

# Genetical studies on flower and fruit characters in an interspecific cross of tomato

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### Abstract

Genetical studies on fruit weight, equatorial diameter and polar diameter of fruit, fruit shape index, locules/fruit, TSS content of fruit juice, length of style, ovary diameter and pollen diameter were made in the F1 and F2 populations of an interspecific cross L. pimpinellifolium × L. esculentum of tomato. The parents represented a wide range of variation for all the characters. Characteristics of F1 and F<sub>2</sub> populations varied in different characters. However, in all the characters genes with negative effect exhibited dominance in both F1 and F2 populations. Group of genes detected for fruit weight were 22-29, for equatorial diameter 11-13, for polar diameter 8-10, for style length 5-7, for pollen diameter 5-8 and 2 groups of genes for locules/fruit and TSS of fruit juice. Only one group of gene was detected for fruit shape index and ovary diameter. Fruits borne by few F2 segregates were medium sized, round to slight flatlish, shiny red and having appreciable TSS content in the fruit juice.

Key words: Lycopersicon esculentum, Lycopersicon pimpinellifolium, flower and fruit characters, degree of dominance.

## Introduction

A large number of wild and semiwild species of cultivated tomato (*Lycopersicon esculentum* Mill.) are being used continuously as genetic material for breeding tomato. *Lycopersicon pimpinellifolium*, the closely related wild relative of tomato belonging to esculentum complex of the genus [1] possesses quantitative trait loci capable of enhancing most fruit quality traits in tomato variety [2]. Other useful fruit characters of this species which have been sought in breeding tomato are large number of fruits per plant (and per cluster), bright red and shiny skin, non-cracking character of fruit and uniformity in fruit ripening.

The present investigation was, therefore, designed to study the genetics of flower and fruit characters with

a view to breeding a high quality tomato variety with the involvement of the wild relative, *Lycopersicon pimpinellifolium*.

#### Materials and methods

The experiment was carried out using parental, F1 and  $F_2$  populations of an interspecific cross. L. pimpinellifolium × L. esculentum. The parents, line C-T-96 of L. pimpinellifolium and variety NDT 11 of L. esculentum used in the cross were pure lines maintained at the Department of vegetable Crops, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur. The female parent, line C-T-98 of L. pimpinellifolium was slender in habit and densely pubescent, having small upright leaves and elongated recemes and bearing large number of very small, round, smooth surfaced and bright, shiny red fruits. The male parent, NDT 11 of L. esculentum was thick stemmed and indeterminate, having comparatively large and deeply lobed leaves and bearing big, flattened, corrugated surfaced and red fruits. The  $F_1$  and  $F_2$  populations along with the parents of the cross were grown at the Horticulture Research Station, Mondouri, Bidhan Chandra Krishi Viswavidyalaya in the winter season of 1998-99. In the experiment, 25 plants spaced 60 cm apart in 5 rows, also spaced by 60 cm, were allotted to each of the  $P_1$ ,  $P_2$  and  $F_1$  100 plants with the same 60  $\times$  60 cm spacing to F<sub>2</sub> populations. The nine flower and fruit characters recorded from all the plant of the four populations were ovary diameter, style length (mean of 5 randomly selected flowers in each plant, in cm), pollen diameter (mean of 25 observations from the composite pollen sample of the 5 selected flowers per plant, in micron), fruit shape index (equatorial diameter : polar diameter), locules per fruit (mean of the same 10 sampled fruits) and total soluble solids (mean of 10 hand refractometer readings, one each from the same 10 sampled fruits, <sup>0</sup>Brix). The data from each plant of the populations

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were used to calculate the means and variances of these populations.

The theoretical arithmetic means for  $F_1$  and  $F_2$ were calculated as  $(P_1 + P_2)/2$  and  $(P_1 + P_2 + 2F_1)/4$ , respectively and geometric mean of  $F_2$  was calculated as antilogarithm of (log  $P_1 + 2 \log F_1 + \log P_2)/4$  [3].

