A NOVEL AHL-DEGRADING RHIZOBACTERIUM QUENCHES THE VIRULENCE OF PECTOBACTERIUM ATROSEPTICUM ON POTATO PLANT

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SUMMARY

Quorum sensing (QS) is a regulatory mechanism that connects gene expression to cell density in bacteria. The expression of numerous genes including those involved in the production of virulence determinants in Pectobacterium atrosepticum are regulated in this way. The signal molecules involved in QS in P. atrosepticum belong to the group of N-acyl homoserine lactones (AHLs). Recently, several soil bacteria were found to degrade AHLs, thereby interfering with the QS system. In this research, twelve strains of AHL-degrading rhizobacteria were isolated from potato rhizosphere. According to ribotyping analysis, these isolates fell into four groups belonging to the genera Bacillus, Arthrobacter, Pseudomonas and Chryseobacterium. All these isolates were capable to degrade both synthetic and natural AHLs produced by P. atrosepticum strain SM1. In this report, Chryseobacterium sp. was isolated as an AHL-degrading bacterium for the first time and shown that it could interfere with QS-dependent bacterial infection of P. atrosepticum SM1. Chryseobacterium sp. and several other tested isolates effectively inhibited maceration of potato tuber tissue by P. atrosepticum. The attenuation of the pathogenicity might be due to the quenching of QS-regulated production of extracellular enzymes by P. atrosepticum SM1. Chryseobacterium sp. isolated in this study might be a useful agent in the biocontrol of bacterial plant diseases.

Key words: AHL degradation, Chryseobacterium sp., Pectobacterium atrosepticum, quorum quenching, quorum sensing.

INTRODUCTION

Bacteria have evolved mechanisms to coordinate gene expression in response to their population density. This occurs via the production and detection of signal molecules in a process called quorum sensing (QS) (Fuqua et al., 1994). Consequently, the concentration of the produced signal in a confined environment reflects bacterial cell density. Each individual bacterial cell produces a basal level of QS signals which then accumulates to a threshold concentration when a certain cell-density is reached. The signal then interacts with the cognate transcription factor to activate gene expression. Several groups of QS signals have already been identified; N-acyl homoserine lactones (AHLs) are to date the most common QS signals found in Gram-negative bacteria. AHL QS regulates the expression of many genes responsible for biofilm formation, bioluminescence, pigmentation, pathogenicity, siderophore production, plasmid conjugal transfer, antibiotic production, and swarming (Whitehead et al., 2001).

It is believed that interfering with QS could be an attractive alternative method to control bacterial infections which does not involve the inhibition of growth, hence minimizing the problem of resistance (Sperandio, 2007). The term quorum quenching (QQ) encompasses various natural phenomena or engineered procedures that lead to the perturbation and eventually attenuate expression of genes related to QS-regulated functions (Dong and Zhang, 2005; Rasmussen and Givskov, 2006; Williams, 2007). Several anti-QS mechanisms have been proposed in recent years (Cirou et al., 2009) via the use of: (i) compounds which accelerate degradation of the AHL-dependent transcription factor and (ii) AHL-degrading enzymes which can affect the accumulation of signal molecules (Dong and Zhang, 2005; Turovskiy et al., 2007). Several rhizobacteria belonging to different genera of Gram-positive (e.g. Arthrobacter, Bacillus, Rhodococcus, Streptomyces) and Gram-negative bacteria (e.g. Agrobacterium, Comamonas, Klebsiella, Pseudomonas, Ralstonia) have been reported to produce AHL-degrading enzymes which can interfere with QS-regulated functions (Angelo-Picard et al., 2005; Faure and Dessaux, 2007).

