

Draft Genome Sequence of *Pseudomonas psychrotolerans* L19, Isolated from Copper Alloy Coins

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We report the draft genome sequence of *Pseudomonas psychrotolerans* strain L19, isolated from a European 50-cent copper alloy coin. Multiple genes potentially involved in copper resistance were identified; however, it is unknown if these copper ion resistance determinants contribute to prolonged survival of this strain on dry metallic copper.

Copper is an essential trace element in most living organisms, including humans. While needed in small amounts, copper can easily become toxic when in surplus. Coins from many countries are made from copper or its alloys. In order to isolate metallic copper-resistant bacteria, European 50-cent coins from general circulation were sampled (3). Coins were kept under sterile conditions for 24 h before bacteria were isolated by plating coins on solidified medium. The Gram-negative *Pseudomonas psychrotolerans* strain L19 was isolated from an LB agar plate. Sequencing of the 16S rRNA gene was performed and the strain was also reexposed to metallic copper for 1, 2, or 7 days. *P. psychrotolerans* strain L19 (classified as *P. oleovorans* L19 in reference 3) was able to survive on copper surfaces for >48 h, which is >5,000 times longer than *Escherichia coli* under identical conditions. The MIC of strain L19 for CuCl₂ was 3.5 mM (3). For further characterization of strain L19, colony morphology, antibiotic resistance, utilization of carbon sources, and enzymatic characterizations were performed (5) and compared with the type strains *P. psychrotolerans* C36^T and its closest relative *Pseudomonas oleovorans* DSM 1045^T (C. Espirito Santo, unpublished results).

Reads were generated by 454 GS FLX sequencing (6), and raw data were assembled using the GS *de novo* assembler (“Newbler”) version 2.5.3 (Roche Diagnostics). The assembled contigs were submitted to the RAST annotation server for subsystem classification and functional annotation (1). Coding sequences (CDSs) were assigned using BLASTp with KEGG Orthology (KO). The G+C content was calculated using an in-house Perl script. The NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) was employed for gene annotation in preparation for submission to GenBank (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>).

The draft genome sequence of *P. psychrotolerans* strain L19 comprises 5,098,787 bases representing a 42-fold coverage of the genome. The assembled genome consists of 46 large contigs (>500 bp) with an average contig size of 110,827 bp and a G+C content of 65.68%. The genome encodes 4,660 putative CDSs, of which 4,641 CDSs have functional predictions. The draft genome sequence contains two ribosomal RNAs, three 5S rRNAs, and 54 tRNAs loci. For the CDSs, 3,887 proteins could be assigned to cluster of orthologous groups (COG) families (7). A total of 2,454 proteins have orthologs (bit score > 60), with 27 of the closest neighbors to strain L19 belonging to eight genera (*Pseudomonas*, *Azotobacter*, *Chromohalobacter*, *Marino-*

bacter, *Shewanella*, *Alcanivorax*, *Hahella*, and *Methylococcus*) as identified by RAST (1).

The *P. psychrotolerans* strain L19 genome carries multiple genes and operons potentially involved in copper resistance, such as the *cus* operon encoding an RND-type efflux system and genes encoding multicopper oxidases typically involved in oxidizing Cu(I) to Cu(II).

Recent publications (2, 4, 8, 9) have focused on the antibacterial mode of action exerted by metallic copper surfaces. It is tempting to speculate that the peculiar membrane composition of *P. psychrotolerans* contributes to the extended survival of this species on metallic copper. In the type strain, diverse unidentified phospholipids, lipids, and aminophospholipids are present (5). Similar compounds in strain L19 constitute promising candidates for further studies.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under accession number [AHBD00000000](https://www.ncbi.nlm.nih.gov/nuccore/AHBD00000000). The version described in this paper is the first version, AHBD01000000.

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