Table S1 Primers used in this study

Primer	Primer sequence (5’ to 3’)	Restriction site[a]
Primers used to identify *Xanthomonas* isolates		
Xan16-23-F1	AAGGAGGTGATCCAGCCGCA	
Xan16-23-F2	CTGAGCCAGGATCAAACTCTTC	
Xan16-23-R	CCTGACCTATCAACCACGTAGT	
Primers used to construct pSJA101		
Xf-DS-*pilA*-F	ATAACACCCGGGTGAATACACACAGCAACACG	XmaI
Xf-DS-*pilA*-R	GTAATATCTAGAGCGCAGGGAAACGATGGAAGGT	XbaI
Primers used to construct pSJA102		
Km^r-F	GCGGCGGGTACCTCGATGAATTGTGTCTCAAAA	KpnI
Km^r-R	AGCAGCCCCGGGTTAGAAAAACTCATCGAGCAT	XmaI
Primers used to construct pSJA103		
Xf-US-*pilA*-F	ATAATAGAGCTCGAGAGCAACCGCGACAATAGCA	SacI
Xf-US-*pilA*-R	GCGGCGGGTACCGTGTATACCTTCAATAAAAAG	Kpn1
Primers used to construct pSJA104		
Xf-*pilA*-F	GCGGCGTCTAGATTCTGGAAGAATGGATCG	XbaI
Xf-*pilA*-R	AGGTGTCTCGAGTTATTTAGCGGCAGTGCA	XhoI
Primers used to construct pSJA105		
Xan-US-*pilA*-F	GCGGCGGCTAGCTTTGAAGACATCTTCGAATTG	NheI
Xan-US-*pilA*-R	ATGGCCAGATCTAATGTACCCCTAGAGATGGTGT	BglII
Primers used to construct pSJA106		
Xan-DS-*pilA*-F	GCGCGCAGATCTGATTCGGTTGGATGGTTTTGAT	BglII

Xan-DS-*pilA*-F	ATAAATAAGCTTTTGACCGGCGCCTTGGCCACGC	HindIII
Primers used to construct pSJA107		
Xan-*pilA*-F	GCGGCGGCTAGCCTTATCCGTCAACACCAT	NheI
Xan-*pilA*-R	GTGAATAAGCTTTTACTGACAGGTCGCCGGGGC	HindIII
Primers used to detect prophage		
Sano-primase-F	AACCTGATCTGGTACGAC	
Sano-primase-R	GGACATTTTTCAGTTCTCTC	
Salvo-primase-F	CAACCTCATCTGGTATGAC	
Salvo-primase-F	GTCTTGGGTAATTTCTTTCT	
Prado-helicase-F	AACTACCTGACAGCGACT	
Prado-helicase-R	CGTACTAGCTTGGCTTCTA	
Paz-helicase-F	AAGAAGCGTGGTTTGTTTGC	
Paz-helicase-R	CTACCGGCTTCCCTAACTCC	

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[a] Restriction sites introduced in the primers are underlined.

TABLE S2 Comparative annotations of phages Sano and Salvo[a]

Gene(s)		% protein identity[b]	Strand[c]	Size (kDa)	Putative function	BcepNazgul homolog locus tag[d]	Evidence[e]
Sano_*01*	Salvo_*01*	52.2	R	10.2, 9.9	hypothetical protein		
Sano_*02*	Salvo_*02*		R	7.1, 17.5	hypothetical protein		
Sano_*03*	Salvo_*03*		R	7.2, 36.8	hypothetical protein		
Sano_*04*	Salvo_*04*		R	13.1, 18.6	hypothetical protein		
Sano_*05*	Salvo_*05*		R	5.0, 15.8	hypothetical protein		
Sano_*06*			R	7.3	hypothetical protein		
Sano_*07*			R	6.8	hypothetical protein		
Sano_*08*			R	20.3	conserved protein		
Sano_*09*	Salvo_*06*	50.1	R	27.9, 22.2	conserved protein		
	Salvo_*07*		R	5.4	hypothetical protein		
Sano_*10*			R	5.3	hypothetical protein		
Sano_*11*	Salvo_*08*	21.4	R	7.3, 6.8	hypothetical protein		

