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IDENTIFICATION OF B-CELL AND T-CELL SPECIFIC PEPTIDE VACCINE FOR MORGANELLA MORGANII.

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ABSTRACT

Introduction: The research tackles the pressing requirement for a specific peptide vaccination against Morganella morganii, a bacteria that poses a considerable risk, particularly to individuals with compromised immune systems. Understanding the drawbacks of conventional antibacterial therapies, attention is now directed toward identifying particular B-cell and T-cell epitopes for a novel peptide vaccine approach.

Objectives: To discover an optimal length range-spanning B-cell epitope that exhibits homology to M.morganii adherence. Identifying the T-cell epitope with the best potential score for increased vaccine efficacy. to emphasize a comprehensive immune response and bring our approach into line with current trends in epitope prediction.

Materials and Methods: To find the best target, protein databases were thoroughly examined. The B-cell epitope TRNMTHYGINDDNRGLTANKTQ was found, and its length and homology were assessed. It was found that the T-cell epitope with the highest score (0.98705) improved the

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vaccine's strategic aspects. Using cutting edge computational tools, epitope predictions were made in accordance with accepted practices in the field.

Results: The B-cell epitope that was chosen demonstrated complete homology to M.morganii and conformed to the optimal length range, making it a promising contender for incorporation into the vaccine. In synergy with current developments in epitope prediction for a stronger immune response, the top-scoring T-cell epitope adds a critical component to the vaccination approach.

Conclusion: This work emphasizes how important epitope identification is as a starting point for developing a targeted peptide vaccine to prevent M.morganii. By improving vaccine efficacy, the chosen epitopes offer a tactical advance in the fight against bacterial infections. But further refinement and validation of these results depend on continuous validation, flexibility, and cooperation between computational and experimental approaches.

Keywords: M.morganii , peptide vaccine, B-cell epitope, T-cell epitope, epitope prediction, Vaccines, Diseases, Universal Health, immune response.

Introduction

A global health crisis is antibiotic resistance (AR). As bacteria develop defense mechanisms against antibiotic attacks, they develop antimicrobial resistance (AR), a subtype of AMR. The continuing abuse of antibiotics can cause AR to evolve naturally.

Morganella morganii is a rod-shaped, facultative anaerobic bacillus that is gram-negative and a member of the commensal microbiota found in the human gut (1).This pathogen is regarded as non-negligent and opportunistic, primarily causing infections such as cellulitis, chorioamnionitis, UTIs, sepsis, and abscesses (2) .Among the most prevalent bacterial infections in kids, UTIs have a substantial short term and long term morbidity rate (2,3).

Vaccination is a great substitute for fighting pathogens caused by AR bacteria. Historically, vaccinations have not been fully utilized as a management tool against AR bacterial pathogens; however, their proven benefits in lowering AMR have been well documented (4).The identification of T and B cell epitopes is aided by immunoinformatics. Using a variety of immunoinformatics techniques occasionally involving viruses and bacteria, the potential of various B and T cell epitopes was discovered and characterized. Potential B and T cell epitopes from the ebolavirus glycoprotein were identified and characterized by Ahmad B. et al (4,5)

In order to create a multi-epitope vaccine, determine how well it binds to components of the host immune system, and assess whether it can provide immune protection against M.morganii, this work combines subtractive proteomics, RV, core genomics, and biophysical methods. Certain pathogen strains are resistant to ampicillin/sulbactam, oxacillin, penicillin, first- and second-generation cephalosporins, macrolides, fosfomycin, colistin, lincosamides, and polymyxin B.(4–

6). To study vaccine binding with various host immune receptors and comprehend its binding mode and interactions, the designed vaccine was subsequently employed in a variety of bioinformatics and biophysics techniques. In order to determine which kind of immunity is essential for eliminating the infection, the host immune system was also simulated in opposition to the vaccine. (7)

Although prior research has been conducted on developing a chimeric vaccine for M.morganii, its data base was small (Ullah et al. 2021). As a result, we concentrated on developing a peptide vaccine that can serve as a universal vaccine by utilizing multiple protein sources.

Materials and methods

Protein Database Analysis.

The https://www.uniprot.org/proteomes server was used to conduct a thorough analysis of protein databases as the first step in the inquiry. The objective was to pinpoint prospective targets that would be appropriate for identifying potential vaccination candidates against M.morganii. A number of factors were taken into consideration to identify proteins with potentially immunogenic qualities, such as protein localization and genomic DNA location.

Selection of Target Protein.

The M.morganii Outer Membrane Protein A (OmpA), which is located in genomic DNA, was identified as a promising candidate for additional research after the protein database analysis. OmpA is an intriguing target for vaccine development because of its crucial role in the pathogen-host interaction.

