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Submission date: 24-Sep-2022 09:11AM (UTC-0400)
Submission ID: 1907779912
File name: 10.33435-tcandtc.1140158-2523751.pdf (563.86K)
Word count: 5182
Character count: 27160

Turkish Computational and Theoretical Chemistry

Turkish Comp Theo Chem (TC&TC)

Volume(Issue): 7(1) – Year: 2023 – Pages: 62-71

e-ISSN: 2602-3237

https://doi.org/10.33435/tcandtc.1140158

Received: 04.07.2022 **Accepted:** 09.09.2022 *Research Article*

Homology Modeling Epitopes of Kirsten Rat Sarcoma (KRAS) G12D, G12V and G12R as Pancreatic Ductal Adenocarcinoma Vaccine Candidates

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Abstract: Pancreatic ductal adenocarcinoma (PDAC) is among the world's deadliest cancers. Multiple studies demonstrated that PDAC is frequently characterized by the presence of Kirsten Rat Sarcoma (KRAS) G12D, G12V, and G12R protein mutants. The mutants are potential immunotherapy targets due to their potential as cancer-specific neoantigens. KRAS G12D, G12V and G12R contain vaccine-immunogenic epitopes. KRAS G12D, G12V and G12R epitopes were presented at major histocompatibility complexes (MHC) class I. The rational design of peptide vaccines to enhance the efficacy of cancer immunotherapy is facilitated by developing a peptide structural data library and knowledge of the MHC and antigen presentation processes. Before predicting peptide activity against MHC, homology modeling must transform the peptide into a three-dimensional structure. In this study, I-TASSER was used to perform homology modeling with the assistance of other applications. In silico methods for predicting epitopes to produce rationally designed peptide vaccines can increase the efficacy of these vaccines. This study yielded four epitope models that are potential PDAC vaccination candidates, KSFEDIHHYR, GIPFIETSAK, VVVGARGVGK and VVVGADGVGK.

Keywords: Homology Modeling, Epitope, KRAS, Vaccine and PDAC.

1. Introduction

In 2020, pancreatic cancer will be the seventh most lethal cancer worldwide. The global incidence of pancreatic cancer is estimated to account for 4.7% of all cancer deaths [1]. Pancreatic cancer is one of the hardest-to-treat cancers with the poorest prognosis [2]. Pancreatic cancer is the development of malignant cells in a portion of the pancreas. This cancer can develop in any part of the pancreas, but approximately 70% of pancreatic cancers are found in the pancreatic head [3].

There are two different types of pancreatic cancer, exocrine and endocrine. The most prevalent form of pancreatic cancer is exocrine pancreatic cancer [4]. Approximately 95% of all cases of pancreatic cancer are pancreatic ductal adenocarcinoma (PDAC) [5]. PDAC is pancreatic duct-originating cancer [6]. When PDAC symptoms first appear in a patient, the cancer advances so rapidly that the average chance of undergoing surgery is only 20% [7]. Due to the relative absence of symptoms in the disease's early stages, PDAC is rarely diagnosed early [8,9]. Several studies have demonstrated that mutations in the Kirsten Rat Sarcoma (KRAS) protein frequently characterize PDAC [10,11].

KRAS plays an important role in PDAC and it is believed to be the main target for treatment [12–14]. KRAS is one of the most frequently mutated proto-oncogenes in human cancer [15–17]. The dominant oncogenic mutation of KRAS is a single amino acid substitution at codon 12 [18,19]. KRAS mutations at codon 12 occur sporadically in normal pancreatic tissue and are detected in 30% of early neoplasms, increasing to almost 100% in late PDAC [20,21]. These mutations occur in 70-95% of PDAC cases and 71% of pancreatic cancer specimens in the COSMICS KRAS database. In PDAC, the most common KRAS mutations are G12D, G12V and

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G12R. The consistency, frequency, and specificity of these "neoantigen" tumors make them attractive therapeutic targets [22,23].

KRAS G12D, G12V, and G12R are prospective immunotherapy targets because they have the potential to be cancer-specific neoantigens. KRAS G12D, G12V and G12R contain immunogenic epitopes suitable for vaccination. The KRAS epitopes G12D, G12V and G12R were presented in major histocompatibility complexes (MHC) class I [22,24,25].

MHC I plays a very important key role in recognition of virus-infected and transformed cells [26,27]. HLA-A*11:01 is one of the MHC I molecules that can bind peptides with KRAS amino acid mutation at codon 12 [22,28,29]. The targeting of KRAS and its downstream signaling pathways can be used as strong immune modulators in cancer immunotherapy [30].

