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The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(10): 1801-1806

www.thepharmajournal.com
Received: 05-08-2023
Accepted: 14-09-2023

Combining ability and gene action studies in chilli (*Capsicum annuum* L.)

Vinay Verma, Amit Vikram, Yash Pal Sharma, Ramesh K Bhardwaj, Rajesh K Dogra, Meenu Gupta and Shalini Singh

Vinay Verma
Department of Vegetable Science, College of Horticulture, Dr. YSP UHF, Nauni, Himachal Pradesh, India

Amit Vikram
Department of Vegetable Science, College of Horticulture, Dr. YSP UHF, Nauni, Himachal Pradesh, India

Yash Pal Sharma
Department of Forest Products (Medicinal and Aromatic Plants), College of Forestry, Dr. YSP UHF, Nauni, Himachal Pradesh, India

Ramesh K Bhardwaj
Department of Vegetable Science, College of Horticulture, Dr. YSP UHF, Nauni, Himachal Pradesh, India

Rajesh K Dogra
Department of Fruit Science, College of Horticulture, Dr. YSP UHF, Nauni, Himachal Pradesh, India

Meenu Gupta
Department of Plant Pathology, College of Horticulture, Dr. YSP UHF, Nauni, Himachal Pradesh, India

Shalini Singh
SMS, Department of Horticulture, KVK Saharanpur, SVPUAT, Meerut, Uttar Pradesh, India

Abstract

Nature of gene action involved in the inheritance of important quantitative and qualitative traits is elucidated by using eight parents in a diallel method without reciprocal to obtain information for selection of the parents and crosses with favorable GCA and SCA effects. The analysis of variance revealed the significant differences among the parents and crosses for all the 14 characters studied. All the characters were exhibited higher magnitude of SCA variances than GCA variances which revealed that non-additive gene action was played an important role in the inheritance of these trait except for pedicel length, fruit weight and 1000 seed weight, where additive gene was responsible for the expression of the trait. According to GCA effects, the genotypes UHF CHI 7, UHF CHI 5, UHF CHI 14 and UHF CHI 15 found to be promising general combiners for yield and yield components. The SCA effects revealed that eleven crosses *viz.*, H6, H17, H7, H10, H8, H26, H3, H25, H14, H1 and H9 were identified as promising hybrids for fruit yield and its yield component characters.

Keywords: *Capsicum annuum*, combining ability, Gene action, GCA, SCA, half diallel

Introduction

Chilli (*Capsicum annuum* L.) is a commercially important vegetable cum spice crop cultivated across the world for its green and ripe fruit. Chilli belongs to the family solanaceae having diploid species with principally 2n = 2x = 24 chromosomes. The domestication of chilli initially occurred in Central America, possibly in North American nation, with secondary centers in Guatemala and Bulgaria (Salvador, 2002) [20]. At a global spice trade, chilli is the second largest traded commodity after black pepper and India has immense potential to export different types of chillies around the world. The productivity of both green and dry chilli in India is low due to extensive use of local landraces or non-selfed seeds of improved varieties, biotic and abiotic stresses, development of new races of pathogens and genetic drift in cultivars. Therefore, in order to increase its yield, quality, and host plant resistance to viral diseases, intensive efforts are required. One of the options to achieve quantum jump in yield is development of heterotic hybrids through hybridization programme. A plant breeder must have knowledge of the relative importance of additive and non-additive gene action in order to develop an effective hybridization program. (Dudley and Moll, 1969) [3] Furthermore, proper parent selection based on combining ability is required to achieve better heterotic effects.

