NOTES

Corynebacterium testudinoris sp. nov., from a tortoise, and Corynebacterium felinum sp. nov., from a Scottish wild cat

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Two unknown Gram-positive, rod-shaped bacteria isolated from a tortoise and a Scottish wild cat were subjected to a polyphasic taxonomic analysis. Chemical analysis revealed the presence of straight-chain and monounsaturated fatty acids and short-chain mycolic acids in the two isolates consistent with the genus Corynebacterium. Comparative 16S rRNA gene sequencing confirmed that the unknown isolates were members of the genus Corynebacterium, with the two organisms displaying greater than 3% sequence divergence from each other and from established species of the genus. The unknown Corynebacterium isolates were readily distinguished from each other and from all recognized species of the genus by biochemical tests. Based on phylogenetic and phenotypic evidence, it is proposed that the unknown organisms from a tortoise and a cat be classified in the genus Corynebacterium as Corynebacterium testudinoris sp. nov. and Corynebacterium felinum sp. nov., respectively. The respective type strains of C. testudinoris and C. felinum are CCUG 41823T and CCUG 39943T.

Keywords: Corynebacterium testudinoris, Corynebacterium felinum, wild cat, tortoise, 16S rRNA

The genus Corynebacterium is one of the largest genera of Gram-positive asporogenous bacteria within the Actinobacteria. Corynebacteria are found in a broad variety of habitats such as soil, plant material, food products and marine and animal sources. During the past decade, a very considerable number of new corynebacterial species have been described (see for example Collins et al., 1999; Fernández-Garayzábal et al., 1997, 1998; Funke et al., 1997, 1998; Riegel et al., 1995). Most of these novel species have come to light primarily as the result of the availability of more precise molecular diagnostic tools (e.g. 16S rRNA gene sequencing) and improved phenotypic criteria (e.g. miniaturized tests and improved databases). The vast majority of these newly described organisms have been recovered from human clinical and veterinary sources, where they occur as cutaneous or mucocutaneous contaminants, whereas others represent hitherto-unrecognized pathogens (Funke et al., 1997). In the course of an on-going study of unusual or taxonomically problematic Actinobacteria from animal sources, we have used molecular chemical and molecular genetic approaches to aid the characterization of two Corynebacterium-like organisms recovered from the mouth of a tortoise and a dead Scottish wild cat. Based on the reported findings, we propose two further new species of the genus Corynebacterium, Corynebacterium testudinoris sp. nov. and Corynebacterium felinum sp. nov.

The unidentified rod-shaped organism designated M935/96/4T (CCUG 41823T) was isolated from necrotic lesions in the mouth of a tortoise. The unknown organism was isolated along with Escherichia coli, a Streptococcus species and a Pseudomonas species. Strain M714/95/5T (CCUG 39943T) was isolated from a Scottish wild cat (Felis sylvestris) that had died from feline influenza. Both unidentified rods were cultured on Columbia blood agar base supplemented with 5% defibrinated sheep blood at 37°C in air plus 5% CO2. The strains were bio-

The GenBank accession numbers for the 16S rRNA gene sequences of strains CCUG 41823T and CCUG 39943T are AJ295841 and AJ401282, respectively.
chemically characterized by using the API CORYNE and API ZYM systems according to the manufacturer’s instructions (API bioMérieux). Cell-wall murein was prepared by mechanical disruption of cells and complete acid hydrolysates, analysed as described by Schleifer & Kandler (1972). Fatty acid methyl esters were prepared and analysed as described by Kämpfer & Kroppenstedt (1996). The presence of mycolic acids was investigated by GLC analysis of trimethylsilylated derivatives (TMS-MAME) (Klatte et al., 1994). The 16S rRNA genes of the isolates were amplified by PCR and sequenced directly using a Taq dye-Deoxy terminator cycle sequencing kit (Applied Biosystems) and an automatic DNA sequencer (model 373A; Applied Biosystems). A phylogenetic tree was constructed according to the neighbour-joining method and the stability of the groupings was estimated by bootstrap analysis (Felsenstein, 1989).

The two unidentified isolates recovered from the mouth of a tortoise and a dead wild cat consisted of Gram-positive, non-motile, non-spore-forming, catalase-positive, diphtheroid-shaped cells. With commercially available API systems, the tortoise bacterium produced acid from glucose, maltose, ribose and sucrose but not from lactose, glycogen, mannotol, N-acetyl-β-glucosamine or D-xylose. Reactions for acid phosphatase (weak), ester lipase C-8 (weak), esterase C-4, leucine arylamidase and β-glucosidase were positive. No activity was detected for alkaline phosphatase, α-galactosidase, β-galactosidase, β-glucuronidase, α-fucosidase, lipase C14, α-mannosidase, valine arylamidase, pyrazinamidase, pyrrolidonyl arylamidase, phosphoamidase, chymotrypsin, esterase activity was detected for alkaline phosphatase, acid amidase and leucine arylamidase were positive but no α-ribose but not from lactose, mannitol, sucrose, the bacterium produced acid from glucose, maltose and ribose and did not hydrolyse gelatin. In contrast, the cat bacterium did not hydrolyse β-galactosidase, β-glucosidase, α-fucosidase, lipase C14, α-mannosidase, valine arylamidase or trypsin. The organism did not hydrolyse aesculin, urea or gelatin and did not reduce nitrate. In terms of their overall morphological and biochemical characteristics, the unidentified isolates somewhat resembled corynebacteria but they did not correspond to any recognized species of this genus.

