

## Table S3: TnXax1-related MICs

### 1) *Acidovorax citrulli* str. AAC00-1 - CP000512

MIC ID	Locus Tag	Coordinates	Length	Orientation	Predicted Product or Feature
<b>MIC A</b> <b>3,740bp</b> <i>No DR</i>	-	2,975,223..2,975,303	84	+	IRL
	-	2,978,700..2,978,785	92	+	IRL
	Aave_2708	2,975,434..2,976,555	1,121	+	type III effector - XopJ2 (IPR005083)
	-	2,978,963..2,978,872	92	-	IRR
<b>MIC B</b> <b>3,740bp</b> <i>No DR</i>	-	3,224,781..3,224,872	92	+	IRL
	Aave_2938	3,227,189..3,228,310	1,121	-	type III effector - XopJ2 (IPR005083)
	-	3,225,044..3,224,959	84	-	IRR
	-	3,228,521..3,228,441	92	-	IRR

### 2) *Xanthomonas citri* subsp. *citri* str. 306, plasmid pXAC33 – NC\_003922

MIC ID	Locus Tag	Coordinates	Length	Orientation	Predicted Product or Feature
<b>MIC A</b> <b>3,738bp</b> [AGATT]	-	12,968..13,059	92	+	IRL
	XACa0022	13,079..16,459	3,380	-	TAL effector – PthA1
	-	16,616..16,706	91	-	IRR
<b>MIC B</b> <b>3,527bp</b> <i>No DR</i>	-	27,219..27,279	63	+	IRL
	XACa0039	27,299..30,589	3,290	-	TAL effector – PthA2
	-	30,836..30,746	91	-	IRR

### 3) *Xanthomonas citri* subsp. *citri* str. 306, plasmid pXAC64 – NC\_003922

MIC ID	Locus Tag	Coordinates	Length	Orientation	Predicted Product or Feature
<b>MIC A</b> <b>3,648bp</b> <i>No DR</i>	-	14,311..14,401	91	+	IRL
	XACb0015	14,558..17,848	3,290	+	TAL effector – PthA3
	-	17,868..17,959	92	-	IRR
<b>MIC B</b> <b>3,758bp</b> [GAG(A/C)(T/G)]	-	54,974..55,064	92	+	IRL
	XACb0065	55,221..58,712	3,491	+	TAL effector – PthA4
	-	58,823..58,732	92	-	IRR

### 4) *Xanthomonas citri* subsp. *citri* str. 29-1, plasmid pXAC33 – NC\_021801

MIC ID	Locus Tag	Coordinates	Length	Orientation	Predicted Product or Feature
<b>MIC A</b> <b>3,518bp</b> <i>No DR</i>	-	5,576..5,636	63	+	IRL
	XAC29_22784	5,656..8,487	2,831	-	TAL effector – PthA1
	-	9,004..9,094	91	-	IRR
<b>MIC B</b> <b>3,657bp</b> [AGATT]	-	24,927..25,018	94	+	IRL
	XAC29_22904	25,038..27,977	2,939	-	TAL effector – PthA2
	-	28,494..28,584	91	-	IRR

5) *Xanthomonas citri* subsp. *citri* str. 29-1, plasmid pXAC64 – NC\_020797

MIC ID	Locus Tag	Coordinates	Length	Orientation	Predicted Product or Feature
<b>MIC A</b>	-	13,749..13,839	91	+	IRL
<b>3,951bp</b>	XAC29_22209	14,356..17,589	3,233	+	TAL effector – PthA3
<i>No DR</i>	-	17,609..17,700	92	-	IRR
<b>MIC B</b>	-	53,945..54,035	91	+	IRL
<b>4,461bp</b>	XAC29_22454	54,552..58,295	3,743	+	TAL effector – PthA4
<i>No DR</i>	-	58,315..58,406	94	-	IRR

6) *Xanthomonas citri* subsp. *citri* str. A<sup>W</sup> 12879 , plasmid pXcaw58 – NC\_020817