Pectobacterium atrosepticum and P. carotovorum are plant pathogenic bacteria responsible for disorders characterized by maceration of tissues, such as the black leg disease of potato, or the soft rot disease of various plants, including cabbage, fritillaria, chili, celery, lettuce, carrot, melon, etc. (Mahmoudi et al., 2007). These pathogens are of economical importance as they cause...
major losses to potato crops in the world (Toth and Birch, 2005). The maceration occurs as the result of a set of bacterial enzymes such as cellulase, pectate lyases and pectin methyl esterase which are responsible for pecto-cellulose wall disruption in plant cells (Toth and Birch, 2005; Grant et al., 2006). Production of virulence factors in Pectobacterium (such as maceration enzymes) are controlled by AHL-dependent QS that relies upon 3-oxo hexanoyl-N-homoserine lactone (3-oxo C6-HSL) or octanoyl homoserine lactone (C8-HSL) signal molecules (Whitehead et al., 2001; Von Bodman et al., 2003; Barnard and Salmond, 2007). To our knowledge, two possible strategies have been developed to control Pectobacterium infection by interference with QS, i.e. using either transgenic plants which degrade AHLs or beneficial plant-associated bacteria naturally interfering with QS of Pectobacterium by degrading AHLs. Importantly, genetically modified P. carotovorum expressing AHL-degrading enzymes, such as a AHL-lactonase or AHL-acylase, have a lower production level of virulence factors (Reimmann et al., 2002; Lin et al., 2003; Dong et al., 2000).

This study was aimed to: (i) isolate and identify potato rhizosphere bacteria which are capable to degrade AHLs and (ii) explore their potential use in antagonizing QS-regulatory processes.

MATERIAL AND METHODS

Bacterial strains, media and culture conditions. Aside from bacterial strains isolated from potato rhizosphere in this study, P. atrosepticum strain SM1 (provided by the Laboratory of Plant Protection, IAU-Science and Research Branch, Tehran, Iran) was used as the source of naturally produced AHL molecules and as soft rot agent of potato. Chromobacterium violaceum CV026 (McClean et al., 1997) (provided by ICGEB, Trieste, Italy) and Agrobacterium tumefaciens NT1 (Shaw et al., 1997) (provided by Y. Dessaux, CNRS, Gif-sur-Yvette, France) were used as indicator strains for AHLs detection. The media used were Luria-Bertani (LB), King-B (KB) (Schaad et al., 2001) and AB minimal medium, which was supplemented when necessary with 2% mannitol (Chilton et al., 1974) or with cycloheximide (50 µg l-1). All bacteria were grown at 27°C, except for AHL biosensors and P. atrosepticum SM1, which were grown at 28°C and 25°C, respectively. All standard AHLs used in this study were purchased from Sigma-Aldrich (USA).

Isolation of bacterial strains. Soils and root samples were collected from commercial potato fields in the Isfahan province (Iran). Soil or root samples (1 g) used for isolating culturable bacteria were resuspended in 10 ml of sterile 0.8% NaCl by very vigorous shaking for 3 min, and the suspension was serially diluted. Appropriate dilutions were spread on KB agar and LB medium (1% tryptone, 0.5% yeast extract, 0.5% NaCl) containing 50 µg ml-1 cycloheximide. Plates were incubated in the dark at 27°C for 72 h, then bacterial colonies with different morphologies were randomly picked from both media, purified and stored in glycerol at -80°C.

Screening of bacterial isolates for N-AHSL degradation activity. As AHLs are sensitive to alkaline pH (Yates et al., 2002), all degradation assays were done in KB and LB media at pH 6.5. Individual colonies (taken from frozen stocks spread onto LB plates) were inoculated in 5 ml LB medium supplemented with each of the standard AHLs at the following concentrations: 5 mg l-1 C6-HSL (N-Hexanoyl-L-homoserine lactone); 5.7 mg l-1 C8-HSL (N-Octanoyl-L-homoserine lactone); 6 mg l-1 C10-HSL (N-Decanoyl-L-homoserine lactone) and 6 mg l-1 C14-HSL (N-Tetradecanoyl-L-homoserine lactone). Cultures were incubated at 27°C for 24 h with shaking. A control experiment using a non-inoculated degradation medium processed as the inoculated media was conducted at the same time as the degradation assays. After this time, bacterial cells were removed by centrifugation at 12,000 rpm for 5 min. The culture supernatant was extracted twice with equal vol of ethyl acetate. The organic phase was evaporated to dryness, the residues were re-dissolved in 50 µl vol of ethyl acetate and stored at -20°C. Components from ethyl acetate extracts were separated by chromatography on C18-reversed phase plate (Sigma Aldrich, USA, Cat. no. Z265446) with a solvent system of methanol-water (60:40, vol:vol). After development, the solvent was evaporated, and the dried plates were overlaid with a culture of the biosensors strains as described by Shaw et al. (1997) and McClean et al. (1997).

