

SUPPLEMENTAL FIGURE LEGENDS

Figure S1. Controls for protein interaction experiments. Protein pull down assays using the indicated beads and the indicated amounts of His-Hag, GST-CsrA, GST, and FliW proteins. Gels were stained with Coomassie blue. “Input” indicates the starting amount of protein in the assays, “supernatant” indicates the proteins that failed to bind to the beads, and “pellet” indicates the proteins that remained bound to the beads following a series of washes. A) FliW was not retained on the GSH-Sepharose beads when the beads were loaded with GST alone. B) FliW was not retained on untreated GSH-Sepharose beads. Note that a small fraction of the His-Hag protein was retained on untreated GSH-Sepharose beads. C) FliW was poorly retained on untreated Nickel-NTA agarose beads. A large fraction of the GST-CsrA protein alone was retained on untreated Nickel-NTA agarose beads for unknown reasons and this combination of protein and beads was not used in Fig 2.

Figure S2. Phylogenetic tree from figure 6 reproduced at higher magnification.

Supplemental Table S1: Plasmids

Plasmid	Genotype	
pCSB9	P_{T7} -CsrA-H ₆ amp	(Yakhnin et al., 2007)
pDP42	amyE::P _{hag} ^{translational} -lacZ spec	
pDG780	kan amp	(Guérout-Fleury et al., 1995)
pDG1515	tet amp	(Guérout-Fleury et al., 1995)
pDG1728	amyE::lacZ spec amp	(Guérout-Fleury et al., 1996)
pDR111	amyE::P _{hyspank} spec amp	(Ben-Yehuda et al., 2003)
pDR183	lacA::mls amp	(Doan et al., 2005)
pJP4	P_{T7} -His ₆ -Hag amp	
pJP87	$\Omega\Delta$ fliW mls amp	
pKB43	P_{T7} -His ₆ -SUMO-FliG amp	
pKB142	lacA::P _{hag} -hag ^{T209C} mls	
pLC108	amyE::P _{hyspank} -fliW spec	
pLC109	amyE::P _{hyspank} -csrA spec	
pMiniMAD	ori ^{BsTs} mls	(Patrick and Kearns, 2008)
pSG35	$\Omega\Delta$ csrA mls amp	
pSG36	$\Omega\Delta$ fliWcsrA mls amp	
pSM6	P_{T7} -GST-CsrA amp	
pSM12	P_{T7} -His ₆ -SUMO-FliW amp	
pTB146	P_{T7} -His ₆ -SUMO amp	(Bendezu et al., 2009)

Supplemental Table S2: Primers

Primer	Sequence
131	gcaggatccaagaagaacaaatcattcttttgaaag
132	ttcggtcgacgtggttaattctcattgtttgtcct
140	aggagatgcagaaatcataaatgcatt
141	gaacaacctgcaccattgcaagaattgattgatttcataggattcctct
142	ttgatcctttttataacaggaattcaatatgattaattttataaaaagcaataaaa
143	tcagaaatataattaacgtttcagct
663	aggaggtagcagaattaaccacaatattgcagcgc
664	ctcctgctagcggcaacgccaaggtcttttataaaa
848	ctcctggatcctgaggaatgattaggagatagaaattt
882	aggaggctctccggtatggcgagacgtgatcaagataag
883	ctcctctcgagtgtggagaaatagatgattctgttta
1541	aggaggtagcccgaagaatcacccgaaaagtaa
1542	ctcctgcatgcaatcgcttctgtttttccgcat
1543	aggaggtagcaggagtagatgctgattttatcgcgaaaata
1544	ctcctgcatccggattgtctctgattttgtaatac
1565	cagttgaaggatcgcagatg
1871	aggaggaattcaaagcgggcagaatgtattgaaatg
1872	ctcctgacaccttcgatgaatgatcattgttcacg
1875	aggaggaattcaacaacgacgcctgccagctaa
1876	ctcctgacgactattttccgataaaaactagcatga
1877	aggaggtagactccgattatcctcacaaaaaagtg
1878	ctcctggatcctacgagactcagcagctgtcaag
1905	aggaggatcccttcgatgaatgatcattgttcacg
1906	ctcctggatccaagcatccgattggaggagaatcat
1907	aggaggtagactgttacgtcaagatcattaactgaat
2093	aggaggaattcgattatgcatagtgttcaaggaaaaat
2140	aggaggatccatgctagttttatcgcgaaaataaac
2141	ctcctgaattctcactttttgtgaggataatgcgg
2230	aggaggctctcaggtatgatcattcacaagtagtacc
2231	ctcctctgaggcaatcacttttacttcaatc
2704	aggaggatccttaacaacgacgcctgccagct
2707	ctcctggatcctacgagactcagcagctgtcaag
2708	caatcgccctatagtgagtcgtaactagcatgattctcctccaatcg
2709	ccagctttgtcccttagtgagtcgcattatcctcacaaaaaag

Supplemental Table S3: β -galactosidase specific activities for Fig. 2C.

Genotype	<i>amyE::P_{hag}^{transcriptional}-lacZ</i> specific activity in MU	<i>amyE::P_{hag}^{translational}-lacZ</i> specific activity in MU
Wild type	1048 \pm 60 (DS793)	7739 \pm 610 (DS278)
Δ <i>fliW</i>	2564 \pm 281 (DS8325)	316 \pm 9 (DS7598)
Δ <i>fliWcsrA</i>	808 \pm 68 (DS8324)	7617 \pm 982 (DS7597)
Δ <i>csrA</i>	772 \pm 46 (DS8323)	6235 \pm 321 (DS7596)

Supplemental Table S4: β -galactosidase specific activities for Fig 6.

Genotype	<i>amyE::P_{hag}^{transcriptional}-lacZ</i> specific activity in MU	<i>amyE::P_{hag}^{translational}-lacZ</i> specific activity in MU
Wild type	1048 ± 60 (DS793)	17027 ± 3686 (DS278)
<i>flgM::tet</i>	1877 ± 602 (DS8345)	8714 ± 877 (DS8340)
<i>csrA::kan</i>	875 ± 38 (DS8341)	17123 ± 1965 (DS8336)
<i>flgM::tet csrA::kan</i>	1123 ± 54 (DS8342)	21158 ± 2362 (DS8337)
<i>flgM::tet Δhag</i>	936 ± 138 (DS8443)	10404 ± 1614 (DS8442)
<i>ΔflhA</i>	170 ± 11 (DS6784)	139 ± 15 (DS8143)
<i>ΔflhA flgM::tet</i>	1543 ± 195 (DS8299)	1098 ± 291 (DS8298)
<i>ΔflhA csrA::kan</i>	139 ± 33 (DS8373)	1520 ± 94 (DS8371)
<i>ΔflhA flgM::tet csrA::kan</i>	1036 ± 86 (DS8297)	18208 ± 2811 (DS8296)
<i>ΔflhA flgM::tet Δhag</i>	740 ± 146 (DS8433)	8355 ± 697 (DS8434)
<i>ΔflgE</i>	114 ± 22 (DS5823)	112 ± 6 (DS7625)
<i>ΔflgE flgM::tet</i>	954 ± 84 (DS8806)	726 ± 127 (DS8927)
<i>ΔflgE csrA::kan</i>	119 ± 33 (DS8343)	880 ± 81 (DS8338)
<i>ΔflgE flgM::tet csrA::kan</i>	788 ± 21 (DS8924)	6065 ± 765 (DS8928)
<i>ΔflgE flgM::tet Δhag</i>	830 ± 61 (DS8435)	8012 ± 695 (DS8436)

SUPPLEMENTAL REFERENCES

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Figure S1