MIC ID	Locus Tag	Coordinates	Length	Orientation	Predicted Product or Feature
<b>MIC A</b>	-	12,492..12,582	91	+	IRL
<b>3,914bp</b>	XCAW_b00018	12,739..16,326	3,587	+	TAL effector - PthAw1
<i>No DR</i>	-	16,346..16,406	63	-	IRR
<b>MIC B</b>	-	22,394..22,485	94	+	IRL
<b>3,853bp</b>	XCAW_b00026	22,505..25,999	3,494	-	TAL effector – PthAw2
<i>No DR</i>	-	26,156..26,247	92	-	IRR

7) *Xanthomonas citri* plasmid pXcB – AY228335

MIC ID	Locus Tag	Coordinates	Length	Orientation	Predicted Product or Feature
<b>MIC A</b>	-	31,463..31,553	91	+	IRL
<b>4,064bp</b>	AAO72098.1	31,719..35,225	3,506	-	TAL effector – PthB
<i>No DR</i>	-	35,461..35,527	68	-	IRR

8) *Xanthomonas axonopodis* pv. *glycines* str. 8ra plasmid pXAG81 – AY80632

MIC ID	Locus Tag	Coordinates	Length	Orientation	Predicted Product or Feature
<b>MIC A</b>	-	22,797..22,887	92	+	IRL
<b>7,618bp</b>	AAX12235	22,448..22,825	377	-	Uncharacterised protein family (IPR011978)
<i>No DR</i>	AAX12236	22,854..23,279	425	-	hypothetical protein
	AAX12237	23,278..23,628	350	+	hypothetical protein
	AAX12238	23,897..24,226	329	-	hypothetical protein
	AAX12239	24,223..24,759	536	-	hypothetical protein
	AAX12240	24,756..25,328	572	-	hypothetical protein
	AAX12241	25,416..26,503	1,087	-	IS <i>Xac2</i> transposase orfA (IS3 ssgr IS407) [complete IS]
	AAX12242	26,237..26,503	266	-	IS <i>Xac2</i> transposase orfB (IS3 ssgr IS407) [complete IS]
	AAX12209	1..3,801	3,801	+	TAL effector – AvrBs3/PthA
	-	3821..3912	94	-	IRR

9) *Xanthomonas campestris* pv. *campestris* str. ATCC 33913 – AE008922

MIC ID	Locus Tag	Coordinates	Length	Ori	Predicted Product or Feature
<b>MIC A</b>	-	2,466,511..2,466,591	91	+	IRL
<b>16,202bp</b>	XCC2094	2,467,727..2,469,457	1,730	+	Tannase/feruloyl esterase (IPR011118)
<i>No DR</i>	XCC2095	2,469,862..2,476,536	6,674	+	Protein of unknown function (IPR025103/ IPR021754)
	XCC2096	2,476,686..2,478,239	1,553	+	Mobilome protein (IPR026487)
	XCC2098	2,478,371..2,478,751	380	-	IS <i>Xac2</i> partial transposase (IS3 ssgr IS407) [Partial IS]
	XCC2097	2,478,711..2,479,607	896	+	Tn <i>Pa43</i> partial transposase (Tn3) [Partial IS]
	XCC2099	2,480,823..2,481,137	314	+	Protein-tyrosine phosphatase-like (IPR029021)
	XCC2100	2,481,228..2,482,565	1,337	+	Type III Effector - avrBs1
	-	2,482,712..2,482,622	91	-	IRR

Comment: MIC A is 100% identical to MIC A from *X. campestris* pv. *campestris* str. 8004

