



Heterosis, combining ability and gene action for yield and quality traits in tomato (*Solanum lycopersicum* L.)

*¹Ankur Agarwal, ²D. N. Arya, ³R. Ranjan, ⁴Zakwan Ahmed

^{1, 2, 3, 4}Defence Institute of Bio-Energy Research, DRDO, Haldwani, Uttarakhand-263145

¹Email: ankurdr@rediffmail.com

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Abstract:

Eight parental lines of diverse origin of tomato were crossed in a 8 × 8 diallel mating design excluding reciprocals. The 28 F₁ hybrids along with their parents were evaluated in a randomized block design with three replications. In the present study, significant and highest general combining ability effect for fruit yield and average fruit weight was recorded in CLN 5915-206 (49.06 and 8.23 respectively), for total soluble solids in CLN 2264H (0.18) and for dry matter content in Best of All (0.32). The highest significant heterosis over better and standard parent was recorded for average fruit weight (74.69 and 117.27) followed by total soluble solids for better parent heterosis. The range of heterosis for fruit yield over better parent was 6.63-35.90% and cross between CLN 5915-206 × CLN 1314G recorded the maximum heterosis over both better (35.90) and standard parent (56.32%) for the trait. Genotype with positive and moderately high gca for dry matter (Pith Sel, DARL-1 and Best of All) and TSS (CLN 2264H and DARL-1) exhibited good specific combining ability for exploiting hybrid vigour for these traits. Genetic components H₁, H₂ were highly significant for all the traits exhibiting the importance of both additive and dominant gene effects in regulating these traits.

Key words: Tomato, heterobeltiosis, total soluble solids, dry matter content, genetic divergence.

Introduction:

Exploring natural diversity as a source of novel alleles to improve the productivity, quality and nutritional value of the crop is the base line of any breeding programme (Fernie *et al.* 2006). Exploitation of hybrid vigour and selection of parents on the basis of combining ability and gene action have been important breeding approaches in crop improvement. The studies of combining ability is essentially useful in connection with testing procedures in which it is desired to study

and compare the performance of a line in hybrid combination. Tomato (*Solanum lycopersicum* L.) is the second most consumed vegetable of the world after potato with a production of 123.6 million tons from 4.5 million ha area. World crop area of tomato has increased by 164% in the last 40 years with a rise in per capita consumption from 14 kg/year during 1985 to 19 kg/year during 2005 (FAO 2008). Considering this, the present investigation was undertaken to generate information on nature of gene action and combining ability in eight parental lines of tomato to assess the prepotency of parents in hybrid combination.

Materials and Methods:

Eight parental lines of diverse origin of tomato were crossed in a 8 × 8 diallel mating design excluding reciprocals. The 28 F₁ hybrids along with their parents viz., DARL-2 (P1), CLN2264J (P2), CLN2264H (P3), CLN5915-206-D4-2-2-0 (P4), CLN1314G (P5), Best of All (P6), DARL-1 (P7) and Pith Sel (P8) were evaluated in a randomized block design with three replications at Defence Institute of Bio-Energy Research, Field station Pithoragarh situated at 1730m above mean sea level in the hills of central Himalayas. Data were recorded on average fruit weight, fruit yield, total soluble solids and dry matter content. For estimation of quality traits, ripe fruits were selected randomly. Total soluble solids (T.S.S. in °brix) was estimated by using hand refractometer and dry matter content (%) by hot air oven drying. Heterosis was calculated as per Allard (1960), combining ability as suggested by Griffing (1956) and genetic parameters by Hayman (1954).

Results and Discussion:

The analysis of variance for combining ability (Table 1) revealed the existence of significant variation for all the four characters indicating wide range of variability among the genotypes. Highly significant variation due to general combining ability (gca) and specific combining ability (sca) indicates the importance of

additive as well as non-additive types of gene action in inheritance of these characters. These findings are in close agreement with Bhatt *et al.* (2004), Premalakshme *et al.* (2006) and Singh *et al.* (2008).

Significant highest gca effect for fruit yield and average fruit weight was recorded in CLN 5915-206 (49.06 and 8.23 respectively), for total soluble solids in CLN 2264H (0.18) and for dry matter content in

Table 1. Analysis of variance of combining ability in 8× 8 diallel cross in tomato.

Source	d.f.	Fruit yield (q/ha)	Ave fruit weight (g)	Total soluble solids (brix)	Dry matter content (%)
Gca	7	9026.2**	559.15**	0.150	1.148**
Sca	28	5322.0**	319.04**	0.384**	0.548**
Component of variation					
Due to gca		867.24	55.31	0.008	0.114
Due to sca		4968.24	313.04	0.317	0.543
Component ratio					
σ^2_g / σ^2_s		0.1746	0.176	0.026	0.210

** denotes significant at $P=0.01$

Table 2. General combining ability (gca) of the parents.

