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Homeostatic Interplay between Bacterial Cell-Cell Signaling and Iron in Virulence

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Abstract

Pathogenic bacteria use interconnected multi-layered regulatory networks, such as quorum sensing (QS) networks to sense and respond to environmental cues and external and internal bacterial cell signals, and thereby adapt to and exploit target hosts. Despite the many advances that have been made in understanding QS regulation, little is known regarding how these inputs are integrated and processed in the context of multi-layered QS regulatory networks. Here we report the examination of the \textit{Pseudomonas aeruginosa} QS 4-hydroxy-2-alkylquinolines (HAQs) MvfR regulatory network and determination of its interaction with the QS acyl-homoserine-lactone (AHL) RhlR network. The aim of this work was to elucidate paradigmatically the complex relationships between multi-layered regulatory QS circuitries, their signaling molecules, and the environmental cues to which they respond. Our findings revealed positive and negative homeostatic regulatory loops that fine-tune the MvfR regulon via a multi-layered dependent homeostatic regulation of the cell-cell signaling molecules PQS and HHQ, and interplay between these molecules and iron. We discovered that the MvfR regulon component PqsE is a key mediator in orchestrating this homeostatic regulation, and in establishing a connection to the QS \textit{rhlR} system in cooperation with RhlR. Our results show that \textit{P. aeruginosa} modulates the intensity of its virulence response, at least in part, through this multi-layered interplay. Our findings underscore the importance of the homeostatic interplay that balances competition within and between QS systems via cell-cell signaling molecules and environmental cues in the control of virulence gene expression. Elucidation of the fine-tuning of this complex relationship offers novel insights into the regulation of these systems and may inform strategies designed to limit infections caused by \textit{P. aeruginosa} and related human pathogens.


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Introduction

Microbes translate environmental cues to coordinate and modulate gene expression such that they can adapt to different niches and overcome hostile environments. Adaptation and coordination of gene expression is particularly important for pathogenic microorganisms that need to colonize dynamic host environments since their ability to sense and respond to host environmental cues is critical for their survival. In bacteria, modulation and coordination of gene expression are also influenced by population density via the regulated production of small molecules that serve as intricate signals impacting the expression of virulence factor genes. Many studies have addressed the role of quorum sensing (QS) communication networks in virulence where by diffusible intercellular auto-inducers factor and environmental signals bacterial cultures mediate pathogenicity by coordinating the expression of a large array of genes [1,2]. Nevertheless, less is known regarding how environmental cues are translated in the context of QS signaling and how environmental cues and QS are integrated to promote the ability of a pathogen to survive and colonize particular niches within their host environments. The processing and integration of environmental inputs in QS becomes even more complex when a pathogen is able to occupy more than one niche. \textit{Pseudomonas aeruginosa} is a ubiquitous and an extremely versatile Gram-negative bacterium with an astounding ability to survive in many different environments and to infect multiple hosts ranging from amoebas to humans [3]. This pathogen has an extensively studied complex QS communication network that facilitates cross-talk between organisms and impacts many \textit{P. aeruginosa} group-related behaviors including virulence [4, 5, 6, 7, 8, and 9]. There are at least three known QS systems in \textit{P. aeruginosa}: two are dependent on the acyl-homoserine-lactone (AHL) QS transcription factors LasR and RhlR [10] and a third is dependent on the 4-hydroxy-2-alkylquinolines (HAQs) LysR-type transcription factor MvfR [11,12]. MvfR activation is mediated by the cell-cell signaling molecules 4-hydroxy-2-heptylquinoline (HHQ) and 3,4-dihydroxy-2-heptylquinoline (PQS), and leads to the positive regulation of many virulence-related factors, a large number of which are also controlled by the QS signal acyl-homoserine-lactone (AHL)–mediated RhlR and LasR circuitry.

The MvfR pathway is a critical virulence component essential for the full virulence of \textit{P. aeruginosa} in multiple hosts [13,14,15].
Bacterial cells can communicate with one another about their surrounding environment. This information can be in the form of small self-secreted molecules acting as signals to activate or inhibit the expression of genes. *Pseudomonas aeruginosa* is an environmental bacterium that infects diverse organisms from plants to humans. Our results show that this pathogen uses two highly sensitive networks, namely MvfR and LasR/RhlR pathways, to modulate its virulence functions by titrating the concentration of the small molecules HHQ and PQS in a manner that depends upon the presence or absence of iron. Via negative and positive feedback loops, this bacterium processes the signaled information to regulate its virulence functions and homeostatically balance the production of the small molecules required for the activation of the MvfR virulence network. Our study sheds light on paradigmatic complex networks that maintain a homeostatic bacterial virulence response.

and is connected to LasR and RhlR by: (i) the dependence of *mvfR* expression at the early growth stages as a result of positive control by LasR [16], (ii) the conversion of HHQ into PQS controlled by PqsH [17,18] whose expression is mediated by LasR [19,20], and (iii) the negative effects of RhlR on the *pqs* operon [16,21], which is responsible for the synthesis of all HAQs [11,14,19,22,23] including the MvfR ligands HHQ and PQS [12,17,21].

The *Q* S regulons MvfR, LasR and RhlR respond not only to Q S signal molecules but also to environmental signals [24], including host factors [25,26,27,28] and other environmental cues such as phosphate [29], magnesium [30] and iron [31,32,33,34,35]. Iron acquisition is controlled by a large set of *P. aeruginosa* genes activated in response to iron starvation [36,37,38], including two siderophore complexes, pyoverdine and pyochelin [39,40], and several ferric uptake regulators, among them are the general iron uptake regulator Fur, Fur-regulated pyoverdine siderophore-specific extracytoplasmic sigma factor PvdS, several ECF sigma factors, and the AraC regulator PchR, which regulates pyochelin uptake [40]. In low iron conditions, PvdS binds to iron-starvation (IS) boxes to induce the transcription of many genes involved in the iron starvation response [41]. The intricate relationship between QS and iron is exemplified by a series of findings demonstrating that iron starvation induced QS systems [26,32,34] and that the *Q* S regulators MvfR [11], LasR/RhlR [42] and VqsR [31,43,44] were found to be responsible for the induction of many iron response genes. Moreover, MvfR contains an IS box in its promoter [36], and *Q* S production is positively-affected by two Fur-regulated small RNAs, Prf1 and 2 [45]. Adding to the complexity of environmental cues such as iron levels affect QS and how iron is integrated into QS to modulate virulence gene expression is the ability of PQS to bind iron [46], to act as an iron trap molecule [47], and to form a toxic complex against the host [48].

