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Assessment of gene action association involved with economic traits of black carrot (*Daucus carota*)

RAMAN SELVAKUMAR[1]*, D C MANJUNATHAGOWDA[2], PRITAM KALIA[1] and R S RAJE[2]

ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India

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ABSTRACT

Carrots (*Daucus carota* L.) are rich sources of vitamins, phytonutrients, bioactive compounds and health promoting properties. Recent increased awareness of nutritional security has resulted in a dramatic increase in carrot consumption, necessitating increased carrot production by farmers and growers. Understanding the genetic design of economic traits including root length, root weight, root diameter, core diameter, and flesh thickness, as well as developing an appropriate breeding plan for these traits, will help accomplish those ambitious goals. Gene action experiments were conducted at ICAR-Indian Agricultural Research Institute during 2012–15 in order to estimate the type and magnitude of gene action in order to develop a breeding strategy for recognizing segregants with desirable horticultural traits. Four inbred lines such as Pusa Asita, Pusa Rudhira, Pusa Kulfi, Pusa Meghali were used to develop three crosses, viz. Pusa Asita × Pusa Kulfi, Pusa Asita × Pusa Meghali, Pusa Asita × Pusa Rudhira to achieve the objectives. The findings confirmed that the exact composition of gene effects varied through crosses and demonstrated the role of additive as well as non-additive gene effects in the inheritance of different traits, with a preponderance of the latter. Due to the parallel function of complementary gene effects, non-epistatic gene interactions for economic yield contributing traits have been found; thus, hybrid exploitation could be efficiently used by heterosis breeding by using favourable positive [*h*] and [*l*] gene interaction and effects. This genetic information is more helpful to formulate suitable breeding methodology for identifying the segregants with desirable horticultural traits.

Keywords: Additive, Carrot, Dominance, Gene, Hybrid

Carrots (*Daucus carota* L.) are a substantial single source of vitamin A, providing 14–17% of total vitamin A diet (Selvakumar *et al.* 2017). They are rich in lycopene, lutein, anthocyanin, tocopherol, carbohydrates and fibre. The uniform root shape, size, colour of root thinner are thick phloem with rich colour carrot is preferred which are most preferred traits for consumers and fetch higher price in the market (Selvakumar *et al*. 2021). Carrot breeding initiatives aim to produce high yielding widely accepted cultivars with good economic features. Breeding for such cultivars requires through understanding of genetic components of carrot. Many breeding techniques have been developed to increase carrot yield, but the finest hybrid combinations are created by crossing huge populations of carrot inbred lines. Before the improvement of high yielding carrot cultivars and/or hybrids it is an important to study the economic components of gene interaction and effects. Biometrics of generation mean analysis is an efficient technique for estimating epistatic gene effects which involved in the expression of horticultural traits in different crosses (Singh and Singh 1992). These genetic analysis provides sufficient information of gene interaction effects of crosses of crops, viz. additive [*d*], dominance [*h*], additive × additive [*i*] (fixable), additive × dominance [*j*] and dominance × dominance [*l*] (non-fixable) (Jadhav and Dhumal 1994). The additive [*d*], dominance [*h*] and epistatic [*i*, *j* and *l*] variance are closely associated with individual, intra-allelic and inter-allelic (non-allelic) genes respectively and it decides the breeding value of genotype (Dudley and Moll 1969). Genetic additive variances of *d* and *h* favour intra-population selection and hybridization. It also aids in the accurate comprehension of genetic components and selection of possible parental crosses. These will also help select early and/or advanced generation parental lines for hybridization with specified features. These best breeding strategies will accelerate to prognosis of new tropical carrot cultivars and hybrids. Therefore, an attempt was made in the present experiment to unravel the nature and magnitude of gene action of distinct economic traits in purple tropical carrot. These genetic studies could help determine the optimum carrot breeding strategy for these features.

Present Address: [1]Centre for Protected Cultivation Technology, ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi; [2]ICAR-Directorate of Onion and Garlic Research, Rajgurunagar, Pune, Maharashtra. *Corresponding author e-mail: selvakumarsingai@gmail.com.

