Novel T Cell Epitope Designing from PPRV HN Protein for Peptide based Subunit Vaccine: An Immune Informatics Approach

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A B S T R A C T

Peste-des-petits Ruminants (PPR) is a disease of small ruminants especially goat and its control and eradication till 2030 wants an extensive research to develop a potent vaccine. The role of surface HN protein in the attachment of the virus to cellular receptors makes it an appropriate target to develop a theranostics against the virus. In this study, cytotoxic T cells epitopes that will bind to MHC class I alleles were predicted out using bioinformatic tools. Ten immunogenic peptides were predicted using IEDB web server based on their binding with cow (BoLA) alleles. Among these predicted peptides, five immunogenic epitopes i.e. 429SVFGPLIPHL438, 86HQTKDVLTPL95, 261RDLGLGPPVF270, 432GPLIPHLSGM441 and 555VRLNFKGNPL564 were selected on the basis of their high percentile score. Predicted three dimensional (3D) models of the PPRV HN protein and SLAM receptor were built and used to dock the immunogenic epitopes. It was used to predict the docked site in the structure. Furthermore, the involvement of these predicted epitopes in experiments may lead to creation of novel potent vaccine and diagnostic tools against the PPR.

Keywords
PPR virus, HN protein, T cell epitope, MHC

Introduction

Peste des petits ruminant (PPR) is an acute, highly contagious and morbid viral disease of goat and other small ruminants caused by PPR virus which comes under genus morbillivirus, affecting livestock of more than 70 countries (Kumar et al., 2014; Prajapati et al., 2019). The occurrence of the PPR virus mainly occurs during winters (Singh et al., 2014) and their seroprevalence were reported throughout the country (Balamurugan et al., 2014a; Hota et al., 2018; Pal et al., 2014; Saritha et al., 2014). The economic impact by the PPR was already reported and its control may help the poor farmers in their growth (Staal et al., 2009; Kamel and El-Sayed, 2019). The surface protein haemagglutinin
neuraminidase (HN) of PPR virus involves in the virus attachment and induces acquired immunity in the host cell (Yu et al., 2017). The inhibition of HN resulting in restriction of its attachment may lead to control the disease. Using conserved epitopes to develop a potent vaccine is a novel concept that applied in control of various harmful diseases (Gershoni et al., 2007; Iurescia et al., 2012; Abu haraz et al., 2017; Tahir et al., 2019). Therefore, prediction and analysis of the novel epitopes of PPRV HN protein is a crucial step to develop a peptide subunit based vaccine, antiviral peptides and diagnostic tools. In this study, cytotoxic T cells epitopes against PPRV HN protein were predicted out using immunoinformatics tools that may interact with MHC class I alleles and their docking has been performed to find their predicted docking site. The main motive of this study is to design a novel antiviral peptides or multiepitopic vaccine that restricts the virus attachment and helps in control and eradication of the PPR.

Materials and Methods

Retrieval of amino acid sequences

The amino acid sequences of hemagglutinin-neuraminidase of PPRV Sungri-96 strain (GenBank accession number: GQ452016.1) and SLAM receptor precursor of Ovis aries (NCBI Reference Sequence: NP_001035378.1) was retrieved from NCBI database (http://www.ncbi.nlm.nih.gov/protein/).

Predictions of T cell epitopes

Immune Epitope Database (IEDB) prediction tools (http://tools.iedb.org/mhci/) were emphasized to predict cytotoxic T lymphocyte (CTL) epitopes of PPRV HN protein using retrieved sequence (609 AA residues) that may interact with MHC (major histocompatibility complex) class I alleles (Lundegaard et al., 2008). Eight different cow alleles i.e. BoLA-T2a, BoLA-T5, BoLA-T2b, BoLA-D18.4, BoLA-T2c, BoLA-JSP.1, BoLA-T7 and BoLA-HD6 were used for analysis using netmhcpan_el4.0 method to predict the binding affinity. The length of amino acids was fixed to 10 and the cut off percentile rank was set in the range of 1-4 during the prediction of T cell epitopes.

