**Natronococcus amylolyticus** sp. nov., a Haloalkaliphilic Archaeon

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The α-amylase-producing haloalkaliphilic archaeon **Natronococcus** sp. strain Ah-36\(^{T}\) (\(T\) = type strain) was isolated previously from a Kenyan soda lake, Lake Magadi. Most cells of strain Ah-36\(^{T}\) occurred in irregular clusters, and the colonies were orange-red. The polar lipids of this organism were composed of \(C_{20} \gamma C_{20} \gamma C_{20} \gamma C_{20} \beta\) and \(C_{20} \gamma C_{20} \gamma C_{20} \beta\) derivatives of phosphatidylglycerol and phosphatidlyglycerophosphate. Phosphatidlyglycero-(cyclo-) phosphate, which is characteristic of **Natronococcus occulatus**, was not detected. The complete nucleotide sequence of the 16S rRNA gene revealed that the closest relative of strain Ah-36\(^{T}\) is **N. occulatus** ATCC43101\(^{T}\) (level of similarity, 96.4%), an extremely halophilic archaeon. However, strain Ah-36\(^{T}\) did not exhibit a significant level of DNA homology to **N. occulatus** ATCC43101\(^{T}\), which represents the only previously described species in the genus **Natronococcus**. We describe a new species for strain Ah-36\(^{T}\), for which we propose the name **Natronococcus amylolyticus**.

**Materials and Methods**

Organisms and growth media. Isolation and preliminary characterization of **Natronococcus** sp. strain Ah-36\(^{T}\) (= JCM6552\(^{T}\) [Japan Collection of Microorganisms, The Institute of Physical and Chemical Research]) have been described previously (6). **Natronococcus occulatus** ATCC 43101\(^{T}\), **Natronobacterium magadii** ATCC 43099\(^{T}\), **Natronobacterium gregoriyi** ATCC 43098\(^{T}\), and **Natronobacterium pharaonis** ATCC 35678\(^{T}\) were obtained from the American Type Culture Collection.

The organisms were grown in natronobacteria medium (1).

Microscopy. Cell size and shape were determined by phase-contrast microscopy. Lipid analyses. Polar lipids were extracted and were analyzed by thin-layer chromatography by using the method of Collins et al. (2).

Molecular cloning of the 16S rRNA gene. The 16S rRNA gene was amplified by PCR by using total DNA from strain Ah-36\(^{T}\) as the template. The following PCR primers were used: 5'-C(C/T)G(G/T)TGATCC(C/T)G(G/C)C(A/G)GA-3' (corresponding to the 16S rRNA at around position 1200). The amplified DNA fragment (length, approximately 1.2 kb) was labeled with digoxigenin-dUTP by using a DNA labeling kit supplied by Boehringer Mannheim Biochemicals. The labeled DNA was used as the probe to detect the 16S rRNA gene in the cloning procedure.

Total DNA which was isolated from strain Ah-36\(^{T}\) by a previously described method (5) was digested with EcoRI and analyzed by Southern hybridization to determine the size of the DNA fragment carrying the 16S rRNA gene. A DNA fragment which was approximately 6.5 kb long and hybridized to the probe was cloned in Escherichia coli MV1184 (ara::Delac-proAB) (Strr-A[396]::Tn5080 lacZAM15 rpsL thi [F lacP lacZAM15 proAB traD36]) with pUC119 as the vector by using a previously described procedure (7).

DNA sequencing. The DNA sequence was determined with an Applied Biosystems model 373A DNA sequencer.

Phylogenetic analysis. A phylogenetic tree based on levels of divergence was constructed by the neighbor-joining method (13) by using the Clustal V package (4). All sites with gaps and all sites where nucleotides were not determined were omitted from the comparison.

The nucleotide sequences of the 16S rRNA genes of the following organisms were obtained from the EMBL database (Release 37) and were used for comparison: **Natronococcus occulatus**, **Natronobacterium magadii**, *Halofexax volcanii*, *Halobacterium halobium*, *Halococcus morrhuae*, *Halococcus marismortui*, *Methanococcus vannielii*, and *Methanobacterium formicicum*.

