Revisiting the quorum-sensing hierarchy in *Pseudomonas aeruginosa*: the transcriptional regulator RhlR regulates LasR-specific factors

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*Pseudomonas aeruginosa* uses the two major quorum-sensing (QS) regulatory systems las and rhl to modulate the expression of many of its virulence factors. The las system is considered to stand at the top of the QS hierarchy. However, some virulence factors such as pyocyanin have been reported to still be produced in las mutants under certain conditions. Interestingly, such mutants arise spontaneously under various conditions, including in the airways of cystic fibrosis patients. Using transcriptional lacZ reporters, LC/MS quantification and phenotypic assays, we have investigated the regulation of QS-controlled factors by the las system. Our results show that activity of the rhl system is only delayed in a lasR mutant, thus allowing the expression of multiple virulence determinants such as pyocyanin, rhamnolipids and C4-homoserine lactone (HSL) during the late stationary phase. Moreover, at this stage, RhlR is able to overcome the absence of the las system by activating specific LasR-controlled functions, including production of 3-oxo-C12-HSL and *Pseudomonas* quinolone signal (PQS). *P. aeruginosa* is thus able to circumvent the deficiency of one of its QS systems by allowing the other to take over. This work demonstrates that the QS hierarchy is more complex than the model simply presenting the las system above the rhl system.

**INTRODUCTION**

*Pseudomonas aeruginosa* is a ubiquitous and versatile bacterium involved in numerous pathogenic infections affecting immunocompromised individuals and those suffering from cystic fibrosis (Marshall & Carroll, 1991; Pier, 1985; Speert, 1985). This bacterium regulates most of its virulence determinants in a cell-density-dependent manner via a mechanism called quorum-sensing (QS). Such global regulatory systems are found in most bacterial species, and control several and diverse biological functions, such as virulence, bacterial conjugation, bioluminescence and biofilm formation (de Kievit & Iglewski, 2000; Donabedian, 2003; Loh et al., 2002; Miller & Bassler, 2001). QS is mediated by diffusible signalling molecules released into the external environment. These signals, when reaching specific concentrations correlated with specific population cell densities, bind to and activate their respective transcriptional regulators. In *P. aeruginosa*, two conventional complete QS systems are known: the synthases LasI and RhlI produce the N-acylhomoserine lactones 3-oxo-C12-HSL and C4-HSL respectively, which induce their cognate LuxR-type transcriptional regulators LasR and RhlR, responsible for the activation of numerous QS-controlled genes (Juhas et al., 2005; Pesci et al., 1997). Among genes activated by these two regulators are those coding for the LasI and RhlI synthases. Since N-acyl-HSLs induce their own production, they are called autoinducers. More recently, a third, distinct QS system has been unveiled. It is composed of a transcriptional regulator from the LysR family, MvfR (PqsR), which directly activates two operons (*phnAB* and *pqsABCDE*) required for the biosynthesis of 4-hydroxy-2-alkylquinolines (HAQs), including molecules involved in 4-quinolone signalling (Déziel et al., 2004; Lépine et al., 2004; Pesci et al., 1999), and for the activation of many QS-controlled genes, via *pqsE* (Déziel et al., 2005; Diggle et al., 2006; Farrow et al., 2008). Among the HAQs, 4-hydroxy-2-heptylquinoline and the *Pseudomonas* quinolone signal (PQS) act as activators of the MvfR regulator, inducing a positive feedback loop typical of QS systems (Xiao et al., 2006a).

