



## Genome Announcement

# Draft genome sequence of *Chryseobacterium limigenitum* SUR2<sup>T</sup> (LMG 28734<sup>T</sup>) isolated from dehydrated sludge

Jure Škraban<sup>a</sup>, Nikos C. Kyrpides<sup>b</sup>, Nicole Shapiro<sup>b</sup>, William B. Whitman<sup>c</sup>,  
Janja Trček<sup>a,d,\*</sup>

<sup>a</sup> University of Maribor, Faculty of Natural Sciences and Mathematics, Department of Biology, Maribor, Slovenia

<sup>b</sup> DOE Joint Genome Institute, Walnut Creek, CA, USA

<sup>c</sup> University of Georgia, Department of Microbiology, Athens, GA, USA

<sup>d</sup> University of Maribor, Faculty of Chemistry and Chemical Engineering, Maribor, Slovenia

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## ABSTRACT

The type strain SUR2 of the novel species *Chryseobacterium limigenitum* was isolated from a dehydrated sludge of the municipal sewage treatment plant in Dogoše near Maribor in Slovenia. The draft genome, with 60 contigs, 4,697,725 bp, 34.4% of G+C content, was obtained using the Illumina HiSeq 2500-1 platform. Joint Genome Institute Microbial Genome Annotation Pipeline (MGAP v.4) has identified 4322 protein-coding sequences including resistance genes against arsenic and other heavy metals. In addition, a subclass B3 metallo-β-lactamase, which confers resistance to penicillins, cephalosporins and carbapenems, was also present in the genome. The genome sequence provides important information regarding bioremediation potential and pathogenic properties of this newly identified species.

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Since its first description two decades ago,<sup>1</sup> the genus *Chryseobacterium* now includes a large number of species often isolated from industrially degraded environments.<sup>2</sup> Many members of the genus are capable of bioremediation of heavy metals and organochlorine pesticides,<sup>3</sup> and some species (*Chryseobacterium indologenes*) cause nosocomial infections.<sup>4</sup> Here we report a draft genome sequence of a new species *Chry-*

*seobacterium limigenitum* (type strain SUR2), which was isolated from dehydrated sludge of the municipal sewage treatment plant in Dogoše near Maribor in Slovenia.<sup>5</sup>

SUR2 was cultured on nutrient agar (NA, Sigma-Aldrich) for 48 h at 30 °C. Genomic DNA was extracted with NucleoSpin Tissue kit (Macherey-Nagel) using the manufacturers protocol. Sequencing was performed at the DOE Joint Genome Institute (JGI) using the Illumina HiSeq 2000-1TB platform, which generated 9,287,994 reads totaling

\* Corresponding author.

E-mail: [janja.trcek@um.si](mailto:janja.trcek@um.si) (J. Trček).

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1393.2 Mbp. The reads were filtered using BBTools software package (<http://sourceforge.net/projects/bbmap>) and assembled with Velvet (version 1.2.07).<sup>6</sup> Wgsim (version 0.3.0) (<https://github.com/lh3/wgsim>) was used to generate 1–3 kbp simulated paired end reads from Velvet contigs longer than 500 bp and finally assembled using Allpaths-LG (version r46652).<sup>7</sup> The final draft assembly contained 60 scaffolds (N50 = 193,444 kb), totaling 4,697,725 bp in size and a coverage of 292.7x. The G+C content was 34.4%. JGI Microbial Genome Annotation Pipeline (MGAP v.4)<sup>8</sup> was used for annotation of the genome's 4322 protein-coding sequences (CDSs), 58 tRNAs, 1 rRNA and 50 ncRNAs.

*C. limigenitum* SUR2 has two operons composed of a transcriptional regulator (ArsR), an unannotated protein of 155 aa, followed by an arsenate reductase (ArsC), and an arsenite efflux pump (ArsB). Arsenate reduction to the more soluble arsenite and its expulsion is a detoxification mechanism by which the strain mobilizes arsenic, which can be deleterious to water environments.<sup>9</sup> However, reduction to arsenite, followed by precipitation by sulfide could be applied for cleaning contaminated areas in the future.<sup>10</sup> Additionally, other heavy metal resistance genes (cobalt-zinc-cadmium resistance protein CzcA) and the corresponding efflux pumps have been identified. These genes are evidence for an adaptation to an environment polluted with heavy metals.

Some members of the genus (*C. indologenes*) cause nosocomial infections due to their resistance against most  $\beta$ -lactams.<sup>4</sup> *C. limigenitum* SUR2 contained a subclass B3 metallo- $\beta$ -lactamase that shares 81% identity to a recently identified CPS-1 lactamase found in *Chryseobacterium piscium* (WP\_063857696.1). CPS-1 efficiently hydrolyses penicillins, cephalosporins, and carbapenems.<sup>11</sup> Additionally, MFS efflux pumps inferring resistance to tetracyclin and fosmidomycin, multidrug resistance transporters of EmrB/QacA subfamily, MATE and DHA2 families are also present. Further analysis of the draft genome will shed more light on the possible bioremediation potential and pathogenic properties of this newly identified species.

The genome sequence has been deposited in the European Nucleotide Archive (ENA) under the accession number FPKW01000000, the version described in this paper is the first version.

### Conflicts of interest

All authors declare, that there are no conflicts of interest regarding the submitted manuscript.

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