

Supporting Information for

Natural and synthetic inhibitors of a phage-encoded quorum-sensing receptor affect phage-host dynamics in mixed bacterial communities

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Figure S1

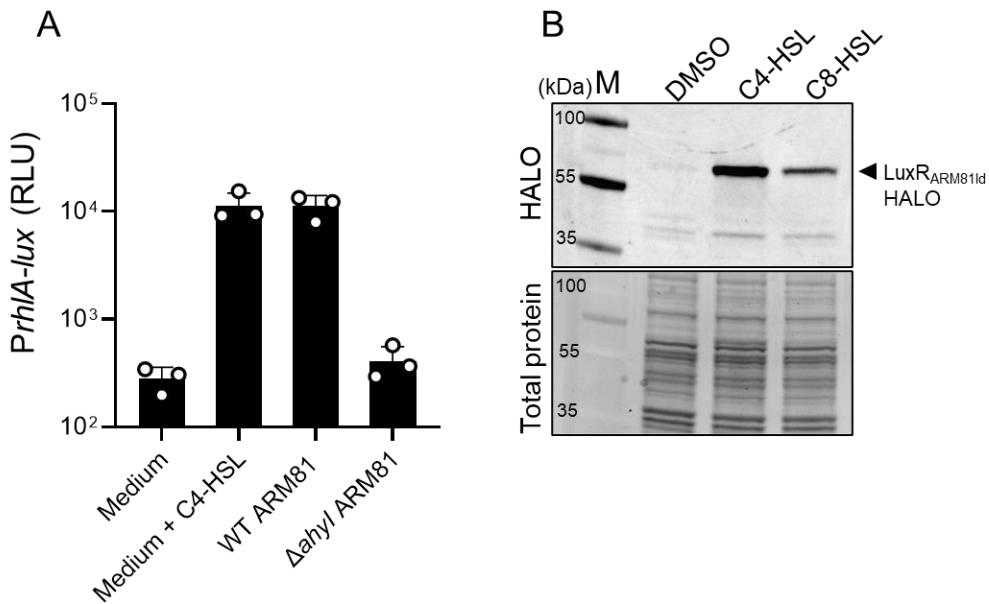


Figure S1. The ARM81 *ahyl* gene encodes the C4-HSL-producing synthase Ahyl and both C4-HSL and C8-HSL solubilize LuxR_{ARM81ld}.

(A) *PrhlA-lux* expression from *E. coli* grown in medium supplemented with C4-HSL, cell-free culture fluids from WT *Aeromonas* sp. ARM81 (C4-HSL⁺), or cell-free culture fluids from Δ ahyl *Aeromonas* sp. ARM81 (C4-HSL⁻). The *E. coli* strain carries a plasmid with *PrhlA-lux* and a second plasmid with arabinose-inducible pBAD-*rhlR*. The *rhlA* promoter and *rhlR* gene both come from *P. aeruginosa*. In this system, *RhlR* only activates *PrhlA-lux* expression when C4-HSL is supplied exogenously. All media contained 0.1% arabinose.

(B) Western blot (top) and total protein (bottom) showing LuxR_{ARM81ld}-HALO in the soluble fractions of *E. coli* supplied with 75 μ M of the indicated HSL or an equivalent volume of DMSO. Detection of the HALO-reactive fluorophore requires that the HALO tag be properly folded. Thus, LuxR_{ARM81ld}-HALO band intensity is a measure of folded LuxR_{ARM81ld} in the soluble fraction of each sample. M denotes molecular weight marker (representative bands are labeled). kDa is kilodalton.

Table S1. Strains used in this study.

