



Genome Announcement

Complete genome sequence of *Thermococcus eurythermalis* A501, a conditional piezophilic hyperthermophilic archaeon with a wide temperature range, isolated from an oil-immersed deep-sea hydrothermal chimney on Guaymas Basin

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ABSTRACT

Thermococcus eurythermalis A501 is a conditional piezophilic hyperthermophilic archaeon, isolated from an oil-immersed hydrothermal chimney located on Guaymas Basin. This isolate is an anaerobic chemoorgano-heterotroph and can grow over wide temperature, pressure and pH ranges. The genome consists of one circular chromosome (2,122,535 bp) and one plasmid (3629 bp) as the extra-chromosome DNA. The genomic information will contribute to studying extreme adaptation in hydrothermal vent and also the development of industrial enzymes with high stability under extreme condition.

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Thermococcus eurythermalis A501 (=CGMCC 7834^T; =JCM 30233^T) is isolated from an oil-immersed chimney sample of a deep-sea hydrothermal vent in the Guaymas Basin (27°04.05' N, 110°24.567' W) at a depth of 2006.9 m, of which the meta-genomic data show that *Thermococcales* (Zillig et al., 1987) are among the dominant microorganisms (He et al., 2013). *T. eurythermalis* A501 is a conditional piezophilic hyperthermophilic archaeon with wild temperature/pressure/pH range. The temperature range of it is 50–100 °C (optimal 85 °C); the pressure range is 0.1–70 MPa (optimal 0.1–30 MPa) and the pH range is 4.0–9.0 (optimal pH 7.0). It is an obligate anaerobic chemoorgano-heterotroph and produces H₂S in the presence of element sulfur while produces H₂ without the sulfur (Zhao et al., 2014). The property of wide growth range makes *T. eurythermalis* A501 a good material for both studying multiple extreme adaptations in hydrothermal vent and development of stable enzyme dealing with extreme condition.

Genomic DNA was prepared by the SDS method (Goldenberger et al., 1995). The genome of *T. eurythermalis* A501 was sequenced by Paired-End strategy with Illumina sequencing platform at

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Shenzhen Huada Genomics Institute (BGI; Shenzhen, China). Almost 1340 Mb of reads were produced from a 500-bp library, and about 1013 Mb of reads were produced from a 5-kb library. Total of them covered approximate 1105-fold of the whole genome. All these reads were assembled by SOAPdenovo (Luo et al., 2012) software package, 11 contigs (size range of 3.5 kb to 543.3 kb) were generated, and gaps were closed and checked by PCR. The RAST Server (Aziz et al., 2008) and IMG ER (Markowitz et al., 2009) were used to predict open reading frames (ORFs) and annotate the genome. The function was verified by BLASTP (Altschul et al., 1990). RNAmmer 1.2 (Lagesen et al., 2007) and tRNAscan-SE 1.21 (Schattner et al., 2005) were used to predict rRNA and tRNA, respectively.

The complete genome of *T. eurythermalis* A501 consists of a circular chromosome of 2,122,535 bp and a plasmid of 3629 bp. It predicted 2095 protein-coding sequences (CDS) which covered about 90.3% of the whole genome. The genome encodes 45 tRNAs and 4 rRNAs which contains 2 copies of 5S rRNA gene, 1 copy of 16S rRNA gene, and 1 copy of 23S rRNA gene (Table 1).

The genome of *T. eurythermalis* A501 encodes an archaeal modified Embden–Meyerhof (EM) pathway (Verhees et al., 2003), a pyruvate degradation pathway, a pentose phosphate synthesis pathway, a propionate utilization pathway and a pseudo-TCA cycle as the central carbohydrate metabolism, and encodes the archaeal RuBisCo (Sato et al., 2007) to fix carbon. For the energy

Table 1
Genome features of *T. eurythermalis* A501.

Features	Chromosome	Plasmid
Length (bp)	2,122,535	3629
G + C content (%)	53.47	46.71
Total genes	2183	5
Protein-coding genes	2095	5
rRNA	4	0
tRNA	45	0
Protein-coding genes with function prediction	1696	1
Protein-coding genes with enzymes	467	0

synthesis, genes encoding a membrane-bound NADH-ubiquinone oxidoreductase, a V-type ATP synthase, and a series of hydrogenases complexes for respiration including MBx, MBh, sulfhydrogenase and formate hydrogenase were found in the genome of *T. eurythermalis* A501. In addition, compared with other *Thermococcus* genomes, *T. eurythermalis* A501 contains more genes for ABC transports, chemotaxis and stress responses, which may be favorable for its survival and growth over wild temperature, pressure and pH range.

Nucleotide sequence accession number: The GenBank/EMBL/DBJ accession number for the complete genome of *Thermococcus eurythermalis* A501 is CP008887–CP008888.

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