The minimum number of genes controlling the expression of the traits was estimated using the formulae of Castle-Wright [4] and Burton [5]. The degrees of dominance,  $h_1$  and  $h_2$  in the  $F_1$  and  $F_2$  populations respectively, were calculated using the potence-ratio method [6] as  $h_1 = (F_1-MP)/D$  and  $h_2 = (F_2-MP)/D$ , where D denotes the mean of the larger parent (*L. esculentum*).

#### **Results and discussion**

The  $F_1$  plants were fully fertile and more like *L. pimpinellifolium* parent bearing large number of fruits per plant (intermediate between the parents). The fruits borne by the  $F_1$  plants, though small, attractive, round, bilocular, smooth skinned, bright red in colour, uniform in ripening and having higher TSS content of fruit juice than that of *L. esculentum*. Most of the  $F_2$  plants had thin long branches, medium sized leaves bearing large number of small sized fruits per plant. Characteristics of  $F_1$  and  $F_2$  populations suggested partial dominance of *L. pimpinellifolium* for most of the characters over *L. esculentum* which was recorded earlier [7].

The mean performance of the two parents,  $F_1$  and  $F_2$  populations for nine flower and fruit characters (Table 1), indicated considerable difference between

Table 1. Mean of the parental,  $F_1$  hybrid and  $F_2$  population for fruit and flower characters

Characters	L. pim-	L. escu-	L. pim-	F <sub>2</sub>
	pine-	lentum	pinelli-	population
	llifolium	(P <sub>2</sub> )	folium × L.	
	(P1)		esculen-	
			<i>tum</i> (F <sub>1</sub> )	
Fruit weight	4.08	59.05	9.21	12.45
Equatorial	2.29	5.34	2.97	3.23
diameter (cm)				
Polar diameter	2.28	4.27	2.64	2.76
(cm)				
Fruit shape index	1.00	1.25	1.14	1.17
Locules/fruit	2.00	4.33	2.17	2.69
Juice TSS	6.30	2.81	4.44	4.04
content ( <sup>0</sup> Brix)				
Length of style	6.33	8.20	6.60	7.04
(mm)				
Ovary diameter	1.10	1.32	0.99	1.09
(mm)				
Pollen diameter	21.00	26.50	21.05	21.65
(micron)				

the two parents, and assumed concentration of (+) and (--) alleles in the parents. The observed, theoretical arithmetic and geometric means and variances of  $F_1$  and  $F_2$  population are presented in Table 2. The theoretical arithmetic means of  $F_1$  is only the mid-parent

Table 2. Observed (O), theoretical arithmetic (A) and geometric means (G) and variances (V) of fruit and flower characters of the cross in  $F_1$  and  $F_2$  populations.

Characters	F1 population			F <sub>2</sub> population			
	0	Α	V	0	Α	G	V
Fruit weight (g)	9.21	31.56	4.83	12.45	20.38	11.96	22.18
Equatorial diameter (cm)	2.97	3.81	0.03	3.23	3.39	3.22	0.13
Polar diameter (cm)	2.64	3.27	0.02	2.76	2.95	2.86	0.08
Fruit shape index	1.14	1.13	0.01	1.17	1.13	1.13	0.01
Locules/fruit	2.17	3.16	0.03	22.69	2.66	2.52	0.42
Fruit TSS content ( <sup>0</sup> Brix)	4.44	4.55	0.03	4.04	4.49	4.32	0.66
Length of style (mm)	6.60	7.26	0.07	7.04	7.26	6.89	0.16
Ovary diameter (mm)	0.99	1.21	0.008	1.09	1.21	1.09	0.02
Pollen diameter (micron)	21.05	23.75	0.62	21.65	22.39	22.28	1.32

