










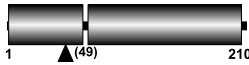










Table 2 - Characterization of XCC mutants<sup>a</sup>

PHENOTYPE CHARACTERIZATION	XCC ID (Psort/SignalP) <sup>b</sup> PRODUCT (gene name) MUTANT(S) DOMAIN STRUCTURE <sup>c</sup>	PHENOTYPE				NB <sup>d</sup>	R <sup>e</sup>	Cf <sup>f</sup>
		WS	HYP	NEC	HR-1			
	XAC0014 (IM/NS) Cardiolipin synthetase (cls) 19C02 / IC02 	ND	ND	ND	+	—	X	II.D.12
	XAC0095 (BC/NS) Xanthomonas conserved hypothetical protein 10H02* 	0	-	+	ND	X	X	VIII.C
	XAC0102 (BC/NS) Conserved hypothetical protein 16G10 	0	-	+	ND	X	—	VIII.A
	XAC0144 (OU+PS/SP) TonB-dependent receptor (iroN) 14E06 	0	-	+	ND	—	—	V.A.7
	XAC0340 (BC/NS) Conserved hypothetical protein 18C05 	0	0	0	0	X	X	VIII.A








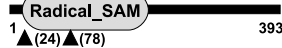


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Table 2 – continued

PHENOTYPE CHARACTERIZATION	XCC ID (Psort/SignalP) <sup>b</sup> PRODUCT (gene name) MUTANT(S) DOMAIN STRUCTURE <sup>c</sup>	PHENOTYPE				NB <sup>d</sup>	R <sup>e</sup>	Cf <sup>f</sup>
		WS	HYP	NEC	HR-1			
	XAC0410 (IM/NS) HrpB4 protein (hrpB4) 02H02 	0	0	0	0	—	X	VII.B
	XAC0618 (IM/NS) Periplasmic glucan biosynthesis protein (hrpM) 14H05 	-	-	0	ND	—	—	VII.G
	XAC0756 (IM/SP) Potassium-transporting ATPase A chain (kdpA) 11G08 	ND	-	+	ND	—	—	V.A.7
	XAC0789 (BC/NS) DGTP-pyrophosphohydrolase Thiamine phosphate synthase 06H10 	0	0	0	0	—	X	III.A.4
	XAC0798 (OM+PS/SP) Alpha-amylase (amy) 10B07 	ND	ND	ND	+	—	—	I.A.1






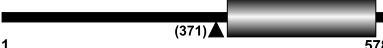

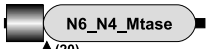


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Table 2 – continued

PHENOTYPE CHARACTERIZATION	XCC ID (Psort/SignalP) <sup>b</sup> PRODUCT (gene name) MUTANT(S) DOMAIN STRUCTURE <sup>c</sup>	PHENOTYPE				NB <sup>d</sup>	R <sup>e</sup>	Cf <sup>f</sup>
		WS	HYP	NEC	HR-1			
	XAC1201 (IM/NS) Conserved hypothetical protein 11C09 / 11D03 	ND	ND	ND	+	—	X	VIII.A
	XAC1266 (BC/NS) HrpX protein (hrpXct) 03C01 	0	0	0	0	—	X	VII.B
	XAC1669 (BC/NS) Histidine kinase-response regulator hybrid protein 18H08 	-	-	+	ND	—	—	I.D.3
	XAC1927 (IM/NS) Fe-S oxidoreductase (aslB) 14H02 / 25D11 	ND	ND	ND	+	X	—	I.C.3
	XAC2047 (BC/NS) PHA synthase subunit 10H09 / 11A04 / 11H07 	ND	ND	ND	+	X	—	IX

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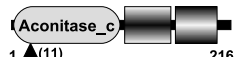






Table 2 – continued

PHENOTYPE CHARACTERIZATION	XCC ID (Psort/SignalP) <sup>b</sup> PRODUCT (gene name) MUTANT(S) DOMAIN STRUCTURE <sup>c</sup>	PHENOTYPE				NB <sup>d</sup>	R <sup>e</sup>	Cf <sup>f</sup>
		WS	HYP	NEC	HR-1			
	<b>XAC2053 (IM/NS)</b> Transcription-related protein (tex) <b>12G12</b> 	ND	ND	ND	+	X	—	I.D.2
	<b>XAC2072 (BC/NS)</b> Sugar ABC transporter ATP-binding protein (ugpC) <b>18H02 / 18H11 / IIA11</b> 	++	++	0	ND	—	—	V.A.3
	<b>XAC2118 (IM/NS)</b> Conserved hypothetical protein <b>17E05</b> 	-	-	+	ND	—	—	VIII.A
	<b>XAC2639 (BC/NS)</b> Site-specific DNA methyltransferase <b>17F02</b> 	0	-	+	ND	—	—	II.A.5
	<b>XAC3136 (BC/NS)</b> Two-component system sensor protein (exsG) <b>14B07*</b> 	ND	ND	ND	+	—	—	I.D.1

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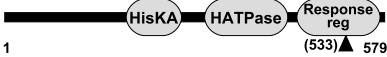





