

Combining ability analysis to identify superior F_1 hybrids for quality improvement in tomato through interspecific hybridization (*Solanum section lycopersicum*)

K. G. Kanjariya^{1*}, A. Parihar²

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Combining ability and gene effects for quality traits in tomato were studied by involving forty cross combinations obtained from crossing five diverse lines with eight testers in line \times tester mating fashion. The analysis of variance revealed that the variance due to line \times tester effects were highly significant for moisture content, total soluble solids, titratable acidity, ascorbic acid and phenol content under study. Combining ability analysis revealed that magnitude of Specific Combining Ability (SCA) variance was greater than General Combining Ability (GCA) variance suggesting the predominance of non-additive gene action for all quality traits. The degree of dominance

revealed that over dominance is the cause of heterosis for these traits. Based on GCA effects of parents, the lines ToLCV RES-3 and DHT-14-8 and the testers EC-520058, IIHR-1966, ATL-10-7, IIHR-1966 and IIHR-2101 were good general combiners for most of the traits under study. The crosses viz., AT-3 \times EC-589496 were found to be superior specific combiners for pericarp thickness. The quality traits, the cross AT-4 \times IIHR-2101 for moisture content, AT-3 \times ATL-10-7 for TSS, (total soluble sugar and titratable acidity), AT-4 \times ATL-10-9 for reducing sugar, ToLCV RES-3 \times ATL-10-9 for ascorbic acid, GT-2 \times IIHR-2101 for lycopene and DHT-14-8 \times IIHR-2101 for Phenol.

Key Words: *Tomato; Interspecific hybridization; Combining ability; Gene action and quality*

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the second most important vegetable crops grown throughout the world because of its wider adaptability, high yielding potential and suitability for variety of uses in fresh as well as processed food industries. The fruits are available year round and eaten raw or cooked for dietary purpose. Tomato in large quantities is used to produce soup, juice, ketchup, puree, paste and powder; it supplies nutrients, adds variety of colors and flavors to the food.

All fruit quality attributes are the expressions of genotypic and environmental effect of interactions. Hence there are need for quality attributes to be considered together for future genetic improvement. Total soluble solids (TSS) and ascorbic acid content were the most desirable attributes for processing industry. There are increase of 1% TSS in tomato fruits results to increase 20% recovery of processed products [1]. The ascorbic acid content adds to improving the nutrition which also helps in the better retention of natural color and flavor of the tomato products. The red color pigment in tomato (lycopene) is now it being considered as the "world's most powerful natural antioxidant" [2]. Therefore, tomato is one of the most important 'protective foods' because, it having special nutritive value. The shelf life is also an important quality trait aspect for marketing, transportation and domestic use. This trait is controlled by genetic as well as environmental factors such as abiotic factors like, temperature. Characters like whole fruit firmness and pericarp thickness are the important parameters contributing towards shelf life besides biochemical changes in tomato fruits [3]. However, pericarp thickness accounts for 64% of fruit firmness [4]. Therefore, development of pericarp thickness is the basic need for longer shelf life.

There is a need to increase the nutritivity of tomato by developing high nutritional varieties through appropriate breeding work to feed the hunger of the billions of the population in the world. The ultimate objective in any crop improvement programme is to identify the best parent(s) for superior hybrid(s). The combining ability is a common tool which is used in the breeding programme for testing the performance of lines in hybrid combinations and for characterizing the nature and magnitude of gene

action involved in the expression of the traits. The Line \times Tester analysis is used for evaluation of genetic stock for utilizing in hybridization programme to identify good combiners, which may be used to build up a population with favourable and which fix the genes for effective quality improvement. This present investigation aimed to evaluate the genetic architecture of quality traits for the development of high quality varieties/hybrids for processing as well as nutritional tomato.

MATERIALS AND METHODS

The present investigation was conducted at Research Center for Distant Hybridization on Field and Fruit crops, Department of Agricultural Biotechnology, Anand Agricultural University, Anand (Gujarat), India, which is situated at 22°35' North latitude and 72°55' East latitude with an altitude of 45.1 meters above the mean sea level. The climate of Anand was classified as humid tropical. The parents used this study was five lines from two different species, eight testers from six different species with two standard check from private companies.

The resultant 40 F_1 's was evaluated along with their parents and two standard checks (Bhagya and Abhinav) in randomized block design which was replicated thrice. Each entry was grown in one row with 10 plants in each row by adopting inter row spacing of 60 cm and intra row spacing of 45 cm. The observations were recorded on five randomly selected plants for viz., pericarp thickness (mm), moisture content (%), TSS ($^{\circ}$ Brix), total soluble sugar (mg/100 mg), reducing sugar (mg/100 mg), titratable acidity (%), ascorbic acid (mg/100 mg), lycopene (mg/100 mg) and phenol (mg/100 mg). Data collected during the growing season for above characters were pooled and analysis of variance and combining ability analysis were done as suggested by Panse and Sukhatme [5] and Kempthorne [6], respectively.

