

Supplementary Information

The *Xanthomonas* RaxH-RaxR two-component regulatory system is orthologous to the zinc-responsive *Pseudomonas* ColS-ColR system

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Figure S1 (following page). Periplasmic domains from select RaxH and ColS sequences. Highlighted residues are: Glu in ExxE motifs (yellow); invariant in all sequences (black); invariant in all RaxH sequences (green); invariant in all ColS sequences (blue); approximate transmembrane segment boundaries (light gray).

Abbreviations:

Xoo	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99 ^A	Rte	<i>Rehaibacterium terrae</i> DSM 25897
Sma	<i>Stenotrophomonas maltophilia</i> K279a	Tca	<i>Thermomonas carbonis</i> KCTC 42013
Aco	<i>Arenimonas composti</i> DSM 18010	Cfl	<i>Chiayiivirga flava</i> DSM 2416
Lgr	<i>Luteimonas granuli</i> Gr-4	Dko	<i>Dokdonella koreensis</i> DS-123
Lyi	<i>Luteimonas yindakuii</i> S-1072	Pae	<i>Pseudomonas aeruginosa</i> PAO1
Len	<i>Lysobacter enzymogenes</i> YC36	Ppu	<i>Pseudomonas putida</i> KT2440
Lgu	<i>Lysobacter gummosus</i> 3.2.11	Pfl	<i>Pseudomonas fluorescens</i> A506
Psp	<i>Pseudoxanthomonas spadix</i> BD-a59	Psy	<i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000
Psu	<i>Pseudoxanthomonas suwonensis</i> 11-1	Pst	<i>Pseudomonas stutzeri</i> A1501

Figure S1. Legend on previous page.