	Salvo_*09*		F	5.2	hypothetical protein
	Salvo_*10*		F	3.9	hypothetical protein
Sano_*12*			R	19.6	hypothetical protein
Sano_*13*	Salvo_*11*	57.1	F	14.7, 15.1	hypothetical protein
Sano_*14*	Salvo_*12*	46.0	F	19.1, 20.0	hypothetical protein
Sano_*15*	Salvo_*13*	31.0	F	66.8, 61.9	hypothetical protein
	Salvo_*14*		F	9.5	hypothetical protein
Sano_*16*	Salvo_*15*	66.2	F	8.7, 9.2	hypothetical protein
Sano_*17*	Salvo_*16*	36.5	F	17.9, 19.2	hypothetical protein
Sano_*18*	Salvo_*17*	89.1	F	11.9, 12.0	conserved protein
Sano_*19*	Salvo_*18*	79.8	F	10.8, 10.8	hypothetical protein
Sano_*20*			F	19.6	hypothetical protein
Sano_*21*			F	6.5	hypothetical protein
Sano_*22*	Salvo_*19*	93.6	F	11.6, 11.7	hypothetical protein
Sano_*23*	Salvo_*20*	67.8	F	22.0, 22.2	hypothetical protein
Sano_*24*			F	5.9	hypothetical protein

Sano_*25*	Salvo_*21*	56.5	F	11.8, 11.8	hypothetical protein		
Sano_*26*	Salvo_*22*	76.6	F	8.2, 7.8	hypothetical protein		
Sano_*27*	Salvo_*23*	34.1	F	12.4, 15.2	hypothetical protein		
Sano_*28*	Salvo_*24*	68.4	F	26.3, 26.6	conserved protein	NP_918968.1(E= 1.24E-09, Dice=19.3)	
Sano_*29*	Salvo_*25*	52.1	F	16.0, 14.8	hypothetical protein		
Sano_*30*	Salvo_*26*	49.4	F	19.5, 18.0	hypothetical protein		
Sano_*31*	Salvo_*27*	57.6	F	24.8, 25.5	hypothetical protein		
Sano_*32*	Salvo_*28*	12.8	F	10.2, 10.3	hypothetical protein		
Sano_*33*	Salvo_*29*	62.5	F	21.9, 22.1	hypothetical protein		
Sano_*34*	Salvo_*30*	76.9	F	17.0, 17.0	conserved protein		IPR012816, PF08719, TIGR02464, SSF143990
	Salvo_*31*		F	12.7	hypothetical protein		
Sano_*35*	Salvo_*32*	53.1	F	27.1, 27.7	conserved protein		SSF52374, SSF52540, (PF13207, Sano only)

						(IPR002891, PF01583 Salvo only)
Sano_*36*			F	11.4	hypothetical protein	
Sano_*37*	Salvo_*33*	75.9	F	34.1, 34.2	conserved protein	(IPR002815, SSF56726, Salvo only)
Sano_*38*			F	9.7	hypothetical protein	
Sano_*39*	Salvo_*34*	30.1	R	11.2, 13.5	o-spanin	(Lipoprotein adjacent to inner membrane spanin component, Sano only) (lipoprotein overlapped with inner membrane spanin component, Salvo only)
Sano_*40*	Salvo_*35*	31.7	R	13.6, 15.4	i-spanin	N-terminal TMD
Sano_*41*	Salvo_*37*		R	17.7, 16.3	holin-antiholin	(Predicted 1 TMD, Sano only) (predicted 2 TMDs,

						Salvo only)
Sano_*42*	Salvo_*38*		R	15.8, 28.6	holin-antiholin	(Predicted 4 TMDs, Sano only) (Predicted 1 TMD, Salvo only)
Sano_*43*	Salvo_*36*		R	21.3, 31.5	endolysin	(IPR024408, PF11860, HHpred hit 3gxr_A prob 97.7% E=4E-05, Sano only) (LipoP, SignalP, HHpred hit 2anv_A prob 100% E=3E-37, Salvo only)
Sano_*44*	Salvo_*39*	46.0	R	37.4, 38.5	tail fiber protein	(IPR001791, SM00282, Sano only) IPR008985, SSF49899, PF13385, Positional evidence, see text

Sano_*45*	Salvo_*40*	72.8	R	34.8, 35.2	conserved tail assembly protein		Positional evidence, see text
Sano_*46*	Salvo_*41*	85.7	R	6.3, 6.3	conserved tail assembly protein		Positional evidence, see text
Sano_*47*	Salvo_*42*	83.9	R	27.2, 27.0	conserved tail assembly protein		Positional evidence, see text
Sano_*48*	Salvo_*43*	75.2	R	90.7, 89.5	conserved tail assembly protein	NP_918976.1 (E=1.45E-60, Dice=25.0)	PF13550, positional evidence, see text
Sano_*49*	Salvo_*44*	78.0	R	30.4, 30.3	conserved tail assembly protein	NP_918979.1 (E=8.65E-18, Dice=26.0)	IPR018964, PF09356, IPR019228, PF09931, Positional evidence, see text
Sano_*50*	Salvo_*45*	75.1	R	64.0, 63.4	conserved tail assembly protein	NP_918980.1(E=1.79E-13, Dice=11.5)	Positional evidence, see text

