

Original Research Article

Epitope based vaccine peptide predictions for fimH gene of *Acinetobacter baumannii*

Abstract:

Background: *Acinetobacter baumannii* is an opportunistic bacterial pathogen that is primarily associated with hospital-acquired infections. Recently, there is a dramatic increase in the incidence of multidrug-resistant (MDR) strains, which has significantly raised the profile of this emerging opportunistic pathogen. MDR is often associated with the formation of biofilms and various other virulence factors. Amidst all the genes, *fimH* gene is our area of interest in this research, because it is an important virulence factor in *A.baumannii* which encodes the Type 1 fimbriae, that helps bacteria bind to the surface of host cells initiating further infection.

Aim: The aim of this study was to assess the epitope based vaccine epitope peptide predictions for the fimH protein of *A. baumannii*.

Materials and methods: The *fimH* gene for epitope prediction was selected. Druggability and physico-chemical properties were analysed. Antigenicity was predicted. Epitope mapping of T-cell MHC class I, Class I immunogenicity, conservancy and toxicity analysis was done. T-cell class II epitopes were further mapped together with the immuno-dominant B-cell epitopes.

Results: From the selected 20 epitopes, 2 best epitopes (AALVASVCL and YSSGANAFT) were selected after analysing their antigenicity and allergenicity. The epitope YSSGANAFT showed better values in association with HLA alleles - HLA-DP, HLA-DQ, HLA-DR and TLR-2.

Conclusion: The finding of the study documents a single immunodominant peptide (sequence) as a promising vaccine candidate to treat infections caused by *A. Baumannii*. However further

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experimental analysis must be performed to assess the immunological memory and response of the peptide in both in-vitro and in-vivo studies.

Keywords: *Acinetobacter baumannii*, novel fimH, vaccine prediction, epitope, environmental strains

Running title: Epitope based vaccine peptide predictions for fimH gene of *Acinetobacter baumannii*.

INTRODUCTION:

Acinetobacter baumannii is an opportunistic bacterial pathogen that is primarily associated with hospital-acquired infections, which is a Gram-negative bacillus, aerobic, pleomorphic and non-motile (1). Recently, there is a dramatic increase in the incidence of multidrug-resistant (MDR) strains, which has significantly raised the profile of this emerging opportunistic pathogen (2). This phenomenon of multidrug-resistant (MDR) pathogens has increasingly become a serious concern with regard to both nosocomial and community-acquired infections (3) (4). The World Health Organization (WHO) has recently identified antimicrobial resistance as one of the three most important problems facing human health (5) (6) (7). The genus *Acinetobacter*, as currently defined, comprises Gram-negative, strictly aerobic, non-fermenting, non-fastidious, non-motile, catalase-positive, oxidase-negative bacteria with a DNA G + C content of 39% to 47% (8). Four species of *Acinetobacter* such as, *A. calcoaceticus*, *A. baumannii*, *Acinetobacter* genomic species 3 and *Acinetobacter* genomic species 13TU have such morphological similarities that they are difficult to differentiate (9) (10). *A. baumannii* specifically targets moist tissues such as mucous membranes or areas of the skin that are exposed through open wounds. Genes such as *bla*_{OXA-66}, *bla*_{OXA-23}, *bla*_{ADC} (11), TEM-1, TEM-2, CARB-5, CTX-M-2, CTX-M-43 (12) (13) etc., show resistance to various drugs like penicillin, carbapenems etc (14) (15). These organisms also have the ability to form biofilms on the surfaces of steel, catheter, as well as human epithelial cells. OmpA is a gene that is responsible for adhesion, resistance and biofilm formation. Various other genes like *CsuA*, *CsuB*, *CsuE*, *fimH*, *Bap* gene (16) (17).

Amidst all the genes, fimH protein is our area of interest in this research. The *fimA* codes for the large secondary unit and the *fimF* and *fimG* codes for small subunits and the *fimH* codes the top of the cilia which are sensitive to the manus and the *fimC* codes for the attached protein (18).

Comment [UdW2]: I suggest to include Bioinformatics as main keyword to make the paper more visible in scientific literature.

This attached protein helps the fim protein that can pass through the periplasmic space (19). *fimD* codes for the outer membrane proteins and *fimI* codes for the structure (20). The *fimH* gene is an important virulence agent for bacteria, which encodes the Type 1 fimbriae, that helps bacteria bind to the surface of host cells and then cause injury (21). Among the virulence factors, the adhesion to human epithelial cells in the presence of fimbriae and/or capsular polysaccharide and ability to grow in iron-chelated medium by secreting iron-regulated siderophores and adhesion to rat bladder tissue what may be a factor contributing to the pathogenicity in the urinary tract or in other tissues (22).

