A LuxR-type Transcriptional Regulator, PsyR, Coordinates Regulation of Pathogenesis-related Genes in *Pseudomonas syringae* pv. *tabaci*

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*Pseudomonas syringae* pathovar *tabaci* is a plant pathogenic bacterium that causes wildfire disease in tobacco plants. In *P. syringae* pv. *tabaci*, PsyI, a LuxI-type protein, acts as an AHL synthase, while primary and secondary sequence analysis of PsyR has revealed that it is a homolog of the LuxR-type transcriptional regulator that responds to AHL molecules. In this study, using phenotypic and genetic analyses in *P. syringae* pv. *tabaci*, we show the effect of PsyR as a quorum-sensing (QS) transcriptional regulator. Regulatory effects of PsyR on swarming motility and production of siderophores, tabtoxin, and N-acyl homoserine lactones were examined via phenotypic assays, and confirmed by quantitative real-time reverse transcription-polymerase chain reaction (qRT-PCR). Further qRT-PCR showed that PsyR regulates expression of these virulence genes in response to environmental signals. However, an upstream region of the gene was not bound with purified MBP-PsyR protein; rather, PsyR was only able to shift the upstream region of *psyR*. These results suggested that PsyR may be indirectly controlled via intermediate-regulatory systems and that auto-regulation by PsyR does not occur.

**Key words** : Electrophoretic mobility shift assay (EMSA), MBP-*psyR* expression, *Pseudomonas syringae*, Quorum sensing, Real-time reverse transcription-polymerase chain reaction (qRT-PCR)

**Introduction**

Bacteria undergo a variety of physiological and morphological adaptations in reaction to physical and chemical changes that arise from the environment. Importantly, some of the most active signaling molecules are not only metabolic wastes but also diffusible molecules released from a bacterial population for cell-to-cell communication [5]. This strategy, called quorum sensing (QS), regulates the specific expression of a group of genes according to the bacterial population density. The QS system coordinates physiological reactions such as virulence, production of secondary metabolites, and antibiotic resistance, based on the local density of the bacterial population [12]. When QS signaling molecules reach a threshold, QS bacteria can detect a QS signaling molecule called an autoinducer, resulting in coordinated expression of specific target genes.

In gram-negative bacteria, various QS systems have been found, such as the *Agrobacterium tumefaciens* TraIR system, the *Erwinia carotovora* CarIR system, and the *Pseudomonas aeruginosa* LasIR and RhlIR systems [14, 23, 43, 46, 49]. The QS systems in gram-negative bacteria are similar to the conventional QS circuit of *Vibrio fischeri* that was described in the early 1970s [29, 30]. The QS system consists of two homologues of *V. fischeri* regulatory proteins, LuxI and LuxR. The LuxI family proteins play a role as AHL synthases and produce a specific AHL known as the QS signaling molecule. The LuxR-type proteins regulate QS-related genes. Most of the LuxR-type regulators act as transcriptional activators, but some act as repressors or play a dual role. The amino-terminal domain of LuxR acts as an AHL-binding domain, while its carboxyl-terminal domain acts as a DNA-binding domain. The DNA-binding domain is assumed to form a helix-turn-helix (HTH) motif with a cluster of four helical structures. The HTH motif binds to the major groove of DNA in the presence of AHL [11, 35, 52]. In the absence of AHL, the LuxR-type protein is in the monomeric, inactive conformation. AHL can interact with the amino-terminal domain of LuxR-type transcriptional regulators; this complex then dimerizes or multimerizes [9, 13]. Consequently, the carboxyl-terminal of AHL-bound LuxR binds to a palindrome promoter region, the lux box, which affects ex-
pression of QS-controlled target genes.

*Pseudomonas* is a noteworthy genus, because it includes a human pathogen (*P. aeruginosa*), a phytopathogen (*P. syringae*), and a nonpathogenic bioremediation agent (*P. putida*). Among these strains, *P. syringae* is an important plant pathogen used for studying plant–bacterial interactions. *P. syringae* is a gram-negative bacterium that causes disease in a wide range of plant species. *P. syringae* consists of more than 50 pathovars, based on host-specificities. *P. syringae* pathovar *tabaci* ATCC 11528 causes wildfire disease in tobacco plants and a hypersensitive response (HR) in non-host plants. The AHL molecules produced in *P. syringae pv. tabaci* are N-(3-oxohexanoyl)-l-homoserine lactone and N-(3-oxooctanoyl)-l-homoserine lactone. In *P. syringae* species, the gene *psyI* has a putative *lux* box sequence with dyad symmetry. In *P. syringae pv. tabaci*, PsyI, a LuxI-type protein, acts as an AHL synthase, while primary and secondary sequence analysis of PsyR has revealed that it is a homolog of the LuxR-type transcriptional regulator that responds to AHL molecules [28, 40].

