FOURIER-TRANSFORM INFRARED SPECTROSCOPY FOR TYPING *Pseudomonas aeruginosa* STRAINS ISOLATED FROM PATIENTS DURING COVID-19 PANDEMIC

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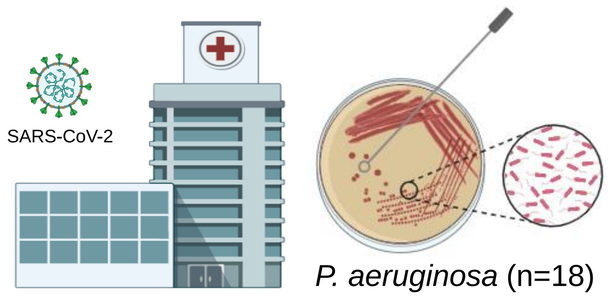
INTRODUCTION

Antimicrobial resistance threatens the effective prevention and treatment of an ever-increasing range of infections caused by bacteria. 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 such as *Pseudomonas aeruginosa*, an emerging multidrug-resistant global opportunistic pathogen, more commonly associated with respiratory infections in humans. The aim of this study was to typing *P. aeruginosa* strains (n=18) isolated from hospitalized patients during COVID-19 pandemic.

METHODOLOGY



P. aeruginosa (n=18)

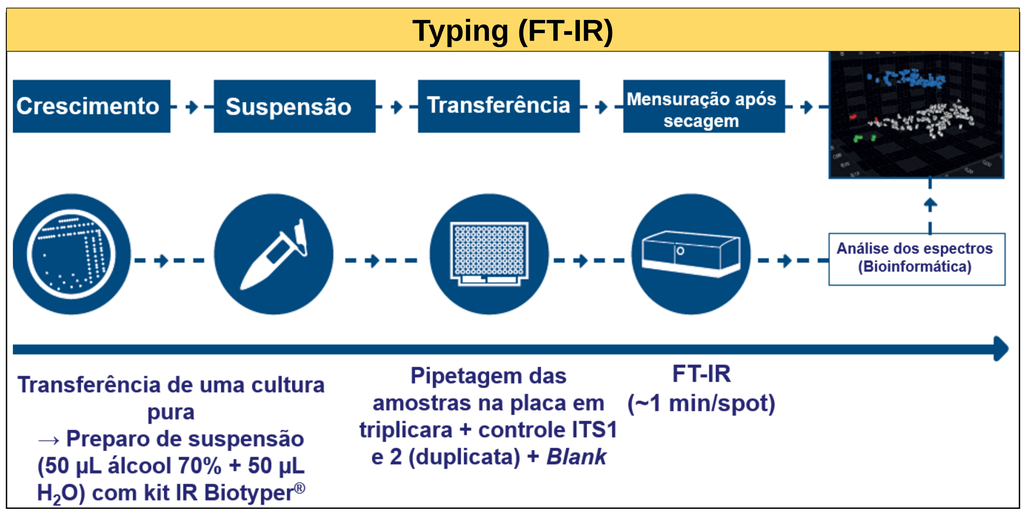
July/2021 to March/2022
Rio de Janeiro/RJ

- 17 patients (11 males and seven females) with ages varying from 45 to 97 years
- 12 with COVID-19 co-infection, four only with *P. aeruginosa*, and two found during Hospital Infection Prevention and Control (HIPC) monitoring;
- Clinical specimens included tracheal secretion (n=9), urine (n=6), rectal swab (n=2), and oral swab (n=1).

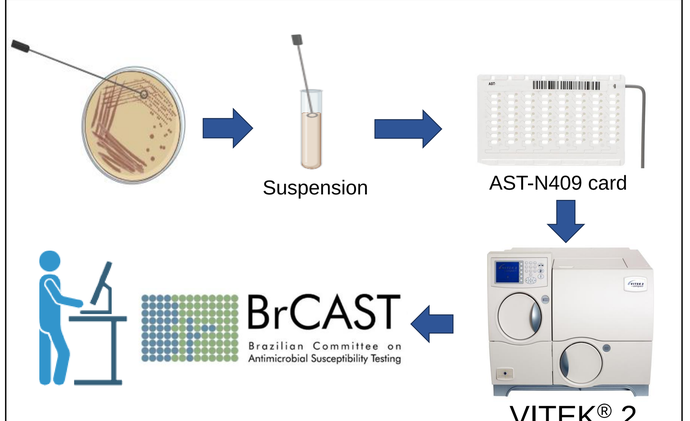
Identification

VITEK® 2 | VITEK® MS | MALDI Biotyper®

Typing (FT-IR)

