**Clostridium jejuense** sp. nov., isolated from soil

Hyunyoung Jeong,1 Hana Yi,1 Yuji Sekiguchi,2 Mizuho Muramatsu,2 Yoichi Kamagata2 and Jongsik Chun1

1School of Biological Sciences, Seoul National University, 56-1 Shillim-dong, Kwanak-gu, Seoul 151-742, Korea
2Institute for Biological Resources and Functions, National Institute of Advanced Industrial Science and Technology (AIST), Central 6, 1-1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan

A strictly anaerobic, mesophilic, endospore-forming bacterium, designated strain HY-35-12T, was isolated from a soil sample in Jeju, Korea. Cells of this isolate were Gram-positive, motile rods that formed oval to spherical terminal spores. Strain HY-35-12T grew optimally at 30 °C, pH 7-0 and 0-0-5 % (w/v) NaCl. The isolate produced pyruvate, lactate, acetate, formate and hydrogen as fermentation end products from glucose. The G+C content of DNA of the isolate was 41 mol%. Phylogenetic analysis based on 16S rRNA gene sequences revealed that the organism formed a monophyletic clade with Clostridium xylanovorans and Clostridium aminovalericum in cluster XIVa of the genus Clostridium. The closest phylogenetic neighbour was C. xylanovorans, with 96-65 % 16S rRNA gene sequence similarity. Several physiological and chemotaxonomic properties were identified that enable strain HY-35-12T to be distinguished from phylogenetically related clostridia. On the basis of polyphasic characteristics, it is proposed that strain HY-35-12T (= IMSNU 40003T = KCTC 5026T = DSM 15929T) represents a novel species, **Clostridium jejuense** sp. nov.

The genus *Clostridium* encompasses Gram-positive, endospore-forming, strictly anaerobic bacteria. At present, the genus comprises over 140 phylogenetically heterogeneous species. Clostridia have been routinely found in soil and are implicated as major players in the decomposition of various organic compounds (Hippe et al., 1992). In this study, a polyphasic characterization of a strictly anaerobic, endospore-forming strain, isolated from soil, is reported. It is proposed that this strain, HY-35-12T, represents a novel species, *Clostridium jejuense* sp. nov.

Strain HY-35-12T was isolated from a soil sample collected in Jeju, Korea (33° 21’ 36-3” N 126° 32’ 05-8” E), using the standard dilution plating method. The isolate was recovered from a reinforced clostridial (RC; Difco) agar plate at 30 °C under anaerobic conditions (N2/CO2/H2, 90:5:5, by vol.). *Clostridium xylanovorans* DSM 12503T and *Clostridium aminovalericum* DSM 1283T were used as reference strains. Test strains were routinely cultured on RC plates and maintained as glycerol suspensions (20 %, w/v) at −80 °C.

Bacterial DNA preparation and PCR amplification and sequencing of 16S rRNA genes were carried out as described previously (Chun & Goodfellow, 1995). The resultant sequences were aligned manually against sequences obtained from GenBank. Phylogenetic trees were inferred using the Fitch–Margoliash (Fitch & Margoliash, 1967), maximum-likelihood (Felsenstein, 1993), maximum-parsimony (Fitch, 1972) and neighbour-joining (Saitou & Nei, 1987) methods. Evolutionary distance matrices were generated according to Jukes & Cantor (1969). The resultant tree topologies were evaluated in bootstrap analyses (Felsenstein, 1985) based on 1000 resamplings. The alignment and phylogenetic analyses were carried out using the programs PHYDIT (available at http://plaza.snu.ac.kr/~jchun/phydit/) and PAUP 4.0 (Swofford, 1998) as described by Chun et al. (2000).