Cell-wall analysis revealed the presence of meso-diaminopimelic acid within the two isolates, consistent with their provisional assignment to the genus Corynebacterium. The cellular fatty acids of the tortoise isolate CCUG 41823\(^{3}\) consisted of C\(_{14:0}\) (2.5 \%), C\(_{16:0}\) (43.6 \%), C\(_{16:1\, \omega 7c}\) (8.7 \%), C\(_{18:0\, \omega 9c}\) (42.7 \%) and C\(_{18:1\, \omega 9c}\) (13 \%), C\(_{17:0\, \alpha 12}\) (2 \%), C\(_{17:1\, \omega 7c}\) (2 \%), C\(_{18:0}\) (14 \%) and C\(_{18:1\, \omega 9c}\) (28 \%), which again resembled corynebacteria. Tuberculostearic acid was not present in either of the isolates. TLC analysis of whole-cell methanolysates and GLC analysis of trimethylsilylated derivatives revealed the presence of short-chain mycolic acids C30 to C36 (major component C32:0) and C32 to C36 (major component C32:0) in the tortoise and cat strains, respectively, confirming their identification as true Corynebacterium species. In order to ascertain the phylogenetic positions of the unknown isolates, their almost complete 16S rRNA gene sequences were determined and subjected to a comparative analysis. Sequence database searches revealed that the unknown bacteria were phylogenetically members of the genus Corynebacterium. Treeing analysis clearly demonstrated that the two unidentified isolates were phylogenetically separate from each other and from all described Corynebacterium species. A tree constructed by the neighbour-joining method, showing the nearest phylogenetic relatives of the unknown organisms, is shown in Fig. 1. The two strains formed distinct sublines associated with a small group of species, which included Corynebacterium argenteoratense, Corynebacterium diphtheriae, Corynebacterium kutscheri, Corynebacterium pseudotuberculosis, Corynebacterium ulcerans and Corynebacterium vitaeaminis.

The results of the polyphasic taxonomic investigation clearly showed that the unknown rod-shaped organisms isolated from necrotic mouth lesions of a tortoise and a dead wild cat represent hitherto unrecognized species within the genus Corynebacterium. Phylogenetically, the two isolates formed distinct lines within a cluster of species that includes C. diphtheriae, the type species of the genus. The two animal isolates clustered together with a bootstrap re-sampling value of 89 \% (500 tree replications), but pairwise analysis

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**Fig. 1.** Unrooted tree based on 16S rRNA showing the phylogenetic relationships of Corynebacterium testudinoris sp. nov. and Corynebacterium felinum sp. nov. Bootstrap values (expressed as percentages of 500 replications) are given at the branching points. Bar, 1 \% sequence divergence.
showed that the isolates represent closely related, albeit distinct, species (96.9–165 rRNA sequence similarity based on a comparison of 1310 bp). C. vitaeruminis displayed highest sequence relatedness to the cat bacterium (97%), with C. diphtheriae and C. ulcerans showing slightly lower levels of similarity (96.8–96.9%). These latter two species also exhibited high sequence relatedness (96.6–96.7%) to the unidentified tortoise bacterium, whereas C. vitaeruminis showed only 96.0% similarity. The results of the tree analysis together with sequence divergence values of 3% or more from other members of the genus therefore demonstrate unequivocally that the two organisms from a tortoise and a cat represent distinct species. Biochemically, the unknown organisms differ from each other and from all recognized members of the genus Corynebacterium. Therefore, based on phylogenetic and phenotypic evidence, we propose that the unknown organisms be classified in the genus Corynebacterium, as Corynebacterium testudinoris sp. nov. and Corynebacterium felinum sp. nov., respectively. Tests that are useful in distinguishing C. testudinoris and C. felinum from their closest phylogenetic relatives are shown in Table 1.

