Identification of Promising CD8 and CD4 T-cell Epitopes for Peptide Vaccine Formulation Against SARS-CoV-2

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Abstract

The novel virus “Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)” has been responsible for the worldwide pandemic causing huge devastation and deaths since December 2019. The disease caused by this virus is known as COVID-19. The present study is based on immunoinformatics approach to develop a multi-epitope loaded peptide vaccine to combat the COVID-19 menace. Here, we have reported the 9-mer CD8 T-cell epitopes and 15-mer CD4 T-cell epitopes, free from glycosylation sites, belonging to three proteins, *viz.* surface glycoprotein, membrane glycoprotein and envelope protein of this virus. Immunogenicity, aliphatic amino acid, antigenicity and hydrophilicity scores of the predicted epitopes were estimated. In addition, other physicochemical parameters namely net charge, Boman index and amino acid contents were also accounted. Out of all the epitopes, three CD8 T-cell epitopes *viz.* PDPSKPSKR, DPSKPSKRS and QTQTNSPRR and three CD4 T-cell epitopes *viz.* ASYQTQTNSPRRARS, RIGNYKLNTDHSSSS and RYRIGNYKLNTDHSS were found to be efficient targets for raising immunity in human against this virus. With the help of our identified potent epitopes, various pharma industries might initiate efforts to incorporate those epitopes with carrier protein or adjuvant to develop a multi-epitope-loaded peptide vaccine against SARS-CoV-2. The peptide vaccines are usually cost effective and therefore, could be administered as a preventive measure to combat the spread of this disease. Proper clinical trials must be conducted prior to the use of identified epitopes as vaccine candidates.

Introduction

Humans are common hosts to a few moderately harmful viruses belonging to Coronaviridae family [1]. On 21st century, three lethal animal-borne coronaviruses namely MERS-CoV, SARS-CoV and SARS-CoV-2 infected humans by traversing animal-human interface [2]. Coronaviruses have the largest RNA genome and SARS-CoV-2 under the genus Beta coronavirus is the seventh species of this family [3–4]. The COVID-19 disease, caused by a single stranded, positive sense virus named SARS-CoV-2, gives rise to troubles in respiratory system, gastrointestinal tract, nervous system and in liver. Difficulties like fever, dry cough, dyspnea, lymphopenia and fatigue manifest in patients. In extreme cases, viral pneumonia develops and eventually it may result in patient death [5] [4] [3]. Bats are regarded as the hosts of SARS-CoV-2, as the whole genome study of the virus revealed that it shared 96% similarity with a bat coronavirus [3].

The genomic study of SARS-CoV-2 revealed its 79% similarity with SARS-CoV and 50% with MERS-CoV, each virus belongs to Betacoronavirus group. Further resemblance of SARS-CoV-2 with its family members is at the level of structural and non-structural proteins. The structural proteins encoded by SARS-CoV-2 are spike protein (S), nucleocapsid phosphoprotein (N), membrane glycoprotein (M) and envelope protein (E) [6]. It was reported that SARS-CoV-2 gene expression occurs when it successfully accesses the host cells, where translation of beneficial accessory proteins allows acclimatization of the virus to the host. The two-third segment of coronavirus genome codes for RNA dependent RNA polymerase (viral polymerase), other transcription enzymes and factors and non-structural proteins [7]

The best preventive measure to combat pathogenic diseases is vaccination [8]. The emergence of recombinant DNA technology and whole genome sequencing of microbes widened the scope of reverse vaccinology. The computational vaccine design through reverse vaccinology approach analyses the proteome expressed by the microorganism of interest. It allows prediction of antigens that can act as most efficient vaccine candidates [9]. Vaccines can be polyvalent by the use of multiple immunogens from a range of serotypes or use of conserved antigens found in those serotypes [8]. Peptide vaccines are immunodominant B-cell and T-cell epitopes that can activate cellular immune response [10]. Synthesis of peptide vaccines is relatively easy, cheaper and the product is stable and non infectious [11].

