

Table S1. Genomic information used for whole genome phylogeny in Figure 4.

Phage name	Host	Family	Size (nt)	GenBank	Order	Family	Genus	Subfamily	Specie
<i>Stenotrophomonas</i> phage DLP4	<i>S. maltophilia</i> D1585	Siphoviridae	63945	MG018224.1	Caudovirales	Siphoviridae	Pamexvirus	unclassified Pamexvirus	
<i>Stenotrophomonas</i> phage IME13	<i>S. maltophilia</i>	Myoviridae	162327	JX306041.1	Caudovirales	Myoviridae	Tulanevirus		<i>Stenotrophomonas</i> virus IME13
<i>Stenotrophomonas</i> phage IME15	<i>S. maltophilia</i>	Podoviridae	38513	JX872508.1	Caudovirales	Autographiviridae	Studiervirinae	Teseptimavirus	<i>Stenotrophomonas</i> virus IME15
<i>Stenotrophomonas</i> phage IME-SM1	<i>S. maltophilia</i>	unclassified	159514	KR560069.1	Caudovirales	Ackermannviridae	unclassified Ackermannviridae		
<i>Stenotrophomonas</i> phage S1	<i>S. maltophilia</i>	Siphoviridae	40287	EU849489.1	Caudovirales	Siphoviridae	unclassified Siphoviridae		
<i>Stenotrophomonas</i> phage Smp131	<i>S. maltophilia</i>	Myoviridae	33525	JQ809663.1	Caudovirales	Myoviridae	Peduovirinae	Simpcentumvirus	
<i>Stenotrophomonas</i> phage vB_SmaS-DLP_1	<i>S. maltophilia</i> D1585	Siphoviridae	42887	KR537872.1	Caudovirales	Siphoviridae	Sep-timatrevirus	unclassified Sep-timatrevirus	
<i>Stenotrophomonas</i> phage vB_SmaS-DLP_2	<i>S. maltophilia</i> D1585	Siphoviridae	42593	KR537871.1	Caudovirales	Siphoviridae	Sep-timatrevirus	unclassified Sep-timatrevirus	
<i>Stenotrophomonas</i> phage vB_SmaS-DLP_6	<i>S. maltophilia</i> D1571	Myoviridae ¹	168489	KU682439.2	Caudovirales	Ackermannviridae	unclassified Ackermannviridae		
<i>Xanthomonas</i> phage Carpasina	<i>X. campestris</i>	Myoviridae	61939	MH059633.1	Caudovirales	Myoviridae	Carpasina-virus		<i>Xanthomonas</i> virus Carpasina
<i>Xanthomonas</i> phage CP1	<i>X. axonopodis</i> pv. citri	Siphoviridae	43870	AB720063.2	Caudovirales	Siphoviridae	Klementvirus		
<i>Xanthomonas</i> phage CP2	<i>X. axonopodis</i> pv. citri	Podoviridae	42963	AB720064.1	Caudovirales	Podoviridae	unclassified Podoviridae		
<i>Xanthomonas</i> phage f20-Xaj	<i>X. arboricola</i> pv. juglandis X-J303	Podoviridae	43851	NC_030928.1	Caudovirales	Autographiviridae	Pradovirus		<i>Xanthomonas</i> virus f20
<i>Xanthomonas</i> phage f29-Xaj	<i>X. arboricola</i> pv.	Siphoviridae	41865	KU595434.1	Caudovirales	Siphoviridae	Jerseyvirus	unclassified Jerseyvirus	