Parents	Fruit yield (q/ha)	Ave fruit weight (g)	Total soluble solids (brix)	Dry matter content (%)
DARL-2 (P1)	-12.75*	1.17	-0.02	-0.78**
CLN 2264J (P2)	-10.16	-7.03**	0.13	0.13**
CLN 2264H (P3)	-10.41	7.53**	0.18*	0.17**
CLN 5915-206 (P4)	49.06**	8.23**	-0.07	-0.13**
CLN 1314G (P5)	39.82**	6.67**	-0.17*	0.17**
Best of All (P6)	-22.91**	-12.77**	-0.06	0.32**
DARL-1 (P7)	4.80	-2.73**	0.11	0.05*
Pith Sel (P8)	-37.46**	-1.07	-0.08	0.08**
SE±	5.564	0.724	0.0762	0.0208

*, ** denote significant at $P=0.05$ and 0.01 respectively

Best of All (0.32) (Table 2). However, none of the parent was best general combiner for all the traits indicating differences in genetic variability for different characters among the parents. These observations revealed that these quality traits with yield could be improved by using these parents in hybrid breeding programme for accumulation of favourable genes. The relative contribution of individual parents to improve the specific trait in the population can be estimated by comparing the general combining ability effects (Lippert 1975). In the present study, parents with positive and high gca

have the capability for increasing the quality traits in the population. Conversely, parents with negative gca effect contribute most to the reduction of TSS and dry matter. The top three crosses selected on the basis of per se performance exhibited higher sca effects in desirable direction and significantly higher standard heterosis involving high × high, high × low and low × low gca parents (Table 3). Manifestation of high sca effects by crosses where both the parents were good general combiners might be attributed to additive × additive gene action. The high × low combinations besides expressing the favourable

additive effect of the high parent, manifested some complimentary gene interaction effects with a higher sca. However, a major part of heterosis exhibited by such crosses may be due to additive × dominance type of gene action. An appreciable amount of the heterosis expressed by low × low crosses might be attributed to dominance × dominance types of non-allelic gene action producing over dominance and are

non-fixable. The highest sca effect for fruit yield was observed in the cross CLN 5915-206 × CLN1314G (188.38), for average fruit weight in Best of All × DARL-1 (39.09) and for both total soluble solids and dry matter content in CLN2264H × Pith Sel (1.60 and 1.47) (Table 3). Shankar *et al* (2013) also reported significant variance due to *gca* and *sca* for all the characters revealing the presence of both additive

Table 3. Range, mean value of parents and F₁ crosses and three heterotic crosses of tomato based on specific combining ability and their heterosis

Characters	Fruit yield (q/ha)	Ave fruit weight (g)	Total soluble solids (brix)	Dry matter content (%)
Range of per se performance				
Parents	178.17 – 343.90	30.0 – 97.00	4.23 – 5.70	4.01 – 5.64
F ₁ s	221.23 – 587.33	42.33 – 100.67	4.00 – 6.33	4.64 – 7.51
SE ±	18.81	2.45	0.258	0.07
Range of heterosis (%)				
Better parent	6.63 – 35.90	0.34 – 74.69	3.70 – 40.74	8.31 – 30.31
Standard parent	13.36 – 56.32	2.16 – 117.27	1.48 – 40.74	1.35 – 60.47
SE ±	6.60	3.465	0.364	0.099
Top three crosses based on Sca and Std heterosis	CLN5915-206 × CLN1314G (188.38**, 56.32**)	Best of All × DARL-1 (39.09**, 103.60**)	CLN2264H × Pith Sel (1.60**, 40.74**)	CLN 2264H × Pith Sel (1.47**, 56.70**)
	CLN5915-206 × Best of All (107.08**, 17.98**)	CLN2264H × DARL-1 (25.13**, 117.27**)	DARL-2 × Best of All (1.15**, 26.67**)	CLN 2264J × Best of All (1.45**, 60.47**)
	CLN2264J × CLN1314G (86.20**, 13.30**)	DARL-2 × CLN1314G (18.43**, 109.35**)	CLN2264J × Best of All (0.97**, 25.93**)	CLN 2264J × DARL-1 (0.95**, 44.02**)

