Corynebacterium pilbarense sp. nov., a non-lipophilic corynebacterium isolated from a human ankle aspirate

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A non-lipophilic coryneform bacterium isolated from an anaerobic Bactec bottle inoculated with an ankle aspirate from a male patient was characterized by phenotypic and molecular taxonomic methods. Chemotaxonomic investigations revealed the presence of short-chain mycolic acids in the cell wall of the bacterium, a feature consistent with members of the genus Corynebacterium. Comparative 16S rRNA gene sequence analysis demonstrated that the isolate displayed 92.0–99.0 % gene sequence similarity with members of the genus Corynebacterium, with Corynebacterium ureicelerivorans as the most closely related phylogenetic species (99.0 % gene sequence similarity). However, the isolate could be genomically separated from C. ureicelerivorans on the basis of DNA–DNA hybridization studies (39.5 % relatedness). Furthermore, the isolate could also be differentiated from C. ureicelerivorans and other species of the genus Corynebacterium on the basis of biochemical properties. Based on both phenotypic and phylogenetic evidence, it is proposed that this isolate be classified as representing a novel species, Corynebacterium pilbarense sp. nov. (type strain IMMIB WACC 658T =DSM 45350T =CCUG 57942T).

The genus Corynebacterium is one of the largest genera within the class Actinobacteria and currently embraces over 82 species, a high proportion of which have been defined over the past decade. Some corynebacteria are well-established pathogens of man and animals, whereas many others occur as part of the normal flora of skin and mucous membranes (Soriano and Fernandez-Roblas, 1988; Coyle & Lipsky, 1990; Colt et al., 1991; Sewell et al., 1995). As some of these diphtheroids show a lipid requirement for growth, which can be supplied by serum or Tween 80, these strains have often been referred to as lipophilic diphtheroids. Attempts to classify these organisms on the basis of biochemical characteristics have been undertaken. The Centers for Disease Control and Prevention (CDC; Atlanta, Georgia, USA) separated lipophilic diphtheroids into groups ANF-1, G-1 and G-2 in addition to groups JK (Corynebacterium jeikeium) and D-2 (Corynebacterium urealyticum) using biochemical tests (Riley et al., 1979; Hollis & Weaver, 1981; Riegel et al., 1992, 1993). After several different taxonomic studies, it was concluded that the strains formerly named as CDC group G-1 represent at least two species, Corynebacterium macginleyi (Riegel et al., 1995) and Corynebacterium accolens (Neubauer et al., 1991). Other glucose-fermenting lipid-requiring strains that do not hydrolyse urea are now known as Corynebacterium tuberculosis (Brown et al., 1984; Feurer et al., 2004). During the course of characterization of bacterial isolates encountered from clinical sources, we found a Gram-positive, pleomorphic to rod-shaped, glucose-fermenting bacterium that did not hydrolyse urea. The API Coryne profile assigned the organism to CDC group G. Further chemotaxonomic and phylogenetic investigations confirmed its assignment to the genus Corynebacterium and indicated that it was different from previously described species of the genus. Based on both phenotypic and phylogenetic evidence, we propose that this strain represents a novel species of the genus Corynebacterium.

Strain IMMIB WACC 658T was isolated from anaerobic Bactec bottles inoculated with ankle aspirate from a 54-year-old man, probably with gout (urate crystals present in the joint fluid) in Pilbara, West Australia. The strain was

The GenBank/EMBL/DBJ accession number for the 16S rRNA gene sequence of strain IMMIB WACC 658T is FN295567.
submitted to the Reference Laboratory of the Institute of Medical Microbiology, University of Bonn, Germany, for identification. The isolate was cultured on Columbia blood agar supplemented with 5% sheep blood to determine its morphological properties. Lipophilic requirement was determined according to standard procedures (Riegel et al., 1994). Fermentation and enzymic tests were performed using the API Coryne, API 20 Strep and the API ZYM systems according to the manufacturer’s instructions (bioMérieux), except for the time of incubation. Enzyme reactions and acid production from carbohydrates, using the API Coryne and API Strep systems, were read after 48 h incubation at 37 °C. The isomeric form of diaminopimelic acid was determined by the methods of Becker et al. (1964) and whole-cell sugars were determined according to the method of Lechevalier (1968). Lipids were extracted using acid methanolyis and mycolic acids were detected with TLC as described by Minnikin et al. (1980). A standard procedure was used to determine the fatty acid profile (Minnikin et al., 1980; Yassin et al., 2007).

For phylogenetic analysis, 16S rRNA genes were amplified by PCR using procedures described previously (Rainey et al., 1996) and directly sequenced using a Taq dye-deoxy terminator cycle sequencing kit (Applied Biosystems) and an automatic DNA sequencer (model 310; Applied Biosystems). The closest relatives of the isolate were determined by performing database searches. Phylogenetic analysis was carried out as previously described (Yassin, 2009) using the ARB-package (Ludwig et al., 2004). DNA–DNA relatedness studies were performed between strain IMMIB WACC 658T and C. ureicelerivorans DSM 4505T. DNA was isolated using a French pressure cell (Thermo Spectronic) and was purified by chromatography on hydroxypatite as described by Cashion et al. (1977). DNA–DNA hybridization was carried out as described by De Ley et al. (1970) with consideration of the modifications described by Huß et al. (1983) using a model Cary 100 Bio UV/VIS-spectrophotometer equipped with a Peltier-thermostatetted 6 × 6 multicell changer and a temperature controller with an in situ temperature probe (Varian).

Strain IMMIB WACC 658T was Gram-positive, non-motile, non-spor-forming and had pleomorphic to short rod-shaped cells. On Columbia blood agar, circular, large colonies (approx. 0.5–2.0 mm diameter) were formed after 24 h incubation at 37 °C. The colonies were non-haemolytic. The organism was facultatively anaerobic and was catalase-positive, but oxidase- and urease-negative. The API Coryne numerical profile was 6100305, which corresponded to the numerical profile for Corynebacterium group G (ID 96.7%). However, the main difference between strain IMMIB WACC 658T and Corynebacterium group G was that the latter includes lipid-requiring strains, whereas strain IMMIB WACC 658T was non-lipophilic. An examination of cell-wall murein acid hydrolysates of the novel strain revealed the presence of meso-diaminopimelic acid as the dibasic amino acid. TLC analysis of cell-wall sugars revealed the presence of galactose and arabinose, i.e. the organism had cell-wall chemotype IV sensu Lechevalier & Lechevalier (1970). Lipid analysis revealed the presence of corynemycolic acids. Examination of the non-hydroxylated long-chain cellular fatty acids of the novel strain showed the presence of straight-chain saturated C16:0 (31.6%), C17:0 (0.5%), C18:0 (10.9%), monounsaturated C16:1ω7c (0.4%), C17:1ω9c (0.1%), C18:1ω9c (56.0%) and cis-9,12-octadecadienoic acid C18:2 (0.4%). Tuberculostearic acid was not detected. These chemotaxonomic characteristics, together with the morphological and biochemical properties of isolate IMMIB WACC 658T, were strongly indicative that the organism belonged to the genus Corynebacterium.

To establish the phylogenetic position of strain IMMIB WACC 658T, its 16S rRNA gene sequence (1486 nt) was determined in this study. Sequence database searches revealed that strain IMMIB WACC 658T was most closely related to species of the genus Corynebacterium (data not shown). Phylogenetic analysis confirmed the placement of strain IMMIB WACC 658T within the genus Corynebacterium. A tree constructed using the neighbour-joining method showing the phylogenetic position of strain IMMIB WACC 658T in relation to members of the genus Corynebacterium is presented in Fig. 1. Comparative 16S rRNA gene sequence analysis unequivocally demonstrated that the isolate represented a hitherto unknown species of the genus Corynebacterium that formed a distinct subline within a subcluster of species including the two subspecies of Corynebacterium afermentans, Corynebacterium coyleae, Corynebacterium mucifaciens and C. ureicelerivorans. Highest sequence similarity values were shown with C. ureicelerivorans (99.0% similarity), the two subspecies of C. afermentans (98.9%), C. coyleae (98.7%), and C. mucifaciens (98.2%). Although the new strain showed close affinity with the aforementioned species, bootstrap resampling analysis showed that this association was not particularly significant. Significantly lower levels of sequence similarity were shown to other members of the genus Corynebacterium (data not shown).

Despite the high sequence similarity between isolate IMMIB WACC 658T and C. ureicelerivorans, the novel strain represented a distinct genomic species. It is now recognized that a 16S rRNA gene sequence similarity range above 98.7–99% should be mandatory for establishing the genomic uniqueness of a novel isolate (Stackebrandt & Ebers, 2006). In addition, the DNA–DNA relatedness study between strain IMMIB WACC 658T and C. ureicelerivorans DSM 4505T clearly demonstrated that the novel strain belonged to a separate genomic species. The mean DNA–DNA relatedness value was 39.5%, a value well below the 70% cut-off point recommended for the assignment of strains to the same genomic species (Wayne et al., 1987). Strain IMMIB WACC 658T could also be distinguished from C. ureicelerivorans using a combination of phenotypic properties (Table 1). In addition, strain IMMIB WACC 658T could be differentiated from the frequently encountered species Corynebacterium amycolatum and...
Corynebacterium minutissimum on the basis of the presence of mycolic acids and absence of tuberculostearic acid, respectively. The novel strain could also be differentiated from Corynebacterium striatum and the less frequently seen Corynebacterium similans on the basis of nitrate reduction.

Thus the 1.0 % 16S rRNA gene sequence divergence between strain IMMIB WACC 658 T and its closest phylogenetic neighbour C. ureicelerivorans, together with the distinctive phenotype of strain IMMIB WACC 658 T (Table 1), clearly demonstrated that this new isolate represents a novel species. Hence, on the basis of both phenotypic and phylogenetic evidence, the new strain merits classification as a novel species of the genus Corynebacterium, for which the name Corynebacterium pilbarense sp. nov. is proposed.

### Description of Corynebacterium pilbarense sp. nov.

Corynebacterium pilbarense (pil.ba.ren’se. N.L. neut. adj. pilbarense pertaining to Pilbara, West Australia, the region from which the strain was isolated).

Cells are Gram-positive, non-spore-forming, non-motile, pleomorphic to short rods. Colonies are creamy, circular and approximately 0.5–2.0 mm in diameter on Columbia blood agar after 24 h incubation at 37 °C. Colonies are non-haemolytic. Facultatively anaerobic, catalase-positive and oxidase-negative. Non-lipophilic. Aesculin, gelatin and hippurate are not hydrolysed. Urease and nitrate reduction are negative. Acid is produced from d-glucose, d-ribose and sucrose. Acid is not produced from L-arabinose, d-fructose, sucrose, or sorbitol. Activity for alkaline and acid phosphatases, leucine arylamidase, pyrazinamidase, pyrrolidonyl arylamidase and naphthol-AS-BI-phospho-esterase is detected. No activity is detected for arginine dihydrolase, esterase C4, ester lipase C8, pyruvate decarboxylase, acetoin production is negative. Mycolic acids are present. Long-chain fatty acids are of the straight-chain saturated and monounsaturated types, with C16:0 and C18:1 predominate; tuberculostearic acid is absent.

The type strain, IMMIB WACC 658 T (≈DSM 45530 T =CCUG 57942 T), was isolated from an anaerobic Bacte vial inoculated with an ankle aspirate from a man who was thought to be suffering from gout.

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References


Physiologic characterization of nine strains isolated from clinical and environmental specimens, and proposal of *Corynebacterium tuberculostearicum* sp. nov. *Int J Syst Evol Microbiol* 54, 1055–1061.


