A Novel Multi-Epitope Vaccine For Cross Protection against Hepatitis C Virus (HCV): An Immunoinformatics Approach

Mokhtar Nosrati, Hassan Mohabatkar *, Mandana Behbahani

Department of Biotechnology, Faculty of Advanced Sciences and Technologies, University of Isfahan, Isfahan, Iran.

Abstract

Background: Hepatitis C virus (HCV) causes acute and chronic human hepatitis infections. Due to the high genetic diversity and high rates of mutations in the genetic material, so far there has been no approved vaccine against HCV.

Materials and Methods: The aim of this study was to determine conserved B- and T-cell epitopes of E1 and E2 proteins from HCV and to construction a chimeric peptide as a novel epitope-based vaccine for cross-protection against the virus. To this end, one B- and one T-cell epitope from both E1 and E2 which were predicted by EPMLR and Propred-1 server and had the highest score and antigenicity in VaxiJen 2.0 and PAP servers were selected for the construction of chimeric protein as a multi-epitope vaccine.

Results: The results of this study showed that the chimeric peptide had a high antigenicity score and stability. Results also showed that most epitopes of E1 were located in two spectra consist of 45-65, 88-107 and 148-182 while the results of B-cell epitopes of E2 showed that this protein had fewer epitopes than E1. The epitopes predicted for E2 were located in (12-24 and 35-54) spectra.

Conclusion: In conclusion, epitope-based vaccine which was designed by immunoinformatics methods could be considered as a novel and effective vaccine for cross-protection against HCV infection.

Keywords: Hepatitis C virus; Immunoinformatics; Epitope prediction

Introduction

Hepatitis C virus (HCV) is a RNA virus causes chronic liver disease and a viral pandemic. The HCV was discovered in the USA in 1989 and it is now known that it has infected infects 3% of the world population (1). Acute HCV infection is usually clinically silent and rarely leads to liver failure. Percentage of patients spontaneously clears the virus within 6 months of infection without any treatment. About 55–85% of people with acute infection develops chronic infection and in 15–30% patients is more likely to develop cirrhosis. On the other hand, acute HCV infection is a short-term illness that occurs within the first 6 months after exposure to the HCV. For most people, acute infection leads to chronic infection (2, 3). HCV is usually spread when blood from a person infected with the HCV enters the body of someone who is not infected. Today, most people become infected with the HCV by sharing needles or other equipment to inject drugs (4). Unlike other Hepatitis viruses various details remain unknown about the exact natural processes of HCV, however the key steps of HCV life cycle include: a) Virus attachment to the surface of liver cells; b) Penetration of virus's core protein into the plasma membrane and entrance to the host cell; c) Release of the viral RNA into the host cell; d) The viral RNA then coopts the host cell's ribosomes; e) RNA transcription and creation of new viral RNA; f) Production of protein-based capsomeres from the viral RNA; g) The completed capsomeres assemble around the new viral RNA into new viral particles; and h) The release of new viruses. Because of the genome heterogenicity, lack of small-animal models and inability to grow the virus in cell culture, our knowledge about the HCV lifecycle has been limited (5).

Recently, many studies have been done to introducing...
Amino acid sequences of E1 and E2 proteins of HCV with 192 and 73 amino acids in length respectively, were retrieved from NCBI (http://www.ncbi.nlm.nih.gov/protein/) with accession numbers of ACN92051.1 and AAX36013.1, respectively. Then these proteins were subjected to the Basic Local Alignment Search Tool (BLAST) against the non-redundant protein database available at UniProt (www.uniprot.org/). Also for determination of conserved area in the proteins multiple sequence alignment was used between different sequences with the highest score and identity.

Table 1. Results of linear B-cell epitope prediction of E1 and E2 proteins of HCV.