The capacity or ability of a genotype to transmit superior performance to its crosses is referred to as combining ability. With regard to combining ability effects, Griffing (1956) [6] reported that, analysis of combining ability is a one of the potential tools for identifying productive parents to develop commercial F1 hybrids. Sprauge and Tatum (1942) [25] have defined the terms ‘general combining ability’ (GCA) and ‘specific combining ability’ (SCA) as a measure of gene action while working with maize. The GCA variance is due to additive whereas SCA variance is due to non-additive gene action. As a result, both serve as important diagnostic tools in the selection of suitable parents. To estimate combining ability, top crossing, line x tester, diallel and partial diallel crossing techniques are used. Among the above techniques Diallel analysis provides the estimates of genetic parameters regarding heterosis and combining ability. It gives additional information on presence or absence of epistasis, average degree of dominance and distribution of dominant and recessive genes in the parents (Rego *et al*., 2009; Nascimento *et al*., 2014) [17, 13]. Therefore, the present investigation was carried out to estimate combining ability effects for yield and its contributing traits.

Corresponding Author:
Vinay Verma
Department of Vegetable Science, College of Horticulture, Dr. YSP UHF, Nauni, Himachal Pradesh, India

Materials and Methods

An experiment was carried out at Vegetable Research Farm, Dr. YS Parmar University of Horticulture and Forestry Nauni, Solan (HP). The experimental material comprised of eight parents (DKC-8, UHF CHI 5, UHF CHI 7, UHF CHI 11, UHF CHI 12, UHF CHI 13, UHF CHI 14 and UHF CHI 15). These parents were crossed in half diallel fashion. The resulting 28 F_1 hybrids along with their 8 parents and standard checks (DKC-8) were evaluated in a Complete Randomized Block Design with three replications of each genotype at a spacing of 45 cm x 45 cm. The crop was raised as per the recommended package of practices. The observations were recorded on ten randomly selected plants for fourteen characters *viz*., days to 50% flowering, plant height (cm), number of branches per plant, plant spread (cm), number of fruits per plant, fruit length (cm), fruit width (mm), pedicel length (cm), fruit weight (g), ripe fruit yield per plant (g), number of seeds per fruit, 1000 seed weight (g), capsaicin (%) and oleoresin (%).

The statistical methods given by Panse and Sukhatme, (1985) [15] and Dabholkar (1992) [2] was used for analysis of variance to test the significance of difference of means for all the characters studied and the combining ability analysis based on mean values over replication was carried out for all characters, using method 2 model I Griffing (1956) [6], which depends on the parental cultivars and their F_1 crosses in one direction.

General combining ability effect (GCA):

$$\text{gi} = \frac{1}{(\text{P}+2)}\left[\sum(\text{Yi.} + \text{Yii}) - \frac{2}{\text{P}}\,\text{Y....}\right]$$

Specific combining ability effect (SCA):

$$\text{Sij} = \text{Yij} - \frac{1}{(\text{P}+2)}(\text{Yi.} + \text{Yii} + \text{Yj.} + \text{Yjj}) + \frac{2}{(\text{P}+1)(\text{P}+2)}\,\text{Y...}$$

Standard errors to test the significance of general and specific combining ability and the difference between two estimates of gca or sca were computed as follows:

1. To test the individual gca effect

$$\text{SE (gi)} = \frac{P-1}{P(P+2)}\,\sigma^2\text{e}$$

2. To test the difference between gca effects

$$\text{SE (gi-gj)} = \frac{2}{P+2}\,\sigma^2\text{e} \qquad (\text{i} \neq \text{j})$$

3. To test the individual sca effects

$$\text{SE (sij)} = \frac{P^2+P+2}{(P+1)(P+2)}\,\sigma^2\text{e} \qquad (\text{i} \neq \text{j})$$

4. To test the difference between sca estimates in the same array or column.

$$\text{SE (sij-sik)} = \frac{2(P+1)}{P+2}\,\sigma^2\text{e} \qquad (\text{i} \neq \text{j, k, j} \neq \text{k})$$

5. To test the difference between sca estimates in the different array or column.

$$\text{SE (sij-skl)} = \frac{2P}{P+2}\,\sigma^2\text{e} \qquad (\text{I} \neq \text{j, k \& l, j} \neq \text{k \& l, k} \neq \text{l})$$

Critical differences were estimated by multiplying the corresponding SE of differences with table value of `t' at error degree of freedom and 5% level of significance.