10) *Xanthomonas campestris* pv. *campestris* str. 8004 – CP000050

MIC ID	Locus Tag	Coordinates	Length	Ori	Predicted Product or Feature
<b>MIC A</b>	-	2,496,533..2,496,623	91	+	IRR
<b>16,202bp</b>	XC_2081	2,496,680..2,498,017	1,337	-	Type III Effector - avrBs1
<i>No DR</i>	XC_2082	2,498,108..2,498,422	314	-	Protein-tyrosine phosphatase-like (IPR029021)
	XC_2084	2,499,638..2,500,534	896	-	Tn <i>Pa43</i> partial transposase (Tn3) [Partial IS]
	XC_2083	2,500,494..2,500,874	380	+	IS <i>Xac2</i> partial transposase (IS3 ssgr IS407) [Partial IS]
	XC_2085	2,501,006..2,502,559	1,553	-	Mobilome protein (IPR026487)
	XC_2086	2,502,709..2,509,179	6,674	-	Protein of unknown function (IPR025103/IPR021754)
	XC_2087	2,509,788..2,511,518	1,730	-	Tannase/feruloyl esterase (IPR011118)
	-	2,512,734..2,512,654	91	-	IRL

Comment: MIC A is 100% identical to MIC A from *X. campestris* pv. *campestris* str. ATCC 33913

11) *Xanthomonas fuscans* subsp. *fuscans* str. 4834-R, plasmid pla – NC\_022539

MIC ID	Locus Tag	Coordinates	Length	Ori	Predicted Product or Feature
<b>MIC A</b>	-	8,706..8,797	92	+	IRL
<b>8,738bp</b>	XFF4834R_pla00140	9,203..10,255	1,052	+	type III effector XopJ2 (IPR005083)
<i>No DR</i>	XFF4834R_pla00150	10,323..11,651	1,328	+	IS <i>XaxI</i> aa1 transposase (IS256 family) [Partial IS]
	XFF4834R_pla00170	11,628..11,897	269	-	toxin-antitoxin module, anti-toxin (IPR010985)
	XFF4834R_pla00190	12,360..12,776	416	+	toxin-antitoxin module, toxin (IPR022907)
	XFF4834R_pla00200	12,784..13,344	560	+	Plasmid pRiA4b – XerD-like (IPR012912)
	XFF4834R_pla00220	13,605..14,153	548	-	DNA topoisomerase, type IA (IPR000380)
	-	14,156..14,247	92	+	IRL
	XFF4834R_pla00230	14,308..15,606	1,298	-	Metalloproteinase (IPR024079/IPR001590)
	XFF4834R_pla00240	15,727..17,046	1,319	-	Pectin lyase/virulence factor (IPR011050)
	-	17,444..17,353	92	-	IRR
<b>MIC B</b>	-	40,014..40,101	91	+	IRL
<b>5,303bp</b>	XFF4834R_pla00510	40,541..45,205	4,664	+	TAL effector – xfutal1
<b>[AGCA]</b>	-	1..93	94	-	IRR

12) *Xanthomonas fuscans* subsp. *fuscans* str. 4834-R, plasmid plc – NC\_022542

MIC ID	Locus Tag	Coordinates	Length	Ori	Predicted Product or Feature
<b>MITE</b> <b>454bp</b> <i>No DR</i>	-	21,844..21,934	91	+	MITE
	-	22,338..22,247	92	-	MITE
<b>MIC A</b> <b>5,536bp</b> <i>No DR</i>	-	26,372..26,462	92	+	IRL
	XFF4834R_plc00330	26,546..27,373	827	-	IS <i>Xcd1</i> transposase (IS3 ssgR IS407) [complete IS]
	XFF4834R_plc00340	27,367..27,633	266	-	IS <i>Xcd1</i> transposase (IS3 ssgR IS407) [complete IS]
	XFF4834R_plc00350	27,958..29,028	1,070	-	type III effector - XopE3
	XFF4834R_plc00360	29,113..30,390	1,277	-	lytic murein transglycosylase – <i>mlt</i> (IPR011757)
	-	30,746..30,837	92	+	IRL
	XFF4834R_plc00380	31,123..31,683	560	+	Plasmid pRiA4b – XerD-like (IPR012912)
-	31,908..31,820	91	-	IRR	
<b>MIC B</b> <b>3,764bp</b> <i>No DR</i>	-	38,186..38,276	91	+	IRL
	XFF4834R_plc00480	38,709..41,843	3,134	+	TAL effector – <i>xfutal2</i>
	-	41,904..41,950	47	-	IRR

Comment: The lytic murein transglycosylase – *mlt* (XFF4834R\_plc00360) is 98% identical (protein level) to XccA and pXAC64 XccA homologues.

