Draft Genome Sequence of *Caloramator australicus* Strain RC3<sup>T</sup>, a Thermoanaerobe from the Great Artesian Basin of Australia<sup>†</sup>  

Christopher D. Ogg and Bharat K. C. Patel*  

*Microbial Gene Research and Resources Facility, School of Biomolecular and Physical Sciences, Griffith University, Brisbane, QLD 4111, Australia  

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*Caloramator australicus* strain RC3<sup>T</sup> (JCM 15081<sup>T</sup> = KCTC 5601<sup>T</sup>) is the type strain of a newly identified thermophilic species, which was isolated from red microbial mats that thrive at 66°C in the runoff channel of a Great Artesian Basin bore (New Lorne bore, registered number 17263) in outback Queensland, Australia. The ability of the *C. australicus* strain to use metals as terminal electron acceptors has led to concerns that it could colonize and enhance corrosion of the metal casing of Great Artesian Basin bore well pipes and that this could subsequently lead to bore failure and loss of water availability for the community which is so reliant on it. The genome of the *C. australicus* strain has been sequenced, and annotation of the ~2.65-Mb sequence indicates that the attributes are consistent with physiological and phenotypic traits.

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* Caloramator australicus* strain RC3<sup>T</sup> (= JCM 15081<sup>T</sup> = KCTC 5601<sup>T</sup>) is a Gram-positive thermoanaerobe of the phylum *Firmicutes* which was isolated from a gelatinous red microbial mat thriving at 66°C in the runoff channel of a Great Artesian Basin (GAB) bore (New Lorne bore, registered number 17263) (2, 5, 6). *C. australicus* and *C. proteoclasticus* are the only members of the 10 species of the genus *Caloramator* which utilize a variety of metals [iron(III), manganese(IV), and vanadium(V)] as the terminal electron acceptor. *C. australicus* therefore is not only an important model organism for understanding the possible role of metal-reducing bacteria in corrosion processes of the Great Artesian Basin bore well pipes but also has potential in microbial fuel cell (MFC) technology. This is the first report on the genome sequence of a *Caloramator* species.

The whole genome of *C. australicus* was sequenced using the Roche 454 Life Sciences GS FLX system at the Interdisciplinary Center for Biotechnology Research (ICBR), University of Florida. The sequence data consisted of two DNA fragment libraries (total of 196,736 reads) and two 8-kb paired-end libraries (total of 86,845 reads). A total of 71,415,765 nucleotides were sequenced to give 27-fold coverage.

A draft assembly of 31 scaffolds (N<sub>50</sub> of approximately 144.4 kb with the largest scaffold size being 358.3 kb) and the total assembly size of 2,579,181 bp were produced using Newbler (version 2.3). A slightly larger, single scaffold of 2,654,716 bp was assembled using Mira (version 3.0.3) and Bambus (version 2.33) using parameters described by Chevreux et al. (4) and Pop et al. (7).

The genome sequence of the single scaffold obtained from the Bambus-Mira assembly was annotated with the online Rapid Annotations Using Subsystems Technology (RAST) server (1) and BASys (9) and verified manually using the NCBI (3) and COG databases (8). The G+C mol% content of the genome was determined to be 32.8%. Three rRNA operons (16S-23S-5S), 2,767 predicted codons, and 62 tRNAs were identified. Putative functions could be assigned to 75% of the encoded proteins, and the remaining 25% could not be placed. The presence of potential homologues to genes involved in iron transport and binding, threonine and glycerol degradation, and polysaccharide biosynthesis was identified and concurs with previously reported physiological data (5). Comparative genome analysis indicated that the closest genomes were those from the mesophilic members of the genus *Clostridium*, family *Clostridiaceae*. The genome sequence of *C. australicus* will contribute to our understanding of extracellular polysaccharide synthesis by microbial mat communities and corrosion processes in the nonvolcanic high-temperature environment of the Great Artesian Basin.

**Nucleotide sequence accession numbers.** The draft genome sequence of *Caloramator australicus* strain RC3<sup>T</sup> reported in this paper has been deposited in the DDBJ database under accession number DRA000322, in GenBank under Genome Project ID number 49895, and in the Genomes OnLine Database (GOLD) as GOLD CARD number Gi06829.

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**REFERENCES**


