

1 **Supplementary Material**

2 **Supporting Tables**

3 **Table S1.** Components of the *X. oryzae* pv. *oryzae* chemotaxis system.

Gene (Paralogs)	Locus Tag [Amino acid length]	Amino acid identity ^a	Extent of deletion in the in-frame deletion mutants ^b (amino acids)	Characteristics			
				Swimming Motility ^c	Chemotactic Response ^d		
					(towards xylem exudate)	(towards L-Glutamine)	(towards L-Methionine)
Xoo (Wild type)	n.a	n.a	n.a	++++	++++	+++++	+++++
<i>cheA</i>							
<i>cheA1</i>	XOO1470 [673]	(43% <i>E.coli</i>)	508 (108 to 615)	++++	+++	++++	++++
<i>cheA2</i>	XOO2624 [552]	(43% <i>E.coli</i>)	366 (101 to 466)	–	–	–	–
<i>cheA3</i>	XOO2836 [669]	(40% <i>E.coli</i>)	633 (35 to 666)	++++	+++	+++++	+++++
<i>cheW</i>							
<i>cheW1</i>	XOO1468 [171]	(30% <i>E.coli</i>)	116 (34 to 149)	+++	+++	+++	+++++
<i>cheW2</i>	XOO2833 [340]	(32% <i>E.coli</i>)	233 (35 to 267)	–	–	–	–
<i>cheW3</i>	XOO2850 [135]	(56% <i>E.coli</i>)	127 (4 to 130)	++++	++	+++	++++

<i>cheY</i> <i>cheY1</i>	XOO2622 [171]	(80% <i>V. cholerae</i>)	92 (51 to 142)	–	–	–	–
<i>cheY2</i>	XOO2835 [121]	(58% <i>V. cholerae</i>)	85 (25 to 109)	++	+++	++	+++
<i>vieA</i>	XOO1467 [433]	(33% <i>P. aeruginosa</i> PAO1)	216 (118 to 333)	++++	++	+++	++++
<i>cheR</i> <i>cheR1</i>	XOO1466 [275]	(41% <i>S. typhimurium</i>)	220 (34 to 253)	+++	+++	++	+++++
<i>cheR2</i>	XOO2857 [288]	(51% <i>S. typhimurium</i>)	196 (93 to 288)	++	–	–	–
<i>cheR3</i>	XOO0644 [569]	(29% <i>B. subtilis</i>)	484 (6 to 485)	++++	+++	++++	++++
<i>cheB</i> <i>cheB1</i>	XOO1465 [379]	(49% <i>S. typhimurium</i>)	278 (34 to 311)	+++	+++	++	++++
<i>cheB2</i>	XOO2859 [358]	(55% <i>S. typhimurium</i>)	250 (1 to 250)	++++	–	–	–
<i>cheD</i>	XOO2858 [198]	(35% <i>Thermotoga maritima</i> MSB8)	192 (5 to 196)	+	+	+	+
<i>cheV</i>	XOO2568 [314]	(29% <i>Syntrophus aciditrophicus</i> SB)	308 (4 to 311)	++	+++	+	+

<i>cheZ</i>	XOO2623 [208]	(28% <i>E. coli</i>)	203 (3 to 205)	+++	+	+	+
<i>mcp2</i>	XOO2848 [753]	(73% <i>E. coli</i>)	741 (5 to 745)	+	+	++++	-
<i>pdeA</i>	XOO2860 [728]	(44% <i>P.aeruginosa</i> PAO1)	500 (135 to 634)	+++	+	+	+
<i>fliC</i>	XOO2581 [422]	(45% <i>Legionella pneumophila</i>)	413 (3 to 415)	-	-	-	-

1 ^a Amino acid identity was determined by blast search with the ORF's corresponding to the locus
2 tag and its deduced polypeptide sequence in the National Center for Biotechnology Information
3 (NCBI) conserved domain protein database.

4 ^b Region of in-frame deletion corresponding to the amino acid residues in the mutants are
5 indicated in bracket.

6 ^c Motility was determined on swim plate assay by quantification of halo diameter compared to
7 the wild type strain. Symbols: -, halo size is equal to that of nonmotile Δ *fliC* mutant; +, halo
8 size is equal to that of wild type strain; ++, halo size 50% as that of wild type strain

9 ^dFor chemotaxis, syringe capillary assay was performed to determine the RCR (Relative
10 Chemotaxis Ratio), which corresponds to ratio of bacteria in the test capillary (containing the
11 chemoattractant) over the number of bacteria in the control phosphate buffer Saline (PBS) for
12 each respective strain compared with wild-type *Xoo* strain. Chemotaxis response was rated as
13 follows; - RCR of < 2; +, RCR of > 4.

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