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Draft Genome Sequence of *Acetobacterium bakii* DSM 8239, a Potential Psychrophilic Chemical Producer through Syngas Fermentation

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***Acetobacterium bakii* DSM 8239 is an anaerobic, psychrophilic, and chemolithoautotrophic bacterium that is a potential platform for producing commodity chemicals from syngas fermentation. We report here the draft genome sequence of *A. bakii* DSM 8239 (4.14 Mb) to elucidate its physiological and metabolic properties related to syngas fermentation.**

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Anaerobic acetogenic bacteria convert syngas, such as CO_2 with H_2 or CO, via the reductive acetyl-coenzyme A (CoA) pathway to acetate as a main product (1). Its autotrophic metabolism can be used for producing biofuels and valuable chemicals with higher catalyst specificity, lower energy cost, and less catalyst poisoning than those with conventional methods (2–6). However, the use of syngas as carbon and energy sources for the bacteria is often limited due to the low solubility of syngas in the liquid phase. For instance, the increasing solubility of hydrogen resulted in increased growth and acetate production by the mesophilic acetogenic bacterium *Acetobacterium woodii* (7). Thus, with its high growth rate at low temperatures, *Acetobacterium bakii* is a potential microbial platform of syngas fermentation (8). In this study, we determined the draft genome sequence of *A. bakii* DSM 8239 to understand its physiological and metabolic properties related to syngas fermentation at low temperature.

A. bakii was cultured under anaerobic conditions at 20°C in DSMZ medium 135 supplemented with 5 g/liter fructose (8). Genomic DNA was isolated using the PowerSoil DNA isolation kit (Mo Bio Laboratories, Carlsbad, CA), followed by fragmentation using Covaris S220 (Covaris, Inc., Woburn, MA). Fragmented genomic DNA was used to construct the Illumina paired-end library using a TruSeq kit (Illumina, Inc., San Diego, CA), and then sequenced using a MiSeq version 2 instrument with the 2 × 150-cycle paired-end read recipe. CLC Genomics Workbench (CLC bio, Aarhus, Denmark) was used to trim the obtained reads using the default parameter, resulting in 8,044,838 reads with an average read length of 139.97 bp. The genome was assembled using the *de novo* program in CLC (minimum contig length, 1,051; automatic bubble size, yes; word size, auto; perform scaffolding, yes). Following assembly, the Rapid Annotations using Subsystems Technology server (9) was used to annotate the draft genome sequence. rRNA and tRNA genes were predicted using RNAmmer 1.2 (10) and tRNAscan-SE 1.31 (11), respectively.

The *A. bakii* draft genome sequence is 4,141,442 bases with 91 contigs, with 41.2% G+C content, 4,024 predicted open reading frames, 48 tRNA genes, and 5 rRNA genes. The assembled genome contains the Wood-Ljungdahl pathway for converting CO_2 to acetyl-CoA. Distinct from other sequenced mesophilic acetogen genomes, *A. bakii* contains a two-component system for membrane fluidity regulation genes, including an autophosphorylatable histidine kinase and a DNA binding response regulator, which activate or regulate the gene expression of membrane lipid composition at different temperatures (12). *A. bakii* contains a metabolic pathway that produces ethanol from pyruvate by the pyruvate decarboxylase (EC 4.1.1.1), alcohol dehydrogenase (EC 1.1.1.1), and propionaldehyde synthesis pathways, producing 1-propanol. Further study of the draft genome sequence will enable *A. bakii* to be used as an industrial producer for syngas fermentation.

Nucleotide sequence accession numbers. The draft genome sequence of *A. bakii* DSM 8239 has been deposited in the DDBJ/EMBL/GenBank database under the accession no. LGYO00000000. The version described in this paper is the first version, LGYO00000000.1.

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