Three dimensional (3D) modeling and docking

Due to non-availability of the crystal structure of PPRV HN protein in PDB format, the predicted 3D model of the PPRV HN protein from the retrieved sequence was built using SWISS-MODEL online server (https://swissmodel.expasy.org/interactive) (Biasini et al., 2014). Similarly predicted 3D model of the SLAM receptor was built from retrieved sequence (338 amino acids) in intensive mode using Phyre 2.0 web server (http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index) (Kelley et al., 2015). Furthermore, docking has been performed between the predicted peptide sequences of the PPRV HN protein and predicted 3D model of SLAM receptor using HPEPDOCK online web server (http://huanglab.phys.hust.edu.cn/hpepdock/) (Zhou et al., 2018).

Results and Discussion

Predicted cytotoxic T cell epitopes

In this study, using MHC-I binding prediction method of IEDB web server, the surface immunogenic epitopes of PPRV HN protein were predicted out. A total of 10 fixed length T-cell epitopes that will interact with various cow (BoLA) alleles were selected along with their percentile rank and position (table 1). Out of ten predicted CTL immunogenic
epitopes, three epitopes viz. SVFGPLIPHL438, HQTKDVLTL95 and VRLNFKGNPL564 were interacted with four BoLA alleles. The four epitopes i.e. VWRSDARDPS243, RDLGLGPPVF270, GPLIPHLSGM441, and three epitopes i.e. RLHRATVGTL68, AHFSELTLTL205 and MLRYITATY529 were predicted to interact with three and two BoLA alleles respectively. The peptide epitope SVFGPLIPHL438 and VRLNFKGNPL564 obtained the highest percentile rank of 3.8 and 3.3 respectively in comparison to other predicted T cell epitopes indicating the most probable potent immunogenic T cell epitopes of PPRV HN protein.

3D modeling of PPRV HN protein and SLAM receptor

The 3D model of PPRV HN protein created by Swiss model revealed the sequence identity of 39.48% with measles virus (MV) haemagglutinin (H) protein using template 2zb5.1 (Crystal structure of the measles virus hemagglutinin) (Fig.1A). Furthermore, the final model posses an overall coverage of 0.76 and sequence similarity of 0.40. Then the QMEAN, Cβ, solvation and torsion values of the model were recorded as -4.89, -1.06, -1.84 and -3.97 respectively under global quality estimation. In addition, the 3D model of SLAM receptor built in intensive mode using Phyre 2.0 revealed 72% of amino acids modeled with greater than 90% confidence using template c2druA (crystal structure and binding properties of the cd2 and cd244(2b4)2 binding protein, cd48) (Fig.1B).

Docking of predicted T cell epitopes on SLAM receptor

From the list of predicted immunogenic epitopes, five epitopes i.e. SVFGPLIPHL438, HQTKDVLTL95, RDLGLGPPVF270, GPLIPHLSGM441 and VRLNFKGNPL564 were selected on the basis of their higher percentile rank and docked as ligands with 3D model of the SLAM receptor on the HEPEDOCK web server. After docking, the binding site model of the epitope with highest docking score was chosen. Among the docked peptides, the epitope SVFGPLIPHL438 docked more efficiently and compactly with the docking score of -183.89. The rest of the epitopes i.e. HQTKDVLTL95, RDLGLGPPVF270, GPLIPHLSGM441, and VRLNFKGNPL564 were also docked successfully and obtained a docking score of -161.267, -170.062, -174.309 and -170.882 respectively (Fig.2).

Discussion

Due to huge economic consequences and morbidity rate, the control and global eradication of the PPR has been initiated. The most effective approach to control and eradicate the PPR is vaccination of livestock. To develop a potent multiepitopic vaccine, accurate prediction of the surface epitopes is a crucial step. Most of the morbilliviruses infection leads to the immunosuppression which may be protected by cell-mediated and humoral immune response against specific surface protein (Naik et al., 1997). In the study, the cytotoxic T cell epitopes were predicted out using cow (BoLA) alleles in order to bind with MHC-I alleles and their docking with SLAM receptor was performed using bioinformatics tools. Earlier studies reported the use of various animal and human alleles to predict the immunogenic T cell epitopes against multiple diseases using immunoinformatics (Patronov and Doytchinova, 2013; Liu et al., 2017; Idris et al., 2018; Abd Albagi et al., 2017; Prabdial-Sing et al., 2012; Ahmad et al., 2019; Prasasty et al., 2019).
### Table 1

