egyptian ministry of agriculture, concerning carrot production were followed.

On December 30, 2024, when the roots of the plants of the previously mentioned populations, reached

the consumption stage, the plants were uprooted from the soil. The individual plants and its roots of the different populations, in each experimental plot, where five plants from each experimental unit were selected randomly for the purpose of chemical analysis, to record the following chemical characters:

1-Root content of total soluble solids (TSS), which was determined in random samples of fresh roots from each of the experimental units of the different populations, by hand refractometer; model Carl Zeiss Jena DDR783295 (A.O.A.C, 2012).

2-Root total sugar content, which was determined in random samples of fresh roots from each of the experimental units of the different populations, using the method described by Plata-Guerrero et al., (2009).

3- Root anthocyanin content, which was determined in random samples of fresh roots from each of the experimental units of the different populations, using the method described by Assous et al., (2014).

4- Root carotene content, which was determined in random samples of fresh roots from each of the experimental units of the different populations, using the method described by Biswas et al, (2011).

Statistical Genetic Analysis:

Several parameters were calculated as follows:

Genotypic Variance (VG)

Genotypic variance was estimated according to the following formula used by Jain (1982):

VG= MSG−MSE/ r

Where, MSG = Mean Square for Genotypes (Populations), MSE = Mean Square for error, r=Number of Replications

Environmental Variance (VE)

Environmental variance was estimated according to the following formula, used by Jain (1982):

VE=MSE

Where, MSE = Mean Square for error

Phenotypic variance (VP)

Phenotypic variance was estimated according to the following formula, used by Jain (1982):

VP= VG + VE

Where, VG = Genotypic variance, VE=Environmental variance

Genotypic coefficient of variation (GCV)

Genotypic coefficient of variation was estimated according to the following formula, used by Sivasubramanian and Menon (1973):

GCV= ($\sqrt{VG}/\bar{x}$) × 100

Where, VG = Genotypic variance, $\bar{x}$ = Grand mean of the character

Phenotypic coefficient of variation (PCV)

Phenotypic coefficient of variation was estimated according to the following formula, used by Sivasubramanian and Menon (1973):

PCV= ($\sqrt{VP}/\bar{x}$) × 100

Where, VP= Phenotypic variance, $\bar{x}$ = Grand mean of the character

Environmental coefficient of variation (ECV)

Environmental coefficient of variation was estimated according to the following formula, used by Sivasubramanian and Menon (1973):

ECV= ($\sqrt{VE}/\bar{x}$) × 100

Where, VE= Environmental variance, $\bar{x}$ = Grand mean of the character

Broad Sense Heritability (H^2_{bs})

Broad Sense Heritability, i.e., ratio of genotypic variance to the phenotypic variance, expressed in percentage according to the following formula, used by Johnson et al. (1955):

H_{bs}= (VG/VP) × 100

Where, VG= Genetic variance, VP= Phenotypic variance

Response to Selection Percentage (RS%)

Response to selection percentage was estimated according to the following formula used by Hamd Alla et al. (2012):

R%= [| ($\bar{x}$2 - $\bar{x}$1) | / $\bar{x}$1] x 100

Where, $\bar{x}$1 and $\bar{x}$2, are the mean of a character in certain generation and the mean of same character in the next generation after selection, respectively.

Genetic Advance (GA)

Genetic Advance (GA), measure the expected genetic gain (improvement) in the next generation by selecting a superior genotype under a certain amount of selection pressure (intensity). Genetic advance (GA) was estimated by the following formula used by Burton (1952):

GA= i x H_{bs} x √ VP

Where i= selection differential, At 5% selection intensity K=2.06, Hbs = Heritability, VP= Phenotypic variance.

Genetic Advance as Percent of Mean (GAM)

Genetic advance as percent of mean, was estimated using the following formula used by Burton (1952):

GAM= (GA/ $\bar{x}$) ×100

Where, GA= Genetic Advance, $\bar{x}$ = Grand Mean

Results and Discussions

The analysis of variance (ANOVA) indicated significant differences for root total sugars (g/100 g. f.w)**,** anthocyanin (mg/100 g. f.w), and carotene (mg/100 g. f.w) contents between the population P0-G (Purple Root Carrot "known also as Balady Cultivar", collected from Giza Governorate), mass selection population after first cycle of mass selection (MS-Cyc.1-G), and mass selection population after second cycle of mass selection (MS-Cyc.2-G), (**Table, 1**).