A nearly complete 16S rRNA gene sequence (1435 bp) of the isolate was obtained and used for the initial BLAST search against GenBank and preliminary neighbour-joining analysis (available as supplementary material in IJSEM Online). Strain HY-35-12T was most closely related to members of cluster XIVa in the genus *Clostridium* (Collins et al., 1994). The closest phylogenetic neighbour was *C. xylanovorans*, with 96-65 % 16S rRNA gene sequence similarity, followed by *C. aminovalericum*, with 93-54 % 16S rRNA gene sequence similarity. To elucidate the phylogenetic relationship between our isolate and other members of *Clostridium* cluster XIVa, phylogenetic trees
were constructed using four different tree-making algorithms. The neighbour-joining tree (Fig. 1) showed that strain HY-35-12T clustered with the type strain of Clostridium with 100% bootstrap support. These two then formed a monophyletic clade with Clostridium aminovalericum with 99% bootstrap support. This relationship was confirmed by all other tree-inferring methods used in this study. On the basis of 16S rRNA gene similarity data and phylogenetic analysis, it is clear that our isolate belongs to a novel genomic species in cluster XIVa of the genus Clostridium.

Gram-staining and the KOH test were carried out according to Johnson et al. (1995) and Powers (1995), respectively. Morphology of cells grown on RC agar plates at 30 °C for 72 h was observed using light microscopy and SEM. Motility of strain HY-35-12T was checked in a Hungate tube (Bellco) containing RC semi-solid medium and sulfite indole motility (Difco) semi-solid medium with 0.5% agar. Flagella type was determined using TEM. Endospores were observed using light microscopy; background staining was done with 10% (v/v) nigrosine (Sigma). The presence of catalase was determined by addition of 10% (v/v) H2O2 to a cell smear on standard microscope slides. The pH, temperature and NaCl ranges for growth were determined using modified tryptic soy broth (mTSB) medium (1%: tryptone, 15 g; soytone, 5 g; NaCl 5 g; cysteine hydrochloride, 0.5 g; resazurin, 0.001 g) in Hungate tubes. Growth was recorded by measuring OD600 in Hungate tubes using a turbidometer (Biolog).

Substrate utilization patterns of test strains were determined at 30 °C and an initial pH of 7.0 according to the procedure of Mechichi et al. (1999). The results were recorded after 2 weeks incubation. Various biochemical tests were carried out using the API 20A system (bioMérieux) according to the manufacturer's instructions.

For detection of fermentation end products, basal medium was prepared based on that of Widell & Pfennig (1981), but slightly modified. It contained the following (1–1 distilled water): NH4Cl, 0.535 g; KH2PO4, 0.136 g; MgCl2.6H2O, 0.204 g; CaCl2.2H2O, 0.147 g; trace element solution (DSMZ medium 318), 1 ml; vitamin solution (DSMZ medium 141), 1 ml; resazurin solution, 1 ml; NaHCO3, 2.52 g; Na2S.9H2O, 0.3 g; and cysteine hydrochloride, 0.3 g (pH 7.0). All cultivations were carried out at 30 °C in 50 ml serum vials containing 20 ml medium under an atmosphere of N2/CO2 (80:20, v/v). Glucose solution was autoclaved and added to the medium prior to cultivation using a sterilized syringe to give a final concentration of 20 mM. Hydrogen was analysed by GC (Shimadzu GC-8AIT) equipped with Unibeads C and a thermal conductivity detector. Argon was used as a carrier at a flow rate of 27 ml min⁻¹. The column and detector temperatures were kept at 60 and 110 °C, respectively. Carboxylic acids were determined by HPLC (Shimadzu LC-6A) equipped with an SCR-101H (Shimadzu) column and a model SPD-6A UV detector. The column was operated at 40 °C and 60% HClO4 was used as eluent at a flow rate of 1.8 ml min⁻¹.

For determination of G+C content, DNA was extracted and purified according to a method described previously (Wolff & Gemmill, 1997) and the G+C content of strain HY-35-12T was determined by HPLC of deoxyribonucleosides as described by Mesbah et al. (1989) using a reverse-phase column (Supelcosil LC-18-S; Supelco).

