**Streptococcus hongkongensis** sp. nov., isolated from a patient with an infected puncture wound and from a marine flatfish

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A bacterium, HKU30T, was isolated from the infected tissue of a patient with wound infection after puncture by a fish fin. Cells are facultative anaerobic, non-spore-forming, non-motile, Gram-positive cocci arranged in chains. Colonies were non-haemolytic. The strain was catalase, oxidase, urease and Voges–Proskauer test negative. It reacted with Lancefield’s group G antisera and was resistant to optochin. It grew on bile aesculin agar and in 5 % NaCl. It was unidentified by three commercial identification systems. 16S rRNA gene sequence analysis indicated that the bacterium shared 98.2, 97.7, 97.4 and 97.1 % nucleotide identities with *Streptococcus iniae*, *Streptococcus pseudoporcinus*, *Streptococcus parauberis* and *Streptococcus uberis*, respectively. The DNA G+C content was 35.6 ± 0.9 mol% (mean ± SD). In view of the occupational exposure of the patient, an epidemiological study was performed to isolate the bacterium from marine fish. Two strains, with similar phenotypic and genotypic characteristics to those of HKU30T, were isolated from a three-lined tongue sole (*Cynoglossus abbreviatus*) and an olive flounder (*Paralichthys olivaceus*) respectively. Phylogenetic analysis of four additional housekeeping genes, *groEL*, *gyrB*, *sodA* and *rpoB*, showed that the three isolates formed a distinct branch among known species of the genus *Streptococcus*, being most closely related to *S. parauberis* (CCUG 39954T). DNA–DNA hybridization demonstrated ≤ 53.8 % DNA relatedness between the three isolates and related species of the genus *Streptococcus*. A novel species, *Streptococcus hongkongensis* sp. nov., is proposed. The type strain is HKU30T (=DSM 26014T = CECT 8154T).

**Streptococcus** is an important bacterial genus comprising diverse species of catalase-negative Gram-positive cocci in chains or pairs. They are traditionally classified into three major groups by their pattern of haemolysis into α-haemolytic, β-haemolytic or non(γ)-haemolytic streptococci. Further identification to species level usually relies on Lancefield grouping and/or biochemical tests. Based on 16S rRNA gene sequences, the various species are divided into six groups including anginosus, equinus, mitis, mutans, pyogenes and salivarius (Kawamura et al., 1995). A recent phylogenetic analysis based on partial sequences of recN also supported the existence of six groups though with slightly different groupings (Glazunova et al. 2010). Since conventional phenotypic tests and commercial identification systems often fail to identify certain species of the genus *Streptococcus* such as the viridans group and rarely encountered species, molecular techniques have been employed to allow accurate species identification and discovery of novel species in clinical microbiology laboratories (Glazunova et al., 2006; Kawamura et al., 1998; Lau et al., 2003; Woo et al., 2001, 2002, 2004b; Zbinden et al., 2012). In this report, we describe the isolation and characterization of a novel non-haemolytic, Gram-positive, catalase-negative, coccus-shaped bacterium, initially from a patient with right thumb wound infection after puncture by a fish fin and subsequently from two marine flatfish.

A 44-year-old previously healthy man was admitted to hospital in July 2010 because of increasing right thumb...
pain and swelling with serous discharge for 3 days. He was a fishmonger who sold fish at a local fish market and had a puncture injury over his right thumb pulp by a fish fin during handling of marine fish one month previously. Examination showed a small wound over the right thumb pulp with surrounding erythema and swelling. X-ray of the right thumb showed the presence of suspected foreign body. The haemoglobin was 13.9 g dℓ⁻¹, total white cell count 5.0 × 10⁹ l⁻¹, with neutrophil count of 3.5 × 10⁹ l⁻¹, lymphocyte count of 1.0 × 10⁹ l⁻¹, monocyte count of 0.4 × 10⁹ l⁻¹ and platelet count of 180 × 10⁹ l⁻¹. Erythrocyte sedimentation rate was elevated to 17 mm h⁻¹. Emergency removal of foreign body and wound debridement was performed, which revealed a 1 cm-fish fin on the radial side of the right thumb pulp. The patient recovered after treatment with oral amoxicillin-clavulanate for 14 days. Samples of his right thumb tissue and fish fin yielded mixed growth of Morganella morganii and a Gram-positive coccus-shaped bacterium (strain HKU30ᵀ) on 5% horse blood agar after 24 h incubation.