MATERIALS AND METHODS

Filial generation (F_1) were developed from these four inbred lines were self-pollinated to produce F_2 generations and backcrossed to get B_1 and B_2 generations for genetic analysis. The experimental carrot field was laid out in Randomized Block Design with three replications. The P_1, P_2, F_1, F_2, B_1 and B_2 populations were grown for performance at the Vegetable Research Farm of Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi, India during 2012–15. The four inbred lines of Pusa Asita, Pusa Meghali, Pusa Meghali and Pusa Rudhira were used in this study. The phenotypic characteristic features of these lines were yellow, purple, red and orange coloured root epidermal layer, phloem and xylem, respectively. These selected lines were steckled and grown under net house for inbred line development. These carrot lines were selfed and harvested to get homozygous seeds. The harvested carrot inbred seeds were grown for hybridization programme. The uniform root epidermal, phloem and xylem colour, size, shape roots of inbred lines were selected and grown under net house for crossing purpose. These selected inbred lines were crossed by manual emasculation and pollination with 10 fertile inbred lines of cross combinations. The crossed F_1 seeds were harvested and. These F_1 carrot roots were harvested and advanced for F_2, B_1 and B_2 generation by selfing of F_1 plants, crossing with female and male parents, respectively. The harvested F_2, B_1 and B_2 seeds were grown for F_2, B_1 and B_2 roots. Each of these populations consists of 50 parental inbred lines, $50F_1$ individuals (3 block) and approximately 300 F_2 and 100 of each backcross. Phenotypic data of roots were recorded on an individual plant of six populations for each cross where 20, 20, 25, 300, 50 and 50 plants were chosen from P_1, P_2, F_1, F_2, B_1 and B_2 generations of three cross combinations, respectively. The scaling test of A, B, C and D were done by Mather (1949) and Hayman and Mather (1955) method in which significance of 'A' and 'B' scale indicate that presence of three non-allelic interaction effects (additive × additive [*i*], additive × dominance [*j*] and dominance × dominance [*l*]), 'C' scale indicate the [*l*] epistatic interaction effects and 'D' scale indicate the [*i*] epistatic interaction effects. When the joint scaling test or three parameter model (mean [*m*], additive [*d*] and dominance [*h*]) of Cavelli (1952) were significant, a six parameter were successfully used to test of fitness of appropriate genetic model as per Mather and Jinks (1982), and Hayman (1958). The significance of m, [*d*], [*h*], [*i*], [*j*] and [*l*] genetic effects were done by '*t*' test at the 0.05 and 0.01 levels of probability (Singh and Singh 1992). The type of epistatic gene interaction were determined by Kearsey and Pooni (1996) as presence of similar sign of [*h*] and [*l*] effects when it is noted as complimentary epistasis while dissimilar sign of [*h*] and [*l*] effects then it is duplicate type of epistatic gene interaction. Genetic analysis were carried out separately for each cross using the plant breeder tools (PBT, 2013) software developed by International Rice Research Institute, Department of Plant Breeding, Genetics and Biometrics, Philippines.

RESULTS AND DISCUSSION

Root length: The scaling test showed that significant of scales A, B and C scales in Pusa Asita × Pusa Meghali, and Pusa Asita × Pusa Kulfi, and A, C and D scales in Pusa Asita × Pusa Rudhira. The significant of joint scaling test revealed that three parameter was inadequate to explain genetic effects (Table 1). The six parameter model was well fitted to explain the presence of epistatic gene interactions and effects which are present in Table 2. The negative *h*, *i*, *j* and dominance × dominance *l* gene effects were highly influencing for root length in the Pusa Asita × Pusa Kulfi cross combination. The estimate of *i*, *j*, *l* effects influencing the gene effects in the mean population (Mather and Jinks 1982). The positive *h*, negative *j*, and *l* gene interactions were highly expressed for traits in Pusa Asita × Pusa Meghali, and Pusa Asita × Pusa Rudhira. Additionally the gene effects were positive *d*, and negative *i* gene interaction effects also influenced in respective crosses. The *h* and *l* effect was same sign revealed the complimentary epistatic interaction for this trait in Pusa Asita × Pusa Rudhira, Pusa Asita × Pusa Meghali crosses. Thus, it can be successfully exploited through development of Pusa Meghali of hybrid combinations, the findings were supported by Karkleliene *et al*. (2005) and Singh *et al*. (1992).

Root weight: The scales of A, B and C in Pusa Asita × Pusa Kulfi, Pusa Asita × Pusa Rudhira and Pusa Asita × Pusa Meghali crosses were highly significant, depicted the epistatic gene interaction (Table 1). The high significance of three parameter model being insufficient, thus digenic six parameter were used for genetic analysis (Table 2). The *h* and *l* gene interaction was significantly governing root weight in the Pusa Asita × Pusa Kulfi, Pusa Asita × Pusa Rudhira, and Pusa Asita × Pusa Meghali. The complimentary type of epistatic interaction was observed in all the crosses due to similar positive sign effects of *h* and *l* gene interactions. Mather (1967) determined that complimentary epistatic interaction inflate variation in advanced F_2 generations, thus exploitation hybrid vigour has strategy of carrot breeding.

