Bacillus infantis sp. nov. and Bacillus idriensis sp. nov., isolated from a patient with neonatal sepsis

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Two Gram-positive bacilli, designated as strains SMC 4352-1T and SMC 4352-2T, were isolated subsequently from the blood of a newborn child with sepsis. They could not be identified by using conventional clinical microbiological methods. 16S rRNA gene sequencing and phylogenetic analysis revealed that both strains belonged to the genus Bacillus but clearly diverged from known Bacillus species. Strain SMC 4352-1T and strain SMC 4352-2T were found to be closely related to Bacillus firmus NCIMB 9366T (98·2 % sequence similarity) and Bacillus cibi JG-30T (97·1 % sequence similarity), respectively. They also displayed low DNA–DNA reassociation values (less than 40 %) with respect to the most closely related Bacillus species. On the basis of their polyphasic characteristics, strain SMC 4352-1T and strain SMC 4352-2T represent two novel species. Strain SMC 4352-1T and strain SMC 4352-2T were found to be closely related to Bacillus infantis sp. nov. (type strain SMC 4352-1T = KCCM 90025T = JCM 13438T) and Bacillus idriensis sp. nov. (type strain SMC 4352-2T = KCCM 90024T = JCM 13437T) are proposed.

The genus Bacillus comprises aerobic or anaerobic, endospore-forming, Gram-positive bacteria. More than 100 bacterial species are included in the genus Bacillus, although many species have been transferred into other genera, e.g. Paenibacillus, Brevibacillus and Alicyclobacillus (http://www.bacterio.cict.fr/b/bacillus.html; Logan & Turnbull, 2003). Most are widely distributed saprophytes, but some are pathogenic, including Bacillus alvei, B. anthracis, B. brevis, B. cereus, B. circulans, B. coagulans, B. licheniformis, B. macerans, B. pumilus, B. sphaericus, B. subtilis and B. thuringiensis (Logan & Turnbull, 2003).

In this paper, we report on the isolation of two bacterial strains, SMC 4352-1T and SMC 4352-2T, from a newborn child. 16S rRNA gene sequencing, DNA–DNA hybridization and biochemical testing showed that these two bacterial isolates constitute two novel species of the genus Bacillus.

A 5-day-old female newborn child was admitted to our neonatal intensive-care unit because of cyanosis after birth. Transthoracic echocardiography showed the presence of a large (35 mm diameter) patent ductus arteriosus. On day 5 of hospitalization, fever and hypotension developed, and two sets of blood cultures were found to harbour Gram-positive bacilli. However, these isolates could not be identified by using conventional methods, such as VITEK (bioMérieux) and Microscan (Dade-Microscan), in the clinical microbiology laboratory.

When the bacterial isolates were tested repeatedly with API 50 CH kits (bioMérieux) to characterize their biochemical traits, they were both found to be positive for D-xylose, galactose, glucose, fructose, mannitol, sorbitol, methyl-α-D-glucoside, N-acetylglucosamine, amygdalin, arbutin, aesculin, salicin, maltose, melibiose, sucrose, trehalose, raffinose, starch, glycogen and gluconate. Cellobiose, lactose and inulin were positive only in the case of strain SMC 4352-1T, whereas glycerol, ribose, mannose, inositol, xylitol, xylobiose and 5-ketogluconate were positive only for strain SMC 4352-2T. Because conventional biochemical tests failed to identify these isolates to given species in the clinical microbiology laboratory, we subjected them to 16S rRNA gene sequence analysis in order to identify them.

Bacterial DNA for the amplification of the 16S rRNA gene was extracted using a boiling lysis method (Ko et al., 2005a, b). Colonies on blood agar plates were suspended in lysis buffer (100 mM NaCl, 10 mM Tris/HCl, 1 mM EDTA and 1 % Triton X-100) and then incubated at 90 °C for 10 min. The mixture was then briefly centrifuged and the aqueous...
phase was used as template for a PCR. The 16S rRNA gene
was amplified using the universal primers 16S-F0 (5′-GA-
TCCTGGCTCAGGACGAAC-3′) and 16S-R0 (5′-CTTGG-
TTACGACTTCAACCCCA-3′) (Hong et al., 2003; Zhu et al.,
2002). Template DNA and 20 pmol each primer were
added to the PCR mixture tubes (AccuPower PCR PreMix;
Bioneer), and the reaction mixtures were then subjected to
35 amplification cycles. Each cycle consisted of 30 s at 95
°C for denaturation, 30 s at 60 °C, and 1 min at 72 °C for
extension, followed by a final extension at 72 °C for 5 min.
Amplified PCR products were purified for sequencing using
a PCR purification kit (CoreOne). Purified PCR products
were sequenced directly using the PCR amplification
primers and primer 16S-F5 (5′-TATTGGGGTTAAAGCC-
AGGC-3′) (Ko et al., 2005a, b). The 16S rRNA gene
sequences of the two novel bacterial strains and those of
other Bacillus species retrieved from GenBank were aligned
using the CLUSTAL X program (Thompson et al., 1997).