MvfR activation by HHQ and PQS leads to the upregulation of the anthranilic acid (AA)-biosynthetic encoding genes *phaIB*, and *phaA*-E operon [11,12,14] that have a conserved genomic organization in *P. aeruginosa* and in HAQs-producing *Burkholderia* species [49], to produce more HAQs leading to the upregulation of the MvfR-regulon in a positive feedback loop. Although the fifth gene of the *pqs* operon *pqsE* (PA14_51380), which encodes a predicted GloB, Zn-dependent hydrolase [50] and member of the metallo-beta-lactamase super family (Piam PF00753), is not required for HAQ synthesis [12,19], it is co-regulated together with the *pqsA-D* genes. We have shown that PqsE is essential for complete *P. aeruginosa* virulence in mice because it controls the expression of a number of MvfR regulon-dependent genes [11]. Although PqsE was previously implicated as the PQS response gene [19,20], it was recently shown to act independently of MvfR and PQS [51]. Thus, the PqsE functions associated with the integration and translation of the QS cell-cell signals has yet to be resolved.

Here we examine the interplay between environmental cues and cell-cell signaling molecules and assess how they are integrated in the modulation of MvfR regulon gene expression. To elucidate the QS multi-layered regulation, we also examine the functional dependency of the MvfR regulon components, especially PqsE, and PQS and HHQ, on the Rhl regulon. The findings presented offer new insights into the highly complex *P. aeruginosa* virulence-associated regulatory loops that may aid in understanding and controlling its pathogenicity.

### Results

**Dissection of the QS MvfR regulon reveals a key component functioning independently of the cell-cell signaling molecules PQS and HHQ**

To elucidate how multi-layered regulatory networks sense and respond to external and internal cell signals to modulate gene expression, we studied the role of MvfR pathway components in integrating and translating signals from PQS and HHQ in the activation of the MvfR regulon genes. To this end, we measured pyocyanin production as an index. This secreted *P. aeruginosa* phenezine was chosen since its production is dependent on the MvfR pathway components, including the cell-cell signaling molecules, PQS and HHQ, and their corresponding biosynthetic enzymes PqsA-D, their AA precursor, PqsE, and on its Phz biosynthetic operons (Figure 1A and [11]). Here we found that overexpression of PqsE under a constitutive promoter (pDN19*pqsE*) in *pqsA- and mvfR* mutant cells not producing HAQs restored pyocyanin production (Figure 1A). In contrast, overexpression of *mvfR* under a constitutive promoter in a *pqsE*-background did not restore pyocyanin production (Figure 1A even when HHQ, PQS, or PA14 cell-free supernatants were added (data not shown). These results highlight the crucial role of PqsE in the regulation of MvfR regulon-dependent factors and demonstrate that PqsE possesses activation properties that are independent of HAQ-mediated signals (Table S1). To assess PqsE mode of action on pyocyanin production, we co-cultured *pqsE*-cells constitutively expressing the phenazine biosynthetic operon *phzA2-G2* with *pqsE*-cells harboring the *phzM* and *phzS* genes essential to pyocyanin synthesis [52] and assessed pyocyanin production. As shown in Figure 1B, approximately 60% of the pyocyanin production was restored, indicating that PqsE participated in pyocyanin production regulation rather than in its synthesis.

Second, we tested whether the precursor of all HAQs, AA was required for PqsE function instead. To this end we used a triple mutant strain deficient in *phaIB*, *topE* and *synBU* (AA* mutant) unable to produce any AA since all three AA synthesis pathways were knocked out [53]. Expression of PqsE in this triple mutant also resulted in high levels of pyocyanin production (Figure 1A) corroborating with the above results and demonstrating that PqsE function did not require AA or any of its derivatives to promote production of the MvfR regulon-dependent factor pyocyanin.

Third, since PqsE controlled the regulation of one of the key MvfR-regulated factors, pyocyanin, we sought to define the impact...
of this factor in the regulation of all MvfR-dependent virulence genes. We carried out whole genome expression studies and compared the expression profiles of a pqsE mutant to those of the PA14 parental strain, an mvfR mutant and to those of PA14 and an mvfR over-expressing pqsE strain (NCBI GEO, accession number #GSE17147). These results showed that PqsE profoundly affected the expression of 90% of the MvfR-regulated genes, including at least thirty-six known and predicted transcription factors (Tables S1B and S2). Of the PqsE-dependent genes, 241 were found to be negatively regulated and 384 positively regulated.
by PqsE (Table S1). At least 75 positively-regulated genes encoded for putative or known virulence factors (Table S1) [11,42]. Importantly, included among the positively-regulated virulence transcriptional factors was the QS AHL regulator rhlR [38] and iron response genes, including the iron starvation sigma factor pvdS and genes involved in the synthesis of the siderophore complex pyochelin (Table S3A).

To confirm that PqsE overexpression also restores virulence functions apart from restoring their expression independently of the signaling molecules PQS and HHQ, we used two assays. The first is based on the observation that virulent P. aeruginosa strains; including PA14 kill yeast [54,55,56]; and the second is based on that P. aeruginosa can infect and kill Drosophila melanogaster [57,58,59], and that pqsE mutant cells exhibit attenuated virulence in flies [57]. As illustrated in Figure 1C–D, a zone of yeast growth inhibition was observed around PA14, but not around the pqsE− or pqsE− mutants following plating of C. neoformans KN99a 5 mm from the bacterial colony on a YPD plate (Figure 1D). The killing zone was restored following PqsE overexpression in pqsE− backgrounds (Figure 1C–D). In agreement flies infected with pqsA− or pqsE− mutants cells exhibited significant delayed in mortality compared to that caused by the WT or the pqsE− cells expressing pqsE (Figure 1E) demonstrating again that PqsE is crucial for P. aeruginosa pathogenicity and independent of PQS and HHQ.