Xoo	MSKQRPLGLRVLVWLMFGYTLMLTLAVFGTAQYLHERA	EHGVRSLSLNSELDSTLERSVQNPDPYHWQSDSDLRLY	74
Sma	MKASKPGPLYRRVWMLLGYLALLSIAVFSVGNVYV	EHAEHAAMRALLNSELDSIVEHTEHEPHYRWQSDSDLRLY	76
Aco	MSARPASLRRRTIVLWLAFTALTVAVIAQGAFW	EYERSVRSLLTVELDHFLERRRTDPAFRWDGTAGIAVY	75
Lgr	MRTRPSLRRRLMQALTAYALLSLVVLVHGTLN	ERAEALVWESLTAEFELLERRSEEPGYGWHDDTLVLF	74
Lyj	MRTRPSLTRQITLGLVYGVLLSVLAFVHGLL	EQAERMVQAMLETSMDLLERRRHPDFGWRNNGRLDLH	74
Len	MATPDRPAAPRPSLRQILLGLFGYTALLSIAWVQGV	ENAEHLVWTSMDTELDFEVERSRIDADYRWTDTALSLY	84
Lgu	MATPAESPDKSKPKGRKTRSLRQILLGLFGYTALLSIAWVQGV	ENAEHLVWTSMDTELDFEVERSRIDADYRWTDTALSLY	89
Psp	MSLPMAIRISLRKRLRWALVYLVWVTGAWLGGEV	ENAEHQVRSLSMRSDLQHFEVRRQADPGYNWIDPAERLY	78
Psu	MKPGGIRSLRGLRARITLWLVYALISLAVFIHGFI	VEAEQLTWSRLKSELAHFVQSAEDPHYHWTDTETVQLY	80
Rte	MNRRTLRARITGLLGYALMAAAIFLHGYIV	EAVERTVRSLLLELDFYQTRRAADPRFEWPQETETALY	73
Tca	MPLRQPHSLHRTIVLWLAFTALTVAVIAQGTAVI	EYERTVRSMLMAELDHFYQTRRAADPRFEWPQETETALY	76
Cfl	MIRSTLSRIAASLFFVSLVAAVLSLGYLV	EDVEAVIWAAVLEPAMERHLAAEGRLETPRVSGRIGTFSV	73
Dko	MKPRWGLRRITVGLIAYAVLSIAVAVHGFV	ENAEHLVWESLHAEMDHLNRRATDPDYRWPDTQLELL	74
Pae	MEYKQSLARRIVIAFMLMTAVGGLFSAGIVGWHII	EEERLISRD LGGELERL RDDLAQGRNPVLDPGMRFFI	74
Ppu	MEFKQSLAQRILIAFALMSALVAGAFAGIVGTVHLV	EEERLISV LGGDLQRLL RMDSVSDWSHRPRPDQLFYF	74
Pfl	MEFKQSLAQRILIAFALMSALVAGAFAMIVATVHLV	EEKLSAGLGGDLQRLL RMDSVSDWSHRPRPDQLFYF	74
Psy	MEFKQSLAQRILIAFALMSALVAGSFAIGIISTVHLV	EEKLSAGLGGDLNRMLMDSVSDWSHRPRPDQLFYF	74
Pst	MLAKQPFARIVIAFTLMTLVSGVFSLGIVAVYF	ESQLVTGELSREL DIVLHEDLPSGRPPRLDAQTRFFS	74
Transmembrane 1 Exxe			
Xoo	HIDDV----	ARAPPVRLTLP	159
Sma	RFDE----	GMPESVRLHPGLH	160
Aco	RGDA----	PALPELSGLAPGLH	158
Lgr	GDA----	RPLPPEVVALPGGLH	156
Lyj	ILDAAD----	ARTPDALRPLAPGLH	159
Len	DSAT----	RPPPRELAALAPGVH	167
Lgu	DDAT----	RPPPELRLSPGLH	172
Psp	FLNTD----	PDVPTKLAALKPGGLH	162
Psu	GDDDD----	SPAPPEFARFGPGGLH	164
Rte	RRPLSETASHLPLALER	PLALERPLGLH	161
Tca	VGADD----	PDLPELRLGLKPGGLH	160
Cfl	RTAAPWP--	TDVPGDLRTLPEGLH	159
Dko	TFPAG----	STIPPLDLTLEPGVH	158
Pae	SDGQGS---	YAMPALDQLDVGFH	158
Ppu	SGGRDD---	FELPKDLRHLDRGFH	158
Pfl	SGPGD---	FELPKDLRHLERGFH	158
Psy	SNPGPD---	FDLPKDLRHLERGFH	158
Pst	TALPD----	YPLPEGFATLPEGFT	157
Transmembrane 2 Exxe			
Xoo	HIDDV----	ARAPPVRLTLP	159
Sma	RFDE----	GMPESVRLHPGLH	160
Aco	RGDA----	PALPELSGLAPGLH	158
Lgr	GDA----	RPLPPEVVALPGGLH	156
Lyj	ILDAAD----	ARTPDALRPLAPGLH	159
Len	DSAT----	RPPPRELAALAPGVH	167
Lgu	DDAT----	RPPPELRLSPGLH	172
Psp	FLNTD----	PDVPTKLAALKPGGLH	162
Psu	GDDDD----	SPAPPEFARFGPGGLH	164
Rte	RRPLSETASHLPLALER	PLALERPLGLH	161
Tca	VGADD----	PDLPELRLGLKPGGLH	160
Cfl	RTAAPWP--	TDVPGDLRTLPEGLH	159
Dko	TFPAG----	STIPPLDLTLEPGVH	158
Pae	SDGQGS---	YAMPALDQLDVGFH	158
Ppu	SGGRDD---	FELPKDLRHLDRGFH	158
Pfl	SGPGD---	FELPKDLRHLERGFH	158
Psy	SNPGPD---	FDLPKDLRHLERGFH	158
Pst	TALPD----	YPLPEGFATLPEGFT	157

Figure S2 (following page). *raxRH* gene neighborhoods in members of the order *Lysobacterales* (formerly *Xanthomonadales*). Non-contiguous genes are on separate lines. Genes are color-coded: *raxR* (dark blue); *raxH* (light blue;); *eptA*, phosphoethanolamine transferase (dark red); *lpxE*, lipid A 1-phosphatase (red); *arnT*, sugar-undecaprenyl phosphate transferase (orange); predicted undecaprenyl phosphate-sugar transferase, and amino-terminal domain in the *Chlamydia* LpxB lipid A-disaccharide synthase (green); predicted sugar nucleotide epimerase (light green); *mdoB*, phosphoglycerol transferase (dark gray); predicted methyltransferase (light gray); LPS heptose kinase (white); and insertion sequence (black rectangle).