Table 1. Analysis of variance (ANOVA), for TSS, total sugars, anthocyanin, and carotene contents of roots, performed on the populations of base population P0-G (Purple Root Carrot "known also as Balady Cultivar", collected from Giza Governorate), mass selection population after first cycle of mass selection (MS-Cyc.1-G), and mass selection population after second cycle of mass selection (MS-Cyc.2-G).

Source of Variance	df	TSS (°Brix)		Total sugars (g/100 g f.w)	
		SS	MS	SS	MS
Replicates	2	0.440	0.220	0.201	0.101
Genotypes (Populations)	2	1.295	0.647^{ns}	6.345	3.172*
Error	4	0.960	0.240	0.118	0.029
Total	8	2.695		6.664	
CV %		6.75		3.82	
Source of Variance	df	**Anthocyanin (**mg/100 g f.w**)**		**Carotene (**mg/100 g f.w**)**	
		SS	MS	SS	MS
Replicates	2	132.982	61.991	0.402	0.201
Genotypes (Populations)	2	878.711	439.355*	3.556	1.778*
Error	4	54.056	13.541	0.356	0.089
Total	8	1056.750		4.313	
CV %		2.48		8.97	

* Significant at 5% level of significance.
^{ns} not significant at 5% level of significance.

In addition, coefficient of variation (CV%) recorded for root total sugars, anthocyanin, and carotene contents were 3.82%, 2.48%, and 8.97%, respectively, (**Table, 1**). These results indicated the presence of sufficient variability in these characters among the different studied populations, i.e., P0-G, MS-Cyc.1-G, and MS-Cyc.2-G, which created a proper condition to use mass selection method for the improvement of total sugars, anthocyanin, and carotene contents of the roots. The importance of high genetic variance in a new population, concerning characters of interest in enhancing the efficiency of mass selection method to improve such characters, has been reported, (**Smith, 1936; Hazel, 1943; Falconer, 1960 & 1981; Kojima. 1961; Wolff, 1972**). The obtained results agreed with those of **Arscott and Tanumihardjo (2010)**, who reported that total anthocyanin concentration in the roots of purple carrots varied widely between cultivars and/or within a cultivar, and with those of **Yadav et al. (2009), and Kulkarni et al. (2019)**, who evaluated different carrot genotypes, and found significant differences concerning root sugars content between the different genotypes; however, **Alasalvar et al. (2001), and Baranski et al. (2012)**, working on carrot genotypes, and found no significant differences among carrot genotypes, opposite to what was found in the present study concerning root sugars content, (**Table, 1**). In addition, **Yadav et al. (2009)**, **Kumar et al. (2010)**, and **Baranski et al. (2012)**, reported significant differences in root carotene content between carrot genotypes, which was similar to what was found in the present study. On the other hand, the obtained result concerning the analysis of variance (ANOVA) for total soluble solids (TSS%) in roots of the plants, showed no significant differences between the P0-G, MS-Cyc.1-G, and MS-Cyc.2-G populations, (**Table, 1**). This result disagreed with those of **Amin et al (2013)**, **Moustafa and Abd El-Wahab (2016)**, **Kumar et al. (2010)**, and **Yadav et al. (2009)**, who evaluated different carrot genotypes and found significant genotype effect concerning root TSS% content. The range values of the root TSS% content recorded for the plants of the different populations, i.e., P0-G, MS-Cyc.1-G, and MS-Cyc.2-G were found to be (6.214-7.652%; mathematical range=1.411), (6.012-7.620%; mathematical range=1.608) and (7.523-8.253%; mathematical range= 0.730), respectively, (**Table, 2**). The range recorded for root TSS% content in the base population P0-G (1.411) was close to the range recorded for the same character in the population MS-Cyc.1-G, while the effect of mass selection in narrowing the variability of root TSS% content was strongly appeared after the second cycle of mass selection where the range recorded in the MS-Cyc.2-G population was 0.730. In addition, the variability of root TSS% content, measured by coefficient of variation (CV%), in the base population P0-G was 3.78%, which was higher than CV% of same character associated with the populations of MS-Cyc.1-G "3.21%", and MS-Cyc.2-G "1.55%"; but, the second cycle of mass selection was more effective, (**Table, 2**). These results indicated that mass selection was effective in reducing variability of TSS% of plant roots in the base population P0-G. In addition, the mean of TSS% in roots of P0-G plants (6.935%) was significantly lower than values associated with roots of both populations of MS-Cyc.1-G (7.049%), and MS-Cyc.2-G (7.790%), (**Table, 2**), which indicated that mass selection had a slight effect on increasing TSS% contents of the roots. These results agreed with those of **Amin et al. (2013)**, and **Kumar et al. (2010)**, who evaluated different carrot genotypes and found high variability among carrot genotypes concerning root TSS% content. In addition, the obtained results concerning the effect of mass selection on reducing the variability, agreed with that of **Abd-Allah and Moussa (2011)**, who reported that using mass selection for two cycles was effective in reducing coefficients of variation by 25%, for most studied characters in the selected genotypes from three base populations of Egyptian Balady radish ecotypes. Concerning the range of the total sugars content of the roots of the plants in the populations P0-G, MS-Cyc.1-G, and MS-Cyc.2-G, were 3.269-3.977 (mathematical range= 0.708 g./100 g. f.w.), 3.822-5.015 (mathematical range=1.193 g./100 g. f.w.), and 5.060-5.977 (mathematical range= 0.917 g./100 g. f.w.), respectively, (**Table, 2**). In addition, the estimated coefficients of variation, CV% of this character, were 6.52%, 5.50%, and 7.37%, for the populations of P0-G, (MS-Cyc.1-G), and (MS-Cyc.2-G), respectively, (**Table, 2**). In spite of that these results did not provide clear trend for the effect of mass selection in reducing variability in root total sugars contents of the plants of the different studied populations, whether measured by the range or by CV%, the recorded means of total sugars content of the roots of the plants of the different studied populations significantly increased with each cycle of mass selection, where these means were 3.545 g./100 g. f.w., 4.341 g./100 g. f.w., and 5.585 g./100 g. f.w., for the populations P0-G, MS-Cyc.1-G, and MS-Cyc.2-G, respectively, (**Table, 2**). Based on these results it can be concluded that mass selection was efficient in improving total sugars content of the roots. The variability in total sugars content of the roots found among the studied populations, (**Table, 2**), was similar to that reported by **Yadav et al. (2009)**, **Kulkarni et al. (2019)**, and **Sitkey et al. (2024)**, who evaluated carrot genotypes, and observed variability among the different genotypes concerning this character.