The phylogenetic relationships among the two novel strains and
other Bacillus species were determined by using the neigh-
bour-joining, maximum-parsimony and maximum-
likelihood methods within PAUP, version 4.0 (Swofford,
1999).

The 16S rRNA gene sequences of strains SMC 4352-1T
(1367 bp) and SMC 4352-1T (1437 bp) showed a pairwise
similarity of 95·2 %, indicating that they belong to the same
genus but to different species. Comparisons with the
GenBank database revealed that their sequences did not
match those of any known bacterium. The bacterium with
the greatest pairwise similarity to strain SMC 4352-1T was B.
firmus NCIMB 9366T (98·2 %), whereas Bacillus cibi IG-30T
most closely matched strain SMC 4352-2T, showing a
pairwise similarity of 97·1 %. Initially, we retrieved and
included the 16S rRNA gene sequences of nearly all Bacillus
species with validly published names. Of these, 19 Bacillus
species found to have a close relationship to the two novel
bacterial strains in the initial analysis were selected and
analysed (Fig. 1). A phylogenetic tree constructed using the
neighbour-joining method suggested that strains SMC
4352-1T and SMC 4352-2T are members of the genus Bacillus
but they represent distinct species. Strain SMC 4352-1T
clustered with B. firmus and Bacillus sira l i s with a
low bootstrap value (<50 %), whereas strain SMC 4352-2T
clustered with B. cibi—a relationship supported by bootstrap
value of 100 %. Other methods of phylogenetic reconstruc-
tion, such as maximum parsimony and maximum like-
ilhood, showed relationships similar to those presented in
Fig. 1.

The cellular fatty acid compositions of the two novel strains
were examined using GC (6890A; Hewlett Packard) and a
MIDI aerobe method (Chem Station, version 4.02) at
MicroID (Seoul, Korea). For fatty acid analysis, the strains
were grown at 35 °C on blood agar for about 24 h. The
cellular fatty acid profiles determined were compared with
published profiles. Analysis of the cellular fatty acid
composition was performed for strains SMC 4352-1T and
SMC 4352-2T, the results of which are shown in Supplementary Table S1 available in IJSEM Online. The
profiles of the two strains differed: in strain SMC 4352-1T,
the predominant fatty acid was isoc15 : 0 (44·0 %), followed
by anteiso-C15 : 0 (30·9 %) and anteiso-C17 : 0 (7·4 %); in
strain SMC 4352-1T, however, the predominant fatty acid
was anteiso-C15 : 0 (26·0 %), followed by iso-C15 : 0 (18·0 %)
and anteiso-C17 : 0 (6·9 %).

DNA–DNA reassociation was measured fluorometrically by
using the microplate hybridization method described by
Ezaki et al. (1989). Strain SMC 4352-1T showed 36 % DNA–
DNA reassociation with B. firmus ATCC 8247T, while strain
SMC 4352-2T showed 23 % DNA–DNA reassociation with
B. cibi KCTC 3880T. The DNA G+C contents of strains
SMC 4352-1T and SMC 4352-2T were determined spectro-
photometrically using the thermal denaturation method
(Marmur & Doty, 1962) and found to be 40·8 and 41·2 mol%,
respectively.

Although these two strains were isolated from a neonate,
their association with neonatal sepsis could not be
determined. In addition to these two isolates, several
other bacterial organisms, such as vancomycin-susceptible
enterococci, Acinetobacter lwoffi, Alcaligenes xylosoxidans

Fig. 1. Neighbour-joining phylogenetic tree, based on almost-
complete sequences of 16S rRNA genes, showing the rela-
tionships among the two novel isolates and species of the genus Bacillus. Bootstrap values are shown as percentages from
1000 replications at branch points. Species names and acces-
son numbers are given as cited in the GenBank database.
Bacillus niacini S147 (GenBank accession no. AY509227)
was used as an outgroup (not shown). Bar, 5 substitutions per
100 nucleotides.
and methicillin-resistant, coagulase-negative staphylococci, were also isolated from the patient. Since these strains were isolated from blood obtained via a central venous catheter, which is prone to contamination, they may not be pathogens but rather contaminants or colonizers. B. firmus and B. cibi, the closest relatives of these two strains, also do not cause human disease (Logan & Turnbull, 2003; Yoon et al., 2005), although their pathogenicity remains to be investigated.