QS regulation is a very complex and extensive network influencing, both positively and negatively, the transcription of perhaps 5–10% of the *P. aeruginosa* genome (Hentzer et al., 2003; Schuster et al., 2003; Wagner et al., 2003). The LasR regulator is known to initiate the QS regulatory system, as it activates the transcription of a number of other regulators, such as rhlR, defining a...
hierarchical QS cascade from the las to the rhl regulons (Latifi et al., 1996; Pesci et al., 1997). Over the last few years, many whole-genome transcriptomic studies have been published with the aim of identifying genes that are under the control of LasR and/or RhlR (Hentzer et al., 2003; Rasmussen et al., 2005; Schuster et al., 2003; Wagner et al., 2003). Specific directly activated genes were clearly identified as belonging to the rhl regulon, such as rhlAB (rhamnolipid biosynthesis), lecA (lectin), hcnABC (HCN production) and both phzABCDEFG operons (phenazine biosynthesis) (Latifi et al., 1995; Schuster et al., 2004; Schuster & Greenberg, 2007; Whiteley et al., 1999; Winzer et al., 2000). However, the situation is not as clear for many LasR-controlled genes, for which it has not been possible to define a single consensus LasR binding site sequence in the promoter region, suggesting that some of these genes are activated indirectly (Schuster et al., 2004; Schuster & Greenberg, 2007). Actually, most QS-regulated factors are more or less influenced by both LasR and RhlR, as is the case for the proteases LasA (staphyloclytic protease) and LasB (elastase) (Freck-O’Donnell & Darzins, 1993; Hentzer et al., 2003; Nouwens et al., 2003; Schuster et al., 2003; Toder et al., 1994; Wagner et al., 2004). Thus QS plays a predominant role in the regulation of virulence determinants in P. aeruginosa. Surprisingly, however, there are increasing reports that lasR mutants occur frequently in the natural environment (Cabrol et al., 2003), in airways from individuals with cystic fibrosis (D’Argenio et al., 2007; Smith et al., 2006), in intubated patients (Denervaud et al., 2004) and in individuals suffering from bacteremia, pneumonia or wound infection (Hamood et al., 1996). This is intriguing, since the LasR regulator is widely considered essential for full P. aeruginosa virulence (Preston et al., 1997; Rumbaugh et al., 1999; Storey et al., 1998).

The LasR transcriptional regulator is generally considered to sit at the top of the QS hierarchy in P. aeruginosa (Latifi et al., 1996). However, we and others have observed that the phenazine pyocyanin is overproduced by lasR mutants at the late stationary phase (Déziel et al., 2005; Diggle et al., 2003). As shown in Fig. 1, a lasR mutant produces less pyocyanin during early growth phases, although at the end of exponential growth and during early stationary phase, pyocyanin begins to be produced. During late stationary phase, after 24 h of cultivation, the lasR mutant cultures contain much more pyocyanin than cultures of the wild-type strain (35 mg l⁻¹ compared to 2.5 mg l⁻¹, respectively). This is unexplained, since pyocyanin production is known to be regulated by QS (Latifi et al., 1995). The regulator of the pyocyanin biosynthesis genes (phz genes) is RhlR (Brint & Ohman, 1995), whose transcription is considered to require LasR (de Kievit et al., 2002; Latifi et al., 1996; Pearson et al., 1997; Pesci et al., 1997). In theory, pyocyanin production is thus expected to be absent in lasR mutants, whereas experimental data show that it is actually only delayed (Fig. 1).

In order to better understand the specific role of LasR and its involvement in expression of virulence factors, we have characterized the expression of QS-controlled determinants in a lasR mutant and have observed that during stationary phase, many QS-regulated virulence factors are expressed. Our data show that at this stage of growth, the RhlR regulon is activated. Moreover, we found that RhlR is able to induce LasR-regulated genes (including some considered specific such as lasI) in the absence of lasR, unveiling a new mechanism for the bacteria to bypass a defect in their QS regulation, allowing RhlR to induce the las system when LasR is non-functional.

**METHODS**

**Strains, plasmids and growth conditions.** Table 1 lists strains and plasmids. Bacteria were routinely grown in Tryptic Soy Broth (TSB) medium at 37 °C in a roller drum, with appropriate antibiotics when required (carbenicillin 300 mg l⁻¹ and tetracycline 75 mg l⁻¹ for P. aeruginosa; carbenicillin 100 mg l⁻¹ and tetracycline 15 mg l⁻¹ for Escherichia coli). TSB plates contained 1.5% agar. For pyocyanin and rhamnolipid detection, King’s A medium was used (King et al., 1954). All measurements of optical density and absorbance were obtained with a Thermo Scientific NanoDrop 1000 spectrophotometer.

An isogenic lasR rhlR double mutant was generated by allelic exchange of the rhlR gene in a lasR background with pSB224.10A using sucrose counterselection (Beaton et al., 2002).