In a previous study done using the *fimH* gene of *Acinetobacter baumannii* it was found to be associated with a catch bond mechanism (23). To analyse the biofilm formation, semi quantitative bio adherent assay together with PCR was performed. By using this gene, new drugs and vaccines can be produced for *A.baumannii* infection. The *fimH* gene was analysed to find the suitable peptides in an antigen to which antibodies bind. This was done using Reverse vaccinology technology, that helps in the examination of the genome of organisms and helps in the development of vaccines (24). For predicting the T-cell epitopes in vaccine production, an immune-informatics approach was used. It scans the epitope sequence to find the MHC binders. Recently various new methods of developing vaccines have come. Among them is the Multi-epitope assembly peptide (MEP), which uses B-cell epitope, T-cell epitope and other parts of other proteins (25).

The vaccine produced using this approach seems to be more effective than other methods. Conventional vaccines are developed from live attenuated or inactivated organisms, which elicit strong humoral and cellular immunity resulting in long lasting immunity (26). However, the use of such vaccines has been questioned due to crucial safety concerns as the used pathogen may become reactivated (27). In addition, the formulation of such vaccines often leads to reactogenic and/or allergic responses that are often not desired (28). The design of epitope-driven or peptide-based vaccines is more attractive; they are comparatively easier to produce and construct, as they lack infectious potential and offer chemical stability (29). However, peptide-based vaccines still present many obstacles including the low intrinsic antigenicity of using individual peptides, and the shortage of suitable delivery routes (30). For proper

engagement of cellular and humoral immunity, the combining task of different peptides and poor population coverage of T-cell epitopes is also challenging (31). The present investigation was thus designed to assess the epitope based vaccine peptide predictions for the fimH protein of *A. baumannii* using the immune-informatics approach.

MATERIALS AND METHODS:

Study setting:

This is an observational in-silico study done in the Department of Microbiology, Saveetha Dental College and Hospital. Institutional approval for the research was obtained from the institutional ethical committee (Ethical approval number - IHEC/SDC/UG-1981/21/156).

Selection of fimH gene for Epitope Prediction:

FASTA sequence of the biofilm associated protein fimH from the clinical strain of *A. baumannii* was retrieved from the NCBI database (NCBI ID QCP20178.1) (32). It was subjected to BLASTp search against non-redundant protein (nr) sequences database of Homosapiens taxid 9606 and the nonhit, non-human homologous proteins were interpreted and recorded.

Analysis on Druggability and Physico- Chemical Properties:

Using the Drug bank database (33), the selected protein fimH was evaluated against all the drug targets (bit score:>100; e-value:<0.0005) for evaluating the potential drug targets. Predictions on the consensus location of the biological location of the druggable protein was assessed using PSORTb and CELLO v2.5 online tools (34) (35). The sequence fimbrial chaperone protein FimH was retrieved from Uniprot database and Subcellular location was predicted using CELLO v.2.5: subCELLular LOcalization predictor tool. Further the physical and chemical properties of the protein were assessed for its molecular weight, theoretical PI, instability index, GRAVY and aliphatic index using Protparam expasy server (36).

Antigenicity Predictions:

At a set threshold of 0.5, fimH was subjected for potent antigenicity predictions using VaxiJen web server to identify whether the selected sequence possesses potent epitopes (37).

T-cell MHC Class-I Epitope Mapping:

Using the NetCTL server (38) for the selected fimH protein, the intrinsic potential was assessed based on the combinatorial scores upon various prediction parameters (at a set threshold value of 0.75). Specificity of the MHC class I binding with the T-cells was evaluated using Immune epitope database analysis resource (IEDBAR) and the HLA alleles were recorded based on the IC50 values and percentile ranks.

Predictions on Class-I Immunogenicity, Conservancy and Toxicity Analysis:

From the predicted T-cell epitopes of fimH, further immunogenicity predictions were made using the positive scores obtained in IEDB-AR MHC class-I immunogenicity prediction tool based on the set default parameters, as this is required to evoke a good immune response. The selected epitopes were subjected to VaxiJen server at a threshold of 0.5 that uses the alignment independent immunogenic antigenic predictions based on the physico-chemical behaviour. Further the degree of conservancy within the genotype sequences was predicted using IEDB-conservancy tool. Finally, setting the parameters at default, the assessment on toxigenicity was predicted using the ToxinPred tool.

T-cell Class-II Epitope Mapping

From the predicted T-cell epitopes, the HLA alleles restricted to MHC class-II binding were evaluated using IEDB MHC class-II epitope prediction tool, which employs a combination of stabilization matrix alignment and average relative binding matrix methods as a consensus approach of prediction.

Cluster Analysis of MHC Restricted Alleles:

To strengthen the predictions, the restricted MHC alleles with the selected T-cell epitopes, MHC cluster v2.0 server is used to identify the clusters (39). The functional relationship between the selected peptides and HLA's was interpreted with the obtained graphical tree and static heat map.

B-Cell Epitope Mapping:

To assess the linear epitopes that can bind to the B-cells to evoke a humoral immune response can be evaluated using the IEDB linear epitope B-cell predictions. This is achieved by subjecting the fimH protein to Kolaskar Tongaonkar antigenicity (40).