	<i>juglandis</i> X-J303								
	<i>X. arbori-</i>								
<i>Xanthomonas</i> phage f30-Xaj	<i>cola</i> pv. <i>juglandis</i> X-J303	<i>Podoviri-</i> <i>dae</i>	44262	NC 03093 7.1	Caudovi- rales	Autographi- viridae	Pradovirus		
<i>Xanthomonas</i> phage KPhi1	<i>X. euvesi-</i> <i>catoria</i>	<i>Myoviri-</i> <i>dae</i>	46077	KY210139 1	Caudovi- rales	Myoviridae	unclassified Myoviridae		
<i>Xanthomonas</i> phage OP1	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Si-</i> <i>phoviri-</i> <i>dae</i>	43785	AP008979 1	Caudovi- rales	Siphoviridae	Xipdeca- virus		
<i>Xanthomonas</i> phage OP2	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviri-</i> <i>dae</i>	46643	AP008986 1	Caudovi- rales	Myoviridae	Naesvirus		<i>Xanthomonas</i> virus OP2
<i>Xanthomonas</i> phage phi Xc10	<i>X. cam-</i> <i>pestris</i> pv. <i>citri</i>	<i>Podoviri-</i> <i>dae</i>	44597	MF375456 1	Caudovi- rales	Autographi- viridae	Pradovirus		
<i>Xanthomonas</i> phage phiL7	<i>X. cam-</i> <i>pestris</i> pv. <i>campestris</i>	<i>Si-</i> <i>phoviri-</i> <i>dae</i>	44080	EU717894 1	Caudovi- rales	Siphoviridae	Eisen- starkvirus		
<i>Xanthomonas</i> phage vB_XveM_DI BBI	<i>X. vesica-</i> <i>toria</i>	<i>Myoviri-</i> <i>dae</i>	49981	JN022534 1	Caudovi- rales	Myoviridae	unclassified Myoviridae		
<i>Xanthomonas</i> phage XacN1	<i>X. citri</i>	<i>Myoviri-</i> <i>dae</i>	38467 0	AP018399 1	Caudovi- rales	Myoviridae	unclassified Myoviridae		
<i>Xanthomonas</i> phage XAJ2	<i>X. ar-</i> <i>boricola</i> pv. <i>ju-</i> <i>glandis</i> <i>X. ar-</i>	<i>Si-</i> <i>phoviri-</i> <i>dae</i>	49241	KU197014 1	Caudovi- rales	Siphoviridae	unclassified Siphoviridae		
<i>Xanthomonas</i> phage XAJ24	<i>boricola</i> pv. <i>ju-</i> <i>glandis</i>	<i>Podoviri-</i> <i>dae</i>	44861	KU197013 1	Caudovi- rales	Autographi- viridae	Pradovirus		
<i>Xanthomonas</i> phage Xoo- sp2	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Si-</i> <i>phoviri-</i> <i>dae</i>	60497	KX241618 1	Caudovi- rales	Siphoviridae	Pamexvirus	unclassi- fied Pamexviri- s	
<i>Xanthomonas</i> phage Xop411	<i>X. oryzae</i>	<i>Si-</i> <i>phoviri-</i> <i>dae</i>	44520	DQ777876 1	Caudovi- rales	Siphoviridae	Xipdeca- virus		
<i>Xanthomonas</i> phage Xp10	<i>X. oryzae</i>	<i>Si-</i> <i>phoviri-</i> <i>dae</i>	44373	AY299121 1	Caudovi- rales	Siphoviridae	Xipdeca- virus		
<i>Xanthomonas</i> phage Xp15	<i>X. cam-</i> <i>pestris</i> pv. <i>pelargonii</i>	<i>Si-</i> <i>phoviri-</i> <i>dae</i>	55770	AY986977 1	Caudovi- rales	Siphoviridae	unclassified Siphoviridae		
<i>Xanthomonas</i> phage XPP1	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviri-</i> <i>dae</i>	46195	MG944227 1	Caudovi- rales	Myoviridae	Vidavervirus	unclassi- fied Vida- vervirus	

Table S2. Comparison matrix for similarities between genomes of the phages sequenced in this study. All sequences were assessed by comparing the percentage of shared 22-mers.

[illegible]

