

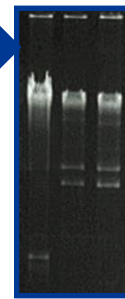
Isolation in PEMBA



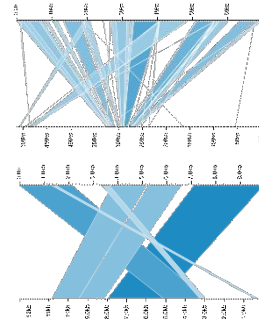
In vitro antagonism against *P. larvae*



Determination of TET, OTC, and MIN resistance

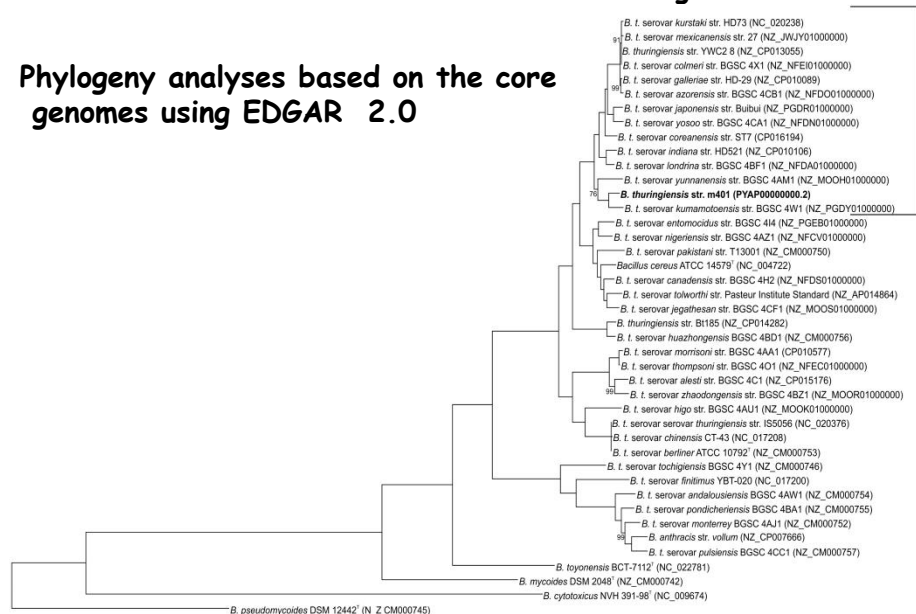


Plasmid patterns

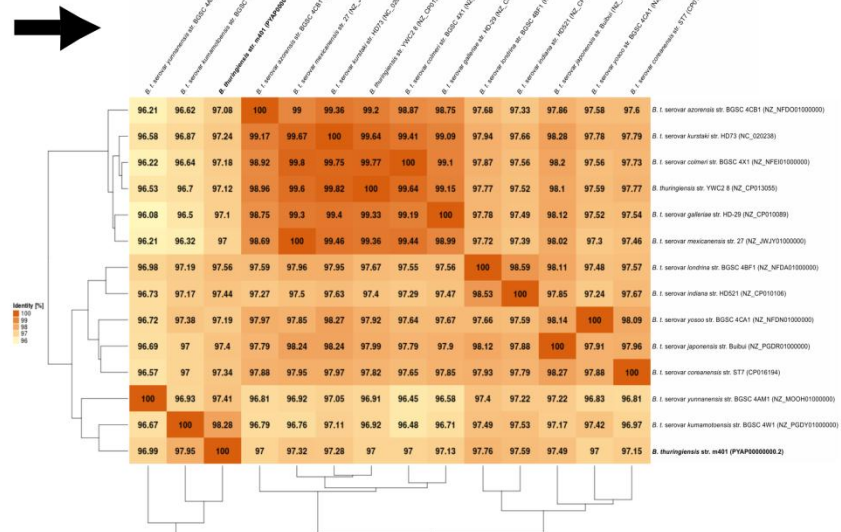


Comparative alignment of plasmids by Kablammo

Phylogeny analyses based on the core genomes using EDGAR 2.0



ANI
analyzes



ANiB Matrix of selected genomes

Table S1 Global statistics of *Bt* m401

Feature	Value
Total sequence length	6,005,135
Total ungapped length	6,004,585
% GC	34.72
Gaps between scaffolds	0
Number of scaffolds	45
Scaffold N50	391,966
Scaffold L50	4
Number of contigs	64
Contig N50	209,993
Contig L50	9
Total number of plasmids	4
Number of component sequences (WGS or clone)	45

