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ELUCIDATION OF GENETIC VARIABILITY, HERITABILITY, CORRELATION AND PATH COEFFICIENT IN CARROT (*Daucus carota* L.)

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ABSTRACT

An experiment was conducted at the Punjab Agricultural University, Ludhiana, India, for 2 years (2019-20 and 2020-21), to study the genetic variability, heritability, correlation and path coefficient analysis in 28 genotypes of Asiatic carrot under 8 environments. The experiment was laid out in RBD with three replications. The analysis of variance showed that the genotype's mean sum of squares was significant for all the traits studied, indicating that significant variation existed among them. A wide range of variation existed for average root length, root weight, root diameter, core diameter and root shoot ratio i.e., 14.5-21.0 cm, 40.9-77.8 g, 2.2-2.7 cm, 0.93-1.56 cm and 0.86 to 1.29, respectively. The average marketable yield of genotypes ranged between 365.55 to 584.55 q ha^{-1}. Vegetative traits like shoot length varied from 42.0-64.7 cm, shoot weight from 44.71-80.14 g, and the number of leaves from 5.4 -7.2 among all genotypes. The magnitude of phenotypic coefficient of variation was greater than the corresponding genotypic coefficient of variation for all the traits indicating that trait expression is environmentally influenced. Root-shoot ratio, shoot length, number of leaves, root length, and root diameter all have exhibited highest heritability and moderate genetic advance that suggested additive gene action. Strong character association of root length, root diameter and root weight with marketable yield suggested as selection criteria for higher yield.

Keywords: Correlation, *Daucus carota*, heritability, path analysis, variability

INTRODUCTION

Carrot (*Daucus carota* L.) 2n = 2x = 18 is a well-known root crop belonging to Apiaceae family which has its origin in Afghanistan (Iorizzo *et al.,* 2013). It is one of the most economically important root vegetable crops which ranks 10th amongst the most cultivated root vegetable crop in the world with a worldwide annual production (carrot and turnips) of 44.76 million tons and a total cultivation area of 1.12 million ha (FAOSTAT, 2021). Roots of this crop are rich source of fibre, β-carotene, minerals, vitamins, phenolics and antioxidants which have been reported to reduce the risk of cancer, cell deterioration and other harmful diseases (Nicolle *et al.*, 2004; Yadav, 2009; Sharma *et al.,* 2012). Improvement in any crop depends upon the magnitude of genetic variability present in the germplasm (Singh *et al.*, 2019). High amount of genetic variation and broad genetic base due to its cross pollinated and protandrous nature makes this crop highly interesting to the breeders (Koul *et al.,* 1989).

Heterosis has been very well exploited word over in carrot. In carrot, root yield and quality traits such as uniformity in shape and size, root colour, core colour, carotene, etc. are some of the most important traits to be improved (Peterson and Simon, 1986, Rubatzky *et al*., 1999). These traits can be enhanced by unravelling the genetic mechanism underlying these traits and their association vary with the genotype (Santhi *et al.,* 2015 and Meghashree *et al.*, 2018b). Most of these traits are polygenic and environmentally controlled having continuous variation (Chakraborty *et al.,* 2017). Higher the amount of variability in the traits, more are the chances of effective selection for better phenotypes. Phenotypic and genotypic coefficients of variation are useful in detecting the amount of variability present in the germplasm. High heritability in broad sense indicated that a large proportion of phenotypic variance are attributable to the genotypic variance and that these character differences among the genotypes are real (Singh *et al.,* 2020). Improvement in the mean genotypic value of the selected families over base population is known as genetic advance. In plant breeding, correlation analysis provides information about yield components and thus helps in the selection of superior genotypes from diverse genetic populations. Most of the correlation studies in past have been conducted on 10 to 15 genotypes in carrot (Yadav *et al.*, 2009, Chakraborty *et al.*, 2017; Kumar *et al.*, 2021); whereas in present study, 28 genotypes have simultaneously been taken under consideration which provides a clear picture to understand the correlation mechanism. The complex inheritance pattern of yield and quality traits necessitate their thorough understanding in order to strengthen the carrot breeding program. The extent and direction of association between yield and quality traits can be ascertained by genetic correlation; but direct and indirect effects of different yield related parameters are determined by path coefficient analysis. Genetic attributes could be ranked according to their contribution by the breeder (Dewey and Lu, 1959). Dewey and Lu (1959) developed a statistical technique for path analysis which helps in understanding the cause of association and provides information about cause and effect situations. Path analysis assists plant breeders in making selection as it dissects the correlation of different traits into direct and indirect effects (Samonte *et al.*, 2005). Direct yield selection may not be particularly successful (Kulkarni *et al.,* 2019), therefore the main objective of this study was to assess the genetic variability and character association, and understand the direct and indirect effects of different traits on the root yield of carrot.

