Genetic analysis of root yield and its contributing traits in tropical carrot (*Daucus carota* L.)

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ABSTRACT

Information on the genetic basis of root yield and quality of different coloured carrot genotypes is essential for planning the breeding strategies for genetic improvement. The objective of this study was carried out during winter and spring-summer season of 2011-15 to determine the gene action involved in the inheritance of economic traits of three carrot hybrids by using six generation mean analysis (P_1, P_2, F_1, F_2, B_1 and B_2). Three crosses of carrot were analyzed to study the gene actions involved in the inheritance of economic traits, *viz.*, root length, root weight, shoulder diameter, root diameter, flesh thickness, core diameter and root to top ratio. The genetics of root weight, root to top ratio and root diameter in the all White Pale crosses were complementary type of gene interaction, which shows the genetic improvement of carrot tropical with respect to these traits can improved through biparental matting followed by mass and cyclic recurrent selection in advanced generation.

Key words: Carrot, complimentary epistasis, duplicate epistasis, gene action, recurrent selection, generation mean analysis.

INTRODUCTION

Carrot (*Daucus carota* L.; 2n = 2X = 18) is a cool weather crop grown in temperate and subtropical regions for its edible storage tap roots both for fresh as well as processed vegetable throughout the world and is most important of all the root crops. The objective of carrot breeding programmes is to evolve high yielding and well adapted cultivar with desirable economic traits. Breeding for such cultivars requires through understanding of genetic components of carrot. Many breeding procedures have been brought up for increasing yield of carrot but in order to bring up best hybrid combinations, a large population of carrot inbred lines are crossed to each other. Before the improvement of high yielding carrot cultivars and/or hybrids, it is important to study the economic components of gene interaction and effects. The genetic component of complex traits plays important role launching a sound breeding strategy. Therefore, the present experiment was undertaken to determine the inheritance pattern of economic traits in carrot involving four phenotypically contrasting tropical carrots. These inheritance studies will help in the understanding of gene interaction and breeding selection of potential parental lines or crosses. Furthermore, these breeding strategies will help to accelerate the tropical carrot breeding with generation of new carrot cultivars and hybrids.

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MATERIALS AND METHODS

The experiment was carried out at Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi in the winter season for four years. The experiment was laid out in a randomized block design with three replications. Four different coloured carrot (*D. carota* L.) inbred lines, *viz.*, White Pale (yellow), IPC-126 (purple), IPC-122 (red) and PM (orange), which were used for development of six generations. Six basic generations (P_1, P_2, F_1, F_2, B_1 and B_2) of three crosses (White Pale × IPC-126, White Pale × IPC-122 and White Pale × PM) were raised and planted in a randomized block design in three replications at vegetable research farm during the November 2014 as four ridges of for each parent and F_1s, ten ridges for B_1 and B_2 each, 15 ridges for F_2 plants. The four parental and 3 F_1 generations were represented by 20 plants within each replication, while each segregating generation, F_2's, B_1 and B_2s were represented by 100 and 50 plants. Data were recorded on an individual plant of six populations for each cross where 20, 20, 25, 300, 50 and 50 plants, which were chosen from P_1, P_2, F_1, F_2, B_1 and B_2 of each crosses respectively, to record the following traits: root length, top height, number of leaves, plant weight, root weight, leaf weight, shoulder diameter, core diameter and root girth-top, bottom and middle. To determine the presence or absence of non-allelic interactions, scaling test as A, B, C and D have been calculated to test adequacy of additive-dominance model in each case (Mather, 10). The best model was selected based on additive and dominance

model using non-significant Chi-square test and lower the standard error. The observed means of the six generations were used to estimate '*m*', '*d*' and '*h*' as per the joint scaling test of Cavalli (1). The joint scaling Mather (10) test was employed to estimate the mean [*m*], additive effect [*d*], dominance effect [*h*], additive × additive [*i*], additive × dominance [*j*] and dominance × dominance [*l*] values. Significance of the scales and gene effects were tested by using the *t*-test of Singh and Singh (15). The type of epistasis was determined as complementary when dominance [*h*] and dominance × dominance [*l*] gene effects have same sign and duplicate epistasis when the sign was different (Kearsey and Pooni, 8). Statistical analyses were carried out separately for each cross using the PBT (12) software developed by IRRI.