MvfR-dependent gene regulation relies on the functional cooperation between RhlR and PqsE

Comparison of the pqsE transcriptome (Table S1) to lasR/rhlR [42] revealed that almost half (46%) of the genes regulated by LasR/RhlR were also regulated by PqsE (Figure S3A) indicating a relationship between AHL- and MvfR-mediated QS regulons. This relationship is also extended to the negative effects that both components have on the transcription of the pqs operon ([16] and Table S1 and Figure 2A). A green fluorescent protein (GFP) reporter gene [32] fused to the pqs operon promoter (Figures 2B), quantitative PCR analysis (Figure S2D) and quantification of HHQ and PQS levels (Figure 2C) further validated the above finding. Moreover, in agreement, Figure 2D shows that HAQ synthesis down-regulation paralleled the accumulation of AA (HAQ precursor) followed by an increase in amyB gene expression that encodes enzymes for AA degradation (Table S1).

To determine whether there was indeed a functional relationship between the respective communication-systems components RhlR and PqsE in the regulation of the MvfR regulon signal production and whether they together affected signal integration, we proceeded to assess whether there was a RhlR-PqsE codependency in the negative regulation of HAQ biosynthesis. Figures 3A and S4B show that overexpression of PqsE in a rhlR− mutant did not result in a downregulation of the promoter-derived expression of the pqs operon in contrast to the overexpression of PqsE in the wild-type (WT) strain PA14 where expression of the pqs operon was downregulated (Figure 2 and Figure S2D). These results indicate that PqsE negative control of the activity of the MvfR regulon depends on RhlR.

Second, we examined whether there was an RhlR-PqsE codependency in signal integration by MvfR-regulon virulence genes downstream of PqsE. To this end, we assessed whether PqsE overproduction in rhlR− cells could restore pyocyanin production since it was completely abolished in both pqsE− [11,19] and rhlR− [38] mutants. Figure 3B shows that PqsE did not restore pyocyanin production in rhlR− while RhlR expression partially (~30%)...
restored pyocyanin production in \( pqsE^- \) mutant cells. This finding suggests that \( PqsE \) also depends on \( RhlR \) in the positive regulation of pyocyanin production and that \( RhlR \) acts downstream of \( PqsE \). Interestingly, Figure S3 shows that pyoverdine levels are higher in \( RhlR^- \) than in PA14 but not in \( pqsE^- \) mutant cells. Moreover, \( PqsE \) or \( RhlR \) overproduction in \( rhlR^- \) or \( pqsE^- \) mutant cells respectively did not fully downregulated pyoverdine production, while \( PqsE \) or \( RhlR \) overproduction in the corresponding mutant cells did (Figure S3). This finding suggests \( RhlR-PqsE \) codependency in the homeostatic regulation of pyoverdine.

Based on the above findings, it is likely that the \( PqsE-RhlR \) activities were not limited to controlling downstream genes associated only with pyocyanin or pyoverdine production if the high number of genes co-regulated by \( PqsE \) and the Las/Rhl system are considered (Figure S3A). This finding suggests \( RhlR-PqsE \) co-dependency in the homeostatic regulation of pyoverdine.

Signal integration studies reveal a homeostatic negative feedback regulation by HHQ and PQS on cell-cell signaling and \( PqsE \)-controlled genes, respectively

The pyocyanin levels produced by the non-HAQs producing mutants \( pqsA^- \), \( msfR^- \) and \( AA^- \) [12,19,22,53] overexpressing \( pqsE \) were higher than the levels produced by the HAQs-producing PA14 parental strain carrying the same plasmid (Figure 1A). This difference raised the question regarding whether the presence and/or levels of HAQs had dose-dependent negative effects on pyocyanin levels. To this end we assessed the effect of exogenously-added HAQs on pyocyanin levels by using 20 mg/L of PQS or HHQ, a concentration corresponding to the approximate maximal physiologic levels reached by PA14 or HHQ, respectively at stationary phase ([17] and Figure S4A). Figure 4A shows that the pyocyanin levels in either \( pqsA::pqsH \) or \( msfR^- \) mutants overexpressing \( pqsE \) were significantly lower in the presence of either HHQ or PQS. Figure 4B shows that PQS concentrations (up to 1 mg/L) induced pyocyanin production in both \( pqsH^- \) and \( pqsA^-::pqsH^- \) cells but concentrations >1 mg/L decreased pyocyanin production in a dose-dependent manner in all strains tested (Figure 4B) without significantly affecting cell growth (data not shown). This concentration-dependent decrease in pyocyanin levels was independent of \( PqsE \) function and \( phz \) operon regulation since it was also observed in \( pqsE^- \) cells constitutively expressing \( phz \) genes (Figure 4C). The PQS-mediated down-regulation was not specific to PA14 cells as it was also observed in the PA01 \( P. aeruginosa \) strain (Figure 4C).

To determine whether high physiological levels of PQS and/or HHQ negatively-impact \( pqsA \) operon gene expression, we conducted experiments using \( pqsA::pqsH^- \) cells harboring the \( pqsA-GFP \) (ASV) reporter gene. Figure 4D shows that 20 mg/L HHQ negatively-impacted \( pqsA \) gene expression compared to 10 mg/L. \( PqsA \) gene expression was not affected by any of the PQS concentrations tested. Interestingly, a negative effect on \( pqsA \) gene expression, similar to that observed following treatment with 20 mg/L HHQ, was also observed when the two HAQs were added together in sub-inhibitory concentrations (1 mg/L PQS +10 mg/L of HHQ). This result is indicating that together HHQ and PQS have synergistic inhibitory effect and implying also that high activation of the \( pqsA \) operon led to its down-regulation.

