**ORT_23 - Polyphasic characterization of Burkholderia cepacia complex strains isolated from a pharmaceutical industry facility**

Giorgio Silva de Santana[1]; Alícia Ribeiro Aguiar[1]; Francisca Letícia de Sousa Sales[1]; Rebeca Vitória da Silva Lage de Miranda[1]; Talita Bernardo Valadão[1]; Luciana Veloso da Costa[1]; Marcelo Luiz Lima Brandão[1].
[1]Fiocruz/Bio-Manguinhos

**Introduction:** The microbial contamination is one of the main risks associated with the production of medicines. The lipopolysaccharide (endotoxin) produced by bacteria from *Burkholderia cepacia* complex (CBc) is very potent, and the presence of these bacteria in the production chain in undesired. Therefore, the correct identification assists in the investigation of possible sources of contamination, enabling preventive actions.

**Objectives:** The aim of this study was to characterize CBc strains isolated from samples collected at different stages of the production chain along the years in an immunobiological facility, through their phenotypic, proteomic, and genotypic profiles.

**Methodology:** A total of 354 strains previously identified by VITEK 2 in CBc were evaluated. The 47 biochemical tests were compiled and profiles with similarity ≥ 85% were grouped into the same cluster. One strain from each cluster was selected and analysis by MALDI Biotyperand 16S rDNA gene sequencing using Sanger method. The sequencing results were obtained by comparison with EZBioCloud database.

**Results:** The 354 lineages identified by VITEK 2 were categorized into 47 groups and 15 singletons, presenting a total of 256 distinct profiles encoded from I-CCLVI. The MALDI-TOF/MS identified 41 lineages with four species as possibilities: *B. cepacia* (75.0%), *B. cenocepacia* (15.4%), *B. lata* (5.8%), and *B. pyrrocinia* (3.8%). Until now, complete sequencing of the 16S rRNA gene was performed in 24 strains, which presented 27 species possibilities: *B. aenigmatica* (4.01%), *B. ambifaria* (4.01%), *B. anthina* (4.01%), *B. arboris* (4.01%), *B. cenocepacia* (4.01%), *B. cepacia* (4.01%), *B. contaminans* (4.01%), *B. diffusa* (4.01%), *B. dolosa* (4.01%), *B. lata* (4.01%), *B. latens* (4.01%), *B. metallica* (4.01%), *B. multivorans* (4.01%), *B. orbicola* (4.01%), *B. puraquae* (4.01%), *B. pyrrocinia* (4.01%), *B. savannae* (4.01%), *B. seminalis* (4.01%), *B. stabilis* (4.01%), *B. territorii* (4.01%), *B. ubonensis* (4.01%), *B. vietnamiensis* (4.01%), *B. stagnalis* (3.83%), *B. catarinensis* (3.64%), *B. glumae* (1.82%), *B. pseudomultivorans* (1.82%), and *B. oklahomensis* (0.73%).

**Conclusion:** The three methodologies applied (VITEK2, MALDI-TOF/MS and 16S rRNA sequencing) were insufficient to identify the CBc at species level. So, other methods must be implemented to achieve this goal. As MALDI Biotyper permits the database expansion, the inclusion of this strains in the database after its species identification, can be an alternative for a cheap and fast identification of CBs strains isolated from pharmaceutical facilities.

**Keywords:** *Burkholderia cepacia* complex; Identification; Pharmaceutical industry