The QS system has been studied intensively in recent years. According to a recent study, the QS system both positively and negatively regulates diverse putative virulence factors. The QS system in *P. syringae pv. syringae* was reported to positively regulate production of extracellular polysaccharides (EPSs), as well as tolerance to oxidative stress and maceration of plant tissue, and also to negatively regulate swarming motility [36, 45]. Other phenotypes are determined by QS upon sensing of environmental cues such as nutrient deficiency or iron limitation [42, 50]. Therefore, the QS system is closely associated with other regulons.

The regulation of virulence genes by several regulators has been studied [6, 7, 24, 51]. The iron-uptake regulator Fur controls the expression of sigma factors and operon genes associated with iron uptake, acid tolerance, oxidative stress response, chemotaxis, and metabolic pathways [4, 27, 34, 44, 47, 48]. GacA, a response regulator of the two-component system, controls a variety of phenotypes, including motility, biofilm formation, and production of secondary metabolites such as antibiotics, siderophores, QS autoinducers, toxins, and extracellular polysaccharides, although the signals that activate the GacS/GacA two-component system have not been identified [8, 28, 37].

Another significant virulence factors are the type III effector proteins that are essential for disease progress in host plants and for the HR in non-host plants. These effector proteins translocate into plant cells via the type III secretion system (TTSS) [10, 16]. According to a recent study, the TTSS in plant pathogens is required for the suppression of plant defense during the first step of interaction with their hosts [19]. Several transcriptional factors that mediate the environmental regulation of *P. syringae* *hrp* genes have been identified; however, transcription of the *hrp* genes is mediated by different mechanisms in different species [17, 18]. The TTSS activator HrpR is required for the expression of *hrp* regulatory genes. The activation of *hrp* regulatory genes, including *hrpA*, which encodes the key *hrp* pil protein, is not understood. A TTSS-linked regulatory system has been elucidated in *Ralstonia solanacearum*. Specifically, it was found that Prhl (an extracytoplasmic function sigma factor), PrhR (a periplasmic domain of the inner membrane protein), and PrhA (an outer membrane receptor for unknown plant signals [26]) comprise this *hrp* gene regulatory cascade. PrhA activates transcription of the *hrp* genes after recognition of tobacco plant cell-contact in *P. syringae pv. tabaci* ATCC 11528 [24]. PrhA transduces the signal to PrhR, which controls *hrp* genes encoding the TTSS, along with Prhl. When PrhR receives the signals, Prhl is released from PrhR into the cytoplasm. The regulatory cascade driving the expression of the type III secretion determinants would therefore start with Prhl [3, 15].

The purpose of this study was to determine the effect of PsyR protein as a transcriptional regulator of various virulence factors in *P. syringae pv. tabaci* ATCC 11528. In this study, phenotypes of the *psyR* deletion mutant were compared with those of the wild-type. We showed that PsyR has effects on pathogenesis, such as production of siderophores, AHLs, tabtoxin, swarming motility, and pathogenicity to tobacco leaf.

**Materials and Methods**

**Bacterial strains, plasmids, and culture conditions**

The bacterial strains and plasmids used in this study are shown in Tables 1 and 2, respectively. *P. syringae pv. tabaci* ATCC 11528 was obtained from the American Type Culture Collection (Manassas, VA, USA). *P. syringae pv. tabaci* was cultured in King’s B (KB) medium at 28°C with aeration via shaking [22]. *Escherichia coli* Top10 and DH5α were used for cloning experiments, *E. coli* S17-1 λpir was used as a donor for conjugation, while *E. coli* BL21 (DE3) was used as host for overexpression of *psyR*; these strains were grown in...
Table 1. Bacterial strains used in this study

<table>
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<th>Strains</th>
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<td>DH5a</td>
<td>Transformation host for cloning vector</td>
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<td>S17-1 λpir</td>
<td>S17-1 derivative, RK2 tra regulon, host for pir-dependent plasmids</td>
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<tr>
<td>BL21(DE3)</td>
<td>Overexpression host for expression vector</td>
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<tr>
<td>BL799</td>
<td>E. coli BL21(DE3)/pBL318 [P. syringae pv. tabaci psyR overexpression (pMAL-c5x)]</td>
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<td>BL792</td>
<td>BL799/pBL337 [P. syringae pv. tabaci psyR overexpression (pMAL-c5x) with psyI expression vector]</td>
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<td>Agrobacterium tumefaciens</td>
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<td>ATCC 11528</td>
<td>Plant pathogen, wild-type strain</td>
<td>ATCC, USA</td>
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<tr>
<td>BL37</td>
<td>ATCC 11528 ΔpsyR (678-bp deletion)</td>
<td>Lab collection</td>
</tr>
<tr>
<td>BL779</td>
<td>BL37 containing pBL336</td>
<td>This study</td>
</tr>
</tbody>
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'Gm', gentamicin resistance.

