

SUPPLEMENTARY MATERIAL

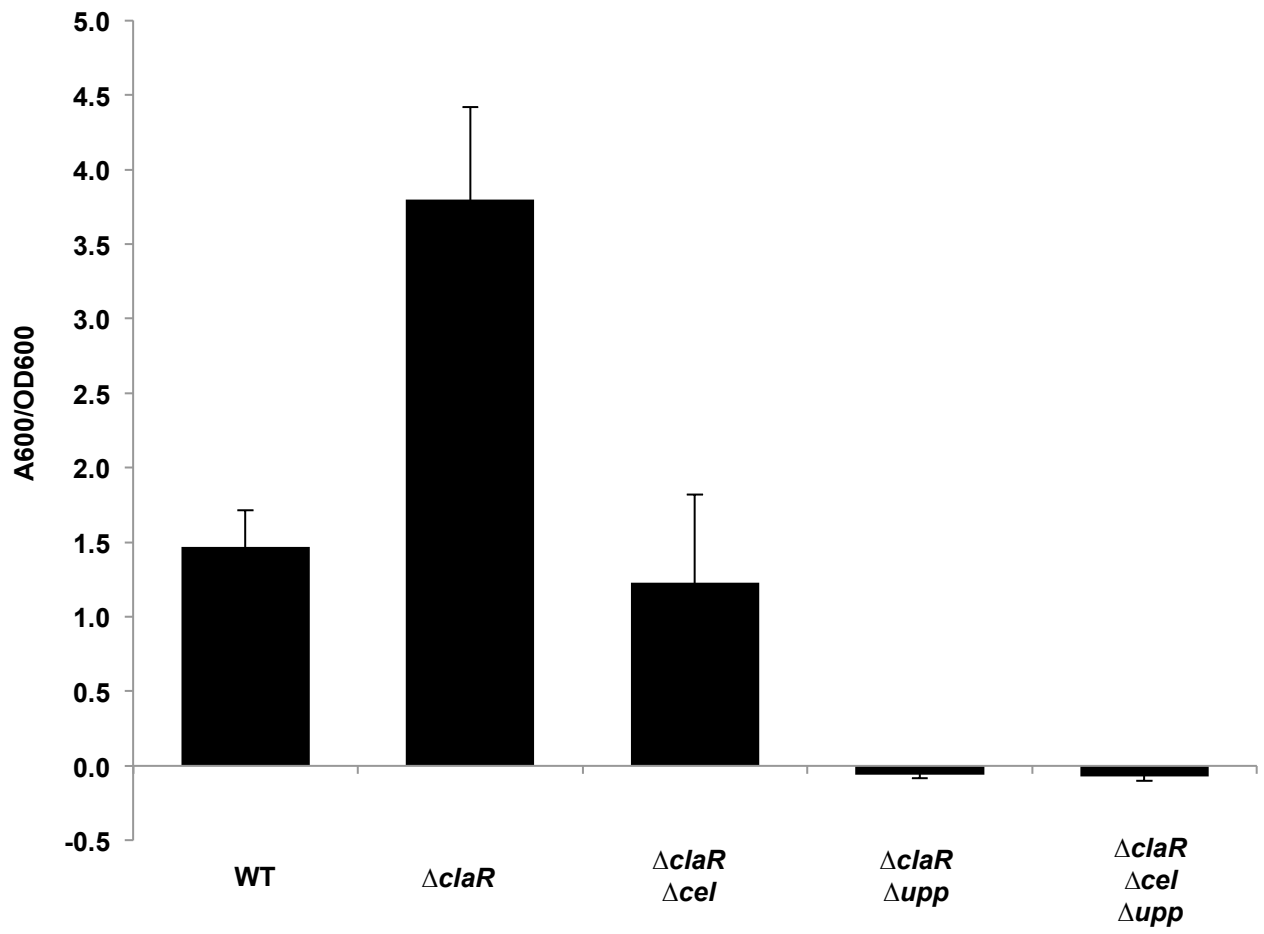
The *Agrobacterium tumefaciens* CheY-Like Protein ClaR Regulates Biofilm Formation

