

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

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

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22 A draft genome sequence of a novel actinobacterium, *Modestobacter* sp. strain VKM Ac-
23 2676, was derived using Ion Torrent sequencing technology. The genome size is 3.88 Mb with
24 average G+C content of 73.40%. The genes encoding properties relevant to adaptability of
25 this bacterium to a sharply continental climate zone were revealed.

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

33

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

36 temperatures up to +40°C, and cold winters, with temperatures down to -40°C. Based on the
37 16S rRNA gene sequence analysis, VKM Ac-2676 is the closest to *M. versicolor* CP153-2^T
38 (99.52% sequence identity).

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40 The genome sequencing was performed with a semiconductor genome analyzer Ion Torrent
41 PGMTM (Thermo Fisher Scientific Inc., USA) using 400-bp sequencing kit and 318 v2 chip. A
42 total of 539,682 raw reads were assembled *de novo* into 2,200 contigs (21.0-fold peak
43 coverage) using Newbler 2.9 (454 Life Sciences Corporation, USA). Genomic contigs were
44 annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP,
45 version 3.3) (https://www.ncbi.nlm.nih.gov/genome/annotation_prok). The genome size is
46 3,884,161 bp with average G+C content of 73.40%. The N50 contig is 2,861 bp, largest contig
47 is 22,534 bp. A total of 2,702 protein-encoding genes (1031 of which are hypothetical
48 proteins), 45 tRNAs, 3 rRNAs and 3 ncRNAs were predicted.

49

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

63

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

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70 **Nucleotide sequence accession number(s).** This Whole Genome Shotgun project has been
71 deposited at DDBJ/ENA/GenBank under the accession MBFF00000000. The version
72 described in this paper is the first version, MBFF01000000.

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