Table 2. Range (R), mean ($\bar{x}$) ± standard error of the mean (S.E.), and coefficient of variation (CV%), for root TSS %, total sugars (g/100 g f.w), anthocyanin (mg/100 g f.w) and carotene (mg/100 g f.w) contents, estimated for the different populations, i.e., base population P0-G (Purple Root Carrot "known as Balady Cultivar", collected from Giza Governorate), mass selection population after first cycle of mass selection (MS-Cyc.1-G), and mass selection population after second cycle of mass selection (MS-Cyc.2-G).

Generations	Parameter (Statistic)	TSS °Brix	Total sugars g/100 g f.w.	Anthocyanin mg/100 g f.w.	Carotene mg/100 g. f.w.
P0-G	R	6.214-7.652	3.269-3.977	114.562-154.563	2.448-3.332
	$\bar{x}$ ± S.E.	6.935±0.16	3.545±0.08	134.423±3.73	2.968±0.09
	CV%	3.78%	6.52%	9.36%	8.89
MS-Cyc.1-G	R	6.012-7.620	3.822-5.015	142.635-165.145	3.476-4.984
	$\bar{x}$ ± S.E.	7.049±0.18	4.341±0.13	152.888±2.76	4.206±0.16
	CV%	3.21%	5.50%	5.76%	11.29
MS-Cyc.2-G	R	7.523-8.253	5.060-5.977	145.584-163.145	2.245-3.788
	$\bar{x}$ ± S.E.	7.790±0.10	5.585±0.12	157.207±2	2.769±0.17
	CV%	1.55%	7.37%	3.58%	18.02%
LSD 5% for mean comparison		0.8913	0.3098	4.646	0.5113

