Genome Sequence of Janibacter hoylei MTCC8307, Isolated from the Stratospheric Air

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Janibacter hoylei MTCC8307 was isolated from stratospheric air at an altitude of 41.4 km over Hyderabad, India. Here, we present the draft genome of Janibacter hoylei MTCC8307, which contains 3,139,099 bp with a G+C content of 72.8 mol%, 2,972 protein-coding genes, and 57 structural RNAs.

The genus Janibacter belongs to the family Intrasporangiaceae of the class Actinobacteria. At the time of writing, the genus Janibacter contained 6 species (11). All the species were isolated from different ecological niches ranging from polluted environment (4), oriental melon (13), sludge (8), and corals (5) to insect gut (6). The strain MTCC8307 was isolated from stratospheric air at an altitude of 41.4 km over Hyderabad, India. Air samples at high altitude were collected using balloon-borne cryosamplers (11). Genome sequencing of MTCC8307 was carried out for the better understanding of how biological processes and bacterial life can be sustained at high altitude. So far, only one genome sequence of Janibacter sp. HTCC2649 (GenBank accession no. PRJNA13546) is available in the public database (12).

The MTCC8307 genome was sequenced using the Ion Personal Genome Machine (PGM) sequencer using 316 chips. PGM sequencing resulted in 2,756,161 reads with a mean read length of 111 bp. This achieved 74× coverage with 122 contigs. A total of 119 contigs with a length of more than 500 bp were obtained. The de novo assembly was done using the MIRA assembler with default parameters (2). De novo assembly was carried out because of the unavailability of a closely related genome sequence (11). Gene prediction and annotation were done using the RAST (1) server and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). Accuracy, consistency, and completeness of RAST are based on the rapidly growing, manually curated library of subsystems (10) and on protein families derived from the subsystems (FIGfams) (9). RAST uses tRNAscan-SE (7) for predicting tRNA genes, search_for_rnas, developed by Niels Larsen, for rRNA-encoding genes, and GLIMMER2 (3) for the initial effort in predicting protein-coding genes (1). Representative sequences from a small set of FIGfams (e.g., tRNA synthase) are used for establishing phylogenetic context. Once the closest phylogenetic neighbors are found, a gene-calling step is repeated using genes of the closest organism as a training set.

The Janibacter hoylei MTCC8307 unclosed draft genome is 3,139,099 bp in length with a G+C content of 72.8 mol%. The genome has a coding density of 87% that contains 2,972 protein-coding genes and 57 rRNA genes. Comparison with genome sequences available in the RAST server revealed that Janibacter sp. HTCC2649 (score, 537), Sanguibacter keddieii DSM10542 (score, 440), and Kytococcus sedentarius DSM20547 (score, 341) were the closest neighbors of strain MTCC8307. The MTCC8307 genome contains putative genes responsible for glycolysis/gluconeogenesis (14), the tricarboxylic acid cycle (14), the pentose phosphate pathway (8), ABC transporters (15), DNA repair (70), osmotic stress (8), oxidative stress (29), cold shock (2), heat shock (11), and resistance to toxic compounds (31). Additionally, Janibacter hoylei MTCC8307 contains putative genes for biotin, thiamine, and histidine biosynthesis which are absent in Janibacter sp. HTCC2649 (12). In-depth comparative genome analysis with other members in the family will reveal a genetic basis for adaptation to its distinctive habitat and the reason for survival of the MTCC8307 strain in the stratosphere.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALWX01000000. The version described in this paper is the first version, ALWX01000000.

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REFERENCES