MATERIALS AND METHODS

Twenty-eight carrot genotypes were procured from various sources *i.e.*, genotypes PC-34, PC-100, PC-160, PC-161, PC-165, PC-171, PC-172, CC-PAU-1, Punjab Black Beauty and Punjab Carrot Red from PAU, Ludhiana, genotype CC-SW-1 from Ludhiana, genotypes CC-J1, CC-J2, CC-J3 and CC-J4 from Jalandhar, genotypes SWO-2 and BMMD from Hoshiarpur, genotypes CC-P-HYB and CC-P-Desi from Patiala, genotypes BJS and Ferozpur Selection from Ferozepur, genotype CC-MH-1 from Maharashtra, genotype CC-Sadhuwali from Rajasthan, genotype Pusa Vristy from IARI New Delhi, genotypes CARTVAR-2 and CARTVAR-6-1 from AICRP-ICAR, and genotypes Long Red and Desi Red from Private sources. The study was conducted at Vegetable Research Farm, Department of Vegetable Science, PAU, Ludhiana (30˚55’ N and 75˚54’ E longitude) during the years 2019-20 and 2020-21. The experiment was laid out in a randomized complete block design with three replications. Seeds were sown in field during August, September, October and November 2019-20 and 2020-2021. Tractor-operated inclined plate planter was used for direct planting of carrot seeds on beds at a spacing of 67.5 cm. The machine planted 4 rows on each bed with 10 cm spacing between rows and 8 cm between plants. All the agronomic practices were followed as per the recommendations of Package and Practices of PAU Ludhiana (Anonymous, 2019).

Root yield and component traits

The roots were harvested 90 to 95 days after seed sowing at proper harvesting stage. The data was recorded for root length (cm), root weight (g), root diameter (cm), core diameter (cm), shoot length (cm), shoot weight (g), root-shoot ratio, number of leaves plant^{-1}, and marketable yield (q ha^{-1}).

Statistical analyses

The traits were statistically analysed with ANOVA on OPSTAT developed by Sheoran *et al.* (1998). The data for variability studies were analysed using ‘R.3.5.1’ software (R Core Team, 2014). Then the variance component and coefficient variation were worked out as per Allard (1960).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{GMSS - EMSS}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = (\sigma^2_g + \sigma^2_e)$$

$$\text{Error variance } (\sigma^2_e) = EMSS$$

Where, σ^2_g = (GV) Genotypic variance, σ^2_p = (PV) Phenotypic variance, and σ^2_e = (EV) Error variance; GMSS = Genotypic mean sum of square, EMSS = Error mean sum of square

The heritability in broad sense and expected genetic advance were computed according to Weber and Moorthy (1952).

$$\text{Heritability } (h^2) = \frac{\sigma 2g}{\sigma 2p} \times 100$$

Where, σ^2_g = Genotypic variance; σ^2_p = Phenotypic variance

Estimates of genotypic and phenotypic coefficient of variance were obtained by using the formulae given by Burton (1952).

$$\text{Genotypic coefficient of variance (GCV)} = \frac{\sigma g}{x} \times 100$$

$$\text{Phenotypic coefficient of variance (PCV)} = \frac{\sigma p}{x} \times 100$$

Where, X = Grand mean of traits, σg = Genotypic standard deviation, σp = Phenotypic standard deviation

The correlation and path analysis were calculated as suggested by Al-jobouri *et al.* (1958) and Dewey and Lu (1959), respectively.

RESULTS AND DISCUSSION

Greater germplasm diversity means a higher possibility of selecting the superior genotypes from the plant population. Since majority of economically important traits are polygenic, hence it is crucial to determine whether genotype variability is heritable or attributable to environmental variables. So, it is critical to separate heritable and non-heritable components of phenotypic variance. The phenotypic (PCV) and genotypic coefficients of variability (GCV) are useful for determining the character divergence. Direct yield selection may not be very effective or precise; that's why correlation provides insight into yield components and promotes genotype selection from a diverse genetic population. The analysis of variance (ANOVA) revealed a significant variation for all the traits studied (Table 1). All the parameters were subjected to further analysis to know the association pattern across the parameters studied.

