Indian J. Genet., **65**(3): 221-222 (2005)

Short Communication

Gene action for fruit yield and its components in tomato (*Lycopersicon esculentum* Mill.)

E. Sulodhani Devi, N. B. Singh, A. Bijaya Devi, N. G. Singh, J. M. Laishram

College of Agriculture, Central Agricultural University, Imphal, Manipur 795 004

(Received: January 2004; Revised: July 2005; Accepted: August 2005)

To provide an estimate of different non-allelic gene actions operating in the inheritance of the quantitative traits and to investigate the genetics of fruit yield per plant and its contributing traits through generation mean analysis , the present study in tomato (*Lycopersicon esculentum* Mill.) was carried out. The study involved six generations, *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 derived from each of the five crosses, namely, Alok × KM, BRH-1 × KM, BRH-2 × KM, TWC-3 × KM and Alok × TWC-3. These populations were grown in compact family block design with three replications during *Rabi* 2000-2001 in the experimental field of the Plant Breeding and Genetics Department of College of Agriculture, Central Agricultural University, Imphal, Manipur. The plant to plant and row to row distances were 40 cm and 60 cm, respectively. Data on ten randomly selected plants from each plot in the parents and F_1, 30 plants per plot in BC_1 and BC_2 and 40 plants per plot in F_2 were recorded for nine characters *viz.*, number of primary branches per plant, plant height, days to first flowering, days to first ripening, number of fruits per plant, fruit weight, equatorial diameter of the fruit, fruit yield per plant and locule number per fruit. The scaling tests A, B, C and D of Mather [1] were performed for all the characters under study to judge the adequacy of the additive - dominance model. The crosses, where the additive-dominance model was inadequate, were subjected to genetic analysis following Hayman [2], using the six-parameter model. In the absence of non-allelic interaction three-parameter model given by Jinks and Jones [3] was employed.

The analysis of the cross, *viz.*, BRH-1 × KM, reveals non-significant estimates of the three types of interaction for number of primary branches per plant (Table 1). Additive and dominance gene effects have been reported in the inheritance of this character [4]. The higher magnitude of dominance effect combined with high magnitude of dominance × dominance component in Alok × TWC-3 indicated the possibility of obtaining taller plants to either of the parents. The dominance and epistatic gene effects appeared to be predominant for plant height in tomato [5]. The study revealed that early flowering and early maturity recombinants could be expected in advanced generations in the crosses Alok × TWC-3 and BRH-2 × KM which was predominantly controlled by additive gene effect combining with high magnitude of additive × dominace component and complementary type of epistasis [4].

Regarding number of fruits per plant, magnitude of additive gene effects was higher than the dominance effects in most of the crosses. In the cross, BRH-2 × KM, complemantary type of gene interaction was observed. The epistatic gene effects were observed in most of the crosses for fruit weight character. The type of epistatic interaction was duplicate. In the crosses, *viz.*, BRH-2 × KM, TWC-3 × KM, and Alok × TWC-3, the additive x dominance and dominance × dominance interaction were significant. Presence of dominance × dominance interaction for fruit weight cannot be exploited through heterosis breeding due to duplicate type of epistasis [6]. Hence, diallel selective mating or recurrent selection for development of open-pollinated variety with higher number of fruits per plants will give better chance.

The dominance × dominance kind of interaction was significant and positive in the crosses *viz.*, BRH-2 × KM, and TWC-3 × KM and Alok × TWC-3 for diameter of the fruit. The dominance × dominance kind of interaction was significant and positive in the crosses *viz.*, BRH-2 × KM and TWC-3 × KM and Alok × TWC-3 for diameter of the fruit. The additive × additive and dominance × dominance digenic interactions were significant and positive in case of Alok × KM, whereas, dominance × dominance were significant and positive in the crosses BRH-2 × KM, TWC-3 × KM and Alok × TWC-3. Earlier workers [4, 5] also reported additive × additive and additive × dominance with duplicate type of epistasis for fruit yield per plant in tomato. Therefore, to exploit both additive and dominance or additive, dominance and epistatic gene effects, reciprocal recurrent selection or biparental mating in F_2 or subsequent generations may be employed for the improvement of this character in the respective crosses, namely, TWC-3 × KM and Alok × TWC-3. As complementary interaction was prevalent in the crosses, namely, Alok × KM and BRH-2 × KM, the development of hybrid may be an alternative.

For locule number per fruit, the dominance × dominance gene effects was found to be positive and

