**Meiothermus hypogaeus** sp. nov., a moderately thermophilic bacterium isolated from a hot spring

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A novel moderately thermophilic, red-pigmented bacterium, designated strain AZM34c11T, was isolated from the bottom of a 1000 m-deep drilled well located in a Japanese hot spring. Cells were Gram-negative and grew optimally at 50 °C, at pH 7.6 and with 0–0.3 % (w/v) NaCl. Analysis of the 16S rRNA gene sequence revealed that the isolate belonged to the genus *Meiothermus*. Levels of 16S rRNA gene sequence similarity between strain AZM34c11T and the type strains of recognized *Meiothermus* species were 88.2–94.8 %. Strain AZM34c11T was distinguished from recognized *Meiothermus* species by its cellular fatty acid profile: iso-C₁₆:₀ was one of the predominant components and hydroxy fatty acids were present only in trace amounts. The strain could also be differentiated based on its growth substrate preferences and characteristic enzyme reactions. On the basis of these results, strain AZM34c11T is considered to represent a novel species of the genus *Meiothermus*, for which the name *Meiothermus hypogaeus* sp. nov. is proposed. The type strain is AZM34c11T (=NBRC 106114T =DSM 23238T).

The genus *Meiothermus* comprises strictly aerobic, non-halophilic and moderately thermophilic heterotrophs. The first species to be described was *Meiothermus ruber*, isolated from the Kamchatka Peninsula (Loginova et al., 1984). *M. ruber, Meiothermus silvanus* and *Meiothermus chliarophilus* were originally described as members of the genus *Thermus* (Tenreiro et al., 1995). However, based on differences in optimal growth temperature range, 2-hydroxy fatty acid content and 16S rRNA gene sequences, they were later reclassified within a separate genus (*Meiothermus* (Tenreiro et al., 1995)). With regard to 16S rRNA gene sequence divergence, phylogenetic analyses indicated that *M. silvanus, M. chliarophilus* and *M. timidus* are distantly related to other species of the genus, including the type species *M. ruber*. This might suggest placing them in a separate genus, but there are no suitable phenotypic differences to separate the two groups (Nobre & da Costa, 2001; Nobre et al., 1996).

We isolated a novel moderately thermophilic, aerobic, *Meiothermus*-like bacterium from a water sample collected from the bottom of a 1000 m-deep drilled well in Hakuba-Himekawa hot spring located in Nagano Prefecture, Japan. The water sample was collected on the surface in June 2008 and its temperature and pH were 48 °C and 7.5. To enrich and isolate bacteria, we used AP13YO liquid medium (approx. pH 7), i.e. AP13 basal medium supplemented with (per litre) 0.1 g Bacto yeast extract (Difco) under a N₂/O₂/C₂O₅ [70:20:10 (v/v/v)] 150 kPa atmosphere. AP13 basal medium had the following composition (per litre):

**Abbreviations:** ML, maximum-likelihood; NJ, neighbour-joining.

The GenBank/EMBL/DDJB accession numbers for the 16S rRNA gene sequences of strain AZM34c11T and *Meiothermus taiwanensis* NBRC 105888T (A and B genes) are AB586707, AB586708 and AB586709, respectively.
0.05 g K2HPO4, 0.09 g KH2PO4, 0.25 g MgSO4.7H2O, 0.15 g CaCl2.2H2O, 0.25 g NH4Cl, 1 ml trace element solution (Mori et al., 2008a) and 0.25 g Na2CO3. The medium was prepared in serum bottles with butyl-rubber stoppers and aluminium caps under N2/CO2/O2 and then autoclaved. For enrichment and routine cultivation, 50 ml serum bottles containing 20 ml liquid medium were used. For primary enrichment of bacteria, 1 ml hot-spring water was inoculated into 20 ml AP13YO medium and incubated at 50 °C. After 1 week of incubation, bacterial growth was confirmed by microscopy and the enrichment culture was repeatedly transferred to fresh AP13YO medium. For single strain isolation, colonies were allowed to form on Gelrite plates prepared with the same medium amended with 1 g MgCl2.6H2O 1−1 and 0.6% (w/v) gellan gum. After 1 week, uniform red colonies (approx. 0.5 mm in diameter) were observed and a single colony was picked and purified by repeating the isolation procedure several times. Strain AZM34c11T was isolated successfully from the enrichment sample. After the isolation procedure, we tested the growth of strain AZM34c11T on Thermus medium (Castenholz, 1969) supplemented with (per litre) 1 g Bacto yeast extract, 1 g Bacto tryptone (Difco) and 1 g sodium glutamate to raise the growth yield, and found positive results: red colonies formed on this agar plate after 1 week of incubation at 50 °C.