Sano_*51*	Salvo_*46*	72.5	R	33.2, 33.0	conserved tail assembly protein		Positional evidence, see text
Sano_*52*	Salvo_*47*	80.8	R	36.4, 36.7	conserved tail assembly protein		Positional evidence, see text
Sano_*53*	Salvo_*48*	77.1	R	156.6, 156.3	tape measure protein		IPR013491, TIGR02675
Sano_*54*	Salvo_*49*	67.8	R	25.6, 25.7	pre-tape measure frameshift protein G-T	NP_918998.2(E= 6.45E-21, Dice=27.0)	Positional evidence, see text
Sano_*55*	Salvo_*50*	63.2	R	18.6, 18.1	pre-tape measure frameshift protein G	NP_918998.2(E= 4.52E-04, Dice=16.1)	Positional evidence, see text, slippery sequence 5’-GGGAAAC-3’
Sano_*56*	Salvo_*51*	79.2	R	28.4, 28.7	conserved virion associated protein	NP_918986.1(E= 8.77E-63, Dice=42.6)	
Sano_*57*	Salvo_*52*	78.9	R	19.2, 18.8	conserved virion	NP_918987.2(E=	

					associated protein	8.60E-22, Dice=30.6)	
Sano_*58*	Salvo_*53*	79.3	R	22.5, 22.8	conserved protein	NP_918988.2(E= 7.56E-32, Dice=38.9)	
Sano_*59*	Salvo_*54*	61.7	R	13.0, 12.6	conserved protein	NP_918989.2(E= 2.26E-20, Dice=32.3)	
Sano_*60*	Salvo_*55*	55.7	R	10.4, 9.8	conserved protein		
Sano_*61*	Salvo_*56*	90.3	R	38.3, 38.5	major capsid protein	NP_918991.1(E= 1.81E-86, Dice=42.0)	IPR005564, PF03864
Sano_*62*	Salvo_*57*	75.4	R	14.2, 13.8	decorator protein	NP_918992.1(E= 1.72E-14, Dice= 28.9)	IPR004195, PF02924
Sano_*63*	Salvo_*58*	66.7	R	14.6, 15.0	scaffold	NP_918993.2(E=	

						4.01E-15, Dice=32.3)	
Sano_*64*	Salvo_*59*	75.2	R	47.8, 47.9	prohead protease	NP_918994.2(E= 1.36E-90, Dice=38.2)	IPR002142, PF01343, PTHR32497, SSF52096
Sano_*65*	Salvo_*60*	83.6	R	62.1, 61.6	portal protein	NP_918995.1(E= 3.37E-168, Dice=45.7)	IPR006429, PF05136, TIGR01539
Sano_*66*	Salvo_*61*	78.1	R	8.0, 8.1	head-to-tail joining protein	NP_918996.1(E= 2.70E-12, Dice=29.1)	IPR004174, PF02831, SSF64210
Sano_*67*	Salvo_*62*	83.6	R	80.4, 79.2	terminase large subunit	NP_918997.2(E= 0, Dice=48.3)	IPR008866, PF05876
Sano_*68*	Salvo_*63*	82.0	R	22.0, 22.4	terminase small subunit	NP_918999.1(E= 4.62E-43, Dice=30.4)	IPR009901, PF07278

Sano_*69*	Salvo_*64*	78.3	R	54.2, 53.9	helicase	NP_919000.2(E=9.34E-66, Dice=29.3)	IPR000330, PF00176, IPR014001, SM00487, SSF52540
Sano_*70*	Salvo_*65*	77.2	R	11.7, 13.7	Holliday-junction resolvase	NP_919001.2(E=3.75E-18, Dice=30.8)	IPR014883, PF08774, SM00990
Sano_*71*	Salvo_*66*	78.6	R	79.1, 77.8	DNA polymerase I	NP_919002.1(E=6.40E-167, Dice=40.2)	IPR001098, PF00476, SM00482, SSF56672
Sano_*72*	Salvo_*67*	44.0	R	31.1, 30.3	ligase	NP_919004.1(E=4.38E-25, Dice=25.4)	IPR012340, SSF50249, IPR022595, PF10991
Sano_*73*	Salvo_*68*	73.7	R	46.6, 44.9	conserved protein	NP_919005.2(E=7.93E-59, Dice=27.9)	IPR021229, PF10926
Sano_*74*	Salvo_*69*	53.8	R	16.7, 16.5	putative lipoprotein		LipoP

Sano_*75*	Salvo_*70*	86.0	F	10.3, 12.2	hypothetical protein		
Sano_*76*	Salvo_*71*	80.5	F	95.5, 95.5	DNA primase	NP_919008.2(E= 1.27E-158, Dice=33.0)	IPR014819, PF08707, IPR015330, PF09250, SM00943, SSF52540, SSF56747
Sano_*77*	Salvo_*72*	52.6	F	10.5, 11.6	hypothetical protein		

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[a] Putative assignable functions and protein molecular masses are shown.

