

GENETIC VARIATION IN TOMATO FOR YIELD AND RESISTANCE TO BACTERIAL WILT

Tomato is a unique vegetable crop, which is highly amenable to genetic improvement owing to its high degree of homogeneity and ease of controlled pollination. Being a crop of Central America, a number of cultivars were introduced to India for genetic improvement work of tomato. Proper and systematic evaluation of genetic resources is essential to understand and estimate the genetic variability, heritability and genetic advance. Bacterial wilt of tomato caused by *Ralstonia solanacearum* EF Smith is one of the most important diseases in the tropics and it severely limits the tomato production in many tropical and subtropical regions (Opena *et al.*, 1990). Identification of sources of resistance to bacterial wilt and combining the resistance to other traits of economic importance is of prime objective for tomato improvement in the tropics. The breeding strategy involves assembling or generating variable germplasm with different sources of resistance and selection of superior genotypes for use in hybridization. With this aim, tomato cultivars and lines of diverse origin were evaluated for yield, fruit quality and resistance to bacterial wilt.

Fifty-two genotypes of tomato were raised in a randomized block design with two replications at the Regional Agricultural Research Station, Ambalavayal, Wayanad during 1999-2000. Each genotype was raised in 6 m long rows with a spacing of 60 cm x 60 cm, accommodating 10 plants per plot. The recommended

packages of practices were adopted (KAU, 1996). Seedlings were also raised in pots and were inoculated with the *Ralstonia solanacearum* following standard procedure for screening against bacterial wilt (Acosta *et al.*, 1964). Following quantitative characters were recorded from five randomly selected plants in each treatment viz., plant height, days to maturity, number of fruits per plant, pericarp thickness, locule number, total soluble solids, average fruit weight, number of harvest per plant and plant yield. The phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability and genetic advance as per cent of mean were estimated according to Burton (1952), Lush (1940) and Govindaswamy *et al.* (1973) respectively.

Analysis of variance revealed highly significant differences among the genotypes for all the 10 characters studied. The range, mean, PCV, GCV, heritability and genetic advance are presented in the Table 1. The important biometric characters such as fruit weight and yield per plant exhibited a range of 1.40-115.00 and 80.00-2370.00 respectively. Similar findings have been reported by Reddy and Reddy (1992). The lowest variation was observed for locule number (2.00-7.00) and total soluble solids (3.20-8.20), which agreed with the results of Pradeepkumar and Tiwari (1999). Genotypic coefficient of variation, which is the true indicator of the extent of genetic variability in a population, was high for all the

Table 1. Mean, range, PCV, GCV, heritability and genetic advance for different characters in tomato

Character	Mean	Range	GCV	PCV	Heritability	Genetic advance (%) mean
Plant height (m)	88.14	42-150	31.03	31.72	95.69	62.54
Days to maturity	108.13	100-131	6.84	7.09	93.18	13.62
No. of fruits/plant	30.86	7-136	58.07	68.21	72.50	101.86
Pericarp thickness (mm)	4.72	1.00-8.50	36.49	38.23	91.10	71.76
Loculenumber	2.94	2-7	38.45	39.93	92.76	76.29
TSS (°Brix)	4.58	3.20-8.20	21.90	22.96	90.99	43.05
Fruit weight (g)	58.12	1.40-115.00	39.74	42.29	88.32	76.95
Bacterial wilt % survival	43.99	0.57-90.00	71.91	72.95	97.19	146.04
Yield/plant (g)	1215.70	80-2370	31.28	40.20	60.54	50.14
No. of harvest	4.88	3-9	28.14	29.23	92.65	55.81

characters except days to maturity. High GCV was observed for bacterial wilt (71.91). Generally, slightly higher PCV values than GCV were obtained for all the characters. The upward estimates of genetic variation and heritability are conceivable since the study was carried out in one environment and the genotype x environment interaction variance is included in the genetic variance. All the characters had higher heritability estimates, indicating lesser influence of environment on them. Plant yield showed a moderate, but higher heritability estimate. Similar findings have been reported by Prasad and Rai (1999). High heritability in broad sense does not always mean better response to selection since it is inclusive of nonadditive genetic variance. High genetic advance as per cent of mean was noticed for all characters except days to ma-

turity which showed that these characters are governed by additive genes and selection will be rewarding improvement of such traits.

High heritability values have been noticed for resistance to bacterial wilt. The magnitude of heritability is largely governed by the amount of genotypic variance present in the population. The germplasm included the known sources of resistance to bacterial wilt from AVRDC, Taiwan as well as the highly susceptible lines such as Pusa Ruby. The high heritability estimates obtained may be due to the divergent genotypes included in the study. Characters such as number of fruits per plant, bacterial wilt with very high genetic advance as per cent of mean, heritability and GCV indicate a possibility of improving these germplasm lines through direct selection.

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