Table 2. Plasmids used in this study

<table>
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<th>Plasmids</th>
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<td>T-blunt</td>
<td>Cloning vector, Ap', Km'</td>
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<td>pDMS197</td>
<td>Suicide vector, Tc'</td>
<td>[6]</td>
</tr>
<tr>
<td>pRK415</td>
<td>Broad host range cloning vector, Tc'</td>
<td>[20]</td>
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<tr>
<td>pMAL-c5x</td>
<td>Expression vector carrying an N-terminal maltose binding protein sequence and lac, Ap'</td>
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<td>pBL108</td>
<td>1.7-kb DNA containing 5' -flanking and 3' -flanking regions of psyR in pGEM-T easy vector, Ap'</td>
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<td>pBL122</td>
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<td>pBL278</td>
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<td>Derivative of pMAL-c5x containing the 749-bp psyR, Ap'</td>
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<td>pBL336</td>
<td>Derivative of pRK415 containing the 1.34-kb wild-type psyR, Tc'</td>
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<tr>
<td>pBL337</td>
<td>Derivative of pRK415 containing the 946-bp wild-type psyI, Tc'</td>
<td>This study</td>
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</table>

'Ap', ampicillin resistance; Km', kanamycin resistance; Tc', tetracycline resistance; DAP; diaminopimelic acid.

DNA manipulation

Plasmid DNA was prepared with a Plasmid Mini Prep kit (Solgent; Daejeon, Korea) and DNA fragments were extracted from agarose gels using a QIAquick Gel Extraction kit (Qiagen; Hilden, Germany). Transformation of E. coli or P. syringae strains was done by either RbCl-CaCl2 heat shock or electroporation (Bio-Rad; Hercules, CA, USA) at 2,500 volts, 200 ohms, and 25 μF. Transfer of the recombinant suicide plasmid to Pseudomonas was accomplished by conjugation with E. coli S17-1 λpir as the plasmid donor.

Oligonucleotide primers used in this study are described in Table 3. Polymerase chain reaction (PCR) amplification was performed with Taq or Pfu polymerase from Solgent, under the following reaction conditions: denaturation at 95°C for 20 s, primer annealing according to melting temper-
Table 3. Primers used in this study

<table>
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<td>TAGAGTCAAGAACCCGKTRACAGATTT</td>
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<td>psyR-C</td>
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<td>Oligonucleotides for quantitative real-time RT-PCR</td>
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<td>qRT-fur</td>
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<td>CACCATGAGTGTCG</td>
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<td>qRT-gacA</td>
<td>AGTCTGAACTCGCCGC</td>
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<td>qRT-psyl</td>
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<td>qRT-prhR</td>
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<td>qRT-prhA</td>
<td>TAGAATTCGTCACTAGTATGACAGTG</td>
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<td>Oligonucleotides for plasmid construction</td>
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<tr>
<td>psyR-P</td>
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<td>CGGATCCCATACCATGGCGCAC</td>
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<td>psyI-P</td>
<td>CGGATCCCTATAGTATGAGGCAGTCTACT</td>
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<td>Oligonucleotides for electrophoretic mobility shift assays</td>
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<tr>
<td>EM-fur</td>
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<td>EM-gacA</td>
<td>CAAGTTGTCAGAGATC</td>
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<td>EM-psyl</td>
<td>GCACATCAGGCAGATTC</td>
<td>CGGATCCCTATAGTATGAGGCAGTCT</td>
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of conjugation [20]. Finally, the complement strain, BL779, was constructed using the above procedures.

Phenotypic tests and plant pathogenicity assays

We performed chrome azurol S (CAS) universal side-phore detection assays, as described by Schwyn and Neilland [39]. Swarming motility was determined using KB agar (0.4% agar) plates [7]. Tabtoxins were detected using standard bioassays with A. tumefaciens NTI as the indicator bacteria. To detect AHLs production in a liquid medium, AHLs extracts were prepared as described by Shaw et al. [41]. The concentrated extracts were characterized by thin-layer chromatography (TLC) using A. tumefaciens NTI as the AHL-sensor strain. Plant pathogenicity assays were performed using tobacco plants (Nicotiana tabacum L. cv. Samsun) as described previously [24]. Each treatment was repeated three times. All assays were repeated in three separate experiments.