Table 1: Analysis of variance of different traits of carrot

Sources	Character d.f.	Root length (cm)	Root weight (g)	Root diameter (cm)	Core diameter (cm)	Marketable yield (q ha^{-1})
RMSS	16	2.189	0.95	2.145	2.414	1.275
GMSS	27	199.229*	587.303*	33.021*	330.674*	899.288*
EMSS	432	1.001	1	1	1	1.001

Sources	Character d.f.	Root: shoot ratio	Shoot length (cm)	Shoot weight (g)	Leaves plants^{-1} (No.)
RMSS	16	0.455	1.877	1.903	1.078
GMSS	27	221.43*	346.605*	1063.136*	186.831*
EMSS	432	1	1	0.999	1

RMSS - Replication mean sum of squares, GMSS - Genotypic mean sum squares, EMSS - Error mean sum of squares; *Significant at P = 0.05

Table 2: Range, grand mean, GCV, PCV, heritability, genetic advance and genetic advance as per cent of mean for different traits of carrot

Characters	Range	GM ± SEm	GCV (%)	PCV (%)	H^2 (%)	Genetic advance (%)	Genetic advance % of mean
Root length (cm)	14.54-21.04	19.50 ± 0.18	6.19	6.41	93.46	2.41	12.34
Root weight (g)	40.89-77.77	67.75 ± 0.42	10.31	10.36	98.93	14.31	21.12
Root diameter (cm)	2.24-2.74	2.49 ± 0.04	6.24	6.71	86.43	0.3	11.95
Core diameter (cm)	0.93-1.56	1.21 ± 0.03	13.12	13.67	92.00	0.31	25.92
Root-shoot ratio	0.86-1.29	1.08 ± 0.01	9.77	9.9	97.37	0.21	19.87
Marketable yield (q ha^{-1})	365.55-584.55	485.27 ± 0.75	10.15	10.19	99.24	30.67	20.83
Shoot length (cm)	42.02-64.66	55.43 ± 0.38	7.97	8.06	97.85	9.01	16.25
Shoot weight (g)	44.71-80.14	65.81 ± 0.28	11.99	12.01	99.61	16.22	24.64
Leaves plant $^{-1}$ (No.)	5.36-7.20	6.23 ± 0.07	8.13	8.37	94.4	1.01	16.28

GM - Grand mean, GCV - Genotypic coefficient of variance, PCV - Phenotypic coefficient of variance, H^2 - Heritability in broad sense

The estimates of genetic parameters of variability, *viz*., phenotypic and genotypic coefficients of variation (PCV and GCV) along with heritability in broad sense (h^2) and genetic advance (GA) as a percentage of the mean for different characters are given in Table 2. For interpretation of the results of genetic variability, heritability and genetic advance, we followed Sharma (1994), Johnson *et al.* (1955) and Deshmukh *et al.* (1986). A wide range of variation existed for average root length, root weight, root diameter, core diameter and root: shoot ratio *i.e.*, 14.5-21.0 cm, 40.9-77.8 g, 2.2-2.7 cm, 0.93-1.56 cm and 0.86 to 1.29, respectively. The average marketable yield of genotypes ranged from 365.55 to 584.55 q ha^{-1}. Vegetative traits such as shoot length varied from 42.0-64.7 cm, shoot weight from 44.71-80.14 g, and the number of leaves from 5.4 -7.2 among all genotypes. Similar reports for variability in germplasms for various horticultural traits in carrots have been reported by Kumar *et al.* (2010), Gupta *et al.* (2012), Meghashree *et al*. (2018b) and Singh *et al.* (2020).

The values of phenotypic coefficient of variation (PCV) were of higher magnitude than that of genotypic coefficient of variation (GCV) for all the characters indicating that the environment played an important role in influencing the expression of traits (Table 2). The results suggested that selection will not be effective on the basis of genotype alone. As per Deshmukh *et al.* (1986), PCV and GCV values > 20% are regarded as high, whereas the values < 10% are considered low and values between 10-20% medium. Genetic variability for the characters revealed moderate variation in terms of both GCV and PCV for characters such as root weight, core diameter, marketable yield and shoot weight.

