In Silico Prediction of Human Parechovirus Epitope-Based Vaccine Candidates

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ABSTRACT

Human parechoviruses (HPeVs) have emerged globally as a potential cause of severe life-threatening illness among neonates and young children. HPeVs, consisting of 17 genotypes causing differential clinical diseases. The most prevalent are HPeV1 and HPeV3. HPeV1 causes primary gastrointestinal infections. Moreover, HPeV3 causes sepsis and disorders of the central nervous system (CNS) in young infants. Although the mortality rate by HPeV infection is rare, it may cause severe neurodevelopmental sequelae. HPeV-3 has been described as the most commonly detected type of HPeV in cerebrospinal fluid (CSF) from hospitalized children. HPeV3 is also a common single cause of aseptic meningitis/meningoencephalitis in infants under 90 days of age, usually seasonal with summer fall. The infection of CNS with HPeV3 usually lack pleocytosis of the CSF. Comparative analysis of HPeV's genomes will help to identify the core characteristics that characterize this virus family's unique properties. HPeV, capsid polyprotein along with the RGD motif, was acquired from a protein database, and we anticipated the most immunogenic epitope for cell-mediated immunity T cells and B cells. FLNFKSMNV, KVFENSYSY, KTKYLTMSTK, SVYASTFNR were the most potent peptides for CD4+, and CD8+ T cells predicted as epitopes. However, EVLNRLTYNY and FAYFTGELNI had the most impressive pMHC-I immunogenicity score and were pursued for their association with HLA particles using silico docking systems to validate the binding cleft epitope. For future planning of an epitope-based peptide immunization against HPeV, we assume this model will help to create and anticipate potential contender for the antibody advancement. In contrast, a phylogenetic analysis may provide details about evolutionary relationships and protein ancestry.

Keywords: Human parechoviruses (HPeVs), RGD motif, Epitopes, Immunogenomics, *Insilico*, Vaccine development, MHC class

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