Interaction Between Protein and TLR2 Receptor :

Possible interactions of the fimH predicted epitopes with the TLR2 receptor was explored using the Galaxy web server. The energy obtained upon interpretations and the number of the hydrogen bonds formed between the complexes will aid in progressing towards the design and optimization of an efficient fimH vaccine.

Identification of MHC Class –II binders (T-cell epitopes):

T MHC class II molecules play an important role in initiation of the antigen-specific immune response (41). The T- cell epitopes of FimH were predicted using the EpiDOCK server which predicts the binding of epitopes to 12 HLA-DR, 6 HLA- DQ, and 5 HLA-DP alleles . The first structure based server for the prediction of MHC class II binding using the Fasta format of sequence as input. Maximum number of epitopes binders (≥ 10) was identified and taken for further analysis.

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Antigenicity and Stability prediction of selected T-cell epitopes

Antigenicity was predicted using Vaxigen v 2.0, instability index of predicted epitopes was calculated using protparam server.

Predicted Epitopes structure prediction and Validation

The structure predicted MHC Class – II binders were predicted using Pepfold server which uses *de novo* approach to predict peptide structures from amino acid sequences. The structure predicted was validated using RAMPAGE tool which predicts the stereochemical properties of given structure. The server assess the quality of modelled epitopes by predicting the amino acids falling in favoured, allowed and disallowed regions of Ramachandran plot.

Molecular Docking of epitopes with HLA-alleles using ClusPro server

The three dimensional structures of HLA-DP - 3LQZ , HLA-DQ - 5KSV, HLA-DR- 4AH2, TLR-2 -6NIG were retrieved from PDB database. The molecular docking analysis of predicted MHC binders with HLA-Alleles were carried out using Clusterpro Server.

B cell epitope prediction

The B cell Epitope prediction of FimH was carried out using Immune Epitope Database (IEDB) using Kolaskar & Tongaonkar Antigenicity Prediction. method.

Evaluation of Antigenicity and allergenicity

The antigenicity of FimH was predicted using VaXiJen v2.0 server. The antigen classification of proteins are based on the physicochemical properties and alignment-based prediction methods. (Doytchinova et al., 2007). Allergenicity of the FimH predicted using AlgPred server which is a web server developed to predict allergenic proteins and for mapping IgE epitopes using mapping of IgE epitope.

Results:

Protein retrieval

The sequence FimH from *Acinetobacter baumannii* was retrieved from Uniprot database and its sequence id was SVK46742.1. The Subcellular location was predicted as Extracellular protein (4.098 *) using CELLO v.2.5: subCELLular LOcalization predictor tool.

Evaluation of Antigenicity and allergenicity

The predicted antigenicity of FimH was predicted using VaXiJen v2.0 server was found to be 0.6896 . The protein was predicted as a non-allergen using Algpred server. Prediction by SVM method based Prediction by mapping of IgE epitope.

Secondary structure

The secondary structure of FimH was predicted using Self-Optimized Prediction Method with Alignment (SOPMA) server. The percentage of α -helix, beta sheet, turns and coils were predicted (Table 1).

Antigenicity and Stability prediction of selected T-cell epitopes

The peptide binders (greater than or equal to 10) were screened for antigenicity and stability analysis. The peptides with antigenicity value greater than 0.4 was predicted using Vaxijen v 2.0 and stability was analysed using protparam (<40) (Table 2). From 20 peptides, 18 peptides were chosen based on antigenicity and stability analysis prediction.

Structure prediction using pepfold and Ramachandran plot evaluation

The structure prediction of Selected Eighteen epitopes were carried out using pepfold server (Fig 1) and based on Ramachandran plot analysis 10 epitopes (Table 3) were taken for further analysis (Fig 2).

B cell epitope prediction - Kolaskar & Tongaonkar Antigenicity Results

The X-axis and Y-axis denote the sequence position and antigenic propensity respectively. The regions above the threshold value are antigenic, and are depicted in yellow (Fig 3).

Molecular Docking of epitopes with HLA-alleles:

The epitope AALVASVCL showed -611.3 for HLA-DP, -684.7 for HLA-DQ, -635.4 for HLA-DR and -887.3 for TLR-2. The epitope YSSGANAFT showed -648.7 for HLA-DP, -701.5 for HLA-DQ, -674.9 for HLA-DR and -919.1 for TLR-2 (Table 4). In those 2 epitopes, YSSGANAFT showed best molecular docking with alleles. The drug interaction between YSSGANAFT and HLA-DP (Table 5), YSSGANAFT and HLA-DQ (Table 6) and YSSGANAFT and HLA-DR (Table 6).

Table 1: Secondary structures obtained using SOPMA tool.