13) *Xanthomonas fuscans* subsp. *fuscans* str. 4834-R – NC\_022541

MIC ID	Locus Tag	Coordinates	Length	Orientation	Predicted Product or Feature
<b>MIC A</b> <b>1,783bp</b> [GCGAA ]	-	1,884,500..1,884,596	97	+	IRL
	XFF4834R_chr16310	1,885,307..1,886,014	707	+	Type III effector – XopJ5
	-	1,886,240..1,886,283	45	-	IRR
<b>MIC B</b> <b>1,330bp</b> [AACTC]	-	2,750,592..2,750,676	85	+	IRL
	XFF4834R_chr23830	2,750,881..2,751,828	947	+	Type III effector - XopT
	-	2,751,831..2,751,922	92	-	IRR
<b>MIC C</b> <b>6,616bp</b> <i>No DR</i>	-	4,939,801..4,939,891	92	+	IRL
	XFF4834R_chr42580	4,940,252..4,940,536	284	-	Toxin-antitoxin system (IPR007712)
	XFF4834R_chr42590	4,940,536..4,940,823	287	-	Ribbon-helix-helix (IPR010985)
	XFF4834R_chr42600	4,940,955..4,941,353	132	-	hypothetical protein
	XFF4834R_chr42610	4,941,389..4,944,418	3,029	-	transposase TnpA (Tn3) (*)
	XFF4834R_chr42620	4,944,415..4,945,008	593	-	transposase TnpR (Tn3) (*)
	XFF4834R_chr42630	4,945,220..4,945,474	254	+	Ribbon-helix-helix (IPR010985)
XFF4834R_chr42640	4,945,471..4,945,755	284	+	PIN domain-like (IPR029060)	
-	4,946,327..4,946,417	91	-	IRR	

(\*) Related with ISPsy30 which is homologous to a Tn5501-like element present in two IncP-1 beta plasmids (accession no. AJ863570 and EF628291); they have a conserved 3.7 kb 3' fragment and a variable configuration of the 5' end. This copy of ISPsy30 in *Pseudomonas syringae* pv. *savastanoi* NCPPB 3335 has entrapped the Type III secretion system effector gene hopAF1. (Source: ISfinder annotation 2011)