Table S2 General overview of plasmids pBTm401a, pBTm401b, pBTm401c, and pBTm401d

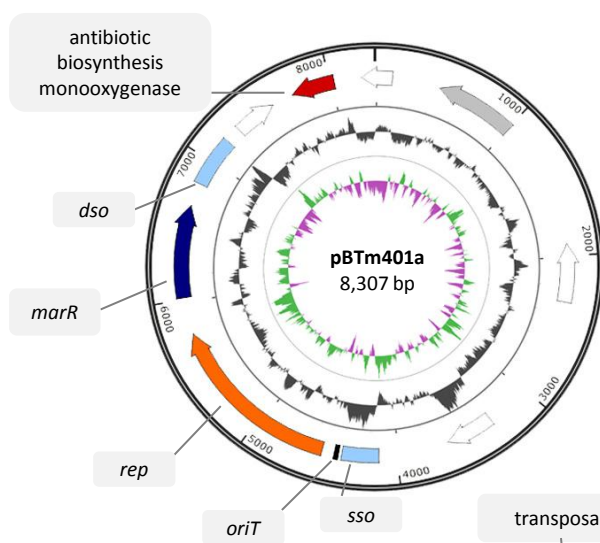
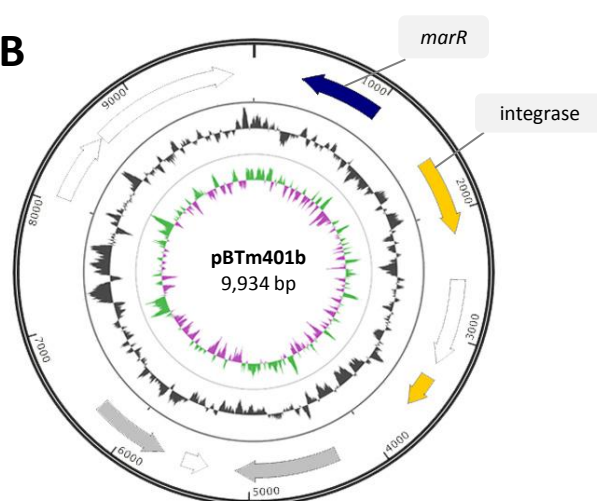
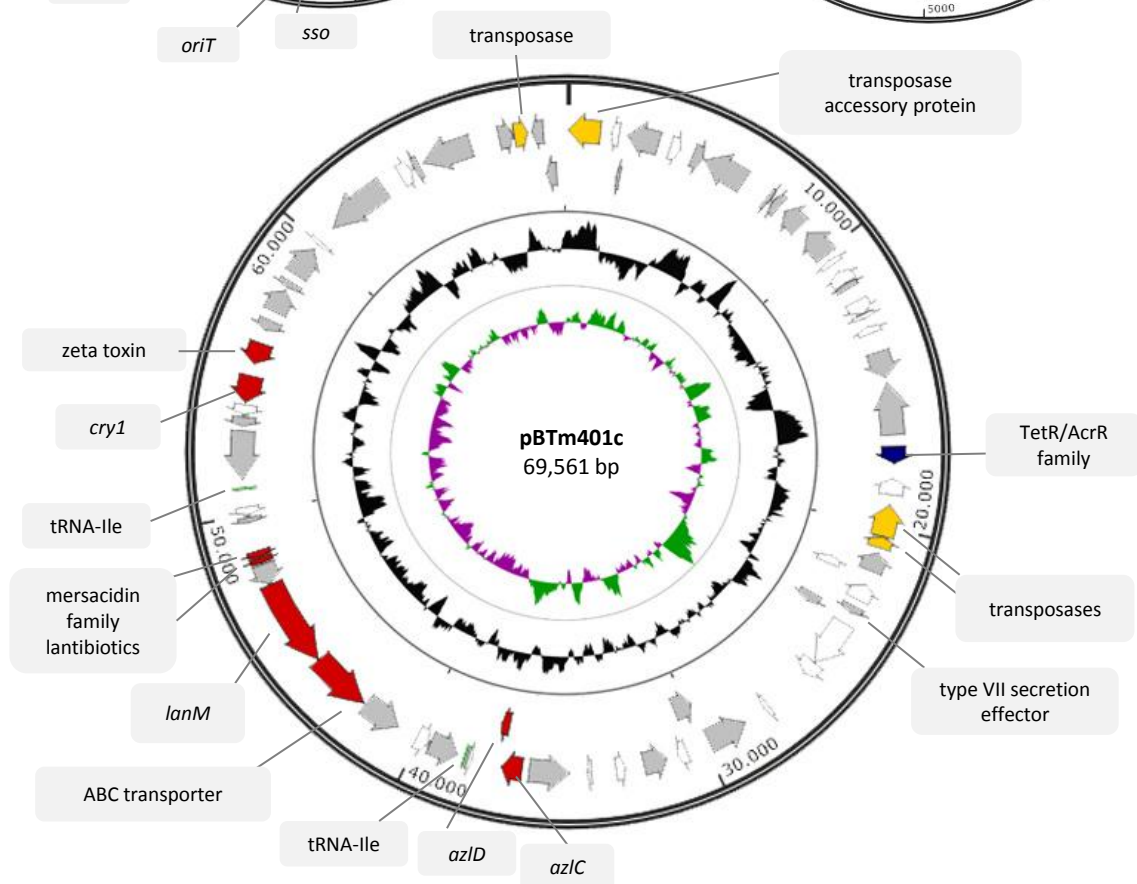
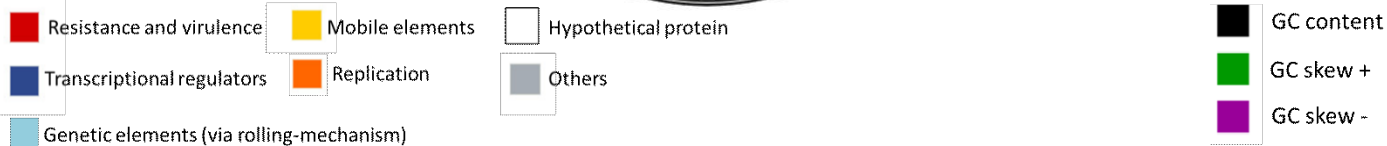
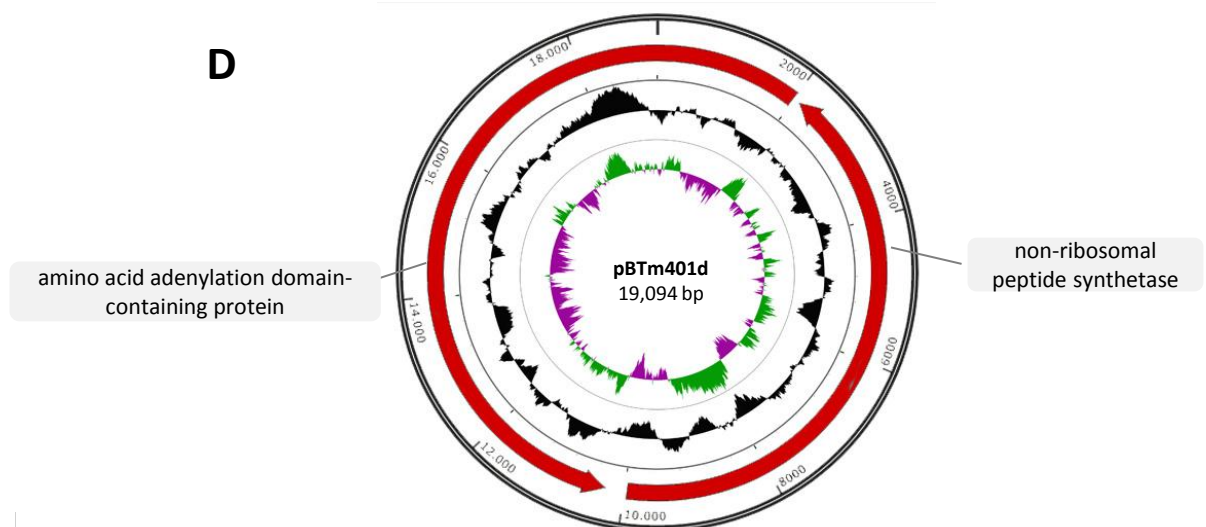
Plasmid name	Size (bp)	% G+C	Number of genes	Number of genes (Kb)	% of genes in + strand	% of genes in - strand	Average gene size (bp)
pBTm401a	8,307	33.04	8	0.96	50	50	495
pBTm401b	9,934	31.09	9	0.91	66.7	33.3	682
pBTm401c	69,591	30.68	71	1.02	29.6	70.4	678
pBTm401d	19,094	31.27	2	0.10	0	100	9,344

