

VAC_18 - Difficulties in identifying Actinomycetota strains isolated from an immunobiological producer in Rio de Janeiro by VITEK 2

Nathalia Gonçalves Santos Caldeira¹; Maria Luiza Soares de Souza¹; Luciana Veloso da Costa¹; Viviane Zahner²; Marcelo Luiz Lima Brandão¹.

¹Fiocruz/Bio-Manguinhos

²Fiocruz/IOC

Introduction: Actinomycetota is a Phylum that comprehends Gram-positive bacteria that exhibits a wide morphological variety of coccoid or coccoid rod to fragmented hyphal forms or branched mycelium. These characteristics cause great difficulty in classifying these microorganisms using Gram staining, as they can easily be confused with the Bacillaceae family. The semi-automated VITEK®2 system, which brings together a series of biochemical tests, has been used for microbial identification in the pharmaceutical industry. However, methodologies based on Gram, as is the case with this system, can result in misidentifications if the card chosen for analysis is wrong.

Objectives: To evaluate the Actinomycetota rods identification using the VITEK®2 system. Identification by full 16S rRNA gene sequencing, which is considered the gold standard for species delineation, was used as a standard.

Methodology: Twenty-nine isolates were selected from an immunobiological producer in Rio de Janeiro, obtained from 2013 to 2020. Identification by VITEK®2 was carried out according to the manufacturer's instructions, using GP and BCL cards, whose databases do not include Actinomycetota phylum bacteria. For full 16S rRNA gene sequencing, the MicroSEQ™ Full Gene 16S rDNA kit was used, according to the manufacturer's instructions.

Results: Nineteen (65.5%) isolates were identified at the genus level and 10 (34.5%) at the species level of Actinomycetota, with the use of full 16S rRNA gene sequencing. VITEK®2, as expected, did not identify 15 (51.7%) and 17 (58.6%) isolates with the GP and BCL card, respectively. However, both cards led to misidentifications. For seven (24.1%) and 12 (41.4%) isolates, with GP and BCL card, respectively, the identification reached genera/species belonging to the Phylum Bacillota, which differed from the standard identification.

Conclusion: We can conclude that, with the use of VITEK®2 with GP and BCL cards, Actinomycetota rods can be misidentified as rods from the Phylum Bacillota, which can compromise preventive and corrective actions in the industry.

Keywords: Actinomycetota; VITEK®2; 16S rRNA gene sequencing