T cell epitopes are exclusively peptides that are either conformational or linear based on their structure and paratope binding. Antigenic peptides complexed with MHC class I or MHC class II molecules are presented to T cells. MHC class I molecules exist on the surface of all nucleated cells, while MHC class II molecules are specifically possessed by specialized antigen presenting cells and lymphocytes. The extracellular peptides of length 8–11 amino acids bind to MHC class I molecules which are recognized by CD8 + T cell receptors. Whereas, 12–25 amino acids long peptides are degraded intracellularly and displayed by MHC class II molecules that are identified by CD4 + T cell receptors. Antigen recognition leads CD8 + T cells to become cytotoxic T lymphocytes and CD4 T-cells become T helper cells. Cell mediated immune responses lead to cytokine production and induction of B-cells for antibody maturation. On epitope presentation and recognition, the T-cells multiply into effectors that can respond to the same antigen displayed by other cells. Subsequently, memory cells are also generated and adaptive immunity is established [11–12] [10] [13].

According to the WHO as on 5th April 2021, the total confirmed cases of COVID-19 were 150M with 3.15M deaths. With an aim to predict the best epitopes of SARS-CoV-2/human/USA/CA-CZB-1053/2020 isolate, it is essential to study the degree of immunogenicity of identified epitopes. In this study, the surface glycoprotein, membrane glycoprotein and envelope protein of the SARS-CoV-2/human/USA/CA-CZB-1053/2020 isolate were retrieved for identification of robust vaccine candidates.

Materials And Methodology

Protein sequence extraction

The protein sequences of three proteins *viz.* surface glycoprotein, membrane glycoprotein and envelope protein of the virus, SARS-CoV-2/human/USA/CA CZB 1055/2020 isolate were selected for the recent study. This set of proteins was extracted from the protein database (<http://www.ncbi.nlm.nih.gov>) having accession number QJW39952.1, QJW39955.1 and QJW39954.1, respectively.

Prediction of antigenic CD8 and CD4 T-cell epitopes

CD8+ T- cells (cytotoxic T-cells) defend the body against foreign attackers and cancerous cells, while CD4+ T-cells (helper T-cells) are the cells of immune system that combats against infections.

Both CD8 and CD4 T-cell epitopes from three proteins of SARS-CoV-2/human/USA/CA CZB 1055/2020 isolate were identified by Hopp and Woods method [14]. Further, the process of N-linked glycosylation, a co-translational process that involves the transfer of an oligosaccharide to any amino acid, may turn it into an ineffective epitope as a vaccine candidate. So, we selected only those epitopes that were devoid of tripeptide sequences *i.e.* Asn-X-Ser/Thr (N-X-S/T), where X stands for any amino acid other than Proline in this study [15].

Immunogenicity score

The immunogenicity score (the potentiality of T-cell to produce antibodies against any antigen) was calculated using AbDesigner algorithm [16]. The immunogenicity score is directly proportional with the immunogenic response *i.e.* with an increase in immunogenicity score the immunogenic response also increases. Different parameters of CD8 and CD4 T-cell epitopes *viz.* immunogenicity, number of aliphatic amino acids, antigenicity and hydrophilicity were enumerated by using a PERL language based computer by our corresponding author SC.

Physiochemical properties of T-cell epitopes

The physiochemical characterisation of T-cell epitopes were predicted with the online tool ExPASy-ProtParam (<https://web.expasy.org/protparam/>). Further, cleavage sites and Boman index value of each epitope were also evaluated with the online tools Peptide cutter (<https://web.expasy.org/peptidecutter/>) and Antimicrobial Peptide Database (APD3) (http://aps.unmc.edu/AP/prediction/prediction_main.php), respectively. If a protein acquires Boman index greater than 2.48kcal/mol, then it is more likely to interact with other proteins.

Results

Investigation of immunogenicity

With the usage of several bioinformatic tools, five 9-mer CD8 T-cell epitopes and five 15-mer CD4 T-cell epitopes from three proteins namely surface glycoprotein, membrane glycoprotein and envelope protein of SARS-CoV-2/human/USA/CA CZB 1055/202 isolate were identified.