RNA isolation and quantitative real-time reverse transcription (qRT)-PCR analysis

Cells were grown to the early (OD$_{600}$ 0.5) and late (OD$_{600}$ 3.5) exponential phases. Total RNA isolation and qRT-PCR were conducted as described previously [6]. Briefly, total RNA was extracted from bacteria using an RNAspin Mini RNA Isolation kit (GE Healthcare; Pittsburgh, PA, USA) according to the manufacturer’s instructions. The total RNA concentration was quantified using a Nanodrop 2000 spectrophotometer (Thermo Fisher Scientific; Waltham, MA, USA). cDNAs were synthesized using a Reverse Transcription Premix kit (ElpisBiotech; Daejeon, Korea) according to the manufacturer’s protocols, using target gene-specific primers, and were stored at -20°C until required for use.

Real-time RT-PCR was carried out using SYBR Primix Ex Taq™ (Takara; Osaka, Japan) with a StepOne Real-Time PCR System (Applied Biosystems; Foster City, CA, USA), as previously described [6]. Specific primer sets used to amplify the genes of interest were designed based on sequences in the GenBank database. The PCR conditions were as follows: 94°C for 5 min, followed by 40 cycles each consisting of 10 s at 94°C, 10 s at 55°C, and 15 s at 72°C, followed by a 7-min incubation at 72°C. To normalize the fold-induction of mRNA, the expression level of 16S rRNA (endogenous control) was quantified and then normalized to the threshold value acquired for the wild-type strain [1]. The relative expression ratios were calculated using a mathe-

matical model, which contained an efficiency correction for the real-time RT-PCR efficiency of each transcript [32]. The data are shown as the average of triplicate samples.

Overproduction and purification of the PsyR protein

The psyR-coding region was amplified from the genomic DNA of P. syringae pv. tabaci by PCR, using the psyR-P forward and reverse primers. The 749-bp DNA fragment was cloned into the T-blunt vector, creating pBL278; this was then digested with NdeI and BamHI and the digested fragment was cloned into the pMAL-c5x vector, resulting in pBL318. To support the production of soluble PsyR protein, a co-expression vector carrying the AHL-encoding psyI was constructed. The psyI fragment, including its promoter region, was amplified by PCR using psyI-P forward and reverse primers. Amplified DNA fragments were cloned into the pGEM-T Easy vector, resulting in pBL186. A 946-bp DNA fragment from pBL186 was digested with EcoRI and cloned into the broad host range cloning vector pRK415, creating pBL337. The integrity of the psyR and psyI sequences was confirmed by DNA sequencing.

For PsyR overexpression, pBL318 expressing the C-terminally maltose-binding protein (MBP)-tagged PsyR proteins, was introduced into E. coli BL21 (DE3) by electroporation, yielding strain BL759. To enhance the production of soluble PsyR protein, pBL337 expressing AHL synthase from psyI was transformed into the BL759 strain. In this way, the PsyR overproduction strain, harboring the pBL318 and pBL337 plasmids, was constructed. The PsyR overproduction strain, BL792, was cultured overnight in 5 ml LB broth containing tetracycline (20 μg/ml), ampicillin (50 μg/ml), and 0.2% glucose. The overnight culture was diluted 100-fold with 50 ml LB medium containing ampicillin (50 μg/ml) and incubated at 37°C. At the exponential phase (OD$_{600}$ 0.4-0.6), the cell cultures were induced with 0.1 mM IPTG and incubated at 15°C for 12 hr. After incubation, cells were harvested by centrifugation and the cell pellet was suspended in 5 ml column buffer (20 mM Tris-HCl, 200 mM NaCl, 1 mM EDTA, pH 7.4). The suspended cells were lysed with 1 mg/ml lysozyme and using an Ultrasonic generator US-300 (Nissei; Osaka, Japan). Cell debris was removed by centrifugation at 20,000*g for 20 min at 4°C. The 1.5×10-cm column, filled with amylose resin (New England Biolabs; Ipswich, MA, USA), was washed with five column volumes of column buffer and the cleared cell lysate was loaded. The column was washed with 12 column volumes of column bu-
fer and subsequently eluted with five column volumes of elution buffer (20 mM Tris-HCl (pH 7.4), 200 mM NaCl, 1 mM EDTA, 10 mM maltose). The protein-containing fractions were concentrated to about 1 mg/ml in an Amicon Ultra-15 (Millipore; Billerica, MA, USA).