61. C15	F	62. 99	0.63. 99	0. 64.	0	65. 1	0.66. 99	0. 67.	0	68. 99	0.69. 25	0.70. 25	0.71. 25	0. 72.	0	73.	0	74. 99	0.75. 99	0.									
76. C17	F	77. 99	0.78. 99	0. 79.	0	80.	1	81.	1	82.	0	83.	1	84. 25	0.85. 25	0.86. 25	0. 87.	0	88.	0	89.	1	90.	1					
91. C23	F	92.	0	93.	0	94.	0	95.	0	96.	0	97.	1	98.	0	99.	0	100.	0	101.	0	102.	0	103.	0	104.	0	105.	0
106. C25	F	107. 99	0.108. 99	0. 109.	0	110.	1	111.	1	112.	0	113.	1	114. 25	0.115. 25	0.116. 25	0. 117.	0	118.	0	119.	1	120.	1					
121. C28	F	122. 25	0.123. 25	0. 124.	0	125. 25	0.126. 25	0. 127.	0	128. 25	0.	129.	1	130. 95	0.131. 75	0. 132.	0	133.	0	134. 25	0.135. 25	0.							
136. C30	F	137. 25	0.138. 25	0. 139.	0	140. 26	0.141. 26	0. 142.	0	143. 26	0.144. 95	0. 145.	1	146. 75	0. 147.	0	148.	0	149. 26	0.150. 26	0.								
151. C39	F	152. 25	0.153. 25	0. 154.	0	155. 25	0.156. 25	0. 157.	0	158. 25	0.159. 75	0.160. 75	0. 161.	1	162.	0	163.	0	164. 25	0.165. 25	0.								
166. C41	F	167.	0	168.	0	169.	0	170.	0	171.	0	172.	0	173.	0	174.	0	175.	0	176.	0	177.	1	178.	0	179.	0	180.	0
181. C44	F	182.	0	183.	0	184.	0	185.	0	186.	0	187.	0	188.	0	189.	0	190.	0	191.	0	192.	0	193.	1	194.	0	195.	0
196. C47	F	197. 99	0.198. 99	0. 199.	0	200. 99	0.201. 99	0. 202.	0	203. 99	0.204. 25	0.205. 25	0.206. 25	0. 207.	0	208.	0	209.	1	210. 99	0.								
211. C57	F	212. 99	0.213. 99	0. 214.	0	215. 99	0.216. 99	0. 217.	0	218. 99	0.219. 25	0.220. 25	0.221. 25	0. 222.	0	223.	0	224. 99	0.	225.	1								

Table S3. Genomic information used for MCP and Terminase_lsu phylogeny (Fig. S3).

Phage name	Host	Family	Size (nt)	GenBank	Major Capsid Protein ID	Terminase Large Subunit Protein ID
<i>Stenotrophomonas</i> phage DLP4	<i>S. maltophilia</i> D1585	<i>Siphoviridae</i>	63945	MG018224.1	ATS92208.1	ATS92199.1
<i>Stenotrophomonas</i> phage IME13	<i>S. maltophilia</i>	<i>Myoviridae</i>	162327	JX306041.1	AFQ22650.1	AFQ22643.1
<i>Stenotrophomonas</i> phage IME15	<i>S. maltophilia</i>	<i>Podoviridae</i>	38513	JX872508.1	AFV51470.1	AFV51483.1
<i>Stenotrophomonas</i> phage IME-SM1	<i>S. maltophilia</i>	<i>unclassified</i>	159514	KR560069.1	AKO61665.1	AKO61658.1
<i>Stenotrophomonas</i> phage S1	<i>S. maltophilia</i>	<i>Siphoviridae</i>	40287	EU849489.1	ACJ24732.1	ACJ24728.1
<i>Stenotrophomonas</i> phage Smp131	<i>S. maltophilia</i>	<i>Myoviridae</i>	33525	IQ809663.1	AFJ75479.1	AFJ75477.1
<i>Stenotrophomonas</i> phage vB_SmaS-DLP_1	<i>S. maltophilia</i> D1585	<i>Siphoviridae</i>	42887	KR537872.1	AKI28799.1	AKI28793.1
<i>Stenotrophomonas</i> phage vB_SmaS-DLP_2	<i>S. maltophilia</i> D1585	<i>Siphoviridae</i>	42593	KR537871.1	AKI28741.1	AKI28735.1
<i>Stenotrophomonas</i> phage vB_SmaS-DLP_6	<i>S. maltophilia</i> D1571	<i>Myoviridae</i> ¹	168489	KU682439.2	AMQ65921.1	AMQ65913.1
<i>Xanthomonas</i> phage Car-pasina	<i>X. campestris</i>	<i>Myoviridae</i>	61939	MH059633.1	AWD92405.1	AWD92396.1
<i>Xanthomonas</i> phage CP1	<i>X. axonopodis</i> pv. <i>citri</i>	<i>Siphoviridae</i>	43870	AB720063.2	BAM29080.1	BAM29076.1
<i>Xanthomonas</i> phage CP2	<i>X. axonopodis</i> pv. <i>citri</i>	<i>Podoviridae</i>	42963	AB720064.1	BAM66438.1	BAM66434.1
<i>Xanthomonas</i> phage f20-Xaj	<i>X. arboricola</i> pv. <i>juglandis</i> X-J303	<i>Podoviridae</i>	43851	NC_030928.1	YP_009275467.1	YP_009275454.1

