

Table S1

General assembly characteristics of the strains

Strain	Xap	Xmi	Xvt
Platform	Roche 454 GS FLX	Roche 454 GS FLX	Roche 454 GS FLX+
Reads	664,349	770,765	726,914
Bases	278,291,163	345,463,238	295,838,728
Coverage	~55	~69	~56
Contigs >500bp	217	195	50

Table S2

List of primers used in the study.

S.NO	Primer ID	Sequence(5'-3')	Length	Purpose
1	XC-UP1	CTACGGCCTGGAGTCATTG	19	Xanthomonadin cluster amplification from Xmi (LMG 941)
2	XC-UP2	CCAACGGCGAGGCGATTCTT	20	
3	XC-UP3	CCAACGGCGAGGCGATTCTTAC	22	
4	XC-LP2	GGTTTCCACAGCGCCCCTATC	21	
5	XC-LP3	TCTGCTCGCCTATGGGGTGATTG	23	
6	XC-LP4	CACGCGCATTGTTGAAGG	18	
7	XC-UP5	ACCTAAAGCA CCTGAAGTCG	20	
8	XC-UP6	CCTGAAGTCG GTAGAGCACA AAT	23	
9	XC-LP5	TGACCTCGAC CAAAACCAAC	20	
10	XC-LP6	GCTGGCCTTG CACCTGTTGA	20	
S.NO.	Primer ID	Sequence (5'-3')	Length(bp)	Purpose
1	XAM F1	GACTCCGGCA AGAACTCAAG AACC	24	Integron cassette amplification from Xmi
2	XAM F2	ACTAGCTCAG GCACGGTCAA	20	
3	XAM R1	ATACGCCAGG TGGGTGTAGC	20	
4	XAM R2	GCTAGTCTGT GCGTCTTGTT A	21	
S.NO.	Primer ID	Sequence (5'-3')	Length(bp)	Purpose
1	XAV F1	GTGATCAGAG CCCTCCCCGA ACA	23	Integron cassette amplification from Xvt
2	XAV F2	CCGAACATGG GACGAAAAT	19	
3	XAV R1	GCAGCATGGC ACCTAACAAT	20	
4	XAV R2	AGCGCCTTGA GTCTGGTGAG TC	22	
S.NO.	Primer ID	Sequence (5'-3')	Length(bp)	Purpose
1	XAP F1	GTCGGGCATG CTCACAATCA G	21	Integron cassette amplification from Xap
2	XAP F2	AAGCCCACCG CCCATTTT	18	
3	XAP R1	CGCTTACGAC GGCAAATACT TCAT	24	
4	XAP R2	CGGATCGAGC TGTTAGTC	18	
5	XAP F3	GCGGCCGAGC TTTGTGGTGA T	21	
6	XAP F4	CCGGTGC GCA GCTTCGACAA T	21	
7	XAP F5	CGCGGATCGG AGAACAAGCA AC	22	
8	XAP R3	GCGGTCAAAG CAGTGGATG	19	
9	XAP R4	CGCACACCAT CAACACCGCA CAT	23	
10	XAP R5	GCTGATGGCG CGTTTGAGGT TG	22	
11	XAP F6	TGCGTCATCT GGGCGTCAAC	20	
12	XAP F7	ACGCAGTGCC ACGACATTG	19	
13	XAP R6	TGCTCCAGGA TGTGAATGTG AT	22	
S.NO.	Primer ID	Sequence (5'-3')	Length(bp)	Purpose
1	LPS F1	GAGAAGCCCT GGCCGACCTA T	21	LPS cassette amplification from Xap
2	LPS F2	GGCCGTGGCA ATGATGCT	18	
3	LPS R1	CGCGCAATCA TCCGTTTACA A	21	
4	LPS R2	TTTTGCGCAA CCACAGTC	18	

Table S3

Relative parameter values for recombination and mutation generated by Clonal Frame

	r/m	ρ/θ
Run 1	1.592	0.180
Run 2	1.629	0.181
Run 3	1.611	0.179
Run 4	1.627	0.182
Run 5	1.595	0.181
Average	1.611	0.181