<table>
<thead>
<tr>
<th>Protein</th>
<th>Rank</th>
<th>Epitope sequence</th>
<th>Score</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>E1</td>
<td>1</td>
<td>MCGAVFLVGQAFTFRPRRH</td>
<td>0.3648</td>
<td>89-107</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>CWTPTPVTAVRYVGAATT</td>
<td>0.7914</td>
<td>134-152</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>RCWTPVTPTVARYVGAATT</td>
<td>0.5710</td>
<td>133-151</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>DMCGAVFLVGAFTFRPRRH</td>
<td>0.5776</td>
<td>159-177</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>NWTPAVGVMVAVQLRLQPS</td>
<td>0.5710</td>
<td>158-178</td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>ADDVILHTPGCIPCVQDG</td>
<td>0.3648</td>
<td>152-159</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>QCTCNCSLYPHLSGHRMA</td>
<td>0.3648</td>
<td>45-89</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>EADDLTHTPGCIPCVQDG</td>
<td>0.3648</td>
<td>46-90</td>
</tr>
<tr>
<td></td>
<td>9</td>
<td>VQTCNCSLYPHLSGHRMA</td>
<td>0.3648</td>
<td>109-118</td>
</tr>
<tr>
<td></td>
<td>10</td>
<td>MNWTPAVGVMVAVQLRLQPS</td>
<td>0.5710</td>
<td>119-128</td>
</tr>
<tr>
<td></td>
<td>11</td>
<td>GAHWGLAGAYGSGEMN</td>
<td>0.5710</td>
<td>119-128</td>
</tr>
<tr>
<td></td>
<td>12</td>
<td>GGAHWMLAGAYGSGEMN</td>
<td>0.5710</td>
<td>119-128</td>
</tr>
<tr>
<td></td>
<td>13</td>
<td>ASVRSHVDDLVGAATMCS</td>
<td>0.5710</td>
<td>119-128</td>
</tr>
<tr>
<td></td>
<td>14</td>
<td>NTRTVGQIARQLQFPRTL</td>
<td>0.5710</td>
<td>119-128</td>
</tr>
<tr>
<td></td>
<td>15</td>
<td>HNTRTVGQIARQLQFPRTL</td>
<td>0.5710</td>
<td>119-128</td>
</tr>
<tr>
<td></td>
<td>16</td>
<td>LFSVGNQNNQILNTNGSW</td>
<td>0.5710</td>
<td>119-128</td>
</tr>
</tbody>
</table>

B-cell epitope prediction
For prediction of linear B-cell epitopes, the full-length sequence of E1 and E2 were subjected to EPMLR analysis with overall sensitivity of 81.8% at...
Multi-Epitope Vaccine against HCV Infection

The cutoff score > 0.15 was selected for all predicted B-cell epitopes and 19mer epitope was selected for prediction.

Table 2. Results of T-cell epitope prediction of E1 and E2 proteins of HCV.

<table>
<thead>
<tr>
<th>Protein</th>
<th>Predicted epitope</th>
<th>Amino acid positions</th>
<th>ProPred1 Log scores</th>
</tr>
</thead>
<tbody>
<tr>
<td>E1</td>
<td>DCPNSSIVY</td>
<td>15</td>
<td>0.9163</td>
</tr>
<tr>
<td></td>
<td>EADDVILHT</td>
<td>24</td>
<td>0.9163</td>
</tr>
<tr>
<td></td>
<td>VTPTVAVRY</td>
<td>51</td>
<td>0.9163</td>
</tr>
<tr>
<td></td>
<td>VGDNCAGAVF</td>
<td>86</td>
<td>0.9163</td>
</tr>
<tr>
<td></td>
<td>RLPSQIFDI</td>
<td>148</td>
<td>4.2042</td>
</tr>
<tr>
<td></td>
<td>MKMNWTPAV</td>
<td>131</td>
<td>3.7029</td>
</tr>
<tr>
<td></td>
<td>DMCAGAVFLV</td>
<td>88</td>
<td>3.3649</td>
</tr>
<tr>
<td></td>
<td>IJMVMSGV</td>
<td>182</td>
<td>2.9639</td>
</tr>
<tr>
<td>E1</td>
<td>RLPSQIFDI</td>
<td>148</td>
<td>4.9357</td>
</tr>
<tr>
<td></td>
<td>IJMVMSGV</td>
<td>182</td>
<td>4.9298</td>
</tr>
<tr>
<td>E2</td>
<td>ILGGAHWGM</td>
<td>156</td>
<td>4.1485</td>
</tr>
<tr>
<td></td>
<td>DMCAGAVFLV</td>
<td>88</td>
<td>3.9172</td>
</tr>
<tr>
<td></td>
<td>MVQAQVLR</td>
<td>141</td>
<td>3.8628</td>
</tr>
<tr>
<td></td>
<td>YVGDNCAGAV</td>
<td>85</td>
<td>3.5835</td>
</tr>
<tr>
<td></td>
<td>KGVIMVMV</td>
<td>179</td>
<td>3.1781</td>
</tr>
<tr>
<td></td>
<td>IJMVMSGV</td>
<td>182</td>
<td>3.0155</td>
</tr>
<tr>
<td>E2</td>
<td>RTVGGQIAR</td>
<td>38</td>
<td>0.2231</td>
</tr>
<tr>
<td></td>
<td>WGVFMGLAY</td>
<td>2</td>
<td>-0.4700</td>
</tr>
<tr>
<td></td>
<td>LLLTAGVDA</td>
<td>24</td>
<td>4.2219</td>
</tr>
<tr>
<td></td>
<td>RQLQPFTRL</td>
<td>46</td>
<td>4.0489</td>
</tr>
<tr>
<td></td>
<td>QPFTRLFSV</td>
<td>49</td>
<td>3.2881</td>
</tr>
<tr>
<td></td>
<td>KVIVIlLT</td>
<td>19</td>
<td>2.4849</td>
</tr>
<tr>
<td></td>
<td>SMQGAWAVK</td>
<td>12</td>
<td>4.4473</td>
</tr>
<tr>
<td></td>
<td>VILLTAGV</td>
<td>22</td>
<td>4.0969</td>
</tr>
</tbody>
</table>