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Figures in the parenthesis indicate specific combining ability (sca) and standard heterosis respectively. ** denotes significant at P=0.01

and non-additive type of gene action for the inheritance of yield and its components in tomato. Highly significant variation due to GCA and SCA indicated the importance of additive as well as non-additive types of gene action of inheritance for all the traits except the number of fruits per plant in tomato (Kumar *et al.*, 2013). A significant and high degree of better and standard parent heterosis for all the traits was observed (Table 3). Fruit yield among

parents varied from 178.17 (Best of All) to 343.90 q/ha (DARL-2) whereas among F₁ crosses fruit yield varied from 221.83 (DARL-2 × CLN2264J) to 587.33 q/ha (CLN2264H × CLN1314G). Parents varied widely in average fruit weight from 30.0 (Best of All) to 97.0 g (CLN1314G) and F₁ crosses varied from 42.33 (Best of All × DARL-1) to 100.67 g (CLN2264J × DARL-1). The highest total soluble

Table 4. Component of variation and genetic parameters of tomato in 8 × 8 diallel crosses

Components	Fruit yield (q/ha)	Ave fruit weight (g)	Total soluble solids (brix)	Dry matter content (%)
D	5256.36* ± 3213	450.57** ± 129.9	-0.0028 ± 0.16	0.293 ± 0.26
F	4408.07 ± 759	473.10 ± 306.9	0.081 ± 0.39	0.192 ± 0.62
H ₁	21660.11** ± 7386.2	1399.28** ± 298.6	1.47** ± 0.38	2.467** ± 0.61
H ₂	18896.30** ± 6426	1165.31** ± 259.8	1.30** ± 0.33	1.969** ± 0.53
h ²	2716.92	15.12	0.056	0.101
H ₁ /D	2.03	1.76	-22.7	2.89
H ₂ /4H ₁	0.218	0.208	0.221	0.199
K _D /K _R	1.52	1.84	4.35	1.25
h ² /H ₂	0.143	0.013	0.043	0.052
Heritability NS (%)	26.06	26.2	9.83	37.55

*, ** denote significant at P=0.05 and 0.01 respectively

solids content was exhibited by Best of All (5.70) whereas among the F₁ crosses the highest value was 6.33 brix (CLN2264J × Pith Sel). Parent CLN1314G exhibited the highest dry matter content (5.64%) and among F₁ crosses DARL-1 × Best of All was the highest with 7.51% dry matter. The highest significant heterosis over better and standard parent was recorded in average fruit weight (74.69 and 117.27) followed by total soluble solids for better parent heterosis. The range of heterosis for fruit yield over better parent was 6.63-35.90%. Cross between CLN5915-206 × CLN1314G recorded the maximum heterosis over both better (35.90) and standard parent (56.32%) for the trait. Bhatt *et al.* (2004), Pandey *et al.* (2006) and Singh *et al.* (2008) also reported significant and high heterosis over better parent in

tomato for dry matter, total soluble solids and fruit yield. Now a day in breeding programme, emphasis is being given to improve yield with quality traits. Exploitation of hybrid vigour for total soluble solid and dry matter content in diallel crosses provides an additional opportunity to improve and develop hybrids for quality along with adaptability for specific environment. In the present study, genotype with positive and moderately high gca for dry matter (Pith Sel, DARL-1 and Best of All) and TSS (CLN2264H and DARL-1) exhibited good specific combining ability for exploiting hybrid vigour for these traits.

In the present study genetic components H₁, H₂ were highly significant for all the traits exhibiting the

importance of both additive and dominant gene effects in regulating these traits (Table 4). Higher value of H_1 and H_2 compared to D show that non-additive gene effects have a greater role than additive gene effects in the genetic control of these traits. The positive estimate of H_2 for these traits suggests that the dominant genes were in the favourable direction and the significant positive H_1 value confirmed the positive direction of dominance. The average degree of dominance over all loci (H_1/D) was more than unity suggesting prevalence of over dominance. The value of F was non-significant for all the traits suggesting symmetrical distribution of dominant and recessive genes among parents. The $H_2/4H_1$ index estimates the frequency of positive and negative alleles showing dominance in the parents. The value of this index was not near to half indicating unequal combinations of genes with positive and negative effects at loci exhibiting dominance among the parents. KD/KR ratio which represents the proportions of dominant and recessive genes in parents was found to be greater than unity indicating excess of dominant genes than recessive genes among the parents. Therefore, it can be concluded that hybrid breeding can be used efficiently to improve yield together with quality traits in tomato.

Conclusion:

Considering higher *per se* performance, significant *sca* effects and non additive gene action for yield per plant, the crosses *viz.*, CLN 5915-206 × CLN 1314G, and CLN5915-206 × Best of All can be further exploited.

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