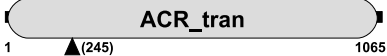




Table 2 – continued

PHENOTYPE CHARACTERIZATION	XCC ID (Psort/SignalP) <sup>b</sup> PRODUCT (gene name) MUTANT(S) DOMAIN STRUCTURE <sup>c</sup>	PHENOTYPE				NB <sup>d</sup>	R <sup>e</sup>	Cf <sup>f</sup>
		WS	HYP	NEC	HR-1			
	<b>XAC3320 (BC/NS)</b> ISxac3 transposase <b>10F08</b> 	ND	ND	ND	+	—	—	VI.C
	<b>XAC3457 (BC/NS)</b> 3-isopropylmalate dehydratase subunit (leuD) <b>15H10</b> 	ND	ND	ND	+	X	—	II.A.2
	<b>XAC3581 (BC/NS)</b> UDP-glucose dehydrogenase (ugd) <b>11G01</b> 	0	-	+	ND	-	—	I.B.11
	<b>XAC3600 (BC/NS)</b> ABC transporter ATP-binding protein (wzt) <b>18A01</b> 	++	++	0	ND	—	—	V.A.7
	<b>XAC3607 (BC/NS)</b> Type II secretion system protein-like protein (uptC) <b>14D01</b> 	ND	ND	ND	+	—	—	IV.A.2

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Table 2 – continued

PHENOTYPE CHARACTERIZATION	XCC ID (Psort/SignalP) <sup>b</sup> PRODUCT (gene name) MUTANT(S) DOMAIN STRUCTURE <sup>c</sup>	PHENOTYPE				NB <sup>d</sup>	R <sup>e</sup>	Cf <sup>f</sup>
		WS	HYP	NEC	HR-1			
	XAC3673 (IM/NS) Histidine kinase 18D06 	0	0	0	0	—	X	I.D.3
	XAC3980 (OM+PS/SP) Protease DO (htrA) 19B06 	0	0	0	0	—	—	III.C.3
	XAC4040 (BC/NS) Delta-aminolevulinic acid dehydratase (hemB) 11D09 	0	0	0	0	—	X	II.D.12
	XAC4160 (IM/SP) Cation efflux system protein (czcA) 02A03 	-	-	0	ND	—	—	VIII.C
	XACb0067 (IM/NS) Tn5045 transposase 12H03 	ND	-	+	ND	—	—	VI.C

<sup>a</sup> Data obtained from *Xanthomonas citri* subsp. *citri* genome web page; <sup>b</sup> Psort (<http://psort.nibb.ac.jp/form.html>) and SignalP (<http://www.cbs.dtu.dk/services/SignalP/>) identification (IN – inner membrane, OM – outer membrane, BC – bacterial cytoplasm, PS – periplasmic space, NS – non-secretory, SP – signal peptide); <sup>c</sup> Pfam domain architecture (names listed below); <sup>d</sup> northern blotting analysis

and <sup>e</sup> reactivation curve in plant and in medium culture (“X” - available; “—” - not available); <sup>f</sup> Functional categorization based on genome annotation (<http://genoma4.fcav.unesp.br/xanthomonas/>). The black triangles identify the site of transposition (EZ::Tn KAN-2) for each mutant, and the number represents the specific site of mutation; PHENOTYPE: WS - water soaking formation; Hyp - hyperplasia, Nec - necrosis, HR-1 - hypersensitive-like response (“ND” - not defined; “+” - induction; “++” - overinduction; “-” - repression; “0” - total absence of symptoms). Domains: PLD - phospholipase D active site motif (PF006140); AHAS1 - activator of Hsp90 ATPase homolog 1-like protein (PF08327); Plug - TonB-dependent receptor plug domain (PF07715); TonB\_dep\_rec - TonB dependent receptor (PF00593); DUF24 - HxlR-like helix-turn-helix (PF01638); Glyco\_transfer2 - glycosyl transferase family 2 (PF00535); kdpA - potassium-transporting ATPase A subunit (PF03814); NUDIX - NUDIX domain (PF00293); TMP-TENIndependent receptor plug domain (PF07715) thiamine monophosphate synthase/TENI (PF02581); Alpha\_amylase - alpha-amylase, catalytic domain (PF00128); HDOD - HDOD domain (PF08668); HD - HD domain (PF01966); HTH-AraC - bacterial regulatory helix-turn-helix proteins, AraC family (PF00165); PAS - PAS fold (PF00989); PAS\_3 - PAS fold (PF08447); PAS\_4 - PAS fold (PF08448); HisKA - histidine kinase A (phosphoacceptor) domain (PF00512) ; HATPase - histidine kinase-, DNA gyrase B-, and HSP90-like ATPase (PF02518); Response\_reg - response regulator receiver domain (PF00072); Radical\_SAM - radical SAM superfamily (PF04055); S1 - S1 RNA binding domain (PF00575); ABC\_tran - ABC transporter (PF00005); TOBE - TOBE domain (PF03459); TOBE\_2 - TOBE domain (PF08402); N6\_N4\_Mtase - DNA methylase (PF01555); HWE\_HK - HWE histidine kinase (PF07536); PG\_binding\_1 - putative peptidoglycan binding domain (PF01471); RHS - RHS repeat (PF05593); rve - integrase core domain (PF00665); Aconitase\_c - aconitase C-terminal domain (PF00694); UDPG-MGDP-dh\_N - UDP-glucose/GDP-mannose dehydrogenase family, NAD binding domain (PF03721); UDPG-MGDP-dh - UDP-glucose/GDP-mannose dehydrogenase family, central domain (PF00984); UDPG-MGDP-dh\_C - UDP-glucose/GDP-mannose dehydrogenase family, UDP binding domain(PF03720); GSPILE - Type II/IV secretion system protein (PF00437); UDG - uracil DNA glycosylase superfamily (PF03167); Trypsin - trypsin (PF00089); PDZ - PDZ domain, also known as DHR or GLGF (PF00595); ALAD - delta-aminolevulinic acid dehydratase (PF00490); ACR\_tran - AcrB/AcrD/AcrF family (PF00873); Transposase\_7 - transposase (PF01526).