Estimates of G.C.A. and S.C.A. variances calculated as follows:

$\sigma^2 g = 1/p+2$ (Mg - Ms)
$\sigma^2 s$ = Ms – M'e
$\sigma^2 e$ = M'e

Results and Discussion

Analysis of variance revealed highly significant mean sum of squares (Table 1) for general and specific combining abilities for all traits studied suggesting that both additive and non-additive gene actions are involved in their genetic expression. However, the variance due to specific combining ability effect have greater in magnitude than general combining ability effects for ripe fruit yield per plant and contributing traits *viz* days to 50% flowering, plant height, number of branches per plant, Plant spread, Number of fruits per plant, fruit length, fruit width and number of seeds per fruit suggesting the predominant role of non-additive gene action for the inheritance of these traits.

Fruit yield per plant is directly correlated with number of fruits per plant and average fruit weight hence, these two traits are the most important yield contributing characters. Among the 8 parents, highest significant GCA effect (Table 2) for ripe fruit yield per plant was found in UHF CHI 7 (204.47), moreover this parent also showed high GCA effects for most of the traits like fruit width (2.80), fruit weight (2.76), number of seeds per fruit (12.06) and 1000 seed weight (0.70). Navhale *et al.* (2014) [14] with seven parents crossed in diallel mating design. In this study revealed that, high gca effects for red fruit yield per plant were exhibited by BC-28 (6.115) and Konkan Kirti (1.474). Siddappa *et al.* (2019) [22] in a Line×Tester analysis involving eleven genotypes identified KCMS-44 (1.18), KCMS-16 (1.20) among lines and H-31 (6.68), Ujjwal (0.79), LCA-234 (0.98) and Arka Lohit (1.46) among testers as good general combiners for average fruit weight. Kranthi Rekha *et al.* (2016) [10] in her study found four parents LCA 625 (4.74), LCA 764 (4.57), LCA 704 (4.98) and LCA 315 (5.76) with good general combining ability for number of seeds per fruit and 0.55 (LCA 704) and 0.36 (LCA 704) for 1000 seed weight. Second highest contributing parent was UHF CHI 14 which showed high significant GCA effects for plant height (13.08), plant spread (5.90) and fruit length (1.76). Janaki *et al.* (2017) [8] in a Line × Testers analysis involving fifteen genotypes identified LCA-504 (7.14), LCA-607 (3.52), LCA-655 (6.60) and LCA-703-2 (10.68) as good general combiners for plant height. Jagtap *et al.* (2015) [7] crossed seven parents in a diallel fashion without reciprocals and found P2 (0.41), P3 (1.73), P4 (1.22) and P6 (0.78) as good general combiners with high positive gca effects for plant spread. Khalil and Hatem (2014) also reported positive GCA effect ranged from 2.97 to 4.43 for fruit length among six parents. For earliness character *viz* day to 50% flowering parent UHF CHI 15 (-1.40) exhibited highest negative significant GCA effect. Jagtap *et al.* (2015) [7] while working in chilli with seven genotypes in diallel mating design, reported negative GCA effect for days to 50% flowering in in P4 (-0.78) and P5 (-0.39). Nagaraja *et al* (2016) [11] also reported significant GCA effect in negative direction in both lines and testers for days to 50% flowering. UHF CHI 5 were showed high GCA effects for number of branches per plant (0.34) and number of fruits per plant (20.57). Patel *et al*. (2003) [16] with three lines and eight testers had found significant gca effects in ACS-98-9 (0.74), BC-14-2 (0.14) and SG-5 (0.58) Singh and Pan (2009) with nine genotypes found HC-8 (22.01), HC-51 (19.51), HC-33 (12.21) and HC-23 (15.16) as good general combiners for number of fruits per plant. For pedicel length DKC-8 (-0.35) showed highest negative GCA effect. Certainly the parent UHF CHI 7 will be the first choice because of highly significant GCA effect for five characters. Naresh *et al.* (2016) [12] in diallel mating design (without reciprocal) involving ten genotypes found significant gca effect for pedicel length and identified parents IHR3453 (-0.37), IHR4506 (-0.225) and IHR 4507 (-0.424) as good general combiners. The next best choice would be UHF CHI 14 which had significant GCA effect for three characters. Involving these parents in hybridization would result in the identification of superior hybrid combinations with favorable genes.