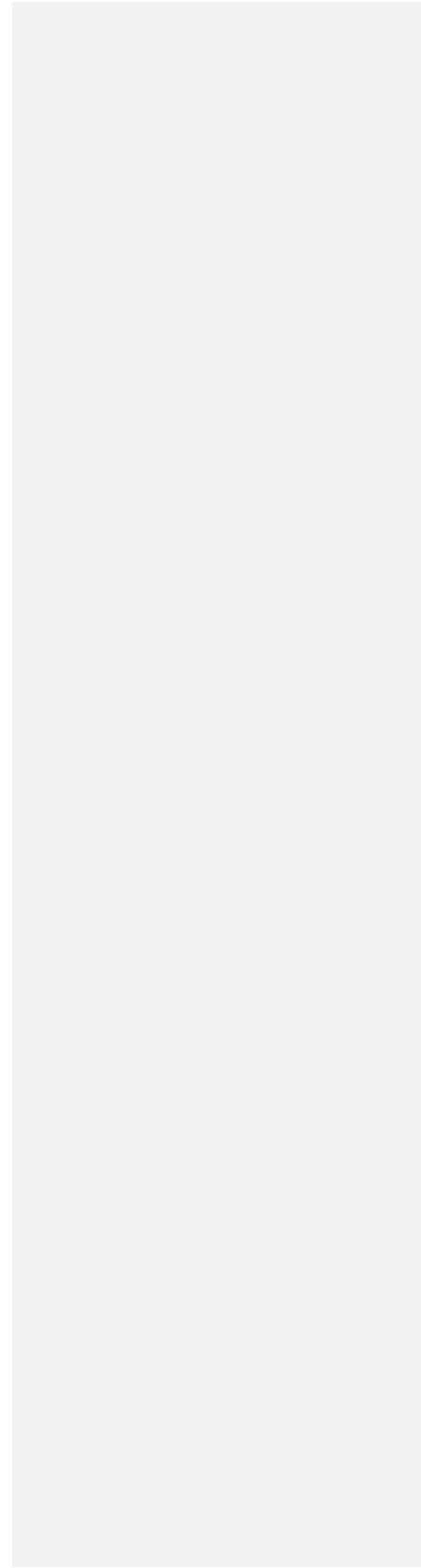
Alpha helix	13.02%
Extended strand	33.97%
Beta turn	7.30%
Random coil	45.71%

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Table 2: Toxigenicity, antigenicity and Class-I conservancy of T-cell epitopes from fimH of *A.baumannii*.

Position of peptide	Sequence	Number of binders to HLA alleles (DP, DQ, DR)	Vaxijen v 2.0	Protparam
1	MTLVSKLKK	16	-0.6349	-13.18
3	LVSKLKKVL	19	-1.1177	-19.41
4	VSKLKKVLK	17	-1.1199	-28.84
5	SKLKKVLKK	13	-0.4651	-28.84

6	KLKKVLKKK	11	-0.1152	-28.84
7	LKKVLKKKE	13	-0.4117	-19.41
8	KKVLKKKEV	11	-0.0171	-9.98
9	KVLKKKEVA	11	-0.0663	-9.98
10	VLKKKEVAA	14	-0.0762	-0.54
11	LKKKEVAAL	19	0.1158	-0.54
13	KKEVAALVA	10	-0.1034	8.89
17	AALVASVCL	11	0.7710	30.29



19	LVASVCLMA	13	0.8136	44.00
28	YSSGANAFT	11	0.8394	20.86
35	FTCKVSATG	17	1.1836	-9.98
53	VYVNLTPSI	10	1.1191	21.91
55	VNLTPSIGV	11	1.3833	30.29

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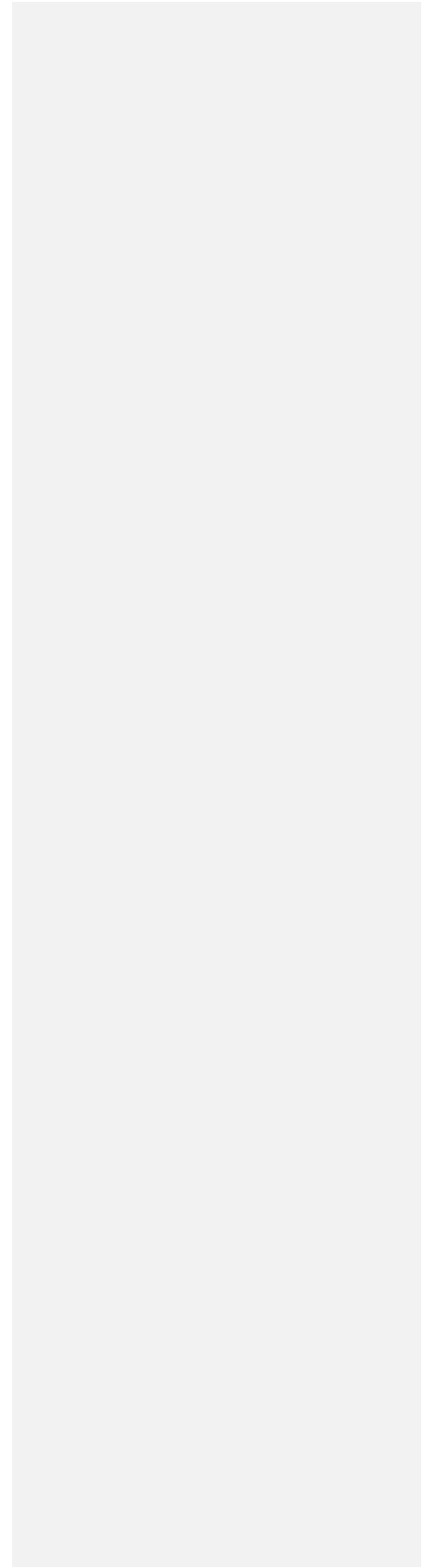