value assuming absence of dominance and that of F<sub>2</sub> is the expected F2 means under the hypothesis of additive - dominance model. In each character, the observed F1 means were lower than observed F2 means because of negative dominance, except for TSS content of fruit juice. To find out the nature and degree of dominance, the observed F1 means were compared with the parental means and with the theoretical arithmetic F1 means. Agreement between observed and theoretical arithmetic F1 means suggests absence of dominance; partial dominance exists when the observed F1 mean stands between the theoretical arithmetic F1 mean and the mean of either parent and overdominance is encountered when the observed F1 mean exceed that of the higher parent or is lower than the lower parent. In the results obtained, significant differences between the observed and theoretical F1 means were found in fruit weight, equatorial diameter, polar diameter, locules/fruit, length of style, ovary diameter and pollen diameter, suggesting dominance gene action. Partial dominance of small fruit size (less fruit weight), less locular condition of fruit, short style, small ovary and pollen diameter characteristics of L. pimpinellifolium was noted because observed F1 means for these characters stood between theoretical F1 means (mid parental values) and means of L. pimpinellifolium parent. Such partial dominance of flower and fruit characters of

Table 3.

*L. pimpinellifolium* over those of flower and fruit characters of *L. esculentum* was pronounced because the observed  $F_1$  means were really inclined towards means for the concerned characters of *L. pimpinellifolium* parent. On the other hand, close agreement between the observed and theoretical  $F_1$  means for fruit shape index and TSS content of fruit juice suggested absence

of dominance, indicating additive gene action.

The extent of agreement between the observed and theoretical F2 means furnishes an indication of the nature of gene action in the inheritance of the particular trait. Arithmetic gene action assumes that the effects of the individual genes are additive, whereas geometric gene action considers that they are multiplicative indicating non-additive action of the genes upon the genotype. In our study, the observed F2 means for fruit weight was in close agreement with the theoretical geometric mean and much lower than the theoretical arithmetic mean (Table 2) indicating overwhelming importance of non-additive gene action in the inheritance of fruit weight. The scaling test 'C' as per Mather (1949) and Hayman and Mather (1955) indicated absence of gene interaction for all the flower and fruit characters under study excepting fruit weight. Pronounced dominance of small fruit size of L. pimpinellifolium over big fruit size of L. esculentum was also apparent in F2 segregation because theoretical geometrical mean of F2 was much lower than theoretical arithmetic mean of F2 and tended towards the mean of L. pimpinellifolium for fruit weight. The small fruited segregates were mostly round fruited as that of L. pimpinellifolium parent. Quantitative trait loci mapping studies conducted elsewhere in BC1 and BC2 populations of L. esculentum × L. pimpinellifolium indicated that alleles from the L. pimpinellifolium reduced the length of fruit, giving round-shaped fruit [8].

The observed  $F_2$  means for all the other eight flower and fruit characters were in close agreement with both theoretical arithmetic and geometric  $F_2$  means (Table 2), which made it difficult to determine the type of gene action in  $F_2$  generation. However, observed  $F_2$  means were more close to the theoretical geometric  $F_2$  means for equatorial and polar diameter of fruit, TSS content of fruit juice, length of style, ovary diameter and pollen diameter which indicated the involvement of non-additive gene action in the inheritance of these traits in  $F_2$  generation. In the same manner, predominance of additive gene action for the inheritance of fruitshape index and locules/fruit was predicted as observed  $F_2$  means were more close to theoretical  $F_2$ means for these characters.

Proportion of the genetic component for the flower and fruit characters were worked out. The estimated degrees of dominance in the  $F_1$  and  $F_2$  population (Table 3) varied in different characters. Moreover, some showed partial dominance in  $F_1$  and over dominance