Similar to GCA effects, the SCA effects of hybrids exhibited variation in direction and magnitude (Table 3). Different parents combined well for different traits. The best specific combiners for days to 50% flowering were H7 (-3.60), H26 (-3.44), H27 (-3.24) and these hybrids were the result of low x high and medium x high GCA effect of their corresponding parents. Janaki *et al.* (2017) [8] also identified nine crosses with significant SCA effect for days to 50% flowering. For plant height cross combinations H6 (10.59), H7 (9.10) and H1 (8.42) had highest significant SCA effect. Similar findings were earlier reported by Spaldon *et al.* (2015) [24] in which they observed that ten out of thirty hybrids in a line x tester design showed significant positive sca effects, being maximum in cross SC-23 × Local (9.988). The best specific combiners with highest significant SCA effects for number of branches per plant were H23 (1.61), H20 (1.48) and H3 (1.37). Similar findings were earlier reported by Aishwarya *et al.* (2020) [1] in which they observed that six out of ten hybrids in a half diallel design showed significant positive sca effects. Cross combinations H3 (8.88), H26 (8.05), H13 (7.06) were showed highest SCA effect for plant spread and these results were due to low x high and high x high GCA effects of their respective parents. The selection for high yielding genotype should be based mainly on the fruits per plant (Gill *et al*., 1973) [5]. The hybrids H24 (68.48), H6 (47.66), H9 (45.18) were found to be superior for number of fruits per plant based on their SCA effects and all these hybrids were the outcome of low x high and high x low GCA effects of their respective parents. Rodrigues *et al.* (2012) [18] in their study of half diallel with five parents reported that, six hybrids exhibited significant positive value of sca effect. Highest value was observed in cross UENF 1624 × UENF 1639 (37.19). Similar results were also reported by Geleta and Labuschagne (2006) [4].

Best performing hybrids in fruit traits based on their highly significant SCA effects were H13 (3.30), H19 (2.06) and H6 (1.51) for fruit length, where parents having high x high, high x low and low x high GCA effects. Patel *et al.* (2003) [16] in which they conducted a Line × Tester analysis with three lines and eight testers and observed high SCA effects in three crosses *viz*., ACS 98-8 × Ba Jochpur (1.46), ACS 98-8 × R. Patti (0.70) and ACS 98-9 × 5GI-5 (1.07). Hybrid H10 (2.79), H3 (1.97) and H28 (1.21) for fruit width with high x low and low x low GCA effects of their corresponding parents. Similar findings were also reported by Nagaraja *et al.* (2016) [11] in which they observed that 11 out of 36 hybrids in a line x tester design showed significant positive sca effects, being maximum in cross CM1112A × NCR1886 (0.14). Hybrid H1 (-0.33), H10 (-0.30) and H24 (-0.26) for pedicle length having high x low and low x high CGA effects in their respective parents.