<i>Xanthomonas</i> phage f29-Xaj	<i>X. arboricola</i> pv. <i>juglandis</i> X-J303	<i>Siphoviridae</i>	41865	KU595434.1	AMM44781.1	AMM44766.1
<i>Xanthomonas</i> phage f30-Xaj	<i>X. arboricola</i> pv. <i>juglandis</i> X-J303	<i>Podoviridae</i>	44262	NC_030937.1	YP_009276308.1	YP_009276349.1
<i>Xanthomonas</i> phage KPhi1	<i>X. euvesicatoria</i>	<i>Myoviridae</i>	46077	KY210139.1	APQ41901.1	APQ41906.1
<i>Xanthomonas</i> phage OP1	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Siphoviridae</i>	43785	AP008979.1	BAE72712.1	BAE72709.1
<i>Xanthomonas</i> phage OP2	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	46643	AP008986.1	BAE72772.1	BAE72777.1
<i>Xanthomonas</i> phage phi Xc10	<i>X. campestris</i> pv. <i>citri</i>	<i>Podoviridae</i>	44597	MF375456.1	ASZ72035.1	ASZ72044.1
<i>Xanthomonas</i> phage phiL7	<i>X. campestris</i> pv. <i>campestris</i>	<i>Siphoviridae</i>	44080	EU717894.1	ACE75746.1	ACE75743.1
<i>Xanthomonas</i> phage vB_XveM_DIBBI	<i>X. vesicatoria</i>	<i>Myoviridae</i>	49981	JN022534.1	AEX65675.1	AEX65672.1
<i>Xanthomonas</i> phage XacN1	<i>X. citri</i>	<i>Myoviridae</i>	384670	AP018399.1	BBA65422.1	BBA65403.1
<i>Xanthomonas</i> phage XAJ2	<i>X. arboricola</i> pv. <i>juglandis</i>	<i>Siphoviridae</i>	49241	KU197014.1	AMW36127.1	AMW36122.1
<i>Xanthomonas</i> phage XAJ24	<i>X. arboricola</i> pv. <i>juglandis</i>	<i>Podoviridae</i>	44861	KU197013.1	AMW36095.1	AMW36109.1
<i>Xanthomonas</i> phage Xoo-sp2	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Siphoviridae</i>	60497	KX241618.1	ANT45254.1	ANT45236.1
<i>Xanthomonas</i> phage Xop411	<i>X. oryzae</i>	<i>Siphoviridae</i>	44520	DQ777876.1	ABK00157.1	ABK00154.1
<i>Xanthomonas</i> phage Xp10	<i>X. oryzae</i>	<i>Siphoviridae</i>	44373	AY299121.1	AAP58676.1	AAP58673.1
<i>Xanthomonas</i> phage Xp15	<i>X. campestris</i> pv. <i>pelargonii</i>	<i>Siphoviridae</i>	55770	AY986977.1	AAX84853.1	AAX84927.1
<i>Xanthomonas</i> phage XPP1	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	46195	MG944227.1	AVO23667.1	AVO23662.1
<i>Xanthomonas</i> phage XPP2	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	46480	MG944228.1	AVO23722.1	AVO23717.1
<i>Xanthomonas</i> phage XPP3	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	49612	MG944229.1	AVO23799.1	AVO23794.1
<i>Xanthomonas</i> phage XPP4	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	47397	MG944230.1	AVO23889.1	AVO23884.1
<i>Xanthomonas</i> phage XPP6	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	46281	MG944231.1	AVO23998.1	AVO23993.1
<i>Xanthomonas</i> phage XPP8	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	46278	MG944232.1	AVO24023.1	AVO24028.1
<i>Xanthomonas</i> phage XPP9	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	48669	MG944233.1	AVO24107.1	AVO24102.1
<i>Xanthomonas</i> phage XPV1	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	46503	MG944234.1	AVO24222.1	AVO24217.1
<i>Xanthomonas</i> phage XPV2	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	45969	MG944235.1	AVO24254.1	AVO24259.1
<i>Xanthomonas</i> phage XPV3	<i>X. oryzae</i> pv. <i>oryzae</i>	<i>Myoviridae</i>	47046	MG944236.1	AVO24390.1	AVO24319.1
<i>Xylella</i> phage Paz	<i>X. fastidiosa</i>	<i>Podoviridae</i>	43869	KF626666.1	AHB12129.1	AHB12142.1
<i>Xylella</i> phage Prado	<i>X. fastidiosa</i>	<i>Podoviridae</i>	43940	KF626667.1	AHB12182.1	AHB12195.1
<i>Xylella</i> Phage Salvo	<i>X. fastidiosa</i>	<i>Siphoviridae</i>	55601	KF626668.1	AHB12256.1	AHB12262.1
<i>Xylella</i> Phage Sano	<i>X. fastidiosa</i>	<i>Siphoviridae</i>	56147	KF626665.1	AHB12081.1	AHB12087.1
<i>Xylella</i> phage Xfas53	<i>X. fastidiosa</i>	<i>Podoviridae</i>	36674	GQ421471.1	ACV41134.1	ACV41131.1