The range of the anthocyanin contents recorded for the roots of the base population P0-G plants was found to be "114.562-154.563; mathematical range = 40.001 mg/100 g f.w.", while the range recorded for the same character in mass selection population after first cycle of mass selection (MS-Cyc.1-G), was "142.635-165.145; mathematical range=22.51 mg/100 g f.w.", and that recorded after the second cycle of mass selection (MS-Cyc.2-G) was "145.584-163.145; mathematical range= 17.561 mg/100 g f.w.", (**Table, 2**). In addition, the coefficient of variation (CV%) for anthocyanin content recorded for the roots of the base population P0-G plants was found to be "9.36%", which was higher than CV%, associated with the population MS-Cyc.1-G "5.76%", and the value associated with the population MS-Cyc.2-G "3.58%", (**Table, 2**). The previously mentioned reduction in the variability of root anthocyanin contents, whether measured by range or CV%, observed in the different studied populations, starting from the base population P0-D, and down to the MS-Cyc.2-D population (**Table, 2**), indicated the efficiency of mass selection method in reducing the variability of this character with the two cycles of selection. The efficiency of mass selection method in reducing the variability of certain quantitative characters of plants in evaluated base populations, has been reported (**Kojima, 1961**; **Abd-Allah and Moussa, 2011**). In addition, the results concerning the variability in root anthocyanin content observed in the present study, agreed with those of **Lazcano et al. (2001)**, **Kammerer et al. (2004)**, **Arscott and Tanumihardjo (2010)**, **Montilla et al. (2011)**, **Iorizzo et al. (2020)**, **Bhandari et al. (2022)**, and **Pérez et al. (2023)**, who evaluated carrot genotypes and found variability in root anthocyanin content between the evaluated carrot genotypes. Concerning means of root anthocyanin content in roots of the plants of the different studied populations, the significantly highest mean value of root anthocyanin content was that associated with the roots of the MS-Cyc.2-G plants (157.207 mg/100 g f.w.), followed by those values associated with MS-Cyc.1-G (152.888 mg/100 g f.w.), and PO-G (134.423 mg/100 g f.w.), (**Table, 2**). This increase in root anthocyanin content with the two cycles of mass selection, indicated the success of mass selection in improving the anthocyanin contents of the roots. The range values of the carotene content recorded for plant roots of the base populations P0-G, MS-Cyc.1-G, and MS-Cyc.2-G, were (2.448-3.332; mathematical range=0.884 mg/100 g. f.w.), (3.476-4.984; mathematical range=1.508 mg/100 g. f.w.) and (2.245-3.788; mathematical range=1.543 mg/100 g. f.w.), respectively, (**Table. 2**). On the other hand, the variability in carotene contents in the roots of the plants of the different populations measured by CV%, was 8.89% in the base population P0-G, while the value associated with the population MS-Cyc.1-G was 11.29%, and that associated with the population MS-Cyc.2-G was 18.02%, (**Table, 2**). Moreover, the average values of carotene content calculated for the roots of the base populations P0-G, MS-Cyc.1-G, and MS-Cyc.2-G, were 2.968, 4.206, and 2.769, respectively, (**Table. 2**). These results indicated the failure of mass selection in reducing the variability in root carotene content, whether measured by the range or CV%, in plant roots of the different populations as expected, which could be attributed to the fact that selection for high root carotene content was not included in the selection index used in the present study. In addition, the cross-pollination nature of carrot could have resulted in new combination of genes, which led to obtaining the previously mentioned results. The formation of new combinations of genes controlling certain quantitative characters in cross pollinated plants exposed to mass selection process has been reported, (**Gardner, 1961**). The variability among carrot genotypes concerning carotene contents of roots has been reported (**Amin et al., 2013**; **Yadav et al., 2009**; **Kumar et al., 2010**; **Ou et al. 2010**; **Kulkarni et al. 2019**; **Sitkey et al. 2024**).

Low estimates for both phenotypic coefficient of variation "PCV %", and genotypic coefficient of variation "GCV %", were found for root TSS% content, i.e., (8.437%), and (5.060%), respectively, (**Table, 3**). In addition, the observed low GCV implied limited potential for genetic improvement of root TSS% content character through mass selection. The importance of high genetic variance existence in a population concerning certain character of interest, to enhance the efficiency of selection for this character, has been reported (**Briggs and Knowles, 1977**; **Hassan, 2012**). Moreover, medium value of broad sense heritability "H^2_{bs}" (36%), and low value of genetic advance as percentage of the mean" GAM" (6.255%), were obtained (**Table, 3**). These results indicated absence of the requirements, i.e., high heritability along with high genetic advance, to approve the suitability of using mass selection to improve root TSS% content. The importance of existing high genetic variance, high heritability, and high genetic advance, concerning characters of interest, in enhancing the expected improvement progress obtained from selection, has been reported (**Smith, 1936**; **Hazel, 1943**; **Falconer, 1960** & **1981**; **Kojima. 1961**; **Wolff, 1972**). On the other hand, the selection response (SR%) for TSS% content of roots, recorded in the populations of the first cycle of mass selection (1.640%), and that recorded in the second cycle of mass selection (10.510%), (**Table, 4**), which indicated that the second cycle of mass selection was more effective in increasing root TSS% content. The obtained results, concerning H^2_{bs}, agreed with that of **Kulkarni et al. (2019)**, and **Hussain et al. (2005)**, who evaluated different carrot genotypes and found medium H^2_{bs} for root TSS%. Concerning root total sugars content, high phenotypic

