

Complete Genome Sequence of Hyperthermophilic Piezophilic Archaeon *Palaeococcus pacificus* DY20341^T, Isolated from Deep-Sea Hydrothermal Sediments

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We report the genome sequence of *Palaeococcus pacificus* DY20341^T, 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* DY20341^T 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* DY20341^T is a single circular 1,859,370-bp chromosome without an extrachromosomal element, with a G+C content of 43.04%. A total of 2,001 protein-coding sequences were predicted by Glimmer version 3.02. Of the genes, 78.11% (1,563/2,001) were assigned to specific Clusters of Orthologous Groups (COG) Database functional gene groups, and 49.83% (997/2,001) were assigned an enzyme classification number. The average gene size is 845 bp, comprising CDSs ranging from 38 to 1,749 amino acids. tRNA genes were predicted using tRNAscan-SE 1.21 and ARAGORN, rRNA genes using RNAmmer version 1.2. Two rRNA loci, and 47 tRNA genes were detected. Three detected tRNA genes 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).

Different with *Pyrococcus* species, *Pa. pacificus* does not contain “saccharolytic gene island” and “maltose and trehalose degradation gene” (5), 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 *Thermococcus* 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](https://doi.org/10.1101/06019).

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