Electrophoretic mobility shift assay
To investigate the interaction of PsyR protein with the virulence gene upstream region, an electrophoretic mobility shift assay (EMSA) was performed using an EMSA kit (Invitrogen; Waltham, MA, USA) [19]. DNA fragments were generated by PCR amplification of the regulatory regions of omisf, psyR, psyI, gacA, fur, prhA, prhI, hrpR, and hrpA using the primer pairs listed in Table 3. As a positive control for the DNA fragment, we used the promoter region of psyI, encoding N-acyl homoserine lactone synthase, whose expression is known to be regulated by PsyR. The EMSA reaction mixture (final volume of 10 μl) contained 0.16 pM DNA, 0·24 nM protein, and 5× binding buffer (50 mM Tris-HCl [pH 7.4], 750 mM KCl, 0·5 mM dithiothreitol, 0·5 mM EDTA), and was incubated at room temperature for 20 min. After the addition of 2 μl of 6× EMSA gel-loading solution, the reaction mixtures were analyzed by electrophoresis in 0·5× TBE buffer (1·1 M Tris-HCl [pH 8·3], 9 M boric acid, 25 mM EDTA). All reactions were loaded onto native 5% polyacrylamide gels (130 bis-acrylamide to acrylamide ratio) at 110 V (15 V/cm) for 55 min at 4°C. The gel was stained in SYBR Green EMSA staining solution at room temperature for 20 min, and then washed twice with sterile distilled water to remove excess stain. The stained DNA gel was visualized using a Lumi-imager F1 (Roche; Basel, Switzerland).

Results
Phenotypes of the psyR deletion mutant
CAS agar plates were used to detect production of siderophores in P. syringae pv. tabaci ATCC 11528. As shown in Fig. 1A, both wild-type (WT) and ΔpsyR mutant (BL37) strains did not produce siderophores under high-iron condition, but produced siderophores under low-iron condition. In the ΔpsyR mutant strain, the orange halo was slightly smaller than in the WT strain. These results suggest that the production of siderophores may be co-regulated by PsyR in P. syringae pv. tabaci ATCC 11528.

Swarming motility is the rapid and coordinated movement of a bacterial population across a semi-solid medium, which is driven by flagella. In comparison with the WT strain, the ΔpsyR mutant strain demonstrated enhanced swarming motility (Fig. 1B). These results indicated that PsyR represses the swarming motility of P. syringae pv. tabaci ATCC 11528, and functions as a negative regulator of this activity.

To determine whether the ΔpsyR mutation affects tabtoxin synthesis, tabtoxin production was measured using the A. tumefaciens NT1 growth inhibition assay. The produced tabtoxin formed zones of inhibition in the case of the WT strain of P. syringae pv. tabaci ATCC 11528 (Fig. 1C). The zones of inhibition of the ΔpsyR mutant strain were slightly greater than that of its parent strain. Therefore, PsyR may be a negative regulator of tabtoxin synthesis in P. syringae pv. tabaci ATCC 11528.

The A. tumefaciens NT1 indicator strain carrying a lacZ-trnC fused plasmid was used for the detection of AHL. Upon TLC analysis, two spots were observed on the TLC plates with a culture of the A. tumefaciens NT1 strain (Fig. 1D). The top spot represented N-(3-oxohexanoyl)-l-homoserine lactone and the bottom spot N-(3-oxooctanoyl)-l-homoserine lactone. In the ΔpsyR mutant strain, production of AHL was considerably reduced as compared to the wild-type strain. These results indicated that synthesis of AHL in P. syringae pv. tabaci ATCC 11528 is regulated by PsyR.

The WT and ΔpsyR mutant strains were observed at 1, 3, 5, and 7 days after inoculation onto tobacco leaves (Fig. 2A). Disease symptoms, such as brown necrotic lesions surrounded by chlorosis, were on the tobacco leaves inoculated with the WT strain. However, inoculation with the ΔpsyR mutant strain resulted in a slight delay in disease symptom development. Consequently, symptom development of wild-fire disease appears to be regulated by PsyR.

The wild-type and ΔpsyR mutant strains were grown in LB medium. As shown in Fig. 2B, the ΔpsyR mutant strain grew slightly faster than did the WT strain.