Although GCV indicates the existence of genetic variation, the estimates of heritability and genetic gain are still needed to find out how much of that variation is heritable. The estimate of heritability acts as a predictive instrument in exercising the reliability of phenotypic value (Johnson *et al.*, 1955). Sharma (1994) classified the heritability value <50% as low, 50-80% as moderate and > 80% as high. The heritability in broad sense was analysed for the nine characters wherein the highest heritability was recorded for all the traits. Tewatia *et al.* (1990), Kumar *et al.* (2011), and Teli *et al.* (2017) also recorded the highest heritability for the root weight, root shoot ratio, yield, shoot weight and number of leaves. Heritability coupled with genetic advance is more useful than heritability alone in predicting the result of selecting the best individual genotype as it suggests the presence of additive gene effects. Genetic advance is a useful indicator of the progress that can be expected as a result of exercising the selection on pedigree. Johnson *et al.* (1955) classified genetic advance as percentage of mean as values from 0-10% are low, 10-20% are moderate and $\geq$ 20% are high. High heritability coupled with high genetic advance was recorded for core diameter, shoot weight, root weight and marketable yield. High heritability with moderate genetic advance in root-shoot ratio, shoot length, number of leaves, root length and root diameter indicating that heritability of these traits is mainly

Table 3: Genotypic and phenotypic correlation coefficient for different traits in carrot

Ch.		RL	RW	RD	CD	RSR	MY	SL	SW	NOL
RL	P	1 **								
	G	1 **								
RW	P	0.894 **	1 **							
	G	0.930 **	1 **							
RD	P	0.491 **	0.6255 **	1 **						
	G	0.559 **	0.6811 **	1 **						
CD	P	0.3521 **	0.5076 **	0.8387 **	1 **					
	G	0.3831 *	0.5248 **	0.9292 **	1 **					
RSR	P	0.1767 NS	0.1965 NS	0.073 NS	0.088 NS	1 **				
	G	0.1794 NS	0.1869 NS	0.0749 NS	0.086 NS	1 **				
MY	P	0.7545 **	0.8186 **	0.5595 **	0.3358 **	0.1964 NS	1 **			
	G	0.7796 **	0.8256 **	0.6014 **	0.3484 NS	0.1976 NS	1 **			
SL	P	0.574 **	0.6079 **	0.3136 **	0.2802 **	-0.5042 **	0.341 **	1 **		
	G	0.5925 **	0.6156 **	0.3501 NS	0.2958 NS	-0.5228 **	0.3482 NS	1 **		
SW	P	0.5901 **	0.6415 **	0.4168 **	0.3005 **	-0.5897 **	0.5014 **	0.906**	1 **	
	G	0.6105 **	0.6474 **	0.4549 *	0.3138 NS	-0.5931 **	0.5049 **	0.9176**	1 **	
NOL	P	0.315 **	0.3742 **	0.2907 **	0.2441 *	-0.697 **	0.285 **	0.8203**	0.8439**	1 **
	G	0.3271 NS	0.3885 *	0.3138 NS	0.259 NS	-0.7262 **	0.2925 NS	0.8519**	0.87**	1 **

Ch. = Characters: RL = Root length, RW = Root weight, SW = Shoot weight, RSR = Root shoot ratio, RD = Root diameter, CD = Core diameter, NOL = Number of leaves, SL = Shoot length, MY = Marketable yield. *Significant at P = 0.05 and **Significant P = 0.01.

owing to additive gene action and phenotypic selection for these traits will be effective (Table 2). Similar results have been reported by Jain *et al.* (2010); Gupta *et al.* (2012); Asima *et al.* (2013) and Singh *et al.* (2019).

The correlation coefficient analysis was performed to understand the association pattern among different traits. Correlation coefficient analysis helps in deciding the component traits on which the trait selection should be made. Genotypic and phenotypic correlation for marketable yield and component traits in carrot are given in Table 3. The genotypic correlations were higher than their corresponding phenotypic correlation coefficients for all traits. These results indicate strong inherent association between these traits which are in agreement with Singh *et al.* (2002), Thakur and Jamwal (2015) and Singh *et al.* (2019). Further, the marketable yield showed strong positive significant correlation with root weight (0.8256 and 0.8186), root length (0.7796 and 0.7545) and root diameter (0.6014 and 0.5595). These results are in line with Gupta *et al.* (2012) and Chakraborty *et al.* (2017). Root length (0.930 and 0.894), shoot weight (0.6474 and 0.6415) and root diameter (0.6811 and 0.6255) exhibited positive and significant correlation with root weight and these characteristics may be considered as a major root yield contributing traits in carrot. Root diameter was significantly correlated with core diameter (0.8387). Hence, for effective crop yield selection should be oriented towards the higher value for these component characters like, root weight, root length and root diameter. Similar results were also reported by Singh *et al.* (2002); Kaurav *et al.* (2018) and Singh *et al.* (2019).