In order to combat the pandemic of SARS-CoV-2, the immunogenicity scores of the five best 9-mer CD8 T-cell epitopes for three proteins *viz.* surface glycoprotein, membrane glycoprotein and envelope protein were investigated and represented in Table 1a. In surface glycoprotein the peptide PDPSKPSKR was found with the highest immunogenicity score of 9.20, in membrane glycoprotein two peptides TDHSSSSDN and NTDHSSSSD had the highest immunogenicity score of 8.72 and likewise, in envelope protein the peptide YSRVKNLNS was found with the highest immunogenicity score of 6.37.

Table 1a

CD8 T-cell epitopes of SARS CoV2/human/USA/CA CZB 1055/2020 isolate showing number of aliphatic amino acids and immunogenicity (Ig) score (Hopp and Woods 1981)

Name of proteins	CD8 T- cell epitopes	Aliphatic amino acids	Ig analysis of epitopes	
			Hydropathy index	Immunogenicity score
Surface glycoprotein	PDPSKPSKR	2	6.97	9.2
	DPSKPSKRS	2	6.88	9.01
	DYNYKLPDD	2	6.53	8.23
	WNSNNLDSK	2	6.34	8.12
	QTQTNSPRR	0	7.09	8.08
Membrane glycoprotein	TDHSSSSDN	0	6.46	8.72
	NTDHSSSSD	0	6.46	8.72
	DHSSSSDNI	1	5.88	7.59
	GNYKLNTDH	3	6.3	7.56
	NYKLNTDHS	2	6.34	7.48
Envelope protein	YSRVKNLNS	3	5.64	6.37
	KPSFYVYSR	2	5.3	5.72
	VYSRVKNLN	4	5.09	5.24
	YSFVSEETG	2	4.94	4.99
	FYVYSRVKN	3	4.96	4.86

The binding efficiency of an epitope is highly enhanced with the presence of aliphatic amino acid sequence on it. Thus, the presence of aliphatic amino acid namely, Gly, Ala, Lys, Ile, Met, Val and Leu in the desired epitopes can lead to proper interactions with lymphocytes. Here, the CD8 T-cell epitopes were analysed for their total number of aliphatic amino acids (Table 1a). Four epitopes of surface glycoprotein *viz.* PDPSKPSKR, DPSKPSKRS, DYNYKLPDD and WNSNNLDSK possessed two aliphatic amino acids each, while epitope QTQTNSPRR did not possess any aliphatic amino acid. In membrane glycoprotein, epitope DHSSSSDNI had only one aliphatic amino acid, epitope NYKLNTDHS had two aliphatic amino acids and epitope GNYKLNTDH had three aliphatic amino acids. Further, in envelope protein, the epitopes KPSFYVYSR and YSFVSEETG possessed two aliphatic amino acids; epitopes YSRVKNLNS and

FYVYSRVKN had three aliphatic amino acids while epitope VYSRVKNLN possessed four aliphatic amino acids.

The immunogenicity scores of the five best 15-mer CD4 T-cell epitopes for three proteins namely surface glycoprotein, membrane glycoprotein and envelope protein were evaluated and reported in Table 1b. Epitopes NSNNLDSKVGGNYNY of surface glycoprotein, GNYKLNTDHSSSSDN of membrane glycoprotein and KPSFYVYSRVKNLNS of envelope protein possessed the highest immunogenicity score of 7.81, 8.14 and 5.70, respectively.

Table 1b

CD4 T-cell epitopes of SARS CoV2/human/USA/CA CZB 1055/2020 isolate showing number of aliphatic amino acids and immunogenicity (Ig) score (Hopp and Woods 1981)

