



Tipo	Periódico
Título	The applicability of gene sequencing and MALDI-TOF to identify less common gram-negative rods (<i>Advenella</i> , <i>Castellaniella</i> , <i>Kaistia</i> , <i>Pusillimonas</i> and <i>Sphingobacterium</i>) from environmental isolates
Autores	Débora Sant' Anna, Jorge Luiz Mello Sampaio, Lais Roberta Deroldo Sommaggio, Dânia Elisa Christofolletti Mazzeo, Maria Aparecida Marin-Morales, Fernando Augusto Lima Marson, Carlos Emílio Levy
Autor (es) USF	Fernando Augusto Lima Marson
Autores Internacionais	
Programa/Curso (s)	Programa de Pós-Graduação Stricto Sensu em Ciências da Saúde
DOI	10.1007/s10482-019-01333-0
Assunto (palavras chaves)	16S rRNA; <i>Advenella</i> ; <i>Castellaniella</i> ; <i>Kaistia</i> ; <i>Pusillimonas</i> ; <i>Sphingobacterium</i>
Idioma	Inglês
Fonte	Título do periódico: Antonie Van Leeuwenhoek (Gedruckt) ISSN: 0003-6072 Volume/Número/Paginação/Ano: v. 113, p. 233-252, 2020
Data da publicação	27 September 2019
Formato da produção	Digital https://doi.org/10.1007/s10482-019-01333-0
Resumo	Our aim was to identify less common non-fermenting gram-negative rods during the bioremediation process. Five genera were found: <i>Advenella</i> , <i>Castellaniella</i> , <i>Kaistia</i> , <i>Pusillimonas</i> and <i>Sphingobacterium</i> , for a total of 15 isolates. Therefore, we evaluated the applicability of four methods currently available for bacteria identification: (1) conventional biochemical methods, (2) the VITEK®-2 system, (3) MALDI-TOF mass spectrometry and (4) 16S rRNA gene sequencing. The biochemical methods and the VITEK®-2 system were reliable only for the <i>Sphingobacterium</i> isolate and solely at the genus level. Both MALDI-TOF mass spectrometry platforms (Bruker and VITEK® MS) did not achieve reliable identification results for any of these genera. 16S rRNA gene sequencing identified eight isolates to the species level but not to the subspecies level, when applicable. The remaining seven isolates were reliably identified through 16S rRNA gene sequencing to the genus level only. Our findings suggest that the detection and identification of less common genera (and species) that appeared at certain moments during the bioremediation process can be a challenge to microbiologists considering the most used techniques. In addition, more studies are required to confirm our results.
Fomento	