Nathan Feirer, DohHyun Kim, Jing Xu, Nico Fernandez,
Christopher M. Waters, and Clay Fuqua

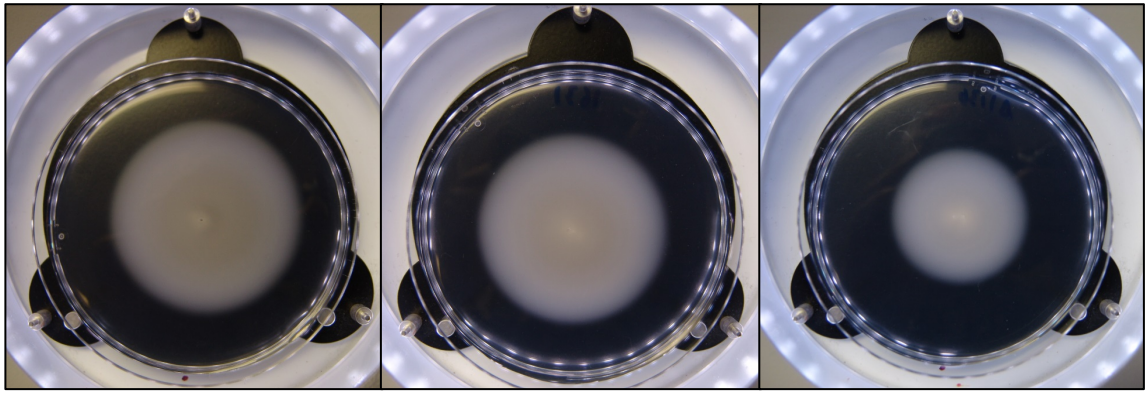
Running title: *Agrobacterium* CheY-type biofilm regulator

- 1) Supplementary Figures – S1-S7
- 2) Supplementary Figure Legends
- 3) Supplementary Tables – S1-S2
- 4) Supplementary References