Name of proteins	CD4 T- cell epitopes	Aliphatic amino acids	Ig analysis of epitopes	
			Hydropathy index	Immunogenicity score
Surface glycoprotein	NSNNLDSKVGGNYNY	5	5.96	7.81
	WNSNNLDSKVGGNYN	5	5.93	7.71
	ASYQTQTNSPRRARS	2	6.31	6.94
	AWNSNNLDSKVGGNY	6	5.58	6.92
	HRSYLTPGDSSSGWT	3	5.61	6.84
Membrane glycoprotein	GNYKLNTDHSSSSDN	3	6.26	8.14
	NYKLNTDHSSSSDNI	3	5.93	7.29
	IGNYKLNTDHSSSSD	4	5.73	7.05
	RIGNYKLNTDHSSSS	4	5.79	6.95
	RYRIGNYKLNTDHSS	4	6.07	6.92
Envelope protein	KPSFYVYSRVKNLNS	5	5.23	5.70
	VKPSFYVYSRVKNLN	6	4.89	5.04
	SLVKPSFYVYSRVKN	6	4.71	4.80
	LVKPSFYVYSRVKNL	7	4.41	4.23
	YSFVSEETGTLIVNS	5	4.27	4.14

Aliphatic amino acids in the epitopes of surface glycoprotein varied from 3 (HRSYLTPGDSSSGWT) to 6 (AWNSNNLDSKVGGNY). In membrane glycoprotein three epitopes (IGNYKLNTDHSSSSD, RIGNYKLNTDHSSSS and RYRIGNYKLNTDHSS) possessed 4 aliphatic amino acids and two epitopes (GNYKLNTDHSSSSDN and NYKLNTDHSSSSDN) had 3 aliphatic amino acids. Further, in envelope protein, the epitopes KPSFYVYSRVKLNLS and YSFVSEETGTLIVNS had 5 aliphatic amino acids, epitopes VKPSFYVYSRVKLN and SLVKPSFYVYSRVKN possessed 6 aliphatic amino acids while epitope LVKPSFYVYSRVKNL had 7 aliphatic amino acids, shown in Table 1b. Epitopes with high immunogenicity scores are usually more immunogenic in nature and thus these peptides could be the potential choice as candidates in vaccine formulation.

Investigation of antigenicity

Five CD8 T-cell epitopes from each of the three proteins were identified and evaluated for antigenicity (Fig 1a). The antigenicity score of 15 epitopes varied within the range from 8.29 (WNSNNLDSK) to 9.77 (FYVYSRVKN). Similarly, for CD4 T-cell epitopes the antigenicity score was evaluated and found to vary from 14.14 (WNSNNLDSKVGGNYN) to 16.66 (LVKPSFYVYSRVKNL) shown in Fig 1b. Epitope with a high antigenicity score normally possesses high antigenic nature and this is considered as a desirable feature of a peptide to be used as vaccine candidate.

Investigation of hydrophilicity

Hydrophilicity score is the average hydrophilicity value of amino acids that is helpful in the prediction of protein structure. The hydrophilicity score of each CD8 T-cell epitope for three proteins was determined having potential to raise immunogenicity in the host [14]. The hydrophilicity score, the epitope position and total net charge of each CD8 T-cell epitope were depicted in Table 1a. Out of five epitopes of surface glycoprotein, the epitope DPSKPSKRS at position 807-815 and net charge 2.00 had the highest hydrophilicity score of 12.90. In case of membrane glycoprotein, two epitopes namely TDHSSSSDN (position 208-216) and NTDHSSSSD (position 207-215) had the highest hydrophilicity score of 6.50, and net charge -1.75. Likewise, in envelope protein, the epitope YSRVKLNLS possessed the highest hydrophilicity score of 1.40, position 59-67 and net charge 2.00.

Similarly, five CD4 T-cell epitopes for each of the three proteins were identified [14] and their hydrophilicity scores were determined as reported in Table 2b. In surface glycoprotein, epitope ASYQTQTNSPRRARS possessed the highest hydrophilicity score of 6.40, position 671-685 and net charge 3.00. Out of five epitopes of membrane glycoprotein, epitope GNYKLNTDHSSSSDN had the highest hydrophilicity score of 5.80, position 202-216 and net charge -0.75. In case of envelope protein, hydrophilicity scores of all the identified epitopes were less than 0, thus these cannot be used as successful vaccine candidates. High hydrophilicity scores of peptides along with their respective locations suggest their hydrophilic sections in the protein molecules and these regions are usually exposed to external surface of the protein molecules.