For ripe fruit weight, hybrids H10 (3.02), H28 (2.31) and H3 (1.19) were showed significant SCA effects and these hybrids were the outcome of high x low and low x low GCA effects of their parents. For 1000 seed weight hybrids H16 (0.88), H3 (0.77) and H23 (0.57) were the best specific combiners. Interestingly for both characters the GCA variance was higher than SCA variance indicating the additive x additive type of gene interaction. As a result, the parents involved in the aforementioned crosses were worthy participants in the varietal improvement program. The high performing hybrids for number of seeds per fruit based on SCA effects were H10 (28.90), H26 (21.86) and H2 (16.02). Ripe fruit yield per plant forms the major objective of the present study and the breeding procedures are focused on increasing the potentiality of this trait. The hybrids H6 (408.30), H17 (407.28) and H7 (230.10) showed high significant positive SCA effects for ripe fruit yield per plant and the SCA effect ranged from -252.83 to 408.30. Janaki *et al*. (2017) [8] in their study of line x tester reported 9 hybrids exhibited significant SCA effects ranged from -49.13 to 64.49 for fruit yield per plant and also found significant SCA effect for seed weight and number of seeds per fruit. Similar results were also reported by Spaldon *et al.* (2015) [24] and Jagtap *et al.* (2015) [7]. Capsaicin is the major component which determines the pungency in chilli fruits. Parents with high significant positive gca effects were considered as good general combiners *viz*. UHF CHI 13 (0.08), DKC-8 (0.07) and UHF CHI 12 (0.03) (Table 4.3.1c). Whereas parents UHF CHI 5 (-0.06), UHF CHI 7 (-0.07), UHF CHI 11 (-0.03) and UHF CHI 14 (-0.03) had significant negative values signifying that these are poor general combiners for capsaicin content. The findings of Sharma *et al.* (2016) [21] support the present results through the combining ability studies in which they found Arka Lohit (0.11), Pusa Jwala (0.22), Pusa Sadabahar (0.08), Kashmir Long (0.04) and LCA206 (0.05) as good general combiners for capsaicin. The findings of Rohini *et al.* (2017) [19] and Janaki *et al.* (2017) [8] are also in conformity with the present findings. Significant positive general combining ability for oleoresin (Table 4.3.1c) was recorded for parents DKC-8 (2.11), UHF CHI 11 (2.36), UHF CHI 12 (0.41) and UHF CHI 13 (2.33), therefore, these parents have good general combining ability. While parents UHF CHI 5 (-2.87), UHF CHI 7 (-2.54), UHF CHI 14 (-0.25) and UHF CHI 15 (-1.55) resulted in poor general combining ability due to the significant negative gca effects. Similar results were reported by Janaki *et al*. (2017) [8] in which they found three parents LCA 615 (3.88), LCA 446 (1.24) and G-4 (2.08) with high gca effects. Aishwarya *et al.* (2020) [1], Sharma *et al*. (2016) [21] and Rohini *et al* (2017) [19] also reported similar findings in different set of genotypes.

Table 1: Analysis of variance (mean squares) for diallel analysis for different components in chilli (*Capsicum annum* L.)

Source of variation	df	Days to 50% flowering	Plant height (cm)	No of branches/ plant	Plant spread (cm)	No of fruits/ plant	Fruit length (cm)	Fruit width (mm)	Pedicel length (cm)	Fruit weight (g)	Ripe fruit yield per plant (g)	Number of seeds per fruit	1000 Seed weight (g)	Capsaicin (%)	Oleoresin (%)
GCA	7	12.40*	726.43*	0.49*	236.79*	2899.26*	15.18*	16.69*	0.66*	19.53*	307814.90*	439.87*	3.41*	0.033*	46.81*
SCA	28	4.74*	75.83*	1.11*	40.65*	1288.88*	1.70*	1.79*	0.03*	1.25*	36018.44*	140.98*	0.28*	0.003*	8.66*
Error	70	0.92	4.51	0.03	6.76	2.18	0.14	0.26	0.01	0.11	1643.91	16.91	0.05	0.00	0.15
σ^2g		0.76	65.06	0.05	19.61	161.03	1.34	1.48	0.06	1.82	27179.65	29.89	0.31	0.003	3.81
σ^2s		3.82	71.31	1.08	33.89	1286.70	1.56	1.53	0.02	1.14	34374.53	124.08	0.23	0.003	8.52
$\sigma^2g/\ \sigma^2s$		0.20	0.91	0.04	0.58	0.13	0.86	0.97	3.00	1.60	0.79	0.24	1.35	1.00	0.45

Table 2: Estimates of general combining ability effects of parents for different horticultural traits in chilli (*Capsicum annuum* L.)