<table>
<thead>
<tr>
<th>S.No.</th>
<th>Peptide</th>
<th>Position</th>
<th>Length</th>
<th>Alleles</th>
<th>Percentile Rank</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>SVFGPLIPHL</td>
<td>429-438</td>
<td>10</td>
<td>BoLA-T2a, BoLA-T2b, BoLA-T5, BoLA-D18.4</td>
<td>2.3, 2.0, 3.8, 2.6</td>
</tr>
<tr>
<td>2.</td>
<td>RLHRATVGTL</td>
<td>59-68</td>
<td>10</td>
<td>BoLA-T2c, BoLA-T7</td>
<td>2.3, 2.0</td>
</tr>
<tr>
<td>3.</td>
<td>HQTKDVLTPL</td>
<td>86-95</td>
<td>10</td>
<td>BoLA-T2c, BoLA-T2b, BoLA-T7, BoLA-T5</td>
<td>2.3, 2.0, 2.7, 2.0</td>
</tr>
<tr>
<td>4.</td>
<td>AHFSELTTLTL</td>
<td>196-205</td>
<td>10</td>
<td>BoLA-HD6, BoLA-JSP.1</td>
<td>1.4, 1.1</td>
</tr>
<tr>
<td>5.</td>
<td>VWRSDARDPS</td>
<td>243-252</td>
<td>10</td>
<td>BoLA-T2c, BoLA-T2b, BoLA-T2a</td>
<td>1.7, 1.8, 2.3</td>
</tr>
<tr>
<td>6.</td>
<td>RDLGLGPPVF</td>
<td>261-270</td>
<td>10</td>
<td>BoLA-HD6, BoLA-T5, BoLA-D18.4</td>
<td>2.3, 2.4, 2.7</td>
</tr>
<tr>
<td>7.</td>
<td>GPLIPHLSGM</td>
<td>432-441</td>
<td>10</td>
<td>BoLA-T2c, BoLA-HD6, BoLA-T7</td>
<td>2.8, 2.7, 2.9</td>
</tr>
<tr>
<td>8.</td>
<td>NRAEVMPHIL</td>
<td>474-483</td>
<td>10</td>
<td>BoLA-D18.4, BoLA-T5, BoLA-T2b</td>
<td>1.5, 2.3, 1.4</td>
</tr>
<tr>
<td>9.</td>
<td>MDLRYTTATY</td>
<td>520-529</td>
<td>10</td>
<td>BoLA-D18.4, BoLA-T5</td>
<td>1.9, 1.7</td>
</tr>
<tr>
<td>10.</td>
<td>VRLNFKGNPL</td>
<td>555-564</td>
<td>10</td>
<td>BoLA-HD6, BoLA-T5, BoLA-T7, BoLA-D18.4</td>
<td>2.0, 2.9, 3.3, 2.7</td>
</tr>
</tbody>
</table>

**Figure 1** Depiction of predicted 3D structure
A) PPR virus HN protein by SWISS MODEL software. Predicted structure consists of six antiparallel beta propeller sheets. B) SLAM receptor by Phyre 2.0 software
Previously, a docking between the MHC I and T cell peptide of chimeric protein of colorectal cancer using HPEPDOCK server was performed and results indicate a successful interaction with a docking score of \(-209.839\) (Hassan et al., 2020). Furthermore, the H protein of the MV is highly homologous to the PPR HN protein and the interaction of the head domain of MV H protein with the SLAM receptor was reported earlier (Hashiguchi et al., 2011). As per reports, due to absence of adequate bioinformatics tools, only 10% of the predicted T cell epitopes were found immunogenic (Zhong et al., 2003).

These findings indicated that the predicted epitopes might be able to bind and restrict the virus attachment and may work as potent antiviral agents. However, in-vitro and in-vivo experiments must be needed to validate and confirm the immunogenic epitopes that potentially binds to the MHC molecules.

In this study, ten immunogenic peptides were predicted as T cell epitopes using IEDB web tool. Out of these predicted peptides, five potent epitopes i.e. \(SVFGLPIPLH\) \(^{429}\), \(HQTKDVLTPL\) \(^{95}\), \(RDLGLGPPVF\) \(^{261}\), \(GPLIPHLSGM\) \(^{432}\), and \(VRLNFKNPL\) \(^{564}\) were identified on the basis of their high percentile score and their probable binding affinity with multiple BoLA alleles. 3D model of the PPRV HN protein and SLAM receptor was built and docking of the predicted immunogenic peptides was done using these predicted models.

Furthermore, experimentation using these predicted epitopes will lead to designing of specific theranostics tools which helps in the control and global eradication of the PPR.

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