

ORT_11 - Diversity of *Burkholderia cepacia complex* found in pharmaceuticals and genotyped by Multi-locus Sequence Typing

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Introduction: The *Burkholderia cepacia complex* is a group of Gram-negative bacteria comprising 9 species. They are related to human infections in immunocompromised and patients with cystic fibrosis (CF). It has clinical relevance due to antibiotic resistance, biofilm formation and ability to grow in pharmaceuticals.

Objective: The aim of this study was to evaluate the *in-silico* data regarding *Burkholderia cepacia complex* strains characterized by multi-locus sequence typing (MLST) available in the PubMLST database isolated between 1944 and 2021.

Methodology: The strains isolated from clinical or industrial samples with complete MLST allelic profile in the database (n=2,726) were analyzed using eBURST algorithm. Simpson's index (SI) was applied to calculate the MLST resolving power for typing.

Results: The strains were assigned to 1,877 STs, a ratio of ~1.01 strains/ST showing high genetic diversity, and the calculated SI was 0,997 indicating that MLST is as efficient typing tool for these pathogens. These species are present in all continents, being the majority in America (n = 1,713), followed by Europe (n = 1,316), Oceania (n = 664), Asia (n = 380) and Africa (n = 61). The vast majority of the eighty-five strains from industrial origin were isolated from Europe (n = 42). Among them, the STs 3, 51, 98, 102, 103, 200, 241, 250, 333, 338, 339, 482, 620, 848 and 1078 were also associated with clinical cases. *B. contaminans* (ST102), that was isolated from a pharmaceutical solution in Argentina, was the only industrial origin ST that has already been related to clinical cases in Brazil, being found in the blood of patients involved in an outbreak of bacteremia in a hemodialysis unit, and the water was considered the main source of contamination. After eBURST, 564 clonal complexes (CC) were formed, 2,726 STs formed 109 groups with double-locus variants and 455 were identified as singletons. ST200, 322, 328, 840, 1893 and 2055 formed a CC with STs already associated with clinical cases.

Conclusion: The presence of clinical origin STs or STs that share the same CC with clinical origin STs in these products warns to the need for further investigation, as these microorganisms may be vehicles of contamination, representing a risk.

Keywords: Epidemiology; *Burkholderia cepacia complex*; MLST