Draft genome sequence of the psychrophilic and alkaliphilic Rhodonellum psychrophilum strain GCM71T

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Cold and alkaline environments are rare on Earth, and knowledge regarding the organisms that thrive in such polyextreme environments is very limited. The submarine ikaite tufa columns in the Ikka Fjord in southwest Greenland (61°11' N, 48°01' W) represent a unique, permanently cold (4 to 6°C), and alkaline (>pH 10) environment (1), and they have been shown to harbor a diverse bacterial community adapted to these conditions (2–4). A large number of bacteria from the ikaite columns have previously been isolated, and the majority of these are psychrotolerant and alkaliphilic or alkalitolerant (2–4). Although a significant number of the isolates display alkaliphilic and psychrotolerant growth properties, only very few true alkaliphilic psychrophiles have been identified. One isolate, *Rhodonellum psychrophilum* GCM71T, was shown to be truly alkaliphilic and psychrophilic, displaying optimal growth at temperatures between 5°C and 10°C and at pH 9.2 to 10 (5). Thus, *R. psychrophilum* is one of very few polyextremophilic bacteria adapted to low-temperature and high-pH conditions, and in this report, we describe the annotated draft genome sequence of *R. psychrophilum* GCM71T, the first genome sequence of an organism adapted to these conditions. The genome sequence is part of research looking into polyextremophily and genome mining for enzymes that are adapted to these conditions.

Genomic DNA was isolated from a liquid culture of *Rhodonellum psychrophilum* strain GCM71T, isolated from the cold and alkaline submarine ikaite columns in the Ikka Fjord in Greenland, displays optimal growth at 5 to 10°C and pH 10. Here, we report the draft genome sequence of this strain, which may provide insight into the mechanisms of adaptation to these extreme conditions.

**REFERENCES**

Research in computational molecular biology. Springer-Verlag, Berlin, Germany.