Root to top ratio: The *h* and *l* gene interactions was highly significant with positive directions for root to top ratio in Pusa Asita × Pusa Kulfi, Pusa Asita × Pusa Rudhira and Pusa Asita × Pusa Meghali. The complimentary type of epistasis noted among all crosses for root to top ratio, could be due to heterotic accumulation of alleles of *h* and *l*. It was partial agreement with those reported in other vegetable crops by earlier researchers Jagosz (2012) and Hussain *et al.* (2006).

Shoulder and root diameter: The scaling test showed significant vales of A, B and C scales in Pusa Asita × Pusa Kulfi, Pusa Asita × Pusa Rudhira and Pusa Asita × Pusa Meghali (Table 1). The three parameter was inadequate to explain gene interaction because of high significant values, further it showed presence of non-allelic gene interaction which were revealed in six parameter model (Table 2). The *d* and *l* type of gene interaction was significantly governing the shoulder and root diameter with positive directions in the Pusa Asita × Pusa Meghali. The positive effects of *h*

Table 1 Estimates of scaling test and Joint scaling test of carrot

Cross	Scaling Test			
	A ± SE	B ±SE	C±SE	D±SE
Root length				
Pusa Asita × Pusa Kulfi	13.05**± 1.32	6.52**± 2.44	14.47**± 2.23	2.54± 1.52
Pusa Asita × Pusa Rudhira	7.23**± 1.39	0.39±1.42	12.4**4± 1.70	-2.41*± 1.04
Pusa Asita × Pusa Meghali	17.17**± 1.64	4.74**± 1.47	20.41**± 1.73	0.74± 1.19
Root weight				
Pusa Asita × Pusa Kulfi	332.80**± 32.39	365.70**±30.05	759.06**± 21.87	-30.28± 23.66
Pusa Asita × Pusa Rudhira	235.10**± 33.74	282.06**±33.65	453.53**± 38.13	31.81± 29.57
Pusa Asita × Pusa Meghali	323.80**±31.41	342.00**±24.56	644.06**±27.38	10.86±23.24
Shoulder diameter				
Pusa Asita × Pusa Kulfi	12.93**±3.45	24.74**± 3.14	73.88**± 3.12	-18.10**± 2.35
Pusa Asita × Pusa Rudhira	17.89**±3.68	17.67**± 2.83	58.22**± 3.42	-11.32**± 2.44
Pusa Asita × Pusa Meghali	10.42**±3.39	4.43±2.67	12.94**±3.31	0.95±2.38
Root diameter				
Pusa Asita × Pusa Kulfi	13.16**± 3.48	25.92**± 3.10	73.88**± 3.12	-17.39**± 2.35
Pusa Asita × Pusa Rudhira	19.05**±3.70	9.53**± 2.96	15.76**± 3.43	6.41**± 2.53
Pusa Asita × Pusa Meghali	10.42**±3.39	4.43±2.67	12.94**±3.31	0.95±2.38
Core diameter				
Pusa Asita × Pusa Kulfi	8.40**±1.63	7.63**±1.31	17.95**±2.17	-0.95±0.67
Pusa Asita × Pusa Rudhira	4.32**±1.26	2.09±1.08	6.37**±1.70	0.02±0.67
Pusa Asita × Pusa Meghali	5.69**±1.21	4.52**±0.93	10.12**±1.67	0.04±0.49
Flesh thickness				
Pusa Asita × Pusa Kulfi	15.06**±3.45	26.30**±3.69	78.36**±3.15	-18.49±2.55
Pusa Asita × Pusa Rudhira	20.03**±3.65	19.95**±2.93	62.70**±3.46	-11.35**±2.47
Pusa Asita × Pusa Meghali	12.55**±3.39	6.71±2.71	17.42**±3.35	0.92±2.38
Root to top ratio				
Pusa Asita × Pusa Kulfi	13.58**± 2.48	13.36**± 1.96	29.12**± 3.27	-1.08± 0.99
Pusa Asita × Pusa Rudhira	10.54**± 2.56	6.34**± 2.16	16.82**± 3.42	0.03± 1.33
Pusa Asita × Pusa Meghali	13.51**±2.34	11.33**±1.82	24.73**±3.15	0.05±0.95