DNA-DNA hybridization. Total DNAs from the haloalkaliphilic archaea were isolated by a previously described procedure (5, 15). DNA-DNA hybridization experiments were performed by the dot blot technique (7). Hybridization was carried out in a solution containing 50% formamide and 5% blocking reagent (Boehringer Mannheim) in 2× SSC (1× SSC is 0.15 M NaCl plus 0.015 M sodium citrate) at 55°C (stringent conditions; denaturation temperature −19°C) by using digoxigenin-labeled total DNAs as the probes. The blots were analyzed with a DIG DNA detection kit supplied by Boehringer Mannheim Biochemicals.

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Morphology. As reported previously (6), strain Ah-36\(^T\) cells are nonmotile cocci that are 1 to 2 \(\mu\)m in diameter and occur in irregular clusters, in pairs, and as single cells. Additional morphological studies of Ah-36\(^T\) revealed that strain Ah-36\(^T\) cells occurred mostly in irregular refractile clusters throughout each culture, while the cells of Natronococcus occultus, the type and only previously described species of the genus Natronococcus, occurred in pairs and as single cells, as shown in Fig. 1. The Ah-36\(^T\) colonies were circular, entire, and orange-red and varied in diameter from 1 to 5 mm, which may have reflected differences in cell numbers in the cell clusters. On the other hand, Natronococcus occultus produced pale brown colonies that were uniform in size (diameter, about 1 mm). The orange-red color of Ah-36\(^T\) colonies suggests that bacterioruberin or another orange-red pigment is present in this organism.

Physiological and biochemical features. Some physiological and biochemical features of strain Ah-36\(^T\) have been described previously (6). In addition, Ah-36\(^T\) did not require a high magnesium ion concentration (>5 mM). Cell growth was observed in the presence of MgCl\(_2\) concentrations of less than 1 mM. This organism was partially susceptible to tetracycline (MIC, 25 \(\mu\)g/ml) while for Natronococcus occultus the MIC was 100 \(\mu\)g/ml; slight growth of strain Ah-36\(^T\) and Natronococcus occultus was observed in the presence of 12.5 and 50 \(\mu\)g of tetracycline per ml, respectively.

Lipids. The polar lipid pattern of Ah-36\(^T\) was the simplest pattern found in the halophilic archaea (Fig. 2). This organism contained \(C_{20}, C_{20}\) and \(C_{20}, C_{30}\) derivatives of phosphatidylglycerophosphate and phosphatidylglycerol. Phospholipid PL2, which is characteristic of Natronococcus occultus (8), was not present in this organism.

16S rRNA gene sequence. The nucleotide sequence of the 16S rRNA gene and its flanking regions is shown in Fig. 3. The 16S rRNA gene was estimated to be 1,474 nucleotides long by comparing it with 16S rRNA genes of other halobacteria and was followed by a putative alanine tRNA gene after a 133-nucleotide space. The sequence GTTAAG, which resembles the boxA sequence found in members of the family Halobacteriaceae ([T/C]TTAAG) (1a), was observed 214 bp upstream of the putative 5' end of the 16S rRNA. In addition, the sequence TTCGA(nnnn)TTAA (n denotes any nucleotide) at positions 268 to 281 was identical to the promoter consensus sequence of ribosomal protein genes in Halobacterium cutirubrum (14). The flanking regions of the 16S rRNA gene could form an extensive double-helix structure which could act as a substrate for an RNase III-like enzyme, as demonstrated in E. coli (16).