Cancer vaccines have the potential as an effective modality for the treatment or even prevention of cancer [31]. T-cell peptide vaccines induce a potent MHC-dependent immune response [32–35]. A rationally designed vaccine epitope can produce a controlled immune response. With the development of the peptide structural data library and greater knowledge of MHC and antigen presentation processes, the rational design of peptide vaccines can increase the effectiveness of cancer immunotherapy [36].

Homology modeling was carried out to predict the protein's three-dimensional (3D) structure, which was expected to be comparable to the experimental results in the presence of the protein sequence data. Homology modeling is a solution to obtain protein structure information in case of failure in the experiment because the protein is too large for NMR analysis and cannot be crystallized for X-ray diffraction [37]. Furthermore, homology modeling can be combined with other computational methods, such as docking to determine potential interactions with substrates, inhibitors or cofactors [38].

2. Computational Method

2.1. Transmembrane Topology Prediction

The test protein used in this study was KRAS protein mutant G12D, G12V and G12R Homo sapiens consisting of 169 amino acids with the allele HLA-A*11:01. KRAS G12D protein was downloaded in FASTA format from NCBI (https://www.ncbi.nlm.nih.gov/protein) with accession number 5XCO_A (Figure 1). The KRAS G12V and G12R proteins can use the FASTA KRAS G12D format by changing codon 12, G to V and G to R. The following is the amino acid sequence of KRAS G12D.

Figure 1. FASTA format from KRAS G12D (5XCO_A) on NCBI

The transmembrane topology of G12D, G12V and G12R proteins was predicted using MEMSAT-SVM and MEMSAT3 (http://bioinf.cs.ucl.ac.uk/psipred/?memsatsvm=1) [39,40].

2.2. Epitope Analysis

Epitope analysis of G12D, G12V and G12R was performed using NetMHC version 4.0 (http://www.cbs.dtu.dk/services/NetMHC/) [41] and IEDB (http://tools.iedb.org/mhci/) [42]. In NetMHC and IEDB, each epitope consists of 10 amino acids [43,44]. The selected epitope from the NetMHC results is the epitope that has the possibility of binding to MHC I, %Rank 0.00 to 2.00 [45,46]. The selected epitopes from the IEDB results are epitopes that have a high binding affinity with MHC I. The binding affinity can be seen from the percentile rank (%Rank). The lower the %Rank signifies the higher the binding affinity of the epitope to MHC 1 [47].

2.3. Antigenicity Prediction

Proteins and epitopes with high binding affinity to MHC I were predicted for their antigenicity using VaxiJen version 2.0 (http://www.ddg-pharmfac.net/vaxijen/VaxiJen/VaxiJen.html). In VaxiJen, epitopes were entered in FASTA format with target tumor organism, threshold 0.4 and auto cross-covariance (ACC) as output [48,49].

2.4. Homology Modeling

Homology modeling of possible epitopes as antigens was carried out using the I-TASSER (Iterative Threading Assembly Refinement) software (https://zhanglab.ccmb. med.umich.edu/I-TASSER/) [50]. Prior to homology modeling, the template identification and alignment of these epitopes with the proteins in the PDB database was carried out using BLASTP® (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Pr

oteins). The two best templates were selected based on sequence identification, query cover and E-value [51]. Epitope alignment with both templates was also carried out using Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo/) which would then be used for homology modeling with I-TASSER [52,53].

On the I-TASSER server, the epitope sequences are entered in FASTA format and the alignment results from Clustal Omega are used as reference templates in epitope modeling. From the results of homology modeling I-TASSER obtained 5 3D models of epitope and selected 1 model with the largest C-score [50].

2.5. Model Validation

Epitope-epitope homology modeling results from Modeller were validated with MolProbity (http://molprobity.biochem.duke.edu/), ProSA (Protein Structure Analysis)-web (https://prosa.services.came.sbg.ac.at/prosa.php) and QMEAN (Qualitative Model Energy Analysis) (https:// swissmodel.expasy.org/qmean/). In MolProbity obtained Clash Score, Poor Rotamers, Ramachandran Favored and MolProbity Score. Meanwhile, ProSA-web and QMEAN produced Z-score and QMEAN Score, respectively [54–57].

