Identifying Canadian Population Allele-Specific Cytotoxic T Cell Epitopes for the Design of Therapeutic Vaccines by Targeting the Fusion Glycoprotein of Human Respiratory Syncytial Virus

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Respiratory syncytial virus (RSV) infection is one of the leading health burdens of Canada and worldwide. Integrated immunoinformatics analysis and protein-protein docking studies are conducted to identify potential Canadian population-specific T cell epitopes for the possible design of therapeutic vaccine against RSV. Population-specific alleles were selected from the HLA allele frequency database and major histocompatibility class-I (MHC-I) binding epitopes were predicted with the NetMHC web interface to neural network algorithms. Different machine learning tools were used to estimate the antigenicity and allergenicity of the cytotoxic T-lymphocyte epitopes (CTL-E). Seven highly antigenic CTL-E were found to bind MHC-I with the fusion glycoprotein of RSV. Protein-protein docking analysis was then performed with selected alleles (HLA-A*02:01 and HLA-B*51:01) and modeled structures of CTL epitopes. The highest binding affinity was found for CTL-E1 (KNNRLLEITREFSV225-238) with HLA-A*02:01 and CTL-E3 (KQLLPIVNKQSCSI200-213) with HLA-B*51:01. The present findings suggest that potent epitope candidates CTL-E1 and CTL-E3 could be used to design a therapeutic vaccine to enhance cellular mediated immunity against RSV infection.