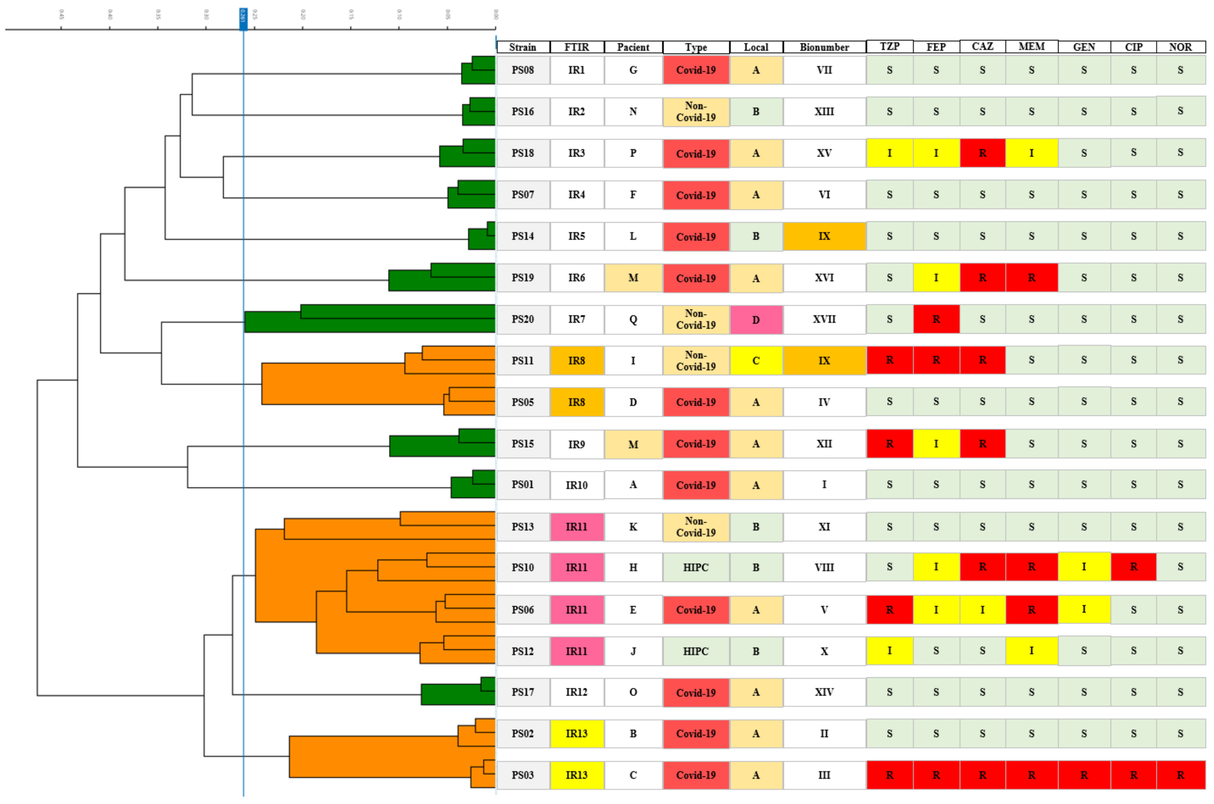


Antimicrobial susceptibility test



RESULTS AND CONCLUSIONS

Thirteen FTIR profiles were obtained with a cut-off of 0.261, a ratio of 1.54 strain/profile (Figure 1). From the three clusters formed, the one that compresences IR13 profile had only COVID-19 co-infections strains from the same local, indicating that they possibly had the same common source. Strains from the IR11 cluster were isolated from HIPC samples and other locals, indicating that this clone may be present in the hospital environment. No correlation could be inferred from the two strains of the IR8 profile. Nine (50.0%) strains were susceptible to all antibiotics tested. No association between the AST and FTIR profiles was observed since resistance and susceptible strains were found in the same cluster. Considering the necessity to use broad-spectrum antibiotics in cases of *P. aeruginosa* infections, the resistance found to four classes of antimicrobial agents (β-lactam, cephems, folate pathway antagonists, and fluoroquinolones) is worrisome. In conclusion, the FTIR seems to be an interesting tool for the evaluation of the clonality of *P. aeruginosa* and a helpful approach to understanding the epidemiology of this bacteria.



Strain	FTIR	Pacient	Type	Local	Bionumber	TZP	FEP	CAZ	MEM	GEN	CIP	NOR
PS08	IR1	G	Covid-19	A	VII	S	S	S	S	S	S	S
PS16	IR2	N	Non-Covid-19	B	XIII	S	S	S	S	S	S	S
PS18	IR3	P	Covid-19	A	XV	I	I	R	I	S	S	S
PS07	IR4	F	Covid-19	A	VI	S	S	S	S	S	S	S
PS14	IR5	L	Covid-19	B	IX	S	S	S	S	S	S	S
PS19	IR6	M	Covid-19	A	XVI	S	I	R	R	S	S	S
PS20	IR7	Q	Non-Covid-19	D	XVII	S	R	S	S	S	S	S
PS11	IR8	I	Non-Covid-19	C	IX	R	R	R	S	S	S	S
PS05	IR8	D	Covid-19	A	IV	S	S	S	S	S	S	S
PS15	IR9	M	Covid-19	A	XII	R	I	R	S	S	S	S
PS01	IR10	A	Covid-19	A	I	S	S	S	S	S	S	S
PS13	IR11	K	Non-Covid-19	B	XI	S	S	S	S	S	S	S
PS10	IR11	H	HIPC	B	VIII	S	I	R	R	I	R	S
PS06	IR11	E	Covid-19	A	V	R	I	I	R	I	S	S
PS12	IR11	J	HIPC	B	X	I	S	S	I	S	S	S
PS17	IR12	O	Covid-19	A	XIV	S	S	S	S	S	S	S
PS02	IR13	B	Covid-19	A	II	S	S	S	S	S	S	S
PS03	IR13	C	Covid-19	A	III	R	R	R	R	R	R	R

Figure 1. Dendrogram obtained by clustering the FTIR spectra of *P. aeruginosa* (n=18). The vertical dashed line represents the cut-off value. Patient identification, type of sample, local, VITEK®2 bionumber profile, and antimicrobial susceptibility profile are given for each strain. FTIR: Fourier-Transform Infrared Spectroscopy; TZP: piperacillin-tazobactam; FEP: cefepime; CAZ: ceftazidime; MEM: meropenem; GEN: gentamicin; CIP: ciprofloxacin; NOR: norfloxacin.

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ACKNOWLEDGMENT

This study was financed in part by CNPq: “Grant Chamada CNPq/MCTI/FNDCT Nº 18/2021 - Faixa A - Grupos Emergentes N.º do Processo 407747/2021-4”. This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001. This project has been approved by the HFAG Research Ethics Committee and is registered on the Brazil Platform with CAAE code: 55303721.0.0000.5250.