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Chryseobacterium treverense sp. nov., isolated from a human clinical source

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Running Title

C. treverense isolated from human clinical source

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Abstract

We report the draft genome sequence of *Chryseobacterium treverense* is isolated from human clinical sources. The genome is 2,379,279 base pairs and contains genes enhancing bacterium survival and evasion of the host's immune system, therefore amplifying broad antibiotic resistance.

Announcement

The Gram-negative *Chryseobacterium treverense* is isolated from Trier City, Germany (49.7501° N, 6.6372° E) (5, 6). It is a yellow-tinged, aerobic, non-spore forming, and non-motile bacterium in soil, plants, human clinical specimens, and food. It potentially causes urinary tract infections and pneumonia (1, 2). Genomic sequencing provided taxonomic revisions, accurately classifying it in the genus *Chryseobacterium* (3). Data from JGI allowed scientists to genomically sequence *C. treverense,* enabling researchers to investigate its impact on eukaryotes (4). *C. treverense* was aerobically grown on Columbia agar, supplemented with 5% sheep blood, and preserved in fetal calf serum by lyophilization (1).

The draft genome of *C. treverense* was generated at DOE JGI using Illumina technology. Illumina HiSeq–2500 1TB platform sequenced a 300 bp insert standard shotgun with the 150-bp paired-end format. Illumina Std PE generated 10,312,988 reads totaling 1,546.9 Mbp. The raw data was filtered using BBDuk. Reads with more than one "N," quality scores averaging less than 8, contigs less than 1 kbp, or reads shorter than 51 bp were discarded. Using BBMAP, the remaining reads were aligned to masked reference genomes of humans, cats, and dogs, discarding those exceeding 95%. The filtered, normalized reads were assembled using SPAdes v3.6.2 (7). The final draft, based on 1,500.0 Mbp of Illumina data with coverage of 625.3X, contained 10 contigs and 10 scaffolds, totaling 2.379 Mbp. The final draft was annotated according to the standard JGI Microbial Genome Annotation Pipeline. The

genome was 17% contaminated with a complete genome of 99.97% (8). DSMZ will provide details on growth and DNA isolation.

The genome had 2,379,279 base pairs. Scaffold N50 is at 1,189,639 base pairs. The average fold coverage was 4.3 with a GC content of 39.46%. There were 2305 genes and 2193 coding sequences with 5 rRNAs and 37 tRNAs (Table 1). The probability of *C. treverense* being a human pathogen is 0.227 with zero matched pathogenic families and 0.68% input of proteome coverage; it is predicted to be non-pathogenic (9). Virulence factors include genes enhancing the probability of bacterium survival and protecting from the host's immune system (VFDB 2022). Using CARD, 95 loose hits and one strict hit were detected in *C. treverense* (10). The bacteria exhibits broad antibiotic resistance, particularly to fluoroquinolones, glycopeptides, oxazolidinones, and tetracyclines. The results of CRISPRCasFinder displayed 10 analyzed sequences and 3 CRISPR sequences with evidence (11). Comparing our results to JGI, no CRISPR sequences were listed. antiSMASH (v 7.0). Analysis revealed type I PKS cluster, indicating possible terpene production.

Feature	**Findings**
Length (bp)	2,379,279
Status	complete
No. of contigs	10
GC content %	39.46
No. of genes	2305
No. of coding sequences	2193
No. of rRNAs	5
No. of tRNAs	37

Table 1: Genome Statistics

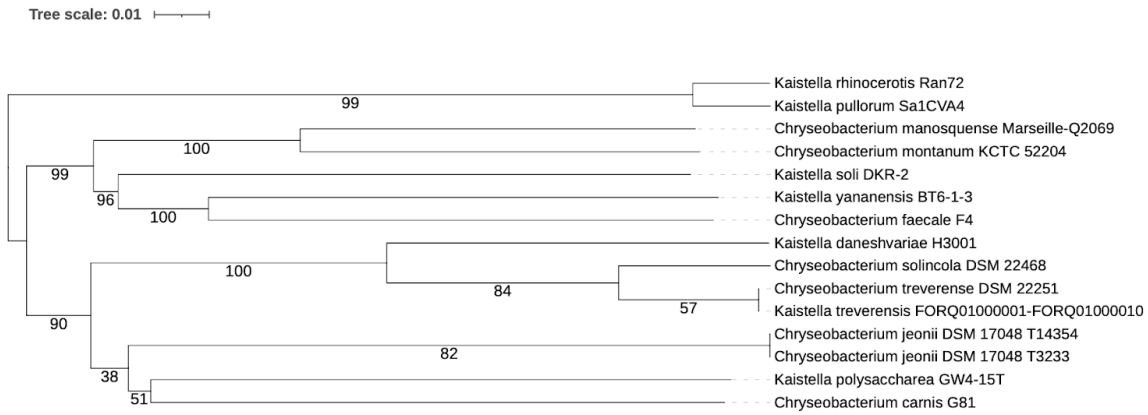

Figure 1: This phylogenetic tree of Chryseobacterium treverense was constructed using the Type Strain Genome Server (TYGS) and Genome BLAST Distance Phylogeny (GBDP) analysis.

Data availability statement

This Whole Genome Shotgun project has been deposited in GenBank under the accession no. FORQ01000001. *The version described in this paper is the first version,* FORQ00000000.1. *Additional information can be found on the JGI Integrated Microbial Genomes and Microbiomes portal under the taxon ID 631455.*

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