Regulation of gene expression by PsyR
To choose regulatory factors related with the regulation of virulence-associated gene expression, qRT-PCR was performed using total RNA from the ΔpsyR mutant and WT strains, which were incubated until the early and late exponential phases. The relative levels of mRNA were determined from the threshold values that were normalized to 16S rRNA gene expression. The genes chosen for this anal-
Fig. 1. (A) Siderophore assay with wild-type (WT), ΔpsyR mutant (BL37), and ΔpsyR mutant harboring pBL336 (BL779) strain of *Pseudomonas syringae* pv. *tabaci* ATCC 11528. *P. syringae* pv. *tabaci* strains were grown overnight and diluted to 2×10^8 CFU/ml in sterile water. Aliquots of 20 μl were spotted on chrome azur S (CAS) agar plates containing high or low iron concentrations. The inoculated plates were incubated for 48 hr at 30°C. (B) Comparison of swarming motility in a wild-type (WT) strain of *P. syringae* pv. *tabaci*, ΔpsyR mutant (BL37), and a ΔpsyR mutant-carrying pBL336 (BL779) strain. Overnight cultures of bacteria were inoculated onto 6-mm sterile filter discs in KB medium containing 0.4% agar. The plates were incubated at 30°C and observed at 24 hr and 48 hr post-inoculation. (C) Detection of tabtoxin-productive capacity with WT, ΔpsyR mutant (BL37), and ΔpsyR mutant-harboring pBL336 (BL779) strain of *P. syringae* pv. *tabaci* ATCC 11528. Overnight cultures of bacteria were inoculated onto 6-mm sterile filter discs in KB agar plates containing *Agrobacterium tumefaciens* NT1 indicator bacteria. The plates were incubated at 30°C and the zones of inhibition were observed at 48 hr. (D) Thin layer chromatography analysis of N-acetyl homoserine lactone (AHL) production. *A. tumefaciens* NT1 was used for the detection of AHL produced in *P. syringae* pv. *tabaci* ATCC 11528 (WT); ΔpsyR mutant (BL37) and the ΔpsyR mutant-harboring pBL336 (BL779) strain. A, N-(3-oxohexanoyl)-l-homoserine lactone; B, N-(3-oxooctanoyl)-l-homoserine lactone.

Fig. 2. (A) Test for disease symptoms on tobacco leaves. Disease symptoms generated by the wild-type (WT), ΔpsyR mutant- (BL37), and ΔpsyR mutant-harboring pBL336 (BL779) strain of *Pseudomonas syringae* pv. *tabaci* ATCC 11528. The tobacco leaves were photographed 1, 3, 5, and 7 days post-inoculation. 1, WT; 2, BL37. (B) Growth characteristics of the WT, BL37, and BL779 *P. syringae* pv. *tabaci* ATCC 11528 strains.
ysis were those encoding a global regulator (gacA), a QS signal synthase (psyI), a ferric uptake regulator (fur), a TTSS regulator, structural components (hrpR, hrpA), and a TTSS-linked regulatory system (pshI, pshA).

The WT and ΔpsyR mutant strains showed a higher transcript level of gacA at the late-exponential phase in comparison to levels at the early exponential phase (Fig. 3A). At the early exponential phase, the mRNA levels of gacA in the ΔpsyR mutant strain were increased approximately 3.9-fold. At the late exponential phase, the expression levels of gacA in the ΔpsyR mutant strain was decreased approximately 0.8-fold compared to that in the WT strain. These results showed that expression of gacA was not significantly different between WT and ΔpsyR mutant strains.

The expression level of psyI in ΔpsyR mutant strain was decreased approximately 160-fold at the late-exponential phase (Fig. 3B). Therefore, expression of psyI at a high cell-density is positively regulated by PsyR.

As shown in Fig. 4A, in the wild-type strain, the fur mRNA levels at the late exponential phase was higher than that at the early exponential phase, indicating that bacterial cell density affects the mRNA expression of fur. At the early exponential phase, the transcript levels of fur were slightly higher in the ΔpsyR mutant strain than in the WT strain.

Fig. 3. The relative mRNA expression levels of gacA and psyI in wild-type (WT) and the ΔpsyR mutant Pseudomonas syringae pv. tabaci ATCC 11528 strains. The relative mRNA levels of each gene were measured by quantitative real-time RT-PCR and normalized to 16S rRNA gene expression as the endogenous control. Bacterial cells were incubated until the early (OD₆₀₀ of 0.5) (A) and late (OD₆₀₀ of 3.5) exponential phases (B). The data are expressed as the average of three replicates ± the standard deviation.

Fig. 4. Relative mRNA expression levels of fur in wild-type (WT) and ΔpsyR mutant Pseudomonas syringae pv. tabaci ATCC 11528 strains (A). Relative fur mRNA levels were measured by quantitative real-time RT-PCR and normalized to 16S rRNA gene expression as an endogenous control. Bacterial cells were cultured until early (OD₆₀₀ of 0.5) and late (OD₆₀₀ of 3.5) exponential phases under low- (B) or high-iron conditions (C). The data are expressed as the average of three replicates ± the standard deviation.
Furthermore, the fur mRNA levels of the ΔpsyR mutant strain at the late exponential phase was slightly higher than that of the WT strain.