HKU30ᵀ appeared as Gram-positive, non-spore-forming cocci arranged in chains. It grew on horse blood agar as non-haemolytic, grey colonies of 0.5–1 mm in diameter after 24 h of incubation at 37 °C in ambient air. Enhancement of growth was observed with 5% CO₂. It also grew in microaerophilic or anaerobic environment and on bile aesculin agar but not MacConkey agar. It grew in 1%, 2, 3, 4 and 5% NaCl but not 6% NaCl. It reacted with Lancefield’s group G but not group A, B, C or D antiserum (Streptex; Remel). It was resistant to optochin, polymyxin B and bacitracin but sensitive to novobiocin. It was non-motile at both 25 and 37 °C. Vitek-2 GPI, API20 STREP and ATB rapid ID32 STREP (bioMérieux Vitek) showed unidentified or unacceptabte profiles (API20 profile number 6173513, ID32 profile number 74336761150).

Because of the inconclusive phenotypic characteristics, PCR and sequencing of nearly complete 16S rRNA gene was performed, using primers listed in Table S1 (available at IJSEM Online), as described previously (Lau et al., 2003; Woo et al., 2003). Pairwise sequence alignment using EzTaxon (Chun et al., 2007) showed that the 16S rRNA gene of HKU30ᵀ possessed 1.8, 2.3, 2.6, 2.9, 2.9 and 3% base differences from that of Streptococcus iniae ATCC 29178ᵀ, Streptococcus pseudoporcinus LQ-940-04ᵀ, Streptococcus parauberis DSM 6631ᵀ, Streptococcus uiberis JCM 5709ᵀ, Streptococcus dysgalactiae subsp. dysgalactiae ATCC 43078ᵀ and Streptococcus isticuluri 707-05ᵀ respectively. Phyllogenetic analysis using the maximum-likelihood method in MEGA version 5.01 (Tamura et al. 2011) revealed that HKU30ᵀ formed a distinct branch being most closely related to S. iniae within the pyogenic group of streptococci (Figs 1 and S1). Phylogenetic trees constructed with the neighbour-joining, minimum-evolution and maximum-parsimony methods also displayed similar topology (data not shown). Similar to previous studies (Kawamura et al., 1995; Glazunova et al., 2010), the diverse species of the genus Streptococcus formed at least six or seven groups based on 16S rRNA gene analysis (Fig. S1). As 16S rRNA gene sequences among some species of the genus Streptococcus may possess low sequence variability and other housekeeping genes, such as groEL, gyrB, rpoB and sodA, have been found to be more discriminative in differentiating members of the genus Streptococcus (Glazunova et al., 2009), the partial sequences of groEL, gyrB, rpoB and sodA were determined to further characterize the phylogenetic position of HKU30ᵀ. The partial groEL sequence of HKU30ᵀ exhibited 11.2, 18.2, 18.7, 19.4 and 21.4% base differences from those of S. parauberis CIP 103956ᵀ, S. urinialis CIP 106463ᵀ, S. iberis CIP 103219ᵀ, S. porcinius CIP 103218ᵀ and S. iniae CIP 102508ᵀ, respectively. The partial gyrB gene sequence exhibited 15.2, 21.1, 21.2, 21.6 and 21.8 % base differences from those of S. parauberis CIP 103956ᵀ, S. porcinius CIP 103218ᵀ, S. urinialis CIP 106463ᵀ, S. iniae CIP 102508ᵀ and S. iberis CIP 103219ᵀ, respectively. The partial rpoB gene sequence exhibited 5.3, 10.2, 10.4, 12.4 and 14.4% from those of S. parauberis CIP 103956ᵀ, S. gallyoticus subsp. pasterianus CIP 107122ᵀ, S. gallyoticus subsp. gallyoticus CIP 105428ᵀ, S. gallyoticus subsp. macedonicus CIP 105683ᵀ, S. iniae CIP 102508ᵀ and S. iberis CIP 103219ᵀ, respectively. The partial sodA gene exhibited 13.4, 17.2, 19, 19.3 and 13.1% base differences from those of S. parauberis CIP 103956ᵀ, S. iniae CIP 102508ᵀ, S. iberis CIP 103219ᵀ and S. canis CIP 103223ᵀ, respectively. Phylogenetic analysis based on partial groEL, gyrB, rpoB and sodA gene sequences using maximum-likelihood, neighbour-joining and maximum-parsimony methods revealed that HKU30ᵀ formed a distinct branch, being most closely related to S. parauberis in all the trees (maximum-likelihood trees shown in Figs S2 to S5).