![Fig. 1. Expression of pyocyanin is delayed in a lasR mutant: P. aeruginosa lasR mutant containing a constitutive rhl (pUCPSK\_rhlR) or lasR (pUCPSK\_lasR) expression vector, or the same vector without rhlR or lasR (pUCPSK), compared with the wild-type and the lasR rhlR mutant.](http://mic.sgmjournals.org)
Table 1. Bacterial strains and plasmids used in this study

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Characteristics</th>
<th>Source or reference</th>
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<td><strong>Bacteria</strong></td>
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<td>E. coli DH5x</td>
<td>supE44 ΔlacU169 (Δ80 lacZAM15) hasD17 recA1 endA1 gyrA96 thi-1 relA1</td>
<td>Hanahan (1983)</td>
</tr>
<tr>
<td>P. aeruginosa/lab no.:</td>
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<td>Rahme et al. (1995)</td>
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<td>Dzeiel et al. (2004)</td>
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<tr>
<td>PA14 lasR rhlR/ED266</td>
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<td>Laboratory strain</td>
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<td><strong>Plasmids</strong></td>
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<td>pMIC61(pUCPSK-lasR)</td>
<td>lasR in pUCPSK with lac promoter as a HindIII–EcoRI fragment (5′–3′ lasR)</td>
<td>John Mattick, Institute of Molecular Bioscience, University of Queensland, Australia</td>
</tr>
<tr>
<td>pMIC62(pUCPSK-rhlR)</td>
<td>rhlR in pUCPSK with lac promoter as a HindIII–EcoRI fragment (5′–3′ rhlR)</td>
<td>John Mattick</td>
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<td>pPCS1002</td>
<td>pLP170 containing rhlR-lacZ</td>
<td>Pesci et al. (1997)</td>
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<tr>
<td>pSB224.10A</td>
<td>pRIC380 suicide vector carrying rhlR::Tc</td>
<td>Beatson et al. (2002)</td>
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<td>pVD1</td>
<td>pDN19 containing lasI with its native promoter, Tc′</td>
<td>This study</td>
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<td>pME3853</td>
<td>pME6010 with a 174 bp lasI upstream fragment and translational lasI::lacZ fusion containing the first 13 lasI codons, Tc′</td>
<td>Pesi et al. (2001)</td>
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<td>pUCPSK</td>
<td>E. coli–P. aeruginosa shuttle vector</td>
<td>Watson et al. (1996)</td>
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<tr>
<td>pLJR50</td>
<td>lasBp-lacZ transcriptional reporter fusion; contains nt −190 to +4 of the lasB promoter region, Cb′</td>
<td>Toder et al. (1994)</td>
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Standard methods were used to manipulate DNA. Plasmid pDN19 (Nunn et al., 1990) was used to construct pVD1, containing the lasI gene under its own promoter. A region spanning from 305 bp upstream to 170 bp downstream of the last ORF was amplified and inserted between the XbaI and HindIII sites in the pDN19 multiple cloning site. The gene fragment was generated from genomic DNA using PCR with primers 5′-GCTCTAGATTTTGGGGCTGTGTTCT-TCTC-3′ and 5′-CCCAAGCTTACTCAGAAGTCAGTGCGGAAA-3′. The construction was confirmed by effective complementation of a lasI mutant. Plasmids were introduced by electroporation (Choi et al., 2006).

lasI mutant subcultures were carried out as follows: a first preculture was made at day 1 and used to inoculate fresh medium for day 2; the latter was used to inoculate fresh medium for day 3. Pyocyanin was measured during each day of culture.

β-Galactosidase activity assay. Bacteria containing the gene reporter fusions were routinely grown overnight from frozen stocks in TSB with appropriate antibiotics, then subcultured in triplicate at a starting OD600 of 0.05 without antibiotic. Culture samples were regularly taken for determination of growth (OD600) and β-galactosidase activity (Miller, 1972). N-Butyl-β-D-homoserine lactone (C12-HSL) was purchased from Sigma-Aldrich and the stock solution prepared in acetonitrile.