To further elucidate the role of PQS on \( PqsE \)-dependent gene regulation, we compared the transcriptional profiles of \( msfR^- \) mutant cells overexpressing \( PqsE \) in the absence or presence of 20 mg/L PQS (Table S1). High PQS concentrations negatively affected the expression of 191 of 625 (31%) \( PqsE \)-regulated genes (Figure 4E and Table S1). This effect was more apparent among the known and putative virulence factors where the expression of 64% of the \( PqsE \)-regulated genes, (including chitinase, halovibrin, cellulase, pyocins, lectin, and elastase genes) was significantly reduced by more than 2-fold upon PQS addition (Table S1). The addition of PQS further increased the expression of only 7 genes; \( fbdA \), the major pyoverdine receptor; \( gatA \), a Glu-tRNA amidotransferase subunit C; \( sucA \), a 2-oxoglutarate dehydrogenase; \( bkdA \), a 2-oxoisovalerate dehydrogenase and of three hypothetical proteins; \( PA642 \), \( PA1343 \) and \( PA2405 \) (Table S1). Interestingly, transcription of \( phz \) operon genes was not modified by the addition of PQS although pyocyanin

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**Figure 3.** MvfR network regulation requires finely tuned cooperation between the MvfR component \( PqsE \) and the AHL QS regulator \( RhlR \). (A) The expression of \( pqsA \) was determined by measuring GFP emission. A \( pqsA-GFP \) (ASV) fusion in the \( rhlR \) mutant harboring pDN19pqsE was used to determine \( pqsA \) expression levels. (B) Pyocyanin levels were measured from various PA14 mutants harboring either pDN19pqsE or pUCP20rhlR plasmids. Empty vector served as control.

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production was affected (Figure 4A), suggesting that PQS may be acting post-transcriptionally in this case.

Homeostatic feedback modulation of the MvfR regulon is fine-tuned by an iron starvation response

As shown in Table S3A, PqsE positively affected the expression of 43 iron starvation-related genes [36,37] including the iron starvation sigma factor PvdS [41,60], the pyochelin regulator PchR [61], pqsR [31,62] and PA2384 [63]. Interestingly, PqsE negatively regulated only 6 iron related genes, bfrB and the siderophore pyoverdine associated genes pvdA, pvdF, pvdJ, pvdN and pvdQ (Table S3A) reflected also in the pyoverdine levels (Figure S5). It is noteworthy that PqsE acted differentially on the siderophores, serving as a positive regulator of pyochelin and a negative regulator of pyoverdine (Figure S5). In addition, Table...
S3A reveal that HAQs are also involved in the control of iron-related genes by PqsE since constitutive expression of pqsE triggered this effect in the mvfR<sup>+</sup> background cells lacking HAQs but not in PA14 cells.

To examine how iron starvation is translated in the context of MvfR signaling, we first examined whether there is a relationship between iron starvation and the regulation of PQS and MvfR regulon genes. We compared pqsA transcription using a pqsA-GFP (ASV) reporter in PA14 cells grown in the absence (D-TSB medium) or presence of high iron levels. Figure 5A demonstrates that iron significantly reduced pqsA transcription. Subsequently, we examined the effect of iron directly on the induction of pqs operon transcription in presence of PQS and not of other HAQs in pqsA<sup>A</sup> pqsH<sup>A</sup> mutant cells. Using 1 mg/L PQS, an amount sufficient to fully induce pqs operon transcription and increasing concentrations of FeCl<sub>3</sub> Figure 5B shows an iron concentration-dependent effect on pqsA gene expression.

We next examined if iron could also counterbalance the downstream effects of PQS on PqsE-dependent genes by assessing the effect of HAQs and iron on pyocyanin production. Figure 5C shows that the addition of iron abolished the reduction in pyocyanin production conferred by PQS (20 mg/L) and restored pyocyanin production to that observed in the presence of 1 mg/L PQS. A similar effect was observed in PA14 cells and pqsA<sup>A</sup> pqsH<sup>A</sup> cells overexpressing PqsE (Figure S6A) where the addition of 20 mg/L PQS decreased pyocyanin levels which were restored in the presence of iron. Since iron alone did not affect pyocyanin production in the experimental conditions used, it suggested that pyocyanin production was affected due to direct effect of iron on PQS. No significant difference in growth was observed between PA14 cells grown in absence or presence of various concentrations of iron (up to 250 μM, Figure S6B). Collectively, these findings indicate that iron counterbalanced PQS-dependent regulation by ‘fine-tuning’ its activity, possibly by reducing PQS activity when it is in a complex with it.

**Discussion**

In this work, we delineated paradigmatically the complex relationships between bacterial multi-layered regulatory QS circuitries, their signaling molecules, and the environmental cues to which they respond.

**Figure 5. Homeostatic interplay between PQS and iron: Iron fine-tunes PQS activities.** The effect of iron on MvfR induction was tested using the pqsA-GFP reporter in PA14 (A) and PA14 pqsA<sup>A</sup> pqsH<sup>A</sup> cells treated with PQS (1 mg/L) (B). The effect of iron on pyocyanin production was tested when PQS was supplied at 1 mg/L or 20 mg/L (C). The cells were grown in low iron medium D-TSB or in media supplemented with iron (FeCl<sub>3</sub> or FeSO<sub>4</sub>, 200 μM). Asterisks show samples that are statistically significant different (P value<0.05) from the PQS 1 mg/L treated sample. doi:10.1371/journal.ppat.1000810.g005
The intracellular communication system of *P. aeruginosa* possesses complex signal transduction systems allowing this versatile pathogen to regulate and coordinate virulence functions in the context of multiple hosts, environments, and competition from other microorganisms [7,64,65,66]. Here we showed that one of these complex signal transduction systems, MvIR, responds to both positive and negative feedback loops that are interconnected with the RhlR QS complex system and that these interactions fine tune the production and concentration of secreted output signals that in turn serve as inputs to preserve a homeostatic regulation. Moreover, our experiments demonstrated that via the finely tuned cooperation and homeostatic interplay between the MvIR circuitry components PqsE, and PQS and HHQ with RhlR and iron, this pathogen governs and balances the intensity of its virulence response.

Although HHQ and PQS principally serve as MvIR ligands [17,18], our results show that once maximal in vitro physiological levels are reached, they negatively impact their own production and the downstream PqsE regulated genes. PqsE, HHQ and PQS are essential molecules in the negative feedback auto-regulatory loops that contribute to this homeostatic regulation. Although the HHQ concentrations shown here are not attained in vitro because HHQ is fully converted into PQS, this effect is most likely relevant in vivo where we have shown that HHQ levels are higher than those of PQS [17]. In addition, in lasR− mutants that accumulated during chronic infections HHQ levels are also higher than PQS since PqsH responsible for the conversion of HHQ to PQS is under the control of LasR [67]. Nevertheless, we show that HHQ and PqsE have together synergistic effects as a negative auto-regulators that down-regulated pqs operon transcription, reducing their own production and that of the other HAQs. Thus, jointly with PqsE, PQS and HHQ most probably contributed to the down-regulation of the pqs and phz operons observed during the late growth phase of *P. aeruginosa* (Figure S1).