14) *Xanthomonas oryzae* pv. *oryzae* str. PXO99A – NC\_010717

MIC ID	Locus Tag	Coordinates	Length	Ori	Predicted Product or Feature
<b>MIC A</b> <b>3,119bp</b> [TGATT]	-	321,285..321,375	92	+	IRL
	PXO_03553	321,508..324,162	2,654	-	Putative type III Effector (IPR027417/IPR016195)
	-	324,403..324,314	91	-	IRR
<b>MIC B</b> <b>19,302bp</b> <i>No DR</i>	-	1,625,939..1,625,971	33	+	IRL
	-	1,626,142..1,626,585	444	+	hypothetical protein
	PXO_00238	1,626,594..1,627,379	786	+	transposase (IS256) [Complete IS]
	PXO_00239	1,627,869..1,627,342	526	-	transposase (IS3 ssgR IS407) [Complete IS]
	PXO_00237	1,628,099..1,627,863	235	-	transposase (IS3 ssgR IS407) [Complete IS]
	PXO_00236	1,631,630..1,628,550	3,079	-	Type III effector - XopU
	PXO_00235	1,633,144..1,632,047	1,096	-	ISXoo14 aa1 transposase (IS5) [Complete IS]
	-	1,633,420..1,633,448	29	+	IRL
	-	1,633,420..1,633,509	91	-	IRR
	PXO_00234	1,635,617..1,633,530	2,086	-	Type III effector - XopX
	PXO_00233	1,636,492..1,637,448	957	+	IS1112 aa1 transposase (IS30) [Partial IS]
	-	1,637,451..1,638,299	849	+	Two component system (IPR011123)
	PXO_00232	1,638,739..1,638,161	577	-	DNA binding – Homeodoamin-like (IPR009057)
	PXO_00231	1,638,833..1,639,975	1,143	+	Membrane fusion protein (IPR006143)
	PXO_00230	1,640,032..1,642,620	2,589	+	Acridiflavin resistance protein – disrupted (IPR001036)
	PXO_00229	1,642,703..1,644,178	1,476	+	ISXoo5 aa1 transposase (IS5 ssgR IS5) [Complete IS]
	PXO_00228	1,644,249..1,644,761	513	+	Acridiflavin resistance protein – disrupted (IPR001036)
	-	1,645,213..1,645,241	29	-	IRR
<b>MIC C</b> <b>4,457bp</b> <i>No DR</i>	-	1,645,151..1,645,242	92	+	IRL
	PXO_00227	1,645,240..1,649,043	3,801	-	TAL effector - PthXo1
	-	1,649,518..1,649,608	91	-	IRR
<b>MIC D</b> <b>3,633 bp</b> [TA]	-	2,359,919..2,360,010	92	+	IRL
	PXO_00567	2,360,008..2,362,440	2,430	-	TAL effector - talC5a
	PXO_05602	2,362,441..2,362,563	120	+	hypothetical protein
	PXO_05603	2,362,535..2,362,690	153	+	hypothetical protein
-	2,363,461..2,363,552	92	-	IRR	
<b>MIC E</b> <b>4,010bp</b> [TA]	-	2,383,272..2,383,323	91	+	IRL
	PXO_00546	2,384,284..2,387,193	2,880	+	TAL effector – talC6a