S1



S2a



WT

Δ *claR*

Δ *pruA*

S2b

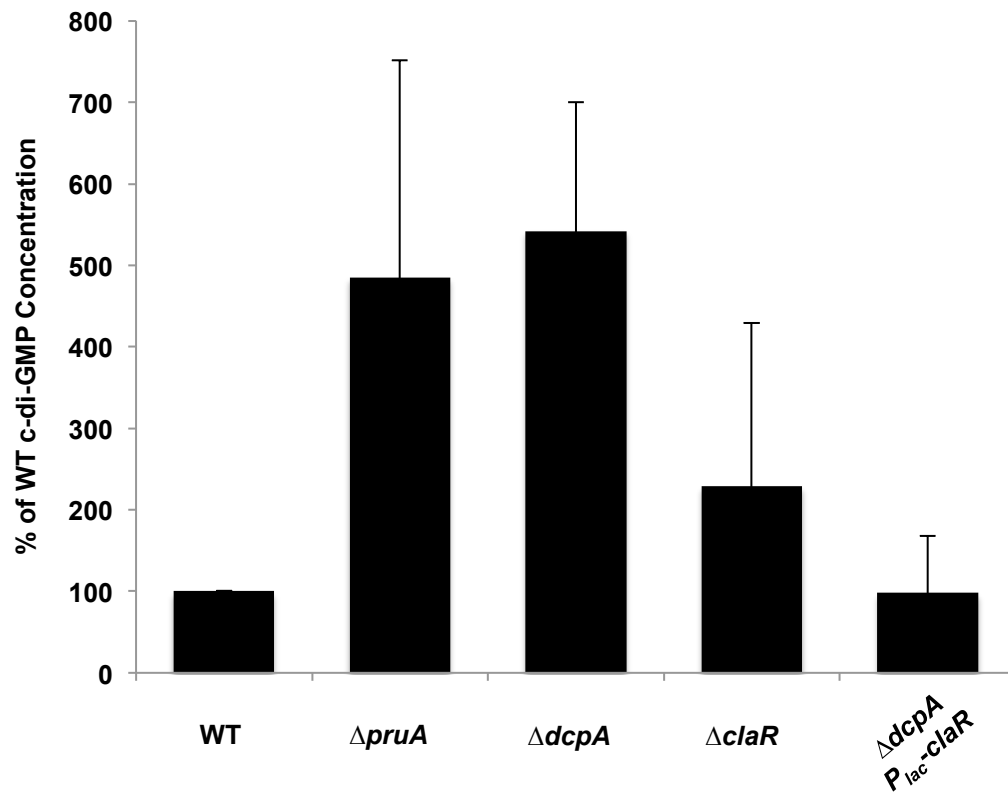


WT

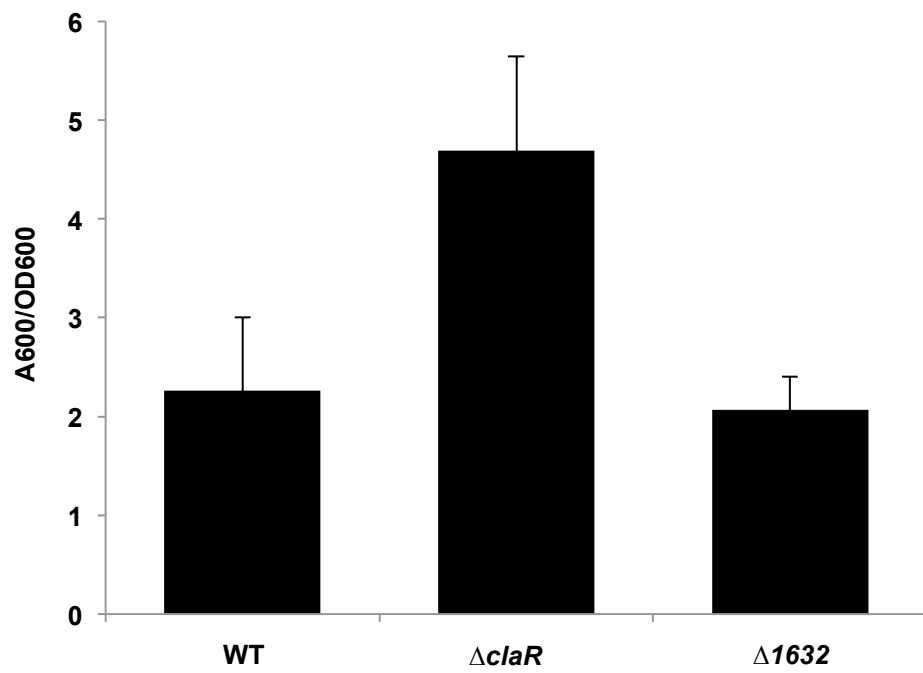