Parents/ character	Days to 50% flowering	Plant height (cm)	Number of branches per plant	Plant spread (cm)	Number of fruits per plant	Fruit length (cm)	Fruit width (mm)	Pedicel length (cm)	Fruit weight (g)	Ripe fruit yield per plant (g)	Number of seeds per fruit	1000 Seed weight (g)	Capsaicin (%)	Oleoresin (%)
DKC-8	1.63*	-9.16*	-0.21*	-7.63*	-6.65*	-1.21*	-0.59*	-0.35*	-0.76*	-101.89*	-7.98*	-0.40*	0.07*	2.11*
UHF CHI 5	-0.37	-0.75	0.34*	2.34*	20.57*	0.96*	0.40*	0.34*	0.44*	180.15*	4.28*	0.46*	-0.06*	-2.87*
UHF CHI 7	-0.03	1.84*	0.06	2.71*	-12.49*	0.34*	2.80*	-0.02	2.76*	204.47*	12.06*	0.70*	-0.07*	-2.54*
UHF CHI 11	-0.80*	12.02*	-0.04	2.70*	-10.46*	0.32*	-0.91*	0.01	-0.86*	-139.88*	-4.35*	0.31*	-0.03*	2.36*
UHF CHI 12	1.57*	-7.77*	-0.17*	-6.15*	-27.07*	-1.27*	-0.27	-0.09*	-0.75*	-215.46*	0.26	-1.01*	0.03*	0.41*
UHF CHI 13	0.27	-5.63*	-0.32*	-2.66*	12.73*	-1.66*	-1.41*	-0.33*	-1.65*	-173.33*	-7.45*	-0.52*	0.08*	2.33*
UHF CHI 14	-0.87*	13.08*	0.18*	5.90*	3.69*	1.76*	0.46*	0.29*	1.08*	170.67*	0.90	0.08	-0.03*	-0.25*
UHF CHI 15	-1.40*	-3.63*	0.16*	2.79*	19.71*	0.75*	-0.49*	0.16*	-0.28*	75.27*	2.26	0.37*	0.00	-1.55*
SE (gi)	0.28	0.62	0.05	0.77	0.44	0.11	0.15	0.04	0.12	15.37	1.49	0.07	0.002	0.11
SE (gi-gj)	0.43	0.94	0.08	1.16	0.66	0.17	0.23	0.06	0.19	23.24	2.25	0.10	0.003	0.17
CD (gi)	0.56	1.24	0.10	1.53	0.88	0.22	0.30	0.08	0.24	30.65	2.97	0.14	0.003	0.22
CD (gi-gj)	0.86	1.87	0.16	2.31	1.32	0.34	0.46	0.12	0.38	46.34	4.49	0.20	0.005	0.34

*Significant at 5% level of significance

Table 3: Estimates of specific combining ability effects of hybrids for different horticultural traits in chilli (*Capsicum annuum* L.)