Table 3: Ramachandran validation showing the most favoured region of peptides

	Peptides	Most favoured region
Epitope 1	AALVASVCL	100%
Epitope 2	YSSGANAFT	85.7%
Epitope 3	FTCKVSATG	28.5%
Epitope 4	VYVNLTPSI	28.5%
Epitope 5	VNLTPSIGV	57.1%

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Table 4: Results of the molecular docking of epitopes in HLA alleles.

Molecular Docking of epitopes with HLA-alleles	Epitopes	HLA-DP	HLA-DQ	HLA-DR	TLR-2
Epitope 1	AALVASVCL	-611.3	-684.7	-635.4	-887.3
Epitope 2	YSSGANFT	-648.7	-701.5	-674.9	-919.1

Table 5: Drug ligand interactions between YSSGANAFT and HLA-DP

		YSSGANAFT		HLA-DP		Distance (Å)
		Residue	atom	Residue	atom	
Hydrogen	Carbon Hydrogen	TYR1	OH	SER7	CB	3.70
Hydrophobic	pi-pi-stacked	PHE8	-	PHE26	-	5.41
	Alkyl/Pi-Alkyl	ALA7	-	PHE52	-	4.82
		ALA5	-	OHE26	-	4.94
Other interactions	Sulfur	PHE8	-	MET31	SD	5.15

Table 6: Drug-ligand interactions between YSSGANAFT and HLA-DQ

		YSSGANAFT		HLA-DQ (atom)		Distance (Å)
		Residue	atom	Residue	atom	
Hydrogen bond	Classical	ASN6	OD1	SER14	HN	2.62
		ASN6	HD22	TYR13	O	1.86
		ASN6	O	ALA82	HN	2.76
		PHE8	O	THR83	HN	2.09
		PHE8	O	THR83	HG1	1.95
		TYR1	HH	SER144	O	1.95
		TYR1	OH	LYS140	HN	1.98
Hydrophobic	pi-sigma	PHE8	CB	PHE113	-	3.80

Pi-pi-T-shaped	PHE8	-	PHE113	-	5.55
Pi-pi-stacked	TYR1	-	HIS143	-	4.20
Alkyl/Pi-Alkyl	ALA5	-	PHE145	-	5.35
	ALA5	-	LEU12	-	4.90

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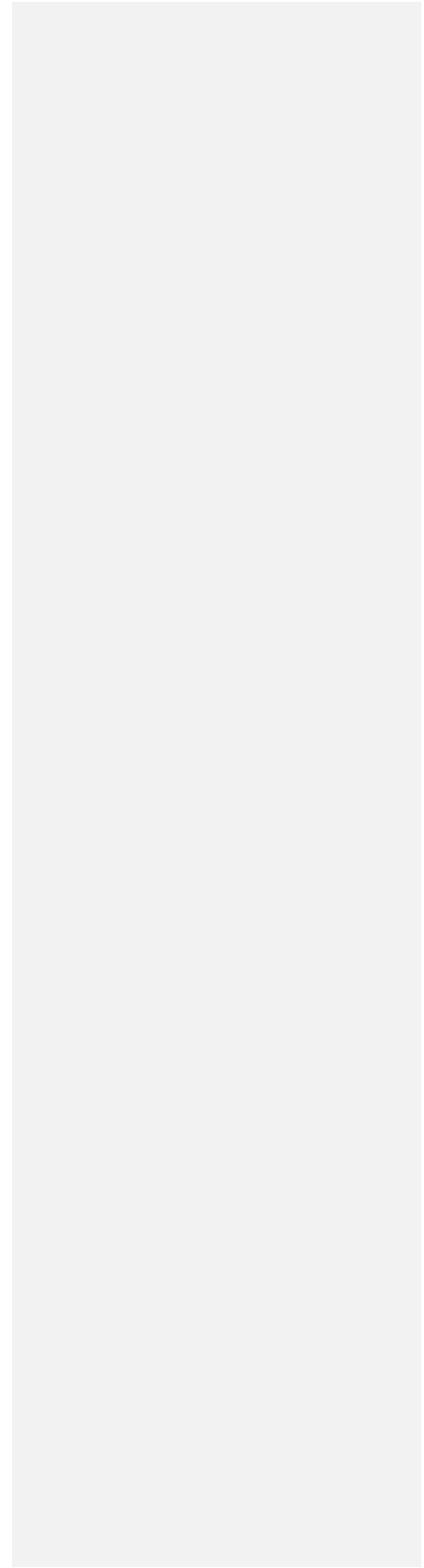