UniProtKB/TrEMBL Accession Retrieval

For M.morganii, the particular UniProtKB/TrEMBL porin protein was found to be (GenBank: CP126137.1). The amino acid sequence required for later epitope prediction studies was obtained using this accession as a foundation.

Amino Acid Sequence Retrieval

The amino acid sequence corresponding to the identified UniProtKB/TrEMBL accession (GenBank: CP126137.1) was obtained from the NCBI database in order to facilitate the prediction of B cell and T cell epitopes. Accurate and focused epitope prediction analyses required this step.

Fasta Sequence Preparation

In order to make the recovered amino acid sequence compatible with epitope prediction software, it was formatted into a Fasta file. This stage prepared the way for using prediction algorithms to find possible immunogenic regions later on.

B Cell Epitope Prediction

For the purpose of predicting B cell immunogenic epitopes within the chosen M.morganii porin protein sequence, Bepipred Linear Epitope Prediction 2.0, an online server program known for its accuracy, was utilized. Bepipred can identify regions that are likely to elicit a strong B cell response by using complex algorithms to improve prediction reliability.

Epitope Analysis

After being obtained through the Bepipred analysis, the resulting B cell immunogenic epitopes were carefully examined. During the evaluation process, variables like antigenicity, conservancy, and possible functional relevance were taken into account. The goal of this thorough analysis was to identify the epitopes that have the best chance of being included in a peptide vaccine against M.morganii.

T Cell Epitope Prediction

A parallel analysis utilizing specialized algorithms or servers for T cell epitope prediction would be carried out in situations where T cell epitopes are of interest. This phase guarantees a thorough comprehension of the immunological response environment, including immunity mediated by both B and T cells.

The materials and techniques described here offer a methodical approach to the identification and evaluation of potential vaccines, and they also highlight the significance of utilizing state of the art bioinformatics tools for epitope prediction in order to improve the chances of developing a targeted vaccine against M.morganii.

Results

Peptide Selection for M.morganii B Cell Epitope

For M.morganii, the peptide TRNMTHYGINDDNRGLTANKTQ was found to be a promising B cell epitope. It is an excellent candidate for a peptide vaccine due to its complete homology to the pathogen and adherence to the recommended length range of 15 to 22 amino acids.

T Cell Epitope Prioritization

Acknowledging the difficulty of short peptides devoid of T cell epitopes, our strategy concentrated on choosing the T cell epitope with the highest score, 0.987505. This calculated decision

guarantees the integration of a strong T cell response, which increases the efficacy of the peptide vaccine.

Comprehensive Vaccine Strategy

A comprehensive peptide vaccine strategy is built on the combination of the top-scoring T cell epitope and the identified B cell epitope. This strategy targets the humoral and cellular immune responses that are essential for a successful defense against bacterial infections and is specifically designed for M.morganii.