2.6. Refinement

Refinement of the validated epitope model was carried out using GalaxyRefine (http://galaxy.seoklab.org/ cgi-bin/submit. cgi? type=REFINE). On GalaxyRefine, epitopes are uploaded in PDB format. GalaxyRefine provides repeated structure perturbations and overall structural relaxation with molecular dynamics simulation. Then obtained 5 epitope models with validation parameters, GDT-HA, RMSD, MolProbity Score, Clash Score, Poor Rotamers and Ramachandran Favored. From the five models, 1 best model was selected with GDT-HA > 60%, RMSD 2, MolProbity Score < 2, Clash Score < 0.4, Poor Rotamers < 0.3% and Ramachandran Favored > 98% [58–60].

3. Results and discussion

Prediction of the transmembrane topology of the KRAS G12D, G12V and G12R Homo sapiens mutants consisting of 169 amino acids using MEMSAT-SVM and MEMSAT3 stated that the KRAS G12D, G12V and G12R mutants is transmembrane proteins with 1 domain. In MEMSAT-SVM results, the helical transmembrane of the KRAS G12D, G12V and G12R protein mutants starts from amino acid 9 to amino acid 24 with N terminal in the cytoplasm and C terminal outside the cell. Meanwhile, the MEMSAT3 prediction results show a helical transmembrane starting from amino acids 92 to amino acids 111 with N terminals outside the cell and C terminals in the cytoplasm (Figure 2).

In the epitopes analysis of KRAS G12D, G12V and G12R using NetMHC, 7 epitopes consisting of 10 amino acids were found that have strong bonds with MHC I. The IEDB produced 5 epitopes consisting of 10 amino acids which intersect with the NetMHC results. The selected epitopes from the results of the NetMHCII and IEDB analysis are epitopes that have high binding affinity with the MHC I allele HLA-A*11:01 Strong binding peptides gave %Rank ≤ 0.50 with affinity threshold ≤ 50 nM and weak binding peptides gave %Rank ≤ 2.00 with affinity threshold ≤ 500 nM (Table 1) [45–47].

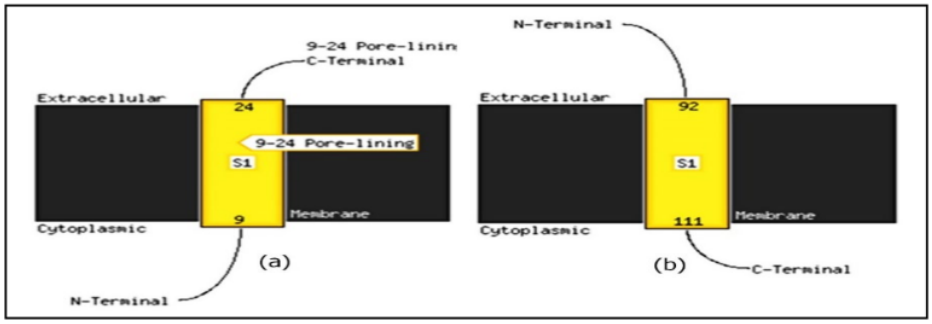

Figure 2. Prediction results of transmembrane topologies KRAS G12D, G12V and G12R (a) MEMSAT-SVM; (b) MEMSAT3.

The epitopes that have strong binding to MHC I were predicted for their antigenicity using VaxiJen with a threshold limit of 0.4. From the results of the prediction of the antigenicity of the epitopes, it was found that 5 epitopes have the possibility of being antigenic and can be used as candidates for the PDAC vaccine, epitopes 1, 3, 5, 6 and 7 (Table 1). However, because the results of the IEDB analysis showed that epitope 6 had a %Rank more than the threshold, homology modeling was not carried out on the epitope.

Table 1. Epitope analysis results and antigenicity prediction of KRAS G12D, G12V and G12R

No.	Sequence	Epitope	NetMHC		IEDB	Antigenicity
			%Rank	Bind Level	%Rank	
1	88-97	KSFEDIHHYR	0.25	SB	1.30	PA
2	79-88	LCVFAINNTK	0.60	WB	>2.00	PNA
3	138-147	GIPFIETSAK	0.80	WB	0.88	PA
4	7-16 (G12V)	VVVGAVGVGK	0.90	WB	0.89	PNA
5	7-16 (G12R)	VVVGARGVGK	1.40	WB	1.40	PA
6	156-165	FYTLVREIRK	1.60	WB	>2.00	PA
7	7-16 (G12D)	VVVGADGVGK	1.70	WB	1.65	PA