T-cell epitope prediction

T-cell epitope prediction was performed using Propred-1 with sensitivity and specificity of 4% as default threshold (47 MHC Class-I alleles) utilizing amino acid position coefficients. This tool was used to identify common epitopes that bind to both the MHC class molecules as well as to count the total numbers of interacting MHC alleles.

Antigenicity of predicted epitopes

Antigenicity of both B- and T-cell epitopes predicted by the tools were determined using VaxiJen 2.0 server with predicted accuracy of 70% to 89% (http://www.ddg-pharmfac.net/vaxijen/VaxiJen/ VaxiJen.html) with 0.4 threshold and Predicting Antigenic Peptides (PAP) server (http://imed.med.ucm.es/Tools/antigenic.pl). Then antigenicity plot of the evaluated proteins was created by PAP based on their sequences.

Allergenicity prediction and IgE epitopes

One of the most important notes about protein and peptide vaccines is that these molecules should not have allergenicity. Therefore, the chimeric peptide was checked for allergenicity by AlgPred server (http://www.imtech.res.in/raghava/algpred/).

Construction of chimeric peptide

In this section, more probable epitopes with the highest score and antigenicity were selected for construction of chimeric peptide as a multi-epitope vaccine. For this, one B- and one T-cell epitope from both E1 and E2 were selected for construction of chimeric peptide.

Table 3. Results of antigenicity determination of predicted B-cell epitope by VaxiJen and PAP servers.

<table>
<thead>
<tr>
<th>Protein</th>
<th>Rank</th>
<th>Epitope sequence</th>
<th>VaxiJen score</th>
<th>PAP score</th>
</tr>
</thead>
<tbody>
<tr>
<td>E1</td>
<td>1</td>
<td>MCGAVFLVQ</td>
<td>0.4101</td>
<td>1.0561</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>CRTVPVPTVAV</td>
<td>0.9165</td>
<td>1.0859</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>RCVTPVPTVAV</td>
<td>1.1220</td>
<td>1.0839</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>DMCAGAVFLV</td>
<td>0.4122</td>
<td>1.0557</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>NWTPAVGMV</td>
<td>0.1183</td>
<td>1.0816</td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>ADDVIIHTPGCI</td>
<td>0.1745</td>
<td>1.0951</td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>QTCNCSLYPGH</td>
<td>0.1367</td>
<td>1.0552</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>EADDVILHTPG</td>
<td>0.0659</td>
<td>1.0938</td>
</tr>
<tr>
<td></td>
<td>9</td>
<td>VQTCNCSLYPG</td>
<td>0.0166</td>
<td>1.0729</td>
</tr>
<tr>
<td></td>
<td>10</td>
<td>MNWTPAVGMV</td>
<td>0.4771</td>
<td>1.0711</td>
</tr>
<tr>
<td></td>
<td>11</td>
<td>GAGHWGLAG</td>
<td>1.0461</td>
<td>0.9888</td>
</tr>
<tr>
<td></td>
<td>12</td>
<td>GAGHWGLAG</td>
<td>0.6814</td>
<td>0.9943</td>
</tr>
<tr>
<td></td>
<td>13</td>
<td>VQTCNCSLYPG</td>
<td>0.3377</td>
<td>1.0968</td>
</tr>
<tr>
<td></td>
<td>14</td>
<td>NTVGGQIAR</td>
<td>0.3304</td>
<td>0.9955</td>
</tr>
<tr>
<td></td>
<td>15</td>
<td>HNTVGGQIAR</td>
<td>0.4465</td>
<td>1.0084</td>
</tr>
<tr>
<td></td>
<td>16</td>
<td>LFSVGPNONIQ</td>
<td>0.9172</td>
<td>1.0087</td>
</tr>
</tbody>
</table>

