Group I
pv. *syringae* included in
the genomospecies 1

Group II
pvs. *aptata*, *avellanae*, *japonica*,
pisi and *syringae* included in the
genomospecies 1

Group III
pvs. *aceris* and *syringae*
included in the
genomospecies 1

Other pathovars
included in different
genomospecies

FIG S1 Distribution and evolution of the *mbo* operon. The neighbor-joining tree was constructed with MEGA5 using the concatenated partial sequences of *rpoD* and *gyrB*. The Tamura-Nei substitution model with gamma correction was used for tree construction. Bootstrap values (1,000 repetitions) are shown on branches. Strain designations are presented on the right. One hundred fourteen strains of different *P. syringae* pathovars were analyzed. Abbreviations for *P. syringae* pathovars are given as: Psv, savastanoi; Ps, *P. syringae* (no pathovar assigned); Pac, aceris; Pan, actinidae; Pae, aesculi; Ptt, aptata; Pco, coronafaciens; Pgy, glycinea; Psj, japonica; Pla, lachrymans; Pma, maculicola; Pmo, mori; Pmp, morsprunorum; Ppi, pisi; Pph, phaseolicola; Psy, syringae; Por, oryzae; Pta, tabaci; Ptg, tagetis; Pto, pv. tomato. The tree was rooted with *P. fluorescens* Pf-5. Evolutionary distances are given in units of nucleotide substitutions per site. The topology was similar for trees produced by the maximum parsimony and maximum likelihood methods. Sequences from some strains were extracted from published genome sequences.

Table S1 Specific oligonucleotide sequences used in this study.

Purpose and primers[a]	Gene	Sequence (5´-3´)	Amplicon size (bp)	Reference
Identification				
mbo9-For	*mboAB*	TCCATAAAGGCGACTGGTTC	653	This study
mbo9-Rev		GGCGGTGTAAGTCTGGTCTC		
mbo15-For	*mboAB*	AGCGTCATATCCTGGAGTGC	795	This study
mbo15-Rev		TATCCGTTTCAGCACGACTG		
mbo21-For	*mboAB*	CATGGGCGAGTTCCATAAAG	663	This study
mbo21-Rev		GCGGTGTAAGTCTGGTCTCC		
mbo24-For	*mboAB*	CAAGGACGAGAAGGATCTGC	692	This study
mbo24-Rev		CGACATTCAAACGACTCAGG		
mbo15-For	*mboAB*	AGCGTCATATCCTGGAGTGC	617	This study
mbo9-Rev		GGCGGTGTAAGTCTGGTCTC		
Insertion site mapping				
mboIS-For	*mboF*	CACGTCGATGTGGTACTG	580	This study
mboIS-Rev		CGTTGACCAGCACCACCA		
mbo operon organisation				
mboAB-For	*mboABC*	TACGGCGACAAGTACAGC	2,128	This study
mboC-Rev		CCAGGTACTCACACAGCG		
mboC-For	*mboCDE*	GTCAAGCCGATCGATATG	2,200	This study
mboDE-Rev		CAGGCTGGTTGATGATGA		
mboDE-For	*mboDEF*	ATAGCAGCGTGCAGTCTC	2,060	This study
mboF-Rev		CAGTACCACATCGACGTG		
rpoD and gyrB sequencing				
rpoDFor2	*rpoD*	ACCGATCCCGTTCGTATGTA	907	Murillo *et al.* (2011)
rpoDRev2		TGGTGTACTTCTTGGCGATG		
rpoDFor3	*rpoD*	GACGCCGATACCGACGAG	1064	This study
rpoDRev3		CGGTATTCGAACTTGTCCAC		
gyrBFor2	*gyrB*	GTCATCATGACCGTGCTCCA	996	Murillo *et al.* (2011)
gyrBRev2		CCCTTCCACCAGGTACAGTT		
gyrBFor3	*gyrB*	GACGACATCAGCATCATCATC	1114	This study
gyrBRev3		CAGCAGAGTCCCCTTCCAC		

[a] For, Forward primer; Rev, Reverse primer.

Table S2 Comparison and similarity matrix of the *mbo* operons between different sequenced genomes of *P. syringae* strains.

Strains		Size (bp)	GC (%)	Identity (%)					
				Ps Cit7	Psy UMAF0158	Psy UMAF0167	Ptt DSM50252	Ppi 1704B	Psy CFBP3388
Group I	Ps Cit7	6,783	55,8						
	Psy UMAF0158	6,784	55,8	99.5					
	Psy UMAF0167	6,774	55,8	99.2	99.4				
Group II	Ptt DSM50252	6,769	55,0	94.2	94.2	94.2			
	Ppi 1704B	6,801	55,3	94.2	94.2	94.2	98.4		
	Psy CFBP3388	6.785	56,1	94.9	94.9	94.9	96.5	96.5	
	Psy FF5	6,770	55,4	94.3	94.4	94.4	98.5	98.4	96.7

[a] Abbreviations are: Ps, *P. syringae*; Ppi, pv. pisi; Psy, pv. syringae; Ptt, pv. aptata.