These sections can easily bind with MHC molecules and the complexes formed might exhibit APCs on the outer regions. The T lymphocytes can easily identify those cells and damage them.

Table 2a

CD8 T-cell epitopes of SARS CoV2/human/USA/CA CZB 1055/2020 isolate showing hydrophilicity score and total net charge (Hopp and Woods 1981)

Name of proteins	CD8 T- cell epitopes	Epitope position	Hydrophilicity score	Net charge
Surface glycoprotein	PDPSKPSKR	806-814	12.60	2.00
	DPSKPSKRS	807-815	12.90	2.00
	DYNYKLPDD	419-427	5.80	-2.00
	WNSNNLDSK	435-443	2.00	0.00
	QTQTNSPRR	674-682	6.10	2.00
Membrane glycoprotein	TDHSSSSDN	208-216	6.50	-1.75
	NTDHSSSSD	207-215	6.50	-1.75
	DHSSSSDNI	209-217	5.10	-1.75
	GNYKLNTDH	202-210	1.40	0.25
	NYKLNTDHS	203-211	1.70	0.25
Envelope protein	YSRVKNLNS	59-67	1.40	2.00
	KPSFYVYSR	53-61	-2.00	2.00
	VYSRVKNLN	58-66	-0.40	2.00
	YSFVSEETG	2-10	-0.10	-2.00
	FYVYSRVKN	56-64	-3.60	2.00

Table 2b

CD4 T-cell epitopes of SARS CoV2/human/USA/CA CZB 1055/2020 isolate showing hydrophilicity score and total net charge (Hopp and Woods 1981)

Name of proteins	CD-4 T- cell epitopes	Epitope position	Hydrophilicity score	Net charge
Surface glycoprotein	NSNNLDSKVGGNYNY	436-450	-0.30	0.00
	WNSNNLDSKVGGNYN	435-449	-1.40	0.00
	ASYQTQTNSPRRARS	671-685	6.40	3.00
	AWNSNNLDSKVGGNY	434-448	-2.10	0.00
	HRSYLTPGDSSSGWT	244-258	-1.60	0.25
Membrane glycoprotein	GNYKLNTDHSSSSDN	202-216	5.80	-0.75
	NYKLNTDHSSSSDNI	203-217	4.00	-0.75
	IGNYKLNTDHSSSSD	201-215	3.80	-0.75
	RIGNYKLNTDHSSSS	200-214	3.80	1.25
	RYRIGNYKLNTDHSS	198-212	3.90	2.25
Envelope protein	KPSFYVYSRVKNLNS	53-67	-1.60	3.00
	VKPSFYVYSRVKNLN	52-66	-3.40	3.00
	SLVKPSFYVYSRVKN	50-64	-3.30	3.00
	LVKPSFYVYSRVKNL	51-65	-5.40	3.00
	YSFVSEETGTLIVNS	2-16	-5.10	-2.00

Boman Index (potential protein interaction)

Boman index of each identified CD8 T-cell epitope in three proteins of SARS-CoV-2 was estimated and shown in Fig 2a. A minimum Boman index of 2.48 kcal/mol is considered for efficient binding with the MHC molecule. From this analysis, we could report efficient CD8 T-cell epitopes that might be presented to APCs and thereby elicit immune response in the host. Notably, Boman indices of most epitopes were >2.48 kcal/mol and thus could be used as vaccine candidates. However, a few epitopes namely KPSFYVYSR, FYVYSRVKN and YSFVSEETG had Boman index <2.48 kcal/mol, thus these epitopes would not be effective as vaccine candidates.

Further, the Boman indices of 15 CD4 T- cell epitopes across three proteins of SARS-CoV-2 were determined and depicted in Fig 2b. Here, the epitopes viz. AWNSNNLDSKVGGNY, KPSFYVYSRVKNLNS, VKPSFYVYSRVKNLN, SLVKPSFYVYSRVKN, LVKPSFYVYSRVKNL and YSFVSEETGTLIVNS possessed Boman index <2.48 kcal/mol and therefore we did not consider them as effective vaccine candidates.

