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Complete genome sequences of two *Bacillus thuringiensis* serovar *kurstaki* strains isolated from Lebanon and Tunisia, highly toxic against lepidopteran larvae

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ABSTRACT *Bacillus thuringiensis*-based products are key in the biopesticides market. *Bacillus thuringiensis* *kurstaki* strains Lip and BLB1 were isolated from Lebanese and Tunisian soils, respectively. These strains are highly toxic against lepidopteran larvae, *Ephestia kuehniella*. Here, we report Lip and BLB1 complete genomes, including their plasmid and toxin contents.

KEYWORDS *Bacillus thuringiensis*, genomes, whole-genome sequencing, PacBio

Bacillus thuringiensis serovar *kurstaki* (*Btk*) strains Lip and BLB1 were isolated from Lebanese and Tunisia soil samples, respectively (1–3). Both strains showed an increased toxicity against the lepidopteran *Ephestia kuehniella* larvae in comparison to the reference strain HD-1. Their entomopathogenic potential was evaluated by *in vivo* toxicity assays and showed a lethal concentration of 50% of the larvae (LC50) of 33.27 and 70 ng of toxin per milligram of flour for Lip and BLB1, respectively (1–3). In the context of IPM-4-Citrus (MSCA RISE, No. 734921, 2017–2023), a project aiming to optimize the culture of these strains on a wheat bran-based medium, a whole-genome sequencing (WGS) approach was adopted to elucidate all genomic aspects of *Btk* Lip and BLB1.

For WGS, strains were grown in liquid Luria-Bertani (LB) medium for 16 h at 30°C, after which DNA was extracted using the Monarch HMW DNA Extraction Kit as per manufacturer instructions. WGS was conducted using a PacBio Sequel II Sequencer (Pacific Biosciences, Menlo Park, CA, USA) (4, 5) at the Gentyane platform (Clermont-Ferrand, France). For PacBio sequencing, library was prepared using a SMRTbell prep kit3, following manufacturer instructions. Genomic DNA was sheared, cleaned of single-strand overhangs, repaired for damage and A A tailed. Then, barcoded overhang adapters were ligated to generate the SMRTBell templates. Fragments above 5 kb were then size selected with 35% AMPure PB Beads. A Fragment Analyzer (Agilent Technologies) and a Qubit fluorimeter (Life Technologies) allowed quantity and quality checks. A ready-to-sequence SMRTBell Polymerase Complex was created using a Binding Kit 3.2 (PacBio) and the Sequel II primer 3.2. A consensus sequencing (CCS) mode was adopted, and reads were later demultiplexed with Bam2fastx software (Bioconda) under default parameters.

The number of CCS reads was 524,791 for Lip and 374,689 for BLB1 (Table 1). Assembly was done with flye v2.5, under default parameters (6). Overlaps were manually removed. The final coverage was 417.3x and 746.6x for Lip and BLB1, respectively. Genome completeness was assessed by BUSCO v5.0, using default parameters (7), and was found to be at 99.78% for Lip and 96% for BLB1. Circular contigs were

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TABLE 1 Sequence features and accession numbers of replicons from *Btk* strains Lip and BLB1

	Replicon	Bioproject/biosample/NCBI SRA accession number	Accession number	Length (bp)	CDS # (total)	# Cry coding genes	GC content (%)	Number of PacBio CCS reads/reads N50	
Lip	Chromosome		CP116313	5,293,947	5,632		35.2	524,791/9,650	
	pLip2189		CP116316	2,189	4		35.3		
	pLip7635		CP116320	7,635	8		32.2		
	pLip7911		CP116321	7,911	9		32.3		
	pLip8513		CP116322	8,513	9		30.8		
	pLip12		CP116314	12,276	21		31.1		
	pLip15		CP116315	15,008	28		34.9		
	pLip69	PRJNA924104/ SAMN32746259/	CP116319	69,004	76		32.2		
	pLip91	SRX20261752	CP116323	91,357	102		31.2		
						2: Cry1Ab;	34.5		
	pLip97		CP116324	97,437	85	Cry1Ac			
	pLip300		CP116317	300,451	267	5: Cry1Aa; Cry1Ac; Cry1Ia; Cry2Aa; Cry2Ab;	33.1		
		pLip457		CP116318	457,481	408		32.7	
	BLB1	Chromosome	PRJNA924104/	CP116325	5,677,911	6,060		35.3	374,689/8,967
pBLB1_7792		SAMN32746260/	CP116333	7,792	9		32.3		
pBLB1_8398		SRX20261751	CP116335	8,398	10		29.8		
pBLB1_8548			CP116336	8,548	8		30.8		
pBLB1_12			CP116326	11,521	9	1: Cry1Ab	40.3		
pBLB1_14			CP116327	14,174	21		32.5		
pBLB1_15			CP116328	15,071	22		31.2		
pBLB1_48			CP116330	47,643	73		35.4		
pBLB1_56			CP116331	56,399	62		32.2		
pBLB1_74			CP116332	73,558	88		30.6		
pBLB1_81			CP116334	80,698	86		33.5		
pBLB1_317			CP116329	317,321	282	5: Cry1Aa; Cry1Ac; Cry1Ia; Cry2Aa; Cry2Ab;	33.2		