Degradation ability of natural AHLs produced by P. atrosepticum. P. atrosepticum strain SM1 (Pa-SM1) was inoculated in 5 ml LB medium on a rotary shaker for 24 h. Bacterial cells were removed by centrifugation at 12,000 rpm for 5 min. The supernatant was extracted twice by equal vol of ethyl acetate and stored at -20°C. Components from ethyl acetate extracts were separated by chromatography on C18-reversed phase plate (Sigma Aldrich, USA, Cat. no. Z265446) with a solvent system of methanol-water (60:40, vol:vol). After development, the solvent was evaporated, and the dried plates were overlaid with a culture of the biosensors strains as described by Shaw et al. (1997) and McClean et al. (1997).

Identification of the selected isolates. To identify the bacterial isolates, the DNA coding regions for the 16S rRNA of each isolate were amplified by PCR using the universal primers pA (5’-AGAGTTTGATCCTG-GCTCA-3’) and pH (5’-GGAGGTGATCCAGCGCA-3’), which allowed the amplification of almost the entire gene (Bruce et al., 1992). DNA extraction for bacterial strains was done as described by Manzano et
PCR runs were performed in a total reaction volume of 50 µl containing 1X PCR buffer, 100 µM of each dNTP, 1.5 mM MgCl₂, 0.1 µM primers, 100 ng DNA extract and 1 U of Taq DNA polymerase (Cinagene, Iran, Cat. no. SN-560011). The following temperature cycle was used: an initial denaturation step of 5 min at 95°C followed by 30 cycles of 1 min denaturation at 95°C, 1 min annealing at 56°C, 1.5 min extension at 72°C and a final extension step of 5 min at 72°C. The amplification yielded a product of ca. 1,500 bp which was analyzed by electrophoresis in 0.8% agarose gel and staining with ethidium bromide (Sambrook et al., 2001). The resulted amplicons were sequenced by a Big Dye Terminator and ABI Prism 3700 Genetic Analyzer (Macrogen, World Meridian Venture Center, Korea), and at least 400 bp were subjected to BLAST analysis within the NCBI database. Though some sequence comparisons authorized identification of isolates at the species level, only the genus level was retained in this study for homogeneity. Additionally, some phenotypic characteristics of bacterial isolates such as Gram reaction and cell morphology were determined.

### Inhibition of the pectinolytic activity of *P. atrosepticum* on potato tubers.

The assay was performed on potato tubers (cv. Agria) essentially as described by Łojkowska et al. (1995). Briefly, potato tubers were washed, surface-sterilized by two consecutive exposures to sodium hypochlorite (1% chlorine) then extensively rinsed with sterile water. The tubers were dried under sterile conditions, sprayed with 70% ethanol, then were dried again and kept for co-inoculation.

Strains used in this assay were Pa-SM1 (pathogen) and EM1, EM2, EM77, EM18, EM22 and EM10 as potential biocontrol agents (quenchers). All strains were cultured overnight at 27°C in LB medium, suspended and diluted in sterile 0.8% NaCl. Each tuber was inoculated with 20 µl of bacterial suspension including the pathogen alone, the pathogen with the quencher and the quencher alone. Four potato tubers were used for each combination of strains. The experiments were repeated twice. After inoculation, potato tubers were incubated in a moist chamber (humidity above 90%) at 25°C. Three days post infection, the tubers were cut in the middle and the results were assessed by visual inspection.

### Table 1. Bacterial strains isolated from the potato rhizosphere identified via 16s rDNA sequencing, their N-acyl-homoserin lactone degradation properties and their effect on tissue maceration of *P. atrosepticum* strain SM1.