rmm.mazums.ac.ir

Amino acid composition and physicochemical properties
Amino acid composition and some physicochemical properties of constructed peptide which consisted of: Size, Molecular weight, Iso-electric point, Extinction coefficient, Net charge at pH 7, Estimated solubility in water, Estimated half-life in the mammalian reticulocytes, Instability index, Aliphatic index, Hydropathy and amphipathicity were determined using ProtParam (http://web.expasy.org/cgi-bin/protparam/protparam), Pepcalc (http://pepcalc.com/), TCDB server (http://www.tcdb.org/progs/Tool=hydro), and Calctool (http://www.calctool.org/).

Table 4. Results of antigenicity determination of predicted T-cell epitope by VaxiJen and PAP servers.

<table>
<thead>
<tr>
<th>Protein</th>
<th>Predicted T-cell epitope</th>
<th>VaxiJen score</th>
<th>PAP score</th>
</tr>
</thead>
<tbody>
<tr>
<td>E1</td>
<td>DCPNSIVY</td>
<td>0.3583</td>
<td>1.0846</td>
</tr>
<tr>
<td></td>
<td>EADDVILHT</td>
<td>-0.2127</td>
<td>1.0671</td>
</tr>
<tr>
<td></td>
<td>VTPTVAVRY</td>
<td>1.1828</td>
<td>1.1210</td>
</tr>
<tr>
<td></td>
<td>VGDMCQAVF</td>
<td>-1.0252</td>
<td>1.0853</td>
</tr>
<tr>
<td></td>
<td>RLPQSFIDF</td>
<td>-0.1844</td>
<td>1.0404</td>
</tr>
<tr>
<td></td>
<td>MKMNWTPAV</td>
<td>2.2262</td>
<td>0.9110</td>
</tr>
<tr>
<td></td>
<td>DMCGAVFLV</td>
<td>-0.5748</td>
<td>1.0958</td>
</tr>
<tr>
<td>E2</td>
<td>IIMVMVSGV</td>
<td>0.0685</td>
<td>1.0760</td>
</tr>
<tr>
<td></td>
<td>ILGGAHWGM</td>
<td>0.8801</td>
<td>1.0108</td>
</tr>
<tr>
<td></td>
<td>MVVAQVLRL</td>
<td>0.2335</td>
<td>1.1471</td>
</tr>
<tr>
<td></td>
<td>KVIIMMVMMV</td>
<td>0.8207</td>
<td>1.0657</td>
</tr>
<tr>
<td></td>
<td>RTVGGQHAR</td>
<td>0.9616</td>
<td>1.0180</td>
</tr>
<tr>
<td></td>
<td>WGMFGLAY</td>
<td>0.6455</td>
<td>1.0319</td>
</tr>
<tr>
<td></td>
<td>LLLTAGVDA</td>
<td>0.2078</td>
<td>1.1058</td>
</tr>
<tr>
<td></td>
<td>RQLQPFTRL</td>
<td>0.4881</td>
<td>1.0112</td>
</tr>
<tr>
<td></td>
<td>QFTRLFSV</td>
<td>-0.5974</td>
<td>1.0381</td>
</tr>
<tr>
<td></td>
<td>VILLLTAGV</td>
<td>0.5098</td>
<td>1.1415</td>
</tr>
<tr>
<td></td>
<td>SMQGAWKVK</td>
<td>-0.0165</td>
<td>0.9597</td>
</tr>
<tr>
<td></td>
<td>KVIVILLT</td>
<td>0.5846</td>
<td>1.2188</td>
</tr>
</tbody>
</table>

Secondary and 3D structure prediction
The secondary structure of constructed peptide was predicted by GORIV (http://cib.cf.ocha.ac.jp/bitool/GOR/GOR.php). Also, 3D structure of the chimeric peptide was generated using Swiss model server (https://swissmodel.expasy.org).

Evaluation of model stability and solvent accessibility
The model stability and structural quality of constructed peptide were validated based on Ramachandran plot using PROCHECK server (http://services.mbi.ucla.edu/PROCHECK/). Solvent accessibility is one of the determining factors in the antigenicity of peptide and protein vaccines. Therefore, the constructed peptide was validated in terms of solvent accessibility using SARpred server (http://www.imtech.res.in/raghava/sarpred/).

