PHENOTYPICAL AND MOLECULAR CHARACTERIZATION OF *Stenotrophomonas maltophilia* STRAINS ISOLATED FROM PATIENTS DURING COVID-19 PANDEMIC

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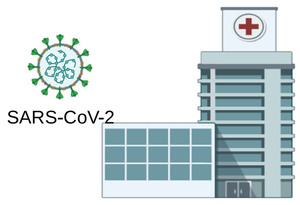
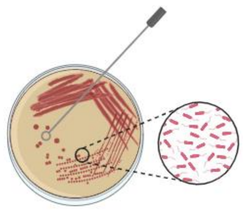
INTRODUCTION

Antimicrobial resistance threatens the effective prevention and treatment of an ever-increasing range of infections caused by bacteria (WHO, 2020). During COVID-19 pandemic, the incidence of bacterial infection in hospitalized COVID-19 patients was high, especially those caused by multidrug-resistant Gram-negative bacteria as *Stenotrophomonas maltophilia* (CHONG et al., 2021). *S. maltophilia* is an emerging multidrug-resistant global opportunistic pathogen, being more commonly associated with respiratory infections in humans. The aim of this study was to characterize *S. maltophilia* strains isolated from hospitalized patients during COVID-19 pandemic.

METHODOLOGY



February-September/2021
Rio de Janeiro/RJ



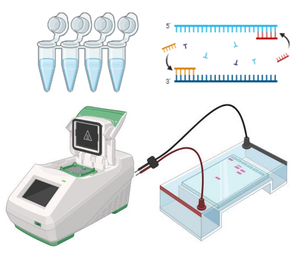
S. maltophilia (n=9)

- nine patients (8 males and 1 female) with ages varying from 64 to 86 years;
- two with COVID-19 co-infection, five only with *S. maltophilia*;
- Clinical specimens included tracheal swab (n=4), blood (n=2), sputum (n=1), lung mass (n=1), and soft tissue fragment (n=1).

Identification

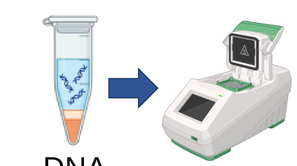
VITEK® 2

VITEK® MS

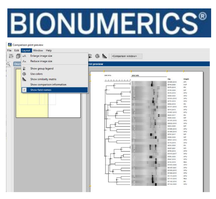


PCR-23S rRNA
(Whitby et al., 2000)

Typing (ERIC-PCR)



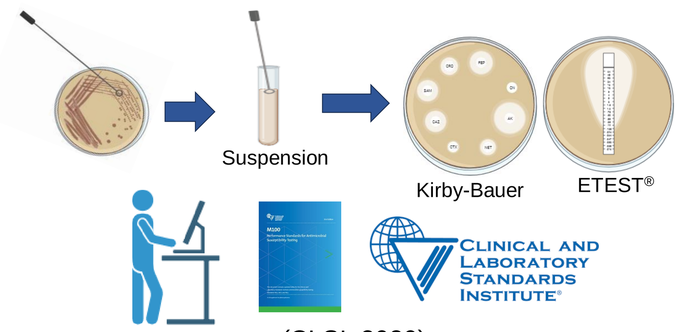
DNA extraction → PCR → Eletroforesis



Dendrogram (UPGMA)

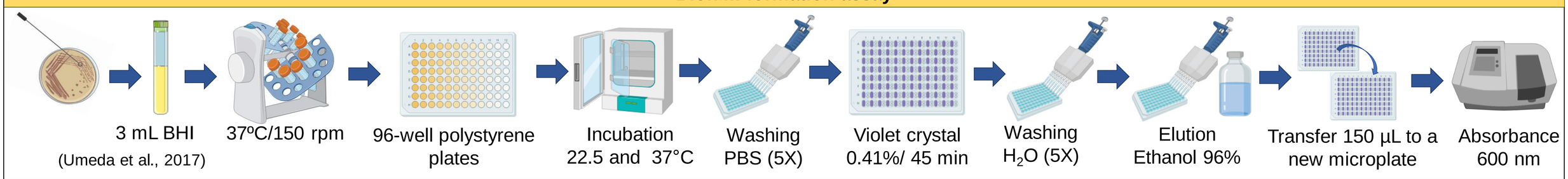
(Versalovic et al., 1991)

Antimicrobial susceptibility test



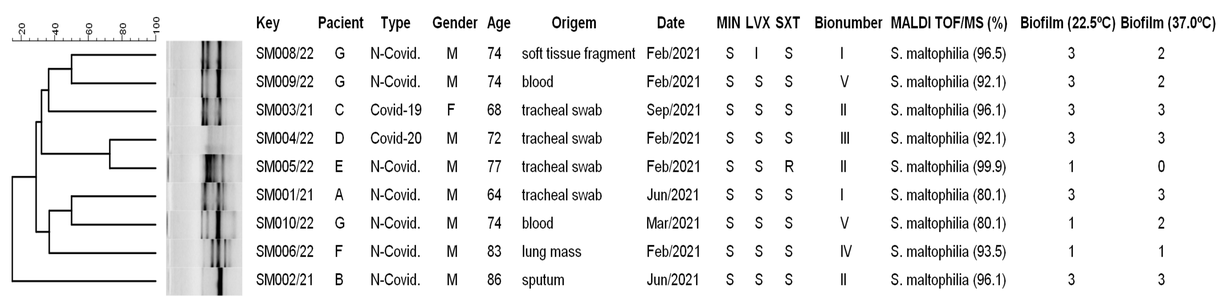
(CLSI, 2020)

