Complete Genome Sequence of Hyperthermophilic Piezophilic Archaeon Palaeococcus pacificus DY20341T, Isolated from Deep-Sea Hydrothermal Sediments

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We report the genome sequence of Palaeococcus pacificus DY20341T, isolated from a sediment sample collected from eastern Pacific Ocean hydrothermal fields, which is the first report of a complete genome for a Palaeococcus species. The genome sequence will help to better understand differentiation phylogenetic relationships and evolution of several Thermococcales species.

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The order Thermococcales is one of the best-studied groups of hyperthermophiles. Over the past 20 years, ~40 species affiliated with three genera (32 Thermococcus, 5 Pyrococcus, and 3 Palaeococcus) have been described in details. The comparative genome analysis results showed that they display a characteristic high level of rearrangements (1). Palaeococcus pacificus DY20341T is a hyperthermophilic piezophilic anaerobic archaeon that was isolated from a sediment sample collected from eastern Pacific Ocean hydrothermal fields (S 1.37° W 102.45°) at a depth of 2,737 m. The Pa. pacificus can grow at temperatures ranging from 50°C to 90°C (optimally at 80°C) and optimally under 30 MPa, showing typical hyperthermophilic and piezophilic features. Phylogenetic analysis based on 16S rRNA gene sequences showed that it was most closely related to Palaeococcus ferrophilus, with a similarity of 95.7% (2).

Pyrosequencing was performed on a Roche 454 GS-FLX Titanium system by Shanghai Hanyu Bio-Tech Company. The contigs were ordered using the Newbler assembler (Roche Diagnostics, Basel, Switzerland), and gap filling and closure was achieved by combinatorial multiplex PCR and sequencing. The genome of Pa. pacificus DY20341T is a single circular 1,859,370-bp chromosome with C-loop introns are tRNA-Lys(ctt) with 1461 bp intron; tRNA-Ser(aga) with 29 bp intron; tRNA-Trp(cca) with 71 bp intron.

Similar with other Thermococcales species, Pa. pacificus possesses an incomplete tricarboxylic acid (TCA) cycle, a modified Embden-Meyerhof pathway to glycolysis and metabolism pathway of proteins and carbohydrates (3–7). The conserved respiration system is also represented by membrane-bound hydrogenase and A0A1-type ATP synthase (8).

Differ from Pyrococcus species, Pa. pacificus does not contain “saccharolytic gene island” and “maltose and trehalose degradation gene” (3), which carries a set of genes responsible for the utilization of cellulose, laminarin, agar, maltose, trehalose, and other β-linked polysaccharides. These genes are also absent in Thermococcales species except Thermococcus sibiricus (5).

Analysis of the repeated sequences and a search against the IS database revealed that a remarkable feature of the Pa. pacificus genome is the absence of mobile genetic elements including transposons, transposases, integrases and virus-related region. It indicates that Pa. pacificus genome has not been subjected to frequent or recent genomic rearrangements during its evolution.

Further comparative genomic studies of several Thermococcales species will provide a foundation to identify the biochemical mechanisms responsible for its adaptation to a hydrothermal vent environment and to understand the systematic evolution of members in this order.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number CP006019.

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