Draft Genome Sequence of *Modestobacter* sp. strain VKM Ac-2676 from soil in the area of sharply continental climate

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Running Head: Draft Genome of *Modestobacter* sp. VKM Ac-2676

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A draft genome sequence of a novel actinobacterium, *Modestobacter* sp. strain VKM Ac-2676, was derived using Ion Torrent sequencing technology. The genome size is 3.88 Mb with average G+C content of 73.40%. The genes encoding properties relevant to adaptability of this bacterium to a sharply continental climate zone were revealed.

The genus *Modestobacter* (family *Geodermatophilaceae*, phylum "Actinobacteria") includes six validly described species (LPSN; <http://www.bacterio.net>) (1). A seventh species has recently been proposed (2). The *Modestobacter* species are aerobic, non-spore-forming, heterotrophic, and able to grow on oligotrophic media. They form orange-red or pink colonies usually turning black with age (2, 3). Members of this genus occur in markedly different ecosystems, including extreme ones (2 - 6).

Strain VKM Ac-2676 was isolated from technogeneous soil collected near Orsk town (Southern Urals, Russia) located in a site characterized by dry and hot summers, with

temperatures up to +40°C, and cold winters, with temperatures down to -40°C. Based on the 16S rRNA gene sequence analysis, VKM Ac-2676 is the closest to *M. versicolor* CP153-2^T (99.52% sequence identity).

The genome sequencing was performed with a semiconductor genome analyzer Ion Torrent PGMTM (Thermo Fisher Scientific Inc., USA) using 400-bp sequencing kit and 318 v2 chip. A total of 539,682 raw reads were assembled *de novo* into 2,200 contigs (21.0-fold peak coverage) using Newbler 2.9 (454 Life Sciences Corporation, USA). Genomic contigs were annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP, version 3.3) (https://www.ncbi.nlm.nih.gov/genome/annotation_prok). The genome size is 3,884,161 bp with average G+C content of 73.40%. The N50 contig is 2,861 bp, largest contig is 22,534 bp. A total of 2,702 protein-encoding genes (1031 of which are hypothetical proteins), 45 tRNAs, 3 rRNAs and 3 ncRNAs were predicted.

WGS analysis revealed that VKM Ac-2676 harbors genes that encode properties relevant to the adaptability of target bacterium to a sharply continental climate. These include genes involved in the heat shock (*hrcA*, *dnaJ* and *dnaK*) and cold shock (Csp family) responses, and also in the trehalose biosynthesis, which play a crucial role in protecting cells against desiccation. The strain has also genes encoding carbon monoxide dehydrogenase (involved in chemolithotrophic metabolism allowing organisms to use CO as a carbon and energy source) (7) and a putative rhodopsin-like protein genes indicative of its probable photoheterotrophic lifestyle. The genome harbors a *recO* gene and four copies of *recQ* DNA helicase that play roles in maintaining genomic stability (8, 9). Strain VKM Ac-2676 also contains genes of multienzyme complex involved in UV resistance, such as *uvrA* and *uvrB*, like that reported for *M. marinus* (NC_017955.1) and *M. caceresii* (NZ_JPMX01000000) (2, 5). The protein sequence of *uvrC* gene of strain VKM Ac-2676 showed high similarity (~95%) to that of a relevant gene in *M. caceresii* 45-2b^T, however PGAAP marks this gene as pseudogene.

VKM Ac-2676 formed a sister branch to *M. versicolor* in the *gyrB* gene tree with 92.90% sequence identity, that is in the range of similarities (84.91%–96.31%) found between other species of this genus. The above data suggest that strain VKM Ac-2676 represent a novel species of *Modestobacter*. The study of biochemical and physiological characteristics of this strain is in progress.

Nucleotide sequence accession number(s). This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession MBFF000000000. The version described in this paper is the first version, MBFF01000000.

ACKNOWLEDGMENTS

Sequencing was performed at the Postgenomics Research Laboratory, SRI PCM FMBA of Russia. We are thankful to Dr. V.V. Babenko and Dr. E.S. Kostryukova for their kind assistance.

Funding information. This work was financially supported by the Russian Federal Agency of Scientific Organizations for fundamental studies at IBPM RAS (topic No. 01201350918).

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