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Genome Sequence of *Gluconacetobacter* sp. Strain SXCC-1, Isolated from Chinese Vinegar Fermentation Starter▽

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***Gluconacetobacter* strains are prominent bacteria during traditional vinegar fermentation. Here, we report a draft genome sequence of *Gluconacetobacter* sp. strain SXCC-1. This strain was isolated from a fermentation starter (Daqu) used for commercial production of Shanxi vinegar, the best-known vinegar of China.**

Vinegar is produced from fermentation of carbohydrates and has been well used as a condiment, food preservative, and medicinal agent (3, 8, 10). In China, Shanxi traditional vinegar is one of the four most famous vinegars. During its production, fermentation starter (Daqu) is the key material, which comprises different filamentous fungi, yeast, and bacteria. Daqu plays great roles in both the anaerobic fermentation (alcohol fermentation by fungi) and aerobic fermentation (acetic acid fermentation by bacteria) steps. From this fermentation starter, a *Gluconacetobacter* sp. designated SXCC-1 was isolated as a prominent bacterium with high acetic acid resistance, and its whole genome was sequenced.

A strategy using combined Roche 454 and Solexa sequencing technology was used to sequence the whole-genome of SXCC-1. Genomic libraries containing 8-kb inserts were constructed, and 357,899 paired-end reads were generated by using the Roche GS FLX system, achieving 40.85-fold coverage of the genome. Genomic libraries containing 3-kb inserts was constructed, and 6,469,064 reads with a depth of approximately 143.76-fold were generated with an Illumina Solexa GA IIx (Illumina, San Diego, CA). We used the Burrows-Wheeler alignment (BWA) tool (4) to map all of the Solexa reads to the scaffolds generated by 454 Newbler (454 Life Sciences, Branford, CT). The inter- and intrascaffold gaps were filled by local assembly of Roche and Solexa reads around. Most of the Roche and Solexa reads were assembled into nine large scaffolds, including 64 contigs. The overall GC content is 62.46%.

The genome of SXCC-1 contains genes that encode pyrroloquinoline quinone (PQQ)-dependent dehydrogenases. They are all membrane-bound enzymes and recognized to be important in the acetic acid fermentation process (15). A gene cluster encoding the dehydrogenase (subunit I) and cytochrome *c* subunit (subunit II) of alcohol dehydrogenase (12, 14) was found. A 15-kDa subunit (subunit III) was also found in a different contig. It was reported that the former two subunits were essential for the enzyme activity (11). Besides these subunit genes, the genome also contains other 10 different alcohol dehydrogenase genes. Two of them are specific for SXCC-1 compared to the genomes of other three *Gluconacetobacter* strains (NC_010125, NC_011365, and BABN00000000). Aldehyde dehydrogenase is another key enzyme during acetic acid fermentation, and a gene cluster responsible for synthesis of all three subunits (AldF, AldG, and AldH) of this enzyme was found (13). Furthermore, there are three other putative aldehyde dehydrogenase genes on the genome. Genes *aarA*, *aarC*, and *aatA*, which are involved in the tricarboxylic acid (TCA) cycle, acetate assimilation, and acetic acid transport, respectively, were found in the genome. All three of these genes are responsible for acetic acid resistance (2, 6). SXCC-1 possesses a glucose dehydrogenase gene which is responsible for flavor formation of vinegar (1). The genome also contains many other functional genes coding for different enzymes involved in enriching nutritional ingredients in vinegar, such as D-sorbitol dehydrogenase (5), gluconate 5-dehydrogenase (9), and glycerol dehydrogenase (7).

Nucleotide sequence accession number. The draft of genome sequence of SXCC-1 has been deposited in GenBank under accession no. AFCH00000000.

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REFERENCES

1. **Cleton-Jansen, A. M., S. Dekker, P. van de Putte, and N. Goosen.** 1991. A single amino acid substitution changes the substrate specificity of quinoprotein glucose dehydrogenase in *Gluconobacter oxydans*. Mol. Gen. Genet. **229:**206–212.
2. **Fukaya, M., et al.** 1990. Cloning of genes responsible for acetic acid resistance in *Acetobacter aceti*. J. Bacteriol. **172:**2096–2104.
3. **Johnston, C. S., and C. A. Gaas.** 2006. Vinegar: medicinal uses and antiglycemic effect. Med. Gen. Med. **8:**61–69.
4. **Li, H., and R. Durbin.** 2009. Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics **25:**1754–1760.
5. **Miyazaki, T., N. Tomiyama, M. Shinjoh, and T. Hoshino.** 2002. Molecular cloning and functional expression of D-sorbitol dehydrogenase from *Gluconobacter suboxydans* IFO3255, which requires pyrroloquinoline quinine and hydrophobic protein SldB for activity development in *E. coli*. Biosci. Biotechnol. Biochem. **66:**262–270.
6. **Nakano, S., M. Fukaya, and S. Horinouchi.** 2006. Putative ABC transporter responsible for acetic acid resistance in *Acetobacter aceti*. Appl. Environ. Microbiol. **72:**497–505.
7. **Prust, C., et al.** 2005. Complete genome sequence of the acetic acid bacterium Gluconobacter oxydans. Nat. Biotechnol. **23:**195–200.

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8. **Salbe, A. D., C. S. Johnston, M. A. Buyukbese, P. D. Tsitouras, and S. M. Harman.** 2009. Vinegar lacks antiglycemic action on enteral carbohydrate absorption in human subjects. Nutr. Res. **29:**846–849.
9. **Salusjärvi, T., et al.** 2004. Cloning of a gluconate/polyol dehydrogenase gene from *Gluconobacter suboxydans* IFO 12528, characterisation of the enzyme and its use for the production of 5-ketogluconate in a recombinant *Escherichia coli* strain. Appl. Microbiol. Biotechnol. **65:**306–314.
10. **Setorki, M., S. Asgary, A. Eidi, A. H. Rohani, and M. Khazaei.** 2010. Acute effects of vinegar intake on some biochemical risk factors of atherosclerosis in hypercholesterolemic rabbits. Lipids Health Dis. **28:**9–10.
11. **Takemura, H., K. Kondo, S. Horinouchi, and T. Beppu.** 1993. Induction by ethanol of alcohol dehydrogenase activity in *Acetobacter pasteurianus*. J. Bacteriol. **175:**6857–6866.
12. **Tamaki, T., et al.** 1991. Cloning and sequencing of the gene cluster encoding two subunits of membrane-bound alcohol dehydrogenase from *Acetobacter polyoxogenes*. Biochim. Biophys. Acta **1088:**292–300.
13. **Thurner, C., C. Vela, L. Thöny-Meyer, L. Meile, and M. Teuber.** 1997. Biochemical and genetic characterization of the acetaldehyde dehydrogenase complex from *Acetobacter europaeus*. Arch. Microbiol. **168:**81–91.
14. **Toyama, H., F. S. Mathews, O. Adachi, and K. Matsushita.** 2004. Quinohemoprotein alcohol dehydrogenases: structure, function, and physiology. Arch. Biochem. Biophys. **428:**10–21.
15. **Yakushi, T., and K. Matsushita.** 2010. Alcohol dehydrogenase of acetic acid bacteria: structure, mode of action, and applications in biotechnology. Appl. Microbiol. Biotechnol. **86:**1257–1265.