Δ *claR*

Δ *pruA*

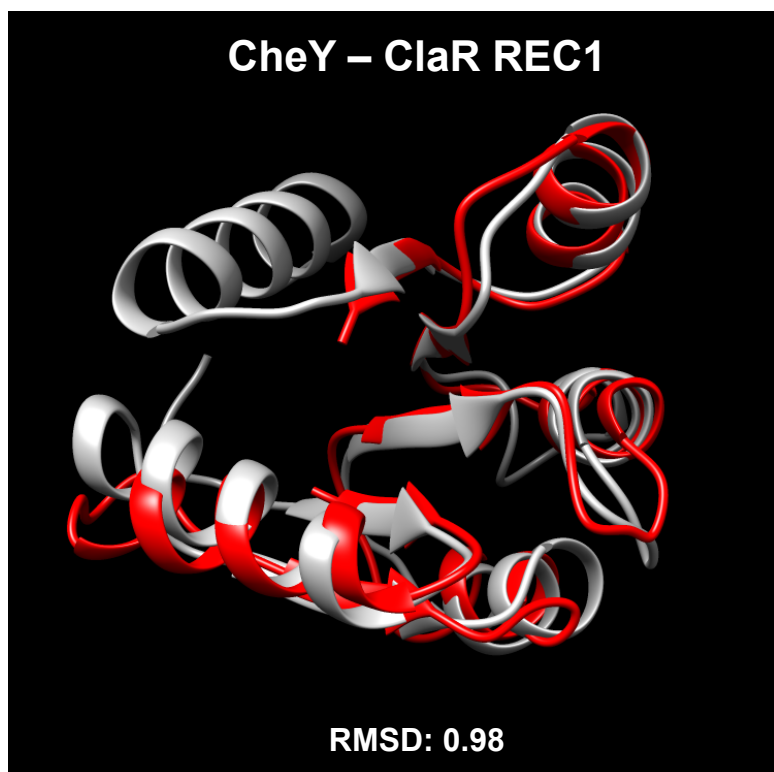
S2c



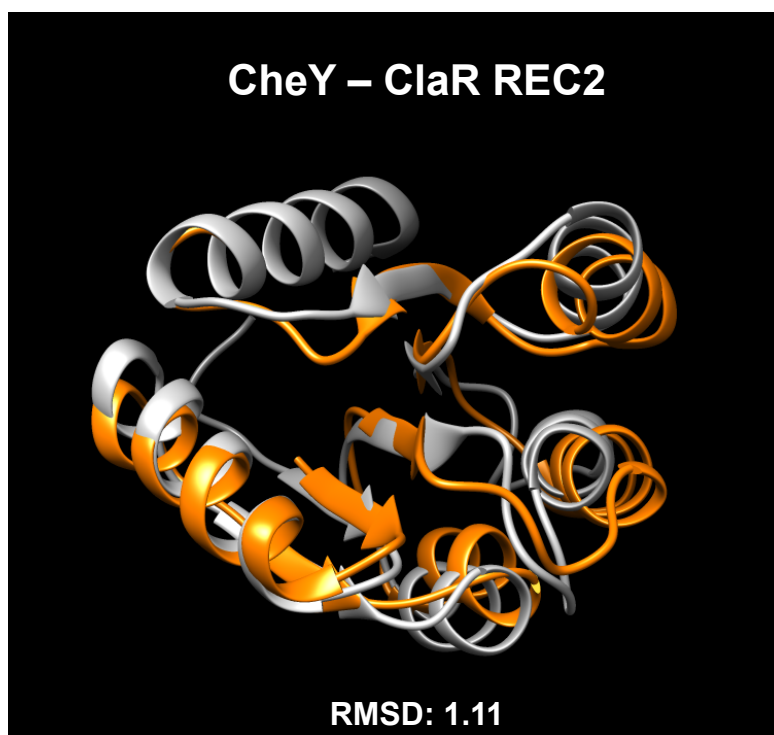
S3



