Data in Brief

Draft genome sequence of *Thermoanaerobacterium* sp. strain PSU-2 isolated from thermophilic hydrogen producing reactor

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**Abstract**

*Thermoanaerobacterium* sp. strain PSU-2 was isolated from thermophilic hydrogen producing reactor and subjected to draft genome sequencing on 454 pyrosequencing and annotated on RAST. The draft genome sequence of strain PSU-2 contains 2,552,497 bases with an estimated G + C content of 35.2%, 2555 CDS, 8 rRNAs and 57 tRNAs. The strain had a number of genes responsible for carbohydrates metabolic, amino acids and derivatives, and protein metabolism of 17.7%, 14.39% and 9.81%, respectively. Strain PSU-2 also had gene responsible for hydrogen biosynthesis as well as the genes related to Ni-Fe hydrogenase. Comparative genomic analysis indicates strain PSU-2 shares about 94% genome sequence similarity with *Thermoanaerobacterium xylanolyticum* LX-11. The nucleotide sequence of this draft genome was deposited into DDBJ/ENA/GenBank under the accession MSQD00000000.

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**Keywords:** Whole genome sequencing, *Thermoanaerobacterium* sp., Hydrogen producing bacteria, Thermophile

**Specifications**

- **Organism/cell line/tissue:** *Thermoanaerobacterium* sp.
- **Strain:** PSU-2
- **Sequencer or array type:** 454 pyrosequencing
- **Data format:** analyzed
- **Experimental factors:** microbrial strain
- **Experimental features:** draft genome analysis and gene annotation of PSU-2
- **Consent:** N/A
- **Sample source location:** Songkhla, Thailand

1. **Direct link to deposited data**

The draft genome sequences could be found at the site [http://www.ncbi.nlm.nih.gov/nuccore/MSQD00000000](http://www.ncbi.nlm.nih.gov/nuccore/MSQD00000000)

2. **Experimental design, materials and methods**

The genus *Thermoanaerobacterium* is a group of anaerobic, gram-positive, rod shaped, reduce thiosulfate to elemental sulfur that belong to *Firmicutes* as previously described by Lee et al. [1]. Genus *Thermoanaerobacterium* are thermophilic that specialize in polysaccharide and carbohydrate fermentation, producing primarily L-lactic acid, acetic acid, ethanol, CO₂, and H₂ [2,3]. The majority of characterized *Thermoanaerobacterium* strains have been isolated from hot springs and other thermal environments [4]; however, they have also been isolated from leachate of a waste pile from a canning factory [5], thermophilic bio-reactor for biohydrogen production [6,7] and deep subsurface environments [8]. This genus has been considered for biotechnological applications, such as conversion of lignocellulosic biomass to ethanol [3], biobhydrogen and other chemicals [9]. *Thermoanaerobacterium* strain PSU-2 is a rod shaped, gram-positive, spore-forming and thermophilic hydrogen producing bacteria belonging to *Firmicutes* that was isolated from a biohydrogen reactor fed with palm oil mill effluent (POME). Phylogenetic analysis based on 16S rRNA genes indicated that strain PSU-2 belonged to the genus *Thermoanaerobacterium* [6]. This genus had been previously studied for hydrogen production from various carbohydrates, such as starch, sucrose and molasses [10]. Strain PSU-2 has a high hydrogen production capacity within a wide range of pH (4.5–8) and temperature (45–70 °C), with the optimal temperature 60 °C and optimal initial pH about 6.25. The strain performed ethanol–acetate type fermentation in inorganic nitrogen amended medium, while it performed butyrate–acetate type fermentation in organic nitrogen amended medium [6].
The draft genome of strain PSU-2 was sequenced with 454 technology using a GS-FLX pyrosequencer at GATC Biotech, Germany (http://www.gatc-biotech.com). A total of 2,552,497 bases were obtained. Assembly into 44 contigs was done with Newbler version 2.9 accessed through the Lifeportal, University of Oslo (http://www.uio.no/english/services/it/research/hpc/lifeportal) and annotation was conducted on RAST [11]. SEED viewer was used for subsystem functional categorization of the predicted open reading frames (ORFs) and visualization [12]. An average nucleotide identity (ANI) was analysis using the online ANI calculator (http://enve-omics.ce.gatech.edu/ani/index). An In Silico genomic DNA:DNA hybridization was performed by genome-to-genome distance calculator (http://ggdc.dsmz.de).

3. Data description

The draft genome of Thermoaerobacterium sp. strain PSU-2 consisted of single DNA chromosome of 2,552,497 bases, a G + C content of 35.2%. The draft genome was predicted to contain 2555 protein-coding sequence, 8 rRNAs and 57 tRNAs. These genes were annotated and classified into 337 subsystems. Most of the annotated genes were involved in carbohydrates metabolic (17.7%), amino acids (14.39%) and derivatives, and protein metabolism (9.81%) (Fig.1). Strain PSU-2 also had gene responsible for hydrogen biosynthesis as well as the genes related to Ni-Fe hydrogenase. Comparative genomic analysis indicates PSU-2 by an average nucleotide identity (ANI) analysis using the online ANI calculator (http://enve-omics.ce.gatech.edu/ani/index) revealed ANI values of 94, when the PSU-2 draft sequence was compared with complete sequences of Thermoaerobacterium xylanolyticum LX-11 species, isolated from geothermal areas of Yellowstone National Park, Wyoming, USA (Fig. 2). This indicates that PSU-2 represents a separate species, as this value is lower than the threshold value of 95%, which corresponds to a genomic DNA:DNA hybridization value of 70% and is a common threshold value for distinction between species [13].

4. Nucleotide accession number

This whole genome project has been deposited at DDBJ/ENA/GenBank under accession no. MSQD00000000. The version described in this paper is version MSQD01000000.

Conflict of interest

The authors clarified that this work and writing has no conflict of interest.

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Fig. 1. Draft genome alignment of Thermoaerobacterium sp. strain PSU-2 with Thermoaerobacterium xylanolyticum LX-11.

Fig. 2. Distribution and counts of genes in COG categories for draft genome of Thermoaerobacterium sp. strain PSU-2.
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