coefficient of variation "PCV %" (23.102%), and high genotypic coefficient of variation "GCV %" (22.789%), were estimated (**Table, 3**). As revealed the PCV % estimate was slightly higher than the estimate of GCV %, which indicated that most of the phenotypic variance observed among the studied populations, i.e., P0-G, MS-Cyc.1-G, and MS-Cyc.2-G, concerning root total sugars content was attributed to total genetic effect. These results were confirmed by the obtained high broad sense heritability estimate "H2bs", i.e., 97.304%, (**Table, 3**). In addition, high genetic advance as a percentage of the mean "GAM" was found (46.302%), (**Table, 3**). The high heritability accompanied by the high GAM %, are dependable genetic parameters which should be used together to predict the expected progress in the improvement of root total sugars content in carrot through selection (**Smith, 1936**; **Hazel, 1943**; **Falconer, 1960** & 1981; **Kojima. 1961**; **Wolff, 1972**). So that, the obtained results indicated that mass selection method was suitable choice to improve root total sugars content, in the present study. This conclusion, was confirmed by the high response to selection percentage (RS%) for root total sugar content recorded in the population of the first cycle of mass selection which was 22.45%, and that recorded in the second cycle of mass selection which was 28.66%, (**Table, 4**). Based on these findings, it can be concluded that mass selection as a breeding method was efficient method to improve root total sugars content of the land race cultivar "Purple Balady Carrot". Concerning the obtained results concerning PCV% and GCV% for root total sugars were similar to those reported by **Yadav et al. (2009)**, who evaluated different carrot genotypes and found that PCV% was higher than GCV%. On the other hand, the obtained result concerning H^2_{bs}, disagreed with that of **Gajewski et al. (2007)**, working on carrot, and found high environmental effects, i.e., low heritability, for root total sugars content. Low estimates for both phenotypic coefficient of variation "PCV %", and Low genotypic of variation "GCV%", were found for root anthocyanin content, i.e., (8.437%), and (8.062%), respectively, (**Table, 3**). In spite of the calculated PCV% and GCV% values were low, the very small difference between the two values indicated that most of the observed variation in the different studied populations, i.e., P0-G, MS-Cyc.1-G, and MS-Cyc.2-G, concerning root anthocyanin content was mainly attributed to the total genetic effects. On the other hand, the estimate of the broad sense heritability "H2bs%", was high, i.e., (91.307%), (**Table, 3**) It is worth mentioning that the genetic variance used in calculating the broad sense heritability "H2bs%" is the total genetic variance which includes both the additive and non-additive gene effects (**Briggs and Knowles, 1977**; **Hassan, 2012**). In addition, the genetic advance as a percentage of the mean-GAM was found to be medium, (15.869%), (**Table, 3**), which could be due to the partial involvement of additive genetic variance in the inheritance of root anthocyanin content. The obtained high H2bs, and medium GAM, (**Table, 3**), can be considered a partial fulfillment of the requirements necessary to use mass selection in improving root anthocyanin content with relatively high efficiency. The importance of high heritability and high genetic advance in enhancing the efficiency of selection for quantitative characters, has been reported (**Smith, 1936**; **Hazel, 1943**; **Falconer, 1960** & **1981**; **Kojima. 1961**; **Wolff, 1972**). The response to selection percentage (RS%) value recorded in the population of the first cycle of mass selection was 13.74%, and that recorded after the second cycle of mass selection was 2.82%, (**Table, 4**), which indicated that the first cycle of mass selection was more effective than the effect of the second cycle.

