

TITLE: DIVERSITY OF *Pseudomonas aeruginosa* ISOLATED BETWEEN 1938 and 2021 AND GENOTYPED BY MULTI-LOCUS SEQUENCE TYPING

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ABSTRACT:

Pseudomonas aeruginosa is considered a waterborne pathogen with clinical relevance due to multi-drug resistance, biofilm production and other virulence factors. Clinical syndromes caused by this bacterium included urinary infection, dermatitis and systemic diseases. The aim of this study was to evaluate the *in silico* data regarding *P. aeruginosa* strains (n= 7,786) isolated and characterized by multi-locus sequence typing (MLST) available in the PubMLST database isolated between 1938 and 2021. Simpson's index (SI) was applied to calculate the MLST resolving power for typing. The strains with complete MLST allelic profile in the database (n= 7,593) were analyzed using eBURST algorithm. The strains were assigned to 3,168 STs, a ratio of ~2.5 strains/ST showing high genetic diversity, and the calculated SI was 0.992 indicating that MLST is an efficient tool for typing of *P. aeruginosa*. After eBURST analysis, 681 clonal complexes (CC) were formed, 3,185 STs formed 192 groups with double-locus variant CCs that shared five or more allelic profiles, and 489 were identified as singletons. This species is present on all continents, with majority from Europe (n=2,456) followed by America (n=1,201), Asia (n=858), Oceania (n=712) and Africa (n=193). Regarding South America, Brazil was the country with the most isolates (n=215, 60.6%). Most Brazilian isolates (n=146, 68%) were from clinical origin. Eight strains were isolated from drinking water in Rio de Janeiro: ST 252 (n=1), ST 1417 (n=1), ST 1605 (n=2), ST 2502 (n=1), ST 2620 (n=1), ST 3078 (n=1) and ST 3312 (n=1). ST 3078 and ST 252 were grouped in two different CCs, and the remaining STs were singletons. ST 252 formed a CC with other 13 STs, being eight associated with human infections. ST 252 was also isolated from a clinical sample in Brazil and other countries. ST 1417 was previously isolated from sputum in Japan and Malaysia. ST 3078 is part of the same CC as ST 1703, that was isolated from a bronchial lavage in France. The presence of STs involved in clinical infections or in the same CC of STs involved in clinical infections found in drinking water needs further investigation as they may be possible vehicles of contamination representing a risk for more vulnerable groups. Molecular characterization represents great importance so that investigations and pathogenic strain routes of contamination can be defined, and control measures can be better planned and implemented.

Keywords: *Pseudomonas aeruginosa*, MLST, epidemiology, molecular characterization.

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