The multi-output incoherent feedforward loop constituted by the transcriptional regulators LasR and RsaL confers robustness to a subset of quorum sensing genes in *Pseudomonas aeruginosa* 

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## SUPPLEMENTAL MATERIAL

- Table S1. Bacterial strains used in this study
- Table S2. Plasmids used in this study
- Table S3. Oligonucleotides used in this study

Strains	Relevant characteristics	<b>Reference/Source</b>
E. coli		
S17.1 λ <i>pir</i>	Conjugative strain for suicide plasmids.	39
SM10 (pFLP2)	Strain carrying the pFLP2 plasmid (FLP; Ap <sup>R</sup> /Cb <sup>R</sup> ) for Flp- mediated recombination.	43
P. aeruginosa		
PAO1	wild type strain ATCC15692.	ATCC
PA14-R3	Biosensor strain for 3OC <sub>12</sub> -HSL quantification.	49
Δvfr	PAO1 mutant strain with in frame clear deletion of the vfr gene.	37
$\Delta rsaL$	PAO1 mutant strain with in frame clear deletion of the <i>rsaL</i> gene, obtained by using the pDM4 $\Delta$ <i>rsaL</i> plasmid (Table S2).	This study
$\Delta rsaL\Delta v fr$	PAO1 double mutant strain with in frame clear deletion of both the <i>rsaL</i> and <i>vfr</i> genes, obtained by using the pDM4 $\Delta$ <i>rsaL</i> plasmid (Table S2) in PAO1 $\Delta$ <i>vfr</i> .	This study
ΔlasR	A 344 bp region encompassing the <i>lasR</i> gene, corresponding to nucleotides 1558474-1558819 of <i>P. aeruginosa</i> PAO1 genome, has been deleted from PAO1 chromosome by using the pEX18 $\Delta$ <i>lasR</i> plasmid (Table S2).	This study
$\Delta las R \Delta rsa L$	A 685 bp region encompassing the <i>lasR</i> and <i>rsaL</i> gene, corresponding to nucleotides 1558473-1559112 of <i>P</i> . <i>aeruginosa</i> PAO1 genome, has been deleted from PAO1 chromosome by using the pDM4 $\Delta lasR\Delta rsaL$ plasmid (Table S2).	This study
lasR <sup>ind</sup>	PAO1 $\Delta lasR$ mutant strain carrying the <i>araC</i> -P <sub>BAD</sub> <i>lasR</i> transcriptional fusion for L-arabinose-dependent induction of <i>lasR</i> , integrated into the chromosome. Generated by using the mini-CTX1- <i>araC</i> -P <sub>BAD</sub> <i>lasR</i> (Table S2).	This study
$\Delta rsaL \ lasR^{ind}$	PAO1 $\Delta lasR\Delta rsaL$ mutant strain carrying the <i>araC</i> -P <sub>BAD</sub> <i>lasR</i> transcriptional fusion for L-arabinose-dependent induction of <i>lasR</i> , integrated into the chromosome. Generated by using the mini-CTX1- <i>araC</i> -P <sub>BAD</sub> <i>lasR</i> (Table S2).	This study

# Table S1. Bacterial strains used in this study

#### Plasmid Relevant characteristics and plasmid construction **Reference/Source** pDM4 Suicide vector for construction of deletion mutants; *sacBR*; 42 oriR6K; Cm<sup>R</sup>. pDM4 $\Delta rsaL$ pDM4-derivative plasmid for in frame clear deletion of the This study rsaL gene. The upstream (UP) and the downstream (DW) DNA regions of rsaL were PCR amplified from P. aeruginosa PAO1 genome using primers FW61G/RV62G and FW63G/RV64G, respectively (Table S3). The UP and DW PCR fragments were subsequently cloned in pDM4 by XhoI-BamHI and BamHI-XbaI restriction, respectively. $pEX18\Delta lasR$ pEX18Tc-derivative plasmid for deletion of the *lasR* gene 44 from nucleotides 1558474-1558819 of P. aeruginosa PAO1 genome. $pDM4\Delta lasR\Delta rsaL$ pDM4-derivative plasmid for deletion of the lasR and rsaL This study genes from nucleotides 1558473-1559112 of P. aeruginosa PAO1 genome. The upstream (UP) and downstream (DW) regions of the genetic locus containing the lasR and rsaL genes was PCR amplified from P. aeruginosa PAO1 genome primers FW675/RV765 and RV62G/FW61G, using respectively (Table S3). The UP and DW PCR fragments were subsequently cloned in pDM4 by SpeI-BamHI and BamHI-XhoI restriction, respectively. mini-CTX1-araC-PBADtolB mini-CTX1-derivative plasmid carrying the araC-P<sub>BAD</sub>tolB 70 cassette from pBEM9, cloned by XhoI/EcoRI restriction. mini-CTX1-araCmini-CTX1-araC-P<sub>BAD</sub>-derivative plasmid containing a 720 This study bp DNA fragment encompassing the lasR gene. lasR was **P**<sub>BAD</sub>lasR PCR amplified from P. aeruginosa PAO1 genome using primers FW763 and RV764 (Table S3) and cloned in the mini-CTX1-*araC*-P<sub>BAD</sub>tolB plasmid by HindIII-EcoRI restriction. Promoter probe vector; IncQ; 15 kb; Sm<sup>R</sup> Cm<sup>R</sup>. pMP190 71