In addition to being activator and auto-down-regulator PQS acted also as a homeostatic agent at high physiological concentrations by down-regulating most PqsE-dependent, downstream genes. Consistently, maximum pyocyanin production occurred only at low PQS concentrations that were sufficient to maximally activate the pqs operon. The homeostatic effect of PQS downstream of the Pqse genes was clearly independent of MvIR, PqsE and of other HAQs given that its effects were still apparent in pqsA− and msvR− backgrounds. Interestingly, this effect appeared also to be post-transcriptional since PQS did not significantly impact phz operon transcription but affected pyocyanin production even when the *phz* operon was constitutively expressed. The mechanism behind this effect remains to be discovered. One intriguing possibility may be that PQS exerts its effect via RsmA and/or on small RNAs like rsmZ or prfE.

Previous studies have suggested that while PqsE is the PQS response protein [19,20], it does not influence PQS production [11,12]. Here we show that PqsE is a crucial player in orchestrating the homeostatic regulation of the signaling molecules HHQ and PQS as well as establishing a connection to the QS RhlR system, underscoring it as a key mediator of MvIR regulon activation and cooperation with the AHL QS system. Our findings also provide initial answers as to why PqsE, although not involved in the synthesis of HAQs in vivo or in vitro [11,19,20], is tightly regulated together with the other *pqs* operon genes. Although our findings are primarily based on trans-regulatory studies, the overexpression of PqsE demonstrated for the first time that PqsE can impact HAQs concentrations by down-regulating their production. In corroboration, are both the AA accumulation and the transcriptional induction of the *antiABC* genes responsible for AA degradation [68,69] and shown to be regulated by *prrF1* and *prrF2* [43]. Since *pqsE* is co-transcribed by MvIR together with *pqsA-D* genes, the reduced production of HAQs mediated by PqsE indicates that *pqsE* gene transcription itself is also downregulated in a negative feedback mechanism that finely balances the regulatory loop.

Although PQS and HHQ signal molecules are critical to MvIR-dependent gene expression, their addition has failed to rescue *pqsE* mutant cells to activate expression of many MvIR-regulated genes or to produce of pyocyanin [11,17,19,20]. Here we found that overexpression of PqsE induced pyocyanin production and transcription of an additional approximately 600 MvIR-regulated genes independently of MvIR, HAQs and AA, demonstrating the crucial role of PqsE in activating MvIR regulon genes independently of the HAQs. Ultimately, expression of PqsE in an *msvR*− or *pqsA*− strain restored *P. aeruginosa* virulence as determined by growth inhibition of yeast and flies feeding assay, indicating that PqsE did not need HAQs to confer virulence in these systems. Corroboratory results were reported by Farrow et al. [51] who showed in a qualitative manner that expression of PqsE in an *msvR*− mutant restored pyocyanin production. These results together indicate that, at least with regard to the genes listed in Table S1, PQS and HHQ only act as inducers of MvIR to express PqsE, that once expressed induces the *P. aeruginosa* virulence response without HAQs or MvIR. Thus, PqsE cannot be designated as the “quinolone signal response protein”. Nevertheless, it is not yet known how PqsE, a protein that belongs to the metallo-beta-lactamase super family without any known DNA binding motifs, regulates the transcription of so many genes. Its predicted hydrolase activity suggests that it may cleave or participate in the synthesis of small molecules. Due to the location of the *pqsE* gene in the *pqs* operon, the immediate candidates likely targeted by PqsE are HAQs. However following extensive LC/MS analyses, we were unable to detect any molecule that accumulated or diminished in concentration in *pqsE*− cultures compared to WT cultures (data not shown). In addition we were unable to complement pyocyanin production in a *pqsE*− culture by exogenously adding HAQs, AHLs or whole PA14 supernatants ([11] and data not shown). Nonetheless, collectively, our results indicate that PqsE is involved in a negative feedback loop that affects the regulation and integration of HAQs-mediated cell-cell signaling molecules and that is functionally dependent on RhlR. The exact nature of the co-dependency between PqsE and RhlR remains unclear. The downregulation of *rhlR* expression by ∼2 fold in a *pqsE* mutant is not sufficient to explain the striking transcriptional and phenotypic effects mediated by PqsE. Since PqsE is not predicted to be a transcriptional factor [50] it is highly likely that it may exert its effect on RhlR post-transcriptionally, and this effect may be perhaps extended to other transcriptional factors.

The MvIR affected gene list has a substantial overlap [11] with the previously published list of Rhl/Las-controlled genes [42], and the expression of almost all MvIR-regulated genes controlled by PqsE. Both PqsE activities (i.e., fine-tuning HAQs production by down-regulating the *pqs* operon, induction of pyocyanin production and downregulation of pyoverdine production) were dependent on RhlR apparently acting downstream but in a tight collaboration with PqsE. Recently, Farrow and colleagues showed that the addition of AHL C12-HSL (a RhlR inducer) to PAO1 *pqsE*− isogenic mutants also restored pyocyanin production [51]. These findings, although we did not reproduce them in PA14 cells, are in agreement with our findings that PqsE and RhlR functions are linked. However, the exact relationship between PqsE and RhlR, that is when or how they cooperate, remains elusive since
RhIR in some cases functions in the absence of PqsE; for example, the RhIR-dependent C4-HSL levels in a pqsE mutant strain were identical to the parental strain (data not shown) as also was OD600 nm. For low iron media the bacteria were grown in D-TSB with sub-cloning and plasmid propagation. The E. coli S17-1 strain was used for conjugation between E. coli and P. aeruginosa by the pEX18Ap-derivative allelic replacement method [75]. Antibiotics used included ampicillin (Amp) (100 μg/ml), carbenicillin (Crb) (300 μg/ml), gentamycin (Gnt) (15/60 μg/ml), kanamycin ((Kan), 50/200), tetracycline (Tet) (15/200 μg/ml) and chloramphenicol (Cam) (15/50 μg/ml) for E. coli and P. aeruginosa respectively.