Quantification of rhamnolipids, pyocyanin, AHLs and HAQs. Detection and measurements were performed by LC/MS. For pyocyanin, AHLs and HAQs, 480 μl culture samples were taken at regular intervals, used for determination of growth (OD600), and mixed with 120 μl acetonitrile containing 50 mg l−1 5,6,7,8-tetradeutero-PQS for a final concentration of 10 mg l−1 as internal standard. After centrifugation, 20 μl aliquots of the supernatants were directly injected for LC separation on an Agilent HP1100 HPLC system equipped with a 3 × 150 mm C8 Luna reverse-phase column (Phenomenex). A 1% acidified water/acetonitrile gradient was used as the mobile phase at a flow rate of 0.4 ml min⁻¹, split to 10% with a Valco Tee. A Quattro II (Waters) triple-quadrupole MS was used for molecule detection. Data acquisition was performed in full scan mode with a scanning range of 130–350 Da. Precise quantification of C₁₂-HSL and 3-oxo-C₁₂-HSL was performed by MS/MS, as described previously (Dzeiel et al., 2005). For rhamnolipid quantification, 500 μl culture samples were taken at regular intervals, used for determination of growth (OD600), and diluted with an equivalent volume of methanol. After centrifugation, 20 μl aliquots of the supernatants were injected for LC/MS analysis as described previously, using 16-hydroxyhexadecanoic acid as internal standard (Dzeiel et al., 1999; Lepine et al., 2002).

Elastase and protease enzymatic assays. TSB plates supplemented with 1% skim milk were inoculated with 10 μl from cultures at OD600 3. Plates were incubated at 37 °C for 3 days. For specific LasB elastolytic activity, we used a protocol adapted from that of Bjorn et al. (1979). Briefly, filter-sterilized culture supernatant samples (100 μl) from late stationary phase cultures were mixed with 5 mg elastin Congo red (Sigma) and 300 μl 0.1 M Tris/HCl pH 7.2. Release of Congo red from degraded elastin was measured as A₄₉₅ after 2 h of incubation at 37 °C followed by centrifugation. For assessment of LasA staphyloytic activity, 4.5 ml of Staphylococcus aureus overnight cultures were boiled for 15 min. and 100 μl was mixed with 300 μl of filtered culture supernatants. The OD₆₀₀ was measured after 2 h of incubation at 37 °C with agitation. All experiments were carried out in triplicate.

RESULTS

The expression of RhlR-regulated factors is only delayed in the absence of LasR

Based on previous observations reporting late pyocyanin production in lasR mutants, we decided to investigate the
mechanism involved in this phenomenon, as an introduction to exploring QS during the stationary phase.

Since RhlR is the known regulator of the *phz* genes, we hypothesized that late pyocyanin production is due to RhlR activity. In the absence of *lasR*, RhlR should activate the expression of the *phz* genes in the late stationary phase, and in its absence, no pyocyanin should be produced. As shown in Fig. 1, unlike the *lasR* mutant, the *lasR rhlR* double mutant does not produce this phenazine at all. Moreover, *lasR*(pUCPSK-*rhlR*), which constitutively expresses *rhlR* from a plasmid, produces pyocyanin at the same time as the wild-type, confirming that RhlR is responsible for the timing of pyocyanin production. As expected, continued expression of *rhlR* results in higher production of pyocyanin. *lasR*(pUCPSK) acts like the *lasR* mutant, confirming that the vector does not influence pyocyanin expression. Finally, *lasR*(pUCPSK*lasR*) does not overproduce pyocyanin, unlike the *lasR* mutant, showing that the *lasR* mutation is responsible for this phenotype. It is also noteworthy that a *lasI* mutant shows the same pyocyanin overproduction phenotype as the *lasR* mutant (data not shown). To ensure that optical density during all growth stages, and particularly during stationary phase, truly reflected the number of living bacterial cells, we also determined the viable cell counts. This showed that the growth rates and survival of the *lasR* mutant and the wild-type were essentially the same (see Supplementary Fig. S1a, available with the online version of this paper), thus confirming that the difference in pyocyanin production is not the result of variations in the number of viable cells.

To ensure that this late pyocyanin production was not due to a spontaneous mutation that might have occurred in the *lasR* background, we subcultured a culture of the *lasR* mutant on three consecutive days in fresh medium, every time monitoring the production of pyocyanin. Consistently, the cultures had to reach the late stationary phase before producing pyocyanin, indicating that this phenotype in not due to accumulation of secondary mutations during cultivation (see Supplementary Fig. S1b).