Concerning root carotene content, high phenotypic coefficient of variation "PCV %" (25.344%), and high genotypic coefficient of variation "GCV %" (23.550%), were estimated (**Table, 3**). As revealed the PCV % estimate was slightly higher than the estimate of GCV %, which indicated that most of the phenotypic variance observed among the studied populations, i.e., P0-G, MS-Cyc.1-G, and MS-Cyc.2-G, concerning root carotene content was attributed to total genetic effect. These results were confirmed by the high broad sense heritability estimate "H^2_{bs}", which was 86.349%, (**Table, 3**). In addition, high genetic advance as a percentage of the mean "GAM" was (45.072%), (**Table, 3**). The high heritability, accompanied by the high genetic advance, have been reported to be useful genetic parameters which can be used to predict the progress concerning the improvement of quantitative characters through selection (**Smith, 1936**; **Hazel, 1943**; **Falconer, 1960** & **1981**; **Kojima. 1961**; **Sprague, 1966**; **Wolff, 1972**; **Aggour, 2024**). On the other hand, high selection response (SR%) was recorded in the populations of the first cycle of mass selection (41.71%) for the root carotene content, while negative response to selection percentage (RS%) was recorded in the second cycle of mass selection, i.e., -34.16%, for root carotene content, (**Table, 4**). The observed decrease in the mean of root carotene content that associated with plants of the population MS-Cyc.2-G comparing to the mean that associated with plants of the population MS-Cyc.1-G, which could be due to the environmental effects and/or to the formation of new combination of genes controlling root carotene content. It is worth mentioning that the selection index used in the present study for mass selection included only physically phenotypic characters, which were easily to select plants carrying such characters in the studied populations, e.g., root external dark purple color as well as good root shape, size, without any deformation (see materials and methods).

Table 3. Phenotypic coefficient of variation (PCV %) [K], genotypic coefficient of variation (GCV %) [K], broad sense heritability (H^2_{bs})[L], expected genetic advance from selection (GA), and genetic advance as percent of mean (GAM) [M], for TSS (), total sugars (g/100 g f.w), anthocyanin (mg/100 g f.w), carotene (mg/100 g f.w) contents of roots, recorded after two cycles of mass selection performed in the base population (P0-G) of the local carrot genotype "Purple Root Carrot", collected from Giza Governorate.

Parameter	TSS °Brix	Total sugars g/100 g f.w	Anthocyanin mg/100 g f.w	Carotene mg/100 g f.w
PCV %	8.437	23.102	8.437	25.344
GCV %	5.060	22.789	8.062	23.550
H^2_{bs} %	36.000	97.304	91.307	86.349
GA	0.454	2.079	23.452	1.436
GAM %	6.255	46.302	15.869	45.072

[K]The phenotypic (PCV %), and genotypic (GCV %) coefficient of variation estimates were categorized as described by ***Chauhan et. al, 2024***, as follows: < 10% = Low; 10 – 20 % = Medium; >20 % = High.

[L]The heritability estimate was categorized as described by ***Robinson et. al.*, 1949**, as follows: < 30% = Low; 30 - 60% = Medium; and >60% = High.

[M]Genetic advance as percent of mean (GAM), was categorized as described by **Burton, 1952**, as follows: < 10% = Low; 10 – 30 % = Medium; >30 % = High

Table 4. Means ($\bar{x}$), for the base population P0-G (Purple Root Carrot "known as Balady Cultivar", collected from Giza Governorate), population of the first cycle of mass selection (MS-Cyc.1-G), and population of second cycle of mass selection (MS-Cyc.2-G), as well as Response to Selection Percentage (RS%) in the populations of the first cycle of mass selection, and second cycle of mass selection, for TSS (°Brix), total sugars (g/100 g f.w), anthocyanin (mg/100 g f.w), and carotene (mg/100 g f.w) contents of roots..

Means ($\bar{x}$) and Response to Selection Percentage (RS%)	TSS °Brix	Total sugars g/100 g f.w	Anthocyanin mg/100 g f.w	Carotene mg/100 g f.w
P0-G - $\bar{x}$	6.935	3.545	134.423	2.968
MS-Cyc.1-G - $\bar{x}$	7.049	4.341	152.888	4.206
RS% After Cyc. 1 of Mass Selection	1.640%	22.45%	13.74%	41.71%
MS-Cyc.2-G - $\bar{x}$	7.790	5.585	157.207	2.769
RS% After Cyc. 2 of Mass Selection	10.510%	28.66%	2.82%	-34.17%

This might unintentionally, led to decrease in root carotene content, because the genes responsible for high carotene production, like the Y and Y2 genes (**Hassan, 2011**), possibly were not closely linked to the characters being included in the selection index applied in the present study. Based on this suggestion it can be mentioned that the selection index applied in the present study was not specifically designed to enhance root carotene content. The negative effects of mass selection on some characters which are not included in a certain selection index, has been reported (**Falconer, 1960** & 1**981**). The results concerning the observed high H^2_{bs} for root carotene content, agreed with that of **Yadav et al. (2009)**, working on carrot genotypes and reported high H2bs for root carotene content. In addition, the obtained results agreed with that of **Priya and Santhi (2015)**, working on carrot genotypes, and found high values for each of heritability, PCV, GCV, and GAM for root carotene content

References

A.O.A.C. (2012). Official Methods of Analysis Association of Official Analytical Chemists International, 19th Ed., Maryland, USA.

