Peptide microarray analysis of in-silico predicted B-cell epitopes in SARS-CoV-2 sero-positive healthcare workers in Bulawayo, Zimbabwe

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Abstract

Immunogenic peptides that mimic linear B-cell epitopes coupled with immunoassay validation may improve serological tests for emerging diseases. This study reports a general approach for profiling linear B-cell epitopes derived from SARS-CoV-2 using an in-silico method and peptide microarray immunoassay, using healthcare workers' SARS-CoV-2 sero-positive sera. SARS-CoV-2 was tested using rapid chromatographic immunoassays and real-time reverse-transcriptase polymerase chain reaction. Immunogenic peptides mimicking linear B-cell epitopes were predicted in-silico using ABCpred. Peptides with the lowest sequence identity with human protein and proteins from other human pathogens were selected using the NCBI Protein BLAST. IgG and IgM antibodies against the SARS-CoV-2 spike protein, membrane glycoprotein and nucleocapsid derived peptides were measured in sera using peptide microarray immunoassay. Fifty-three healthcare workers included in the study were RT-PCR negative for SARS-CoV-2. Using rapid chromatographic immunoassays, 10 were SARS-CoV-2 IgM sero-positive and 7 were SARS-CoV-2 IgG sero-positive. From a total of 10 SARS-CoV-2 peptides contained on the microarray, 3 (QTH34388.1-1-14, QTN64908.1-135-148, and QLL35955.1-22-35) showed reactivity against IgG. Three peptides (QSM17284.1-76-89, QTN64908.1-135-148 and QPK73947.1-8-21) also showed reactivity against IgM. Based on the results we predicted one peptide (QSM17284.1-76-89) that had an acceptable diagnostic performance. Peptide QSM17284.1-76-89 was able to detect IgM antibodies against SARS-CoV-2 with area under the curve (AUC) 0.781 when compared to commercial antibody tests. In conclusion in silico peptide prediction and peptide microarray technology may provide a platform for the development of serological tests for emerging infectious diseases such as COVID-19. However, we recommend using at least three in-silico peptide prediction tools to improve the sensitivity and specificity of B-cell epitope prediction, to predict peptides with excellent diagnostic performances.