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
pBTm401d	1	2,005	2,005	amino acid adenylation domain-containing protein	<i>B. thuringiensis</i>	WP_192402335	100
	2,108	9,961	7,854	MULTISPECIES: non-ribosomal peptide synthetase	<i>B. cereus</i> group	WP_033694187	100
	10,267	19,094	8,828	amino acid adenylation domain-containing protein	<i>B. cereus</i>	EOP94530.1	100

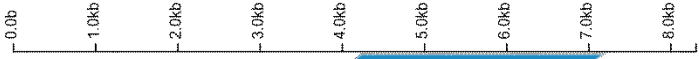
Table S4 Predicted virulence factors of *Bacillus thuringiensis* m401

Gene	Location	Accession	Locus tag	Genome position
HBL Complex				
<i>hblB</i>	chromosomal	PYAP02000008.1	C5676_016000	378,291-379,418
<i>hblA</i>	chromosomal	PYAP02000008.1	C5676_016005	379,794-381,194
<i>hblD</i>	chromosomal	PYAP02000008.1	C5676_015995	377,034-378,254
<i>hblC</i>	chromosomal	PYAP02000008.1	C5676_015990	375,653-376,972
Cytotoxin K				
<i>cytK</i>	chromosomal	PYAP02000006.1	C5676_007580	237,152-238,162
Enterotoxin FM				
<i>entFM</i>	chromosomal	PYAP02000007.1	C5676_011360	143,241-144,521
Non-hemolytic enterotoxin				
<i>nheA</i>	chromosomal	PYAP02000007.1	C5676_011035	73,929-75,089
<i>nheB</i>	chromosomal	PYAP02000007.1	C5676_011040	75,127-76,335
<i>nheC</i>	chromosomal	PYAP02000007.1	C5676_011045	76,443-77,522
δ-endotoxins				
<i>cry1</i>	pBTm401c	PYAP02000003.1	C5676_000375	53,883-54,806
Zeta toxin	pBTm401c	PYAP02000003.1	C5676_000380	55,246-55,992
Other virulence factors				
thiol-activated cytolysin	chromosomal	PYAP02000009.1	C5676_017000	180,826-182,364
immune inhibitor A	chromosomal	PYAP02000014.1	C5676_022580	145,118-147,517
metalloprotease	chromosomal	PYAP02000007.1	C5676_010775	15,785-17,047

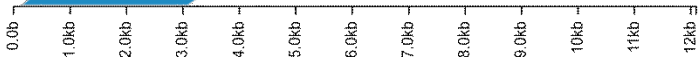
A**B****C****D**

A

Plasmid pBTm401a
(PYAP02000001.1)