Table S4List of CRISPR elements identified in *X.axonopodis* strains

CRISPR		Contig number	CRISPR start position	CRISPR end position	CRISPR length	Direct repeat consensus	Direct repeat length	Number of spacers
Xap	I	15	50335	50633	298	TGGAAACGGTCAATGGCAGCATC	23	5
	II	14	51991	52808	817	GTTTCAATCCACGCGCCCGTGAGGGCGCGAC	31	12
Xvt	I	6	181084	181436	352	GATGCTGCCGTTGACCGTTTCCA	23	6
Xag	I	253	3546	3844	298	TGGAAACGGTCAATGGCAGCATC	23	5
Xmi	I	2	68069	68421	352	GATGCTGCCGTTGACCGTTTCCA	23	6
Xcaw	I	NA	27400	27698	398	TGGAAACGGTCAATGGCAGCATC	23	5
	II	NA	5157634	5158851	1217	GTCGCGCCCTCACGGGCGCGTGGATTGAAAC	31	18
	III	NA	5155349	5155579	230	GGTCGCGCCCTCACGGGCGCGTGGATTGAAAC	32	3
Xac29	I	NA	27439	27737	298	TGGAAACGGTCAATGGCAGCATC	23	5
	II	NA	4530049	4530804		GTCGCGCCCTCACGGGCGCGTGGATTGAAAC	31	11
Xac	I	NA	27399	27697	298	TGGAAACGGTCAATGGCAGCATC	23	5
	II	NA	4522475	4523694	1219	GTCGCGCCCTCACGGGCGCGTGGATTGAAAC	31	18
Xml2388	I	13	101241	101593	352	GATGCTGCCGTTGACCGTTTCCA	23	6
Xml-x20	I	2	13267	13565	298	TGGAAACGGTCAATGGCAGCATC	23	5
Xml-X18	I	1	27395	27693	298	TGGAAACGGTCAATGGCAGCATC	23	5
Xml1386	I	6	81424	81722	298	TGGAAACGGTCAATGGCAGCATC	23	5
Xf1	I	215	9610	9915	305	GATGCTGCCGTTGACCGTTTCCACCCGCC	30	5
Xf2	I	178	25078	25374	296	GTGGAAACGGTCAACGGCAGCATC	24	5

Table S5

Blast matches of Condensation (C) domain and Ketosynthase (KS) domain

	Query id	Database match id	percent identity	align length	e-value	pathway product	domain class	Pathway type
Condensation (C) domains								
C1	contig00013_3_7_1102_1404	bleom4_C2_modAA	55	297	1.00E-96	bleomycin	modAA	NRPS
C2	contig00013_2_6_29_320	compl1_C1	33	274	2.00E-20	complestatin	C	NRPS
C3	contig00013_3_10_11_305	cyclo1_C8_LCL	29	291	6.00E-22	cyclosporin	LCL	NRPS
C4	contig00013_3_14_270_566	cyclom1C3_LCL	36	301	1.00E-24	cyclomarin	LCL	NRPS
C5	contig00013_2_13_158_459	liche1_C3_LCL	27	302	1.00E-20	lychenicin	LCL	NRPS
C6	contig00013_2_13_1243_1534	cdaps2_C3_LCL	33	299	5.00E-18	calcium-dependent antibiotic	LCL	NRPS
C7	contig00013_1_17_633_913	fengy4_C2_LCL	26	189	4.00E-14	fengycin	LCL	NRPS
C8	contig00013_1_17_1659_1952	bleom4_C2_modAA	31	293	3.00E-32	bleomycin	modAA	NRPS
C9	contig00013_2_16_247_532	bacit3_C4_DCL	26	299	1.00E-18	bacitracin	DCL	Hybrid
C10	contig00013_2_17_104_397	cdaps1_C6_LCL	33	302	2.00E-28	calcium-dependent antibiotic	LCL	Hybrid
Ketosynthase (KS) domain								
KS1	contig00013_1_9_19_446	bleom_AAG02357_H	51	432	1.00E-104	bleomycin	Hybrid KS	Hybrid

