Immunoinformatic Design and Evaluation of a Multi-Epitope Peptide Vaccine Targeting SARS-CoV-2 Structural and Nonstructural Antigens

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As the effort for SARS-CoV-2 vaccine development continues, characterization of SARS-CoV-2 immune memory has indicated that the Spike (S) protein, the target of most SARS-CoV-2 vaccines, elicits a narrow T cell response compared to SARS-CoV-2 infection. In recognition of this research, a multi-epitope peptide vaccine was designed to better capture the full extent of the immune response towards SARS-CoV-2. Beginning with a large pool of experimentally-identified T cell epitopes from SARS-CoV-2 structural and nonstructural antigens, T cell epitopes were selected based on computational Major Histocompatibility Complex binding affinity predictions and antigenicity predictions. Likewise, experimentally-identified B cell epitopes from the S protein were evaluated through literature review for their ability to induce neutralizing antibody responses, and a vaccine construct comprised of 19 CD8 T cell epitopes, 19 CD4 T cell epitopes, and four B cell epitopes was produced by linking these epitopes with linker sequences. This construct was then evaluated for its allergenicity, immunogenicity, and physicochemical properties using computational tools. The strong immunogenic profile of the chosen epitopes and the computationally-determined characteristics of the vaccine construct suggest that this vaccine will theoretically induce a strong T cell response towards multiple SARS-CoV-2 antigens as well as neutralizing antibodies towards the S protein that together, could confer robust SARS-CoV-2 immunity. This is the first peptide-based vaccine construct towards SARS-CoV-2 produced with experimentally-identified epitopes derived from structural and nonstructural antigens, and with further experimental validation, this novel construct could be a strong SARS-CoV-2 vaccine candidate.

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