DNA manipulations

The plasmid overexpressing PqsE was generated by PCR amplification of the pqsE gene from PA14 genomic DNA using primer pairs GX119 and GX120 (Table S4). The PCR product was digested with HindIII/Xbal and sub-cloned into the pDN19 plasmid vector under the puc promoter to generate pDN19pqsE that constitutively expresses pqsE. Construct integrity was confirmed by DNA sequencing. Plasmids were introduced into E. coli or P. aeruginosa PA14 by electroporation. Non polar deletions were generated by pEX18AP allelic replacement using sucrase selection. Fragments with the size of about 1 kb flanking the desired genes were cloned into the pEX18Ap plasmid vector and introduced into E. coli by electroporation followed by conjugation to P. aeruginosa. Alternatively, the I-Red recombinase method was used to generate chromosomal deletions or insertions [53].

Materials and Methods

Bacterial strains, growth conditions, and plasmids

Table S4 lists bacterial strains and plasmids used in this study. P. aeruginosa were routinely grown in Luria Bertani (LB) broth at 37°C for 18 h, and diluted to OD600 nm 0.05 and grown to the desired OD600 nm. For low iron media the bacteria were grown in D-TSB medium [36] that was treated with Chelex 100 beads (Bio-Rad, Hercules, CA) and for high iron FeCl3 or FeSO4 were added at concentrations of 200 μM. The E. coli M1109 strain was used for sub-cloning and plasmid propagation. The E. coli S17-1 strain was used for conjugation between E. coli and P. aeruginosa by the pEX18Ap-derivative allelic replacement method [75]. Antibiotics used included ampicillin (Amp) (100 μg/ml), carbenicillin (Crb) (300 μg/ml), gentamycin (Gnt) (15/60 μg/ml), kanamycin ((Kan), 50/200), tetracycline (Tet) (15/200 μg/ml) and chloramphenicol (Cam) (15/50 μg/ml) for E. coli and P. aeruginosa respectively.

Environmental and QS Cooperation

The existence of a tight interconnection between iron concentrations, QS, and virulence in P. aeruginosa is likely due to iron conditions encountered in vivo [71,72] serving as a signal indicating a hostile environment requiring expression of virulence or fitness-related genes. When host tissues become damaged as a consequence of virulence factor production, the resulting increase in iron concentrations should down-regulate virulence factor concentrations, thereby reducing bacterial virulence that may favor host survival and potentially chronic infection.

A complete understanding of the regulation of the multiple P. aeruginosa virulence networks, in particular the mechanisms of the homeostatic and down-regulation processes (Figure 6), will be essential for the development of drugs targeting QS inhibition [73,74]. The findings presented in this study may aid in the design of anti-infective therapies tailored to interfere with virulence pathways and provide a paradigm for understanding the complex QS networks of other bacterial pathogens besides that of P. aeruginosa.

 Reporter genes

Two kinds of reporter genes were used: 1) translational and transcriptional fusions to lacZ where the β-galactosidase activity assay was performed in triplicate as described [76]; and 2) a pqsA-GFP (ASV) fusion consisting of a pqsA promoter upstream to a short-lived GFP that allows for the detection of pqs operon up or down regulation carried on the plasmid pAC37 [32]. Overnight cultures were diluted to an OD600 nm of 0.05 in black, clear bottom sterile 96-well assay plates (Corning Inc., Corning, NY). The plates were incubated for 50 h at 37°C in an Infinite F200 plate reader (Tecan Group Ltd, Mannedorf, Switzerland). Every 30 min the plates were shaken for 2 min and read at 600 nm and fluorescence detected by excitation at 485 nm and emission at 535 nm. The results are expressed as an average of 3-6 observations that were normalized to a strain that did not carry the plasmid pAC37.

RNA isolation, generation and analysis of transcriptome data

Bacteria were respectively grown overnight at 37°C, diluted to an OD600 nm of 0.05 in 25 ml LB with the corresponding antibiotics at 37°C until the OD600 nm reached 3.0. The total RNA was isolated with the RNeasy Mini kit (QIAGEN Inc., Valencia, CA) and cDNA synthesis and labeling performed according to the manufacturer’s instructions (Affymetrix, Santa Clara, CA). The P. aeruginosa PAO1 GeneChip® Genome array (Affymetrix) was used for hybridization, staining, washing and scanning according to the manufacturer’s instructions. Experiments were independently performed in triplicate. Affymetrix DAT files were processed using the Affymetrix Gene Chip Operating System (GCOS) to create .cel files. The raw intensity .cel files were normalized by robust multi-chip analysis (RMA) (Bioconductor release 1.7) with PM-only models. Array quality control metrics generated by the Affymetrix Microarray Suite 5.0 were used to assess hybridization quality. Normalized expression values were analyzed with SAM (Significance Analysis of Microarray) using the permuted unpaired two-class test. Genes...
whose transcript levels exhibited either a 2-fold or up or down regulation and had a q value $<6\%$ were further analyzed. The results of the GeneChip® arrays were imported to GeneSpring 7.3 (Agilent Technologies, Inc., Palo Alto, CA) and the expression signals of the GeneChip® arrays were normalized to the constant value of 1.0 and the ratio cut-off was set to 2-fold. Annotations were performed using the database http://pseudomonas.com/.