Investigation of amino acid contents

The amino acid content of CD8 T-cell epitopes of SARS-CoV-2 was analysed and represented in Fig 3a. Distributions of amino acids were found to be different across different epitopes. Interestingly, a few amino acids *viz.* Pro, Ser, Asp and Asn in surface glycoprotein comprised of 33% of the total composition, while Ser amino acid in membrane glycoprotein consisted of 44% of the total peptide composition.

Likewise, the amino acid composition for CD4 T-cell epitopes for SARS-CoV-2 proteins was analysed and shown in Fig 3b. The epitopes exhibited different patterns of amino acid compositions. Most CD4 T-cell epitopes possessed amino acid to the tune of 6% in terms of total composition, while a few other amino acids were found to vary from 13 to 33% contents.

Moreover, the identified CD8 T-cell and CD4 T-cell epitopes, if used as vaccine candidates, against SARS-CoV-2 might be amenable to cleavage by several chemicals and enzymes inside host cell, the results of their cleavage sites are depicted in supplementary files (S1, S2).

Discussion

In current investigation, the efficient peptide sequences for potential use as vaccine candidates were identified in three proteins *viz.* surface glycoprotein, membrane glycoprotein and envelope protein of SARS-CoV-2/human/USA/CA CZB 1055/2020 isolate. All the peptides identified as epitopes were evaluated using several bioinformatics tools. A few peptides were discarded in the study for not fulfilling the criteria for vaccine formulation. While, a few epitopes were reported to fulfil the selected criteria and thus we could conclude that these epitopes might generate immune response in the host against SARS-CoV-2. These potential epitopes might be considered in the development of a novel peptide vaccine for fighting the pandemic through prophylactic measure.

Alkhurma hemorrhagic fever virus is mostly prevalent in human beings of sub-tropical and tropical regions. This virus of Flaviviridae family was considered as a major public health concern. A study reported a total of 25 T-cell (MHC-II=17, MHC-I=8) and 5 B-cell epitopes from the envelope protein of alkhurma hemorrhagic fever virus that could be efficiently used as epitope-based peptide vaccine against this virus [17].

Lassa virus (LASV), assigned to Arenaviridae virus family, is mainly responsible for fatal hemorrhagic fever disease known as lassa fever disease (LASV). The virus is transmitted to humans by *Mastomys natalensis*, a rodent and it had infected a large number of people in western Africa leading to 5000–10,000 deaths per annum. A common potential B-cell and T-cell epitope SSNLYKGVY that would induce immunity was identified as an efficient vaccine candidate against LASV [18].

Aichi virus 1 (AiV-1) of Picornaviridae family causes gastroenteritis in humans and it is hazardous for children in the developing countries. From a study on this virus, three B-cell epitopes *i.e.* PPLPTP,

LPPLPTP and PLPPDT and one T-cell epitope FSIPYTSPL (binds to both MHC- α and MHC- β) were found to be efficient targets for boosting immunity against this virus [19].

Chikungunya virus (CHIKV), transmitted by *Aedes* mosquitoes, causes an infectious viral disease *i.e.* Chikungunya infection. Based on *in-silico* analysis, the T-cell and B-cell epitopes, capable of inducing immune response, were identified in the proteins of the viral strains. The potential T-cell epitopes identified were KKKPGRRERMCMKIE, AEEEREAEEL and DAEKEAEEEREAEELT, likewise the potential B-cell epitopes identified in this virus were SSKYDLECAQ and QVLKAKNIGL [20].

Merkel cell polyomavirus (MCPYV) is associated with Merkel cell carcinoma [21], a type of deadly skin malignancy. MCPYV, a member of Polyomaviridae family, under the genus *Orthopolyomavirus* mostly affects the light-complexioned, older and immunosuppressed individuals (diagnosed with AIDS). A study predicted three B-cell epitopes *viz.* QEKTVYP, QEKTVY and KTVYPK and T-cell epitopes *viz.* LLVKGGVEV, SLFSNLMPK and LQMWEAISV (binding to MHC- α alleles) and ISSLINVHY, IELYLNPRM and NSLFSNLM (binding to MHC- β alleles) as efficient components for peptide vaccine against MCPYV [22].