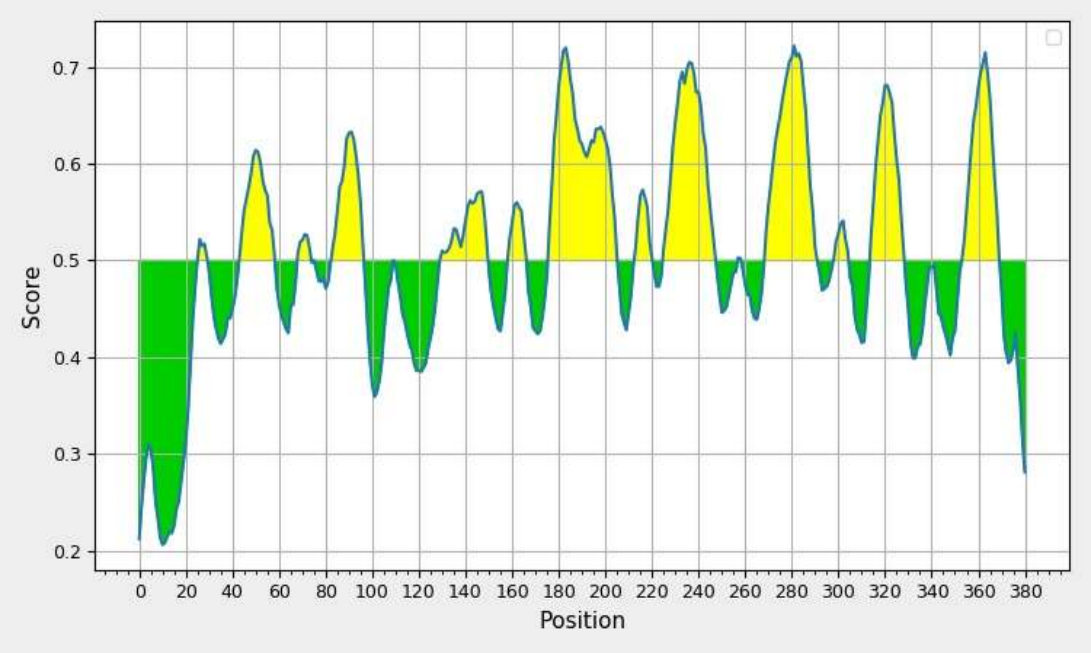

Figure 1: Epitope Analysis

Immunogenic epitopes are highlighted in yellow in this graphic representation, while non-immunogenic areas are shown in green. Making use of this, a peptide vaccine targeting the immunogenic regions of M.morganii was developed, identifying particular B and T cell epitopes. This focused approach guarantees a customized reaction, improving the vaccine's accuracy in producing strong protection against infections with Morganella morganii.

No	Start	End	Peptide	Length
1	26	30	NKDGN	5

2	44	59	FSDNDHYGDSQNGDDS	16
3	69	74	TQITDQ	6
4	76	76	T	1
5	84	97	EIKTNGTEGDNKNK	14
6	110	110	F	1
7	130	150	DVLPIFGNDTMTQTDVYMTGR	21
8	160	167	SDFFGYVD	8
9	177	206	GANDDNSISSRGTSDFRDPTSYDNTANGDG	30
10	214	221	DIGWGVSV	8
11	226	248	SSSARPDGQKYNQASGALGDRAE	23
12	258	259	AN	2
13	270	291	TRNMTHYGINDDNRGLTANKTQ	22

14	299	305	YQFDFGL	7
15	315	329	KGKSLSGGYGDDQDL	15

Table 1: Peptide Selection for Morganella morganii B Cell Epitope

The choice of an ideal B cell epitope is crucial for the development of a successful peptide vaccination strategy. Because of its complete homology to Morganella morganii, the peptide TRNMTHYGTNDDNRGLTANKTQ was found to be an excellent candidate. Most importantly, its length—which ranges from 15 to 22 amino acids perfectly matches the requirements set forth by experts for an efficient B cell epitope. This deliberate choice, which combines length with sequence specificity, increases the peptide's potential to function as a strong building block for an effective vaccination against M.morganii infections.

allele	**sequence number**	**start**	**end**	**length**	**peptide**	**score**	**percentile rank**
HLA-B*40:01	2	23	31	9	GETQITDQL	0.987505	0.01
HLA-A*01:01	4	29	28	10	TSDFRDPTSY	0.979173	0.01
HLA-A*02:01	7	13	21	9	ALIDYKINL	0.973832	0.02
HLA-B*44:03	5	29	38	10	AEAWNFGAKY	0.96388	0.01

HLA-B*35:01	3	30	38	9	LPIFGNDTM	0.944215	0.02
HLA-A*31:01	3	48	56	9	RAANLLTYR	0.929963	0.01
HLA-B*08:01	6	35	43	9	YLQSKGKSL	0.919303	0.01
HLA-A*02:06	7	13	21	9	ALIDYKINL	0.919281	0.03
HLA-B*44:02	5	29	38	10	AEAWNFGAKY	0.913205	0.02
HLA-A*02:03	6	28	36	9	GLRPSIAYL	0.905063	0.03
HLA-A*01:01	3	5	13	9	FAEFGSLDY	0.90474	0.03
HLA-A*02:03	7	13	21	9	ALIDYKINL	0.904	0.03
HLA-A*01:01	6	47	56	10	YGDDQDLVKY	0.891307	0.04
HLA-B*58:01	4	49	57	9	FSTAYDIGW	0.887676	0.07

HLA-B*15:01	6	14	23	10	TONIELVAQY	0.875474	0.03
HLA-A*02:06	4	5	13	9	YVDGLSFAL	0.843106	0.06
HLA-A*24:02	3	25	33	9	AWTDVLPIF	0.836603	0.04
HLA-B*35:01	4	45	53	9	DGFGFSTAY	0.824771	0.07
HLA-A*23:01	3	25	33	9	AWTDVLPIF	0.822135	0.04
HLA-B*44:03	5	50	58	9	GETRNMTHY	0.817678	0.07
HLA-B*15:01	5	10	18	9	SARPDGQKY	0.807106	0.06
HLA-B*35:01	5	30	38	9	EAWNFGAKY	0.806914	0.08
HLA-B*57:01	4	49	57	9	FSTAYDIGW	0.804798	0.2
HLA-A*01:01	5	9	18	10	SSARPDGQKY	0.80452	0.06