Fig.S1

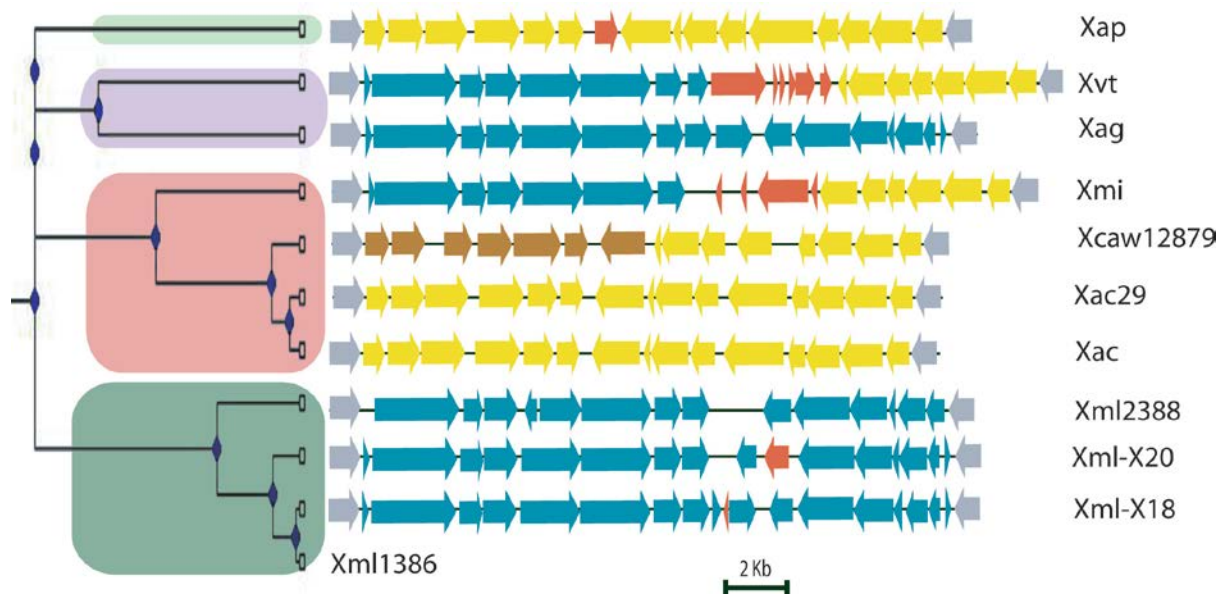


Fig.S1. Comparison of Lipopolysaccharide coding gene cluster in *X. axonopodis* pathovars to their evolutionary relationship predicted by clonal frame. Comparison of nucleotide sequences encoding LPS is shown in *X. axonopodis* pv. punicae LMG 859 (Xap), *X. campestris* pv. viticola LMG 965 (Xvt), *X. axonopodis* pv. glycines str. 12-2 (Xag), *X. citri* pv. mangiferaeindicae LMG 941 (Xmi), *X. citri* subsp. citri Aw12879 (Xcaw12879), *X. axonopodis* Xac29-1 (Xac29), *X. axonopodis* pv. citri str. 306 (Xac), *X. axonopodis* pv. malvacearum str. GSPB2388 (Xml2388), *X. citri* pv. malvacearum strain X20 (Xml-20) and X18 (Xml-X18). Different LPS cassettes are coloured differently. All maps are approximately to scale. Red coloured ORFs represent transposable elements.