For phylogenetic analysis, protein sequences of the Major Capsid Protein (MCP) and Terminase Large subunit (Terminase_Lsu) of the *Caudovirales* bacteriophages infecting *Xanthomonadales* were downloaded from the Genbank database (Table S2). Sequence alignments were performed using ClustalW, and cladograms were built using the MEGA-X software [1]. Aminoacid sequence data set were concatenated using Mesquite Version 2.6 [2]. Then, trees were inferred based on the maximum-likelihood Statistical method using MEGA-X and bootstrap values were calculated from 1,000 bootstrap replications. Genetic distances were determined by the Jones-Taylor-Thornton (JTT) model [3].

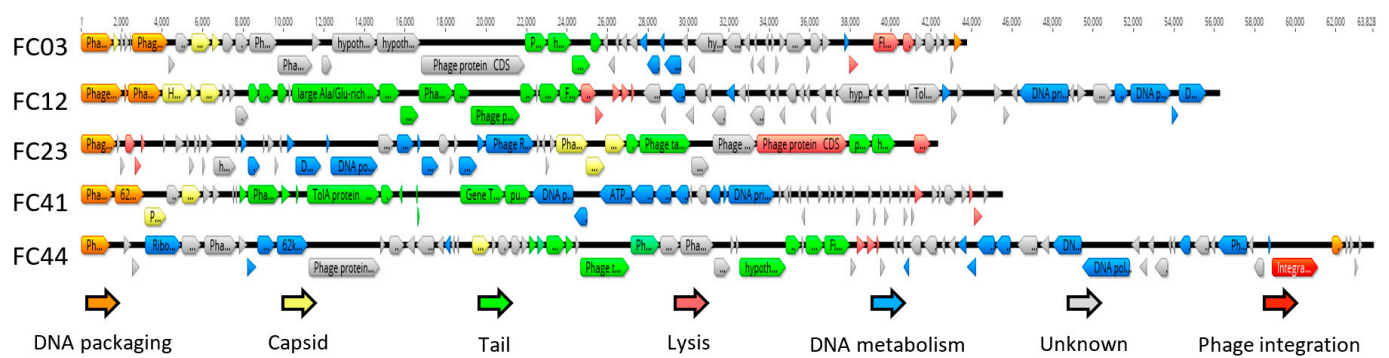


Figure S1. Genomic organization and main functions encoded by FC03-Usme, FC12-Bacata, FC23-Cota, FC41-Suba and FC44-Bosa phage genomes, the type phages of the 5 PCR groups defined in this study. .