first highlighted by the Flye assembler repeat graphs and then further identified as plasmids via a database similarity search using a nucleotide BLAST+ (2.12.0+ [8]) executable *blastn* command. This allowed to search for identified plasmids against the complete *Bacillus thuringiensis* genomes from NCBI assembly (NCBI:txid1428). Additional checks of completeness, identity, and circularity of plasmids were done by multiple sequence alignment comparison with several reference *Btk* strains: HD-1 (ASM71753v1 [9]), YBT-1520 (ASM74754v1), and HD73 (ASM33875v1 [10]).

Each strain carried 11 different plasmids ranging between 2 and 457 kb. pLip15 was identified as a linear tectiviral prophage, quite similar to GIL16, a tectivirus also isolated from a *Bacillus thuringiensis* strain (11).

Genome annotation was done with NCBI's automated annotation pipeline Prokaryotic Genome Annotation Pipeline (PGAP) (12). Toxin content was mined using t.BLAST.n with the toxin protein sequences recovered from the Bacterial Pesticidal Protein Resource Center (<https://www.bpprc-db.org> [13]). Genes encoding toxins from the Cry1 and Cry2 families were detected in Lip on plasmids pLip300 and pLip97, and BLB1 on pBLB1_317 and pBLB1_12 (Table 1).

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Nancy Fayad, Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Software, Validation, Visualization, Writing – original draft, Writing – review and editing | Rita Barssoum, Formal analysis, Methodology, Writing – review and editing | Nathalie Marsaud, Formal analysis, Methodology, Writing – review and editing | Rayan Nasserredine, Methodology, Writing – review and editing, Resources | Nouha Abdelmalek, Investigation, Methodology, Writing – review and editing | Souad Rouis, Writing – review and editing, Resources, Funding acquisition | Marie Ange Teste, Investigation, Writing – review and editing | Vincent Pailler, Methodology, Software, Writing – review and editing, Resources | Veronique Gautier, Methodology, Writing – review and editing, Resources | Elodie Belmonte, Investigation, Writing – review and editing, Resources | César Arturo Aceves Lara, Investigation, Writing – review and editing, Funding acquisition | Julien

Cescut, Investigation, Writing – review and editing, Funding acquisition | Luc Fillaudeau, Writing – review and editing, Resources, Funding acquisition, Project administration | Mireille Kallassy Awad, Conceptualization, Investigation, Writing – review and editing, Resources, Funding acquisition, Project administration, Supervision

DATA AVAILABILITY

Whole-genome sequences for *Bacillus thuringiensis* serovar *kurstaki* strains Lip and BLB1 are available in NCBI's GenBank under the bioproject number [PRJNA924104](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA924104) for both strains and the accession numbers [CP116313](https://www.ncbi.nlm.nih.gov/nuclseq/CP116313) to [CP116324](https://www.ncbi.nlm.nih.gov/nuclseq/CP116324) for Lip and [CP116325](https://www.ncbi.nlm.nih.gov/nuclseq/CP116325) to [CP116336](https://www.ncbi.nlm.nih.gov/nuclseq/CP116336) for BLB1. Raw reads are also available on the NCBI SRA database under the bioproject number [PRJNA924104](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA924104).

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