### Table S2. Plasmids used in this study

Plasmid	Relevant characteristics and plasmid construction	Reference/Source
pP <i>lasI</i> 190	A DNA fragment encompassing the lasI promoter region	19
	(PlasI) was PCR amplified and cloned in the pMP190	
	plasmid upstream of the promoterless <i>lacZ</i> gene.	
pP <i>lasR</i> 190	A DNA fragment encompassing the lasR promoter region	This study
	(PlasR) was PCR amplified from P. aeruginosa PAO1	
	genome with primers FW324 and RV325 (Table S3) and	
	cloned by SalI-BglII restriction in the pMP190 plasmid	
	upstream of the promoterless <i>lacZ</i> gene.	

Name	Sequence (5'-3') <sup>a</sup>	Position <sup>b</sup>	<b>Restriction site</b>
FW324	NNNACGC <u>GTCGAC</u> GGTCGCACGCGTGGCG	1557812	SalI
RV325	NNNNGGA <u>AGATCT</u> CAACCAAGGCCATAGCGC	1558166	BglII
FW675	GG <u>ACTAGT</u> ACCTATGCGCCGCCGTTG	1557572	SpeI
RV676	CGC <u>GGATCC</u> AGCGCTACGTTCTTCTTAAACT	1558149	BamHI
RV765	GCG <u>GGATCC</u> ACTCGTGCTGCTTTCGCGT	1558454	BamHI
FW763	TAT <u>AAGCTT</u> ATGGCCTTGGTTGACGGTTT	1558171	HindIII
RV764	TAT <u>GAATTC</u> TCAGAGAGTAATAAGACCCAAA	1558869	EcoRI
FW61G	CCG <u>CTCGAG</u> CGCATCGCCTCCAGCGT	1559614	XhoI
RV62G	TAT <u>GGATCC</u> GTGTGAAGCCATTGCTCTG	1559111	BamHI
FW63G	TAT <u>GGATCC</u> TTGCATTTCTATATAGAAGG	1558932	BamHI
RV64G	TGC <u>TCTAGA</u> CTGGGAACCGTCCATCTAC	1558441	XbaI

Table S3. Oligonucleotides used in this study

<sup>a</sup> Engineered restriction sites are underlined.

<sup>b</sup> Position with respect to *P. aeruginosa* PAO1 chromosome (www.pseudomonas.com).<sup>72</sup>

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- A. Lo Sciuto, R. Fernández-Piñar, L. Bertuccini, F. Iosi, F. Superti and F. Imperi. The periplasmic protein TolB as a potential drug target in *Pseudomonas aeruginosa*. *PLoS One*, 2014, 9(8), e103784. doi:10.1371/journal.pone.0103784.
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- 72. G. L. Winsor, D. K. Lam, L. Fleming, R. Lo, M. D. Whiteside, N. Y. Yu, R. E. Hancock and F. S. Brinkman. *Pseudomonas* Genome Database: improved comparative analysis and population genomics capability for *Pseudomonas* genomes. *Nucleic Acids Res.*, 2011, **39**, D596-600.

<sup>a</sup> Please note that other references cited in this Supplemental Material file are listed in the Reference Section of the manuscript main body.