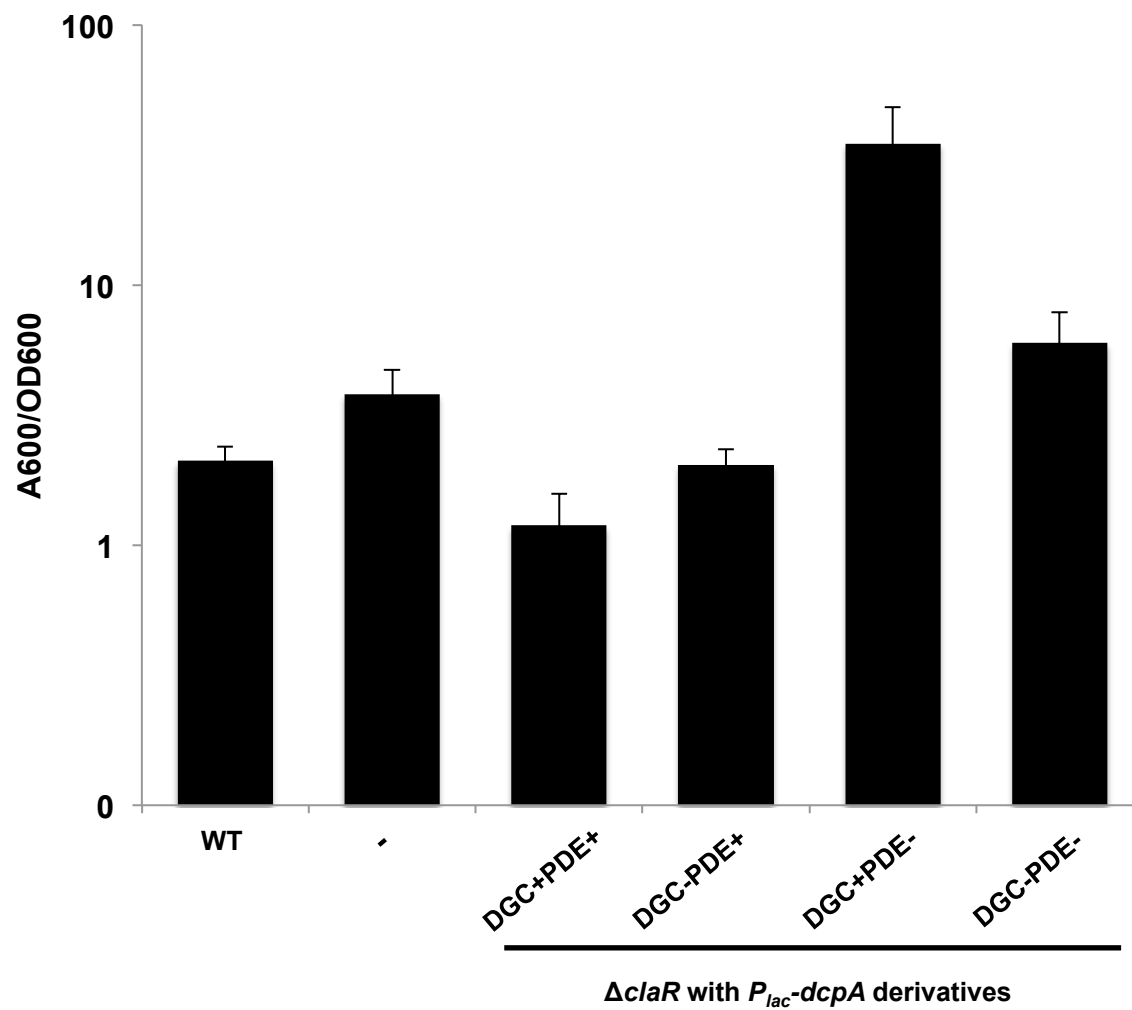
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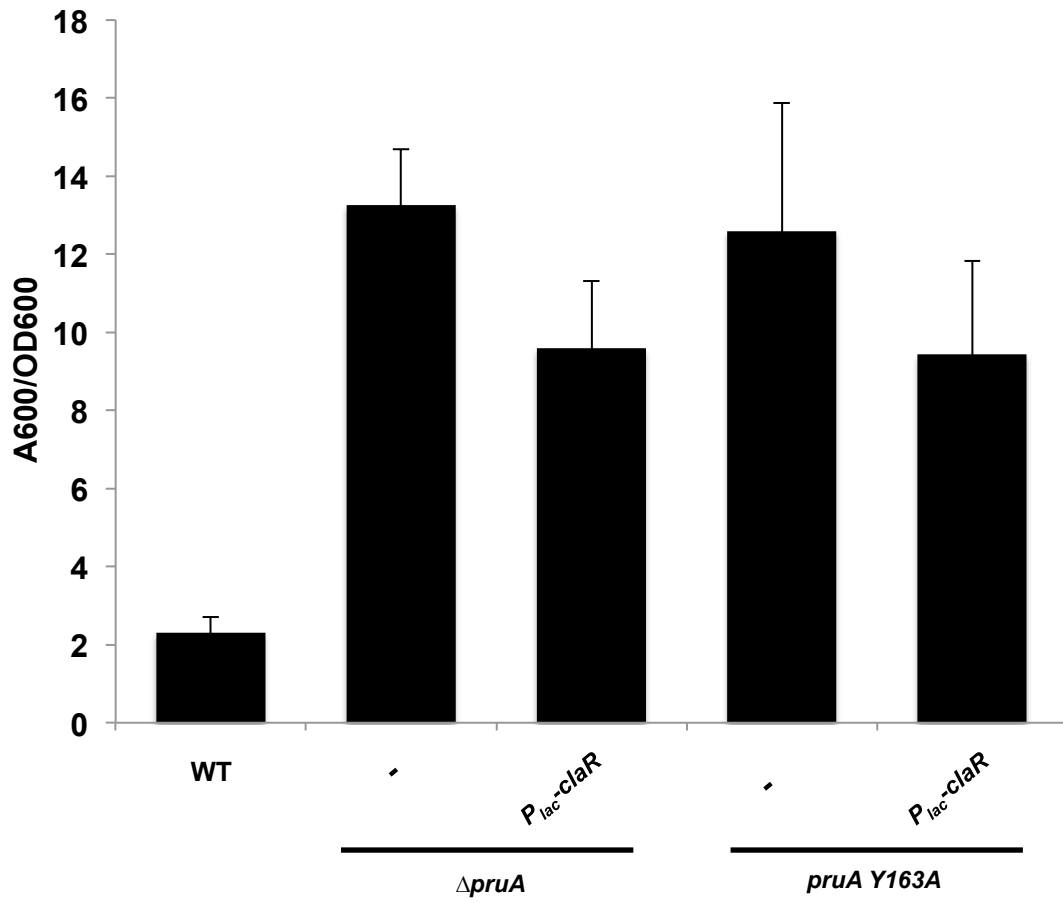
S5b