Comparisons with 16S rRNA sequences from other haloalkaliphilic archaea revealed that Natronococcus occultus is the closest relative of strain Ah-36\(^T\) (Fig. 4), indicating that this strain belongs to the genus Natronococcus. However, the low level of sequence similarity (96.4%) may indicate that strain Ah-36\(^T\) is a representative of a new species. Strain Ah-36\(^T\) exhibited levels of sequence similarity...
of 92.9, 90.0, 89.6, 89.4, and 88.6% with *Natronobacterium magadii*, *Halofex volcanii*, *Halobacterium halobium*, *Halococcus morrhuae*, and *Haloarcula marismortui*, respectively (Table 1). DNA-DNA homology. Ah-36T did not exhibit significant levels of DNA-DNA homology with *Natronococcus occultus*, *Natronobacterium magadii*, *Natronobacterium gregoryi*, and *Natronobacterium pharaonis* as determined by dot blot hybridization experiments (Fig. 5). Under the same experimental conditions, *Halobacterium halobium* CCM2090 gave strong hybridization signals with *Halobacterium salinarium* CCM2148 and NCMB764 (levels of DNA-DNA homology, 60 and 77%, respectively) (data not shown) (12).

**FIG. 3.** Nucleotide sequence of the 16s rRNA gene from *Natronococcus* sp. strain Ah-36T. The 16s rRNA sequence and the alanine tRNA sequence are shown in capital letters. Nucleotide substitutions in *Natronococcus occultus* are shown above the sequence. The parts of the nucleotide sequence that are similar to the promoter consensus sequence of the extremely halophilic archaea are underlined.

**DISCUSSION**

On the basis of morphological, physiological, and genetic properties, Ah-36T is a member of the genus *Natronococcus*,...
but this strain differs from the only previously described species, Natronococcus occultus as follows: (i) the colonies of Ah-36 are orange-red, while Natronococcus occultus produces pale brown colonies; (ii) Ah-36 cells occur mostly in irregular clusters (Fig. 1); (iii) starch is hydrolyzed by Ah-36 and gelatin is not liquefied (6), while Natronococcus occultus liquefies gelatin and does not hydrolyze starch; (iv) the polar lipids of Ah-36 consist of only C\textsubscript{20}, C\textsubscript{22}, and C\textsubscript{25} derivatives of phosphatidylglycerol and phosphatidylglycerophosphate, and the minor polar lipid phosphatidylglycerol-cyclophosphate is not detected; (v) the 16S RNA gene sequences of Ah-36 and Natronococcus occultus exhibit a level of similarity of only 96.4%; and (vi) no DNA-DNA homology is observed between Ah-36 and Natronococcus occultus. Thus, we propose that Ah-36 should be designated the type strain of a new species, Natronococcus amylolyticus.

Description of Natronococcus amylolyticus Kanai, Kobayashi, Aono, and Kudo sp. nov. Natronococcus amylolyticus (am.y.lyt.icus. Gr. n. amylum, starch; Gr. adj. lyticus, dissolving; M.L. adj. amylolyticus, starch dissolving). Cells are nonmotile cocci that are 1 to 2 \( \mu \)m in diameter and occur mostly in irregular clusters. Colonies are circular and orange-red. Cell lysis does not occur in distilled water. Extremely halophilic; growth occurs in the presence of NaCl concentrations between 8 and 30% and optimum growth occurs in the presence of 15 to 20% NaCl. The temperature range for growth is 22 to 50°C, and the optimum temperature is 40 to 45°C. The pH range for growth is 8.0 to 10.0, and the optimum pH is around 9.0. The polar lipids consist of C\textsubscript{20}, C\textsubscript{22}, and C\textsubscript{25} derivatives of phosphatidylglycerol and phosphatidylglycerophosphate. Does not contain phosphatidylglycerol-cyclophosphate. Chemoorganotrophic. Obligatory aerobic. Nitrate and nitrite reduction positive. Starch is hydrolyzed. Gelatin is not liquefied. Susceptible to anisomycin, bacitracin, erythromycin, novobiocin, and tetracycline. Resistant to ampicillin, chloramphenicol, polymyxin B, and streptomycin. The G+C content of the DNA is 63.5 mol%. Inhabits a Kenyan soda lake, Lake Magadi.

The type strain is Natronococcus amylolyticus Ah-36 (= JCM 9655).

ACKNOWLEDGMENTS
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\(^a\) Sites with gaps and sites where nucleotides were not determined were not included in the comparison.

\(^b\) The 16S ribosomal DNA sequence of the type strain was used.

\(^c\) The \textit{mra} gene sequence was used.
We thank Michael Travisano for carefully reading the manuscript.

REFERENCES