RESULTS AND DISCUSSION

The scale estimates of root length (Table 1) showed that the adequacy of six parameter model in explaining the inheritance of root length. Preponderance of additive × additive gene [*i*] action as well as dominance × dominance [*l*] gene interaction was found to play an important role in governing the inheritance of this trait in White Pale × IPC-126 and White Pale × IPC-122 cross combinations. Significant values of dominance [*h*] and dominance × dominance [*l*] with same signs indicated that epistatic interaction of complimentary type explained the inheritance of root length in White Pale × PM cross. This interaction inflates the variation in the segregating population. Similar results have been reported earlier by Dixit *et al.* (3), Holland (5), Iqbal *et al.* (6), Novoselovic *et al.* (11), Srivastava *et al.* (17) and Wu *et al.* (19). The positive direction of [*d*], [*l*] and complimentary type epistatic gene interactions in White Pale × PM cross showed the intermating of these parents and selection in filial generation for improvement for this trait. The results are in agreement with those of Checa *et al.* (2), Iqbal *et al.* (6), Singh *et al.* (14), Srikanth *et al.* (16), Srivastava *et al.* (17) and Stuber *et al.* (18).

As given in the Table 2 for root weight gene interaction, the significant [*h*] and [*l*] effects showed the epistatic interaction in the inheritance of root weight in a cross of White Pale × IPC-126, whereas the sign of [*h*] and [*l*] were of same sign due to the interaction of complimentary epistasis type. The digenic non-allelic epistasis of [*i*], [*j*] and [*l*] were considered the major contributors in the inheritance of these traits in crosses of White Pale × IPC-122 and White Pale × PM. Significance of [*j*] for root weight traits in the both White Pale × IPC-126 and White Pale × PM crosses revealed that selection through selfing is not effective for improvement of these traits

because among the digenic interactions, additive × dominance type is more fixable and more useful for carrot breeders. These results are comparable with Jenson (7), Novoselovic *et al.* (11), Rodriguez *et al.* (13), Singh *et al.* (14), Srikanth *et al.* (16), Stuber *et al.* (18) and Wu *et al.* (19).

Joint scaling and simple scaling test were significant for all crosses showing that adequacy of six parameter model to explain shoulder and root diameter (Table 1). It indicated that presence of non-allelic interaction (Table 2), the effect of dominance [*h*] and additive × dominance [*j*] were significant and positive in the cross White Pale × IPC-126, whereas in White Pale × PM there were significant effect of additive [*d*], dominance × dominance [*l*] and additive × dominance [*j*] gene interactions. The negative additive [*d*] effects lead to non-dispersal of gene(s) between parents. The additive [*d*] and dominance [*h*] gene interactions played an important role in the inheritance of these traits in a cross of White Pale × IPC-122. Similarly, results on these traits were confirmed with Checa *et al.* (2), Dixit *et al.* (3), Gamble (4), Holland (5) and Srikanth *et al.* (16). Complimentary type of gene interaction were expressed in all three crosses, which implied that heterosis breeding can be exploited for improvement of this trait.

Three crosses with respect to core diameter exhibited significance for either A, B, C, or D scales indicating the presence of inter-allelic interaction (Table 2). The magnitude of [*h*] effects was comparatively higher than that of [*d*] effects in non-interacting cross. The additive gene [*d*] and dominance × dominance [*l*] gene effect were significant in White Pale × IPC-126 cross and White Pale × IPC-122 with negative and positive values, respectively. Duplicate type of epistasis were governing core diameter in White Pale × IPC-126 and White Pale × IPC-122, which showed that early selection may not be useful for this trait and advanced generation selection will be useful for uniform core diameter. The results are in agreement with those of Jenson (7), Novoselovic *et al.* (11), Srikanth *et al.* (16), Srivastava *et al.* (17), Stuber *et al.* (18) and Wu *et al.* (19). Negative additive [*d*], additive × dominance [*j*] and positive dominance × dominance [*l*] gene interactions expressed significantly in White Pale × PM cross for core diameter in heterosis breeding will be more useful due to complimentary type of epistatic interaction.

