

## Complete Genome Sequence of the Obligate Piezophilic Hyperthermophilic Archaeon *Pyrococcus yayanosii* CH1

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### Abstract:

*Pyrococcus yayanosii* CH1 is the first obligate piezophilic hyperthermophilic archaeon isolated from the deep-sea hydrothermal site Ashadze on the mid-Atlantic ridge at a depth of 4,100 m. This organism grows within a temperature range of 80 to 108°C and a hydrostatic pressure range of 20 to 120 MPa, with optima at 98°C and 52 MPa, respectively. Here, we report the complete genome sequence (1,716,817 bp, with a G+C content of 51.6%) of the type strain *P. yayanosii* CH1<sup>T</sup> (= JCM 16557). This genomic information reveals a systematic view of the piezoadaptation strategy and evolution scenario of metabolic pathways in *Thermococcales*.

*Pyrococcus yayanosii* CH1 is the first obligate piezophilic hyperthermophilic archaeon isolated from the deep sea hydrothermal site named "Ashadze" located on the mid-Atlantic ridge at a depth of 4100 m. *P. yayanosii* CH1 was cultivated in TRM medium (2, 7) under the optimal growth conditions (98°C and 52 MPa) for two days. Cells were collected by centrifugation then the genomic DNA was prepared using alkaline lysis method. The genome of CH1 has been sequenced respectively by Solexa in Beijing Genomics Institute and 454 pyrosequencing in Chinese National Human Genome Center at Shanghai to ensure good accuracy.

From Solexa sequencing, results 11 scaffolds ranging from 5.3 kb to 458 kb to give ~374-fold coverage of the genome. In the case of 454 pyrosequencing, 17 contigs were generated (size range between 6.5 kb to 336 kb) to give ~68.5-fold coverage of the genome. These sequencing data were combined and gaps were closed by PCR sequencing.

The genome consists of a circular DNA molecule of 1,716,817 bp with a G+C% of 51.6% that is higher than in other related *Pyrococcus species* like *P. abyssi*, *P. horikoshii*, and *P. furiosus* (3, 5, 6).

A total of 1926 coding sequences (CDSs) were predicted by Glimmer 3.02 and tRNAscan-SE 1.21. The average size of gene is 816 bp, comprising CDSs ranging from 37 to 1,405 amino acids. There are two predicted copies of the 5S, one 16S, and one 23S rRNA genes and 46 predicted tRNAs. The genome sequence was annotated by integrated Blast analysis against KEGG, UniProt and Clusters of Orthologous Groups (COG) databases.

The genome was categorized into 168 subsystems by authorized annotation using the RAST (Rapid Annotation using Subsystem Technology) server (1). Reconstructed metabolic network includes a modified Embden-Meyerhof pathway, partial pentose phosphate pathway (Enter-Doudoroff) and rTCA cycles.

Amino acid composition and codon usage bias of all the predicted *P. yayanosii* CH1 ORFs were analyzed using software Acua version 1.0. Observations of the asymmetries in the amino acid substitution in 200 pairs of orthologous proteins from *P. furiosus* and *P. yayanosii* CH1 were made. Piezophily in the physicochemical properties of amino acids and in the genetic code could be ranked by PAI (Pressure Asymmetry Index) after comparison of proteins from *P. furiosus* and *P. abyssi* as assumed by Massimo D. Giulio (4). Our data show that both alanine and arginine have higher PAI value and the ratio of appearances in the genome of *P. yayanosii* CH1 is higher than that in other *Pyrococcus species*. This result suggests that piezophilic amino acids be prone to have small molecular weight and higher polarity.

Taking together the results from genome annotation, physiological and genetic characterization and high throughput transcriptomic, proteomic, and metabolomic comparisons, a systematical view of the piezo-adaptation strategy and evolution scenario of metabolic pathways in *P. yayanosii* CH1 could be reached.

### **Nucleotide sequence accession number**

The final annotated genome of *P. yayanosii* strain CH1 reported in this paper is now accessible in GenBank under accession number CP002779.

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