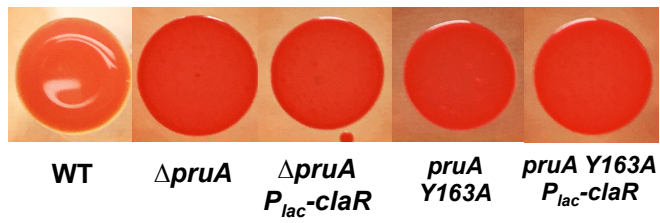
S6



S7a



S7b



Supplemental Figure Legends

Figure S1. Polysaccharide dependence of ClaR biofilm phenotypes. 48 hr PVC coverslip biofilms quantified as described in Fig. 2A. Δcel strains are unable to produce cellulose and Δupp strains are unable to produce the UPP. Values are result of two independent biological replicates consisting of three technical replicates each. Error bars: +/- 1 standard deviation.

Figure S2. Additional ClaR phenotypes. (A) *A. tumefaciens* soft agar motility assay. Indicated strains were grown to mid-exponential phase and spotted into ATGN plates containing 0.3% (w v⁻¹) Bacto agar. Plates were dried and placed in room temperature Tupperware container alongside beaker of saturated potassium sulfate. Plates were incubated for 5 days, at which time pictures were taken. (B) Calcofluor staining phenotypes of *A. tumefaciens* colonies. Indicated strains were grown to mid-exponential phase, normalized to an OD₆₀₀ of 0.5 and spotted onto LB plates containing 20 µg/ml calcofluor white (fluorescent white) dye. Spots were dried and photographs taken under UV light exposure in a light cabinet after 48 hours of growth at 28°C. (C) Intracellular c-di-GMP concentrations of *A. tumefaciens* mutants. Indicated strains were grown to early stationary phase, normalized for OD followed by nucleotide extraction. Measurements of c-di-GMP with LC-MS-MS as described in *Materials and Methods*. As with previous experiments, the extended version of ClaR (*claR-Ext.*) was utilized for overexpression studies. Values are the result of two independent biological replicates consisting of three technical replicates each. Error bars: +/- 1 standard deviation.

Figure S3. Atu1632 Doesn't Regulate *A. tumefaciens* biofilm formation. 48 hr PVC coverslip biofilms quantified as described in Fig. 2A. Values are the result of three independent biological replicates consisting of three technical replicates each. Error bars: +/- 1 standard deviation.