Cells of strain AZM34c11T were Gram-negative rods (0.4 μm wide and 1.7–10.0 μm long). Spore formation and motility were not observed. Cells were catalase-negative and oxidase-positive (Tamaki et al., 2003).

Strain AZM34c11T was unable to grow in the presence of nitrate (10 mM), nitrite (2 and 5 mM), fumarate (10 mM), thiosulfate (10 mM), sulfate (10 mM), sulfate (2 and 5 mM) or elemental sulfur (2%) as an elemental acceptor in the AP13 medium with (per litre) 0.1 g Bacto yeast extract and 3.4 g sucrose under N2/CO2 [80:20 (v/v); 150 kPa]. Accordingly, strain AZM34c11T was considered to be strictly aerobic, and neither fermentative growth nor respiration was observed under anaerobic conditions. Nitrate was reduced to nitrite (Dobrogosz, 1981), although no cell growth occurred. A reduced sulfur compound (thiosulfate) was not required for growth of strain AZM34c11T in the liquid medium. Yeast extract (0.1 g l−1) was necessary for growth. Strain AZM34c11T utilized several single carbon sources for growth (Table 1). The optimum temperature, pH and NaCl concentration ranges for growth in Thermus medium with (per litre) 1 g Bacto yeast extract, 1 g Bacto tryptone and 3.4 g sucrose were determined by examining the time course of optical density (temperature gradient incubator with a bio-photorecorder, model TN-2612; ADVANTEC). The experiments were performed in duplicate. Strain AZM34c11T was able to grow at 35–57 °C, with optimum growth around 50 °C. The pH range for growth was pH 5.9–8.7, with optimum growth at pH 7.6. The isolate grew optimally at NaCl concentrations of 0–0.3% (w/v), and no growth was observed above 0.6% NaCl.

Hydrolysis of casein, starch (Mania & da Costa, 1991) and gelatin (Smibert & Krieg, 1981) and degradation of arbutin, aesculin (Mania & da Costa, 1991), elastin, hide-powder azure and fibrin (Hudson et al., 1986) were tested by using Thermus medium. Strain AZM34c11T was positive for hydrolysis of starch and gelatin and for the degradation of hide-powder azure, but was negative for the other reactions. Additional enzyme activities were tested and identified by using the API ZYM system (bioMérieux) at 50 °C; the strain showed positive reactions for several enzymes.

Respiratory quinones were extracted from cells of strain AZM34c11T by using the protocol described by Nakagawa & Yamasato (1993) and analysed with an LCMS-QP 8000alphalpha spectrometer (Shimadzu). This respiratory quinone was menaquinone-8, which has been found in all described members of the phylum Deinococcus-Thermus. Cell fatty acids of strain AZM34c11T grown at 50 °C were prepared by using the method of Sasser (1990) and were analysed with the MIDI microbial identification system (Microbial ID; Agilent Technologies); M. cerbereus NBRC 106473T, M. granaticius NBRC 107808T and M. rufus NBRC 107809T were also analysed by using the same procedure. Strain AZM34c11T possessed mainly iso- and anteiso-branched fatty acids (see Supplementary Table S1, available in IJSEM Online); 2- and 3-hydroxy fatty acids were detected in very minor amounts. The polar lipids of strain AZM34c11T, M. cerbereus NBRC 106473T, M. granaticius NBRC 107808T and M. rufus NBRC 107809T were extracted and examined by two-dimensional TLC by using a previously described method (Hamada et al., 2010), and the patterns were visualized by spraying the TLC plates with 5% phosphomolybdic acid, Dittmer–Lester reagent (Dittmer & Lester, 1964) and anisaldehyde. The polar lipid pattern of strain AZM34c11T mainly comprised one phospholipid and one glycolipid, designated PL-2 and GL-1b, respectively (Nobre & da Costa, 2001), as with the profiles of M. cerbereus NBRC 107809T and M. granaticius NBRC 107808T, but in contrast to that of M. cerbereus NBRC 106473T, which contained two glycolipids (not shown). The genomic DNA G+C content was determined by HPLC with a Shodex ODS pack F-411 (Showa Denko K.K.), after an initial nuclease P1 treatment (Yamas et al., 1997) and identified by using the API ZYM system (bioMe´rieux) and with the maximum-likelihood (ML) method via the MOLPHY program version 2.3b3.
The sequence determined indicated that strain AZM34c11T belonged to the genus *Meiothermus* in the family *Thermaceae*. The NJ tree constructed on the basis of the 16S rRNA gene sequence of the new isolate and those of related strains is shown in Fig. 1. The result obtained with the ML method was similar to that obtained with the NJ method (not shown). Levels of 16S rRNA gene sequence similarity calculated by the CLUSTAL X program between strain AZM34c11T and the type strains of recognized *Meiothermus* species were as follows: *M. ruber*, 93.7 %; *M. silvanus*, 88.4 %; *M. chlorophilus*, 88.2 %; *M. cerbereus*, 94.8 %.