If RhlR is present and active during the late stationary phase in a *lasR* mutant, then we should be able to detect RhlR-regulated factors other than pyocyanin. The *rhLAB* and *rhlC* genes, coding for enzymes involved in rhamnolipid biosynthesis, and *rhlI*, coding for the C$_4$-HSL synthase, are all directly regulated by RhlR (de Kievit et al., 2002; Medina et al., 2003). We precisely quantified rhamnolipids and C$_4$-HSL in *lasR*, *lasR rhlR* and *lasR*(pUCPSK-*rhlR*) cultures. As shown in Fig. 2(a, b), the *lasR rhlR* double mutant was unable to synthesize rhamnolipids or C$_4$-HSL, while the *lasR* mutant produced these molecules with a delay, essentially in late stationary phase. These results support the hypothesis that expression

![Fig. 2. Expression of RhlR-controlled factors is delayed in a *lasR* mutant. *P. aeruginosa* wild-type and *lasR* mutant containing or not a constitutive *rhlR* expression plasmid (pUCPSK-*rhlR*) are compared. Production of (a) rhamnolipids and (b) C$_4$-HSL.](http://mic.sgmjournals.org)
of the rhl regulon is only delayed in a lasR mutant. The production of C4-HSL and rhamnolipids was restored to levels similar to wild-type when the lasR mutant was transformed with an rhlR expression vector, confirming that RhlR is responsible for these phenotypes. These results show that the delayed expression of RhlR-controlled phenotypes in a lasR background can be restored by expressing rhlR.

In order to obtain additional evidence that RhlR is indeed expressed in a lasR mutant, we evaluated the transcription of rhlR with a lacZ fusion reporter. As shown in Fig. 3, maximal rhlR transcription occurs at the early stationary phase in the wild-type strain. Furthermore, it follows a similar expression pattern in the lasR mutant background, but at lower levels. Still, during late stationary phase, rhlR expression slightly increases in the lasR mutant, while it decreases in the wild-type. These data support the significant presence of RhlR in lasR mutants during late stationary phase, as previously reported (Diggle et al., 2003).

It is well established that the production of proteolytic enzymes such as LasA and LasB, responsible for staphyloytic and elastolytic activities respectively, is under LasR regulation (Rust et al., 1996; Storey et al., 1998; Toder et al., 1991). However, there are indications that production of these enzymes might also be under partial RhlR control (Brint & Ohman, 1995; Diggle et al., 2003; Pearson et al., 1997). To evaluate global protease activity of the strains, we inoculated on solid medium containing skim milk. Protease activity was visible for the lasR mutants while the double mutant was unable to degrade milk proteins (see Supplementary Fig. S2). Since this test only indicates general proteolytic activity, it was interesting to target specific proteases. Fig. 4(a) shows that the lasR mutant is able to activate lasB expression late in stationary phase, while the double lasR rhlR mutant cannot. Detection of LasB activity confirmed these results. During late stationary phase, the lasR mutant shows significant elastolytic activity, which is nearly as high as that in lasR(pUCPSK-rhlR) (Fig. 4b). Finally, Fig. 4(c) shows that the wild-type and the lasR mutant, complemented with rhlR or not, express LasA activity, while the lasR rhlR double mutant does not. Taken together, all these results indicate that the expression of many QS-controlled factors is only delayed when LasR is defective.

