ORT_10 - Identification of *Acinetobacter* species isolated in a pharmaceutical industry by phenotypical characterization and 16S rRNA sequencing

Samara Verly da Silva¹; Luciana Veloso da Costa¹; Rebeca Vitória da Silva Lage de Miranda¹; Cristhiane Moura Falavina dos Reis¹; Lygia Maria Paulo da Silva Braga¹; Josiane Machado Vieira Mattoso¹; Igor Barbosa da Silva¹; Maria Helena Simões Villas Bôas²; Marcelo Luiz Lima Brandão¹; Luiza Vasconcellos¹. ¹Fiocruz/Bio-Manguinhos;

²Fundação Oswaldo Cruz (Fiocruz).

Introduction: Microorganisms of the genus *Acinetobacter* belong to the *Moraxellaceae* family and contains more than 70 described species. The most clinically relevant species of the genus *Acinetobacter* belong to the *Acinetobacter calcoaceticus–baumannii* complex. The genus can be found in water, animal and soil, and the isolation in pharmaceutical industries environments was already reported. Information retrieved from microorganism identification can be extremely relevant in investigating sources of microbiological contamination from a product or process, especially when specified limits are exceeded.

Objective: The aim of this study was to identify strains isolated from a pharmaceutical industry that has been previously identified by Vitek[®] 2 as "*Acinetobacter baumannii* group" by 16S rRNA sequencing and compare the results.

Methodology: Thirty-eight strains isolated from different types of samples from 2015 to 2020 were selected. Strains were identified by 16S rRNA gene Sanger sequencing analysis using MicroSEQTM Full Gene 16S rDNA kit and analyzed on the 3500 Series Genetic Analyzer. The sequences were processed using DNA Star LaserGene SeqMan software v.7.0.0, and identification results were obtained from the website https://www.ezbiocloud.net/. Only results retrieved with identification \geq 96% were considered valid and only those species whose identification was \geq 98.7% were considered identified.

Results: Twenty-eight (73.8%) were identified as *A. seifertii/ pitti/ nosocomialis*, four (10.5%) as *A. seifertii/ pitti/ nosocomialis/ lactucae*, four (10.5%) as *A. baumannii*, one (2.6%) as *A. seifertii/ nosocomialis*, and one (2.6%) as *A. vivianii/ courvalini*. As "Acinetobacter baumannii group" identified by Vitek 2 includes the species *A. baumannii*, *A. calcoaceticus*, *A. nosocomialis*, and *A. pittii*, only the *A. vivianii/ courvalini* strain was incorrectly identified.

Conclusion: Vitek® 2 identification of *Acinetobacter baumannii* group presented 97.4% of sensitivity comparing to 16S rDNA sequencing. The last method was able to identify just four (10.5%) strains at the species level (*A. baumannii*). Therefore, the use of other methodologies are necessary in order to improve *Acinetobacter* species identification in pharmaceutical industries.

Keywords: Acinetobacter baumannii complex; Microbiological control; 16S rRNA gene