Figure S2. Legend on previous page.

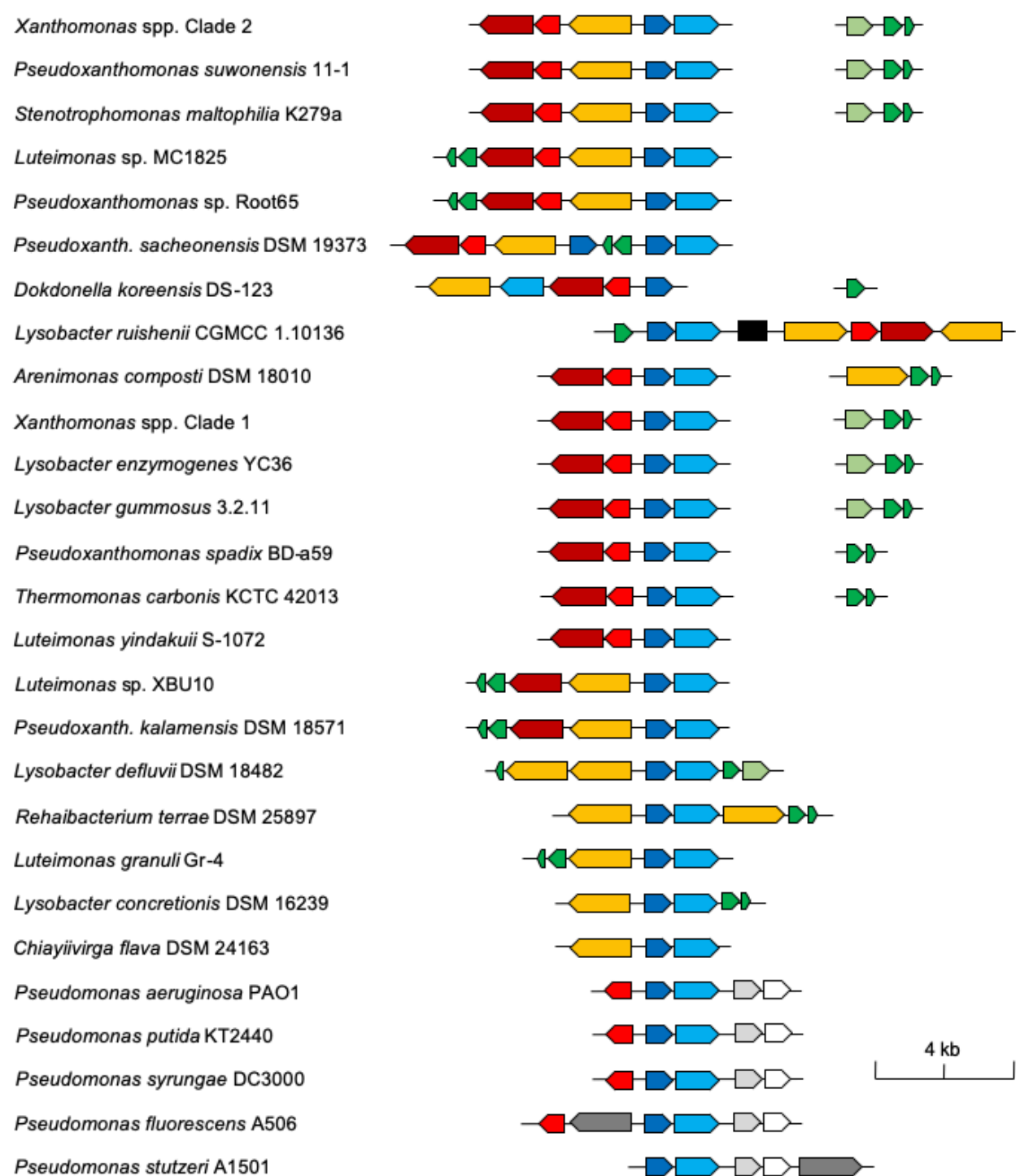


Figure S3. Percent G+C across the *gcvP*-*minCDE* region in *Xoo* PXO99^A. The plot was constructed in MegAlign. The red line shows the median G+C value for the PXO99^A genome.