Flesh thickness revealed that the estimates for either of simple scales, A, B, C, or D were significant for all the crosses. The additive gene [*d*] effect was significant in cross White Pale × IPC-122 with positive values and White Pale × IPC-126, White Pale × PM with negative values. The highest magnitude of additive gene [*d*] effects was found in cross White

Table 1. Estimates of scaling test and Joint scaling test of three white pale crosses for economic traits.

Trait	Cross	Scaling test				Joint Scaling Test		
		A ± SE	B ± SE	C ± SE	D ± SE	m ± SE	d ± SE	h ± SE
Root length (cm)	I	7.55** ± 1.34	13.76** ± 1.60	13.85** ± 2.53	3.72** ± 1.08	26.13** ± 0.40	1.82** ± 0.37	-1.04** ± 0.81
	II	9.93** ± 1.61	8.18** ± 2.23	10.25** ± 1.85	3.93** ± 1.38	23.44** ± 0.37	-0.10** ± 0.39	5.62** ± 0.68
	III	10.84** ± 2.20	7.14** ± 1.50	15.93** ± 1.63	1.03 ± 1.40	22.02** ± 0.33	-0.95** ± 0.36	8.75** ± 0.52
Root weight (g)	I	434.70** ± 25.43	279.00** ± 30.53	772.14** ± 23.52	-29.22 ± 22.00	211.47** ± 3.69	-63.78** ± 3.79	193.12** ± 5.16
	II	295.23** ± 33.28	378.28** ± 28.97	526.90** ± 31.20	73.30** ± 26.28	281.94** ± 2.18	-3.94 ± 2.20	130.15** ± 4.83
	III	503.49** ± 24.38	307.87** ± 34.73	689.66** ± 28.56	60.85* ± 25.15	241.58** ± 1.88	-36.56** ± 1.90	189.35** ± 3.60
Shoulder dia. (mm)	I	51.25** ± 2.76	7.75* ± 3.36	63.19** ± 3.39	-2.09 ± 2.32	41.77** ± 0.68	-4.71** ± 0.71	7.94** ± 1.08
	II	6.08* ± 3.02	5.91 ± 5.91	12.92** ± 3.33	-0.45 ± 2.51	43.40** ± 0.54	-5.00** ± 0.57	13.64** ± 0.89
	III	25.61** ± 3.07	0.65 ± 3.74	17.48** ± 3.00	4.38 ± 2.68	42.37** ± 0.41	-4.93** ± 0.43	12.31** ± 0.72
Root dia. (mm)	I	51.32** ± 2.55	7.66* ± 3.35	63.22** ± 3.28	-2.11 ± 2.25	36.02** ± 0.69	-4.55** ± 0.73	12.46** ± 0.98
	II	6.08* ± 3.02	5.91 ± 3.25	12.92** ± 3.33	-0.45 ± 2.51	40.19** ± 0.54	-5.00** ± 0.57	13.64** ± 0.89
	III	25.61** ± 3.07	0.65 ± 3.74	17.48** ± 3.00	4.38 ± 2.68	39.16** ± 0.41	-4.93** ± 0.43	12.31** ± 0.72
Core dia. (mm)	I	2.22 ± 0.41	1.17* ± 0.57	3.10** ± 0.78	0.14 ± 0.21	4.40** ± 0.16	-0.00** ± 0.13	-0.77* ± 0.32
	II	6.37** ± 1.28	6.29** ± 1.10	0.53 ± 2.04	6.07** ± 0.75	8.54** ± 0.28	-1.49** ± 0.25	0.56** ± 0.61
	III	8.66** ± 0.80	4.74** ± 0.96	11.79** ± 1.36	0.81 ± 0.53	6.30** ± 0.24	-0.74** ± 0.22	-1.03* ± 0.49
Flesh thickness (mm)	I	53.38** ± 2.76	10.03** ± 3.40	67.67** ± 3.41	-2.12 ± 2.33	36.35** ± 0.70	-4.23** ± 0.75	9.95** ± 1.09
	II	5.83* ± 3.052	4.82 ± 3.29	31.59** ± 2.96	-10.471** ± 2.4	30.97** ± 0.58	-5.74** ± 0.64	15.35** ± 0.82
	III	27.67** ± 3.21	4.39 ± 3.68	21.96** ± 2.98	5.05* ± 2.70	38.10** ± 0.45	-4.60** ± 0.47	13.06** ± 0.71
Root to top ratio	I	14.12** ± 1.37	10.38** ± 2.10	23.38** ± 2.52	0.56 ± 0.84	6.93** ± 0.56	-1.23* ± 0.52	-1.53* ± 1.06
	II	14.12** ± 1.37	10.38** ± 2.10	23.38** ± 2.52	0.56* ± 0.84	8.61** ± 0.40	-2.31** ± 0.37	-1.13* ± 0.87
	III	18.60** ± 1.60	10.11** ± 1.92	25.65** ± 2.72	1.53 ± 1.03	7.32** ± 0.51	-1.19** ± 0.47	-1.84** ± 1.03