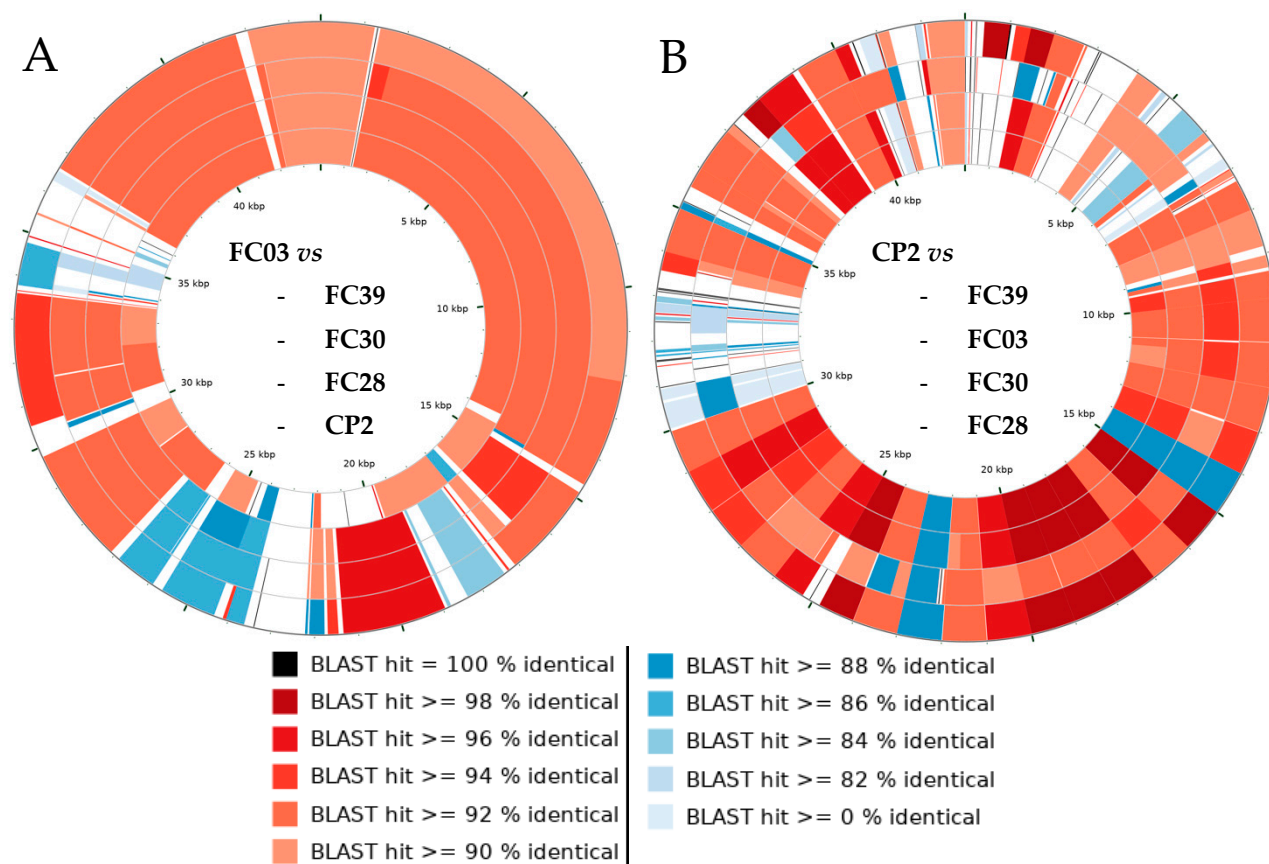


Figure S2. Visualization of BLAST-pairwise comparisons of genome sequences of FC03-Usme-like phages and *Xanthomonas axonopodis* phage CP2. Genomic sequences of isolated phage FC03-Usme, and *X. axonopodis* phage CP2 were cut in 1 kb-length fragments. Conservation of each fragment of a query genome was searched in the others using the BLASTN algorithm. The CGVIEW analytic tool [4] was used to represent the results, with the order of phage genome given from the external to the internal circles. The color scale indicates the level of identity. White stripes indicate fragments from the query genome that are absent in the others. A- Pairwise comparisons of FC03-Usme versus FC39-Tenjo, FC30-Tabio, FC28-Sopo and *X. axonopodis* phage CP2; B- Pairwise comparisons of *X. axonopodis* phage CP2 versus FC39-Tenjo, FC03-Usme, FC30-Tabio and FC28-Sopo.