Based on the clinical history, an epidemiological study on marine fish was carried out to identify the source of the bacterium. A total of 101 marine fish of 29 species were sampled from local retail markets. Organ tissues and swabs, where available, were obtained as described previously (Lau et al., 2007; Woo et al., 2004a). Homogenized tissue samples and swabs were plated onto horse blood agar containing Streptococcus-selective supplement (Oxoid) for isolation of streptococci (Petts, 1984) and inoculated into an enrichment broth (brain heart infusion broth with 3% sodium chloride and 100 μg neomycin ml⁻¹) for DNA extraction, after incubation in 5% CO₂ at 37 °C for 48 h. PCR was performed to detect the specific 16S rRNA gene of the potentially novel species of the genus Streptococcus, using primer sequences (Table S1) tested to be specific to the novel strains using strains from related species of the genus Streptococcus, as described previously with modifications (Lau et al., 2007). PCR was positive in two skin swab samples from two marine fish of different species, Cynognusss abbreviatus (three-lined tongue sole) and Paralicthys olivaceus (olive flounder). Two isolates of catalase-negative, non-haemolytic, Gram-positive cocci were detected on the blood agar inoculated with these two samples, strain FSHK1 from P. olivaceus and strain FSHK2 from C. abbreviatus. They possessed similar phenotypic characteristics to those of strain HKU30ᵀ.
(Table 1). Their 16S rRNA gene and partial groEL, gyrB, rpoB and sodA gene sequences were identical to those of strain HKU30T (Figs 1 and S2 to S5). Antimicrobial susceptibility using Kirby Bauer disk diffusion, with results interpreted according to the Clinical and Laboratory Standards Institute for α-haemolytic streptococci (Clinical and Laboratory Standards Institute, 2010), showed that strains HKU30T, FSHK1 and FSHK2 were sensitive to penicillin (MICs 0.032–0.064 mg l⁻¹ by E-test), clindamycin, ofloxacin, levofloxacin and vancomycin, except for strain HKU30T being resistant to clindamycin. Whole-cell protein content was analysed by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) as described previously (Lau et al., 2012). The distance dendrogram constructed using MALDI Biotyper 3.0 (Bruker Daltonics) illustrates that strain HKU30T, FSHK1 and FSHK2 were closely related to each other with identical mass spectra, but were distinct from other related species of the genus Streptococcus (Fig. S6).

The G+C content of the genomic DNA of strain HKU30T, as determined by thermal denaturation (Marmur & Doty, 1962) in triplicates and calculated by the formula: (G+C)% = 2.44Tm − 169, was 35.6 ± 0.9 mol% (mean ± se), which lies within the characteristic range of the genus Streptococcus (34–46 mol%) (Spellerberg & Brandt, 2011). To determine the DNA–DNA relatedness of the three isolates and their close phylogenetic neighbours, DNA–DNA hybridization studies were performed using genomic DNA extracted from HKU30T, FSHK1 and FSHK2 and type strains of closely related species, including S. iniae CCUG 27303T, S. paraheris CCUG 39954T, S. uberis CCUG 17930T, S. porcinus CCUG 27628T, Streptococcus dysgalactiae subsp. dysgalactiae CCUG 43079T (AB002485) and S. ictaluri CCUG 52536T, which shared 97% nucleotide identity in their 16S rRNA gene sequences to that of strain HKU30T. Preparation of