Molecular docking study
In order to validate the binding affinity of the chimeric peptide to MHC1 (with PDB entry 1HLA) and MHCII (with PDB entry 1DLH), molecular docking study was carried out by HEX 6.0 software. The selected parameters for docking study were FFT Mode–3D fast life, Distance Range – 40, Twist range – 360, Correlation type –Shape only, Grid Dimension – 0.6, Receptor range – 180 and Ligand Range –180.

Results
Sequence Retrieval and Homology Analysis
The BLAST of E1 and E2 amino acid sequences revealed 88-99% and 66-78% similarity between E1 and E2 among the different subtypes of HCV, respectively. The results of multiple sequence alignments of E1 and E2 residues showed high degree of conservation among different subtypes of HCV.

B-cell epitope prediction
The results of B-cell epitope prediction of E1 and E2 proteins are shown in Table1. The results indicated that E1 had more B-cell epitopes than E2. Most epitopes of E1 were located in two spectra of 88-107 and 45-65. The predicted epitopes in mentioned spectra had the highest score and could be the main epitopes for humoral immune stimulation.

Unlike E1, the results of B-cell epitopes of E2 showed that this protein had fewer epitopes than E1. Most epitopes predicted for E2 were located in 35-54 spectra so this range in E2 similar to E1 could be considered as stimulating the humoral response of the immune system.

T-cell epitope prediction
The results of T-cell epitopes prediction of E1 and E2 proteins are presented in Table 2. The results showed that these two proteins have multiple T-cell epitopes with high scores. E1 had three predicted epitopes consisted of RLPQSFIDF, IIMVMVSGV, and ILGGAHWGM with the highest score that was located in 148-182 spectra. On the other hand, unlike E1, E2 had fewer T-cell epitopes than E1 and in general the predicted epitope for E2 had a lower score.

However, three epitopes consisted of (SMQGAWA KV, VILLLTAGV, and LLLTAGV A) were the most probable epitopes of E2 that were located in 12-24 spectra. Further comparative studies of E1 and E2
showed that although the number of epitopes predicted for E1 was more than E2, E2 was more immunogenic due to the number of epitopes on the total number of amino acids.

**Figure 1.** Antigenic plot of E1.

**Antigenicity of predicted epitopes**

To ensure the results of B- and T-cell epitope prediction, antigenicity of predicted epitopes was investigated by VaxiJen and PAP servers. The results of antigenicity of predicted B- and T-cell epitopes are given in Tables 3 and 4, respectively. Based on the results, it was found that most B- and T-cell epitopes that had a high score in Propred and EPMLR received high marks in terms of antigenicity.

**Figure 2.** Antigenic plot of E2.

Also, it became clear that two B-cell epitopes consists of (RCWTPVTPTAVRYVGATT and HNRTTVGQIARQLQPFR) were the most antigenic epitopes of E1 and E2, respectively. In this regard, it was found that the most antigenic T-cell epitopes of E1 and E2 were MKMNWTPAV and RTVQGQIAR, respectively.

**Table 5.** Physicochemical properties of E1 and E2 proteins of HCV (MW is Molecular weight, Ii: Instability index, Ai: Aliphatic index and Ec is Extinction coefficient)

<table>
<thead>
<tr>
<th>Protein</th>
<th>Size (nm)</th>
<th>PI</th>
<th>Net-charge</th>
<th>MW (Da)</th>
<th>Solubility</th>
<th>Half-life (h)</th>
<th>Ii</th>
<th>Ai</th>
<th>Ec (M⁻¹cm⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td>E1</td>
<td>38.4903</td>
<td>6.63</td>
<td>-0.9</td>
<td>20830.01</td>
<td>poor</td>
<td>5.5</td>
<td>21.7</td>
<td>90.31</td>
<td>43100</td>
</tr>
<tr>
<td>E2</td>
<td>28.0062</td>
<td>11.18</td>
<td>3.3</td>
<td>8024.13</td>
<td>poor</td>
<td>3.5</td>
<td>21.46</td>
<td>96.16</td>
<td>18350</td>
</tr>
<tr>
<td>Chimeric</td>
<td>25.4818</td>
<td>11.83</td>
<td>5.1</td>
<td>6044.03</td>
<td>poor</td>
<td>1</td>
<td>32.13</td>
<td>100.89</td>
<td>12660</td>
</tr>
</tbody>
</table>

The antigenic plot of E1 and E2 are shown in Figures 1 and 2, respectively. These plots represent the average of antigenicity of proteins based on the sequences. The antigenicity plot of E1 and E2 showed that three positions in E1 and one position in E2 had high antigenicity. These positions were in accordance with the core of the predicted epitopes with high score and antigenicity.