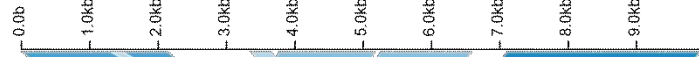


Plasmid pFR12 (EU362917)
from *Bt* strain INTA FR7-4

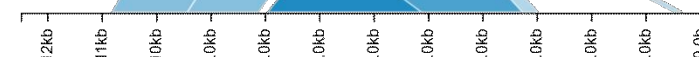


B

Plasmid pBTm401b
(PYAP02000002.1)

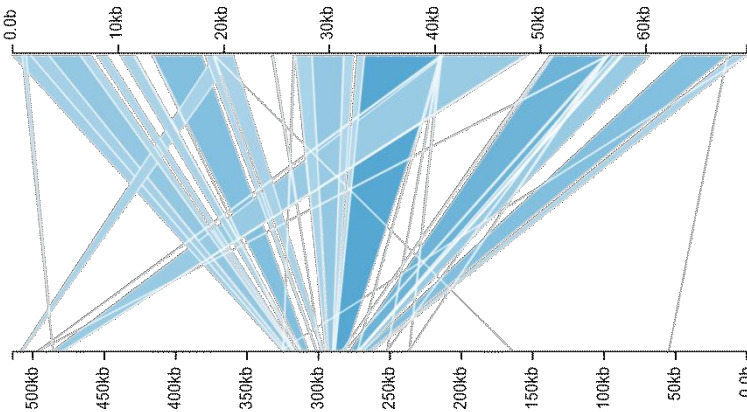


Plasmid pBT1850012
(CP014288) from *Bt* strain 185

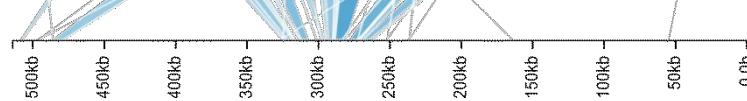


C

Plasmid pBTm401c
(PYAP02000003.1)



Plasmid Unnamed 1 (CP042875)
from *B. cereus* strain 09

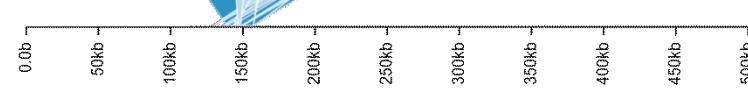


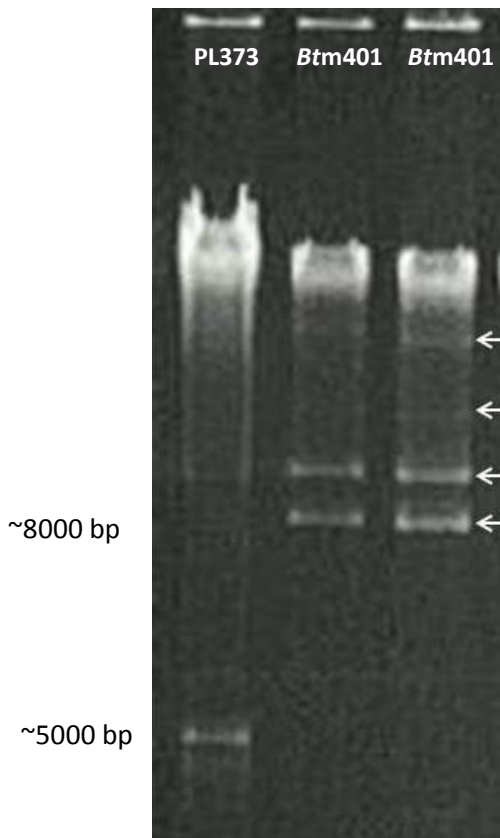
D

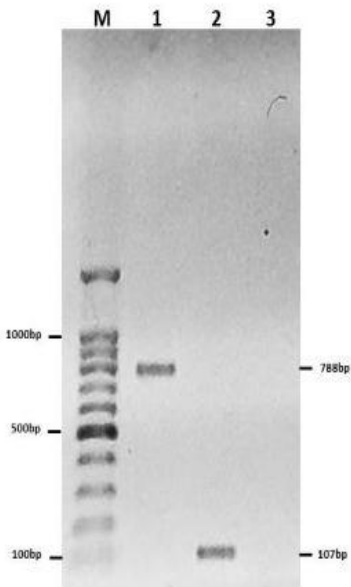
Plasmid pBTm401d
(PYAP02000004.1)