<table>
<thead>
<tr>
<th>Strains</th>
<th>GenBank accession No.</th>
<th>Gram</th>
<th>Colony and cell morphology</th>
<th>C₆-HSL</th>
<th>C₈-HSL</th>
<th>C₁₀-HSL</th>
<th>C₁₄-HSL</th>
<th>Pa-SM1 AHL</th>
<th>Effect on maceration ability of Pa-SM1</th>
</tr>
</thead>
<tbody>
<tr>
<td>EM1</td>
<td>Bacillus sp.</td>
<td>EU977693.1</td>
<td>+</td>
<td>White, rod-shaped, motile</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
</tr>
<tr>
<td>EM2</td>
<td>Bacillus sp.</td>
<td>HM748447.1</td>
<td>+</td>
<td>As above</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
</tr>
<tr>
<td>EM77</td>
<td>Bacillus sp.</td>
<td>EU240440.1</td>
<td>+</td>
<td>As above</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
</tr>
<tr>
<td>EM13</td>
<td>Bacillus sp.</td>
<td>HM188452.1</td>
<td>+</td>
<td>As above</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
</tr>
<tr>
<td>EM84</td>
<td>Bacillus sp.</td>
<td>FJ866738.1</td>
<td>+</td>
<td>As above</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
</tr>
<tr>
<td>EM93</td>
<td>Bacillus sp.</td>
<td>AY948211.1</td>
<td>+</td>
<td>As above</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
</tr>
<tr>
<td>EM36-1</td>
<td>Bacillus sp.</td>
<td>HM748430.1</td>
<td>+</td>
<td>Pink, rod-shaped, motile</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
</tr>
<tr>
<td>EM18</td>
<td>Arthrobacter sp.</td>
<td>AY444858.1</td>
<td>+</td>
<td>Yellow, rod-shaped, non-motile</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>+</td>
<td>++</td>
</tr>
<tr>
<td>EM22</td>
<td>Arthrobacter sp.</td>
<td>AY635865.1</td>
<td>+</td>
<td>As above</td>
<td>++</td>
<td>++</td>
<td>+</td>
<td>+</td>
<td>++</td>
</tr>
<tr>
<td>EM12</td>
<td>Pseudomonas sp.</td>
<td>AJ969084.1</td>
<td>-</td>
<td>White, rod-shaped, fluorescent on King-B, motile</td>
<td>+</td>
<td>+</td>
<td>++</td>
<td>++</td>
<td>+</td>
</tr>
<tr>
<td>EM40</td>
<td>Pseudomonas sp.</td>
<td>HM134290.1</td>
<td>-</td>
<td>As above</td>
<td>+</td>
<td>+</td>
<td>++</td>
<td>++</td>
<td>+</td>
</tr>
<tr>
<td>EM10</td>
<td>Chryseobacterium sp.</td>
<td>DQ530068.1</td>
<td>-</td>
<td>Light yellow, rod-shaped, non-motile</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
<td>++</td>
</tr>
</tbody>
</table>

Nd.: not determined.

*a* AHL degrading ability of tested strains reflected by non pigmentation of bio-indicator strains (see text).

*b* *P. atrosepticum* strain SM1 was used as N-AHL production source, +: low degrading ability, ++: high degrading ability.

*c* effect on potato tubers maceration ability of *P. atrosepticum* SM1, +: weak, ++: strong, +++: extensive, Nd.: not determined.
Inhibition of the Black leg disease on potato plants. Mini-tubers of potato cv. Agria were washed, surface-sterilized by dipping in 10% ethanol for 5 min, rinsed in sterile distilled water and air-dried overnight. Tubers were then sown in 20-cm diameter pots placed in a greenhouse at 25°C. After 6 weeks, potato plants were inoculated with bacterial suspension. Strains used in this assay were _P. atrosepticum_ SM1 as pathogen and EM10 as AHL degrading agent (quenchers). Strains were cultured overnight at 25°C in LB medium, suspended and diluted in sterile 0.8% NaCl. One stem per potato plants, 5 cm above the base, was injected with 100 µl of bacterial suspension including pathogen alone, pathogen along with quencher and quencher alone. The injection site was covered by mineral oil Tween 20. Inoculated plants were incubated in a greenhouse at 27°C with high humidity for 3-4 days. The size of rotting tissue was visually measured and disease severity was estimated by its progression in the stem.