Significant at A, B involves three type of non-allelic-gene interactions; Significant at C involves Dominance × Dominance; Significant at D- involves Additive × Additive; Significant at C and D- involves Additive × Additive and Dominance × Dominance, *Significance at 5%; **Significance at 1%.

and *l* type of gene interactions were highly influencing for shoulder and root diameter than the negative effects of *i*, and *j* gene interactions in the Pusa Asita × Pusa Rudhira. The value of *h* and *l* were influence the association of genes in heterotic condition, whereas *l* negative values participate indirectly (Mather 1967, Selvakumar *et al*. 2017, 2019, 2021). The *d*, *h* and *l* type of gene interactions were significantly noticed from the cross Pusa Asita × Pusa Kulfi, the other gene effects were *i* and *j* gene interactions observed significantly with positive directions. The fixable [*d*+*i*] effects was involving in the gene dispersion but due to negative values it promotes dominance effects in this trait (Mather and Jinks 1982).The complimentary epistasis was observed from all crosses for shoulder and root diameter. It was supported that accumulation of favourable alleles in heterotic conditions between the parents and value of *h* and *l* were increased the function. This favours for hybrid exploitation by utilizing non-fixable alleles in the populations for this trait (Holland 2011).

Core diameter: Table 1 shows joint scaling test estimates and the magnitudes of several genetic components for core diameter. The A, B, and C scales were extremely significant in Pusa Asita × Pusa Kulfi, Pusa Asita × Pusa Rudhira, and Pusa Asita × Pusa Meghali, indicating the presence of non-allelic epistatic gene interactions (Table 2). The presence of complementary type digenic non-allelic interactions in the inheritance of this trait in the Pusa Asita × Pusa Kulfi, Pusa Asita × Pusa Rudhira, and Pusa Asita × Pusa Meghali was indicated by genetic components of *h* and *l* with the same signs and significant magnitudes. In all crossings of Pusa Asita, significant values of *h* and *l* demonstrated the relevance of dominance, as well as non-allelic interactions

Table 2 Estimation of gene effects based on six generation mean analysis in carrot

