

Recent Progress in Mapping Begomovirus Resistance and Marker-Assisted Selection for Bacterial Wilt Resistance in Tomato at AVRDC – The World Vegetable Center

P. Hanson¹, P. Kadirvel², R. Schafleitner¹, R. de la Peña⁴, S. Geethanjali³, L. Kenyon¹, W-S Tsai¹, J-F Wang¹, Fang-I Ho¹, S. Huang¹, C-W Tan¹

¹AVRDC – The World Vegetable Center, PO Box 42, Shanhua, Tainan 74199, TAIWAN, ²Directorate of Oil-seeds Research, ICAR, Rajendranagar, Hyderabad 500030, INDIA, ³Coconut Research Station, TNAU, Aliyarnagar, Pollachi, Coimbatore 642101 INDIA, ⁴East-West Seed, 50/1 Moo 2, Sanoi-Bangbuathong Road, Sainoi, Nonthaburi 11150 THAILAND



Bacterial wilt caused by *Ralstonia solanacearum* and diseases caused by begomoviruses are major tomato production constraints in the tropics. Developing inbred lines resistant to both diseases is an objective of tomato breeding at AVRDC – The World Vegetable Center. Significant diversity exists among the begomoviruses and the bacterial wilt pathogen, complicating the development of lines with broad-based resistance. Mapping of resistance and the design/validation of protocols for linked molecular markers facilitates breeding strategies such as pyramiding. The genetics of resistance to the begomovirus *Tomato yellow leaf curl Thailand virus* Taiwan strain (TYLCTHV-[TW]) in a highly resistant tomato line FLA456 was studied through quantitative trait loci (QTL) analysis. Four QTLs named *qTy4.1*, *qTy6.1*, *qTy10.1* and *qTy11.1* were detected on chromosomes 4, 6, 10, and 11, respectively, through evaluation of an F₆ recombinant inbred line (RIL) population derived from a cross between FLA456 (resistant) and CLN1621L (susceptible). The four QTLs collectively contributed about 60.5% of the phenotypic variation in resistance against TYLCTHV-[TW]. Of the four QTLs identified in this study, *qTy10.1* mapped to the lower part of chromosome 10 and contributed the most towards resistance to TYLCTHV. ‘Hawaii 7996’ (H7996) is the best known source of bacterial wilt resistance in tomato and a recent mapping study supports the presence of two major genomic regions conditioning bacterial wilt resistance—one on chromosome 6 and the other on chromosome 12. The resistance factor on chromosome 12, called *Bwr-12*, is

linked to SSR markers SLM12-2 and SLM12-10. Near isogenic lines (NIL) with or without *Bwr-12* were developed from segregating AVRDC lines CLN3125A-24 and CLN3125L; greenhouse experiments with pathogen isolate Pss4 (Phylotype I and race 1) were conducted to validate markers SLM12-2 and SLM12-10 in breeding and to assess the effect of *Bwr-12*. The differences between NIL group means with (RR) or without (SS) *Bwr-12* were 41-52% in summer 2012 and 27.5-28.9% in summer 2011. Results indicated that the two markers delimit *Bwr-12*. Routine application of markers for tomato yellow leaf curl disease and bacterial wilt resistance by AVRDC and other institutions will enable efficient development of varieties resistant to both diseases.

