

Draft Genome Sequence of *Bacillus subtilis* ALBA01, a Strain with Antagonistic Activity against the Soilborne Fungal Pathogen of Onion *Setophoma terrestris*

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***Bacillus subtilis* is a nonpathogenic bacterium that lives in soil and has long been used as biological control agent in agriculture. Here, we report the genome sequence of a *B. subtilis* strain isolated from rhizosphere of onion that shows strong biological activity against the soilborne fungal pathogen *Setophoma terrestris*.**

Received 13 April 2016 Accepted 22 April 2016 Published 2 June 2016

Citation Albarracín Orio AG, Tobares RA, Ducasse DA, Smania AM. 2016. Draft genome sequence of *Bacillus subtilis* ALBA01, a strain with antagonistic activity against the soilborne fungal pathogen of onion *Setophoma terrestris*. *Genome Announc* 4(3):e00455-16. doi:10.1128/genomeA.00455-16.

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Biocontrol is a reliable alternative to chemical fungicides, which have raised serious concerns regarding food contamination and environmental pollution. Biocontrol is eco-friendly, safe, and may provide long-term protection to a crop (1). Plant growth-promoting rhizobacteria (PGPR) are naturally occurring soil microorganisms that colonize plant roots and benefit plants by increasing growth and/or reducing disease impact. Several *Bacillus* spp. representing typical PGPR have been widely studied and applied as efficient and stable biocontrol agents due to their ability to form heat- and desiccation-resistant spores (2). Bacteria belonging to the genus *Bacillus* are considered to be safe microorganisms that hold the remarkable ability to synthesize a vast array of beneficial substances for agronomical and industrial purposes (3). We have isolated a strain of *Bacillus subtilis* subsp. *subtilis* from the rhizosphere of onion plants (Bahía Blanca, Argentina) that was capable of strongly inhibiting the growth of *Setophoma terrestris* in vitro. We named it *B. subtilis* strain ALBA01. Interestingly, we observed a high growth inhibition of *S. terrestris* on plates containing cell-free supernatant of *B. subtilis* ALBA01 previously grown in the presence of the fungus (4). No antagonistic activity against two other onion pathogens, *Fusarium oxysporum* f. sp. *cepae* and *Fusarium proliferatum*, was observed. To gain insight into the features of *B. subtilis* ALBA01, we sequenced and annotated its genome sequence. Whole-genome sequencing was performed using a paired-end (PE) 2 × 100-bp library on an Illumina HiSeq 1500 (INDEAR Genome Sequencing facility, Argentina). The A5 pipeline (5) was used to execute *de novo* assembly. Reads were assembled into 28 scaffolds, with an average scaffold size of 147,128 bp. Annotation of the genome was done by uploading the scaffolds to the Rapid Annotations using Subsystems Technology (RAST) server (6) and by using the SEED-based method on this server. The genome sequence of *B. subtilis* ALBA01 is composed of 4,119,571 bp, with a mean G+C content of 44%. The annotation revealed 4,303 open reading frames (ORFs). Three families of *Bacillus* lipopeptides (surfactins, iturins, and fengycins) have mostly

been studied for their antagonistic activity against a wide range of potential phytopathogens, including fungi (7). Then, we decided to analyze the genome for the presence of genes encoding antimicrobial peptide synthetases. Four ORFs showed high identity levels to those from the *sfA* locus required for the production of the lipopeptide antibiotic surfactin. We also found an ORF with 98.77% identity to *pksD*, a gene encoding an enzyme involved in polyketide synthesis, and another with 80.66% identity to the fengycin synthetase gene, *fenB*. No coding sequences were found to be related to *ituD* (iturin A synthetase D), *bamA* (bacillomycin D synthetase A), *bmyA* (bacillomycin L synthetase A), and *mycA* (mycosubtilin synthase subunit A).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. [LVYH000000000](https://www.ncbi.nlm.nih.gov/nuclink/LVYH000000000). The version described in this paper is version LVYH01000000.

ACKNOWLEDGMENTS

We thank the Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Agencia Nacional de Promoción Científica y Tecnológica (ANPCyT, grant PICT 2013-2592 to A.G.A.O.), and Santiago Revale (Indear) for bioinformatics support.

FUNDING INFORMATION

This work, including the efforts of Andrea Georgina Albarracín Orio, was funded by MINCYT | Agencia Nacional de Promoción Científica y Tecnológica (ANPCyT) (PICT 2013-2592).

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