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Genome Sequence of *Corynebacterium glutamicum* S9114, a Strain for Industrial Production of Glutamate

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Here we report the genome sequence of *Corynebacterium glutamicum* S9114, an industrial producer widely used in production of glutamate in China. Preliminary comparison with the sequences of the *Corynebacterium glutamicum* strains ATCC 13032 and R revealed some notable mutagenesis that might be related to the high yield of glutamate.

Corynebacterium glutamicum, a fast-growing and aerobic Gram-positive microorganism able to secrete large amounts of glutamate under suitable conditions (10, 16), has a long history of use for the industrial production of various primary metabolites, including amino acids and nucleotides (5, 6). The complete genome sequences of two variants of *C. glutamicum* ATCC 13032 have been published (7, 8). Genome sequences have been reported for some other closely related microorganisms, such as *Corynebacterium efficiens* YS-314 (14) and *Corynebacterium glutamicum* R (17). Here we report the genome sequence of *Corynebacterium glutamicum* S9114, an industrial producer generated by conventional mutagenesis (18) which has been widely used in production of glutamate in China. Strain S9114 has a high resistance to high sugar and glutamate concentrations, which could be applied in glutamate production under biotin limitation or an excess of biotin with addition of penicillin.

The genome was sequenced using the Illumina Solexa GA IIx instrument at the Beijing Genomics Institute (BGI; Shenzhen, China). A library containing 500-bp inserts was constructed. Sequencing was performed with the paired-end strategy of 90-bp reads to produce 327 Mb of filtered sequences, representing a 95.5-fold coverage of the genome. The sequences were assembled into 67 contigs and 47 scaffolds using the SOAPdenovo package (12). Some remaining gaps in scaffolds were closed by Sanger sequencing of PCR products.

Genome annotation was performed at the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP). Open reading frames (ORFs) were identified by Glimmer 3.02 (4) and Genemark (2). The GenBank NR database, as well as the KEGG (9) and COG (15) databases, was employed for BLASTP identification (1). tRNA and rRNA genes were detected by tRNAscan-SE (13) and RNAmmer (11), respectively.

The chromosome of *Corynebacterium glutamicum* S9114 is 3,292,392 bp in length, with an average G+C content of 53.93%. In the genome sequence, 3,098 ORFs, 54 tRNA genes, and 1 rRNA fragment were identified. Fourteen pseudogenes were also detected, which coincided with the fact that *Corynebacterium glutamicum* S9114 was selected by a random mutagenesis process. Moreover, four potential prophage sites were found using Prophage Finder (3).

A brief comparative analysis on some genes related to the glutamate synthesis pathway was conducted on S9114, ATCC 13032, and *Corynebacterium glutamicum* R. Functions of those genes include serving as a key enzyme in the biosynthesis pathway (*pyc*, *pdh*, *pepC*, *odhA*, and *gltB*), nutrient assimilation (*sugR*, *lldR*, and *amtR*), cell wall biosynthesis and glutamate transport (*murE*, *ftsI*, and *dtsR*), and metabolic regulation (*odhI*, *pknG*, *dtxR*, and *ripA*). The preliminary results showed that some notable mutagenesis might lead to the high glutamate yield of S9114. A detailed report will be included in a future publication, including the results of a complete sequence and functional validation of some mutated proteins.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AFYA00000000. The version described in this paper is the first version, AFYA01000000.

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