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Complete Genome Sequence of 11 type-species from the *Thermococcus* genus of hyperthermophilic and piezophilic Archaea

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1 We report the genome sequences of the type strains of the species *Thermococcus barossii*, *T. celer*, *T.*
2 *chitonophagus*, *T. gorgonarius*, *T. pacificus*, *T. peptonophilus*, *T. profundus*, *T. radiotolerans*, *T. siculi*,
3 *T. thioreducens* and the prototype of a possible type strain of a novel *Thermococcus* species, strain
4 P6.

5

6 *Thermococcus celer* were isolated from surface hydrothermal vent systems in the Mediterranean (1).
7 *Thermococcus* sp. Strain P6 was isolated in 1997 by Pr. M. Thomm (University of Kiel, Germany) in 1997
8 from an hydrothermal site off Palaeochori Bay (Milos, Aegean Sea, Greece). *T. thioreducens* was isolated
9 from the Rainbow hydrothermal vent system on the Mid-Atlantic ridge, 2600m below the ocean surface
10 (2). All other species were isolated from hydrothermal vents systems in the Pacific ocean (3-9). All species
11 exhibit very similar growth characteristics, with optimal conditions for growth ranging from 83 and 88°C
12 (T), pH 5.8 and pH 7 and salinity between 2 and 3%.

13 DNA was extracted from cells grown in TRM medium to late exponential phase. Whole-genome
14 shotgun sequencing was carried out by a combination of IonTorrent PGM (800 bp fragment library, 318
15 Chip, HiQ chemistry) and Illumina HiSeq run (500bp library, 100bp paired reads), which generated at
16 least 583k reads with a mean 389 bp length (IonTorrent) and 13 million paired 100 bp reads after QC
17 check and trimming (10-11) for each species. The IonTorrent data were assembled de novo with Newbler
18 2.8 (12). The paired-end Illumina data was assembled de novo with velvet (13). The pooled IonTorrent
19 and Illumina data was assembled de novo with MIRA (14) and Newbler. The hybrid data assembly
20 yielded between 1 and 6 contigs which were connected by PCR.

21 Chromosome sizes range from 1.52Mb in *Thermococcus* sp. strain P6 to 2.07Mb in *Thermococcus*
22 *thioreducens*. which is similar to known genomes from this family. Only two species, *T. peptonophilus*
23 and *T. profundus*, harbor an extrachromosomal element. The *T. profundus* plasmid belongs to the
24 pTBMP1 family of plasmid described in the piezophilic archaeon *T. barophilus* (15). To the exception of
25 *T. chitonophagus*, the GC% ranges between 51.7 and 56% Similar to previously sequenced
26 *Thermococcales*, all genomes harbor a single copy of the 16S-23S operon, two copies of 5S operons and
27 45 to 48 tRNA genes, large CRISPR loci associated with *cas* genes (*cas1*, *cas2*, *cas3*, *cas4*, *cas5*, *cas6*,
28 *cas2*), indicating multiple contacts with mobile elements of viral or plasmidic origin. Sinteny analyzes
29 confirm the plasticity of *Thermococcales* genomes. The gene content is consistent with an anaerobic and
30 heterotrophic lifestyle. The genome of *T. barossi* encodes the capacity for hydrogenogenic growth on
31 carbon monoxide, as identified previously in *T. onnurienus* and *T. barophilus*.

32 The genome sequence of *T. peptonophilus* (GC%, core genome phylogeny) confirms previous
33 reports that it may have been misplaced into the *Thermococcus* genus, and that it should be placed in the
34 *Pyrococcus* genus instead. Strain P6 is most closely related to *Thermococcus celer* strain Vu 13 (1), as
35 indicated by *in silico* DNA-DNA hybridization of their genomes (predicted value = 28.90% using the
36 genome-to-genome distance calculator GGDC2.0 (16). This genomic distance suggests that strain P6
37 defines a novel species inside the *Thermococcus* genus.

38 **Nucleotide sequence accession number.** These whole Genome Shotgun project has been deposited in
39 GenBank under the accession numbers CP014750, CP014751, CP014854, CP014855, CP014862,
40 CP014863, CP015101, CP015102, CP015103, CP015104, CP015105, CP015106, and CP015193.

41

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