Figure S4. Alignment of ClaR Homologs. Alignment of ClaR (Annotated and Extended) to closely related Rhizobial bi-directional best-hit homologs. *A. radiobacter* K84 ACM26930.1 (79% aa identity vs ClaR), *R. leguminosarum* WP_012757872 (79% aa identity vs ClaR), and *A. vitis* WP_015916382.1 (77% aa identity vs ClaR). Alignment performed with ClustalX software (www.clustal.org) using multiple alignment mode.

Figure S5. Secondary structure alignment of predicted ClaR REC domains with experimentally determined CheY structure from *E. coli*. Predicted REC domain Phyre tertiary structures described in Fig. 3 computationally aligned to published *E. coli* crystal structure (3CHY). Alignments performed and visualized using UCSF Chimera (<https://www.cgl.ucsf.edu/chimera/>) with Needleman-Wunsch alignment algorithm. Coloring as follows: (A) CheY: grey, ClaR REC1: red. (B) CheY: grey, ClaR REC2: orange. Root mean-square deviation (RMSD) values overlaid on alignment images.

Figure S6. DcpA PDE activity can decrease biofilm formation of *claR* mutant. 48 hr PVC coverslip biofilms quantified as described in Fig. 2a. Values are the result of three independent biological replicates consisting of three technical replicates each.

Error bars: +/- 1 SD. DcpA variants containing catalytic site mutations GGDEF->GGDAF (DGC-) and EAL->AAL (PDE-) were examined.

Figure S7: ClaR does not regulate attachment in a PruA catalytic site mutant. (A)

48 hr PVC coverslip biofilms quantified as described in Fig. 2A. Values are the result of three independent biological replicates consisting of three technical replicates each.

Error bars: +/- 1 standard deviation. Dash represents strain without plasmid inserted.

(B) Congo red colony phenotypes of indicated *A. tumefaciens* strains, as described by Fig. 5B.

Table S1
Strains and plasmids

Strain/plasmid	Relevant features	Reference
<i>E. coli</i>		
DH5 α / λ pir	λ pir ; cloning strain	(1)
TOP10 F'	Cloning strain	Invitrogen
S17-1/ λ pir	λ pir ; Tra ⁺ , cloning host	(2)
<i>A. tumefaciens</i>		
C58	Nopaline type strain; pTiC58; pAtC58	(3)
NF001	<i>pruA</i> Y163A allelic replacement	(4)
NF003	Δ <i>pruR</i>	(4)
NF009	Δ Atu1632	This study
NF011	Δ <i>claR</i> Δ <i>cel</i>	This study
NF012	Δ <i>claR</i> Δ <i>upp</i>	This study
NF013	Δ <i>claR</i> Δ <i>cel</i> Δ <i>upp</i>	This study
JX136	Δ <i>claR</i>	This study
JX137	Δ <i>pruA</i>	(5)
JX138	Δ <i>dcpA</i>	(5)
Plasmids		
pGEM-T easy	PCR cloning vector; Ap ^R	Promega
pNPTS138	ColE1 suicide plasmid; <i>sacB</i> ; Km ^R	Gift of M. Alley
pSRKGm	Broad host range <i>P</i> _{lac} expression vector; <i>lacIQ</i> ; Gm ^R	(6)
pNF030	pSRKGm carrying <i>P</i> _{lac} - <i>dcpA</i> E308A; Gm ^R	(4)
pNF031	pSRKGm carrying <i>P</i> _{lac} - <i>dcpA</i> E431A; Gm ^R	(4)
pNF032	pSRKGm carrying <i>P</i> _{lac} - <i>dcpA</i> E308A E431A; Gm ^R	(4)
pNF054	pSRKGm carrying <i>P</i> _{lac} - <i>claR</i> Ext.; Gm ^R	This study
pNF058	pSRKGm carrying <i>P</i> _{lac} - <i>claR</i> Ext. D193A Allele; Gm ^R	This study
pNF059	pSRKGm carrying <i>P</i> _{lac} - <i>claR</i> Ext. D193N Allele; Gm ^R	This study
pNF078	pNPTS138 carrying <i>Atu1632</i> SOE deletion fragment; Km ^R	This study
pJX131	pNPTS138 carrying <i>claR</i> SOE deletion fragment; Km ^R	This study
pJX148	pSRKGm carrying <i>P</i> _{lac} - <i>claR</i> Annot.; Gm ^R	This study
pJW168	pSRKGm carrying <i>P</i> _{lac} - <i>dcpA</i> ; Gm ^R	(5)