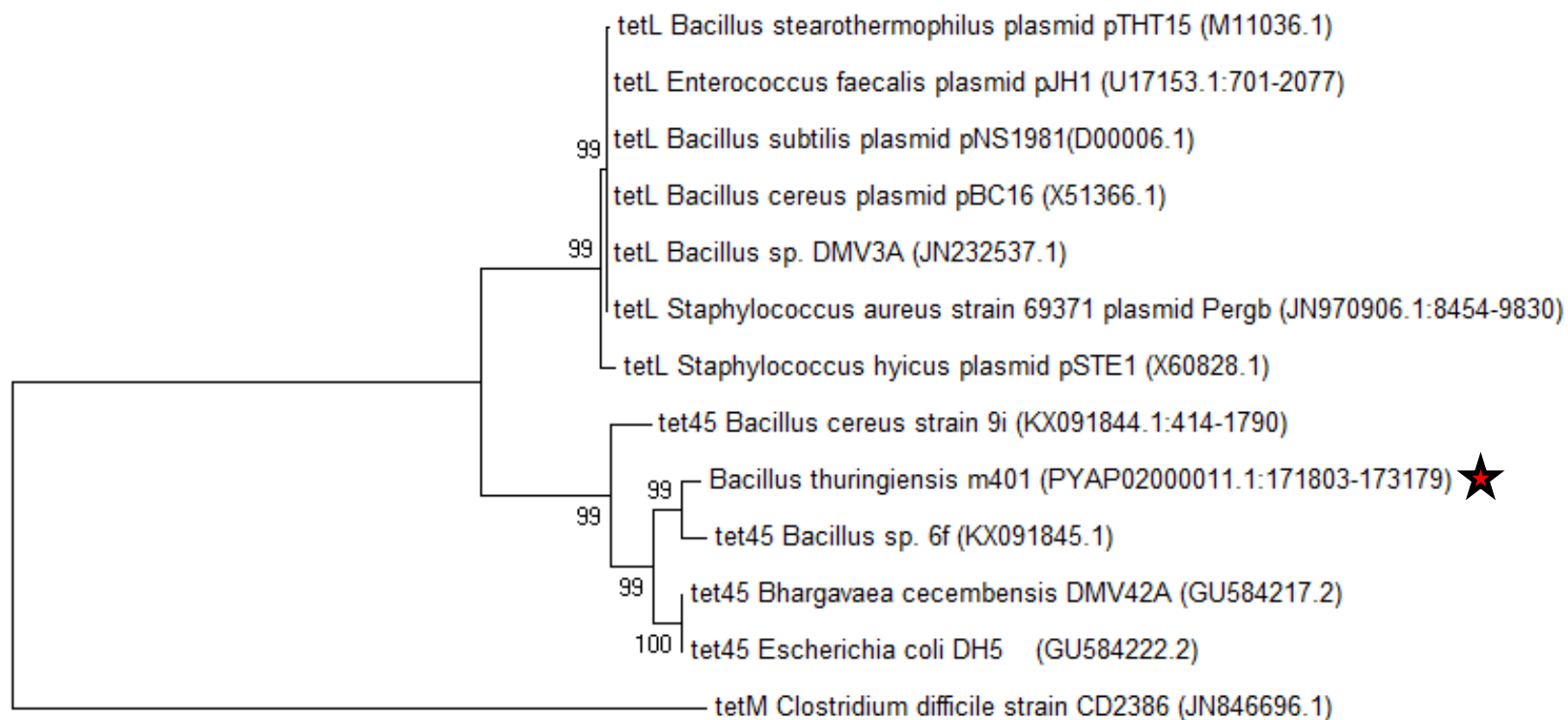


Plasmid p1 (CP053657)
From *B. cereus* strain CTMA_1571









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