**Table 1. Characteristics that differentiate C. felinum and C. testudinoris from their nearest phylogenetic relatives**

Biochemical reactions were determined with the API CORYNE system. Characteristics are scored as: +, positive; + (−), most strains positive; −(+), most strains negative; −, negative; v, variable. REV CAMP, Reverse Christie–Atkins–Munch–Petersen reaction.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>C. felinum</th>
<th>C. testudinoris</th>
<th>C. argen toratense</th>
<th>C. diphtheriae</th>
<th>C. kutscheri</th>
<th>C. pseudotuberculosis</th>
<th>C. ulcerans</th>
<th>C. vitaeruminis</th>
</tr>
</thead>
<tbody>
<tr>
<td>Major cellular fatty acids</td>
<td>C16:0 C16:1</td>
<td>C16:0 C16:1</td>
<td>C16:0 C16:1</td>
<td>C16:0 C16:1</td>
<td>C16:0 C16:1</td>
<td>C16:0 C16:1</td>
<td>C16:0 C16:1</td>
<td>C16:0 C16:1</td>
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<tr>
<td>Lipophilic</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>v</td>
<td>−</td>
<td>−</td>
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<tr>
<td>Nitrate reduction</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>v</td>
<td>v</td>
<td>−</td>
<td>v</td>
<td>v</td>
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<td>Urease</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>v</td>
<td>−</td>
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<tr>
<td>Hydrolysis of aesculin</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>v</td>
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<td>Pyrazinamidase</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
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<td>Alkaline phosphatase</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>v</td>
<td>v</td>
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<tr>
<td>Pyrrolidonyl arylamidase</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>v</td>
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<td>Production of acid from:</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>v</td>
<td>−</td>
<td>−</td>
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<td>Maltose</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<td>Sucrose</td>
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<td>+</td>
<td>+</td>
<td>−</td>
<td>v</td>
<td>v</td>
<td>+</td>
<td>+</td>
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<td>Other characteristics</td>
<td>−</td>
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<td>−</td>
<td>−</td>
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Description of *Corynebacterium felinum* sp. nov.

*Corynebacterium felinum* (fe.li’num. L. neut. adj. felinum pertaining to cats).

Cells are Gram-positive, non-motile, non-spore-forming diphtheroids. Facultatively anaerobic and catalase-positive. Non-haemolytic. Acid is produced from glucose, maltose and ribose but not from lactose, mannitol, sucrose, N-acetyl-β-glucosamine or d-xylose. Activity is detected for z-glucosidase, pyrazinamidase, pyrrolidonyl arylamidase and leucine arylamidase. No activity is observed for alkaline phosphatase, acid phosphatase, chymotrypsin, ester lipase C-8 and esterase C-4. Activity is detected for d-glucosidase, a-galactosidase, b-galactosidase, b-glucuronidase, a-fucosidase and sulfatase. Activity is detected for alkaline phosphatase and esterase C-4. Activity is detected for a-galactosidase, b-galactosidase, b-glucuronidase and N-acetyl-β-glucosaminidase. Activity is detected for a-mannosidase, valine arylamidase, pyrazinamidase, phosphoamidase, pyrrolidonyl arylamidase, urease or trypsin. β-Glucosidase may or may not be produced. Aesculin is hydrolysed but gelatin is not. Nitrate is reduced. Cell wall contains meso-diaminopimelic acid. Long-chain fatty acids are of the straight-chain saturated and monounsaturated types, with C16:0 and C18:1 ω9c predominating. Tuberculostearic acid is not present. Mycolic acids are present (C30 to C36). Isolated from necrotic lesions in mouth of a tortoise. Habitat is unknown. The type strain is M935/96/2T, which has been deposited in the Culture Collection of the University of Göteborg as strain CCUG 41823T and in the Collection of Bacterial Strains of Institut Pasteur as CIP 106763T.

Description of *Corynebacterium testudinoris* sp. nov.

*Corynebacterium testudinoris* (tes.tu.din.o’ris. L. n. testudo tortoise, L. gen. neut. n. oris of the mouth, N. L. gen. neut. n. testudinoris of the mouth of a tortoise).

Cells are Gram-positive, non-motile, non-spore-forming diphtheroids. Yellow pigmented. Facultatively anaerobic and catalase-positive. Non-lipophilic. Acid is produced from glucose, maltose, ribose and sucrose but not from fructose, lactose, mannitol or d-xylose. Activity is detected for acid phosphatase, a-galactosidase, a-fucosidase and leucine arylamidase. Activity is detected for a-glucosidase, a-galactosidase, b-glucuronidase and N-acetyl-β-glucosaminidase. Activity is detected for a-mannosidase, valine arylamidase, pyrazinamidase, phosphoamidase, pyrrolidonyl arylamidase, urease or trypsin. β-Glucosidase may or may not be produced. Aesculin is hydrolysed but gelatin is not. Nitrate is reduced. Cell wall contains meso-diaminopimelic acid. Long-chain fatty acids are of the straight-chain saturated and monounsaturated types. Tuberculostearic acid is not present. Mycolic acids are present (C30 to C36). MK-8(H2) is the predominant menaquinone. Isolated from a dead Scottish wild cat (*Felis sylvestris*). Habitat is unknown. The type strain is M714/95/5T, which has been deposited in the Culture Collection of the University of Göteborg as strain CCUG 39943T.
and in the Collection of Bacterial Strains of Institut Pasteur as CIP 106740 T.

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**References**