RESULTS AND DISCUSSION

Analysis of variance revealed significance differences due to parents (lines \times testers), crosses and line \times tester interaction for all the characters viz., Moisture content, TSS, Titratable acidity, Aescorbic acid, Phenol. Mean

¹Main Sorghum Research Station, NAU, Surat, Gujarat-395007, India; ²Department of Genetics and Plant Breeding, AAU, Anand, Gujarat-388110, India

Correspondence: K. G. Kanjariya, Main Sorghum Research Station, NAU, Surat, Gujarat-395007, India, E-mail: kgkanjariya@gmail.com

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squares due to lines were significant for Moisture content, Total soluble sugar, TSS, Titratable acidity, Ascorbic acid and Phenol. Mean squares due to testers were non-significant for all characters at 0.01 probability level. The analysis of variances for combining ability revealed that the SCA variances were greater than GCA variances for all characters (Table 1). These results suggested the contribution of heritable and non-heritable genetic causes in characters' manifestation. However, higher values of variances due to SCA (σ^2_{sca}) than variances due to GCA (σ^2_{gca}) indicated that non-additive variances prevailed in genetic determination of all traits under study. The ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ being less than one, indicated the prevalence of over-dominance for these characters. The ratio of $\sigma^2_{GCA\ male}/\sigma^2_{SCA}$ was <1 for all the characters, suggesting predominance of non-additive type gene action, as followed by Hannan et al., [7].

General combining ability

General combining ability which refers to the average performance of a line in a series of cross combinations and it is attribute to fixable (additive) gene action. The estimates of GCA effects provides general combining ability of each genotype, so it aids in selection of superior ones as parents for breeding programmes.

In the present study, all the female and male parents displayed highly positive significant values all parents. In this parents were found to exhibit negative proving to be a good combiner for low moisture as negatively significant MC value showed high shelf life of parents. For Total Soluble Solids (TSSs) all the male and female parents expressed significant except ToLCV RES-3, parents AT-3 and DHT-14-8 expressed high and positive value, remaining parents displayed negative significance value this result concordant with Figuiredo et al., [8]. For the Total Soluble Sugar (TSS), the parents IIHR-2101, AT-3 and DHT-14-8 expressed high and positive significant values, while the remaining parents displayed either negative significance except GT-2 were non-significance, and this is also concordant with Mondal et al., [9] and Dusyanta et al., [10]. Similarly, for Reducing Sugar (RS), only five parents AT-3, ToLCV RES-3, DHT-14-8, IIHR-1966 and IIHR-2101 showed highly positive and significant while the remaining parents exhibited negative significant values. These findings were supported by the study of Figuiredo et al., [8]. The Titratable Acidity (TA) displayed a positive or negative significant GCA value for all parents. This is in accordance with the good combiner for titratable acidity studied by Figuiredo et al., [8] and Mondal et al., [9]. For the Ascorbic Acid (AA), parents were found significant for all the parents and thus, these parents may be good combiners for tomato quality.

These results are in accordance with the studies of Mali et al., [11] and Figuiredo et al., [8]. Similarly, Lycopene (LYC), all parents showed highly positive and negative significant values which is highly desirable for lycopene content for tomato quality. These findings were supported by the study of Mondal et al., [9] and Figuiredo et al., [8]. The Phenol (PHE) displayed negative significant GCA value for seven parents, GT-2, AT4, EC-589496, EC-520058, ATL-10-7, ATL-10-9, WIR-5032 and IIHR-1966. The low value of phenol is highly desirable for the tomato quality. This is in accordance with the good combiner for fruit weight studied by Pradheep et al., [12] and Figuiredo et al., [8].

Specific combining ability

For TSSs, chronologically high and positive significant values were found in the top tree crosses of AT-3 × ATL-10-7, GT-2 × IIHR-1966 and ToLCV RES-3 × ATL-10-9. The total soluble solids were high in most crosses, similar findings as reported by Mondal et al., [9]. Among the 40 F₁'s, TSS show positive significant values 15 cross combinations. This result may be a guide to any breeder who avoids developing the TSS characters by using interspecific crosses. Similar results were reported by Mondal et al., [9]. For the TA total 19 cross combination could show a significant value, like, AT-3 × ATL-10-7, followed by AT-4 × ATL-10-9 and ToLCV RES-3 × IIHR-2101. The similar findings by Kumar et al., [13]. For RS, chronologically high and positive significant values were found in the top tree crosses of AT-4 × ATL-10-9, DHT-14-8 × EC-520058 and ToLCV RES-3 × WIR-5032. The high in reducing sugar in most of crosses, similar findings as reported by Figuiredo et al., [8]. Besides flavour point of view, AA was also an interesting character for developing a good hybrid by tomato breeders. In the present study, the SCA effect 19 crosses was positive significant value for yield traits. The top tree cross combinations exhibited significant results on yield for SCA effects are ToLCV RES-3 × ATL-10-9, AT-3 × ATL-10-7 and DHT-14-8 × EC-520058. The best cross combiners for ascorbic acid were reported in many studies [8,11,14]. For the nutritional composition LYC, 17 cross combinations could show a significant value, viz., GT-2 × IIHR-2101, GT-2 × ATL-10-7 and AT-4 × IIHR-2101. Similar results of best cross combiners for lycopene was reported by Mondal et al., [9] and Figuiredo et al., [8]. Besides taste point of view, PHE was also an interesting character for developing a good hybrid for disease resistance as well as taste. In this study, the SCA effect 15 crosses was positive significant value for yield traits. The top tree cross combinations exhibited significant results on yield for SCA effects are ToLCV RES-3 × IIHR-2101, DHT-14-8 × ATL-10-7 and DHT-14-8 × EC-IIHR-2101 (Table 1).

