Strain 1860, a novel member of the genus *Pyrobaculum*, is a hyperthermophilic organotrophic crenarchaeon growing anaerobically with various electron acceptors. The complete genome sequence reveals genes for several membrane-bound oxidoreductases, the Embden-Meyerhof and Entner-Doudoroff pathways for glucose metabolism, the tricarboxylic acid cycle, the glyoxylate cycle, and the dicarboxylate/4-hydroxybutyrate cycle.

Members of the genus *Pyrobaculum* within the crenarchaeal order *Thermoproteales* were among the first hyperthermophilic archaea described (5). Most *Pyrobaculum* spp. are facultative chemolithoautotrophs growing anaerobically with a wide range of electron acceptors (1, 6), whereas *Pyrobaculum aerophilum* is a facultative microaerophile (10) and *Pyrobaculum ogunense* is a facultative aerobe (8). The complete genome sequences of five representatives of the genus *Pyrobaculum* are known, *P. aerophilum* (3), *Pyrobaculum arsenaticum*, *Pyrobaculum calidifontis*, *Pyrobaculum islandicum*, and *Thermoproteus neutrophilus* (to be reclassified within the genus *Pyrobaculum*).

Strain 1860 was isolated from Lake Fumarolic (84°C, pH 6.8) in the Uzon Caldera in Kamchatka, Russia. Strain 1860 is an obligate anaerobe able to grow on different organic substrates. Nitrate, arsenate, thiosulfate, soluble ferric iron citrate, and insoluble ferric iron oxide may be used as respiratory electron acceptors. To understand the physiological properties of strain 1860 and its possible ecological role, its complete genome sequence was determined.

The genome of strain 1860 was sequenced using the Roche 454 GS FLX pyrosequencing platform. We obtained a library of 240,992 single-strand reads; the reads were assembled into 17 contigs by Newbler Assembler 1.1 (454 Life Sciences, Branford, CT). The genome was finished by filling gaps with sequencing and primer walking of PCR products with an ABI 3730 capillary sequencer (Applied Biosystems).

The complete genome of strain 1860 consists of 2,467,972 bp in a single circular chromosome with an average G+C content of 56.97%. The sequences of the 16S rRNA exons of strain 1860 are 97 to 98% identical to those of other *Pyrobaculum* species, suggesting that it belong to this genus. A total of 2,840 protein coding genes were predicted by Glimmer (2), covering 91% of the genome. The complete genome sequence reveals genes for several membrane-bound oxidoreductases, including those for nitrate, arsenate, and thiosulfate reduction, as well as the gene encoding a putative membrane-bound polyheme c-type cytochrome, may account for the respiratory versatility of this archaeon. Making the genome sequence of *Pyrobaculum* sp. 1860 available will allow comprehensive comparisons with other members of the genus *Pyrobaculum* and enable further investigation of the respiratory pathways in the members of the *Crenarchaeota*.

Nucleotide sequence accession number. The complete genome sequence of *Pyrobaculum* sp. 1860 was deposited in GenBank under accession number CP003098.

ACKNOWLEDGMENTS

This work was performed using the scientific equipment of the Core Research Facility of the Bioengineering Center, Russian Academy of Sciences, and was supported by the Ministry of Education and Sciences of Russia (contract 16.512.11.2234) and the Russian Foundation for Basic Research (grant 11-04-00671).

REFERENCES

new genus of neutrophilic, rod-shaped archaebacteria from continental solfataras growing optimally at 100°C. Arch. Microbiol. 149:95–101.