Abd-Allah, A. A., & Moussa, M. (2011). Efficiency of mass selection on improving characteristics of native radish (*Raphanus sativus* L.). *Alexandria Science Exchange Journal*, 32(JULY-SEPTEMBER), 346-353.

Aggour, A. Reda. 2024. Notes of Post-Graduate Course "Advanced Vegetable Breeding". College of Agriculture; Department of Horticulture; Benha University.

Alasalvar, C., Grigor, J. M., Zhang, D., Quantick, P. C., & Shahidi, F. (2001). Comparison of volatiles, phenolics, sugars, antioxidant vitamins, and sensory quality of different colored carrot varieties. *Journal of agricultural and food chemistry*, 49(3), 1410-1416.

Amin, A., Singh, P. K., & Wani, K. P. (2013). Genotypic Variation for Quantitative and Qualitative Traits in Asiatic and European Carrot (Daucus carota L. var. sativa). *Indian Journal of Plant Genetic Resources*, 26(02), 151-154.

Arscott, S. A., & Tanumihardjo, S. A. (2010). Carrots of many colors provide basic nutrition and bioavailable phytochemicals acting as a functional food. *Comprehensive reviews in food science and food safety*, 9(2), 223-239.

Assous, M. T. M., Abdel-Hady, M. M., & Medany, G. M. (2014). Evaluation of red pigment extracted from purple carrots and its utilization as antioxidant and natural food colorants. *Annals of Agricultural Sciences*, 59(1), 1-7.

Baranski, R., Allender, C., & Klimek-Chodacka, M. (2012). Towards better tasting and more nutritious carrots: Carotenoid and sugar content variation in carrot genetic resources. *Food research international*, 47(2), 182-187.

Bhandari, S. R., Choi, C. S., Rhee, J., Shin, Y. K., Song, J. W., Kim, S. H., ... & Lee, J. G. (2022). Influence of root color and tissue on phytochemical contents and antioxidant activities in carrot genotypes. *Foods*, 12(1), 120.

Biswas, A. K., Sahoo, J., & Chatli, M. K. (2011). A simple UV-Vis spectrophotometric method for determination of β-carotene content in raw carrot, sweet potato and supplemented chicken meat nuggets. *LWT-Food Science and Technology*, *44*(8), 1809-1813.

Briggs F. N. and Knowles. (1977). Introduction to Plant Breeding. Reinhold Publishing Corporation. USA. pp 426.

Burton. (1952) George Washington. Proceedings of the Sixth international Congress of Agriculture; 1:277-283.

Falconer, D. S. (1960). Introduction to quantitative genetics. Oliver and Boyd. Edinburgh and London, 365 pp.

Falconer, D. S. (1981). Introduction to quantitative genetics. Ed. 2. Longmans Green, London/ New York.

Gajewski, M., Szymczak, P., Elkner, K., Dabrowska, A., Kret, A., & Danilcenko, H. (2007). Some aspects of nutritive and biological value of carrot cultivars with orange, yellow and purple-colored roots. Journal of Fruit and Ornamental Plant Research, 67(1), 149-161.

Gardner, C. O. (1961). An evaluation of effects of mass selection and seed irradiation with thermal neutrons on yield of corn. *Crops, Vol*. 1: 241-245.

Hamd Alla, W. A., Bakheit, B. R., Abo-El Wafa, A. & El-Nahrawy, M. A. (2012). Effect of mass selection for root characteristic on forage yield and some of its components in alfalfa. Egypt. Journal. Plant Breed. 16 (3):1 – 18.

Hassan, A. A. (2011). Vegetable crop breeding. Al-Dar Al-Arabia Lil-Nashr wa Tawzee, Cairo, 808 pp.

Hassan, A. A. (2012). Fundamentals of plant breeding. Al-Dar Al-Arabia Lil-Nashr wa Tawzee, Cairo, 685 pp.

HAZEL, L. N. (1943). The genetic basis for constructing selection indexes. *Genetics* 28:476-490.

Hussain, K., Singh, D. K., Ahmed, N., Gazala Nazir, G. N., & Rafiqua Rasool, R. R. (2005). Genetic variability for qualitative and quantitative traits in carrot (*Daucus carota* L.). *J. Environment and Ecology*, 23(3), 644-647.

Iorizzo, M., Curaba, J., Pottorff, M., Ferruzzi, M. G., Simon, P., & Cavagnaro, P. F. (2020). Carrot anthocyanins genetics and genomics: Status and perspectives to improve its application for the food colorant industry. *Genes*, *11*(8), 906.

