Extremophiles are important potential resources for industrial applications, and many researchers have focused on this field (2, 9–11).

There are 10 genera and 18 species in the family Planctomycetaceae (http://www.bacterio.cict.fr/p/planctomycetaceae.html). Whole-genome sequences have been reported for species in six genera (GenBank accession numbers AANZ00000000.1, ABGO00000000.1, NC_013720.1, NC_014962.1, NC_014148.1, and NC_005027.1). In this report, we sequenced three species in the remaining genera, including Singulisphaera acidiphila (DSM 18658T) (4), Schlesneria paludicola (DSM 18645T) (5), and Zavarzinella formosa (DSM 19928T) (3). All the strains were isolated from acidic wetlands in northern Russia, and we purchased them from Deutsche Sammlung von Mikroorganismen und Zellkulturen Gmbh (DSMZ).

Singulisphaera acidiphila is an aerobic, nonmotile sphere that occurs singly or in shapeless aggregates and attaches to surfaces by means of a holdfast material. The major fatty acids are C16:0, C16:1ω7c, and C18:2ω6c,12c (4). Schlesneria paludicola is a budding, ellipsoid-shaped and rosette-forming bacterium. The major fatty acids are C16:0 and C16:1ω7c (5). Zavarzinella formosa is an aerobic, pink-pigmented, budding and rosette-forming bacterium. The major fatty acids are C18:0, C18:1ω9c, and C16:1ω5c (3). The major quinine produced by these three strains is menaquinone-6 (MK-6) (3–5). Also, it was reported that some of these microbes were able to degrade polymers or showed halophilia, cold resistance, or acidophilia (3–5).

Genomic DNAs were extracted from the above-named three species by using a conventional phenol-chloroform extraction method and were sequenced by using Illumina Hiseq 2000 at BGI-Shenzhen, China. About 1.5 Gb of data were generated for each sample. The pair-end reads were assembled using SOAPdenovo (7) into 621, 106, and 594 contigs for Singulisphaera acidiphila, Schlesneria paludicola, and Zavarzinella formosa, respectively.

Gene prediction was determined by using Glimmer 3.0 (1). Genes coding tRNA were determined through tRNAscan-SE (8), and rRNA genes were identified by using RNAmer (6). The G+C (mole percent) contents were calculated according to the genome sequences.

The three draft genome sequences were 9.72, 8.70, and 10.09 Mb in size and contained 8,972, 8,626, and 10,112 genes with G+C contents of 62.16%, 55.66%, and 59.10% for Singulisphaera acidiphila, Schlesneria paludicola, and Zavarzinella formosa, respectively. Singulisphaera acidiphila has 63 tRNA genes with a total length of 4,773 bp and 8 rRNA loci. The other two strains, Schlesneria paludicola and Zavarzinella formosa, have 74 tRNA genes and 53 rRNA loci each and total lengths of 5,596 and 5,533 bp, respectively.

The genes were blasted against the COG, NR, KEGG, SWISSPORT, and TREMBLE databases. For Zavarzinella formosa, Singulisphaera acidiphila, and Schlesneria paludicola, respectively, nearly 3,015, 2,404, and 2,371 gene families and 22, 22, and 21 Clusters of Orthologous Groups (COG) categories (A to V) were identified. The metabolic networks comprised about 155, 169, and 166 subsystems, respectively, according to KEGG analysis. Five, 11, and 13 resistance proteins were annotated from the SWISSPORT database; in addition, 8, 53, 64, 76, and 155; 14, 47, 73, 111, and 131; and 11, 52, 69, 76, and 128 genes, respectively, were associated with cell cycle control/cell division/chromosome partitioning, cell defense mechanisms, lipid transport/metabolism, cell wall/membrane/envelope biogenesis, and signal transduction mechanisms. Aside from these findings, most of the predicted genes in the three species were involved in carbohydrate metabolism.

Nucleotide sequence accession numbers. These Whole Genome sequencing projects have been deposited at GenBank under the accession numbers AIAB00000000, AHZQ00000000, and AHZR00000000 for Zavarzinella formosa, Singulisphaera acidiphila, and Schlesneria paludicola, respectively. All the accession number versions described in this paper are the first version.

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