A rigorous evaluation of optimal peptide targets for MS-based clinical diagnostics of Coronavirus Disease 2019 (COVID-19)

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INTRODUCTION

The COVID-19 pandemic has wrought immense suffering worldwide, with over 110 million cases and nearly 2.5 million deaths as of February 2021. Rapid diagnosis of SARS-CoV-2 infection is the key to identification and early treatment of patients and minimizing the spread of the disease.

Targeted mass spectrometry (MS) represents a potential complementary mode of detecting SARS-CoV-2 that doesn’t rely on amplification of the viral RNA.

To maximize the ability of targeted MS assays to detect and quantify SARS-CoV-2, target peptides should be selected for detection that have the greatest likelihood of being reliably observed in patient samples.

A selection of COVID-19 datasets were analyzed to build a panel of potential SARS-CoV-2 peptide targets.

SARS-CoV-2 panel was assessed against COVID-19 datasets to determine the quality of peptide spectral matches.

Four peptides were selected as the best candidate target for MS-based detection of SARS-CoV-2 in patient samples.

EXPERIMENTAL METHODS

Cell culture experiments and analytical patient samples were searched against SARS-CoV-2 protein FASTA files from Uniprot.

Search/Query/PepShaker results were searched against human proteomes in PepQuery and filtered to leave only viral peptides.

SUMMARY

- Peptides from SARS-CoV-2 were evaluated to determine their suitability for diagnosis of COVID-19 through targeted mass spectrometry.
- Analysis of cell culture and patient datasets established a panel of 639 SARS-CoV-2 peptides which covered most of the viral proteomes.
- Seventy-five peptides from the nucleocapsid protein were found to have high confidence in their PepQuery validation, high-quality spectra, and most present in most patient samples.
- The selected target peptides are specific to SARS-CoV-2.

This work is available as a pre-print on MedRxiv https://www.medrxiv.org/content/10.1101/2021.02.25.21254142

REFERENCES


Our manuscript was submitted to EMBO Journal as an open-source publication, and we are currently working on the final version to be submitted to a journal for publication.

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