In addition, the fur mRNA levels were also assayed in *P. syringae* pv. *tabaci* strains grown under high- or low-iron conditions (Fig. 4B and 4C). Under low-iron conditions, the mRNA levels of fur in the ΔpsyR mutant strain at the early exponential phase were higher than that in the WT strain. However, these mRNA expression levels were reversed at the late exponential phase. A lower amount of fur mRNA was observed in the ΔpsyR mutant strain grown under high-iron conditions in comparison with the WT strain, but this was again reversed at the late exponential phase.

In order to investigate the correlation between TTSS-associated regulatory factors and the QS regulator PsyR, qRT-PCR was conducted as described previously [6]. *P. syringae* pv. *tabaci* PrhI, corresponding to *R. solanacearum* PrhI, exhibited sequence similarity to other sigma factors.

The expression levels of prhA in the WT strain at the early exponential phase were greater than that at the late exponential phase (Fig. 5A). In comparison with the WT strain, the prhA mRNA levels in ΔpsyR mutant strain were increased approximately 0.8-fold at the early exponential phase; slightly greater levels of prhA mRNA were also observed at the late exponential phase. These results showed that the mRNA expression levels of prhA are not significantly different between WT and ΔpsyR mutant strains. For prhl, the mRNA levels in the WT strain were increased at the late exponential phase (Fig. 5B). As compared with the WT strain, the ΔpsyR mutant strain exhibited higher levels of this transcript at the early exponential phase. The mRNA levels of prhl in the ΔpsyR mutant strain were decreased at the late exponential phase. Therefore, expression of prhl is regulated optimally by PsyR in a cell density-dependent manner.

Along with PrhA and Prhl, TTSS regulatory factors influencing expression of HrpR (an activator of TTSS) and HrpA (a major protein of TTSS pili) were investigated in the WT and ΔpsyR mutant strains (Fig. 5C). In the WT strain, the mRNA levels of hrpR decreased at the late exponential phase. In general, lower hrpR mRNA levels were observed in the ΔpsyR mutant strain as compared with the WT strain. However, the mRNA expression levels of hrpR were not significantly different between WT and ΔpsyR mutant strains.

The WT strain showed a higher hrpA mRNA levels at the late exponential phase (Fig. 5D). In the ΔpsyR mutant strain, the mRNA levels of hrpA at the late exponential phase was greater than that of the WT strain. These observations suggested that PsyR may repress hrpA expression at a high cell density. Therefore, hrpA expression at the late exponential
phase was negatively regulated by PsyR.

**Putative promoter region related to virulence genes of *P. syringae pv. tabaci* ATCC 11528**

A specific palindromic sequence, called a *lux* box, has been reported in the promoter regions of many QS-regulated genes [31]. In this study, we searched for a putative *lux* box sequence in the promoter regions of eight genes of interest (Fig. 6). Interestingly, this regulatory box lies between the -35 and -10 position, and overlaps the putative -10 sequence. Thus, all these genes have a putative *lux* box with homologous dyad symmetry.

**DNA-binding activity of PsyR**

PsyR was purified from BL792 containing the plasmids pBL318 and pBL337, as described in the Materials and Methods. Protein samples from each phase of purification, as well as the eluted protein fractions, were analyzed by SDS-PAGE (Fig. 7). The molecular weight of the purified MBP-PsyR was determined as being about 70 kDa, which matched the predicted molecular weights of this protein.

The ability of *P. syringae pv. tabaci* 11528 PsyR to bind the *lux* box in vitro was investigated using EMSA (Fig. 8). The purified MBP-PsyR caused a band mobility shift of the PCR fragment on a 5% polyacrylamide gel. The DNA fragment was amplified from the upstream region of virulence-related genes in assays using as little as 160 fM of the purified DNA fragment. PsyR derived from the BL792 harboring pBL318 and pBL337 was not able to shift DNA fragments containing the *lux* box of any of the genes, except for the upstream region of *psyI*. These results confirmed that PsyR binds specifically to the *lux* box region in *psyI*, but does not directly regulate virulence-related genes.

**Discussion**

*Pseudomonas syringae pv. tabaci* is a plant pathogenic bacterium that causes wildfire disease in tobacco plants. Studies on the genetic basis of the pathogenesis of *P. syringae* pathovars has been reported, and have revealed the role of TTSS-related genes, global regulatory genes, and motility and virulence-associated factors such as various phytotoxins, EPSs, and siderophores [3]. *P. syringae pv. tabaci* exhibits QS that is based on the production of diffusible signal molecules; however, the role of QS in this organism has not yet been clearly defined. In this study, the effect of PsyR protein as a QS transcriptional regulator was demonstrated using phenotypic and genetic analyses in *P. syringae pv. tabaci* ATCC 11528. We investigated the regulation of virulence-related genes by PsyR and observed differences in the patterns of regulation of *psyI*, *fur*, *prhI*, and *hrpA* in the ΔpsyR mutant strain as compared to that in the WT strain.