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**Fig. 1.** Phylogenetic tree showing the relationship of S. hongkongensis sp. nov. to related species within the S. pyogenes group using 16S rRNA gene sequence analysis. The tree was constructed by the maximum-likelihood method using Kimura’s two-parameter correction (Kimura, 1980) with Streptococcus mutans ATCC 25175T as the outgroup. A total of 1178 nt positions was included in the analysis. Bootstrap values were calculated as percentages from 1000 replicates and only values ≥ 70% were shown. The scale bar indicates the estimated number of substitutions per 100 bases. Names and accession numbers are given as cited in GenBank.
Streptococcus hongkongensis sp. nov.

Table 1. Differential biochemical characteristics between S. hongkongensis sp. nov. and the related species S. iniae, S. parauberis, S. uberis and S. pyogenes

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1*</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Resistance to bacitracin</td>
<td>+</td>
<td>–</td>
<td>(v)</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Resistance to novobiocin</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Bile aesculin agar</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>– (v)</td>
</tr>
<tr>
<td>Hippurate hydrolysis</td>
<td>–</td>
<td>–</td>
<td>+ (v)</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Voges–Proskauer</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Utilization of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glycogen</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>v</td>
<td>+</td>
</tr>
<tr>
<td>Inulin</td>
<td>–</td>
<td>–</td>
<td>+ (v)</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Lactose</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Melezitose</td>
<td>–</td>
<td>+</td>
<td>– (v)</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Sorbitol</td>
<td>–</td>
<td>–</td>
<td>+ (v)</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Tagatose</td>
<td>–</td>
<td>–</td>
<td>+ (v)</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Production of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>α-Glucosidase</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>β-Galactosidase</td>
<td>+</td>
<td>– (v)</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>β-Glucuronidase</td>
<td>–</td>
<td>+</td>
<td>– (v)</td>
<td>+ (v)</td>
<td>(v)</td>
</tr>
<tr>
<td>N-acetyl-β-glucosaminidase</td>
<td>+</td>
<td>– (v)</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

*Strains HKU30T, FSHK1 and FSHK2 have identical biochemical characteristics except a delayed positive result in the production of α-glucosidase was observed in strain FSHK2.

Genomic DNA was performed using Qiagen Genomic tip 100-G (Qiagen) and DNA–DNA dot blot hybridization using DIG High Prime DNA Labelling and Detection Starter kit II (Roche Diagnostics) in triplicate. Genomic DNA probe was DIG High Prime DNA Labelling and Detection Starter kit II 100-G (Qiagen) and DNA–DNA dot blot hybridization using genomic DNA was performed using Qiagen Genomic tip 100-G (Qiagen) and DNA–DNA dot blot hybridization using DIG High Prime DNA Labelling and Detection Starter kit II (Roche Diagnostics) in triplicate. Genomic DNA probe was DIG High Prime DNA Labelling and Detection Starter kit II 100-G (Qiagen) and DNA–DNA dot blot hybridization using Genomic tip 100-G (Qiagen) and DNA–DNA dot blot hybridization using 12344T. –, Negative, +, positive; (v), variable among tested or previously reported strains; (†), weak and delayed positive reaction (Bentley et al., 1993; Lau et al., 2003a, 2006; Nho et al., 2009; Whiley & Hardie, 2009). All data were obtained by the same methodology using the same culture conditions except for S. pyogenes, in which the data were extracted from literature.

We report the isolation and characterization of a novel species of the genus Streptococcus, S. hongkongensis sp. nov., from the infected thumb wound of a patient and two marine fish. Its 16S rRNA gene is most closely related to that of S. iniae, while sequence analysis of four additional housekeeping genes, groEL, gyrB, sodA and rpoB, showed that it is most closely but distantly related to S. parauberis. Such an incongruent phylogenetic position has been described in other species of the genus Streptococcus and may reflect the different evolutionary rates of the 16S rRNA gene and the housekeeping genes or represent the result of horizontal gene transfer between streptococcal species (Schouls et al., 2003; Zhang et al., 2012). DNA–DNA hybridization studies demonstrated ≤53.8% DNA relatedness between S. hongkongensis and closely related species of the genus Streptococcus. Based on their unique phylogenetic positions and genetic characteristics, the three isolates should be classified as a separate species among the genus Streptococcus.