Biofilm formation assay



RESULTS AND CONCLUSIONS

All strains were identified as *S. maltophilia* by VITEK®2 and MALDI-TOF (Fig 1) and were positive using 23S PCR. Nine distinct band profiles were obtained by ERIC-PCR (Fig. 1). All strains were susceptible to cefiderocol, minocycline, and resistant to ceftazidime. Five (55.5%) were resistant to ticarcillin-clavulanate and four (44.5%) susceptible, increased exposure. Three (33.3%) were resistant to chloramphenicol and six (66.7%) intermediate. One (11.1%) strain was resistant to trimethoprim-sulfamethoxazole and one (11.1%) to levofloxacin. Six (66.7%) strains were classified as strongly adherent and three were weakly adherent at 22.5ºC. Four (44.5%) strains were classified as strongly, three (33.3%) as moderately, one weakly and one non-adherent at 37.0°C (Fig 2).



Key	Pacient	Type	Gender	Age	Origem	Date	MIN	LVX	SXT	Bionumber	MALDI TOF/MS (%)	Biofilm (22.5ºC)	Biofilm (37.0ºC)
SM008/22	G	N-Covid.	M	74	soft tissue fragment	Feb/2021	S	I	S	I	S. maltophilia (96.5)	3	2
SM009/22	G	N-Covid.	M	74	blood	Feb/2021	S	S	S	V	S. maltophilia (92.1)	3	2
SM003/21	C	Covid-19	F	68	tracheal swab	Sep/2021	S	S	S	II	S. maltophilia (96.1)	3	3
SM004/22	D	Covid-20	M	72	tracheal swab	Feb/2021	S	S	S	III	S. maltophilia (92.1)	3	3
SM005/22	E	N-Covid.	M	77	tracheal swab	Feb/2021	S	S	R	II	S. maltophilia (99.9)	1	0
SM001/21	A	N-Covid.	M	64	tracheal swab	Jun/2021	S	S	S	I	S. maltophilia (80.1)	3	3
SM010/22	G	N-Covid.	M	74	blood	Mar/2021	S	S	S	V	S. maltophilia (80.1)	1	2
SM006/22	F	N-Covid.	M	83	lung mass	Feb/2021	S	S	S	IV	S. maltophilia (93.5)	1	1
SM002/21	B	N-Covid.	M	86	sputum	Jun/2021	S	S	S	II	S. maltophilia (96.1)	3	3

Figure 1. Cluster analysis of *S. maltophilia* strains (n=9) patterns resolved by ERIC-PCR. The dendrogram was evaluated using Dice coefficient and Unweighted Pair-Group Method with Arithmetic mean (UPMGA) with BioNumerics software. Legend: Male (M), Female (F), Susceptible (S), Intermediate (I), Resistant (R), Levofloxacin (LVX), Minocycline (MIN), Sulfamethoxazole-trimethoprim (SXT), Matrix-assisted laser desorption/ionization time-of-flight (MALDI TOF/MS).

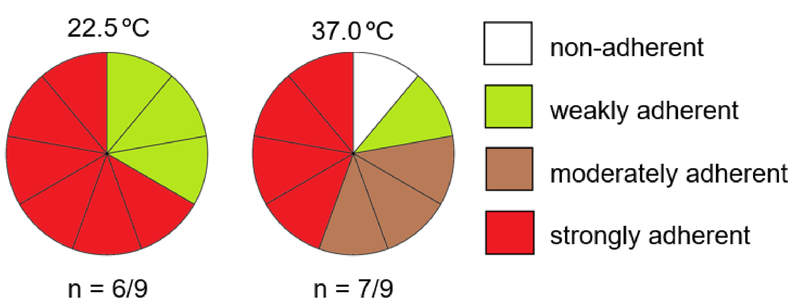


Figure 2. Biofilm formation of *S. maltophilia* strains (n=9) in 96-well polystyrene plates in at 22.5 and 37.0ºC.

The Antimicrobial susceptibility test was similar between strains, neither with they were from patients co-infected with COVID-19 or not. All strains presented different ERIC-PCR profiles, indicating that they were not clonal, and possible have different origins. Considering the necessity to use broad-spectrum antibiotics in cases of bacterial infections, especially in cases of co-infection with COVID-19, the resistant found to four classes of antimicrobial agents (β-lactam, cephems, folate pathway antagonists, and fluoroquinolones) is worrisome. In conclusion, the continuing monitoring of the antimicrobial susceptibility profile and clonality of *S. maltophilia* is important to understand the epidemiology of this bacteria.

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