**RhlR controls factors generally considered to be solely regulated by LasR**

Another observation we and others have made is that not only pyocyanin but also PQS is produced during late stationary phase by a lasR mutant (Déziel et al., 2004; Diggle et al., 2003). This was unexpected, since the final step in PQS synthesis is catalysed by the lasR-dependent FqsH enzyme (Déziel et al., 2004; Gallagher et al., 2002; Whiteley et al., 1999; Xiao et al., 2006b). It is of note that there is a close correlation between the timing of production of both PQS and pyocyanin in lasR mutant backgrounds (Déziel et al., 2005; Diggle et al., 2002, 2003). To test if RhlR might also be responsible for this effect, we quantified PQS production by the wild-type and the lasR, lasR rhlR and lasR(pUCPSK-rhlR) mutants. As shown in Fig. 5(a), during the exponential and early stationary growth phases, PQS production is totally absent in the double mutant and barely detectable in the lasR mutant unless rhlR is expressed, which leads to a substantial reduction in the delay observed for that mutant. The same reduction of PQS is observed in a lasI mutant, and can also be restored by overexpressing RhlR in that mutant (data not shown). At the late stationary phase, however, the concentration of PQS in lasR mutant cultures is similar to the wild-type, while the double mutant still shows no detectable production. These data explain the late PQS production in a lasR mutant by the activity of RhlR.

We then asked whether lasI, probably the most specific LasR-regulated gene, which codes for the autoinducer synthase producing 3-oxo-C12-HSL, might also be regulated by RhlR. As expected from the above data, we found that 3-oxo-C12-HSL production is greatly increased in lasR(pUCPSK-rhlR) compared to the wild-type strain, at the same optical density (Fig. 5b). It also shows that 3-oxo-C12-HSL is eventually produced in a lasR mutant at late stationary phase, but is totally absent if rhlR is also defective.

![Fig. 3. rhlR transcription in a lasR mutant increases during late stationary phase. β-Galactosidase activity using the pSC1002 vector containing the rhlR-lacZ transcriptional reporter.](image-url)
Fig. 4. LasA and LasB are activated late in a lasR mutant but not in a lasR rhlR double mutant. (a) Transcription of the lasB gene; (b) elastolytic (LasB) activity; (c) staphylolytic (LasA) activity.

Fig. 5. Production of PQS (a) and 3-oxo-C_{12}^– HSL (b) requires rhlR in the absence of lasR. LC/MS analysis from culture supernatants.
RhlR controls lasI in a heterologous system

In order to further identify RhlR as an alternative activator of lasI transcription in the absence of a functional LasR, we constructed a heterologous system in E. coli. A vector (pME3853) carrying the lasI-lacZ gene reporter was introduced into E. coli DH5α. In the presence of the rhlR gene constitutively expressed on another compatible plasmid, and with addition of its autoinducer C4-HSL, β-galactosidase activity was greatly enhanced in the E. coli strain, while only basal expression was detected in absence of rhlR or C4-HSL (Fig. 6a). To confirm 3-oxo-C12-HSL production through activation by RhlR, a vector containing lasI under its native promotor was introduced into E. coli DH5α. 3-Oxo-C12-HSL was detected in this heterologous system only in the presence of both RhlR and its autoinducer C4-HSL (Fig. 6b).

DISCUSSION

P. aeruginosa is an opportunistic pathogen that relies on its impressive ability to coordinate gene expression in order to compete against other species for nutrients or colonization. QS appears essential for this bacterium for competitiveness in clinical or environmental niches. The QS LasR is known to control a wide array of virulence-associated factors, C4-HSL and rhamnolipids. Others might be involved in that production, although no evidence was presented (Diggle et al., 2003). Here we present evidence for the role of the RhlR regulator in the delayed production of virulence factors such as pyocyanin in a lasR mutant, since no evidence can be observed in a lasR rhlR double mutant and production is advanced in a lasR mutant complemented with rhlR.

The activity of RhlR during stationary phase in a lasR mutant was confirmed by the delayed production of other RhlR-controlled factors, C4-HSL and rhamnolipids. Others

Fig. 6. LasI is activated by RhlR in a heterologous E. coli DH5α system in the presence of either or both C2-HSL (5 mg L⁻¹) and rhlR (pUCPSK-rhlR). (a) lasI-lacZ expression (pME3853); (b) 3-oxo-C12-HSL production in the presence of the lasI gene with its native promoter (pVD1).
have noticed the presence of rhamnolipids during this stage. Van Delden et al. (1998) proposed that environmental factor(s) could be responsible for the induction of some virulence factors in a lasR mutant, and that this induction should be mediated by RhlR. In another study, Kohler et al. (2001) reported rhamnolipid production by lasR and lasI mutants. Interestingly, the delayed production of pyocyanin and rhamnolipids in a lasR mutant background observed in our work seems to correlate with the delayed accumulation of C4-HSL and PQS. These signals both positively upregulate the rhl system. Our results provide new evidence that LasR mainly acts as an exponential growth phase activator on several RhlR-dependent factors. The expression of the rhl system is maintained in a lasR mutant