RESULTS

Screening of bacterial isolates degrading N-AHLs. Among sixty five bacterial strains isolated from rhizospheric soil and root samples, 12 isolates completely degraded 5 mg l⁻¹ of C6 HSL after 20 h, as indicated by the absence of violacein induction in the CV026 biosensor (Table 1). To further characterize the AHL degradation patterns of selected isolates, four synthetic unsubstituted AHLs and crude cell culture extracts of _P. atrosepticum_ strain SM1 were used. Results revealed that all 12 tested strains degraded all AHLs types under same conditions with either high or low degradation activity (Table 1). In fact, the degradation properties of the various strains differed with respect to their substrate preferences. For instance, strains EM1, EM2, EM36-1 and EM10 completely degraded all AHLs as well as the culture extract of Pa-SM1 after 20 h (Fig. 1). These isolates, excluding EM10, were identified as _Bacillus_ spp., which are known to have high AHL-degrading activity (Dong et al., 2000, 2002). EM12 and EM40 strains also completely degraded 6 mg l⁻¹ C10 and C14-HSL after 20 h. However, some C6 and C8-HSL remained in cell culture supernatant as indicated by slight production of the blue pigment induced by NT1 biosensor. Additionally, all tested strains, excluding EM12 and EM40, efficiently degraded natural AHLs produced by Pa-SM1. These results indicated that all tested isolates were able to degrade various AHLs albeit with different abilities.

Identification of the AHL-degrading isolates. In order to characterize the isolated bacterial species, the 16S rRNA region of all putative bacterial AHL degraders was amplified by PCR using pA and pH primers as de-

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**Fig. 1.** (A) Thin layer chromatogram for degradation of AHLs produced by _Pectobacterium atroseptium_ strain SM1. PaSM1 inoculated LB medium and after 24 h incubation, free cell culture supernatant was extracted with ethyl acetate. The extract was added to fresh LB medium and selected strains were cultured. After 24 h, culture supernatant was extracted with ethyl acetate and AHL disappearance was revealed using the biosensor strain *Chromobacterium violaceum* CV026 as described in methods. Pa extr: natural AHL extracted from culture media containing _P. atrosepticum_ strain SM1, St.: Synthetic C6-HSL standard. (B) N-AHL production by _P. atrosepticum_ strain SM1. Pa-SM1 was streaking cultured on LB medium and biosensor strain, _C. violaceum_ CV026, was cultured adjacent PaSM1. Appearance of violet pigment in CV026 colony revealed the production of violacein by CV026 as well as production of N-AHL by Pa-SM1.
scribed in Materials and Methods. DNA sequences were compared to those found in the DNA databank using the online FASTA search engine (http://www.ncbi.nlm.nih.gov). All the 16S rRNA sequences exhibited 80-100% similarity with described genera. Alignment with sequences from GenBank database indicated that the isolates belong to four different genera. Seven isolates including EM1, EM2, EM77, EM133, EM84, EM93 and EM36-1 belonged to *Bacillus* sp., thus possibly harboring the *aiiA* gene (Dong et al., 2000). Isolates EM12 and EM40 showed 99% similarity with *Pseudomonas* sp. Strains belonging to *Arthrobacter*, which included EM18 and EM22, were also isolated. Isolate EM10 had a high similarity with *Chryseobacterium* sp. To our knowledge, there are no reports of AHL degradation ability by bacteria belonging to this genus.

**Biocontrol of* P. atrosepticum* by AHL-degrading bacteria.** The biocontrol activity of tested isolates (Table 1) was assessed against Pa-SM1, the virulence of which relies on QS via the 3-oxo-C8HSL signal (Smadja et al., 2004). Inoculation of potato tubers with *P. atrosepticum* SM1 resulted in extensive tissue maceration. Co-inoculation of Pa-SM1 with AHL-degrading bacteria provided substantial reduction in tissue maceration compared to the pathogen alone (Fig. 2). The biocontrol activity of the *Chryseobacterium* sp. was more effective than that of the other tested isolates. Co-inoculation of *Chryseobacterium* sp. as novel AHL-degrading bacterium produced a significant reduction of tuber maceration compared to the rotting area when potato tubers were inoculated with the pathogen alone as well as with other tested bacteria (Fig. 3). Additionally, the ability of Pa-SM1 to macerate potato tuber tissue was attenuated by EM18, EM22 (identified as *Arthrobacter* sp.) and significantly reduced also by EM1, EM2, EM77 (identified as *Bacillus* sp.) when co-inoculated with Pa-SM1 at 10⁶ CFU/ml (Fig. 2). In a greenhouse assay, *P. atrosepticum* SM1 failed to cause or caused only minor blackleg disease symptoms in the presence of *Chryseobacterium* sp. EM10 (Fig. 3).