Cross: I = White Pale × IPC-126, II = White Pale × IPC-122, III = White Pale × PM
Significant at A & B = involves three type of non-allelic-gene interactions; Significant at C = involves D × D; Significant at D = involves A × A; Significant at C and D = involves A × A and D × D
m = mean, [d] = additive, [h] = Dominance
*Significant at 5 and 1% levels; D = Duplicate epistasis; C = Complementary epistasis

Table 2. Estimation of gene effects based on six generation mean analysis in three White Pale crosses of carrot.

Trait	Cross	Gene interaction						Type of epistasis
		m ± SE	[d] ± SE	[h] ± SE	[i] ± SE	[j] ± SE	[l] ± SE	
Root length (cm)	I	25.52** ± 0.40	0.48 ± 0.72	-4.62 ± 2.38	-7.45** ± 2.17	6.21* ± 1.69	28.76** ± 3.85	D
	II	25.60** ± 0.29	-0.69 ± 1.25	-1.09 ± 2.85	-7.87** ± 2.77	-1.74 ± 2.63	25.99** ± 5.33	D
	III	24.31** ± 0.31	-1.00 ± 1.25	6.34* ± 2.85	-2.05 ± 2.80	-3.70 ± 2.61	20.05** ± 5.26	C
Root weight (g)	I	159.59** ± 5.27	-47.60* ± 19.31	239.19** ± 44.31	58.44 ± 44.01	-155.70** ± 39.45	655.26** ± 80.76	C
	II	235.90** ± 7.39	43.77** ± 21.72	8.13* ± 52.80	-146.61** ± 52.57	83.04 ± 43.68	820.13** ± 92.34	D
	III	181.71** ± 6.90	-57.05** ± 21.01	83.04* ± 50.43	-121.70* ± 50.30	-195.61** ± 42.21	933.07** ± 88.79	D
Shoulder dia. (mm)	I	37.30** ± 0.64	-20.08** ± 1.94	13.60** ± 4.78	4.18 ± 4.64	-43.49** ± 4.22	54.82** ± 8.46	C
	II	48.17** ± 0.70	4.52* ± 2.08	14.82** ± 5.10	0.91 ± 5.02	-0.17 ± 4.34	11.08** ± 8.98	C
	III	45.72** ± 0.65	-6.94** ± 2.34	4.35* ± 5.42	-8.77 ± 5.37	-24.95** ± 4.77	35.03** ± 9.86	C
Root dia. (mm)	I	33.46** ± 0.63	-20.43** ± 1.87	13.87** ± 4.63	4.23 ± 4.51	-43.66** ± 4.13	54.74** ± 8.17	C
	II	44.96** ± 0.70	4.52* ± 2.08	14.82** ± 5.10	0.91 ± 5.02	-0.17 ± 4.34	11.08** ± 8.98	C
	III	42.51** ± 0.65	-6.94** ± 2.34	4.35* ± 5.42	-8.77 ± 5.42	-24.95** ± 4.77	35.03** ± 9.86	C
Core dia. (mm)	I	3.97** ± 0.06	-0.35* ± 0.17	-0.13* ± 0.571	-0.29 ± 0.43	-1.05 ± 0.57	3.68** ± 1.059	D
	II	10.14** ± 0.26	1.18* ± 0.53	-9.29** ± 1.74	-12.14** ± 1.51	-0.07 ± 1.22	24.82** ± 2.96	D
	III	5.51** ± 0.16	-0.82* ± 0.42	0.99* ± 1.22	-1.62 ± 1.06	-3.91** ± 1.00	15.03** ± 2.17	C
Flesh thickness (mm)	I	32.54** ± 0.64	-20.12** ± 1.94	13.79** ± 4.79	4.24 ± 4.66	-43.34** ± 4.26	59.18** ± 8.50	C
	II	33.32** ± 0.60	3.97* ± 2.10	34.72** ± 4.93	20.94 ± 4.86	-1.01** ± 4.43	-10.28** ± 8.93	D
	III	40.96** ± 0.65	-6.21** ± 2.36	3.13* ± 5.45	-10.11 ± 5.40	-23.27** ± 4.83	42.18** ± 9.92	C
Root to top ratio	I	5.58** ± 0.23	-1.41* ± 0.71	-0.96* ± 2.05	-1.12 ± 1.69	-3.73 ± 2.25	25.62** ± 3.79	D
	II	7.90** ± 0.29	1.97* ± 0.88	0.96* ± 2.52	-5.17 ± 2.12	-0.79 ± 1.95	28.73** ± 4.61	C
	III	5.80** ± 0.31	-1.97* ± 0.82	2.30* ± 2.40	-3.06 ± 2.07	-8.48** ± 2.02	31.77** ± 4.27	C