^aAll *A. tumefaciens* strains are C58 derivatives

Table S2. Oligonucleotides

Primer	Sequence
D193A P1	GTCTCGTCGTGACC GCC TATAATATGCCCCG
D193A P2	CGGGCATATTATA GGC GGTCACGACGAGAC
D193N P1	GTCTCGTCGTGACC AAC TATAATATGCCCCGATATT
D193N P2	CAATATCGGGCATATTATA GTT GGTCACGACGAGA
De1631-P1	(SpeI) actagt CGTTTGCATGAATTGCGTTCGCAG
De1631-P2	<i>aagcttggtaccgaattc</i> GCCGGGTTTTCCCGTCAAAGCTGA
De1631-P3	<i>gaattcggtagc</i> caagcttCACATTGCTGTCTTCCGCCAG
De1631-P4	(PstI) ctgcag AAGTCGATTGCACTTGCCATGCTC
1632 Del P1	(SpeI) gaactagt taaGTCGCCTCATGGAAGGTGCTG
1632 Del P2	<i>caggggtctgtaa</i> atgaagacaCGCGCAT AAGATCATTCCCTC
1632 Del P3	<i>gaggg</i> aatgatcttatg cgcg TGTCTTCATT TACAGAACCCTG
1632 Del P4	(NheI) ga gctagcgttCGAATTGCGTTTCCACCTTGC
1632 Del P5	GCACATGATGGCGGTGATTGGTG
1632 Del P6	CTTCTGTGCGGGA ACTGGACG
1631 new 5'	(Nde1) gcg catATG AATTTCTGGGCATTAC
Com1631-P1	(SpeI) actagt TCAGCTTTGACGGGAAAACCCGGC
M13-F	CGCCAGGGTTTTCCAGTCACGAC
M13-R	TCACACAGGAAACAGCTATGAC

Upper case sequence anneals to target sequences; lower case are engineered into oligonucleotides but do not anneal with target sequences in genome

Italicized sequences are complementary among paired oligonucleotides

Engineered restriction endonuclease cleavage sites are indicated in parentheses and highlighted in yellow

Bases altered for site-specific mutagenesis highlighted in red

References

1. **Chiang SL, Rubin EJ.** 2002. Construction of a mariner-based transposon for epitope-tagging and genomic targeting. *Gene* **296**:179-185.
2. **Kalogeraki VS, Winans SC.** 1997. Suicide plasmids containing promoterless reporter genes can simultaneously disrupt and create fusions to target genes of diverse bacteria. *Gene* **188**:69-75.
3. **Xu J, Platt TG, Fuqua C.** 2012. Regulatory linkages between flagella and surfactant during swarming behavior: lubricating the flagellar propeller? *J Bacteriol* **194**:1283-1286.
4. **Feirer N, Xu J, Allen KD, Koestler BJ, Bruger EL, Waters CM, White RH, Fuqua C.** 2015. A Pterin-Dependent Signaling Pathway Regulates a Dual-Function Diguanylate Cyclase-Phosphodiesterase Controlling Surface Attachment in *Agrobacterium tumefaciens*. *mBio* **6**.
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6. **Khan SR, Gaines J, Roop RM, 2nd, Farrand SK.** 2008. Broad-host-range expression vectors with tightly regulated promoters and their use to examine the influence of TraR and TraM expression on Ti plasmid quorum sensing. *Appl Environ Microbiol* **74**:5053-5062.