S. hongkongensis also exhibits phenotypic characteristics distinct from related species of the genus Streptococcus, which may be useful for species identification in clinical laboratories (Table 1). Most notably, S. hongkongensis belongs to Lancefield group G, while S. iniae, S. parauberis and S. uberis are usually non-groupable, although some S. parauberis isolates may react with Lancefield group E, P or U antiserum and some S. uberis isolates with Lancefield group E, C, D, P or U antiserum (Bentley et al., 1993; Spellerberg & Brandt, 2011). Moreover, S. hongkongensis is non-haemolytic, while S. iniae is known to display rainbow or β-haemolysis. It is also different from S. iniae in its ability to grow on bile aesculin agar and utilize lactose, but
**Table 2. DNA–DNA relatedness between *S. hongkongensis* sp. nov. and related members of the genus Streptococcus**

Results from reciprocal experiment are given in parentheses.

<table>
<thead>
<tr>
<th>Source of unlabelled DNA</th>
<th>Results with labelled probe of <em>S. hongkongensis</em> sp. nov. HKU30&lt;sup&gt;†&lt;/sup&gt;</th>
<th>Relative binding ratio%&lt;sup&gt;*&lt;/sup&gt;</th>
<th>SD†</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>S. hongkongensis</em> HKU30&lt;sup&gt;T&lt;/sup&gt;</td>
<td>100.0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td><em>S. hongkongensis</em> FSHK1</td>
<td>101.1 (98.8)</td>
<td>18.0 (2.1)</td>
<td></td>
</tr>
<tr>
<td><em>S. hongkongensis</em> FSHK2</td>
<td>104.5 (97.7)</td>
<td>8.1 (0.5)</td>
<td></td>
</tr>
<tr>
<td><em>S. iniae</em> ATCC 29178&lt;sup&gt;T&lt;/sup&gt;</td>
<td>24.2 (29.0)</td>
<td>6.7 (17.4)</td>
<td></td>
</tr>
<tr>
<td><em>S. parauberis</em> CCUG 39954&lt;sup&gt;T&lt;/sup&gt;</td>
<td>29.4 (53.8)</td>
<td>8.3 (12.7)</td>
<td></td>
</tr>
<tr>
<td><em>S. uberis</em> ATCC 19436&lt;sup&gt;T&lt;/sup&gt;</td>
<td>38.0 (20.3)</td>
<td>17.8 (11.3)</td>
<td></td>
</tr>
<tr>
<td><em>S. porcinus</em> ATCC43138&lt;sup&gt;T&lt;/sup&gt;</td>
<td>49.1 (18.8)</td>
<td>2.0 (2.7)</td>
<td></td>
</tr>
<tr>
<td><em>S. dysgalactiae</em> subsp. <em>dysgalactiae</em> ATCC 43078&lt;sup&gt;T&lt;/sup&gt;</td>
<td>4.0 (27.5)</td>
<td>7.5 (6.2)</td>
<td></td>
</tr>
<tr>
<td><em>S. ictaluri</em> 707-05&lt;sup&gt;T&lt;/sup&gt;</td>
<td>48.7 (47.0)</td>
<td>5.9 (4.3)</td>
<td></td>
</tr>
</tbody>
</table>

*RBR* (relative binding ratio) was determined by the following equation: (dot intensity of labeled DNA probe bound in unlabeled DNA from target strains)/(dot intensity of labeled DNA probe of strain bound with unlabeled DNA of itself) × 100.

†SD calculated from three independent experimental replicates.

inability to utilize melezitose and produce β-glucuronidase. It is different from *S. parauberis* and *S. uberis* by its negative Voges–Proskauer reaction and ability to produce β-galactosidase. It is also different from *S. parauberis* in its ability to utilize glycerol and different from *S. uberis* in its inability to utilize sorbitol and tagatose. Isolation of non-haemolytic group G streptococci, especially from patients with a history of marine exposure, should raise the suspicion of *S. hongkongensis*. Analysis 16S rRNA gene or other housekeeping gene targets, is a reliable approach for definitive identification, which is important in understanding the prevalence and epidemiology.