	-	2,387,191..2,387,282	92	-	IRR
<b>MIC F</b> <b>4,938bp</b> <i>No DR</i>	-	2,387,192..2,387,220	29	+	IRL
	PXO_00545	2,387,462..2,387,656	192	+	hypothetical protein
	PXO_00544	2,387,749..2,387,874	123	-	hypothetical protein
	-	2,387,936..2,388,026	91	+	IRR
	PXO_05608	2,388,813..2,388,953	132	-	hypothetical protein
	PXO_05609	2,388,988..2,392,041	3,051	+	TAL effector - talC6b (pseudogene)
-	2,392,039..2,392,130	92	-	IRR	
<b>MIC G</b> <b>3,854bp</b> [TACTC]	-	2,682,578..2,682,668	91	+	IRL
	PXO_05633	2,683,629..2,686,343	2,712	+	TAL effector - talC7A
	-	2,686,341..2,686,432	92	-	IRR

Comment: MIC B is 99% identical (nucleotide level) to MIC J and MIC G from Xo MAFF and Xo KACC respectively.

14) *Xanthomonas oryzae* pv. *oryzae* str. PXO99A – NC\_010717 (Continuation)

MIC ID	Locus Tag	Coordinates	Length	Ori	Predicted Product or Feature
<b>MIC H</b> <b>3,854bp</b> [TACTC]	-	2,894,665..2,894,755	91	+	IRL
	PXO_06229	2,895,716..2,898,430	2,712	+	TAL effector - talC8a
	-	2,898,428..2,898,519	92	-	IRR
<b>MIC I</b> <b>5,531bp</b> [TACTC]*	-	4,104,802..4,104,830	29	+	IRL
	PXO_02171	4,105,147..4,105,266	117	+	hypothetical protein
	PXO_02263	4,105,270..4,105,569	297	+	hypothetical protein
	PXO_02170	4,105,359..4,105,484	123	-	hypothetical protein
	-	4,105,546..4,105,636	91	+	IRL
	PXO_05714	4,105,793..4,110,244	4,449	+	TAL effector - talC9b
<b>MIC J</b> <b>4,490bp</b> [TACTC]*	-	4,110,242..4,110,333	92	-	IRR
	-	4,110,243..4,110,271	29	+	IRL
	PXO_05715	4,110,513..4,110,707	192	+	hypothetical protein
	PXO_05716	4,110,800..4,110,925	123	-	hypothetical protein
	-	4,110,987..4,111,077	91	+	IRL
	PXO_05717	4,111,863..4,112,003	138	-	hypothetical protein
	PXO_05718	4,112,038..4,114,644	2,604	+	TAL effector - avrXa27
<b>MIC K</b> <b>4,088bp</b> [TACTC]*	-	4,114,642..4,114,733	92	-	IRR
	-	4,114,643..4,114,671	29	+	IRL
	PXO_05719	4,114,913..4,115,107	192	+	hypothetical protein
	PXO_05720	4,115,200..4,115,325	123	-	hypothetical protein
	-	4,115,387..4,115,477	91	+	IRL
	PXO_05721	4,116,263..4,116,403	138	-	hypothetical protein
<b>MIC L</b> <b>2,202bp</b> [TACTC]*	PXO_02269	4,116,438..4,118,642	2,202	+	TAL effector - talC9d
	-	4,118,640..4,118,731	92	-	IRR