The transcriptome results were (in part) validated by assessing b-HAQs Iron Starvation box MvfR regulon genes siderophores AA Synthesis HAQs PQS Low Synthesis HAQs PQS

Figure 6. Schematic of the positive and negative homeostatic interplay among the MvfR regulon components PqsE, and PQS and HHQ with RhlR and iron. PqsE (green), HHQ and PQS (blue) and iron (red) play a dual role in up- or down-regulating the MvfR regulon. The outcome—that is the level of downstream gene expression translated into the bacterial virulence response—is the integrated sum of these interactions. Positive loops (thin lines): (1) MvfR is induced by HHQ and its derivative PQS to express phn and pqs operons, which are in turn (2) responsible for the synthesis of HAQs. PqsE is not required for HAQ synthesis and does not need AA or its derivatives for its "bottleneck" function, (3) controlling the expression of many virulence factors in cooperation with the AHL regulator RhlR. (4) PqsE also controls many iron starvation response genes, such as PvdS and siderophores. (5) PvdS in turn up-regulates the transcription of mvfR via an iron starvation box. (6) Low iron conditions also contribute to the induction of PvdS and other iron-related regulators to activate the iron response including (7) uptake of iron into the cell by siderophores as well as (8) induction of the virulence response. Negative loops (thick lines): (9) PqsE in cooperation with RhlR down-regulates the expression of the phn and pqs operons, thus reducing HAQ production. When a threshold concentration of HHQ is reached, (10) HHQ down-regulates the pqs operon. (11) PQS at high physiological levels in turn counterbalances the expression of PqsE-controlled genes, including many virulence factors. High levels of iron in presence of low levels of PQS, reduce P. aeruginosa virulence, at least in part, by (12) binding and inactivating PQS. In contrast, when PQS is at high physiological levels its inactivation by iron will increase virulence by reducing the negative PQS counterbalance and thus sustain the positive loops that include (13) iron starvation as a result of PQS trapping iron. (14) The integration of these processes enforces a fine-tuning of MvfR regulon gene expression levels, therefore determining the magnitude of virulence.

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galactosidase expression and RT-PCR of selected genes (Figure S2). The data are deposited in NCBI GEO with accession number GSE17147.

**Quantitative real-time RT-PCR**

Cells from each triplicate experiment were harvested at an OD_{600 nm} of 2, 3 and 4. Total RNA was subsequently isolated using the RiboPure-Bacteria RNA Isolation kit (Ambion, Austin, TX) according to the manufacturer’s instructions. cDNAs were synthesized with random reverse primers using the Reverse Transcription RETROscript kit (Ambion) according to the manufacturer’s instructions. Specific primers (Table S4) for the amplification of products of approximately 200 base pairs were designed using the Primer3 algorithm (http://frodo.wi.mit.edu/primer3/) and analyzed by In Silico simulation of PCR amplifications (http://insilico.ehu.es/) and by the Primer Analysis Software NetPrimer (Premier Biosoft International, http://www.premierbiosoft.com/netprimer/index.html) for the detection of expressed pqsA, pqsE and rpoD that served as the normalizer genes [77]. Quantitative RT-PCR was carried out using the Brilliant II SYBR Green QPCR Master Mix (Stratagene) with a RT Fluorescence Detection System MX3005P (Stratagene, La Jolla, CA) in a 25 μl final volume. The efficiency of each pair of primers was determined by a standard curve of 8 dilutions of 1:4 of PA14 genomic DNA. The relative expression ratios were calculated and analyzed using MXPro analysis software, version 4.01 (Stratagene) using a mathematical model that included an efficiency correction. The fold induction of mRNA was determined from the threshold values that were first normalized to the WT strain harboring the pDN19 plasmid at OD_{600 nm} of 2 that served as the calibrator. The data are expressed as the average of triplicate samples.

**HAQs detection**

The quantification of HAQs concentration in bacterial culture supernatants and in vivo from rectus abdominis muscle of burned and infected mice was performed by LC/MS as described previously [17,78]. The HAQs were separated on a C18 reverse-phase column connected to a mass spectrometer using a water/acetonitrile gradient [78]. Positive electrospray in the MRM mode with 2×10^{-5} mTorr argon and 30 V as the collision gas were employed to quantify HAQs using the ion transitions HHQ 244>159, HHQ-D4 246>163, HQNO 260>159, PQS 260>175, and PQS-D4 264>179. The pseudomolecular ions of each compound were monitored in full scan mode using the unsaturated PA14 HAQs response factors.

**Pyocyanin production assay**

Samples of 5 ml were spun down and the supernatants mixed with equal volumes of chloroform. The lower blue phase was collected and its OD_{520 nm} was measured. The concentration of pyocyanin was determined by the formula: mg/L = OD_{520 nm}×17.072 normalized to cell counts and the statistical significance was assessed using the Student’s 2 tailed t-test assuming equal variance [79]. In order to assess the production of pyocyanin by expression of the plc genes we used a co-culture of cells harboring the pUCP-2AG2 and pUCP-MS plasmids [80]. All experiments were performed in triplicate.

**Pyoverdine production detection**

D-TSB medium was used to grow 200 μl of bacterial cells in 96 wells plate. Production of pyoverdine was assessed using a plate reader ( Infinite F200, Tecan Group Ltd, Mannedorf, Switzerland). Pyoverdine levels were determined every 30 minutes using excitation at 400 nm and emission at 460 nm and the values obtained were normalized to cell growth ( OD_{600 nm} ). Pyoverdine concentrations were calculated using a calibration curve of fluorescence of a range of concentrations of pyoverdine (Sigma Aldrich, US).

**Yeast killing assay**

Yeast (Cryptococcus neoformans KN99 α, Candida albicans ATCC #90028 DAY185 strain or Saccharomyces cerevisiae YJM310 strain) were plated for 2 days on YPD agar (Difco) plates at 30°C. A colony was picked and grown for 18 h in liquid YPD media (Difco) at 30°C with shaking (200 rpm). The yeast was diluted 1:100 in 4 ml soft YPD agar (0.6% agar) and poured onto an YPD plate that was dried for 30 min in a laminar flow hood. A 1 μl drop of an overnight culture of the desired bacterial strain was put on top of the yeast lawn and the plate incubated for 2–3 days at 30°C. A dead yeast zone was formed around a by PA14 bacterial colony but not around mutants such e.g., mviR−, pqsA− and pqsE−. The viability of yeast in these zones was tested by plating yeast from distance of 5 mm from the bacterial colonies on YPD plates.

**Fly infection**

Fly infection feeding assay was performed as previously described in [58,59]. Briefly, 45 female Oregon-R flies per group, 5–7 days old, were fed with a mixture of 4 ml of LB bacterial culture at OD_{600 nm} 3.0 with 1 ml of 20% sucrose. Thus, feeding mix contained a final concentration of 80% LB containing ~2×10^{9} bacterial cells per ml and 4% sucrose. An autoclaved cotton ball was placed at the bottom of each fly vial and was impregnated with 5 ml of the feeding mix. The 45 flies per treatment group were sub-divided in three fly vials (15 flies each), sealed with a clean cotton ball, and incubated at 25°C. Fly survival was recorded twice a day until all flies succumbed to the infection. Statistical analysis of the survival curves was performed using the log-rank test (Mantel-Haenszel) of the Kaplan-Meier estimate of survival using the software MedCalc (http://www.medcalc.be/). Two independent experiments gave similar results.