Jain JP. (1982). Statistical techniques in quantitative genetics. Tata Mc Graw Hill Publishing Company, New Delhi;103.

Johnson, H.W., Robinson, H.F., & Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybean. Agriculture. Journal. 47:314-318.

Kammerer, D., Carle, R., & Schieber, A. (2004). Quantification of anthocyanins in black carrot extracts (Daucus carota ssp. sativus var. atrorubens Alef.) and evaluation of their color properties. *European Food Research and Technology*, *219*, 479-486.

Kojima, K. (1961). Effects of dominance and size of population on response to mass selection. *Journal of Genetic Research, Campus*. Pp. 177-188

Kulkarni, C. C., Manikanta, D. S., Poleshi, C. A., Cholin, S. S., Raghavendra, G., Ambika, D. S., & Patil, B. B. (2019). Genetic Variability, Heritability and Genetic Advance for Economic Root Traits in Asiatic and European Type Carrot Germplasm Lines (Daucus carota L.). international journal of current applied microbiology science, 8(7), 2553-2563.

Kumar, R., Vashisht, P., Gupta, R. K., Singh, M., & Kaushal, S. (2010). Characterization of European carrot genotypes through principal components and regression analyses. *International Journal of Vegetable Science*, *17*(1), 3-12.

Lazcano, C. A., Yoo, K. S., & Pike, L. M. (2001). A method for measuring anthocyanins after removing carotenes in purple colored carrots. *Scientia Horticulturae*, *90*(3-4), 321-324.

Montilla, E. C., Arzaba, M. R., Hillebrand, S., & Winterhalter, P. (2011). Anthocyanin composition of black carrot (Daucus carota ssp. sativus var. atrorubens Alef.) cultivars Antonina, Beta Sweet, Deep Purple, and Purple Haze. *Journal of Agricultural and Food Chemistry, 59*(7), 3385-3390.

Moustafa, Y., Abd El-Aal, H., & Abd El-Wahab, M. (2016). Introduction of purple and deep purple F1 carrot hybrids to Egypt showed high antioxidant activity and high content of total flavonoids and phenols. *Journal of Basic and Applied Research in Biomedicine*, *2*(2), 148-156.

Ou, C. G., Deng, B. T., Bao, S. Y., Zhao, Z. W., Hu, H., Zhuang, F. Y., & Mao, S. M. (2010). QTL mapping for contents of main carotenes and lycopene in carrot (Daucus carota L.). *Yi Chuan= Hereditas*, *32*(12), 1290-1295.

Pérez, M. B., Carvajal, S., Beretta, V., Bannoud, F., Fangio, M. F., Berli, F., & Cavagnaro, P. F. (2023). Characterization of purple carrot germplasm for antioxidant capacity and root concentration of anthocyanins, phenolics, and carotenoids. *Plants*, *12*(9), 1796.

Plata-Guerrero, R., Guerra-Hernandez, E., & Garcia-Villanova, B. (2009). Determination of reducing sugar and asparagine in potatoes. *Journal of Liquid Chromatography & Related Technologies,* 32(17), 2556-2568.

Priya, P. A., & Santhi, V. P. (2015). Variability, character association and path analysis for yield and yield attributes in carrot (Daucus carota L.). *Electronic Journal of Plant Breeding*, *6*(3), 861-865.

Sitkey, V., Cicova, I., Docolomansky, P., Havrlentova, M., Ivanisova, E., & Belajova, E. (2024). Comparison of the chemical composition and morphological characteristics of different carrot. *Journal of microbiology, biotechnology and food sciences*, e10779-e10779.

Sivasubramanian S, Menon M. (1973). Genotypic and phenotypic variability in rice. Madras Agriculture journal. 60:1093-1096

Smith, H. F. (1936). A discriminant function for plant selection. *Annals of eugenics*, *7*(3), 240-250.

Sprague, G. F. (1966). Quantitative Genetics in Plant Improvement. In: Kenneth J. Fry (ed.); Plant Breeding. Iowa State University Press, Ames, Iowa. pp. 315-347.

WOLFF F. (1972). Mass Selection in Maize Composites By Means of Selection Indices. *Mededelingen Landbouwhogeschool. Wageningen* 72-1. Doi. 633.15:631.527.2

Yadav, M., Tirkey, S., Singh, D. B., Chaudhary, R., Roshan, R. K., & Pebam, N. (2009). Genetic variability, correlation coefficient and path analysis in carrot. *Indian Journal of Horticulture*, *66*(3), 315-318.