[b] Protein identities between Sano and Salvo homologs were calculated by the Dice method using BLASTp alignment identity scores.

[c] F/R, coding region on forward or reverse strand, respectively.

[*d*] E value and Dice identity reported for phage BcepNazgul homologs in Sano.

[e] Evidence includes detected conserved domains or motifs, HHpred hits, or other evidence as detailed in text.

TABLE S3 Comparative annotations of *Xylella* phages Prado and Paz[a]

Gene(s)		% protein identity[b]	Strand[c]	Size (kDa)	Putative function	Phage Cd1 homolog locus tag[d]	Evidence[e]
Prado_*01*	Paz_*01*	26.9	F	9.2, 10.3	hypothetical protein		
Prado_*02*	Paz_*02*	20.6	F	20.9, 19.6	conserved protein	ADD21636.1(E=8E-10, Dice=25.4)	
Prado_*03*	Paz_*03*	21.4	F	18.1, 16.8	conserved protein		
Prado_*04*			F	32.9	conserved protein		
	Paz_*04*		F	6.6	hypothetical protein		
Prado_*05*	Paz_*05*		F	5.0, 22.2	hypothetical protein		
Prado_*06*	Paz_*06*		F	8.2, 13.9	hypothetical protein		
Prado_*07*	Paz_*07*		F	19.5, 21.2	hypothetical protein		
Prado_*08*	Paz_*08*		F	11.3, 10.8	hypothetical protein		
Prado_*09*			F	13.5	hypothetical protein		
Prado_*10*	Paz_*09*	24.7	F	12.3, 15.8	hypothetical protein		
Prado_*11*	Paz_*10*	29.0	F	15, 15.8	conserved protein	ADD21644.1(E=5.10	

						E-08, Dice=22.1)	
	Paz_*11*		F	6.9	hypothetical protein		
Prado_*12*	Paz_*12*		F	8.1, 11.8	hypothetical protein		
Prado_*13*	Paz_*13*	50.5	F	31.1, 31.8	DNA primase	ADD21651.1 (E= 9.66E-47, Dice=35.0)	cd01029
	Paz_*14*		F	18.1	hypothetical protein		
Prado_*14*	Paz_*15*	38.4	F	48.4, 49.8	DNA helicase	ADD21652.1 (E=9.62E-109, Dice=40.9)	PF13481, (SSF52540 Paz only)
Prado_*15*	Paz_*16*	25.3	F	10.6, 12.3	hypothetical protein		
Prado_*16*			F	7.5	hypothetical protein		
Prado_*17*	Paz_*17*	51.9	F	92.5, 88.9	DNA polymerase A	ADD21653.1(E=0, Dice=51.4)	IPR001098, PF00476, SM00482, IPR002298, PR00868, PTHR10133,

							SSF56672
Prado_*18*	Paz_*18*	40.1	F	32.1, 31.7	conserved protein	ADD21654.1(E=5.07 E-54, Dice=35.3)	
Prado_*19*	Paz_*19*	52.1	F	34.4, 35.1	5'-3' exonuclease	ADD21655.1(E=2.63 E-72, Dice=38.5)	IPR020045,SSF47807
Prado_*20,*	Paz_*20*	70.2	F	14.1, 12.8	DNA endonuclease VII	ADD21656.1(E=6.39 E-34, Dice=45.9)	IPR004211, PF02945, SSF54060
Prado_*21*	Paz_*21*	79.2	F	31.8, 32.2	3' to 5' exonuclease		IPR012337, SSF53098
Prado_*22*	Paz_*22*	30.3	F	22.1, 23.7	conserved protein		
Prado_*23*	Paz_*24*	75.2	F	8, 8.1	conserved protein		
Prado_*24*			F	8.2	hypothetical protein		
Prado_*25*	Paz_*23*	20.3	F	11.4, 9.3	conserved protein		
Prado_*26*	Paz_*25*	35.0	F	33.3, 37.6	ATP-dependent DNA ligase	ADD21659.1(E=2.41 E-47, Dice=36.3)	(IPR012310, PF01068 Prado only) IPR012340,