Cross	Gene interactions						Epistasis
	m ± SE	[*d*] ± SE	[*h*] ± SE	[*i*] ± SE	[*j*] ± SE	[*l*] ± SE	
Root length							
Pusa Asita × Pusa Kulfi	25.59** ± 0.42	-0.64 ± 1.25	-1.81 ± 3.13	-5.09* ± 3.04	-6.53** ± 2.66	24.66** ± 5.51	Duplicate
Pusa Asita × Pusa Rudhira	26.86** ± 0.31	-0.62 ± 0.84	9.97** ± 2.17	4.82** ± 2.09	-6.84** ± 1.93	2.79 ± 3.77	Complementary
Pusa Asita × Pusa Meghali	24.58** ± 0.33	-2.74** ± 0.98	4.43 ± 2.44	-1.49 ± 2.38	-12.43** ± 2.16	23.40** ± 4.30	Complementary
Root weight							
Pusa Asita × Pusa Kulfi	168.36** ± 4.82	-13.80 ± 21.60	252.31*8 ± 47.61	60.56 ± 47.33	32.90 ± 43.95	637.94** ± 89.15	Complementary
Pusa Asita × Pusa Rudhira	254.36** ± 9.10	-4.52 ± 23.31	151.87* ± 59.43	-63.62 ± 59.15	46.96 ± 47.33	580.78** ± 100.75	Complementary
Pusa Asita × Pusa Meghali	184.23** ± 6.37	19.60 ± 19.42	225.76** ± 46.75	-21.73 ± 46.48	18.20 ± 39.63	687.53** ± 82.40	Complementary
Shoulder diameter							
Pusa Asita × Pusa Kulfi	33.95** ± 0.52	4.50* ± 2.10	45.73** ± 4.84	36.20** ± 4.70	11.81** ± 4.55	1.46 ± 8.96	Complementary
Pusa Asita × Pusa Rudhira	37.87** ± 0.63	-1.50 ± 2.09	32.17** ± 5.02	22.64** ± 4.89	-0.22 ± 4.53	12.92 ± 9.03	Complementary
Pusa Asita × Pusa Meghali	47.36** ± 0.67	1.14 ± 1.95	15.04** ± 4.85	-1.90 ± 4.76	-5.98 ± 4.28	16.75** ± 8.50	Complementary
Root diameter							
Pusa Asita × Pusa Kulfi	30.74** ± 0.52	4.98* ± 2.10	44.31** ± 4.84	34.79** ± 4.70	12.75** ± 4.55	4.30 ± 8.96	Complementary
Pusa Asita × Pusa Rudhira	40.44** ± 0.67	-1.41 ± 2.01	2.72 ± 5.17	-12.82* ± 5.06	-9.52* ± 4.71	41.40** ± 9.22	Complementary
Pusa Asita × Pusa Meghali	44.15** ± 0.67	1.14 ± 1.95	15.04** ± 4.85	-1.90 ± 4.76	-5.98 ± 4.28	16.75** ± 8.50	Complementary
Core diameter							
Pusa Asita × Pusa Kulfi	4.93** ± 0.13	-0.61 ± 0.62	3.89* ± 1.70	1.91 ± 1.34	-0.77 ± 1.68	14.12** ± 3.29	Complementary
Pusa Asita × Pusa Rudhira	5.96** ± 0.18	-0.09 ± 0.56	3.57* ± 1.54	-0.04 ± 1.34	-2.23 ± 1.40	6.46* ± 2.82	Complementary
Pusa Asita × Pusa Meghali	3.87** ± 0.13	0.38 ± 0.406	3.14** ± 1.26	-0.09 ± 0.98	-1.16 ± 1.22	10.31** ± 2.33	Complementary
Flesh thickness							
Pusa Asita × Pusa Kulfi	29.20** ± 0.53	4.10 ± 2.31	46.634** ± 5.23	36.99** ± 5.10	11.23** ± 4.94	4.38 ± 9.78	Complementary
Pusa Asita × Pusa Rudhira	33.11** ± 0.64	-1.54 ± 2.11	32.35** ± 5.07	22.71** ± 4.94	-0.07 ± 4.56	17.28 ± 9.12	Complementary
Pusa Asita × Pusa Meghali	42.61** ± 0.67	1.10 ± 1.96	15.22** ± 4.87	-1.84 ± 4.77	-5.84 ± 4.28	21.11* ± 8.55	Complementary
Root to top ratio							
Pusa Asita × Pusa Kulfi	5.61** ± 0.18	-0.56 ± 0.91	5.24* ± 2.54	2.17 ± 1.98	-0.21 ± 2.53	24.78** ± 4.92	Complementary
Pusa Asita × Pusa Rudhira	8.47** ± 0.36	-0.17 ± 1.12	7.33** ± 3.09	-0.06 ± 2.67	-4.19 ± 2.81	16.95** ± 5.64	Complementary
Pusa Asita × Pusa Meghali	6.20** ± 0.25	0.72 ± 0.80	6.48** ± 2.42	-0.11 ± 1.91	-2.18 ± 2.47	24.96** ± 4.50	Complementary

m=Mid parent value, [*d*]=additive, [*h*]=dominance, [*i*]=additive × additive, [*j*]=additive × dominance, [*l*]= dominance × dominance; *Significance at 5%, **Significance at 1% .

of dominance *l* with positive directions in the inheritance of this trait. The *h* and *l* effect values increased the effects of the dominant allele in the population, resulting in heterotic generation (Holland 2007, Selvakumar *et al*. 2021).

Flesh thickness: The scaling test revealed that A, B, C and D scales in Pusa Asita ×Pusa Rudhira, A, B and C scales in Pusa Asita × Pusa Kulfi cross, A and C scales in Pusa Asita × Pusa Meghali were significant value and digenic interactions (Table 1). The *h* gene was significantly higher than *i*, *j*, and *l* type of interactions in Pusa Asita × Pusa Kulfi. The *h*, *j*, and *l* type of gene interactions was significantly govern the flesh thickness in the Pusa Asita × Pusa Rudhira. The positive effects of *d* and *h* were significantly exhibited in the cross Pusa Asita × Pusa Kulfi in which the negative effects of *j* and *l* type of gene interactions for flesh thickness, whereas the *h* and *l* gene interactions was controlling this trait in Pusa Asita × Pusa Meghali. The values of *h* and *l* were positively enhancing the performance of traits which resulted into variation in F_2 and subsequent generations (Holland 2011, 2007). The present results were in line with the other vegetable crops such as brinjal (Singh *et al*. 2002), tomato (Causse *et al*. 2007) and pea (Dixit *et al.* 2006).