(\*) The DRs are located flanking the second IRL and the IRR (includes only the TALE gene).

15) *Xanthomonas oryzae* pv. *oryzae* str. MAFF311018 – NC\_007705

MIC ID	Locus Tag	Coordinates	Length	Ori	Predicted Product or Feature
<b>MIC A</b> 3,746bp [C/GAGTA]	-	1,232,692..1,232,783	92	+	IRL
	XOO_1134	1,232,781..1,236,191	3,408	-	TAL effector - AvrBs3/Pth
	-	1,236,348..1,236,438	91	-	IRR
<b>MIC B</b> 4,784bp [G/CAGTA]	-	1,237,092..1,237,183	92	+	IRL
	XOO_1136	1,237,181..1,241,629	4,446	-	TAL effector - AvrBs3/Pth
	-	1,241,786..1,241,876	91	-	IRR
<b>MIC C</b> 4,058bp [AGTAC]	-	2,205,565..2,205,656	92	+	IRL
	XOO_1998	2,205,654..2,209,376	4,260	-	TAL effector - AvrBs3/Pth
	-	2,209,533..2,209,623	91	-	IRR
<b>MIC D</b> 7,575bp <i>No DR</i>	-	2,210,920..2,210,989	72	+	IRL
	XOO_2000	2,211,006..2,212,328	1,320	-	IS <i>Xoo5</i> aa1 transposase (IS5 ssg IS5) [Complete IS]
	-	2,212,619..2,212,645	27	-	IRR
	XOO_2001	2,212,644..2,216,771	4,125	-	TAL effector - AvrBs3/Pth
	XOO_2002	2,217,060..2,218,379	1,317	-	IS <i>Xo15</i> aa1 transposase (IS701)) [Complete IS]
-	2,218,433..2,218,495	60	-	IRR	
<b>MIC E</b> 4,191bp <i>No DR</i>	-	2,352,097..2,352,188	92	+	IRL
	XOO_2127	2,352,186..2,356,040	3,845	-	TAL effector - AvrBs3/Pth
	-	2,356,197..2,356,288	92	-	IRR
<b>MIC F</b> 3,635bp [TAG]	-	2,356,941..2,357,032	92	+	IRL
	XOO_2129	2,357,030..2,360,329	3,297	-	TAL effector - AvrBs3/Pth
	-	2,360,486..2,360,576	91	-	IRR
<b>MIC G</b> 4,055bp [TACTG]	-	3,219,386..3,219,476	91	+	IRL
	XOO_2865	3,219,633..3,223,352	3,717	+	TAL effector - AvrBs3/Pth
	-	3,223,350..3,223,441	92	-	IRR
<b>MIC H</b> 4,787bp <i>No DR</i>	-	3,224,095..3,224,185	91	+	IRL
	XOO_2866	3,224,342..3,228,793	4,449	+	TAL effector - AvrBs3/Pth
	-	3,228,791..3,228,882	92	-	IRR
<b>MIC I</b> 4,676bp <i>No DR</i>	-	3,229,536..3,229,626	91	+	IRL
	XOO_2868	3,229,783..3,234,123	4,338	+	TAL effector - AvrBs3/Pth
	-	3,234,121..3,234,212	92	-	IRR
<b>MIC J</b> 18,244bp <i>No DR</i>	-	3,234,122..3,234,150	29	+	IRL
	XOO_2869	3,233,116..3,234,604	511	-	Acridiflavin resistance protein – disrupted (IPR001036)
	XOO_2870	3,234,413..3,236,413	1,476	-	IS <i>Xoo5</i> aa1 transposase (IS5 ssg IS5) [Complete IS]
	XOO_2871	3,237,332..3,236,744	2,587	-	Acridiflavin resistance protein – disrupted (IPR001036)
	XOO_2872	3,238,501..3,239,389	1,111	-	Membrane fusion protein (IPR006143)
	XOO_2873	3,238,626..3,241,204	579	+	DNA binding – Homeodoamin-like (IPR009057)
	XOO_2874	3,241,065..3,242,189	1,122	-	Two component system (psedogene) (IPR011123)
	XOO_2875	3,242,691..3,244,778	2,088	+	Type III effector - XopX
	XOO_2876	3,243,194..3,246,186	993	+	IS <i>Xoo14</i> aa1 transposase (IS5) [Complete IS]
	-	3,244,797..3,244,886	91	-	IRL
	XOO_2877	3,244,677..3,249,757	3,081	+	Type III effector - XopU
	XOO_2878	3,248,208..3,250,444	237	+	transposase (IS3 ssg IS407) [Complete IS]
	XOO_2879	3,248,525..3,250,965	441	+	transposase (IS3 ssg IS407) [Complete IS]
	XOO_2880	3,249,713..3,250,928	784	-	transposase (IS256) [Complete IS]
XOO_2881	3,250,165..3,251,722	442	-	Hypothetical protein	
-	3,252,334..3,252,366	33	+	IRR	
<b>MIC K</b> 2,232bp <i>No DR</i>	-	4,763,458..4,763,547	91	+	IRL
	XOO_4215	4,763,699..4,764,424	723	+	Polymerase/histidinol phosphatase-like (IPR016195)
	XOO_4216	4,764,376..4,765,467	1,089	+	P-loop containing nucleoside triphosphate hydrolase (IPR027417)
	-	4,765,600..4,765,690	92	-	IRR

