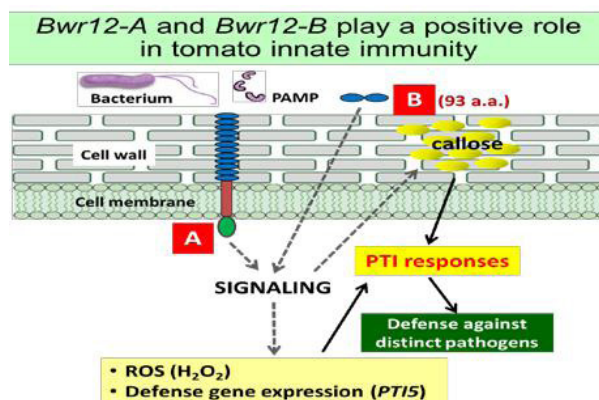


Study of the mechanisms underlying tomato innate immunity mediated by two *Bwr12* genes

Chiu-Ping Cheng and Ching-Jung Lin
National Taiwan University, Taiwan

Bacterial wilt (BW) caused by *Ralstonia solanacearum* (Rs) is a devastating disease of many crops, and breeding for durable resistance is urgent and important for disease control. Tomato cultivar Hawaii 7996 (H7996) is currently the most stable resistance source for BW control. Although various BW-resistance-associated quantitative trait loci (QTLs) have been mapped on H7996 chromosomes, the involved molecular mechanisms and the gene identities remain undetermined. Our studies showed that H7996 possesses strong PTI responses, and the major QTL associated with the H7996 resistance against Rs phylotype I strains, namely *Bwr12*, is involved in PTI. Functional genetic and gene expression analyses further revealed positive roles of *Bwr12-A* and *Bwr12-B* in PTI and defense against distinct pathogens. Transient expression assay suggested that *Bwr12-A* localizes on the plasma membrane of *Nicotinana benthamiana* (Nb), while *Bwr12-B* might localize on the cell membrane, nucleus or be secreted to the apoplast. Overexpression of *Bwr12-B* in transgenic Nb increased H₂O₂ accumulation and resistance to Rs and *Pectobacterium carotovorum* subsp. *carotovorum* (Pcc). These results along with future studies are projected to shed light on H7996 defense mechanisms.



Biography

Plants constantly encounter a wide range of diseases, leading to tremendous crop losses. Plant bacterial wilt (BW), caused by *Ralstonia solanacearum*, is a deadly and complex soil-borne vascular disease of many agronomically important crops worldwide. Control for this disease via traditional practices has been very ineffective. To gather important information and resources potentially useful for disease control, our researches aim to gain insights into molecular mechanisms and signaling pathways involved in the interactions among plants, *R. solanacearum* and biocontrol agents. Through systematic genomic screening, we currently focus on studying the functions and the involved mechanisms of a group of plant and *R. solanacearum* genes which play crucial roles in plant-pathogen interactions. In addition, resources have been collecting from tentative biocontrol agents, including bacteriophages and symbiotic fungi.

chiupingcheng@ntu.edu.tw

Notes: