Potential misidentification of a new *Exiguobacterium* sp. as *Oerskovia xanthineolytica* isolated from blood culture

F. KENNY*, J. XU†, B. C. MILLAR†, R. B. McCLURG* and J. E. MOORE†

Department of Microbiology, Sligo General Hospital, Sligo, Ireland; and †Northern Ireland Public Health Laboratory, Department of Bacteriology, Belfast City Hospital, Belfast BT9 7AD, Northern Ireland, UK

Blood culture of a male patient attending Sligo General Hospital became positive with a coryneform-like Gram-positive rod, and phenotypic identification of the organism by the API Coryne kit (bioMerieux, France) yielded *Oerskovia xanthineolytica* (isolate identifier: 290703/S6645SLIGO). The isolate grew aerobically on blood agar at 37°C. However, given the relatively poor phenotypic identification obtained, the isolate subsequently was forwarded for molecular identification through polymerase chain reaction (PCR) amplification and direct sequencing of a large but partial region of the 16S rRNA gene, as previously described by this group.[1–3]

The resulting sequence obtained (1024 bp) was compared with those stored in the GenBank Data system using FASTA alignment software (www.ebi.ac.uk), and was deposited in GenBank (accession number: AY360351). On BLAST analysis in combination with previously reported criteria used for interpretation of partial 16S rRNA gene sequences,[4] the sequence gave a 99% identification for *Exiguobacterium* sp. (AY205564), bacterium Str61610 (AF227839), 98% identity with *E. aurantiacum* (X70316), 96% identity with *E. undae* (AJ344151) and 92% identity with *Bacillus hackensackii* (AY148429), as illustrated in Figure 1.

Although the isolated organism was not believed to be clinically significant, it presented difficulties in its correct and reliable phenotypic identification and gave the identification of *O. xanthineolytica* with the API Coryne scheme. At present, there are four species described in the genus *Exiguobacterium*, including *E. acetylicum*, *E. antarcticum*, *E. aurantiacum* and *E. undae*.

The genus *Exiguobacterium* was first described by Collins *et al*.[5] in 1983, with *E. aurantiacum* as the type strain, isolated from potato processing effluent. Previously, the organism has been misidentified as the former CDC coryneform group A-5; however, cell wall and cellular fatty acid analyses clearly separate this genus from other genera most likely to be misidentified, particularly *Microbacterium* spp.[6]

Until recently, the clinical significance of members of this genus was confined to a few sporadic reports of the organism being found in various clinical sources, including skin, wounds and cerebrospinal fluid.[7] However, a recent report has suggested that *Exiguobacterium* sp. is an important agent in periodontal disease.[8]

This short report highlights the benefits of the integration of a sequence-based typing approach employing partial regions of the 16S rRNA gene in the identification of difficult-to-identify bacterial isolates. Continued routine adoption of such techniques by clinical diagnostic laboratories may prove beneficial for the correct identification of bloodborne infections, as well as for the correct epidemiological characterisation of unusual causal agents of bacteraemia.

Correspondence to: Dr. John E. Moore
Northern Ireland Public Health Laboratory, Department of Bacteriology, Belfast City Hospital, Lisburn Road, Belfast BT9 7AD, Northern Ireland.
Email: jemoore@niphl.dnet.co.uk

References

1 Millar BC, Xu J, Moore JE. Risk assessment models and contamination management: implications for broad-range ribosomal DNA PCR as a diagnostic tool in medical bacteriology. *J Clin Microbiol* 2002; **40:** 1575–80.

2 Xu J, Smyth CL, Buchanan JA *et al*. Employment of 16S rDNA gene sequencing techniques to identify culturable environmental eubacteria in a tertiary referral hospital. *J Hosp Infect* 2004; **57**: 52–8.

3 Campbell PW 3rd, Phillips JA 3rd, Heidecker GJ, Krishnamani MR, Zahorchak R, Stull TL. Detection of *Pseudomonas (Burkholderia) cepacia* using PCR. *Pediatr Pulmonol* 1995; **20:** 44–9.

4 Goldenberger D, Kunzli A, Vogt P, Zbinden R, Altwegg M. Molecular diagnosis of bacterial endocarditis by broad-range PCR amplification and direct sequencing. *J Clin Microbiol* 1997; **35:** 2733–9.

5 Collins MD, Lund BM, Farrow JAE, Schleifer KH. Chemotaxonomic study of an alkalophilic bacterium, *Exiguobacterium aurantiacum* gen. nov., sp. nov. *J Gen Microbiol* 1983; **129:** 2037–42.

6 Funke G, von Graevenitz A, Clarridge JE 3rd, Bernard KA. Clinical microbiology of coryneform bacteria. *Clin Microbiol Rev* 1997; **10:** 125–59.

7 Hollis DG, Weaver RE. Gram-positive organisms: a guide to identification. Special Bacteriology Section. Atlanta: Centers for Disease Control, 1981.

8 Zijnge V, Harmsen HJ, Kleinfelder JW, van der Rest ME, Degener JE, Welling GW. Denaturing gradient gel electrophoresis analysis to study bacterial community structure in pockets of periodontitis patients. *Oral Microbiol Immunol* 2003; **18:** 59–65.

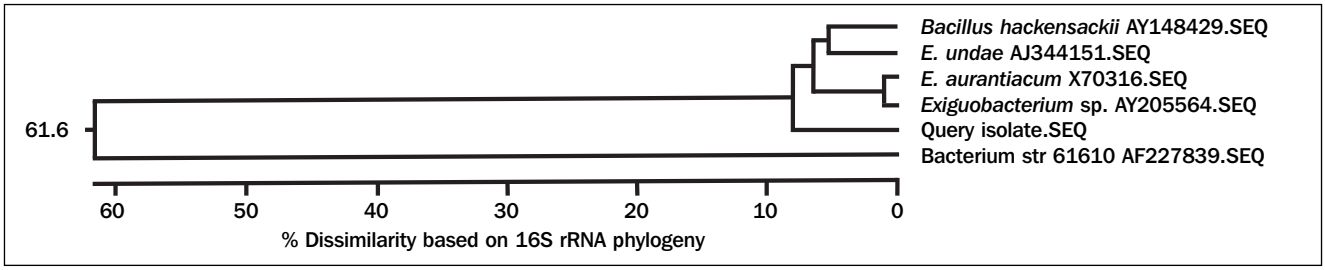

Fig. 1. Phylogenetic relatedness of query isolate to closest neighbours based on 16S rRNA homology.