



# Genome Sequence of *Oxalobacter formigenes* Strain SSYG-15

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**ABSTRACT** Colonization of the intestine with *Oxalobacter formigenes* reduces urinary oxalate excretion and lowers the risk of forming calcium oxalate kidney stones. Here, we report the genome sequence of *Oxalobacter formigenes* SSYG-15, a strain isolated from a stool sample from a healthy Chinese boy.

*Oxalobacter formigenes*, an anaerobe that is extremely sensitive to oxygen with substrate specificity for oxalate, was first isolated in 1985 by Milton J. Allison and then was identified as a new genus and species (1). This microorganism has a potential effect on oxalate metabolism in the human body (2, 3).

We isolated one *Oxalobacter formigenes* strain from the feces of a healthy Chinese boy who resided in Shanghai, China. We serially diluted 1 g of the feces sample and then spread it over ATCC medium 1352 with 7% agar and incubated it in an anaerobic environment at 37°C for 7 days. One white colony growing on the plates after 7 days of incubation was identified as *Oxalobacter formigenes* (99.6% identity to the 16S rRNA gene of *Oxalobacter formigenes* OXCC13) based on 16S rRNA gene sequencing. This strain was named *Oxalobacter formigenes* SSYG-15 (4), and it grew optimally at 37°C, with a doubling time of 7 days.

For genomic DNA extraction, a single colony was inoculated in ATCC medium 1352 broth and cultured in an anaerobic environment at 37°C until saturation. Genomic DNA was isolated using the MagAttract high-molecular-weight (HMW) DNA kit (Qiagen) according to the manufacturer's instructions (for Gram-negative bacteria). Library preparation was performed with the SMRTbell template prep kit 1.0 (Pacific Biosciences, USA), followed by single-molecule real-time (SMRT) sequencing on the Pacific Biosciences RS II platform (5).

A single SMRT cell produced a total of 2.52 Gb in 56,490 polymerase reads, and the  $N_{50}$  value of 66.16 kb was used for *de novo* assembly with the PacBio SMRT Analysis 5.1.0 assembly protocol, resulting in one circular chromosome with a single contig of 2,491,742 bp. The chromosomal contig showed an average G+C content of 49.56%.

Genome annotation was completed by submission to the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP). A total of 2,255 predicted genes, 6 rRNAs, 47 tRNAs, and 4 noncoding RNAs were obtained. AntiSMASH2.0.2rc1 analysis (6) resulted in the prediction of a secondary metabolite biosynthesis prediction gene cluster of formic acid. Meanwhile, antibiotic resistance gene analysis with Resistance Gene Identifier (RGI) (7) predicted a gene associated with resistance to macrolide, penicillin, trimethoprim, aminoglycoside, and chloramphenicol. Default parameters were used for all software programs unless otherwise stated.

*Oxalobacter formigenes* strain SSYG-15 was archived in the China Center for Type Culture collection in 2016 and was assigned CCTCC number M2016183.

**Data availability.** The complete genome sequence of *Oxalobacter formigenes* SSYG-15 is available from GenBank under the accession number [CP042242](https://doi.org/10.1128/MRA.01059-19). The raw sequence reads have been deposited in the NCBI Sequence Read Archive under the BioProject number [PRJNA556554](https://doi.org/10.1128/MRA.01059-19) and accession number [SRR10007720](https://doi.org/10.1128/MRA.01059-19).

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We declare no conflict of interest.

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