Comment: MIC J is 99% identical (nucleotide level) to MIC B and MIC G from Xo PXO99A and Xo KACC10331 respectively.

16) *Xanthomonas oryzae* pv. *oryzae* str. KACC 10331 – NC\_006834

MIC ID	Locus Tag	Coordinates	Length	Ori	Predicted Product or Feature
<b>MIC A</b> <b>4,058bp</b> [AGTA]	-	2,226,583..2,226,674	92	+	IRL
	XOO2128	2,226,672..2,230,478	3,804	-	TAL effector - AvrBs3/Pth
	-	2,230,551..2,230,641	91	-	IRR
<b>MIC B</b> <b>7,583bp</b> No DR	-	2,231,938..2,232,007	72	+	IRL
	XOO2130	2,232,024..2,233,529	1,503	-	ISXoo5 aa1 transposase (IS5 ssgR IS5) [Complete IS]
	XOO2131	2,233,670..2,237,881	4,209	-	TAL effector - AvrBs3/Pth
	XOO2132	2,238,086..2,239,468	1,380	-	ISXo15 aa1 transposase (IS701) [Complete IS]
	-	2,239,482..2,239,521	40	-	IRR
<b>MIC C</b> <b>3,767bp</b> No DR	-	2,377,246..2,377,337	92	+	IRL
	XOO2264	2,377,335..2,380,850	3,513	-	TAL effector - AvrBs3/Pth
	-	2,380,923..2,381,013	91	-	IRR
<b>MIC D</b> <b>4,907bp</b> [TACTC]	-	2,401,741..2,401,831	91	+	IRL
	XOO2276	2,401,778..2,405,743	3,963	+	TAL effector - AvrBs3/Pth
	XOO2277	2,405,806..2,406,252	444	+	Transposase (IS5) [Partial IS]
	-	2,406,604..2,406,648	45	-	IRR
<b>MIC E</b> <b>5,498bp</b> [TACTC]	-	3,224,429..3,224,519	91	+	IRL
	XOO3014	3,224,466..3,229,838	5,370	+	TAL effector - AvrBs3/Pth
	-	3,229,836..3,229,927	92	-	IRR
<b>MIC F</b> <b>3,965bp</b> No DR	-	3,230,581..3,230,671	91	+	IRL
	XOO3015	3,230,618..3,234,457	3,837	+	TAL effector - AvrBs3/Pth
	-	3,234,455..3,234,546	92	-	IRR
<b>MIC G</b> <b>18,266bp</b> No DR	-	3,234,456..3,234,484	29	+	IRL
	XOO3016	3,235,450..3,234,938	511	-	Acriflavin resistance protein – disrupted (IPR001036)
	XOO3017	3,237,011..3,235,521	1,489	-	ISXoo5 aa1 transposase (IS5 ssgR IS5) [Complete IS]
	XOO3018	3,239,682..3,237,094	2,587	-	Acriflavin resistance protein – disrupted (IPR001036)
	XOO3019	3,240,851..3,239,739	1,111	-	Membrane fusion protein (IPR006143)
	XOO3020	3,240,976..3,241,554	579	+	DNA binding – Homeodoamin-like (IPR009057)
	XOO3021	3,242,189..3,242,752	947	-	Two component system (IPR011123)
	XOO3022	3,243,040..3,245,127	2,088	+	Type III effector - XopX
	-	3,245,146..3,245,187	42	+	IRL
	XOO3023	3,245,513..3,246,178	666	+	ISXoo14transposase (IS5) [Disrupted IS]
	XOO3024	3,246,142..3,246,615	474	+	ISXoo14 transposase (IS5) [Disrupted IS]
	XOO3025	3,247,032..3,248,423	1,392	+	Type III effector – XopU (pseudogene)
	XOO3025	3,248,395..3,250,113	1,719	+	Type III effector – XopU (pseudogene)
	XOO3026	3,250,564..3,250,800	237	+	transposase (IS3 ssgR IS407) [Complete IS]
	XOO3027	3,250,794..3,251,321	528	+	transposase (IS3 ssgR IS407) [Complete IS]
	XOO3028	3,252,069..3,251,284	784	-	transposase (IS256) [Complete IS]
XOO3029	3,252,521..3,252,078	442	-	Hypothetical protein	
-	3,252,690..3,252,722	33	-	IRR	
<b>MIC H</b> <b>3,116bp</b> [AATCA]	-	4,767,482..4,767,569	91	+	IRL
	XOO4472	4,767,721..4,770,375	2,652	+	Polymerase/histidinol phosphatase-like (IPR016195)
	-	4,770,508..4,770,598	92	-	IRR

Comment: MIC G is 99% identical (nucleotide level) to MIC B and MIC G from Xo PXO99A and Xo KACC respectively.

17) *Xanthomonas oryzae* pv. *oryzicola* str. BLS256 – NC\_017267



MIC ID	Locus Tag	Coordinates	Length	Ori	Predicted Product or Feature
<b>MIC A</b> <b>7,407bp</b> <i>No DR</i>	-	2,548,617..2,548,706	91	+	IRL
	XOC_2512	2,549,003..2,550,064	1,059	+	ISXoo14 (IS5) [complete IS]
	XOC_2513	2,550,471..2,553,551	3,078	+	type III effector - XopU
	XOC_2516	2,553,877..2,554,584	705	+	transposase (IS1404) [partial IS]
	XOC_2515	2,554,547..2,554,705	156	-	disrupted transposase (IS256) – Partial N terminus
	XOC_2517	2,554,705..2,555,220	513	-	disrupted transposase (IS256) – Partial C terminus
	XOC_2518	2,555,622..2,555,981	357	+	partial transposase (Tn3)
	-	2,555,991..2,556,024	34	-	IRR