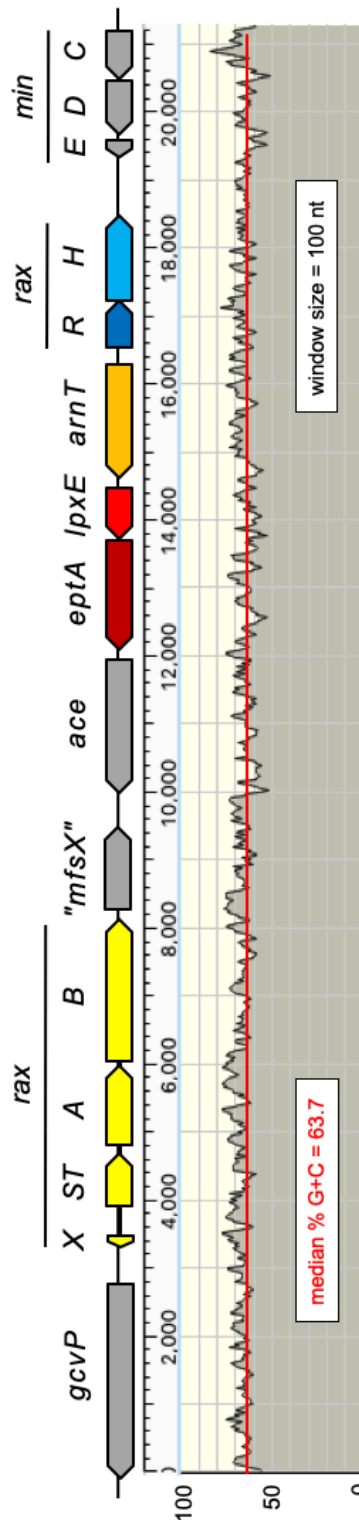


Table S1. Locus tags and accession numbers.

Symbol	Strain ^a	Locus Tag	Accession	Length
ColR	<i>Pae</i>	PA4381	WP_003094039.1	227
DetR	<i>Xoo</i>	PXORS_05125	WP_002811889.1	237
RaxR	<i>Xoo</i>	PXORS_06050	WP_011409239.1	238
VgrR	<i>Xoo</i>	PXORS_18925	WP_011407833.1	225
ColS	<i>Pae</i>	PA4380	WP_003094037.1	426
ColS	<i>Ppu</i>	PP_0902	AAN66527.2	436
ColS	<i>Pfl</i>	PSEBR_a4371	CAA70932.1	425
ColS	<i>Pst</i>	PST_0914	WP_011912104	422
ColS	<i>Psy</i>	PSPTO_4373	WP_003380966	429
DetS	<i>Xoo</i>	PXORS_05130	WP_027704202.1	423
RaxH	<i>Xoo</i>	PXORS_06055	WP_027703305.1	430
VgrS	<i>Xoo</i>	PXORS_18935	WP_027704076.1	439
EptA	<i>Xoo</i>	PXO_RS06035	WP_041182603.1	556
EptA	<i>Pae</i>	PA1972	WP_003113468.1	567
EptA	<i>Nmb</i>	NMB1638	WP_002216735.1	544
LpxE	<i>Xoo</i>	PXO_RS06040	WP_011409241.1	254
LpxE	<i>Pae</i>	PA4382	WP_003112760.1	264
LpxE	<i>Ret</i>	—	WP_011654039.1	244
ArnT	<i>Xoo</i>	PXO_RS06045	WP_027703306.1	577
ArnT	<i>Pae</i>	PA3556	WP_038403631.1	549
ArnT	<i>Cme</i>	Rmet_4828	ABF11690	575
—	<i>Xoo</i>	PXO_RS2226	WP_011407452.1	240
ArnC	<i>Pae</i>	PA3553	WP_003112880.1	339
—	<i>Xoo</i>	PXO_RS14680	WP_011408225.1	348
FlmF1	<i>Fno</i>	FTN_1403	ABK90273.1	314
FlmF2	<i>Fno</i>	FTN_0545	ABK89440.1	318