Cross: I = White Pale × IPC-126, II = White Pale × IPC-122, III = White Pale × PM
m = mean, [d] = additive, [h] = Dominance, [i] = additive × additive, [j] = additive × dominance, [l] = dominance × dominance
*, **Significant at 5 and 1% levels; D = Duplicate epistasis; C = Complementary epistasis

Pale × IPC-126. Dominant [*h*] gene effects were highly significant with positive values for flesh thickness was found in the White Pale × IPC-126 and White Pale × IPC-122 crosses. Among the interaction of gene effects, additive × dominance [*j*] gene effects were highly significant in White Pale × IPC-126, White Pale × IPC-122 and White Pale × PM cross with negative estimates. Dominant × dominant interaction [*l*] was highly significant in White Pale × IPC-126 and White Pale × PM crosses with positive direction. White Pale × IPC-126 and White Pale × PM crosses showed complimentary type of epistasis as indicate by positive signs of [*h*] and [*l*] genetic parameters, whereas, White Pale × IPC-122 cross expressed duplicate type of epistasis as indicated by negative signs of [*h*] and [*l*] genetic parameters. Similar findings have been observed by Holland (5), Srivastava *et al.* (17), Stuber *et al.* (18) and Wu *et al.* (19).Therefore, heterosis breeding will be utilized for improving flesh thickness due to negative [*d*], [*j*] which leads to non-dispersal of alleles in White Pale × IPC-126 and White Pale × PM crosses, whereas recurrent and mass selection through intermating of parents could be exploited for improvement of this trait in White Pale × IPC-122 cross.

The root to top ratio estimates for scaling tests and gene effects (Table 2) revealed that the estimates for either of simple scales, A, B, C, and D were significant for all White Pale crosses. Additive gene effects [*d*] were observed to be significant in a cross White Pale × IPC-122 with positive estimates, which were in desirable direction, whereas in White Pale × IPC-126 and White Pale × PM crosses were additive gene effects with negative values. The positive dominance × dominance [*l*] and negative additive gene [*d*] effect was controlling root to top ratio trait in White Pale × IPC-126 and White Pale × PM and *vice-versa* in White Pale × IPC-122 cross for this trait. The dissimilar signs of [*h*] and [*l*] gene action and duplicate type of epistatic effects was observed in White Pale × IPC-126 in which selection breeding methodology can be advanced generation through intermating of parents followed by mass selection and recurrent selection. Heterosis would be exploited for applicable for root diameter, length, flesh thickness and core diameter traits in White Pale × IPC-122 and White Pale × PM crosses indicated predominance of complementary type of epistasis due to non-fixable gene effects. The negative additive [*d*] gene effects leads to non-dispersal of gene between parents, which confirm well with the findings of Ma *et al.* (9), Checa *et al.* (2), Gamble (4), Holland (5), Iqbal *et al.* (6) and Srikanth *et al.* (16). The generation mean analysis revealed that complimentary and duplicate type of epistatic gene interaction was inherited for economic traits.

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