### Table 1. Differential characteristics between strain AZM34c11T and recognized *Meiothermus* species

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* Determined by HPLC (a) or Tm (b).
**Meiothermus hypogaeus sp. nov.**

Meiothermus hypogaeus (hy.po.ga‘e.us. L. masc. adj. hypogaeus underground, living under the ground).

Cells are rod-shaped (0.4 μm wide and 1.7–10.0 μm long), red-pigmented, non-motile and non-sporulating. Gram reaction is negative. Catalase-negative and oxidase-positive. Nitrate is reduced to nitrite. Positive for hydrolysis of starch and gelatin and degradation of hide-powder azure. Negative for hydrolysis of casein and degradation of arbutin, aesculin, elastin and fibrin. API ZYM tests were negative for hydrolysis of casein and degradation of arbutin, aesculin, elastin and fibrin.

**Description of Meiothermus hypogaeus sp. nov.**

Meiothermus hypogaeus sp. nov. was characterized by the following phenotypic and chemotaxonomic characteristics. The predominant components (Supplementary Table S1). However, the amount of hydroxy fatty acids in strain AZM34c11T was very low, which is a feature seen only in *M. rufus and M. granaticius* in the entire genus *Meiothermus* (Albuquerque et al., 2009, 2010). In addition, iso-C₁₆:0 was present in larger quantities in strain AZM34c11T than in recognized species of the genus *Meiothermus*. These phenotypic differences support the phylogenetically distinct position of strain AZM34c11T in the genus *Meiothermus*. Based on the data presented above, we suggest that strain AZM34c11T represents a novel species of the genus *Meiothermus*, for which the name *Meiothermus hypogaeus* sp. nov. is proposed.

As reported by some researchers (Nobre & da Costa, 2001; Nobre et al., 1996; Pires et al., 2005), phylogenetic analysis based on 16S rRNA gene sequences indicated that *M. silvanus, M. chlorophilus* and *M. timidus* were distant from the other *Meiothermus* species at a high replicate/resampling value (Fig. 1) and levels of sequence similarity between the type strains of the three species and other *Meiothermus* species were less than 91.5%. Although it may be reasonable to erect a new genus for the three species based on phylogenetic analysis, this is not supported by phenotypic and chemotaxonomic characteristics. The isolation of additional novel representatives related to *M. silvanus, M. chlorophilus* and *M. timidus* will be important in this regard.

**Fig. 1.** NJ phylogenetic tree based on 16S rRNA gene sequences of strain AZM34c11T and relatives. Bootstrap percentages ≥50% are indicated at branch points (NJ/ML); −, <50%. GenBank/EMBL/DDBJ accession numbers are shown in parentheses. Bar, 0.02 substitutions per nucleotide position.
arylamidase, valine arylamidase, cystine arylamidase, trypsin, 
\( x \)-galactosidase, \( \beta \)-glucuronidase, \( N \)-acetyl-\( \beta \)-glucosaminidase, 
\( x \)-mannosidase and \( \alpha \)-fucosidase. Cells are aerobic and 
chemoheterotrophic, requiring yeast extract for growth. 
Sulfur compounds are not required for growth in liquid 
medium. Utilizes D-glucose, D-fructose, D-mannose, D-
galactose, melibiose, maltose, lactose, trehalose, sucrose, 
cellobiose, D-xylene, glycerol, pyruvate, L-asparagine and 
L-glutamate as carbon and energy sources, but not raffinose, 
D-arabinose, L-rhamnose, ribitol, D-mannitol, D-sorbitol, 
citrate, succinate, malate, myo-inositol, L-glutamine, L-
serine, L-proline or L-arginine. Grows at 35–57 \(^\circ\)C; optimum 
growth at 50 \(^\circ\)C. The pH range for growth is 5.9–8.7, with 
optimum growth at pH 7.6. Grows optimally with 0–0.3 
(\( w/v \)) NaCl; no growth occurs with more than 0.6% (\( w/v \)) 
NaCl. Menaquinone-8 is the major respiratory quinone. The 
major cellular fatty acids are iso-C\(_{15:0}\) and iso-C\(_{16:0}\). The 
major polar lipids are PL-2 and GL-1b. The genomic DNA 
G + C content of the type strain is 63.4 mol%.