While *S. hongkongensis* probably shares similar aquatic habitats to the related species, *S. parauberis* and *S. iniae*, its pathogenic potential remains to be elucidated. *S. parauberis* is an important causative agent of bovine mastitis as well as olive flounder streptococcosis in aquaculture industries (Bentley et al., 1993; Nho et al., 2009). *S. iniae*, apart from being an important fish pathogen (Pier & Madin, 1976; Shoemaker et al., 2001), can cause invasive infections in humans (Weinstein et al., 1997, Koh et al., 2004, 2009; Lau et al., 2003, 2006). In contrast to invasive *S. iniae* infections, the present patient did not have features suggestive of systemic infection, which may be explained by his young age and absence of underlying disease. The two marine fish, from which *S. hongkongensis* was isolated, also did not exhibit gross abnormalities suggestive of disease. Interestingly, the three related streptococci, *S. hongkongensis*, *S. iniae* and *S. parauberis*, have been isolated from olive flounder, a common flatfish native to the northwestern Pacific Ocean and raised in aquaculture in Asia (Nho et al., 2009). Moreover, both fish positive for *S. hongkongensis* belonged to the order *Pleuroectiformes* (flatfish), suggesting that flatfish may be a common reservoir of these aquatic streptococci. The ability of *S. hongkongensis* to grow in 5% NaCl is also compatible with its survival in marine environment, in contrast to freshwater-associated bacteria such as *Laribacter hongkongensis*, which only grew in 2% NaCl (Woo et al., 2004a). Similar to the situation in infections caused by other aquatic bacteria (Koh et al., 2009; Lau et al., 2003, 2011; Weinstein et al., 1997), the Asian population may be at higher risk for *S. hongkongensis* infections because of their cultural preference for freshly killed whole fish for cooking. In our patient, the bacterium had probably gained entry through the wound during injury while he was handling fish for sale. The Asian population should be aware of the chance of acquiring infections from injury during preparation of fish.

**Description of Streptococcus hongkongensis** sp. nov.

*S. hongkongensis* (hong.kong.en’sis N.L. masc. adj. hongkongensis of or belonging to Hong Kong, the place where the type strain was isolated).

Cells are facultatively anaerobic, Gram-positive, non-motile, non-spore-forming cocci (0.5–1.0 μm). It grows on blood agar as small (0.5–1.0 mm), opaque, convex, non-haemolytic colonies after 48 h of incubation at 37°C in ambient air. Enhancement of growth was observed with 5% CO<sub>2</sub>. Also grows in microaerophilic or anaerobic environments and on bile esculin agar but not MacConkey agar. Grows in 1, 2, 3, 4 and 5% NaCl but not 6% NaCl. Cells react with Lancefield’s group G antisera. Does not produce catalase. Hydrolyses esculin and arginine but not hippurate. It is negative for Voges-Proskauer, oxidase and urease. Utilizes amygdalin, galactose, glycogen, lactose, maltose, mannitol, mannose, methyl-β-D-glucopyranoside, N-acetyl-D-glucosamine, pullulan, ribose, salicin, sucrose, starch and trehalose. Produces alanine arylami-
dase, alanine–phenylalanine–proline arylamidase, alkaline phosphatase, β-galactopyranosidase, β-galactosidase, β-glucosidase, β-mannosidase, glycy1-tryptophan arylamidase, leucine arylamidase, N-acetyl-β-glucosaminidase, pyrrolidonyl arylamidase and tyrosine arylamidase. Cells are resistant to optochin, polymyxin B and bacitracin, but sensitive to penicillin, vancomycin, ofloxacin, levofloxacin and novobiocin.

The type strain, HKU30^T (=DSM 26014^T=CECT 8154^T), was isolated from the infected tissue of a patient with a puncture injury of the right thumb in Hong Kong, China. The G+C content of the DNA of the type strain HKU30^T is 35.6 ± 0.9 mol% (mean ± sd).

Two reference strains of this novel species, FSHK1 and FSHK2, were isolated from marine fish.

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