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# GENOME ANNOUNCEMENTS

## Genome Sequence of *Corynebacterium nuruki* S6-4$^T$, Isolated from Alcohol Fermentation Starter$^\nabla$

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***Corynebacterium nuruki* S6-4$^T$, isolated from Korean alcohol fermentation starter, is a strictly aerobic, nonmotile, Gram-positive, and rod-shaped bacterium belonging to the genus *Corynebacterium* and the actinomycete group. We report here the draft genome sequence of *C. nuruki* strain S6-4$^T$ (3,106,595 bp, with a G+C content of 69.5%).**

*Corynebacterium nuruki* strain S6-4$^T$ was described as a Gram-positive, strictly aerobic, irregular rod-shaped, and nonmotile bacterium (6). The strain was isolated from alcohol fermentation starter named "nuruk" in Korean, which is used for the manufacture of Korean traditional rice wine. Phylogenetic analysis based on 16S rRNA gene sequences showed that *Corynebacterium nuruki* strain S6-4$^T$ was most closely related to *C. variabile* DSM 20132$^T$, with 98.1% similarity. The genus *Corynebacterium* is currently composed of more than 100 type species, and 24 genome sequences have been reported to the NCBI database. The genetic information of the genus *Corynebacterium* has been enlarged over recent years, owing to its importance in the clinical aspect and food industry. The genome sequencing of *C. diphtheriae* NCTC13129, for instance, provided the knowledge about the etiology of diphtheria (2), and the genome sequencing of *C. glutamicum* ATCC 13032 confirmed the broad metabolic diversity related to fermentative production of L-amino acids for the food industry (3). To verify the role of the organism *C. nuruki* during alcohol fermentation, the sequencing project was initiated. Here, we present the genome of *Corynebacterium nuruki* strain S6-4$^T$ in the family *Corynebacteriaceae*.

The genome sequence of *Corynebacterium nuruki* strain S6-4$^T$ was determined using paired-end sequencing technology (3-kb library) and performed with Roche 454 GS (FLX Titanium) pyrosequencing by Macrogen, Inc. (Seoul, Republic of Korea). The library preparation, sequencing reaction, and sequencing run were carried out with Roche software, according to the manufacturer's instructions. A total of 297,994 reads (81,128,322 bp) and 68 large contigs were generated to give 26-fold coverage. Assembly into scaffolds was performed using the GS Assembler software (version 2.5.3). The average size of the 9 scaffolds was 349,144 bp. The largest scaffold size was 1,619,955 bp, and the total assembly size was 3,142,299 bp.

The unclosed draft genome was 3,106,595 bp in length and had a G+C content of 69.5%. Two rRNA genes (5S-16S) and 56 tRNA genes in the draft assembly were identified by tRNAscan-SE 1.23 (5) and RNAmmer 1.2 (4), respectively. Open reading frames (ORFs) of large contigs were predicted by six-reading-frame translation (7) and annotated against the COG database (RPS-BLAST, E value of $<10^{-3}$) (1) with the CAMERA server, version 2.0.6.3 (http://camera.calit2.net/). Consequently, 2,832 coding sequences (CDSs) and 109 subsystem features were predicted with 18 COG categories (J, K, L, D, V, T, M, U, O, C, G, E, F, H, P, Q, R, and S). It contains 10 predicted genes for amino acid transport and metabolism and 9 predicted genes for carbohydrate transport and metabolism. These results perhaps reflect the food-grade ecological niche of the organism presented in the alcohol fermentation starter for amylolytic machinery.

**Nucleotide sequence accession numbers.** The draft genome sequence of *Corynebacterium nuruki* strain S6-4$^T$ reported in this paper has been deposited in DDBJ/EMBL/GenBank under accession number AFIZ00000000 and in GenBank under Genome Project ID number 66913. The version described in this paper is the first version, accession number AFIZ01000000.

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