^a *Cme*, *Cupriavidus metallidurans* CH34; *Fno*, *Francisella novicida* U112; *Nmb*, *Neisseria meningitidis* MC58; *Ret*, *Rhizobium etli* (*leguminosarum*) CFN42; *Pae*, *Pseudomonas aeruginosa* PAO1; *Pfl*, *Pseudomonas fluorescens* WCS365; *Ppu*, *Pseudomonas putida* KT240; *Psy*, *Pseudomonas syringae* pv. *tomato* DC3000; *Pst*, *Pseudomonas stutzeri* A1501; *Xoo*, *Xanthomonas oryzae* pv. *oryzae* PXO99^A

Table S2. Genome sequences used for gene neighborhood analysis.

Species	Strain	Accession
Order Lysobacterales (formerly Xanthomonadales)		
Family Rhodanobacteraceae		
<i>Chiayiivirga flava</i>	DSM 24163	NZ_JACHHP000000000.1
<i>Dokdonella koreensis</i>	DS-123	NZ_CP015249.1
Family Lysobacteraceae (formerly Xanthomonadaceae)		
<i>Arenimonas composti</i>	DSM 18010	NZ_AUFF000000000.1
<i>Luteimonas granuli</i>	Gr-4	NZ_CP042218.1
<i>Luteimonas yindakuii</i>	S-1072	NZ_CP039383.2
<i>Luteimonas</i> sp.	MC1825	NZ_CP061714.1
<i>Luteimonas</i> sp.	XBU10	NZ_VTFT000000000.1
<i>Lysobacter concretionis</i>	DSM 16239	NZ_AVPS000000000.1
<i>Lysobacter defluvii</i>	DSM 18482	NZ_AUHT000000000.1
<i>Lysobacter enzymogenes</i>	YC36	NZ_CP040656.1
<i>Lysobacter gummosus</i>	3.2.11	NZ_CP011131.1
<i>Lysobacter ruishenii</i>	CGMCC 1.10136	NZ_VLKP000000000.1
<i>Pseudoxanthomonas kalamensis</i>	DSM 18571	NZ_PDWQ000000000.1
<i>Pseudoxanthomonas sacheonensis</i>	DSM 19373	NZ_PDWS000000000.1
<i>Pseudoxanthomonas spadix</i>	BD-a59	NC_016147.2
<i>Pseudoxanthomonas suwonensis</i>	11-1	NC_014924.1
<i>Pseudoxanthomonas</i> sp.	Root65	NZ_LMHA000000000.1
<i>Rehaibacterium terrae</i>	DSM 25897	NZ_JACHHX000000000.1
<i>Stenotrophomonas maltophilia</i>	K279a	NC_010943.1
<i>Thermomonas carbonis</i>	KCTC 42013	NZ_BMZL000000000.1
Clade 1 Xanthomonas spp. with raxX-raxSTAB		
<i>Xanthomonas translucens</i> pv. <i>cerealis</i>	CFBP 2541	NZ_CM003052.1
<i>Xanthomonas translucens</i> pv. <i>translucens</i>	DSM 18974	NZ_CAPJ000000000.1
<i>Xanthomonas translucens</i> pv. <i>undulosa</i>	ICMP 11055	NZ_CP009750.1
Clade 1 Xanthomonas spp. without raxX-raxSTAB		
<i>Xanthomonas albilineans</i>	GPE PC73	NC_013722.1
<i>Xanthomonas hyacinthi</i>	DSM 19077	JPLD000000000.1
<i>Xanthomonas sacchari</i>	R1	NZ_CP010409.1
<i>Xanthomonas theicola</i>	CFBP 4691	NZ_CP049017.1
Clade 2 Xanthomonas spp. with raxX-raxSTAB		
<i>Xanthomonas alfalfae</i>	GEV-Rose-07	MIKD000000000.1
<i>Xanthomonas axonopodis</i> pv. <i>manihotis</i>	UA536	AKEQ000000000.1
<i>Xanthomonas cucurbitae</i>	CFBP 2542	NZ_MDED000000000.1
<i>Xanthomonas dyei</i>	CFBP 7245	NZ_MDEE000000000.1
<i>Xanthomonas euvesicatoria</i>	85-10	NC_007508.1

Table S2 (continued). Genomes used for gene neighborhood analysis.

