NOTE

Corynebacterium capitovis sp. nov., from a sheep

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An unknown Gram-positive rod-shaped bacterium was isolated from skin scrapings from the infected head of a sheep and subjected to a polyphasic taxonomic analysis. Chemical analysis revealed the presence of straight-chain and monounsaturated fatty acids and short-chain (C12-C16) mycolic acids consistent with the genus Corynebacterium. Comparative 16S rRNA gene sequencing confirmed that the unknown rod was a member of the genus Corynebacterium, with the organism forming a distinct sub-line and displaying greater than 3% sequence divergence with established species. The unknown Corynebacterium isolate was readily distinguished from recognized species of the genus by biochemical tests and electrophoretic analysis of whole-cell proteins. Based on phylogenetic and phenotypic evidence, it is proposed that the unknown bacterium from a sheep be classified in the genus Corynebacterium, as Corynebacterium capitovis sp. nov. The type strain of Corynebacterium capitovis is CCUG 39779T (= CIP 106739T).

Keywords: Corynebacterium capitovis, sheep, taxonomy, phylogeny, 16S rRNA

The genus Corynebacterium currently contains over 50 species, the vast majority of which have been isolated from man or other animals. During the past decade, the number of recognized Corynebacterium species has increased dramatically due in the main to the use of higher precision molecular-based diagnostic methodologies. In particular, 16S rRNA gene sequencing in conjuction with molecular chemical approaches such as whole-cell protein profiling have proved invaluable not only for the recognition of new diversity, but in combination with improved phenotyping for the delineation of novel taxa (see for example Collins et al., 1999; Fernandez-Garayzabal et al., 1997, 1998; Funke et al., 1997, 1998; Riegel et al., 1995). In this article, we have used molecular chemical and molecular genetic approaches to aid the characterization of an unusual Corynebacterium-like organism recovered from the infected head of a sheep. Based on the reported findings, we propose yet another new species of the genus Corynebacterium, Corynebacterium capitovis sp. nov.

An unidentified rod-shaped organism designated S108/98/2 (CCUG 39779T) was isolated from skin scrapings of the infected head of a sheep. The unknown organism was isolated along with Arcanobacterium pyogenes, Fusobacterium necrophorum and Peptococcus magnus. The unidentified rod was cultured on Columbia Blood agar base supplemented with 5% defibrinated horse blood at 37 °C, in air plus 5% CO2. The strain was biochemically characterized by using the API CORYNE and API ZYM systems according to the manufacturer’s instructions (API bioMérieux). Preparation of cellular protein extracts for PAGE analysis, densitometric analysis, normalization of the protein profiles and numerical analyses were performed as described by Pot et al. (1994) using the GelCompar 3.0 software package (Applied Maths, Kortrijk, Belgium). The similarity between all pairs of traces was expressed by the Pearson product moment correlation coefficient converted for convenience to a percentage similarity value. Cell wall murein was prepared by mechanical disruption of cells and complete acid hydrolysates were analysed as described by Schleifer & Kandler (1972). Fatty acid methyl esters were prepared and analysed as described by Kämpfer & Kroppenstedt (1996) and the presence of mycolic acids was investigated by GLC analysis of trimethyl-silylated derivatives (TMS-MAME) (Klatte et al., 1994). The 16S rRNA genes of the isolate were amplified by PCR and directly sequenced using a Taq

The GenBank accession number for the 16S rRNA gene sequence of strain CCUG 39779T is AJ297402.
The unidentified isolate recovered from a polymicrobial infection of the head of a sheep consisted of Gram-positive, non-motile, non-spore-forming, diphtheroid-shaped cells. Using commercially available API systems, the isolate produced acid from glucose but not from lactose, maltose, mannitol, sucrose, N-acetyl-β-glucosamine, ribose or D-xylose. Reactions for alkaline phosphatase, acid phosphatase, esterase C8, esterase C4, leucine arylamidase and lipase C14 were positive. No activity was detected for α-glucosidase, β-galactosidase, α-glucosidase, β-glucosidase, β-glucuronidase, χ-fucosidase, χ-mannosidase, valine arylamidase, pyrrollidonyl arylamidase, phosphoamidase, chymotrypsin, trypsin or urease. The organism did not hydrolyse ascinul or gelatin and did not reduce nitrate. In terms of its overall morphological and biochemical characteristics, the unidentified bacterium somewhat resembled corynebacteria but did not appear to correspond to any recognized species of this genus. Cell wall analysis revealed the presence of meso-diaminopimelic acid within the isolate, consistent with its provisional assignment to the genus *Corynebacterium*. The cellular fatty acids of the isolate consisted of C16:0 (23%), C16:1ω9c (3%), C18:0 (61%) and C18:1ω9c (67-8%), which again resembled corynebacteria. Tuberculostearic acid was not present. TLC analysis of whole-cell methanolsates and GLC analysis of trimethylsilylated derivatives revealed the presence of short-chain mycolic acids (C32:0, C32:1, C34:0, C34:1, C36:0 and C36:2) in the strain, confirming its identification as a true *Corynebacterium*. PAGE analysis of whole-cell proteins of the unknown sheep bacterium was performed and the generated profile was compared with a comprehensive database maintained by the Culture Collection of the University of Göteborg. The unidentified organism from sheep was found to be distinct from other *Corynebacterium* species (data not shown) and failed to show a specific affinity with any recognized species. The nearest species on PAGE analysis to the unknown isolate corresponded to *Corynebacterium mastitidis*, with the isolate joining the latter at less than 50% correlation. To ascertain the phylogenetic position of the unknown isolate, its almost complete 16S rRNA gene sequence was determined and subjected to a comparative analysis. Sequence database searches revealed that the unknown bacterium was phylogenetically a member of the genus *Corynebacterium* but was distinct from all described species. A tree constructed using the neighbour-joining method depicting the phylogenetic placement of the unidentified organism within a subset of the genus *Corynebacterium* is shown in Fig. 1 and unequivocally shows that it represents a new species. The unknown sheep isolate formed a distinct sub-line, associated with a small group of species, which included *Corynebacterium auris*, *Corynebacterium mycetoides* and *Corynebacterium lipophiloflavum*.

