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Short Communication

Triple test cross analysis of tomato leaf curl virus resistance in tomato (*Lycopersicon esculentum* Mill.)

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Tomato Leaf Curl Virus (ToLV) is a major viral disease limiting the cultivation and production of tomato during summer in South India and autumn in North India causing substantial yield loss besides affecting the quality of fruits (1). In a survey of 174 farmers in Karnataka state conducted during 1997, 89% stated that ToLCV was a serious problem, particularly in the hot season (Warburton et al., unpublished report). Infection in early crop growth stages results in the highest yield losses (2). The present study has been undertaken to analyse the inheritance pattern of ToLCV resistance using triple test cross analysis which allows for the unambiguous testing of additive, dominance and epistatic genetic variations (3).

The material consisted of true breeding testers, 148 (resistant) and Arka Abha (susceptible) (referred hereafter as cross 1) and ATY-1 (resistant) and Arka Sourabh (susceptible) (referred here after as cross-2) were selected on the basis of phenotypically extreme expression of ToLCV symptoms. Resistance in 148 and ATY-1 was derived from an accession of *L. hirsutum f. glabratum* (4). These testers and their F_1s were crossed individually with 10 randomly selected F_2 plants in both the crosses to generate the experimental material for the triple test cross analysis and were evaluated in randomized block design with two replications during the summer season of 2000 at Main Research Station, University of Agricultural Sciences, Bangalore. In order to ensure infection, 7 days old nursery plants were exposed to viruliferous whiteflies, *Bemisia tabaci* (GENN) under muslin cloth nets. Observations were recorded on five randomly chosen plants in each replication for ToLCV symptom severity and the percent disease incidence. Co-efficient of infection which takes into account both percent disease incidence and severity of infection was calculated as outlined by Banerjee and Kalloo (5). The data so generated was subjected to triple test cross analysis as per Kearsey & Jinks (3) and Jinks and Perkins (6).

The mean sum of square for the comparison ($L_{1i} + L_{2i} - 2L_{3i}$) used to test the presence of epistasis, where L_{1i}, L_{2i} and L_{3i} are the means of the i^th^ family in respect of the tester concerned, was found to be non-significant in both the crosses (Table 1).

Table 1. Analysis of variance for coefficient of ToLCV infection in two crosses of tomato

Parameter	Source	Cross	df	M.S.	F value
Epistasis	Epistasis	1	10	4.670	1.636
($L_{1i} + L_{2i} - 2L_{3i}$)		2	10	0.926	0.463
	Within family	1	240	2.85	
	Within replicates	2	240	2.01	
Additive	Additive	1	9	5.060	2.826**
($L_{1i} + L_{2i} + L_{3i}$)		2	9	3.983	1.991**
	Within family	1	240	2.85	
	Within replicates	2	240	2.00	
Dominance	Dominance	1	9	3.430	1.309
($L_{1i} - L_{2i}$)		2	9	2.385	1.131
	Within family	1	160	2.62	
	Within replicates	2	160	2.11	

**Significant at $P \leq 0.01$ level; Cross-1 : Arka Abha × 148; Cross-2 : Arka Sourabh × ATY-1

Analysis of variance for sums ($L_{1i} + L_{2i} + L_{3i}$) and difference ($L_{1i} - L_{2i}$) in the absence of epistasis showed significant mean squares due to sums while it was non-significant due to difference in both the crosses. This indicates the importance of additive (D) genetic variance for ToLCV resistance. The presence of additive genetic component observed in this study is in agreement with Jalikop (7).

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The significant correlation between sums and differences (r = 0.71 in cross-1 and r = 0.94 in cross-2) and value of F being negative in both the crosses indicated that alleles with decreasing effect were important in contributing towards dominance for coefficient of ToLCV infection (8).

As the contribution of epistasis component to ToLCV resistance was either absent or too low to be detected in the material analyzed, estimates of D and H components might be considered unbiased. The magnitude of additive genetic component (D) was found to be relatively higher than the dominance component (H) (Table 2). Apparently, sufficient additive genetic variation exists in the germplasm analyzed, providing an opportunity for selection of the resistant genotypes. On the basis of these results pedigree selection may be recommended for the development of ToLCV resistant cultivars. Further, progress can be enhanced if additional ToLCV resistant parents are involved in multiple crosses and reasonably large populations are sampled in each filial generation. Recurrent selection in the populations so derived shall lead to the development of lines with increased ToLCV resistance.

Table 2. Estimates of genetic variances, degree of dominance, F value and correlation co-efficient between sums and differences for coefficient of ToLCV infection in tomato

Components	Co-efficient of ToLCV infection	
	Cross-1	Cross-2
Additive (D)	07.49**	03.33**
Dominance (H)	–00.09	02.26
Degree of dominance $(H/D)^{1/2}$	–00.10	00.82
F value	–36.60	–28.42
Correlation$_{\text{(sums/differences)}}$	00.71	00.94

**Significant at P ≤ 0.01 level; Cross-1 : Arka Abha × 148; Cross-2 : Arka Sourabh × ATY-1

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