

DIVERSITY OF STENOTROPHOMONAS MALTOPHILIA ISOLATED BETWEEN 1958 AND 2020 AND GENOTYPED BY MULTI-LOCUS SEQUENCE TYPING

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RESUMO

Stenotrophomonas maltophilia is an opportunistic pathogen associated with respiratory infections in humans. This microorganism has clinical relevance due to the emergence of multiresistance strains decreasing susceptibility to common use antibiotics. In addition, *S. maltophilia* produces biofilm that provides more protection against several external threats and makes it difficult to remove it from surfaces. The objective of this study was to evaluate the *in silico* data regarding *S. maltophilia* strains (n=931) isolated and characterized by multi-locus sequence typing (MLST) available in the PubMLST database isolated between 1958 and 2020 (last access 22/01/2021). The strains with complete MLST allelic profile in the database (n=929) were analyzed using eBURST algorithm. The Simpson's index (SI) was applied to calculate the MLST resolution power for typing *S. maltophilia* strains. The 929 strains were assigned to 674 STs, a ratio of 1.4 strain/ST, and the calculated SI was 0.998. This specie is present on five continents, the majority (n=417, 44.8%) from Asia followed by Europe (n=243, 26.1%), America (n=212, 22.8%), Oceania (n=51, 5.5%), Africa (n=7, 0.75%) and one (0.1%) from an unknown country. Regarding the source of isolation, 811 (87.1%) were from humans, 67 (7.1%) from environment, 39 (4.1%) from animal, eight (0.8%) from clinical environment, and six (0.6%) from unknown sources. After eBURST analysis, 674 STs formed 90 groups (n=505) with single-locus variant (SLV) and/or double-locus variant clonal complexes which shared five or more allelic profiles, and 331 STs (n=424) were identified as singletons. Five hundred and eighty (86.0%) STs were associated with human infections, being isolated from clinical specimens as blood, sputum, conjunctivitis, vascular ulcer and surgical wound. Regarding America, Brazil was the only South America country with deposited strains (n=10, 1.1%). The strains were isolated in the southeast and northeast region and seven STs were identified: ST144 (n=1), ST172 (n=1), ST173 (n=1), ST264 (n=4), ST473 (n=1), ST474 (n=1), and ST552 (n=1). Four STs (ST144, ST172, ST173, and ST264) were isolated from human infections in São Paulo and Rio de Janeiro and are unique in the database. ST473, ST474 and ST552 were isolated from animal and environmental sources. ST144 belongs to Group 31 and it is the dominant ST. It is a SLV of ST107 and ST408, both isolated from humans in South Korea and China, respectively. The others STs were identified as singletons and are unique in the database. ST264 was the most prevalent in Brazil and was isolated from the sputum of a single non-hospitalized cystic fibrosis

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pediatric patient in Rio de Janeiro, and several resistance genes were identified. In conclusion, *S. maltophilia* strains showed a high genetic diversity when characterized by MLST that is a powerful tool for epidemiological investigations. Molecular characterization represents great importance so that investigations and pathogenic strains routes of contamination can be defined and control measures can be better planned and implemented.

PALAVRAS-CHAVE: epidemiology, M L S T , molecular characterization, *Stenotrophomonas maltophilia*.

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