The above results can be explained by the fact that RhlR is expressed in a lasR mutant, as confirmed by a transcriptional rhlR-lacZ reporter, showing reduced but sustained transcription of rhlR. This finding contradicts the prevailing concept that the rhl system is inactive in the absence of a functional LasR (Latifi et al., 1996). However, the available literature on the QS system in P. aeruginosa is largely based on experiments carried out during early growth stages. Indeed, Van Delden et al. (1998) had previously noticed significant rhlR expression in a lasR mutant background during the stationary phase, using the same reporter that we did. Perhaps the lacZ reporter used by Latifi et al. (1996) was less sensitive or a difference in growth conditions modified the response. Nevertheless, our results agree that the rhl system is indeed underexpressed during the exponential and early stationary growth phase in a lasR mutant, but importantly seems to maintain a higher level of activity than in the wild-type during late stationary phase when lasR is absent. Still, our results are in agreement with induction of the rhl system by LasR (Latifi et al., 1996). Most probably, basal rhlR and rhlI transcription leads to the autoinduction of the rhl QS system in a lasR mutant background. It is also possible that environmental conditions are involved in that induction, since factors such as starvation (Van Delden et al., 1998), phosphate and iron (Jensen et al., 2006) have an influence on RhlR activation.

Fig. 7. Proposed model for the influence of RhlR on the las regulon. Basal expression of lasI leads to weak production of 3-oxo-C12-HSL. This signalling molecule binds to some LasR regulators produced due to basal transcription of lasR. Once LasR is bound to its autoinducer, it activates the las regulon, leading to increased lasI transcription and activation of the rhl regulon. Our present work reveals an overlap between the las and rhl regulons where the las system is activated by the RhlR regulator. In the presence of a lasR mutation leading to loss of its function, residual rhlI and rhlR transcriptions, perhaps combined with environmental factors, will allow activation of the rhl regulon, but with a marked delay due to lack of rhlI and rhlR transcriptional activation by LasR. Eventually, when the bacteria reach stationary phase, RhlR is present and functional to activate numerous virulence factors such as pyocyanin, rhamnolipids, proteases and signalling molecules including PQS and 3-oxo-C12-HSL.
RhIR partially controls LasR-specific factors in the absence of a functional LasR regulator

Some LasR-dependent factors can be expressed in the absence of this regulator, RhIR apparently acting as a surrogate activator. Indeed, PQS was detected in late stationary phase of a lasR mutant (Déziel et al., 2005; Diggle et al., 2003). Using a heterologous system, we found that the gene coding for the specific autoinducer synthase of LasR, lasI, is also transcriptionally activated by RhIR, and this is accompanied by the production of the corresponding AHL. It has previously been observed that some activities known to be LasR regulated are also affected by RhIR. Numerous proteolytic enzymes responsible for elastolytic (via the lasB gene) and staphylolytic (via the lasA gene) activities were initially reported to be specifically under the control of LasR (Rust et al., 1996; Storey et al., 1998; Toder et al., 1991), although these activities were also reported to be also partially under RhIR regulation (Brintr & Ohman, 1995; Diggle et al., 2003; Pearson et al., 1997). The absence of a correlation between lasR and lasB transcription in some clinical and environmental P. aeruginosa strains was noted by Cabrol et al. (2003). Our data suggest that this is explained by the additional control of lasB by RhIR.