Cells of strain HY-35-12T in exponential growth phase occurred singly and were straight to slightly curved rods. Endospore formation was observed in a liquid culture of mTSB medium containing fructose. The cells swelled to a cell smear on standard microscope slides. The pH, temperature and NaCl ranges for growth were determined using modified tryptic soy broth (mTSB) medium (1%: tryptone, 15 g; soytone, 5 g; NaCl 5 g; cysteine hydrochloride, 0.5 g; resazurin, 0.001 g) in Hungate tubes. Growth was recorded by measuring OD600 in Hungate tubes using a turbidometer (Biolog).
**Clostridium jejuense sp. nov.**

**Description of Clostridium jejuense sp. nov.**

*Clostridium jejuense* (je.ju.en’s.e. N.L. neut. adj. jejuense pertaining to Jeju Island, Korea, geographical origin of the type strain of the species).

Gram-positive, strictly anaerobic, mesophilic bacterium. Cells are straight to slightly curved rods, 1.8–4.5 μm long and 0.5 μm wide, motile by means of peritrichous flagella. Forms slightly oval to almost spherical terminal endospores. Colonies on RC agar plates are 1–2.5 mm in diameter, circular, entire, flat, translucent to opaque, greyish and smooth after 72 h. Cells grow at 10–40 °C, pH 5–9:5 and 0–1.5 % (w/v) NaCl; optimum growth occurs at 30 °C, pH 7–0 and 0–0.5 % (w/v) NaCl. The doubling time under optimum conditions is 10–5 h. Catalase is absent and indole is not produced. Aesculin is hydrolysed, but not gelatin or urea. Utilizes D-cellulose, D-glucose, lactose, D-maltose, D-mannose, sucrose, D-trehalose, D-fructose, D-galactose, D-ribose, L-arabinose, D-raffinose, D-xylene and cellulose, but not D-sorbitol, D-mannitol, peptone (0–1 %, w/v) or yeast extract (0–2 %, w/v). Fermentation end products from glucose include pyruvate, lactate, acetate, formate and H₂. The G+C content of the DNA is 41 mol%. Detailed biochemical characteristics are given in Table 1. Phylogenetically, the organism belongs to cluster XIVa of the genus *Clostridium sensu* Collins et al. (1994).

The type strain is HY-35-12T (= KCTC 5026T = DSM 15929T), isolated from soil in Jeju, Korea.

**Acknowledgements**

This work was supported, in part, by a grant (M1-0219-00-0018) to J.C. from the Strategic National R&D Program through the Genetic Resources and Information Network Center, MOST and a grant (MG02-0101-001-2-1-0) to J.C. from the 21C Frontier Microbial Genomics and Applications Center Program.

**References**


**Table 1. Characteristics that differentiate strain HY-35-12T from phylogenetically related *Clostridium* species**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>G+C content (mol%)</td>
<td>41</td>
<td>40†</td>
<td>33†</td>
</tr>
<tr>
<td>Optimum growth temperature (°C)</td>
<td>30</td>
<td>37‡</td>
<td>37‡</td>
</tr>
<tr>
<td>Presence of catalase</td>
<td>−</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Utilization of:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>L-Arabinose</td>
<td>+</td>
<td>−</td>
<td>W</td>
</tr>
<tr>
<td>Lactose</td>
<td>+</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>D-Raffinose</td>
<td>+</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>D-Sorbitol</td>
<td>−</td>
<td>−</td>
<td>W</td>
</tr>
<tr>
<td>D-Xylose</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Cellulose</td>
<td>W</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>D-Mannitol</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Yeast extract (0–2 %)</td>
<td>−</td>
<td>−</td>
<td>W</td>
</tr>
</tbody>
</table>

*Results from Mechichi et al. (1999).*

†Results from Hardman & Stadtman (1960).

‡Results obtained using the method of Mechichi et al. (1999).