**Construction of chimeric peptide**

*Multi-Epitope Vaccine against HCV Infection*
As it was mentioned, a peptide that was composed by more probable B- and T cell epitopes with the highest antigenicity and the one located in more conserved area of E1 and E2 sequence was introduced as a candidate vaccine. This peptide composed of 56 amino acids with the following sequence: RCWTPVTPTAVRYVGATTHNTRTVGQIARQLQF TR ILGGAHWGM VILLLTAGV.

**Amino acid composition and physicochemical properties**

The results of physicochemical properties of E1, E2 and chimeric peptide are shown in Table 5. Results of this section indicated that all three proteins had poor water solubility. Also in term of electrostatic charge, E1 had negative net charge while this parameter was determined as +3.3 and +5.1 for E2 and chimeric peptide, respectively.
Secondary and 3D structure prediction
The secondary and 3D structure prediction of chimeric peptide are illustrated in Figure 6 (a, b) respectively. The results indicated that the percentage of random coils (51.79%) was more than that of beta-sheets (39.29%) and alpha-helices (8.93%). Also, tertiary structures of chimeric peptide modeled by Swiss model based on homology (similarity) with the N-terminal domain of HCV envelope glycoprotein E1 as the template, showed that this peptide organized in two beta strands, one short helix, and one long coil.

Evaluation of model stability and Solvent accessibility
Ramachandran plot of the chimeric peptide is depicted in Figure 7. The results revealed that 96.9% of amino acid residues from modeled structure generated by Swiss model incorporated in the favored regions of the plot. Results also showed that 3.1% of residues were located in allowed regions while there was no amino acid in the outlier region. The results of solvent accessibility prediction are presented in Table 6. Results showed that chimeric peptide has high level of solvent accessibility, especially in the central area. In addition, it was found that certain amino acids such as Arg1 (58%), Cys2 (48%), Gly55 (39%), Val56 (36%), and Val6 (34%) gave a high relative solvent accessibility when compared to other amino acids in the chimeric construct.

Allergenicity prediction and IgE epitopes
The result of allergenicity prediction of chimeric peptide revealed that this peptide did not contain IgE epitope and was considered as non-allergen. Allergenic potential of mentioned peptide was determined -0.5 (threshold was -0.4). Furthermore, positive and negative predictive values were 18.21% and 71.24%, respectively.

Molecular docking studies
The results of molecular docking study confirmed that chimeric peptide had high affinity to both MHCI and MHC II. Results revealed that chimeric peptide had more affinity to MHCII with e-value of -100.3 while e-value was determined -90.7 for MHCI.

Discussion
The results of the study revealed that designed chimeric peptide composed of conserved B- and T-cell epitopes of E1 and E2 protein of HCV had a high level of antigenicity and affinity to MHC I and MHC II. So, it can be considered as a novel vaccine for cross-protection against HCV infection. In recent years, great efforts have been done to introduce effective vaccine against HCV infection. In this regard Kumar et al. introduced new hepatitis C virus-like particles (HCV-LPs) encoding structural proteins for genotype 3a. This vaccine was designed for Indian patients and was not effective against other serotypes(14). Zhu et al. constructed novel adenovirus particles (AAV) vectors expressing the full-length NS3 or NS3/4 protein of HCV genotype 1b. This candidate vaccine could well stimulate the immune system but was limited to a specific serotype (15). However, due to the high genetic diversity and high rates of mutations in the genetic material, so far there is no approved vaccine against HCV. Immunoinformatics as a branch of bioinformatics is a new approach with a variety of tools and databases for in silico analysis and modeling of immunological data. One of the major applications of
immunoinformatics that in recent years has been highly regarded is the design of epitope-based vaccines (16-22).

Table 6. Results of solvent accessibility prediction for chimeric peptide.