Table 2. KRAS G12D, G12V and G12R epitope templates from BLASTP®

Epitope	PDB Code Template	Query Cover	E-value	Sequence Identity
1	4DSO_A	100%	3e-06	100.00%
	5UQW_A	100%	3e-06	100.00%
3	3CON_A	100%	9e-07	100.00%
	4DSO_A	100%	9e-07	100.00%
5	4QL3_A	100%	6e-04	100.00%
	421P_A	100%	6e-04	100.00%
7	4DSO_A	100%	6e-04	100.00%
	5US4_A	100%	6e-04	100.00%

SB = Strong Binding; WB = Weak Binding; PA = Probable Antigen; PNA = Probable Non-Antigen

In the identification and alignment of the PDAC vaccine candidate epitopes with the proteins in the PDB database using BLASTP®, 2 templates were obtained for each epitope. The two templates have a query cover alignment percentage with an epitope of 100%, sequence identity 100% and the lowest E-value of all database sequence alignments (Table 2). Multiple alignment of epitopes with the two templates was also carried out using Clustal Omega which will then be used for homology modeling with I-TASSER.

Homology modeling for 4 epitopes was performed using I-TASSER. I-TASSER is an on-line application for predicting the 3D structure of proteins with high quality from amino acid sequences. Structural templates were identified from PDB by the multiple threading approach, LOMETS. Alignment-specific template information can be added to target templates. Then the modeling is done by iterative threading assembly simulation which is extended to annotation of structure-based functions by matching the predicted structure with known functional templates [50].

The 3D epitopes model from I-TASSER homology modeling was validated using MolProbity, ProSA-web and QMEAN. In the validation of the epitope model, there are several aspects that need to be considered, the position of the residue, the interaction between the residues and the atoms that make up the residue [38].

In MolProbity, the validation of the steric interaction of all atoms in the residue is shown by the Clash Score. Clash score is the number of collisions per 1000 atoms. A good model is a model that has a small Clash Score [37]. Geometric analysis is also an indicator that determines whether a model is good or bad. Poor Rotamer and Ramachandran Favored are parameters that can be used for geometric analysis of epitope models. Poor

Rotamer is used to see the location of the multidimensional distribution of residues. A residue is said to be Poor Rotamer if it has a branch chain χ rotamer angle below 1% of the set χ value level. MolProbity Score is a combination of Clash Score, Poor Rotamer and Ramachandran Favored [54,61].

ProSA was used to evaluate the accuracy of the protein model. The analysis was carried out based on statistical analysis of experimental protein structures, both by X-ray crystallography and NMR spectroscopy in PDB. The results of the validation of the 3D epitope structure with ProSA are in the form of a Z-score. The 3D epitope structure is said to be accurate if it has a Z-score that falls into the Z-score range of the experimental protein structure [55]. The four epitopes produced Z-scores that fall into the Z-score range of protein structures as a result of experiments with NMR spectroscopy (Figure 3).

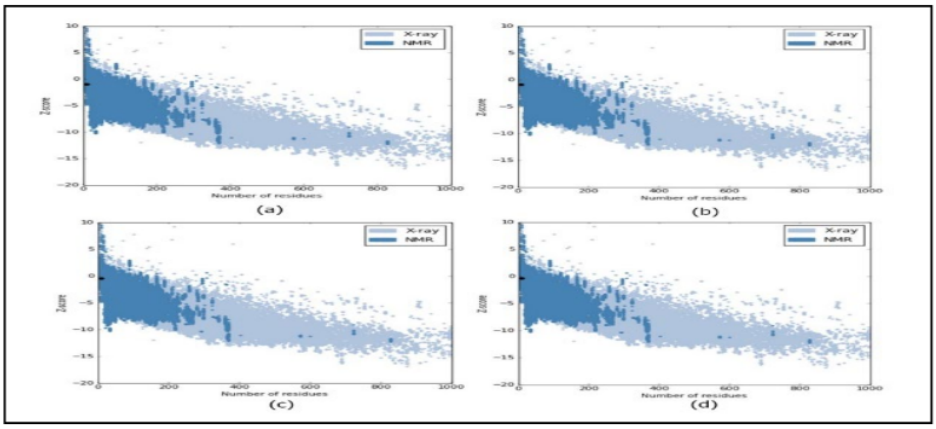

Figure 3. Plot Z-score of (a) epitope 1; (b) epitope 3; (c) epitope 5; (d) epitope 7 model in ProSA-web.