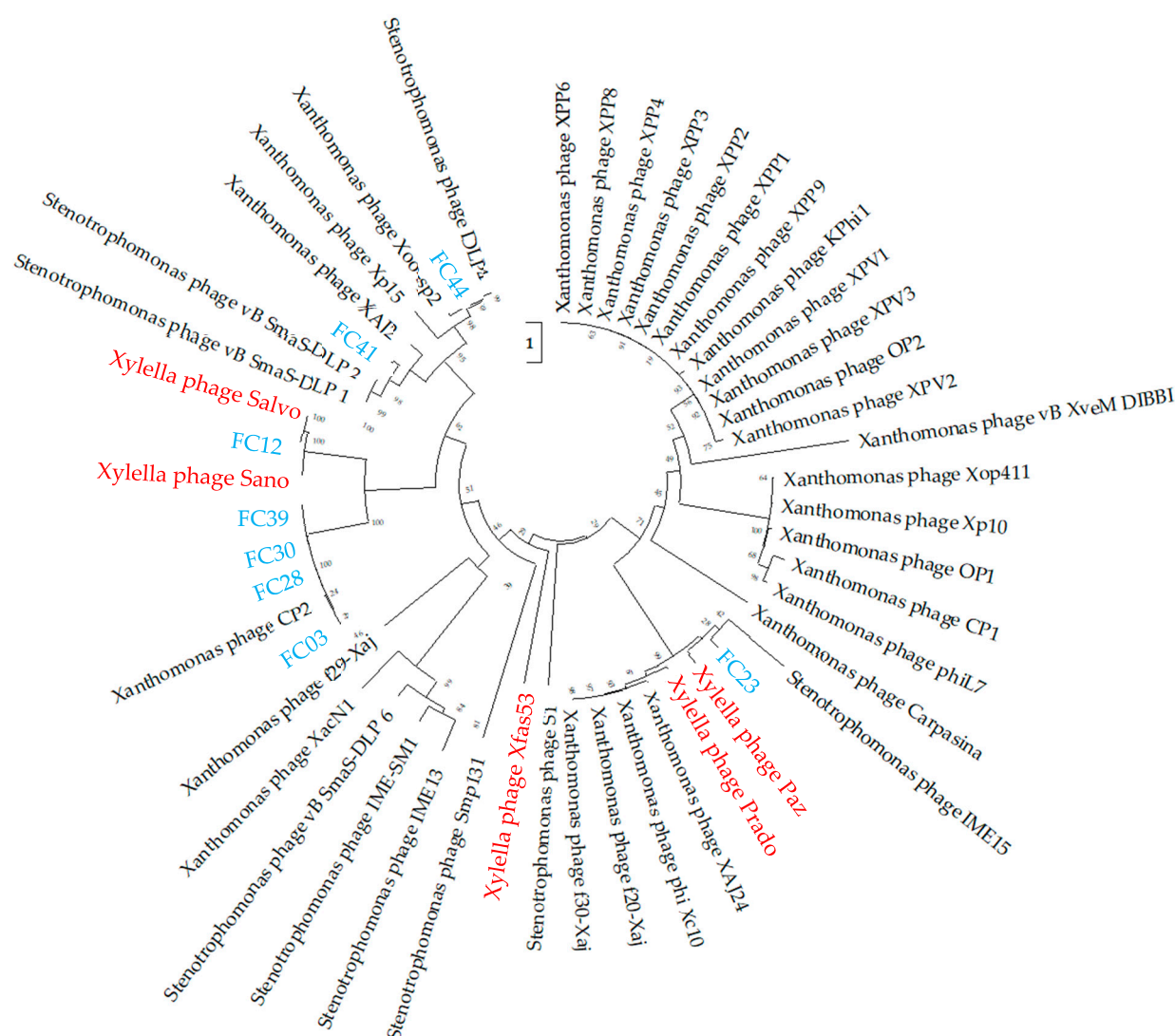


Figure S3. Phylogeny of phages infecting Xanthomonads. Circular cladograms showing the relationships between amino acid sequences obtained in this study and the isolated Caudovirales phages active on various species of the genera *Xanthomonas* and *Stenotrophomonas*. The Neighbor Joining trees based on the concatenated alignment of the conserved Major Capsid Protein and the Terminase large subunit protein with the highest log likelihood - (-100895.80) are shown. Initial tree for the heuristic search was obtained automatically by applying Neighbor-Join to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. This analysis involved 51 amino acid sequences. A total of 2214 positions were analyzed in the final dataset. Numbers indicated on branches indicate the number of substitutions per site. Red labels highlight referenced bacteriophages that are active on *X. fastidiosa* and blue labels highlight bacteriophages isolated in this study.

Supplemental References:

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