According to the results of the genetic investigation of the black carrot population, there is a prevalence in the interaction and non-interaction inheritance of economic traits. In the Pusa Asita crosses, non-allelic gene interaction was operative for root length, root weight, root to top ratio, shoulder and root diameter, core diameter, and flesh thickness. Thus, exploiting heterosis by non-fixable effects increases the positive effects of *h* and *l* gene effects, allowing Pusa Asita to create carrot hybrids. The higher frequency of gene dispersal alleles between these parents were detected in duplicate non-allelic gene interaction, so restricting selection in earlier generations and favouring homozygosity of alleles, breeding needs to be advanced generation through inter-mating. This genetic information would aid in developing appropriate breeding strategies for particular economic traits. Thus, increasing the frequency of favourable genes in carrot populations can help future tropical carrot development programmes.

REFERENCES

Akhilesh Sharma, Pooja Kapur and Viveka Katoch. 2012. Generation mean analysis to estimate genetic parameters for desirable horticultural traits in garden pea (*Pisum sativum*). *Indian Journal of Agricultural Sciences* **82**(3): 201–06.

Causse M, Chaïb J, Lecomte L, Buret M and Hospital F. 2007. Both additivity and epistasis control the genetic variation for fruit quality traits in tomato. *Theoretical and Applied Genetics* **115**(3): 429–42.

Cavalli L L. 1952. An analysis of linkage in quantitative inheritance. *Quantitative Inheritance,* p 135–44. HMSO, London.

Dixit G P, Tanveer H and Chandra S. 2006. Generation mean analysis for grain yield related traits in field pea (*Pisum sativum* L.). *Indian Journal of Genetics* **66**: 147-48.

Hayman BI and Mather K. 1955. The description of genetic interactions in continuous variation. Biometrics **11**: 69–82

Holland J B. 2011. Epistasis and plant breeding. *Plant Breeding Reviews* **21**: 27–91.

Hussain K, Singh D K, Ahmed N and Gazal Nazir. 2006. Multivariate analysis in carrot (*Daucus carota* L.). *Environment and Ecology* **24**(1): 37–41.

Jadhav M G and Dhumal S A. 1994. Genetic studies of some quantitative characters in chilli. *Journal of Maharashtra Agricultural University* **19**(1): 62–64.

Jagosz B. 2012. Combining ability of carrot (*Daucus carota* L.) lines and heritability of yield and its quality components. *Folia Horticulturae* **24**(2): 115–22.

Karklelienë R, Bobinas È and Stanienë G. 2005. Combining ability of morphological traits and biochemical parameters in carrot (*Daucus sativus* Rohl.) CMS lines. *Biologija* **3**: 15–18.

Mather K and Jinks J L. 1982. *Biometrical Genetics*, 3rd edn. Chapman and Hall, London

Plant Breeding Tools (PBT). 2013. Plant breeding, genetics and biotechnology, International Rice Research Institute, Philippines.

Selvakumar R, Pritam Kalia, Sureja A K and Raje R S. 2019. Genetic analysis of structural traits in tropical carrot (*Daucus carota* L.)**.** *EC Agriculture* **5**(1): 4–14.

Selvakumar R, Pritam Kalia and Raje R S. 2017. Genetic analysis of root yield and its contributing traits in tropical carrot (*Daucus carota* L.)**.** *Indian Journal Horticulture* **74**(2): 214–19.

Selvakumar R, Pritam Kalia and Raje R S. 2019. Genetic analysis of nutritional traits in tropical carrot (*Daucus carota* L.). *Genetika* **51**(2): 641–60.

Selvakumar R, Dalasanuru Chandregowda Manjunathagowda, Pritam Kalia and Raje R S. 2021. Genetic analysis of root traits in tropical carrots (*Daucus carota* L.). *Genetic Resources Crop Evolution*. https://doi.org/10.1007/s10722-021-01188-3.

Singh H V, Singh S P, Singh M and Singh S. 2002. Genetic analysis of quantitative traits in brinjal (*Solanum melongena* L.). *Vegetable Science* **29**(1): 84–86.

Singh O, Gowda C L, Sethi S C, Dasgupta T and Smithson J B.1992. Genetic analysis of agronomic characters in chickpea. I. Estimates of genetic variances from diallel designs. *Theoretical Applied Genetics* **83**: 956–62.

Singh R P and Singh S.1992. Estimation of genetic parameters through generation mean analysis in bread wheat. *Indian Journal of Genetics and Plant Breeding* **52**: 369–75.