F_1 Combinations	D50F	PH	NBPP	PS	NFPP	FL	FW	PL	FWT	RFYPP	NSPF	SW	Cap (%)	Oleo (%)
H1	-1.30*	8.42*	-0.74*	-4.42*	42.58*	0.07	-1.32*	-0.33*	-0.73*	75.97*	1.31	0.05	0.07*	3.05*
H2	-0.30	-1.77*	-0.26*	3.77*	9.04*	1.12*	0.26	-0.01	-0.03	-58.73*	16.02*	0.12	0.04*	0.03
H3	-0.20	0.05	1.37*	8.88*	8.80*	0.60*	1.97*	0.05	1.19*	160.55*	8.10*	0.77*	0.04*	4.34*
H4	0.10	8.34*	0.90*	5.90*	13.62*	-1.02*	0.19	0.10*	-0.65*	-25.47	-16.71*	0.25*	-0.03*	0.87*
H5	2.73*	-7.37*	1.12*	-10.36*	-38.18*	-1.00*	-3.41*	0.06	0.39*	-126.53*	0.60	-0.11	0.01*	2.07*
H6	-0.80*	10.59*	-1.64*	5.62*	47.66*	1.51*	0.52*	0.15*	0.85*	408.30*	1.92	-1.01*	0.01*	0.41*
H7	-3.60*	9.10*	0.70*	4.36*	33.64*	-0.13	0.60*	0.09	0.58*	230.10*	13.82*	-0.08	-0.01*	-1.84*
H8	1.03*	-7.04*	0.13	1.57	24.22*	0.84*	-1.00*	-0.01	-0.76*	182.69*	-17.30*	0.27*	0.04*	-1.25*
H9	1.13*	-3.26*	-0.11	1.05	45.18*	-0.30	-0.68*	0.04	-0.94*	53.58*	13.64*	0.09	0.05*	-2.65*
H10	0.10	-3.67*	0.96*	6.34*	-12.40*	1.09*	2.79*	-0.30*	3.02*	211.69*	28.90*	0.15	-0.06*	-3.42*
H11	1.06*	-20.51*	-2.10*	2.04*	8.80*	0.50*	-0.45*	0.06	-0.81*	-64.27*	-0.19	-0.47*	-0.02*	2.24*
H12	1.20*	7.08*	0.88*	4.02*	-22.76*	-0.81*	-0.06	0.34*	-1.01*	-252.83*	-10.34*	-0.23*	-0.03*	2.99*
H13	2.73*	2.36*	-0.44*	7.06*	-29.18*	3.30*	-0.77*	-0.01	0.22	-75.14*	-5.10*	-0.15	-0.08*	0.56*
H14	0.46	-5.31*	1.04*	-1.90	22.84*	0.16	0.15	0.07	-0.80*	77.32*	4.72*	0.00	-0.03*	3.24*
H15	1.76*	-9.95*	0.10	6.56*	2.86*	0.44*	-3.27*	-0.09	0.30	0.32	12.12*	0.27*	-0.05*	-4.13*
H16	-1.94*	4.40*	-1.55*	1.76	-31.34*	1.09*	0.98*	0.11*	0.53*	-45.99*	-7.24*	0.88*	-0.08*	2.25*
H17	3.20*	-3.50*	-0.11	-2.36*	35.70*	-0.29	-0.67*	0.36*	-0.04	407.28*	-13.25*	-0.74*	-0.00	0.49*
H18	-0.94*	-2.69*	0.24*	-0.98	-10.32*	-0.49*	-0.41*	-0.17*	-0.77*	-64.83*	-1.42	-0.23*	0.07*	-0.87*
H19	0.86*	3.17*	-0.54*	5.64*	-14.78*	2.06*	-0.56*	0.13*	0.18	-50.49*	-3.71	-0.87*	-0.04*	1.80*
H20	0.50	7.72*	1.48*	0.27	-30.58*	-0.01	0.27	-0.03	-0.45*	-126.51*	5.50*	-0.24*	0.04*	-3.74*
H21	-1.70*	0.12	-0.95*	-9.21*	-15.74*	-0.58*	-0.19	0.04	-0.75*	-192.95*	-4.64*	0.25*	-0.06*	-0.86*
H22	-0.17	-3.97*	-0.27*	1.53	-8.16*	-0.46*	-0.06	-0.09	-0.62*	-77.52*	-5.61*	0.23*	-0.01*	3.60*
H23	2.13*	-10.09*	1.61*	-13.50*	-27.56*	-1.63*	0.17	-0.21*	0.34*	-13.06	-10.10*	0.57*	0.07*	3.23*
H24	-2.74*	5.67*	-0.82*	2.54*	68.48*	-0.43*	-0.50*	-0.26*	-2.46*	16.86	-9.12*	-0.34*	0.06*	2.10*
H25	0.13	-3.58*	0.60*	-2.91*	20.06*	0.77*	-0.08	-0.02	0.17	132.40*	5.05*	-0.89*	-0.09*	1.52*
H26	-3.44*	-6.14*	-0.07	8.05*	-6.32*	1.49*	0.90*	0.14*	1.08*	167.06*	21.86*	0.43*	0.06*	-5.37*