In agreement with the work presented here, evidence for production of 3-oxo-C12-HSL in some lasR mutants was reported by Sandoz et al. (2007). However, they suggested that this phenotype was due to compensatory mutations, while this is not the case in the present work. Production of 3-oxo-C12-HSL in a lasR mutant would suggest that the bacterium is wasting resources, since no LasR protein is present to be activated by this autoinducer. However, it is known that this molecule also plays a role in P. aeruginosa pathogenicity as a virulence factor inducing inflammation in vivo (Qazi et al., 2006; Shiner et al., 2006; Smith et al., 2002) and accelerates apoptosis in macrophages and neutrophils (Tateda et al., 2003; Vikstrom et al., 2005). N-Acyl-HSLs are also signalling molecules involved in intra- and inter-species communication, which allow P. aeruginosa to compete or collaborate with other bacterial species (Eberl & Tummler, 2004; Juhas et al., 2005; Qazi et al., 2006; Riedel et al., 2001; Shiner et al., 2005; Williams, 2007). Interestingly, another QS regulator, QscR, can bind to 3-oxo-C12-HSL (Ledgham et al., 2003) and requires this signalling molecule to regulate some genes (Lee et al., 2006; Lequette et al., 2006). 3-Oxo-C12-HSL can thus be valuable even in absence of the LasR regulator. PQS production in a lasR mutant is also important, since it allows the activation of the third QS system in P. aeruginosa (Diggle et al., 2006; Xiao et al., 2006a), which affects expression of multiple virulence factors (Calfee et al., 2001; Déziel et al., 2005; Xiao et al., 2006b), with a positive effect on the rhl regulon (Diggle et al., 2003; Jensen et al., 2006; McKnight et al., 2000).

LasR is a direct and indirect regulator of QS-controlled genes

In light of these elements, it appears that at least some of the known LasR-regulated genes are not strictly controlled only by this regulator. Although direct binding of LasR to some promoters such as that from lasB has been reported (Schuster et al., 2004), here we confirm that at least lasA, lasB, pqsH and lasI (Pearson et al., 1997; Pesci et al., 1997; this study) can also be controlled via RhIR, and are activated late in the absence of LasR. Although unique binding sites have been identified in several LasR-regulated promoters (Schuster et al., 2004), it has not been possible to define a single consensus binding site sequence in the promoter of QS-controlled genes, or to differentiate LasR vs RhIR-specific promoters (Anderson et al., 1999; Schuster et al., 2003; Wagner et al., 2003; Whiteley et al., 1999; Whiteley & Greenberg, 2001). Our data suggest that RhIR can efficiently recognize LasR boxes, since RhIR is able to activate some LasR-specific genes.

Finally, considering the fact that 3-oxo-C12-HSL production begins to decrease early and thus does not correlate with lasB transcriptional activation or PQS production, and that LasR is inactive in absence of its autoinducer (Schuster et al., 2004), it is reasonable that other regulators are able to take over and/or supplement LasR in order to express these factors. Since C4-HSL, unlike 3-oxo-C12-HSL, accumulates during growth, it appears that RhIR is active and functional for a much longer period than LasR. RhIR is thus a good candidate to itself activate some LasR-regulated factors.

Finally, it is noteworthy that we have repeated most of the experiments reported here with different P. aeruginosa PA01 strains, leading to the same conclusions. We have therefore no indication that our results are restricted to the PA14 strain.

Spontaneous emergence of lasR mutants during infections would preclude targeting the las system for antivirulence QS therapy

Understanding why supposedly non-virulent mutants might be selected in infected patients is an intriguing question. After quantification of pyocyanin, rhamnolipids and protease activities, our results show that during late stationary phase, a lasR mutant is able to produce at least as much of these virulence factors as the wild-type. This might help to explain the occurrence of such mutants among clinical isolates (Heurlier et al., 2006).

Over the last few years, research has been carried out to identify drugs targeting QS to prevent virulence instead of bacterial survival, in order to circumvent the risks of resistance observed with antibiotic treatments (Hentzer et al., 2002, 2003; Smith et al., 2003; Wu et al., 2004). Until now, these therapies have mostly targeted the las system, because blocking the activity of LasR is thought to inactivate all P. aeruginosa QS. However, we have shown here not only that the rhl system is expressed late in a lasR mutant but also that RhIR is able to overcome the las system when the latter is deficient, by activating specific LasR-controlled functions. This suggests that P. aeruginosa
can circumvent the deficiency of one of its QS systems by allowing the other to take over. This should be taken into account in the light of new therapies directed against QS in *P. aeruginosa*. In this respect, targeting other levels of the QS circuitry, such as PQS/4-quinolone signalling (Lesic et al., 2007) or the RhlR/C4-HSL system, might represent interesting alternatives.

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