<table>
<thead>
<tr>
<th>Number of residue</th>
<th>Residue</th>
<th>Relative solvent accessibility</th>
<th>% Relative solvent accessibility</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>R</td>
<td>0.58</td>
<td>58</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>0.48</td>
<td>48</td>
</tr>
<tr>
<td>3</td>
<td>W</td>
<td>0.16</td>
<td>16</td>
</tr>
<tr>
<td>4</td>
<td>T</td>
<td>0.29</td>
<td>29</td>
</tr>
<tr>
<td>5</td>
<td>P</td>
<td>0.29</td>
<td>29</td>
</tr>
<tr>
<td>6</td>
<td>V</td>
<td>0.34</td>
<td>34</td>
</tr>
<tr>
<td>7</td>
<td>T</td>
<td>0.33</td>
<td>33</td>
</tr>
<tr>
<td>8</td>
<td>P</td>
<td>0.28</td>
<td>28</td>
</tr>
<tr>
<td>9</td>
<td>T</td>
<td>0.17</td>
<td>17</td>
</tr>
<tr>
<td>10</td>
<td>V</td>
<td>0.19</td>
<td>19</td>
</tr>
<tr>
<td>11</td>
<td>A</td>
<td>0.11</td>
<td>11</td>
</tr>
<tr>
<td>12</td>
<td>V</td>
<td>0.15</td>
<td>15</td>
</tr>
<tr>
<td>13</td>
<td>R</td>
<td>0.12</td>
<td>12</td>
</tr>
<tr>
<td>14</td>
<td>Y</td>
<td>0.16</td>
<td>16</td>
</tr>
<tr>
<td>15</td>
<td>V</td>
<td>0.19</td>
<td>19</td>
</tr>
<tr>
<td>16</td>
<td>G</td>
<td>0.22</td>
<td>22</td>
</tr>
<tr>
<td>17</td>
<td>A</td>
<td>0.19</td>
<td>19</td>
</tr>
<tr>
<td>18</td>
<td>T</td>
<td>0.23</td>
<td>23</td>
</tr>
<tr>
<td>19</td>
<td>T</td>
<td>0.17</td>
<td>17</td>
</tr>
<tr>
<td>20</td>
<td>H</td>
<td>0.18</td>
<td>18</td>
</tr>
<tr>
<td>21</td>
<td>N</td>
<td>0.14</td>
<td>14</td>
</tr>
<tr>
<td>22</td>
<td>T</td>
<td>0.19</td>
<td>19</td>
</tr>
<tr>
<td>23</td>
<td>R</td>
<td>0.24</td>
<td>24</td>
</tr>
<tr>
<td>24</td>
<td>T</td>
<td>0.17</td>
<td>17</td>
</tr>
<tr>
<td>25</td>
<td>V</td>
<td>0.15</td>
<td>15</td>
</tr>
<tr>
<td>26</td>
<td>G</td>
<td>0.20</td>
<td>20</td>
</tr>
<tr>
<td>27</td>
<td>G</td>
<td>0.18</td>
<td>18</td>
</tr>
<tr>
<td>28</td>
<td>Q</td>
<td>0.21</td>
<td>21</td>
</tr>
<tr>
<td>29</td>
<td>I</td>
<td>0.18</td>
<td>18</td>
</tr>
<tr>
<td>30</td>
<td>A</td>
<td>0.18</td>
<td>18</td>
</tr>
<tr>
<td>31</td>
<td>R</td>
<td>0.23</td>
<td>23</td>
</tr>
<tr>
<td>32</td>
<td>Q</td>
<td>0.29</td>
<td>29</td>
</tr>
<tr>
<td>33</td>
<td>L</td>
<td>0.17</td>
<td>17</td>
</tr>
<tr>
<td>34</td>
<td>Q</td>
<td>0.20</td>
<td>20</td>
</tr>
<tr>
<td>35</td>
<td>F</td>
<td>0.28</td>
<td>28</td>
</tr>
<tr>
<td>36</td>
<td>F</td>
<td>0.23</td>
<td>23</td>
</tr>
<tr>
<td>37</td>
<td>T</td>
<td>0.20</td>
<td>20</td>
</tr>
<tr>
<td>38</td>
<td>R</td>
<td>0.18</td>
<td>18</td>
</tr>
<tr>
<td>39</td>
<td>I</td>
<td>0.28</td>
<td>28</td>
</tr>
<tr>
<td>40</td>
<td>L</td>
<td>0.21</td>
<td>21</td>
</tr>
<tr>
<td>41</td>
<td>G</td>
<td>0.19</td>
<td>19</td>
</tr>
<tr>
<td>42</td>
<td>G</td>
<td>0.20</td>
<td>20</td>
</tr>
<tr>
<td>43</td>
<td>A</td>
<td>0.18</td>
<td>18</td>
</tr>
<tr>
<td>44</td>
<td>H</td>
<td>0.24</td>
<td>24</td>
</tr>
<tr>
<td>45</td>
<td>W</td>
<td>0.13</td>
<td>13</td>
</tr>
<tr>
<td>46</td>
<td>G</td>
<td>0.17</td>
<td>17</td>
</tr>
<tr>
<td>47</td>
<td>M</td>
<td>0.13</td>
<td>13</td>
</tr>
<tr>
<td>48</td>
<td>V</td>
<td>0.07</td>
<td>7</td>
</tr>
<tr>
<td>49</td>
<td>I</td>
<td>0.10</td>
<td>10</td>
</tr>
<tr>
<td>50</td>
<td>L</td>
<td>0.10</td>
<td>10</td>
</tr>
<tr>
<td>51</td>
<td>L</td>
<td>0.17</td>
<td>17</td>
</tr>
<tr>
<td>52</td>
<td>L</td>
<td>0.17</td>
<td>17</td>
</tr>
<tr>
<td>53</td>
<td>T</td>
<td>0.20</td>
<td>20</td>
</tr>
<tr>
<td>54</td>
<td>A</td>
<td>0.25</td>
<td>25</td>
</tr>
<tr>
<td>55</td>
<td>G</td>
<td>0.39</td>
<td>39</td>
</tr>
<tr>
<td>56</td>
<td>V</td>
<td>0.36</td>
<td>36</td>
</tr>
</tbody>
</table>

