Draft Genome Sequence of an Oxalate-Degrading Strain of *Clostridium sporogenes* from the Gastrointestinal Tract of the White-Throated Woodrat (*Neotoma albigula*)

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The gastrointestinal tract of the white-throated woodrat *Neotoma albigula* harbors a diverse microbial population that functions in the degradation of ingested plant secondary compounds. Here, we present the draft genome sequence and annotation of *Clostridium sporogenes* strain 8-O, a novel oxalate-degrading bacterium isolated from the feces of *N. albigula*.

In some habitats, *Neotoma albigula* consumes a diet consisting primarily of *Opuntia cactus* which is rich in oxalate (1). Like all mammals, *N. albigula* is not capable of metabolizing oxalate, and relies on bacterial populations in their gut to degrade oxalate. Previous work has demonstrated that *N. albigula* houses multiple oxalate-degrading taxa throughout its gastrointestinal tract, and many of these oxalate-degrading taxa have been cultured and their oxalate-degrading capabilities quantified (2). Bacterial isolation and oxalate-degrading capabilities were previously described in Miller et al. (2). In brief, gut contents of the foregut, stomach, small intestine, cecum, and large intestines were collected along with the feces isolated from *N. albigula* and were serially diluted in sterile deionized water. Dilutions were then plated onto brain heart infusion (BHI) agar supplemented with 20 mM sodium oxalate and 1 g/L calcium chloride. Cultures were incubated at 37°C for 48 h under anaerobic conditions (Anaeropack system, Mitsubishi Gas Chemical Company). Individual colonies were selected for further enrichment by the presence of a zone of clear-lawn around the colony, indicating the degradation of oxalate. To evaluate *in-vitro* oxalate degradation, isolates were inoculated into BHI broth supplemented with 20 mM sodium oxalate and incubated for 48 h. The oxalate concentration of the medium after the incubation period was then determined by titration. Isolates that showed significant oxalate degradation were identified by 16S sequencing (2) and the resulting oxalate degradation was examined by the accession number LUAU0000000. The version described in this paper is version LUAU0000000. The version described in this paper is version LUAU0000000.

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REFERENCES


Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number LUAU00000000. The version described in this paper is version LUAU0000000. 

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