TITLE: VALIDATION OF A MALDI-TOF MS METHOD FOR SARS-COV-2 DETECTION ON NASO/OROPHARYNGEAL SWABS

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ABSTRACT

Introduction: The COVID-19 pandemic caused by the SARS-CoV-2, has spread around the world overloading health systems and testing capacity in almost all countries. Recently, Iles et al. (2020) have published a Clinical MALDI-TOF Mass Spectrometry Assay for SARS-CoV-2 on gargle samples. Objectives: Evaluate the performance of SARS-CoV-2 MAPSciences Gargle Test for naso/oropharyngeal sample and identify SARS-CoV-2 variants based on MALDI-TOF spectra analysis. Materials and methods: A total of 47 samples (13 positive and 34 negative by RT-qPCR) were analysed. A volume of 500 µL was added in an eppendorf tube in a 1:1 ratio with ice cold acetone and centrifuged at 16,000g/30 min./4ºC. The pellet was resuspended in 50 µL of LBSD-X buffer and vortexed. The MALDI target plate was prepared with a first layer of 15 mg/mL sinapinic acid (SA) matrix followed by 1 µL of sample plus another 1 µL of SA and placed into the Bruker microflex® MALDI-TOF MS (Bruker Daltonics Inc.) for data acquisition with optimized parameters. The spectra were processed and analysed by a bioinformatics workflow. Samples with S1 peak intensity >400 a.i were classified as positive by MALDI-TOF MS. Correlations were calculated by linear regression. Results and Discussion: Our samples (Br) presented the S1 peak at 81-84 Km/z differently than those observed in gargle samples (78-81 Km/z) from the United Kingdom (UK) and United States (USA). The S1 peak was detected in 43/47 samples, with higher intensity in positive samples (8/13; average = 864 a.i) than negative samples (9/34; average = 272 a.i). The expected S2 peak at 68 to 72 Km/z, previously detected in the UK and USA, was not detected here. A different peak at 106 Km/z was detected and correlated with positive samples (6/13; R2 = 0.7935) and higher intensity levels (> 400 a.i) of S1 peak. Another unexpected peak at 92 Km/z was correlated with negative samples (7/34; R2=0.7996). These samples were identified as SARS-CoV-2 positive by the MALDI-TOF MS. In addition, the S1 peak intensity showed correlation with IgA peak intensity (IgA1 heavy chain detected at approx. 57 Km/z) for Br RT-qPCR positive samples. Interestingly, these samples showed no correlation with the IgA peak intensity.

These findings may suggest a possible characterization of a new variant of SARS-CoV-2 which was not detected by RT-qPCR and may have the ability to evade mucosal immunity. Conclusion: The MALDI-TOF method was able to identify the SARS-CoV-2 with 70-80% agreement with RT-qPCR results. Furthermore, our findings suggest that the MALDI-TOF MS can identify new SARS-CoV-2 variants not recognized by the RT-qPCR test. The data set is being expanded and correlations with full sequencing data is underway.

Keywords: SARS-CoV-2; COVID-19; MALDI-TOF MS; diagnostics.

Development Agencies: FIPE/HCPA, CAPES