


Draft Genome Sequence of *Streptacidiphilus oryzae* TH49^T, an Acidophilic Actinobacterium Isolated from Soil

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The draft genome sequence of *Streptacidiphilus oryzae* strain TH49^T, an acidophilic actinobacterium, was obtained. The draft is composed of six scaffolds totaling 7.8 Mbp, and it contains 6,829 protein-coding genes and 91 RNA genes. Genes related to respiratory nitrate reduction, siderophore production, and biosynthesis of other secondary metabolites were identified.

Received 22 May 2015 Accepted 22 May 2015 Published 25 June 2015

Citation Kim YR, Park S, Kim T-S, Kim M-K, Han J-H, Joung Y, Kim SB. 2015. Draft genome sequence of *Streptacidiphilus oryzae* TH49^T, an acidophilic actinobacterium isolated from soil. *Genome Announc* 3(3):e00703-15. doi:10.1128/genomeA.00703-15.

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The family *Streptomyces* was proposed by Waksman and Henrici (1) and comprises 3 genera, *Streptomyces*, *Kitasatospora*, and *Streptacidiphilus* (1, 2). The genus *Streptacidiphilus* is the most recently described member among them and currently encompasses 10 acidophilic species, which typically grow in a pH range between 3.5 and 6.5, with optimum values around pH 4.5 to ~5.5 (2). *Streptacidiphilus* is widely distributed in a variety of terrestrial habitats, such as coal mine waste, acid mine drainage soils, and acidic forest soils (3–5). Acidophilic actinobacteria, such as streptacidiphili, are considered a good source of antibiotics and acid-stable enzymes (6, 7). Soil acidophilic actinobacteria may have higher potential than their neutrophilic counterparts for some activities, for example, antifungal activity (8, 9).

Recently, the genome sequences of selected streptacidiphili, *S. albus* NBRC 100918^T, *S. anmyonensis* NBRC 103185^T, *S. carbonis* NBRC 100919^T, *S. jiangxiensis* NBRC 100920^T, *S. melanogenes* NBRC 103184^T, and *S. neutrinimicus* NBRC 100921^T, were analyzed. In this study, the genome sequence of *Streptacidiphilus oryzae* was determined, and some basic features were analyzed.

S. oryzae TH49^T is an isolate from an acidic rice field soil sample and grows optimally at pH 5.0 to ~5.5 (10). The biomass of *S. oryzae* TH49^T (NCBI taxonomy identification no. 1449353) was obtained from a culture in ISP2 broth after incubation at 30°C for 3 days. High-quality genomic DNA was prepared using a DNA prep kit (SolGent), and the construction of a DNA library by PacBio 10-kb and sequencing on a PacBio RS platform (Pacific Biosciences) were performed at the Joint Genome Institute (JGI).

The analyzed draft genome sequence is composed of 6 DNA scaffolds covering 7,806,543 bp, with 73.36% G+C content, and contains 6,829 protein-coding genes and 91 RNA genes. The number of copies of rRNA genes for each subunit was between 7 and 8. *S. oryzae* TH49^T possessed genes related to anaerobic respiration, namely, the alpha, beta, and gamma subunits of respira-

tory nitrate reductase and respiratory nitrate reductase chaperone.

Genes for the biosynthesis of secondary metabolites were found in the genome, including genes for siderophore production and those related to the synthesis of type II polyketides, terpenoid backbones, and aminoglycosides.

Nucleotide sequence accession number. The annotated draft genome sequence of *S. oryzae* TH49^T has been deposited in DDBJ/EMBL/GenBank under the accession no. [JQM000000000](https://www.ncbi.nlm.nih.gov/nuccore/JQM000000000).

ACKNOWLEDGMENTS

The work conducted by the U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User Facility, is supported by the Office of Science of the U.S. Department of Energy under contract DE-AC02-05CH11231. This research was also supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education, Science and Technology (grant no. NRF-2013R1A1A2013821).

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