Species	Strain	Accession
<i>Xanthomonas maliensis</i> *	M97	NZ_AQPR00000000.1
<i>Xanthomonas perforans</i>	91-118	NZ_CP019725.1
<i>Xanthomonas phaseoli</i> pv. <i>dieffenbachiae</i>	LMG 695	NZ_JPYB00000000.1
<i>Xanthomonas phaseoli</i> pv. <i>phaseoli</i>	CFBP 412	NZ_CP020964.2
<i>Xanthomonas prunicola</i>	CFBP 8353	NZ_PHKV00000000.1
<i>Xanthomonas oryzae</i> pv. <i>leersiae</i>	NCPPB 4346	LHUK00000000.1
<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	AXO1947	NZ_CP013666.1
<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	PXO99 ^A	NC_010717.2
<i>Xanthomonas oryzae</i> pv. <i>oryzicola</i>	BLS256	NC_017267.2
<i>Xanthomonas vasicola</i> pv. <i>musacearum</i>	NCPPB 4392	AKBI00000000.1
<i>Xanthomonas vasicola</i> pv. <i>vasculorum</i>	NCPPB 206	AKBM00000000.1
Clade 2 <i>Xanthomonas</i> spp. without <i>raxX-raxSTAB</i>		
<i>Xanthomonas arboricola</i> pv. <i>juglandis</i>	Xaj 417	NZ_CP012251.1
<i>Xanthomonas bromi</i>	CFBP 1976	NZ_MDCE00000000.1
<i>Xanthomonas campestris</i> pv. <i>campestris</i>	8004	NC_007086.1
<i>Xanthomonas campestris</i> pv. <i>raphani</i>	756C	NC_017271.1
<i>Xanthomonas cannabidis</i> pv. <i>cannabidis</i>	NCPPB 2877	JSZE00000000.1
<i>Xanthomonas cassavae</i>	CFBP 4642	NZ_ATMC00000000.1
<i>Xanthomonas citri</i> pv. <i>citri</i>	306	NC_003919.1
<i>Xanthomonas codiae</i>	CFBP 4690	NZ_MDEC00000000.1
<i>Xanthomonas floridensis</i>	WHRI 8848	NZ_LXNG00000000.1
<i>Xanthomonas fragariae</i>	LMG 25863	AJRZ00000000.1
<i>Xanthomonas hortorum</i> pv. <i>gardneri</i>	ICMP 7383	NZ_CP018731.1
<i>Xanthomonas massiliensis</i>	SN8	NZ_FCOY00000000.1
<i>Xanthomonas melonis</i>	CFBP 4644	NZ_MDEH00000000.1
<i>Xanthomonas nasturtii</i>	WHRI 8853	NZ_LYMI00000000.1
<i>Xanthomonas pisi</i>	CFBP 4643	NZ_MDEI00000000.1
<i>Xanthomonas populi</i>	CFBP 1817	NZ_MDEJ00000000.1
<i>Xanthomonas retroflexus</i>	Sp953	FRDD00000000.1
<i>Xanthomonas vesicatoria</i>	LMG 911	NZ_CP018725.1
Order <i>Pseudomonadales</i>		
Family <i>Pseudomonadaceae</i>		
<i>Pseudomonas aeruginosa</i>	PAO1	NC_002516.2
<i>Pseudomonas fluorescens</i>	A506	NC_021361.1
<i>Pseudomonas putida</i>	KT2440	NC_002947.4
<i>Pseudomonas stutzeri</i>	A1501	NC_009434.1
<i>Pseudomonas syringae</i> pv. <i>tomato</i>	DC3000	AE016853.1

* Intermediate between clades 1 and 2