On the basis of their biochemical characteristics and cellular fatty acid profiles, the two isolates were demonstrated to represent two different species (Table 1 and Supplementary Table S1); this was confirmed by the results of 16S rDNA gene sequence comparisons and DNA–DNA hybridizations. The 16S rRNA gene sequence of strain SMC 4352-1 T showed the highest level of pairwise similarity to that of the type strain of B. firmus (98·2 %), while that of strain SMC 4352-2 T showed the highest level of pairwise similarity to that of the type strain of B. cibi (97·1 %). These pairwise similarities are sufficient to consider strains SMC 4352-1 T and SMC 4352-2 T as belonging to novel species, as many Bacillus species having sequence pairwise similarities > 98·5 % are considered as different species. For example, the 16S rRNA gene sequences of the type strains of Bacillus bataviensis, B. soli, B. dretensis, B. novalis and B. vireseti, which are distinct species, show 98·7–99·6 % pairwise similarity, whereas the type strains of B. mojavensis, B. subtilis, B. amylobiqufaciens, B. valismortis and B. atrophaeus show 98·5–99·6 % pairwise similarity and yet they are regarded as distinct species. In addition, DNA–DNA hybridization results supported species differentiation of the two strains, because their values for DNA–DNA reassociation with the closest species were below 40 %. Phenotypically, strain SMC 4352-1 T could be differentiated from B. firmus in that it was positive for utilization of glycogen, inulin and salicin (Table 1). Strain SMC 4352-2 T was positive for utilization of mannitol and salicin, while B. cibi was negative for both (Table 1). Thus, our data suggest that the two isolates represent novel Bacillus species.

On the basis of the above biochemical data, cellular fatty acid compositions and molecular phylogenetic results, strains SMC 4352-1 T and SMC 4352-2 T represent two novel species of Bacillus, for which we propose the names Bacillus infantis sp. nov. and Bacillus idriensis sp. nov.

**Description of Bacillus infantis sp. nov.**

Bacillus infantis (in.fan’t.is. L. gen. n. infantis of an infant, baby, the putative source of the type strain).

Aerobic, Gram-positive, catalase-positive, oxidase-negative bacillus. Grows well on blood agar at 37 °C. When assayed with the API 50 CH system, it is positive for utilization of D-xylose, galactose, glucose, fructose, mannitol, sorbitol, methyl α-D-glucoside, N-acetylgalactosamine, amygdalin, arbutin, aesculin, salicin, maltose, melibiose, sucrose, trehalose, raffinose, starch, glycogen, gluconate, cellobiose, lactose and inulin and is negative for utilization of glycerol, ribose, mannose, inositol, xylitol, gentiobiose and 5-ketogluconate. The major fatty acid is iso-C_{15:0} (44·0 %), followed by anteiso-C_{15:0} (30·9 %) and anteiso-C_{17:0} (7·4 %), and its 16S rDNA gene sequence shows most similarity (98·2 %) to that of the type strain of B. firmus. DNA–DNA reassociation with B. firmus ATCC 8247 T is 36 %. The DNA G+C content is 40·8 mol%.

The type strain, SMC 4352-1 T (= KCCM 90025 T = JCM 13438 T), was isolated from a newborn with sepsis.

**Description of Bacillus idriensis sp. nov.**

Bacillus idriensis (id.ri.en’sis. N.L. masc. adj. idriensis arbitrary specific epithet pertaining to IDRI, the Infectious Disease Research Institute, where this study was performed).

Aerobic, Gram-positive, catalase-positive, oxidase-negative bacillus. Grows well on blood agar at 37 °C. When assayed with the API 50 CH system, it is positive for utilization of D-xylose, galactose, glucose, fructose, mannitol, sorbitol, methyl α-D-glucoside, N-acetylgalactosamine, amygdalin, arbutin, aesculin, salicin, maltose, melibiose, sucrose, trehalose, raffinose, starch, glycogen, gluconate, glycerol, ribose, mannose, inositol, xylitol, gentiobiose and 5-ketoglucunate, but negative for utilization of cellobiose, lactose and inulin. The predominant fatty acid is anteiso-C_{15:0} (26·0 %), followed by iso-C_{15:0} (18·0 %) and anteiso-C_{17:0} (6·9 %), and its 16S rDNA gene sequence shows most similarity (97·1 %) to that of the type strain of B. cibi. DNA–DNA reassociation with B. cibi KCTC 3880 T is 23 %. The DNA G+C content is 41·2 mol%.

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**Table 1.** Comparison of the biochemical characteristics of strains SMC 4352-1 T and SMC 4352-2 T and related species

<table>
<thead>
<tr>
<th>Biochemical reaction</th>
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<th>5</th>
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<td>V</td>
<td>−</td>
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<tr>
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<td>+</td>
<td>+</td>
<td>−</td>
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<td>+</td>
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<td>V</td>
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</table>

Two novel Bacillus species from a patient
The type strain, SMC 4352-2<sup>T</sup> (=KCCM 90024<sup>T</sup>=JCM 13437<sup>T</sup>), was isolated from a newborn child with sepsis.

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**References**