H27	-3.24*	7.77*	-0.26*	3.49*	-4.14*	-0.52*	0.81*	0.17*	-0.63*	-88.49*	-6.84*	-0.08	0.02*	-2.93*
H28	-1.77*	1.47	1.05*	1.17	-58.50*	1.35*	1.21*	0.04	2.31*	-149.29*	11.75*	-0.22*	-0.06*	-3.73*
SE (sij)	0.87	1.91	0.17	2.36	1.34	0.35	0.46	0.11	0.38	47.13	4.56	0.21	0.0051	0.35
SE (sij-sik)	1.29	2.82	0.25	3.49	1.98	0.51	0.69	0.17	0.57	69.73	6.74	0.31	0.0075	0.52
SE (sij-skl)	1.21	2.66	0.23	3.29	1.87	0.48	0.65	0.16	0.54	65.74	6.36	0.29	0.0071	0.49
CD (sij)	1.73	3.81	0.34	4.70	2.67	0.70	0.92	0.22	0.76	93.98	9.10	0.42	0.010	0.70
CD (sij-sik)	2.57	5.62	0.50	6.96	3.95	1.02	1.37	0.34	1.14	139.04	13.44	0.62	0.015	1.04
CD (sij-skl)	2.41	5.30	0.46	6.56	3.73	0.96	1.30	0.32	1.08	131.08	12.68	0.58	0.014	0.98

*Significant at 5% level of significance

D50F (Days to 50% flowering), PH (Plant height), NBPP (Number of branches per plant), PS (Plant spread), NFPP (Number of fruits per plant), FL (Fruit length), FW (Fruit width), PL (Pedicel length), FWT (Fruit weight), RFYPP (Ripe fruit yield per plant), NSPF (Number of seeds per fruit), SW (1000 seed weight), Cap (Capsaicin), Oleo (Oleoresin)

Conclusion

The diallel analysis revealed that parents UHF CHI 7 and UHF CHI 14 were good general combiners for ripe fruit yield per plant together with plant height, plant spread, fruit length, fruit width, fruit weight, number of seeds per fruit and 1000 seed weight. All these characters were governed by dominance gene effects. Hence, biparental mating, recurrent selection, heterosis breeding, and modified diallel mating are the best breeding strategies to exploit non-additive gene actions. Additive gene effects are more important in controlling the fruit weight and 1000 seed weight, suggesting that simple selection is the best strategy for improving these traits. For ripe fruit yield per plant eleven hybrid combinations were showed significant positive SCA effect in positive direction. SCA variance was higher than GCA variance for ripe fruit yield per plant suggesting the trait was controlled by dominance gene action. Hence potential cross combination can be used for the identification of superior hybrids for commercial exploitation of heterosis.

Acknowledgement

This work is a part of Ph.D. thesis of Vinay Verma. The authors thank Dr Yash Pal Sharma (Principal Phytochemist), Department of Forest Products (Medicinal and Aromatic Plants), Dr YSP UH&F Nauni (HP) for their support during the lab work which leads to completion of this thesis.

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