

**Table S3** Most relevant genes and genetic elements found in the plasmids of *Bacillus thuringiensis* m401

Plasmid denomination	Start	End	Size (bp)	Blastx product	Highest homology with bacterial species	Accession Number	Identity (%)
pBTm401a	454	1,014	560	DUF 23967 domain-containing protein	<i>B. thuringiensis</i>	WP_109139815.1	100
	4,513	5,752	1,240	plasmid recombination protein	<i>B. toyonensis</i>	WP_098985545.1	87
	6,014	6,665	651	MULTISPECIES: MarR family transcriptional regulator	<i>B. cereus</i> group	WP_002035308.1	100
	7,728	8,030	303	MULTISPECIES: antibiotic biosynthesis monooxygenase	<i>Bacillus</i> sp.	WP_016107055	100
pBTm401b	378	1,019	642	MarR family transcriptional regulator	<i>B. thuringiensis</i>	WP_129542643	99
	1,555	2,178	624	tyrosine-type recombinase/integrase	<i>Bacillus thuringiensis</i>	WP_109139820	100
	4,304	5,111	807	uracil permease	<i>B. thuringiensis</i>	WP_098223429	96
pBTm401c	1	1,119	1,119	IS200/IS605 family element transposase accessory protein TnpB	<i>B. thuringiensis</i>	WP_000593068.1	98
	17,213	17,782	570	MULTISPECIES: TetR/AcrR family transcriptional regulator	<i>B. cereus</i> group	WP_000593068.1	100
	20,349	20,747	399	MULTISPECIES: IS200/IS605 family transposase	<i>B. cereus</i> group	WP_000762720.1	100
	22,923	23,195	273	MULTISPECIES: TIGR04197 family type VII secretion effector	<i>B. cereus</i> group	WP_061663104	100
	34,727	36,115	1,389	MULTISPECIES: PLP dependent aminotransferase family	<i>B. cereus</i> group	WP_098279451	100
	36,344	37,057	714	azaleucine resistance protein AzIC	<i>B. thuringiensis</i>	WP_109139837.1	100
	37,054	37,389	336	branched-chain amino acid transporter permease-putative AzID-	<i>Bacillus</i> sp.	WP_000178819	99
	40,832	42,190	1,359	S8 family serine peptidase	<i>B. thuringiensis</i>	WP_109139839	100
	42,246	44,381	2,136	peptidase domain-containing ABC transporter	<i>B. thuringiensis</i>	WP_109139840.1	100
	44,404	47,478	3,075	type 2 lantipeptide synthetase LanM family protein	<i>B. thuringiensis</i>	WP_109139841.1	100
	47,494	48,204	711	NAD(P)H-dependent oxidoreductase	<i>B. thuringiensis</i>	WP_100616756.1	100
	48,275	48,463	189	mersacidin family lantibiotic – putative Class II	<i>B. toyonensis</i>	WP_097821240.1	100
	48,479	48,706	228	MULTISPECIES: mersacidin family lantibiotic – putative Class II	<i>B. cereus</i> group	WP_100616759.1	100
	49,707	49,901	195	MULTISPECIES: Helix-turn-helix transcriptional regulator	<i>B. cereus</i> group	WP_100616760.1	100

	51,218	52,900	1,683	DUF 2075 domain-containing protein	<i>B. thuringiensis</i>	WP_109139842.1	100
	53,048	53,377	330	MULTISPECIES: Nucleotide pyrophosphohydrolase	<i>B. cereus</i> group	WP_109139843.1	100
	53,883	54,806	924	Cry1 -HNH endonuclease	<i>B. thuringiensis</i>	WP_109139845.1	100
	55,246	55,992	747	zeta toxin family protein	<i>B. thuringiensis</i>	WP_109139846.1	100
	58,095	58,319	225	M4 family metallopeptidase	<i>B. thuringiensis</i>	WP_109139848.1	100
	64,097	64,312	216	alpha/beta-type small acid-soluble spore protein	<i>B. thuringiensis</i>	WP_172555819	99
	67,727	68,198	472	Transposase for IS660	<i>B. cereus</i>	EEL61710.1	100
	1	2,005	2,005	amino acid adenylation domain-containing protein	<i>B. thuringiensis</i>	WP_192402335	100
pBTm401d	2,108	9,961	7,854	MULTISPECIES: non-ribosomal peptide synthetase	<i>B. cereus</i> group	WP_033694187	100
		19,09				EOP94530.1	
	10,267	4	8,828	amino acid adenylation domain-containing protein	<i>B. cereus</i>		100