AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™

PROKARYOTES

Draft Genome Sequence of *Bacillus altitudinis* Lc5, a Biocontrol and Plant Growth-Promoting Endophyte Strain Isolated from Indigenous Black Rice of Manipur

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ABSTRACT We report here the 3.6-Mb draft genome of *Bacillus altitudinis* Lc5, a potential plant growth promoter and an active antagonistic endophyte of black rice. This genome study will provide better insights into the strain's mechanisms for plant growth promotion and biocontrol, thus facilitating its application in organic agriculture.

Bacillus altitudinis Lc5 was isolated by conventional microbial isolation techniques from an effectively sterilized leaf tissue of healthy indigenous black rice of Manipur, India. To our knowledge, this is the first *Bacillus altitudinis* endophyte strain reported from black rice. The strain could tolerate abiotic stress when grown in different experimental conditions and produce major defensive enzymes and growth-promoting factors like beta-1,3-glucanase, siderophore, protease, chitinase, cellulase, P-solubilizing ability, indole acetic acid, nitrogen-fixing ability, and antagonistic activity against the phytopathogens *Fusarium oxysporum*, *Rhizoctonia solani*, *Sclerotium oryzae*, *Pyricularia oryzae*, and *Pythium ultimun*. At present, a total of 14 genome sequences of *B. altitudinis* strains with various functional activities, including biocontrol and plant growth-promoting traits (1–3), have been deposited in GenBank.

The genome sequencing was performed on the Illumina HiSeq 2500 platform. Libraries were prepared with Illumina technology, and the adapter sequences were removed using Cutadapt version 1.8 (4). All low-quality ($Q < 30$) data were filtered out using Sickle version 1.33 (5), and the cleaned reads were subjected to KmerGenie (6) to predict the optimal *k* value and assembly size, which were found to be 27 and 3,760,383 bp, respectively. *De novo* assembly was performed using ABySS version 2.0.1 (7). The draft genome assembly obtained after trimming the paired-end reads comprised 91 scaffolds, with a total length of 3,741,201 bp in 91 scaffolds, with a largest contig size of 885,254 bp, a contig N_{50} size of 691,681 bp, and a G+C content of 41.89%. Genes were predicted from the ABySS-assembled contigs using Glimmer version 3.02 (8). The number of predicted genes was 3,950, and the number of genes with a significant BLASTx match (E value $\leq 1 \times 10^{-5}$ and similarity score ≥40%) was 3,286. The NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (https://www.ncbi.nlm.nih.gov/genome/annotation_prok) was used for automatic annotation and prediction of the assembled contigs, which predicted 69 contigs ($L_{50} = 6$), 3,824 genes, 3,679 protein-coding sequences, 74 tRNAs, 24 rRNAs, and 145 pseudogenes.

Annotation of the Lc5 genome revealed several genes and biosynthetic pathways, including antioxidant enzymes, such as catalase, peroxidase, and superoxide dismutase, that support the strain's potential role as a biocontrol agent against factors such as

Received 30 May 2018 **Accepted** 30 May 2018 **Published** 28 June 2018

Citation Potshangbam M, Sahoo D, Verma P, Verma S, Kalita MC, Indira Devi S. 2018. Draft genome sequence of *Bacillus altitudinis* Lc5, a biocontrol and plant growth-promoting endophyte strain isolated from indigenous black rice of Manipur. Genome Announc 6: e00601-18. https://doi.org/10.1128/genomeA.00601-18.

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temperature stress, salinity stress, drought stress, and oxidative stress. Also present in the annotation were gene clusters and pathways related to phosphorous solubilization, iron uptake, cellulose degradation, chitinolytic activity, glucanase, acetoin dehydrogenase, protease, trehalose metabolism, exopolysaccharides, cytokinin, and tryptophan biosynthesis, as well as nitrogen-fixing proteins and genes responsible for sporulation, motility, chemotaxis, and quorum sensing.

Antibiotics and secondary metabolites were analyzed using antiSMASH version 4.1.0 (9). Also predicted were 26 gene cluster types comprising a terpene-siderophore, type III polyketide synthase, bacteriocin, nonribosomal peptide synthetase, sactipeptide, and biosynthetic gene clusters of bacilysin, pseudomonine, fengycin, surfactin, and lichenysin. Thus, we conclude that *B. altitudinis* Lc5 harbors important putative genes, and further exploration will lead to significant contributions toward its sustainable application in organic agricultural practices.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. QCWN00000000. The version described in this paper is the first version, QCWN01000000.

ACKNOWLEDGMENTS

We gratefully acknowledge the financial support of the Department of Science and Technology and the Department of Biotechnology, Government of India.

The AgriGenome Labs Private Limited, Kerela, India, provided technical assistance for the genome sequencing.

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