**Supporting Information**

**Figure S1** Transcription profile of mviR and pqsA−E. The transcription profile was determined from the transcriptome analysis of PA14 cultures along the growth curve in LB at 37°C. Found at: doi:10.1371/journal.ppat.1000810.s001 (0.85 MB EPS)

**Figure S2** Microarray data validation. The effect of PqsE on the expression of various differentially-expressed genes in the transcriptome (Table S1) was further confirmed by β-galactosidase assays derived from transcriptional fusions of the tested genes with lacZ(A-C) and by quantitative PCR (D). The levels of pqsA− and pqsE− gene expression by PCR were determined from PA14 cultures harboring pDN19pqsE (+PqsE) or the control vector pDN19. The PA14 sample at OD_{600 nm} of 2 served as the calibrator. Found at: doi:10.1371/journal.ppat.1000810.s002 (1.12 MB EPS)

**Figure S3** PqsE and RhlR cooperate in the regulation of the pqs operon and of PqsE downstream genes. (A) A Venn diagram showing the number of genes co-regulated by PqsE (Table S1) and by the Las/Rhl system [42]. (B) Constitutively-expressed PqsE does not reduce the expression of pqsA in a rhlR− mutant. The expression of the pqsA gene in an rhlR− mutant constitutively expressing PqsE or harboring the empty vector was assessed by
quantitative PCR reaction. An OD$_{600}$ reading of a sample from rhf$^-R$ served as the calibrator. 

**Figure S4** $pqsE$ is not required for HAQs production. The levels of HHQ$_2$, PQS and HQNO were assessed by LC/MS from PA14 (circles) and $pqsE^+$ mutant (squares) cultures at various growth stages in LB at 37°C. Found at: doi:10.1371/journal.ppat.1000810.s004 (0.68 MB EPS)

**Figure S5** Pqse downregulates pyoverdine production in a RhfR dependent manner. The effect of PqsE and RhfR on pyoverdine production was assessed by measuring the pyoverdine production in PA14 and mutants harboring pDN19pqsE (PqsE) or the empty vector pDN19 cells as control. Cells were grown in D-TSB medium in 96 wells plate and were incubated at 37°C with shaking for 1 minute every 30 minutes. The results shown are averages of 6 wells. Found at: doi:10.1371/journal.ppat.1000810.s005 (4.36 MB EPS)

**Figure S6** Iron counteracts PQS-mediated activity. (A) The effect of iron and PQS was assessed by measuring pyocyanin production in PA14 and a PA14 $pqsA::PqsE$ double-mutant constitutively expressing PqsE. PQS was added at 20 mg/L and iron at 200 μM. Asterisks show samples that are statistically significantly different (P value<0.01) from the untreated sample of PA14 (*) and $pqsA::PqsE$ (**). (B) The effect of iron is not a consequence of growth impairment. Growth curves were performed with PA14 cells in D-TSB media supplied with various concentrations of FeCl$_3$ in 96 wells plate incubated at 37°C with shaking for 1 minute every 30 minutes. The results shown are averages of 6 wells. Found at: doi:10.1371/journal.ppat.1000810.s006 (0.93 MB EPS)

**Table S1** The PqsE controlled genes list. A list of genes comprising the PqsE regulated genes was generated from our transcriptional data (NCBI GEO accession number #GSE17147). The values represent ratios of differential expression between the $pqsE^+$ mutant vs. PA14 ($pqsE^+$), $mvfR^+$ vs. PA14 ($mvfR^+$), $mvfR^+$ harboring pDN19pqsE vs. $mvfR^+$ with pDN19 ($mvfR^+$ + PqsE), $mvfR^+$ harboring pDN19pqsE treated with PQS (20 mg/L) vs. untreated ($mvfR^+$ + PqsE + PQS) and PA14 harboring pDN19pqsE vs. PA14 harboring the empty vector pDN19 ($mvfR^+$ + PqsE). The expression results were validated using reporter genes and quantitative PCR (Figure S2). Found at: doi:10.1371/journal.ppat.1000810.s007 (0.08 MB PDF)

**Table S2** Transcriptional regulators controlled by the MvfR pathway. The data on the differential expression of transcription regulators was adapted from Table S1. Found at: doi:10.1371/journal.ppat.1000810.s008 (0.07 MB XLS)

**Table S3** The interplay between the pqx operon and iron. The $mvfR$ regulon components controlling (A) or controlled by (B) iron related regulators. (A) The data was adapted from Table S1. The values represent fold changes in the $pqsE^+$ mutant vs. PA14 ($pqsE^+$), $mvfR^+$ vs. PA14 ($mvfR^+$), $mvfR^+$ harboring pDN19pqsE vs. $mvfR^+$ with pDN19 ($mvfR^+$ + PqsE), $mvfR^+$ + PqsE treated with PQS (20 mg/L) vs. untreated ($mvfR^+$ + PqsE + PQS) and PA14 harboring pDN19pqsE vs. PA14 with pDN19 (PA14 + PqsE). (B) Iron related regulators controlling the MvfR regulon component. Fold change in expression of $mvfR$, $pqsA-E$, and $phnB$ were retrieved from previously published studies of iron-related conditions and regulators 1, 2, 3, 6, 8, 9. Found at: doi:10.1371/journal.ppat.1000810.s009 (0.07 MB XLS)

**Table S4** Strains, plasmids and primers. The P. aeruginosa strains, plasmids and primers that were used in this study. Found at: doi:10.1371/journal.ppat.1000810.s10 (0.07 MB DOC)

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**Author Contributions**

Conceived and designed the experiments: RH GX LG. Performed the experiments: RH JH GX VD YA BL CA FL. Analyzed the data: RH VD TJK LN. Contributed reagents/materials/analysis tools: ED FL LGR. Wrote the paper: RH LGR.

**References**


