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Studies on the ATP-dependent protease, Lon of Pseudomonas syringae pv. tabaci

Hyun Ju Yang, Ji Young Cha, So Young Park, Jun Seung Lee and Hyung Suk Baik

Division of Biology Sciences, Pusan National University, 609-735, Busan, Korea

Pseudomonas syringae is a plant pathogen whose pathogenicity and host specificity are thought to be determined by effectors injected into plant cells by type III secretion system (TTSS). P. syringe pv. tabaci causes wildfire on tobacco and elicits hypersensitive response (HR) in nonhost plants.

Lon protease functions as a negative regulator of TTSS by degrading HrpR, activator of *hrp* regulon in *Pseudomonas syringae*. Lon-associated regulation of the TTSS also involves proteolysis of effectors prior to secretion. Thus Lon protease is thought to play a significant role in regulation of *P. syringae* pathogenesis.

In this study we confirmed that like other P. syringae strains, TTSS of P. syringae pv. tabaci also is expressed in hrp-inducing medium similar to plant tissue environment by transformation of hrpA promoter transcriptional fusion.

We amplified *lon* gene of *P. syringae* pv. *tabaci* by PCR using designed primer and identified it by sequencing. The sequence of the *lon* gene has 90~93% homology with other *P. syringae*. We cloned and constructed *lon* mutant using homologous recombination. In addition, we overexpressed the *lon* gene in *E. coli* and identified Lon by SDS-PAGE.