The QMEAN scoring function estimates the global quality of the model based on a linear combination of 6 structural descriptors. Four of the descriptors represent statistical potential averages, namely local geometry analyzed with torsion angle potentials of 3 consecutive amino acids, 2 distance-dependent interaction potentials based on the Cβ atom with all atoms, and solvation potential. The other two descriptors reflect agreement between the calculation and prediction of secondary structure and solvent accessibility. QMEAN Score 0-1 reflects the predicted global model [56,57].

Refinement of the epitope models that have been selected from the validation results is carried out using GalaxyRefine. In the evaluation with GalaxyRefine, the accuracy of the global and local structures was changed. GalaxyRefine initially reestablished the conformation of all side chains and relaxed the structure repeatedly through short molecular dynamics simulations for 0.6 and 0.8 ps with a time step of 4 fs after structure perturbation [58].

GDT-HA (Global Distance Test High Accuracy) and RMSD (Root Mean Square Deviation) values were used to measure the accuracy of the global structure. Meanwhile, the MolProbity score is used to measure the accuracy of the local structure as a result of the refinement. GDT-HA is a high-accuracy global quality measure of the repair of the backbone position of multi-superposition structures by calculating the percentage of the average residual distance with the Cα atom of the experimental structure with a range of 0-1. The higher the GDT-HA value, the better the accuracy. In contrast to GDT-HA, a lower RMSD value indicates better accuracy. In measuring the accuracy of local structures, a lower MolProbity Score indicates a more physically realistic model as explained in the model validation section [60]. The refinement results from GalaxyRefine for the four epitopes can be seen in Table 3.

Table 3. The validation results of 3D epitope model KRAS G12D, G12V and G12R

Parameter	A				B				Requirement
	1	3	5	7	1	3	5	7	
Clash Score	0	0	0	0	0	0	0	0	< 0.4 Å
Ramachandran Favored	100.0	75.0	62.5	37.5	100.0	100.0	100.0	87.5	> 98%
Poor Rotamers	30.00	0.00	16.67	16.67	10.00	12.50	0.00	0.00	< 0.3%
MolProbity Score	1.620	1,290	2.330	2.460	1.260	1.333	0.500	1.110	< 2 Å
Z-score	-0.99	-0.87	-0.48	-0.39	NA	NA	NA	NA	-
QMEAN Score	-1.91	-3.96	-5.28	-6.45	NA	NA	NA	NA	0-1
GDT-HA	37	NA	NA	NA	97.5	85.O	97.5	92.5	> 60%
RMSD	NA	NA	NA	NA	0.401	0.711	0.315	0.625	≤ 2 Å

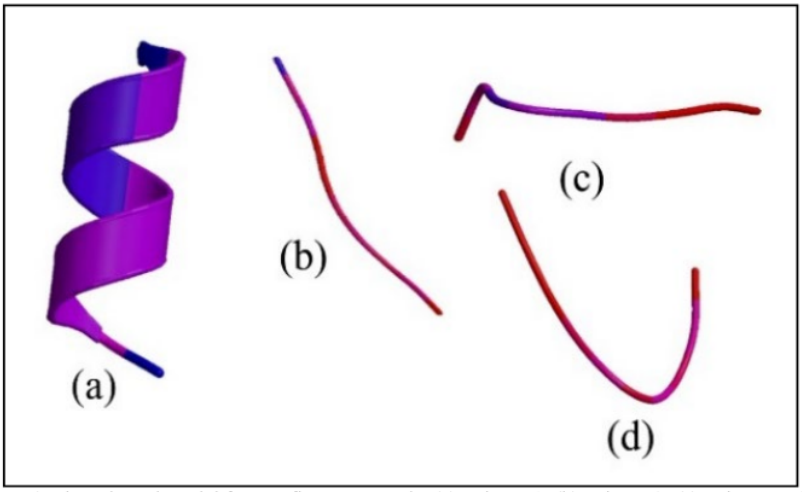

Figure 4. The selected model from refinement results (a) epitope 1; (b) epitope 3; (c) epitope 5; (d) epitope 7.

Out of the requirements; A = Epitope models before refinement; B = Epitope models after refinement; NA = Not analyzed

4. Conclusions

KSFEDIHHYR, GIPFIETSAK, VVVGARGVGK, and VVVGADGVGK are four epitope models that exhibit substantial binding affinity with MHC I and the potential to be antigenic, allowing them to be employed as vaccine candidates for PDAC based on the results of the research.

Acknowledgment

Research and Development Institute of Universitas Muhammadiyah Prof. DR. HAMKA deserves special thanks for the assistance.

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