Table 1. Estimates of gene effects and interactions for different characters

Characters	Crosses	m	[d]	[h]	[i]	[j]	[l]	Type of interaction
Number of primary branches/plant	ALOK × KM	0.499	−2.260	0.953				
	BRH-1 × KM	17.541*	−1.160	−0.640	−0.980	−1.796	0.777	
	BRH-2 × KM	17.541*	−1.160	−0.640				
	TWC-3 × KM	1.256	0.628	0.528				
	ALOK × TWC-3	0.716	−1.746	1.524				
Plant height (cm)	ALOK × KM	13.586*	−0.160	0.011				
	BRH-1 × KM	3.672*	0.494	1.400				
	BRH-2 × KM	2.271*	1.682	0.081				
	TWC-3 × KM	3.572*	1.542	0.575				
	ALOK × TWC-3	8.090*	−11.199*	1.517	1.161	−1.388	1.421	
Days to first flowering	ALOK × KM	137.500*	0.707	0.5117	1.633	−4.212*	0.106	-
	BRH-1 × KM	43.716*	−0.447	−0.338	0.000	−1.309	0.045	-
	BRH-2 × KM	77.657*	4.999*	−1.845	−0.957	6.364*	−1.969	-
	TWC-3 × KM	103.562*	−1.511	−2.360*	−1.336	−6.920*	0.164	Duplicate
	ALOK × TWC-3	100.275*	−2.141*	2.819*	4.445*	-12.365*	5.669*	Complementary
Days to first ripening	ALOK × KM	321.449*	−6.343*	−0.736	0.023	−15.483*	0.653	-
	BRH-1 × KM	8.278*	2.794*	−0.109				
	BRH-2 × KM	1.020	0.431	−1.340	−3.254*	1.215	−2.364*	Complementary
	TWC-3 × KM	183.337*	−0.605	−2.532*	−1.223	−0.099	0.791	Duplicate
	ALOK × TWC-3	75.704*	3.335*	2.522*	4.213*	3.275*	−5.897*	Duplicate
Number of fruits per plant	ALOK × KM	0.455	1.461	1.705				
	BRH-1 × KM	18.467*	−1.011	−0.991				
	BRH-2 × KM	23.410*	1.805	4.163*	3.809*	−1.084	0.866	Complementary
	TWC-3 × KM	1.614	1.559	0.398				
	ALOK × TWC-3	5.559*	1.162	0.921	0.802	1.186	−1.006	-
Fruit weight (g)	ALOK × KM	11.005*	3.919*	1.899	1.414	0.562	−1.641	
	BRH-1 × KM	0.438	25.813*	75.542				
	BRH-2 × KM	22.685*	−0.277	−0.801	−2.626*	0.215	3.507*	Duplicate
	TWC-3 × KM	77.436*	0.553	−5.762*	−8.638*	2.253*	8.931*	Duplicate
	ALOK × TWC-3	6.014*	−0.827	−0.671	−1.275	−2.923*	2.576*	Duplicate
Equatorial diameter of the fruit (cm)	ALOK × KM	24.218*	1.413	3.930*	3.564*	0.109	2.687*	Complementary
	BRH-1 × KM	7.734*	0.376	1.547				
	BRH-2 × KM	11.293*	−0.558	−0.209	−1.273	0.196	2.119*	Duplicate
	TWC-3 × KM	8.683*	0.072	−1.323	−1.415	1.010	2.736*	Duplicate
	ALOK × TWC-3	6.694*	−1.149	−0.933	−1.587	−3.468*	0.282	-
Fruit yield per plant (g)	ALOK × KM	18.619*	4.579*	9.258*	7.920*	3.420	7.554*	Complementary
	BRH-1 × KM	1.478	0.765	0.231				
	BRH-2 × KM	10.208*	−0.042	1.445	−0.528	1.442	3.783*	Complementary
	TWC-3 × KM	19.241*	−0.102	−7.694*	−9.240*	−0.351	8.350*	Duplicate
	ALOK × TWC-3	19.214*	−0.016	−7.695*	−9.240*	3.481*	8.350*	Duplicate
Locule number per fruit	ALOK × KM	3.745*	−3.15*	−1.12	−0.826	−1.671	0.203	
	BRH-1 × KM	15.037*	−5.317	−0.194	−0.826	−1.671	0.203	-
	BRH-2 × KM	28.001*	0.408	0.924	0.708	1.407	0.033	-
	TWC-3 × KM	24.249*	−2.026*	1.078	1.703	0.067	−0.964	
	ALOK × TWC-3	12.077*	1.059	−1.538*	−2.722*	−0.410	2.627*	Duplicate

* 5% Level of significance

significant for Alok × TWC-3. The predominace of non-additive gene action was also reported [5]. A critical perusal of all the crosses for the different characters under study suggests that no general breeding methodology can be followed for all the crosses. There is need to develop specific breeding strategy for each cross. In general, when parents are really diverse intermating in a backcross or F_2 is suggested to break undesirable linkage which in addition to cause bias in estimate also helps in getting desirable segregants as well as in increasing fixable effects like additive and additive × additive gene effects.

References

1. **Mather K.** 1949. Biometrical Genetics. The study of continuous variation. Methuen and Co., Ltd., London.
2. **Hayman B. I.** 1958. The separation of epistasis from additive and dominance variation in generation means. Heredity, **12**: 371-390.
3. **Jinks J. L. and Jones R. M.** 1958. Estimation of the components of heterosis. Genetics, **43**: 223-234.
4. **Kanthaswamy V., Koder Mohideen M. and Thamburaj S.** 1995. A study of generation means analysis in tomato (*Lycopersicon esculentum* Mill.). South Indian Hortic., **43**: 25-29.
5. **Padmini K. and Vadivel E.** 1995. Genetic analysis in tomato (*Lycopersicon esculentum* Mill.). South Indian Hortic., **44**: 71-74.
6. **Dhaliwal M. S., Gupta A., Singh S. and Cheema D. S.** 2001. Assessment of genetic potential for economically important characters in an inter varietal cross of tomato: P-4-5-2 × UC 82-B. Indian J. Genet., **61**: 178-179.