The type strain, AZM34c11\(^T\) (=NBRC 106114\(^T\) =DSM 
23238\(^T\)), was isolated from hot-spring water collected 
from the bottom of a 1000 m-deep drilled well in Hakuba-
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**References**

chimpanzee separation in the mitochondrial DNA tree: heterogeneity 

Albuquerque, L., Ferreira, C., Tomaz, D., Tiago, I., Verissimo, A., da 
new slightly thermophilic red-pigmented species and emended description 

*Meiothermus granaticus* sp. nov., a new slightly thermophilic red-
pigmented species from the Azores. Syst Appl Microbiol 33, 243–246.


taiwanensis* sp. nov., a novel filamentous, thermophilic species 

Chung, A. P., Rainey, F., Nobre, M. F., Burghardt, J. & da Costa, M. S. 
(1997). *Meiothermus cerberus* sp. nov., a slightly thermophilic 
species with high levels of 3-hydroxy fatty acids. Int J Syst Bacteriol 
47, 1225–1230.

Dittmer, J. C. & Lester, R. L. (1964). A simple, specific spray for the 
detection of phospholipids on thin-layer chromatograms. J Lipid Res 
15, 126–127.

General Bacteriology, pp. 365–392. Edited by P. Gerhardt, R. G. E. Murray,
Washington, DC: American Society for Microbiology.

Ekman, J., Kosonen, M., Jokela, S., Kolari, M., Korhonen, P. & 
deposit-forming *Meiothermus* spp. in paper industry processes and 

Hamada, M., Iino, T., Iwami, T., Harayama, S., Tamura, T. & Suzuki, K. 
(2010). *Mobilicoccus pelagius* gen. nov., sp. nov. and *Piscicoccus intestinalis* 
gen. nov., sp. nov., two new members of the family *Dermatophilaceae*, and 
reclassification of *Dermatophilus chelone*. (Masters et al. 1995) as *Austwickia 

human-ape splitting by a molecular clock of mitochondrial DNA. 

The Thermacetogenium phaeum gen. nov., sp. nov., a strictly anaerobic, 
thermophilic, syntrophic acetate-oxidizing bacterium. Int J Syst Evol 
Microbiol 50, 1601–1609.


196.

499.

Ludwig, W., Strunk, O., Westram, R., Richter, L., Meier, H., 
Yadhukumar, Buchner, A., Lai, T., Steppi, S. & other authors 
Res 32, 1363–1371.

halotolerant *Thermus* isolates from shallow marine hot springs on 

*Archaeoglobus infectus* sp. nov., a novel thermophilic, chemolithohe-
terotrophic archaean isolated from a deep-sea rock collected at 
Suiyo Seamount, Izu-Bonin Arc, western Pacific Ocean. Int J Syst 
Evol Microbiol 58, 810–816.

Mori, K., Sunamura, M., Yanagawa, K., Ishibashi, J., Miyoshi, Y., Iino, T., 
investigation of a bacteria affiliated with the candidate phylum OP5 
from hot springs. Applviron Microbiol 74, 6223–6229.

Nakagawa, Y. & Yamasato, K. (1993). Phylogenetic diversity of the 
genus *Cytophaga* revealed by 16S rRNA sequencing and menaquinone 
analysis. J Gen Microbiol 139, 1155–1161.

Nobre, M. F. & da Costa, M. S. (2001). Genus II *Meiothermus* Nobre, 
Trüper and da Costa, 1996b, 605\(^V\). In Bergey's Manual of Systematic 
Bacteriology, 2nd edn, vol. 1, pp. 414–420. Edited by D. R. Boone, 

1995), and *Thermus chlorophilus* (Tenreiro et al. 1995) to *Meiothermus* 
gen. nov. as *Meiothermus ruber* comb. nov., *Meiothermus silvanus* comb. 
nov., and *Meiothermus chlorophilus* comb. nov., respectively, and 

Pires, A. L., Albuquerque, L., Tiago, I., Nobre, M. F., Empadinhas, N., 
a new slightly thermophilic yellow-pigmented species. FEMS Microbiol 
Lett 245, 39–45.