**Fig. 2.** Quench of the maceration capacity of *Pectobacterium atrosepticum* strain SM1 (Pa-SM1) by selected rhizobacteria strains assessed by visual inspection of the percentage of maceration zones 3 days after inoculation. Co-inoculation of Pa-SM1 with selected isolates EM1 (*Bacillus* sp.), EM2 (*Bacillus* sp.), EM77 (*Bacillus* sp.), EM18 (*Arthrobacter* sp.), EM22 (*Arthrobacter* sp.) and EM10 (*Chryseobacterium* sp.). The results represent a mean value of trial with four replications (4 potato tubers) per each treatment.

**Fig. 3.** Biocontrol activity of AHL degrading rhizobacteria against plant tissue maceration activities in *Pectobacterium atrosepticum* strain SM1. A, negative control consisting of a tuber treated with 0.8% NaCl; B, Inoculation of 20 µl of Pa-SM1 alone at about 10⁶ CFU per tuber; C, co-inoculation of Pa-SM1 at about 10⁶ CFU per tuber along EM10 (*Chryseobacterium* sp.); D, inhibition of *P. atrosepticum* SM1 pathogenicity in greenhouse by AHL degrading rhizobacterium *Chryseobacterium* sp. EM10.
DISCUSSION

The microenvironment of the rhizosphere is relatively rich in nutrient substances exuded by the plant and, consequently, is inhabited by many different bacterial species. The composition of specific root exudates varies depending on the plant species, genus, cultivar, and growth stage (Savka et al., 2002). The first aim of this work was to recover and identify bacterial isolates from the potato rhizosphere able to degrade AHL molecules. Out of 65 identified isolates, 12 had AHL degradation capability.

Bacteria that inactivate AHL signal molecules are taxonomically diverse (α,β-proteobacteria, firmicutes and actinobacteria) and may represent 10-20% of the total cultivable bacteria in soil (Dong et al., 2000; Angelo-Picard et al., 2004; Jafra et al., 2006). In this study, we isolated 12 AHL-degrading bacteria that were identified using some morphological approaches and 16S rRNA homology. Among them, seven isolates belonged to Bacillus sp., a Gram-positive bacterium that has AHL-degradation activity and carries a lactonase gene called aiiA, which is common among most Bacillus strains (Dong et al., 2000, 2002; Lee et al., 2002). Other bacterial isolates were less abundant in the rhizosphere and were classified as Arthrobacter, Pseudomonas, and Chryseobacterium. Previous studies by Dong et al. (2000), Molina et al. (2003) and Park et al. (2003) revealed that Bacillus, Pseudomonas and Arthrobacter isolates possess AHL-degrading properties. But, to our knowledge, we now provide the first report of an AHL-degrading activity in a member of the genus Chryseobacterium.

Chryseobacterium is a Gram-negative and aerobic bacterial genus with rod-shaped and non-motile cells, described by Vandamme et al. (1994). Chryseobacterium strains are distributed in a wide variety of habitats such as water, plant roots, sewage, marine sediments, clinical samples, and materials from food processing industry. Many species of this genus have been found associated with plants and are known as plant growth promoting bacteria. These studies, as well as the data presented in this paper, highlight a promising strategy for the biocontrol and prevention of infectious diseases through AHL signal degradation.

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Recently, several authors have proposed interference of QS regulation as a way to develop innovative approaches for the control of plant, animal or human pathogens (Sperandio, 2007). AHL degrading rhizobacteria could be potentially used for the biological control of AHL-producing plant pathogenic bacteria. The success of their application will depend on the population density of the antagonists and the efficiency with which AHLs are inactivated (Jafra et al., 2006). Therefore, the identification and evaluation of the antagonistic ability of these AHL-degrading agents is the first step in this procedure. Dong et al. (2002), Molina et al. (2003) and Morohoshi et al. (2009) reported the attenuation of P. carotovorum virulence to potato using QS-interfering bacteria. These studies, as well as the data presented in this paper, highlight a promising strategy for the biocontrol and prevention of infectious diseases through AHL signal degradation.


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