							SSF50249, SSF56091
Prado_*27*	Paz_*26*	43.9	F	6.7, 6.4	hypothetical protein		
Prado_*28*	Paz_*27*	56.3	F	95.6, 91.7	DNA-dependent single-subunit RNA polymerase	ADD21661.1(E=0, Dice=51.0)	IPR002092, PTHR10102, PF00940, SSF56672
Prado_*29*	Paz_*28*	26.8	F	7.1, 6.5	conserved protein	ADD21662.1(E=2.80 E-06, Dice=23.6)	
Prado_*30*			F	15.2	conserved protein	ADD21663.1(E=2.42 E-16, Dice=24.5)	
Prado_*31*	Paz_*29*	30.1	F	12.1, 11.3	conserved protein	ADD21664.1(E=3.00 E-05, Dice=31.1)	
Prado_*32*	Paz_*30*	47.2	F	56.5, 56.5	head-tail connector	ADD21666.1(E=2.43 E-154, Dice=44.5)	IPR020991, PF12236
Prado_*33*	Paz_*31*	22.2	F	28.9, 26.3	scaffold	ADD21667.1(E=4.29 E-06, Dice=18.5)	(PHA01929 Prado only)

Prado_*34*	Paz_*32*	57.1	F	36.3, 36.3	major capsid protein	ADD21668.1(E=2.91 E-84, Dice=43.2)	cl18086
Prado_*35*	Paz_*33*	19.4	F	7.4, 7.9	hypothetical protein		
Prado_*36*	Paz_*34*	33.6	F	23.9, 24.0	tail tubular protein A	ADD21669.1(E=4.31 E-35, Dice=29.3)	cl10205
Prado_*37*	Paz_*35*	42.0	F	91.5, 93.8	tail tubular protein B	ADD21670.1(E=0, Dice=36.8)	
Prado_*38*	Paz_*36*	38.8	F	31.4, 30.2	internal virion protein	ADD21671.1(E=6.34 E-21, Dice=21.7)	
Prado_*39*	Paz_*37*	28.0	F	85.0, 85.1	internal virion protein	ADD21672.1(E=5.50 E-29, Dice=12.0)	
Prado_*40*	Paz_*38*	34.4	F	176.3, 147.1	internal virion protein with transclycosylase activity	ADD21673.1(E=2.85 E-120, Dice=18.9)	IPR023346, SSF53955
Prado_*41*	Paz_*39*	46.0	F	39.8, 39.7	tail fiber protein	ADD21674.1(E=1.57 E-15, Dice=7.6)	IPR005604, PF03906

Prado_*42*	Paz_*40*	32.8	F	44, 43.3	tail fiber protein		See text
Prado_*43*	Paz_*41*	24.5	F	33.6, 34.7	tail fiber protein		See text
Prado_*44*	Paz_*42*	36.2	F	21.2, 20.7	tail fiber protein		See text
Prado_*45*	Paz_*43*	38.2	F	7.3, 7.0	holin		Predicted 2 TMDs, see text
Prado_*46*	Paz_*44*	27.7	F	10.1, 10.2	terminase small subunit	ADD21677.1(E=1.80 E-05, Dice=21.9)	
Prado_*47*	Paz_*45*	59.8	F	65.8, 65.7	terminase large subunit	ADD21678.1(E=0, Dice=54.9)	
Prado_*48*	Paz_*46*	41.9	F	8.5, 7.2	hypothetical protein		
	Paz_*47*		F	29.8	conserved protein		
Prado_*49*	Paz_*48*	49.3	F	19.2, 18.3	endolysin	ADD21680.1(E=1.52 E-25, Dice=32.0)	IPR002196, PF00959, IPR023346, SSF53955
Prado_*50*	Paz_*49*	17.1	F	11.2, 10.8	i-spanin		N-terminal TMD

Prado_*51*	Paz_*50*	41.9	F	10.7, 10.2	o-spanin	ADD21682.1(E=1.25 E-05, Dice=20.1)	Lipoprotein overlapped with inner membrane spanin component
Prado_*52*	Paz_*51*	39.7	F	15.1, 14.1	conserved protein		

[a] Putative assignable functions and protein molecular masses are shown.

[b] Protein identities between Prado and Paz homologs were calculated by the Dice method using BLASTp alignment identity scores.

[c] F/R, coding region on forward or reverse strand, respectively.

[d] E value and Dice identity reported for phage Cd1 homologs in Prado.

[e] Evidence includes detected conserved domains or motifs, HHpred hits, or other evidence as detailed in text.