Table 7: Drug - ligand interactions between YSSGANAFT and HLA-DR

		YSSGANAFT		HLA-DR (atom)		Distance (Å)
		Residue	atom	Residue	atom	
Hydrogen bond	Classical	PHE8	O	THR83	HN	2.03
		GLY4	O	THR113	HG1	1.89
		ASN6	OD1	ASN15	HN	2.47
		SER2	HN	GLU11	O	2.46
		SER2	HG	ASP66	OD1	2.07
		SER2	HG	ASP66	OD2	2.01
		TYR1	HH	PHE137	O	1.91

	Carbon Hydrogen	GLY4	CA	HIS143	O	3.28
		ASN6	OD1	LEU14	CA	3.58
		SER2	OG	PHE12	CA	3.48
Hydrophobic	Pi-sigma	TYR1	-	ALA10	CB	3.93
	Alkyl/Pi- Alkyl	TYR1	-	PRO139	-	4.56
		PHE8	-	LEU144	-	4.87
		ALA5	-	PHE145	-	5.10
		ALA5	-	PHE12	-	4.89

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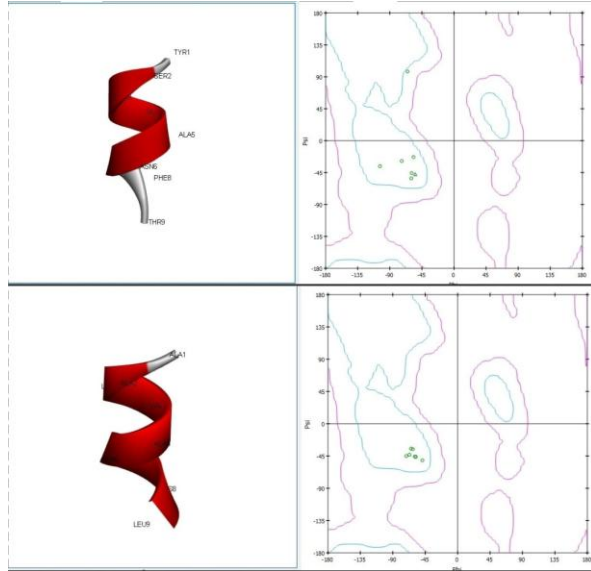


Figure 2: Ramachandran plot depicting the structure of the predicted epitopes.

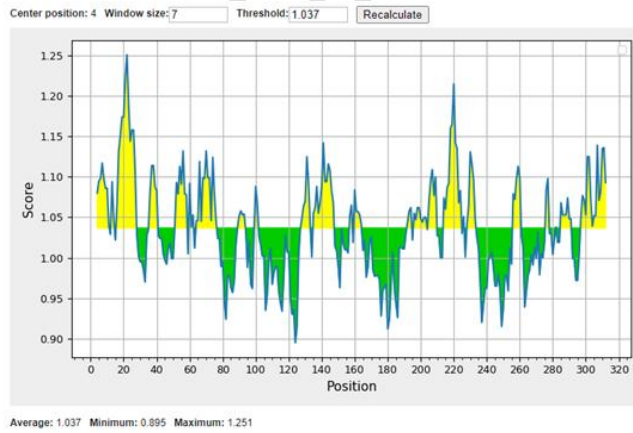


Figure 3 : Kolaskar & Tongaonkar Antigenicity Results of FimH showing the B-cell dominant epitopes

DISCUSSION:

Acinetobacter baumannii is known for its multi-drug resistance property among hospitalised patients. Hence implementing novel methods to combat the infection is important. For the prophylaxis for *A.baumannii*, a study was designed as an observational and in silico experimental analysis against the fimH gene of *A.baumannii*, to arrest biofilm formation. Selection of possible and suitable targets is the first vital step in vaccine construction. It may further significantly bind with the immunological receptors and is considered highly crucial to evoke and elicit both humoral and cell-mediated immune responses. Its multi-drug resistant property imposing serious threat amidst hospitalized patients, implementation of novel strategies to combat the infections caused by *A.baumannii* is mandatory. Considering the prophylaxis as the best alternate strategy for *A.baumannii*, with the advent of bioinformatics, the study was designed as an observational and in-silico experimentation analysis in the design and evaluation of vaccine candidates against the fimH of *A.baumannii* and to arrest the formation of biofilms (42). Predictions of promiscuous fimH vaccine peptides were thus successfully achieved in the present study by the immuno-informatics approach utilizing the available genomic and proteomic reservoirs under a single computational platform comprising various databases and tools.

A significant approach targeting fimH was made to suggest the considerable relevance in the predictions that can lead to the immunotherapies against the biofilm formation associated with virulence in *A.baumannii*. fimH was detected in both gram positive and gram negative bacteria and was found to possess multiple tandem repeats as a common feature and is located on the cell surface contributing its role in adhesion and biofilm formation (43). fimH was thus selected as an antigenic component amidst many biofilm associated operons in the present immuno-informatics vaccine peptide construction analysis. Selection of specific protein being the initial step in *fimH* vaccine peptide analysis, it was noteworthy that the selection was good and was done based on the analysis of the non-redundant protein for further epitope predictions.

