70. Dosage effect of the genomic region harboring the *Ty-1* locus on the phenotypic expression of the resistant reaction to the bipartite species Tomato severe rugose virus (*Begomovirus*) in tomato

Daniela D.X.Ferro, Maria Esther de N. Fonseca and Leonardo Silva Boiteux
EMBRAPA-Vegetable Crops, Brasília-DF, Brazil
Email: leonardo.boiteux@embrapa.br

The begomoviruses are among the most important tomato diseases in Brazil. The most promising strategy for disease control is the employment of cultivars with genes of resistance/tolerance to this group of pathogens. The dominant locus *Ty-1* (introgressed from the wild species S. chilense) has been one of the most important sources of resistance in tomato breeding programs throughout the world. Accessions and inbred lines carrying this locus display high levels of resistance to monopartite begomovirus species of the Tomato yellow leaf curl virus (TYLCV) complex and also against some viruses of the bipartite species complex from Brazil, including Tomato severe rugose virus (ToSRV). The objective of the present work was to evaluate the effect on the phenotypic expression after inoculation with one ToSRV isolate in tomato plants carrying distinct dosages/allelic states of the locus *Ty-1* (homozygous resistant, heterozygous, and homozygous recessive). For this analysis was employed a segregating F2 population of 586 plants derived from a cross between two near isogenic lines contrasting for the *Ty-1* locus. Inoculation was carried out with 20-day-old plants using Bemisa tabaci adults. Two evaluations were carried out (44 and 87 days after inoculation) aiming to characterize the reaction to ToSRV. Evaluation was done by using a disease severity scale ranging from absence of symptoms to severe stunting. Codominant cleaved amplified polymorphic sequence (CAPS) markers obtained with the primer pair UWTy1F/UWTy1R (in tight linkage with Ty-1 locus in chromosome 6) were employed to categorize the dosage of this genomic region. The group of plants with double dominant locus dosage (homozygous resistant) obtained a disease grade significantly lower than that of heterozygous plants in both evaluations. Heterozygous plants had also superior performance when compared with plants displaying double recessive locus dosage (ty-1/ty-1). Therefore, the association of the locus *Ty-1* with the high levels of ToSRV tolerance was confirmed, indicating that this tomato genomic region might have either one or a cluster of genes that control large-spectrum resistance/tolerance against distinct species within the genus Begomovirus. Our results also indicate to breeding programs that F1 hybrids should have, whenever possible, both parental lines with the *Ty-1* locus in homozygous condition in order to have the best phenotypic tolerance/resistance expression against ToSRV isolates.