Although Immunoinformatics-based vaccine design is able to achieve cost-efficient, effective, cross-protective and particular development of vaccines these methods have some weak points such as restricted immunoinformatics tools to the linear epitopes, deficiency of B-cell epitope servers, deficiency of conformational epitope servers, and restrictions of the servers predictor of overlapping epitopes (12, 18, 23, 24).

So obtaining the useful results from immunoinformatics methods requires epitope database updating and should be coupled with experimental techniques.

In recent years, numerous studies have been conducted to introduce the effective peptide vaccines against infectious diseases. In this regard, Nazarian et al. introduced chimeric multi-subunit vaccine based on the B- and T-cell epitopes of virulence factors of enterotoxigenic Escherichia coli (25). In a similar study Hasan and his colleagues introduced novel peptide for cross protection against Saint Louis encephalitis virus infection (26). In another study Farhadi et al. designed a novel peptide that was composed of discontinuous (conformational) B cell and linear CD4+ T cell epitopes of the Outer membrane proteins (Omps) of Klebsiella pneumoniae to protect against this pathogenic bacterium (27). In the same context, Badawi et al. introduced a novel universal multi-epitope peptide vaccine in the whole spike glycoprotein of Middle East Respiratory Syndrome Coronavirus (MERS COV) (28). Due to the high efficiency and specificity of epitope-based vaccines for protection against infectious diseases, numerous attempts have been made to introduce epitope map of HCV virulence factors and effective epitope-based vaccines for protection against HCV infection. Huang et al. introduced a HCV dataset consisting of 774 linear B-cell epitopes and 774 non B-cell epitopes and revealed that PDREMVLYQE could be a conserved promising vaccine candidate for protection against HCV infection. But this peptide had no high antigenicity score in the present study (29). In a similar study, Ikram et al. confirmed that many epitopes from E2 protein are conserved in HCV 3a genotypes and HCV gpE2 is an ideal target for HCV vaccine design (30). In another study more probable and conserved T- and B-cell epitopes of E1 protein from HCV isolated in Pakistan were introduced as potential B- and T-cell epitopes that can raise the desired immune response against HCV (31). In this regard Gededzha et al. who predicted antigenic T-cell epitopes that bind HLA class II and HLA class I also showed that the highest number of HLA class I and HLA class II binding epitopes were predicted within the NS3 (63%) and NS3 (30%), respectively (32). In this study, we became eager to
design a novel chimeric peptide that can stimulate humoral and cellular immune responses to different serotypes of HCV. For this, more studied surface proteins of HCV were selected for determination of the conserved area of mentioned protein and construction of the chimeric peptide. The results showed that some areas of E1 and E2 proteins are conserved between different serotypes of HCV. More probable epitopes from mentioned proteins that were located in the conserved area were selected for construction of the chimeric peptide. So this peptide could be a good candidate for cross-protection against different serotypes of HCV.

Conclusion
The aim of this study was to determine B- and T-cell conserved epitopes of E1 and E2 proteins from HCV and to construct a chimeric peptide as a novel epitope-based vaccine for cross-protection against HCV. The results of this study showed that the chimeric peptide had high antigenicity score and stability. In conclusion epitope-based vaccine that is designed by immunoinformatics methods can be considered as a novel and effective platform of vaccines for cross-protection against HCV infection.

Acknowledgements
This work was supported by a grant from the University of Isfahan, Iran.

Authors’ contributions
M Nosrati participated in study designing, data collection, interpretation and manuscript writing. H Mohabatkar, data analysis and manuscript writing. M Behbahani, data interpretation and final approval of the manuscript.

Conflict of interest
The authors have no competing interests.

References