The preliminary evaluation of the fimH protein for localization using PSORTb and CELLO V2.5 tools aids in the filtration and optimization of the vaccine peptides (44). The instability index in the present study was found to be ≤ 40 . In a previous study conducted by

Iraj Rasooli et al., the instability index of Oma87 was 29.44 (proteins with instability index of < 40 are stable) (45). This result correlates with the present study. In another study done in the OmpA gene, the instability index was 30.58 (≤ 40) (46). In another study, the instability index being <40 (7.78) suggests the protein to be a stable protein (47).

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In the present study, the secondary structures were predicted using Self-Optimized Predicted Method with Alignment (SOPMA) server. The percentage of α helix, beta sheet, turns and coils were predicted. In a previous study, SOMPA analysis revealed alpha helix more than random coil or beta strand. In the present study, the allergenicity of the *fimH* gene was predicted using AlgPred by mapping the IgE epitope. The results showed that it was a non-allergen. In a previous study, based on different allergen prediction approaches in AlgPred, the PLD protein was not detected as an allergen (48)

The predicted antigenicity of *fimH* was predicted using Vaxijen V2.0. The obtained result was 0.6896. Vaxijen is an appropriate server for prediction of protective antigens and can be used in silico screening of genome information for vaccine development by Doytchinova. In a previous study conducted by Hadise Bazmara et al, the antigenicity score of FepA was 0.8136. In that study, out of twelve proteins, four of them, *AtpA*, *OmpW*, *Bfr* and hypothetical protein *AIS_I295* obtained less value. Hence it was omitted (49). In another study, The score obtained for Bap_{Ab} was 0.7086 seems to be promising for the protein to be a probable antigen (50). In another study, a threshold of > 0.4 showed all the five peptides (E1–E5) as potential vaccine candidates with E1-HTEQTEEDLRRTLDTLVQN showing the highest score, 0.9803 (51). These antigenicity prediction tools were also used for analysing and eliminating the proteins with low values.

In our study, out of 20 epitopes, 18 epitopes were used for antigenicity and stability prediction. Out of which only 5 epitopes were selected for further analysis. This is because those epitopes showed positive values for Vaxijen and Protparam. This was done using the Ramachandran plot. In a previous analysis, 6 out of 10 epitopes of B0VMD0 protein and 8 out of 12 epitopes of B0VUZ6 contain the positive value score (52). In another study, out of 10 epitopes, 5 epitopes with high score were selected for further analysis of antigenicity. Out of 5 epitopes, 2 epitopes

were predicted as probable antigens with the antigenic score of > 0.5 (53). In another study, out of 10 epitopes, 3 epitopes were selected since it showed positive values (54).

In the present study, the B-cell epitope was predicted using Kolaskar & Tongaonkar Antigenicity. A graph was obtained which represents peaks in yellow and green. The regions above the threshold are antigenic and are depicted in yellow (Fig 3). In addition to cellular immunity, evoking a humoral immune response is also essential for any vaccine candidate. Thus we performed the B-cell epitope evaluation in the present investigation. The protein elicited highest affinity and lowest percentile marks. Those were considered as good binders. Among those 5 epitopes, 2 epitopes showed higher ranges of most favoured regions. The epitope AALVASVCL showed a rank of 100%. The epitope YSSGANAFT showed a rank of 85.7%. The functional interaction between three alleles HLA-DP, HLA-DQ, HLA-DR and TLR-2 are shown (Fig 1). These alleles are in correspondence to bacteria. The epitope AALVASVCL showed -611.3 for HLA-DP, -684.7 for HLA-DQ, -635.4 for HLA-DR and -887.3 for TLR-2 (55). The epitope YSSGANAFT showed -648.7 for HLA-DP, -701.5 for HLA-DQ, -674.9 for HLA-DR and -919.1 for TLR-2 (Table 4). In those 2 epitopes, YSSGANAFT showed best molecular docking with alleles. In a previous study, “FYLNQPV” of polysaccharide export outer membrane protein (EpsA) and “LQNNTRRMK” of chaperone-usher pathway protein B (CsuB) as broad-spectrum peptides for induction of targeted immune responses (56). In a previous study, molecular docking of four peptides were performed with six different HLA alleles. 1A6A(HLA-DR B1*03:01), 3C5J(HLA-DR B3*02:02), 1H15 (HLA-DR B5*01:01), 2FSE(HLA-DR B1*01:01), 2Q6W(HLA-DR B3*01:01), and 2SEB(HLA-DRB1*04:01) were performed using PatchDock to show HLA-peptide interactions. The interaction between the alleles and peptides were analysed. The distance between YSSGANAFT and HLA-DP was 3.70 Å, HLA-DQ was 2.62Å, HLA-DR was 2.03Å and TLR-2 was 2.78Å. This shows that the relation between them is good and can act as a good antigen. The limitation of the present study was that the predictions of the epitope was done using in-silico tools. Thus the future prospects are set to observe the immunological memory and response using in-vitro and in-vivo study models. Similarly the same methodology can be used for the prediction of potential dental pathogens like Enterococci sp., and viruses like Corona virus (57) (58) (59) (60).