We also investigated the regulatory effects of PsyR on swarming motility and production of siderophores, tabtoxin, and AHLs, as well as symptoms of wildfire disease in tobac-
Electrophoretic mobility shift assays (EMSA) of binding of MBP-PsyR to the putative promoter-containing regions of target genes: (A) psyI, (B) psyR, (C) fur, (D) gacA, (E) prhA, (F) prhl, (G) hrpR, (H) hrpA. All lanes contained 160 fM of DNA and the indicated concentration of MBP-PsyR. The DNA–protein reaction mixtures were loaded onto 5% polyacrylamide gels.

Our results demonstrated that PsyR coordinated the production of tabtoxin. In addition, swarming motility was increased in the ΔpsyR mutant strain, indicating that PsyR

leaves by comparing the mutant and WT strains. Previous studies of tabtoxin reported that tabtoxin causes chlorosis around necrotic lesions and assists the development of lesions.
was involved in the regulation of swarming motility. The ΔpsyR mutant strain caused a delay in the development of disease symptoms compared to the WT strain. However, PsyR did not affect the growth rate of *P. syringae* pv. *tabaci* 11528. Thus, the phenotypic characteristics of the ΔpsyR mutant may not be due to differences in growth rates.

Furthermore, the ΔpsyR mutant strain produced less siderophores than the WT strain under low-iron conditions and did not produce siderophores under high-iron conditions. This was confirmed by the results from real-time RT-PCR. Under low-iron conditions, the fur mRNA level in the ΔpsyR mutant strain at the early exponential phase was higher than that in the WT strain, suggesting that the expression of fur repressed production of siderophores and may be positively regulated by PsyR. Moreover, the fur mRNA level in the ΔpsyR mutant strain was lower under high-iron conditions than in the WT strain. This may suggest that expression of fur in the presence of high iron concentrations is controlled by PsyR, using another mechanism.

Production of AHL was regulated by PsyR in response to cell density; this finding was supported by the real-time RT-PCR results. The psyI mRNA levels in the ΔpsyR mutant strain were significantly reduced at the late exponential phase. These results suggested that expression of psyI at a high density of bacteria is positively controlled by PsyR. Thus, psyI expression is tightly controlled by PsyR in response to bacterial cell density. There was no marked difference in the gacA mRNA levels between WT and ΔpsyR mutant strains. Previous studies have reported that GacA positively controls QS signaling and PsyR [6, 8, 31]. More specifically, GacA regulates expression of psyR, according to a recent study, but PsyR does not regulate expression of gacA. Expression levels of prhI in the ΔpsyR mutant strain were higher at the late exponential phase. In addition, the mRNA levels of *hrpA* at the late exponential phase were greater than those in the WT strain. These results showed that prhI and *hrpA* are expressed via regulation by PsyR in response to bacterial cell density; thus, QS influences expression of TTSS genes. These results suggest that PsyR has a dual role as an activator or repressor.

To determine whether PsyR binds upstream of pathogenesis-related genes in order to regulate their expression, EMSA was performed. A PsyR-overproduction strain was constructed specifically for use in EMSA in this study. A recent study reported that cognate AHLs are necessary for protein stability and solubility during the purification of several LuxR-type regulators [21]. *psyI*, encoding an AHL synthase, was co-expressed in the PsyR-overproduction strain to enhance the production of soluble protein. Soluble PsyR proteins were successfully overproduced when the overproduction strain harbored both *psyI* and *psyR*. The identification of cis-regulatory sequences and the binding of PsyR to the upstream region of each virulence gene provided evidence of their involvement in the regulation of these genes. No binding of a purified MBP-PsyR protein to the upstream region of these genes, except *psyI*, was detected. Surprisingly, PsyR did not bind to the upstream region of *psyR*. These results suggested that PsyR may be indirectly controlled via intermediate-regulatory systems and that auto-regulation by PsyR does not occur.

In conclusion, this study shows that PsyR controls production of the effectors by modulating transcript levels. These findings indicate that PsyR-mediated regulation plays important roles in infection of plants by *P. syringae* pv. *tabaci*. Integration of the regulatory network including PsyR is required in order to obtain a better understanding of the pathogenetic mechanism common to all *P. syringae* pathovars and to identify the major components of each regulatory system. Elucidating pathogenetic mechanisms in phytopathogens will offer valuable insight into diseases caused by plant pathogens and will lay the basis for studies into antimicrobial therapies, as well as in the medical, food, and agriculture industries.

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초록: *Pseudomonas syringae pv. tabaci*에서 LuxR-type 전사조절자인PsyR에 의한 병원성 유전자들의 조절

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