Estimates of maximum number of genes according

to Castle-Wright formula (N) and formula of Burton

		of dominand characters	ce for F1	(h1) and F2
Characters	N	n	h1	h <sub>2</sub>
Fruit weight	21.77	28.97	-0.813	-1.391
Equatorial diameter	11.09	12.79	-0.554	-0.770
Polar diameter	8.08	9.74	-0.639	-1.034
Fruit shape index	1.28	1.29	0.123	0.714
Locules/fruit	1.76	2.40	-0.856	-0.811
Juice TSS content	2.41	2.42	0.067	0.594
Length of style	5.26	6.61	-0.716	-0.472
Ovary diameter	0.36	1.07	-1.985	-2.139
Pollen diameter	5.39	8.00	-0.983	-1.53

in the F<sub>2</sub> population (e.g., fruit weight and pollen diameter and polar diameter of fruit). In both F<sub>1</sub> and F<sub>2</sub> populations, overdominance was expressed for ovary diameter and partial dominance for equatorial diameter of fruit, locules/fruit and style length. In F<sub>1</sub> population, dominance was complete for fruit weight, locules/fruit and pollen diameter (h<sub>1</sub> = -0.81 to - 0.98). In all characters excepting fruit shape index and TSS content of fruit juice, genes with negative effect exhibited dominance in both F<sub>1</sub> and F<sub>2</sub> populations. The polygenes with such negative effect in F<sub>1</sub> and F<sub>2</sub> populations were presumed to have been contributed by the *L. pimpinellifolium* parent.

Minimum number of gene groups was estimated for each flower and fruit character following both the formulae of Castle Wright [4] and Burton [5]. Such estimations based on the two formulae agreed well. As high as 22-29 groups of gene were detected for fruit weight and as low as one group of gene for fruit shape index and ovary diameter and 2 groups of genes for locules/fruit and juice TSS were estimated. Number of genes groups for equatorial diameter of fruit were 11-13, for polar diameter of fruit 8-10, for style length 5-7 and for pollen diameter 5-8 (Table 3). The quantitative trait loci mapping of a back cross population of a L. esculentum × L. pimpinellifolium cross using 151 RFLP markers identified 4-10 guantitative trait loci for fruit weight, polar and equatorial diameters of fruit, fruit shape and total soluble solids and however, seven such studies altogether identified at least 28 quantitative trait loci for fruit weight and 32 for total soluble solids [9]. Our experiment based on phenotypic observations agreed well to the earlier genomic fingerprint studies by Chen et al [9] with regard to identification of number of guantitative genes for the character concerned.

#### References

- 1. **Lebeda A. and Mieslerova B.** 1998. Genetic resources of genus *Lycopersicon* and their exploitation in tomato resistance. Zahraadnictivi, **25**: 53-65.
- Tanksley S. D, Grandillo S., Fulton T. M., Zamir D., Eshed Y. Petiard V., Lopez J. and Bukbunn T. 1996. Advanced backcross QTL analysis in a cross between elite processing line of tomato and its wild relative L. pimpinellifolium. Theor. Appl. Genet., 92: 213-214.
- Paul N. K. 1978. Genetic architecture and components of yield in mustard (*Brassica juncea*) Theor. Appl. Genet., 53: 233-237.
- 4. **Castle W. E.** 1921. An improved method of estimating the number of genetic factors concerned in case of blending inheritance. Science, **54**: 223.

- 5. **Burton G. W.** 1951. Quantitative inheritance in pearl millet (*Pennisetum glaucum*). Agron J., **43**: 409-417.
- Romero G. E. and Frey K. J. 1973. Inheritance of semi dwarfness in several wheat crosses, Crop Sci., 13: 33-337.
- Pal B. P. and Singh H. B. 1943. A note on the economic possibilities of the cross, *Lycopersicon esculentum* × *Lycopersicon pimpinellifolium*. Indian J. Genet., 3: 115-119.
- Grandillo S., Hsin Mel. Ku, Tanksley S. D. and Ku H. M. 1996. Characterization of fs 81, a major QTL influencing fruit shape in tomato. Molecular Breeding, 2: 251-260.
- 9. **Q. F. Chen, Foolad M. R., Hyman J., St. Clair D. A. and Beelaman R. B.** 1999. Mapping of QTLs for lycopene and other fruit traits in a *L. esculentum × L. pimpinellifolium* cross and comparison of QTLs across tomato species. Molecular Breeding, **5**: 183-299.