## 69. Molecular mapping and chromosomal localization of the recessive tcm-1 locus associated with resistance to Tomato severe rugose virus (ToSRV) in tomato

Mariana Machado, Maria Esther de N. Fonseca, Daniela D.X.Ferro and Leonardo Silva Boiteux EMBRAPA-Vegetable Crops, Brasília-DF, Brazil

Email: leonardo.boiteux@embrapa.br

Due to the huge variability of the Begomovirus species infecting tomato (Solanum lycopersicum L.), the most effective breeding strategies have been the incorporation into elite inbred lines of as many as possible resistance factors as well as the search and characterization of largespectrum resistance genes. In this regard, the inbred line 'TX-468-RG' derived from S. lycopersicum 'Tyking' is one of the most important sources of wide-spectrum resistance, being effective against a range of begomovirus isolates from both bipartite species from Brazil and monopartite species from Europe. This was the first monogenic recessive source of resistance characterized (locus tcm-1). To increase the efficiency of the pyramidization process of genes controlling identical phenotype, the establishment of a marker assisted selection system to all known (dominant and recessive) begomovirus resistance loci is necessary. However, no molecular markers are available for the tcm-1 locus so far and even its genomic location is yet unknown. In the present work, molecular markers were developed in association with tcm-1 and anchored in the reference tomato genome, aiming to develop efficient marker-assisted selection systems for this locus. Co-segregation analyses of a segregating population evaluated with an isolate of the bipartite Tomato severe rugose virus (ToSRV) and a panel of SCAR and CAPS markers indicated that tcm-1 is located in the top of chromosome 6, in linkage with a the wellknown resistance gene cluster encompassing the Ty-1 and Mi loci. More recently, a recessive resistance to Florida isolates of the monopartite Tomato yellow leaf curl virus was characterized in inbred lines also derived from the hybrid 'Tyking'. This gene and one allelic variant (located in chromosome 4) have been tentatively named as Ty-5/ty-5. Even though polymorphic in our mapping population, the molecular markers linked with the Ty-5/ty-5 genomic region segregated independently from the resistant reaction to ToSRV. Therefore, our results indicated that tcm-1 and Ty-5/ty-5 are distinct resistance factors and that 'Tyking' most likely represent a pyramid of distinct Begomovirus species-specific recessive genes that in association in a same genotype might confer an effective resistance against a range of both monopartite and bipartite species.