The results of the polyphasic taxonomic analysis clearly show that the unknown rod-shaped bacterium isolated from the infected head of a sheep represents a hitherto unrecognized species within the genus *Corynebacterium*. Phylogenetically the bacterium forms a distinct sub-line, with *C. auris*, *C. mycetoides* and *C. lipophiloflavum* as its nearest relatives. However, bootstrap resampling did not reveal a particularly significant affinity with any of the aforementioned species and sequence divergence values of more than 3% unequivocally demonstrate that the sheep bacterium represents a distinct species. The distinctiveness of the unknown species was also very evident from the whole-cell protein profiling analysis and from its biochemical traits. Therefore, based on both phylogenetic and phenotypic evidence, we propose that the unknown sheep bacterium be classified in the genus *Corynebacterium*, as *Corynebacterium capitovis* sp. nov. Tests which are useful in distinguishing *C. capitovis* from its closest phylogenetic relatives and from some other veterinary and human clinically relevant *Corynebacterium* species are shown in Table 1.

**Description of Corynebacterium capitovis** sp. nov.

*Corynebacterium capitovis* (ca.pit.oˈvis. L. gen. n. capitis of a head; L. gen. n. ovis of a sheep; N.L. gen. n. capitis of a sheep’s head).

Cells are Gram-positive, non-motile, non-spore-forming diphtheroids. Colonies are circular, entire, convex and approximately 0.5 mm diameter after 24 h at 37°C on blood agar. Colonies are lemon-pigmented and non-haemolytic. Facultatively anaerobic and catalase-positive. Non-lipophilic. Acid is produced from glucose but not maltose, mannitol, ribose, sucrose or D-xylose. Activity for alkaline phosphatase, acid phosphatase, esterase C4 (weak),...
**Corynebacterium capitovis** sp. nov.

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<table>
<thead>
<tr>
<th>Species</th>
<th>Fermentation/oxidation</th>
<th>Lipophilism</th>
<th>Nitrate</th>
<th>Urease</th>
<th>Pyrazinamidase</th>
<th>Alkaline phosphatase</th>
<th>Acid production</th>
<th>Other characteristics</th>
</tr>
</thead>
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<tr>
<td><em>C. capitovis</em></td>
<td>F</td>
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<td></td>
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<td></td>
<td>Glu</td>
<td>Mal, Suc</td>
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<td><em>C. lipophiloflavum</em></td>
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*Negative according to API CORYNE system database.

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*Fig. 1.* Unrooted tree based on 16S rRNA showing the phylogenetic relationships of *Corynebacterium capitovis* sp. nov. Bar, 1% sequence divergence.

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**Table 1.** Characteristics that differentiate *Corynebacterium capitovis* from other veterinary and human clinically relevant *Corynebacterium* species

Glu, glucose; Mal, maltose; Suc, sucrose; v, variable; +, positive; −, negative.

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ester lipase C8, lipase C14 (weak) and leucine arylamidase is detected. No activity is detected for cystine arylamidase, chymotrypsin, α-fucosidase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, β-glucuronidase, α-mannosidase, N-acetyl-β-glucosaminidase, valine arylamidase, pyrazinamidase, phosphoamidase, pyrrolidonyl arylamidase, urease or trypsin. Aesculin and gelatin are not hydrolysed. Nitrate is not 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 (C$_{32}$–C$_{36}$). Isolated from infected head of a sheep. Habitat is unknown. The type strain is CCUG 39779$^T$ (= CIP 106739$^T$).

**Acknowledgements**

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**References**

of Corynebacterium auric平is sp. nov. J Clin Microbiol 37, 3443–3447.