Conclusion:

An attempt on detecting few vaccine peptides for the cessation of *fimH* based virulence in *A.baumannii* using an immune-informatics approach suggests promising results in the present study. However, the proposed vaccine peptides needs further experimentation in animal models for its application against *A.baumannii* associated infections for its assessments on the suitable immunological response and memory. Further progress from the available *fimH* vaccine peptide data, it is evident to design chimeric vaccine constructs to combat the menace of *A.baumannii* infections.

Comment [UdW7]: Conclusions must be more wide. Review results and objectives to write a little bit more.

COMPETING INTERESTS DISCLAIMER:

Authors have declared that no competing interests exist. The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

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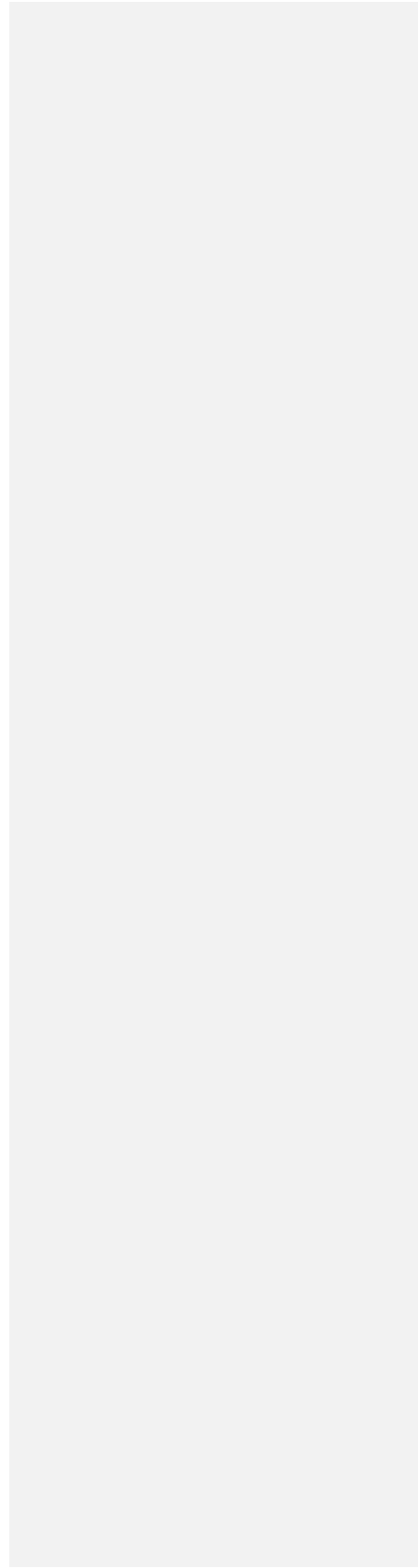
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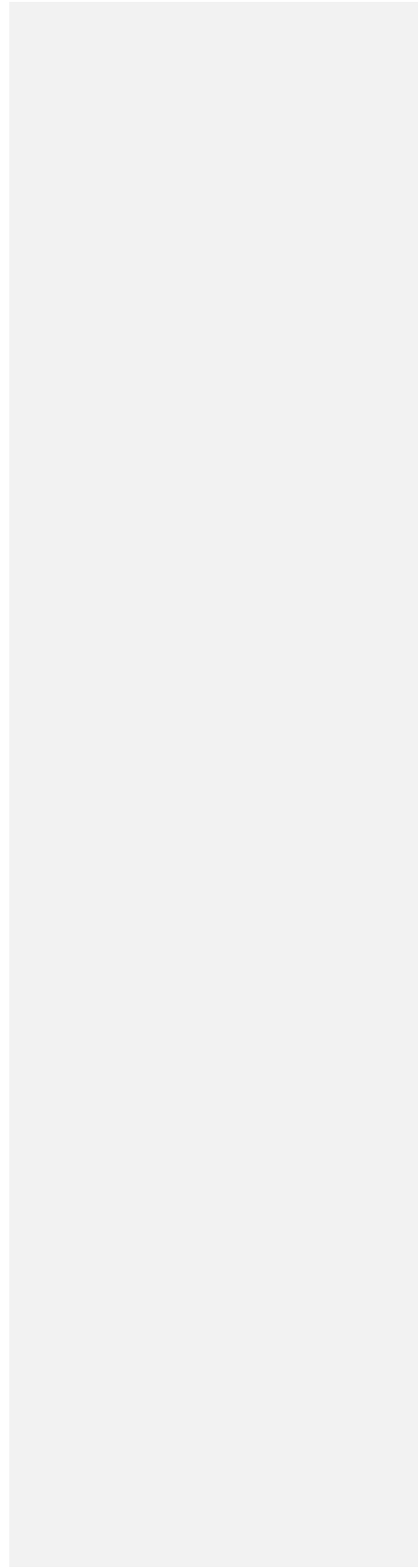
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