Conclusions

From the current study using an *in silico* approach, we identified a few potential CD8 T-cell and CD4 T-cell epitopes in three proteins (*viz.* surface glycoprotein, membrane glycoprotein and envelope protein) for use as components in peptide vaccine formulation against SARS CoV-2/human/USA/CA CZB 1055/2020 isolate. In order to design an effective vaccine, primary criterion is to identify the epitopes with high immunogenicity score, as it would induce higher immune response in the host. Out of 15 epitopes identified as CD8 T-cell epitopes, only three 9-mer peptides namely PDPSKPSKR, DPSKPSKRS and QTQTNSPRR of surface glycoprotein were found to have high scores for immunogenicity, antigenicity, hydrophilicity, Boman index and hydropathy and we concluded that these epitopes have great potential as vaccine candidates. In membrane glycoprotein, the epitopes *i.e.* GNYKLNTDH and NYKLNTDHS possessed high immunogenicity, antigenicity, Boman index and hydropathy index, however their hydrophilicity scores were low, so we did not consider them as potential vaccine candidate. Likewise, in envelope protein, the epitope YSRVKNLNS possessed high values of immunogenicity, antigenicity and hydropathy index, however their hydrophilicity and Boman index were low and therefore we excluded them as vaccine candidates. Further, the epitopes possessing net negative charge were discarded from our analysis.

In the case of 15-mer CD4 T-cell epitopes, we observed that the epitopes ASYQTQTNSPRRARS of surface glycoprotein; RIGNYKLNTDHSSSS and RYRIGNYKLNTDHSS of membrane glycoprotein possessed high scores of immunogenicity, antigenicity, hydrophilicity, Boman index and hydropathy index and hence we identified them as effective vaccine candidates. While, in the case of envelope protein the hydrophilicity scores of all the five epitopes were very low and thus none of them could qualify as potential component of peptide vaccine.

Pharma industries might use these identified CD8 T-cell epitopes viz. PDPSKPSKR, DPSKPSKRS and QTQTNSPRR and CD4 T-cell epitopes viz. ASYQTQTNSPRRARS, RIGNYKLNTDHSSSS and RYRIGNYKLNTDHSS for developing a multi- epitope loaded peptide vaccine by combining in various proportions with a carrier protein or strong adjuvant. These epitopes could be administered as a prophylactic vaccine, following proper clinical trials to confirm their efficacy and safety in host. This might prevent the devastating spread of the virus by boosting immunity in human.

In view of recent outbreak of SARS-CoV-2 an endless struggle for survival is continuing worldwide. It is, therefore, imperative to construct peptide vaccine comprising different sets of epitopes in various combinations. Immunity against SARS-CoV-2 could be induced in human through the large scale use of peptide vaccine as a prophylactic measure in human populations across the globe.

Declarations

Conflicts

Authors declare no conflict of interests in the manuscript.

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Figures

Figure 1

(a) Antigenicity of CD8 T-cell epitopes of SARS-CoV-2/human/USA/CA CZB 1055/2020 isolate, (b) Antigenicity of CD4 T- cell epitopes of SARS-CoV-2/human/USA/CA CZB 1055/2020 isolate

Figure 2

(a) Boman index of CD8 T-cell epitopes of SARS-CoV-2/human/USA/CA CZB 1055/2020 isolate, (b) Boman index of CD4 T- cell epitopes of SARS-CoV-2/human/USA/CA CZB 1055/2020 isolate

Figure 3

(a) Composition of amino acids of each CD 8 T-cell epitope of SARS-CoV-2/human/USA/CA CZB 1055/2020 isolate, (b) Composition of amino acids of each CD4 T-cell epitopes of SARS-CoV-2/human/USA/CA CZB 1055/2020 isolate

Supplementary Files

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