Knowledge of correlation alone is often misleading as the correlation observed may not always be true. Correlation only measures the mutual association without considering causation while the path coefficient analysis not only measures the relative importance of the characters but also specifies the cause (Verma *et al.,* 2018). Path coefficient analysis is a very powerful statistical tool that indicates the effect of independent variables (causes) on dependent variables (marketable yield), while recognizing the impacts of multi-collinearity (Akanda *et al.,* 1996). Therefore, path analysis was used to partition the correlation coefficient of studied traits into the direct and indirect effect on marketable yield. Direct and indirect effects of all the traits on marketable yield were computed at the genotypic level and presented in Table 4. The data revealed that root weight (0.870 and 0.800) had the maximum

Table 4: Genotypic and phenotypic direct and indirect effects of different traits in carrot

Ch.		RL	RW	RD	CD	RSR	SL	SW	NOL	SY
RL	P	0.013	0.778	0.085	-0.086	-0.015	-0.368	-0.064	0.002	0.408
	G	-0.142	0.743	0.361	-0.251	0.01	-0.284	-0.105	0.017	0.431
RW	P	0.012	0.87	0.11	-0.124	-0.016	-0.389	-0.069	0.002	0.424
	G	-0.132	0.8	0.44	-0.344	0.01	-0.295	-0.111	0.02	0.439
RD	P	0.006	0.545	0.175	-0.203	-0.005	-0.201	-0.045	0.001	0.285
	G	-0.079	0.545	0.646	-0.61	0.004	-0.168	-0.078	0.016	0.326
CD	P	0.005	0.442	0.145	-0.24	-0.005	-0.18	-0.032	0.001	0.2
	G	-0.054	0.42	0.6	-0.656	0.005	-0.142	-0.054	0.013	0.217
RSR	P	0.002	0.172	0.01	-0.014	-0.08	0.324	0.064	-0.003	-0.277
	G	-0.025	0.149	0.048	-0.056	0.0531	0.251	0.102	-0.038	-0.287
SL	P	0.008	0.529	0.055	-0.069	0.042	-0.641	-0.097	0.004	0.51
	G	-0.084	0.492	0.226	-0.194	-0.028	-0.48	-0.158	0.044	0.529
SW	P	0.008	0.558	0.073	-0.073	0.049	-0.58	-0.108	0.004	0.569
	G	-0.087	0.518	0.294	-0.206	-0.031	-0.44	-0.172	0.045	0.584
NOL	P	0.004	0.326	0.052	-0.059	0.058	-0.526	-0.091	0.005	0.515
	G	-0.046	0.311	0.203	-0.17	-0.039	-0.409	-0.15	0.052	0.54

Ch = Characters: RL - Root length, SL - Shoot length, RW - Root weight, SW - Shoot weight, RSR - Root shoot ratio, RD - Root diameter, CD - Core diameter, NOL - Number of leaves, RY - Root yield, SY - Shoot yield, MY - Marketable yield, GY - Gross yield; Phenotypic residual effect: 0.1079; Genotypic residual effect: 0.066

positive direct effect on marketable yield followed by root diameter (0.175 and 0.646) and number of leaves (0.005 and 0.052). The root length exhibited a positive indirect effect through root weight (0.778 and 0.743), root diameter (0.085 and 0.361) and number of leaves (0.002 and 0.017) on marketable yield. Root weight of carrot contributed positively to marketable yield indirectly through root diameter (0.110 and 0.440) and number of leaves (0.002 and 0.020). Besides this, root diameter also had positive indirect effect through root weight (0.545 and 0.545) and number of leaves (0.001 and 0.016); whereas core diameter showed positive indirect effect via root weight (0.442 and 0.420), root diameter (0.145 and 0.600) and number of leaves (0.001 and 0.013). Besides these traits number of leaves positively contribute to the yield via root weight (0.326 and 0.311) and root diameter (0.052 and 0.203) The phenotypic and genotypic residual effect in the path coefficient was 0.1079 and 0.0666, respectively which explained most of the traits involved in the expression of variability have been taken into the consideration in this study. Positive direct effect of root weight on yield was also reported by Priya and Santhi (2015). Similarly, Yadav *et al.* (2009) reported the negative direct effect of shoot length and shoot weight on the yield of carrot.

Conclusion: The study revealed that the genetic variation was available among most of the studied traits, which can be exploited by selection or hybridization. High heritability with genetic gain also implies that the selection can be effective tool to bring genetic improvement as traits are controlled by additive gene action. Hence, due consideration needs be given to the diversity of these traits in future for the improvement of yield and its contributing traits.

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