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Short Communication

MODIFIED TRIPLE TEST CROSS ANALYSIS FOR YIELD AND ITS COMPONENT IN TOMATO (*LICOPERSICAN ESCULENTUM MILL.*)

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Among several vegetables, tomato (*L. esculentum Mill*) a member of family Solanaceae is one of most important crop next to potato cultivated throughout the world. Some reports on analysis of genetic variance for quantitative traits in tomato are available in literature but these are invariably based on either generation mean analysis involving a few crosses or models of second degree statistics developed assuming absent of epistasis. The Modified Triple Test Cross analysis of Ketat et al. (1976a & b) following Jinks et al. (1969) detects epistasis and estimates of additive (D) dominance (H) components of genetic variance with a high degree of precision using large sample of crosses.

Therefore, an attempt was made to find out the role of various component of genetic variance in the inheritance of the ten important traits in tomato using II[nd] Modified Triple Test Cross analysis.

Two extreme parents (BT–17 and PS–1) were chosen for this experiment in spring–summer season of 1994–95. A cross was made between to testers (where BT–17 referred as L_1 and PS–1 as L_2) and F_1(Bt-17x PS-1) were developed (referred as L_3) during 1995. Fifteen pure breeding lines viz. H–24, TC–1, S–12, Pant T–4, BT–3, NDT–11, Sel–7, Pusa Ruby, Angoor Lata, H–36, NDT–4, Azad T–2, EC–31515, EC–1154 and EC–223 were crossed with L_1, L_2 and L_3 to generate 45TTC progenies (15L_1, 15L_2 and 15L_3). All the 15 set of TTC progenies (15 L_1i + 15L_2i + 15L_3i); along with 3 testers (L_1, L_2 and L_3) and 15 pure breeding lines were transplanted in randomized block design with three replications during autumn–winter season of 1996. The families and progenies within family were randomized in each replication. The progenies were grown in row of 3m width at inter row and intra row spacing of 60 and 50 cm, respectively.

Analysis of variance of modified triple test cross to detect epistasis revealed that significant epistasis was present for all the characters except plant height, number of branches/plant, fruit set % and number of fruits/plant. The epistasis x block interaction was non significant for all the characters (Table–1).

The analysis of variance for sums (L_1i + L_2i) showed that variance due to sums was important for all the traits. However, interaction of sums x block was non significant for all the characters. When variances due to sums of these traits were again tested with interaction item, it was found that sum item was not significant for number of branches/plant, fruit set % and number of fruit/plant. Thus, within family variance were the appropriate error items for testing the significance of major components.

The test of significance of difference item (L_1i – L_2i) was also important for all the traits except plant height, number of branches/plant, fruit set % and number of fruits/plant. The interaction component was not

Table – 1 : Analysis of variance for the test of epistatsis in II[nd] modified Triple Test cross models for different characters in tomato.

Source	d.f.	Plant height	No. of branches/ plant	Days to flowering	No. of flowers/ cluster	No. of fruit/ cluster	Fruits set %	No. Fruit/ plant	Fruit size	Fruit weight	Yield/ plant
Epistasis ($L_{1i}+L_{2i}$–Pi)	14	444.75	2.43	36.87**	0.45**	0.39**	7.17	228.06	0.42*	68.33*	0.64*
Epistasis x Blocks	28	47.78	1.03	5.14	0.03	0.05	3.50	19.41	0.06	7.66	0.07
Within Families	540	201.36	2.87	5.61	0.09	0.11	21.70	135.53	0.15	21.76	0.26

*, ** :- Significant at P = 0.05 and P = 0.01 respectively.

Table – 2 : Analysis of variances for sums and differences in II[nd] modified Triple Test Cross model in Tomato.

