Yenjit Raruang 2006: Selection of Bacterial Wilt Resistance Tomato Using High Density Map and Testing of Near Isogenic Lines Containing Bacterial Wilt Resistance Genes. Master of Science (Agriculture), Major Field: Horticulture, Department of Horticulture. Thesis Advisor: Assistant Professor Julapark Chunwongse, Ph.D. 140 pages. ISBN 974-16-1578-7

The high density map of the long arm terminal of tomato chromosome 2 was constructed to determine the recombination breakpoints between DNA markers TG48 and TG332 using 1,200 F_2 plants derived from the cross between SD3 and L285.Two hundred and forty plants were identified as recombinant plants and were used further in analysis. The DNA markers located between TG48 and TG332 i.e. TG462, SSR32, SSR598, SSR26 and TG373 were used for studying the locations of the recombinations events. Fourteen recombinations were found between TG332 and TG462 (4 cM), 9 recombinants were found between TG462 and SSR32 (2.5 cM). There was no recombination between SSR32 and SSR598. Three recombinants were found between SSR598 and SSR26 (0.9 cM), 41 recombinants were found between SSR26 and TG373 (11.7 cM) and 4 recombinants were found between TG373 and TG48 (1.1 cM). Among all of the recombinant plants, 28 were oval fruit shape as in SD3. There were significant differences between the genotypic classes of SD3 and the L285 at the DNA markers TG332, TG373 and TG48, but with the representation of the graphical genotype, the ovate fruit shape gene should be located in the vicinity of the DNA marker SSR26 and TG373. Forty seven homozygous recombinant plants were inoculated with the RS160 strain of the bacterial wilt disease by using scalpel leaf-clipping technique. Some of the recombinant plants showed resistant to the bacterial wilt disease that was correlated with the DNA markers TG332, TG373 and TG48 on chromosome 2.

Near isogenic lines (NILs) of tomato 'Seedathip3' that contained resistant genes were created through successive backcrossing for six generations with the selections using DNA marker associated with 4 resistant gene on 3 chromosomes, i.e., chromosome 2, 6 and 10. The NILs for 2 and 3 genes were the combined by crossing the single resistant gene NILs and selected using DNA markers. These 11 lines of NILs were inoculated with the strains of the bacteria *Ralstonia solanacearum*, namely, RS27, RS140, RS145 and RS160 using leaf-clipping (2 trials) and drenching (2 trials) techniques. The result indicated the resistant of each QTL to be strain-specific. Environmental effect was found to be substantial. The pyramiding of individual QTL resulted in gene interaction in both positive and negative directions. The inoculation techniques and strain types were found to have effects on resistance response of QTLs.

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