Fig.S2

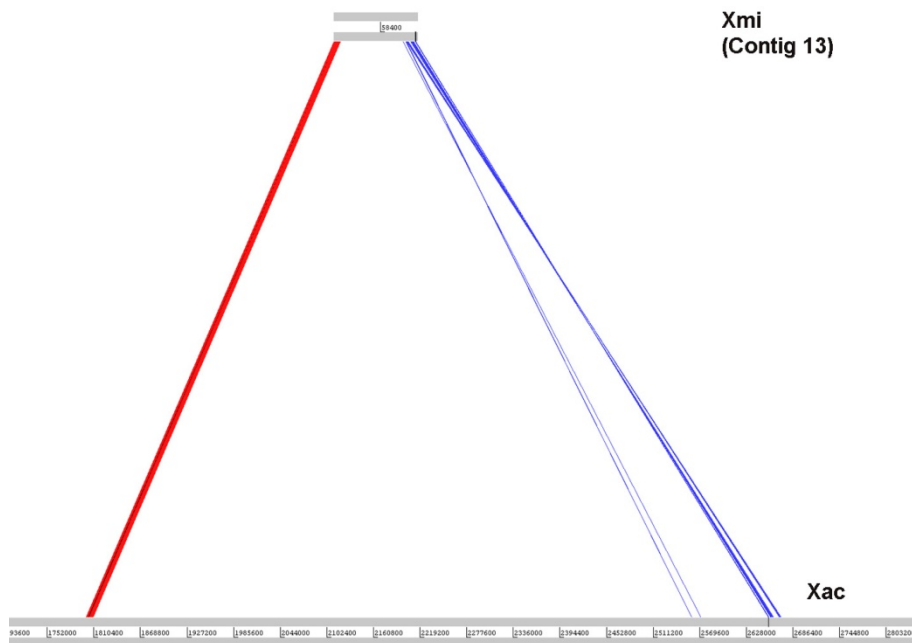


Fig. S2. Artemis comparison of Hybrid NRPS-PKS system carrying contig in *X. citri* pv. *mangiferaeindicae* LMG 941 and *X. axonopodis* pv. *citri* str. 306 (Xac). Red colour shows the region of forward matches and blue colour shows the regions of reverse matches.

Fig.S3

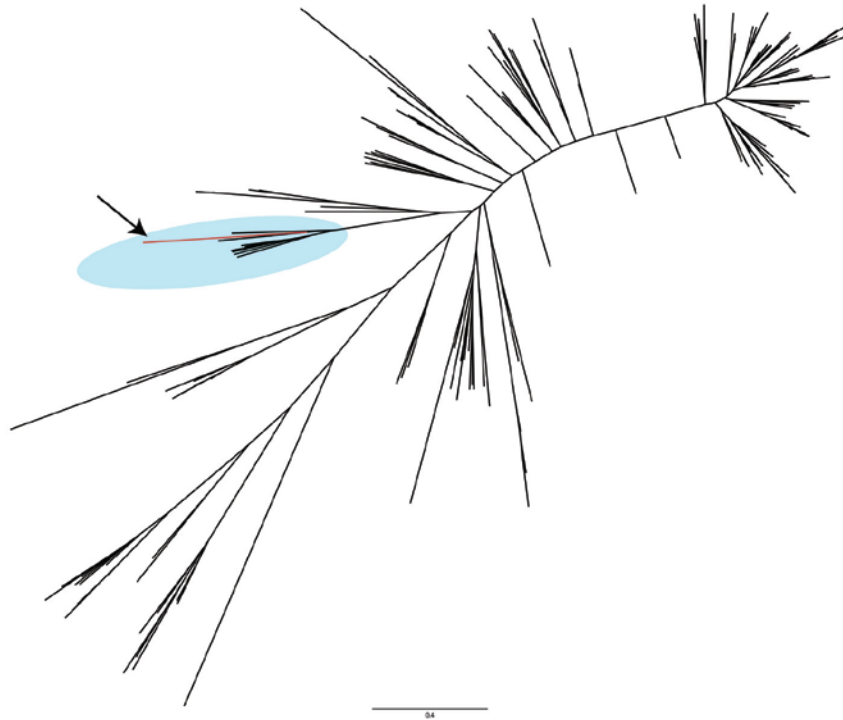


Fig.S3. Phylogenetic tree obtained on conserved Ketosynthase (KS) domain of PKS system. Tree was obtained using NaPDoS server taking all database sequences. Clade highlighted in cyan shows the KS domains belonging to Hybrid NRPS-PKS pathways. KS domain of NRPS-PKS system of *X. citri* pv. *mangiferaeindicae* LMG 941 (present study) is coloured in red and marked by a solid black arrowhead.