Source	d.f.	Plant height	No. of branches/ plant	Days to flowering	No. of flowers/ cluster	No. of fruit/ cluster	Fruits set %	No. Fruit/ plant	Fruit size	Fruit weight	Yield/ plant
Sums($L_{1i}+L_{2i}$)	14	1174.85**	3.81	69.94**	1.14**	0.92**	11.89	142.98	1.12**	144.98**	0.81*
Sums x Blocks	28	54.26	0.88	4.96	0.06	0.07	7.29	25.07	0.08	10.27	0.12
Differences ($L_{1i}+L_{2i}$)	14	251.29	3.96	57.79**	0.62**	0.51**	13.95	192.41	1.02**	119.84**	0.89*
Differences x Blocks	28	50.99	0.85	5.00	0.05	0.06	3.73	16.46	0.06	5.35	0.04
Within Families	360	235.25	3.22	5.41	0.11	0.13	27.12	149.09	0.17	20.76	0.29

*, ** :- Significant at P = 0.05 and P = 0.01 respectively.

Table – 3 : Estimates of additive (D), dominance (H) genetic component of variances and other estimates in Modified Triple Test Cross Model in tomato.

Parameter	Plant height	No. of branches/ plant	Days to flowering	No. of flowers/ cluster	No. of fruit/ cluster	Fruits set %	No. Fruit/ plant	Fruit size	Fruit weight	Yield/ plant
D	1228.80**	0.79	86.04**	1.37**	1.05**	–20.31	–8.15**	1.27**	165.69**	0.69
H	–2.61	0.99	69.84**	0.68**	0.51**	–17.56	57.76**	1.13**	132.11**	0.80*
F	28.42	0.38	–1.56	0.09	0.002	1.23**	8.64	0.04	7.45	0.01
r(RF)	–0.10	–0.19	0.04	–0.17	–0.005	–0.27**	–0.09	–0.04	–0.09	–0.02
$(H/D^{½}$	0.05	1.13	0.90	0.49	0.69	0.93	2.66	0.94	0.89	1.08

Note : RF = 'r' value to show the significance of 'F' parameter.

*, ** :- Significant at P = 0.05 and P = 0.01 respectively.

important for any traits. But when these interaction items were used as denominator for testing the significance of difference variance, the significance of difference item was confirmed for all the characters except plant height, number of branches/plant, fruit set % and number of fruits/plant.

The variances due to sums ($L_1i + L_2i$) were used for estimating additive (D) component of genetic variation, whereas the variances due to difference ($L_1i – L_2i$) item were used for estimation of dominance (H) component (Table–3). The estimates of both additive and dominance components were significant for all the characters, except number of branches/plant, fruit set % for both and yield /plant for additive and plant height for only dominance component. In general, the estimates of additive component were greater in magnitude than the dominance component for most of the characters, except number of branches/plant, fruit set %, number of fruits/plant and yield/plant. The presence of common alleles in the testers increases the magnitude of additive component.

The directional element F was estimated from the covariance of sum and differences and its significance was tested indirectly as the correlation r(RF) of sums and differences. When the value of r(RF) and F were considered together it was found that estimates of the directional element (F) was important and significant for fruit set %. This revealed isodirectional nature of dominance, suggesting that genes with increasing effect were most predominant for this traits. The positive and non significant value of F for plant height, number of branches/plant, number of flower/cluster, number of fruit/plant, fruit size, fruit weight and yield /plant suggested anbidirectional nature of dominance.

It may be argued that epistasis or dominance do not have much of the directional element. Nanda et al. (1942) also did not observed the confounding effect of F with dominance for most of the traits in triple test cross analysis in wheat. However, the possibility of confounding of directional element with epistasis and dominance cannot be underrated as the component F was present along with a high coefficient of dominance and epistasis assessed for plant height, fruit set %, number of fruit/plant and fruit weight.

The dominance $(H/D)^{½}$ was in the range of partial dominance for most of the fruits. Tall plant, more flower and fruit number/cluster, large fruit size and heavy fruit weight appear to be dominant in the present investigation. Similar result were also reported for most of the character in TTC analysis in pea. (Singh et al. 1986). The additive component (D) was important for number of branches/plant and yield/plant and dominance had no role in the expression of this traits. the overall degree of dominance suggested that most of the character studies are controlled predominantly by additive gene effects, however, dominance and epistatic components played a major role in controlling the expression of different traits which was also reported in pea (Singh et al. 1986 & 1987).

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