Strain	Genotype	Reference
<i>E. coli</i> TOP10	F- <i>mcrA</i> Δ(<i>mrr-hsdRMS-mcrBC</i>) φ80 <i>lacZΔM15 ΔlacX74 recA1 araD139</i> Δ(<i>ara-leu</i>)7697 <i>galU galK</i> λ- <i>rpsL</i> (<i>Str^R</i>) <i>endA1 nupG</i>	Invitrogen
<i>E. coli</i> BL21	<i>fhuA2</i> [<i>lon</i>] <i>ompT gal</i> [<i>dcm</i>] Δ <i>hsdS</i>	Invitrogen
<i>Aeromonas</i> sp. ARM81 (JSS-3155)	WT	(Dziewit and Radlinska, 2016)
<i>Aeromonas</i> sp. ARM81 (JSS-3388)	Δ <i>ahyl</i>	This study
<i>Vibrio fischeri</i> ES114	WT	Bassler lab strain collection
	Δ <i>luxI</i>	Bassler lab strain collection
	Δ <i>ainS</i>	Bassler lab strain collection
	Δ <i>luxI</i> Δ <i>ainS</i>	Bassler lab strain collection

Table S2. Primers used in this study.

Name	Sequence (5' - 3')	Purpose; Template
JSO-2192	GTTTGCAGGCCGACGTTTTACCCCC CCAAAGCC	<i>ahyl</i> upstream flanking DNA for insert into pFOG with NotI site; from <i>Aeromonas</i> sp. ARM81
JSO-2193	TTAACACTCTGTTATTACAAATGAGCA AAAAAAGTCCGGGA	<i>ahyl</i> upstream flanking DNA for insert into pFOG; from <i>Aeromonas</i> sp. ARM81
JSO-2194	TTTGTAAATAACAGAGTGTTAATT	<i>dhfr</i> cassette amplification; from EZ-DHFR Tn5
JSO-2195	TTAATTAAGCCTGGCACAGCGG	<i>dhfr</i> cassette amplification; from EZ-DHFR Tn5
JSO-2196	CGCTGTGCCAGGCTTAATTAACATT ATGCCCTCTCCATTCA	<i>ahyl</i> downstream flanking DNA for insert into pFOG; from <i>Aeromonas</i> sp. ARM81
JSO-2197	GTTTGTTAACACATGGGATGCG TTCCTGTGA	<i>ahyl</i> downstream flanking DNA for insert into pFOG with Pmel site; from <i>Aeromonas</i> sp. ARM81
JSO-1566	CATTAATTAACCTCCTGAATT CGGAA GCGAT	pT7 backbone amplification for Gibson assembly; pH6HTN plasmid
JSO-2035	TAATAGTCAACCGCTGAGCAATAACT AGC	pT7 backbone amplification for Gibson assembly; pH6HTN plasmid
JSO-2176	GCTTTGTATATGCCACCTA	qPCR; phage ARM81ld
JSO-2177	GCAATCAGACATCAGTGCCAAG	qPCR; phage ARM81ld
JSO-2106	CTTCTCTCCGAGCGTTACGAC	qPCR; <i>Aeromonas</i> sp. ARM81 host (<i>rpoB</i>)
JSO-2107	GGTCGATATCGTCCACTTCGTC	qPCR; <i>Aeromonas</i> sp. ARM81 host (<i>rpoB</i>)

Table S3. Plasmids used in this study.

Plasmid name (informal)	Strain ID (formal)	Relevant fragment	Marker, Origin	Source
pTetA- <i>xre_{ARM81ld}-luxR_{ARM81ld}</i>	JSS-3237	<i>xre_{ARM81ld}-luxR_{ARM81ld}</i>	Amp, pBR322	(Silpe et al., 2022)
pTetA- <i>xre_{ARM81ld}-luxR_{ARM81ld}</i>	JSS-3326	<i>xre_{ARM81ld}-luxR_{ARM81ld}</i>	Cm, p15A	(Silpe et al., 2022)
PsmORF _{ARM81ld} - <i>lux</i>	JSS-3235	PsmORF _{ARM81ld} - <i>lux</i>	Kan, p15A	(Silpe et al., 2022)
pFOG- Δ ahyl::dhfr	JSS-3387	Δ ahyl::dhfr	Gent, oriR6ky	This study
pH6HTC-pT7- <i>luxR_{ARM81ld}-HALO-HIS</i>	JSS-1868	<i>luxR_{ARM81ld}-HALO-HIS</i>	Amp, pBR322	(Silpe and Bassler, 2019)