TABLE 1
Analysis of variance (mean squares) and estimates of combining ability for various characters

Source	D.F	PT	MC	TSSs	TSS	RS	TA	AA	LYC	PHE
Replications	2	0.01	2.81	0.06	0.26	0.16	783.28**	0.01	0.10	9.95**
Lines (L)	4	0.35	16.47**	3.43*	10.99**	1.87	8.21**	11.32**	0.85	434.29**
Testers (T)	7	0.83	95.85**	53.17**	152.01**	6.10**	9.97**	51.40**	21.67**	1985.57**
Lines x Testers	28	0.46	9.32**	0.90	2.09*	1.15	469.57**	8.56**	1.04	168.11**
Error	78	0.007	0.89	0.03	0.04	0.01	0.0004	0.19	0.03	4.41
σ^2_{gca} (Females)	4	0.01	0.15**	0.03**	0.03**	0.02	0.00	0.07**	0.03	0.33**
σ^2_{gca} (Males)	7	0.02	0.20**	0.04**	0.04**	0.02**	0.00	0.09**	0.04**	0.44**
σ^2_{gca} (Pooled)	-	0.02	0.18**	0.04**	0.04**	0.02**	0.00	0.08**	0.04**	0.40**
σ^2_{sca}	28	0.04	0.40**	0.08	0.09*	0.04	0.01**	0.18**	0.08	0.88**
$\sigma^2_{gca}/\sigma^2_{sca}$	-	0.50	0.45	0.50	0.44	0.50	0.00	0.44	0.50	0.45

Note: *, ** Significant at 5 % and 1% levels, respectively, PT=pericarp thickness, MC=moisture content, TSSs=total soluble solids, TSS=total soluble sugar, RS=reducing sugar, TA=titratable acidity, AA=ascorbic acid, LYC=lycopene, PHE=phenol.

Gene action

The variance due to GCA and SCA were found to be significant for all the traits except PT, TSSs, TA, RS and LYC revealing the presence of both additive and non-additive type of gene action for the inheritance of quality traits. In case of TSSs, RS and LYC, the SCA variance alone was significant indicating that only non-additive genetic component is involved in the inheritance of this character. Non additive genetic variance had greater estimates than additive genetic variance and the ratio of additive variance and non-additive genetic variance is less than 1, establishing the predominance of non-additive gene action in the inheritance of these traits viz., PT, TSSs, TSS, TA and LYC by Mondal et al., [9]. RS, AA and PHE by Figueiredo et al., [8,15].

CONCLUSION

Based on results, it was concluded that the following parents were good general combiners for various characters namely, GT-2 (TA, PHE), AT-3 (MC, TSSs, TSS, RS, TA, AA, LYC), AT-4 (TA, PHE), ToLCV RES-3 (PT, MC, RS, AA, LYC), DHT-14-8 (PT, MC, TSSs, TSS, RS, TA, LYC), EC-589496 (TA, AA, LYC, PHE), EC-520058 (PT, TA, AA, LYC, PHE), EC-500047 (TA, AA, LYC), ATL-10-7 (PT, TA, AA, LYC, PHE), ATL-10-9 (TA, AA, LYC, PHE), WIR-5032 (AA, LYC, PHE), IIHR-1966 (PT, RS, TA, AA, LYC, PHE) and IIHR-2101 (MC, TSS, RS). In case of SCA most of the characters were found to be better in various crosses namely TSSs, TSS, TA and AA, (AT-3 × ATL-10-7), PT (AT-3 × EC-589496), MC (AT-4 × IIHR-2101), RS (AT-4 × ATL-10-9), LYC (GT-2 × IIHR-2101) and PHE (ToLCV RES-3 × IIHR-2101). The presence of non-additive gene action for these quality traits requires maintenance of heterozygosity in the population. Hence, it need to follow modified breeding methods such as bi-parental cross or triple test cross design or any other form of recurrent selection method in early generations, which is used for exploitation of non-additive gene action in order to recover transgressive segregates by breaking linkages, releasing concealed variability, improving the concentration of favorable genes and changing linkage equilibrium or the heterosis breeding would be a main breeding method in improvement of these traits.

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