						9	
HLA-A*26:01	5	30	38	9	EAWNFGAKY	0.792462	0.04
HLA-A*24:02	1	24	32	9	IYNKDGNKL	0.774851	0.06
HLA-B*35:01	5	10	18	9	SARPDGQKY	0.770675	0.09

Table 2: T Cell Epitope predicted for M. morganii

Short peptides present a challenge for the development of peptide vaccines because they lack T cell epitopes, which are essential for MHC restriction. In order to address this, we determined that the T cell epitope with the highest score, 0.987505, was a strong contender for our peptide vaccination. This rigorous selection procedure guarantees the incorporation of a strong T cell response, addressing an important factor in the development of a complete and successful peptide vaccine.

Discussion

A major risk to human health is the emergence of bacterial pathogen strains that are resistant to multiple drugs (8). The effectiveness of the current list of antibiotics is especially at risk because of this. This has an effect on the creation of new medications as well, since the pharmaceutical industries have not demonstrated much interest due to difficult regulatory requirements and diminished financial incentives (9). Traditional vaccination methods have a number of drawbacks, including a long processing time, a developed vaccine that produces erroneous immune responses, high costs, decreased safety, decreased specificity, increased sensitivity, and decreased stability (10). We now have access to a sizable amount of genomic data that will aid in determining which antigenic proteins are most appropriate for the creation of novel vaccines.(11). In order to create vaccines that are both safe and effective, it has become more appealing to combine the B cell and T cell peptide vaccine.

The current work represents a major step forward in the effort to create a peptide vaccine to prevent M.morganii infection. We carefully considered our options and chose the B cell epitope TRNMTHYGTNDDNRGLTANKTQ, which is 100% homologous to the pathogen and has an ideal length range of 15 to 22 amino acids. This careful selection guarantees the vaccine's possible success by conforming to established standards for a successful B cell response. Furthermore, by giving priority to the T cell epitope with the highest score (score: 0.987505), our approach tackles the problem of T cell epitope absence in short peptides. Our vaccine is positioned as a comprehensive and promising contender in the ongoing fight against M.morganii infections because of its dual focus on B and T cell epitopes.

A prior study on the design of an in silico multi-epitope vaccine demonstrated that the vaccine could elicit potent immune responses against invader Enterobacteriaceae. The study assessed the vaccine potency using various computer-aided vaccine strategies (12). The creation of a chimeric vaccine against Proteus mirabilis was the subject of a related study, which discovered that broad-spectrum multi-antigenic, non-redundant, conserved, and surface localized peptides can elicit precise and targeted immune responses. In the process of developing a vaccine, they examined three distinct protein types (AtfC, PMI2533, and PMI1466). Each of these proteins met the requirements for a vaccine and could be a viable candidate for a subunit vaccine (13).Additionally, a computer-aided vaccine design approach was employed in a different study to combat Klebsiella pneumonia (14), Streptococcus pneumoniae (14,15), Providencia rettgeri(16), and Pseudomonas aeruginosa (17), Morganella morganii (17,18) A major factor in the quick development of computational vaccine design techniques is the exponential increase in genomic data. These analyses can direct the development of a safe vaccine against a variety of microbial pathogens and are very specific and effective.(19) These revelations highlight the difficulty in developing vaccines and call on scientists to combine experimental validation with computational forecasts for a more reliable method.(20)

To sum up, our peptide vaccine appears to be a promising option for treating infections caused by M.morganii due to its emphasis on epitope prediction, the deliberate selection of B and T cell epitopes, and the incorporation of a comprehensive immune response. Similar computational strategies are found in comparisons with other studies, highlighting the significance of diverse immune responses(21) Challenges and constraints, however, highlight the necessity of a cautious and flexible approach in vaccine development. The development of computational and experimental methodologies in tandem will be essential to the field's advancement toward the development of potent bacterial peptide vaccines.

Conclusion

We conclude that the identification of particular B-cell and T-cell epitopes is critical as it lays the groundwork for the creation of a targeted peptide vaccine against M.morganii. An additional factor supporting the chosen B-cell epitope's candidacy for the vaccine is its homology to the pathogen

and adherence to the ideal length range. The vaccine approach's strategic dimensions are further enhanced by the inclusion of the highest-scoring T-cell epitope (score: 0.987505), which is in line with current trends in epitope prediction for a stronger immune response. Although we find similarities with similar studies, we also recognize that vaccine design presents inherent challenges and stresses the continuous need for validation and flexibility. Although our designed vaccine is a promising tool in the fight against M.morganii infections, more work between computational and experimental methods is needed to make it suitable for widespread use. This field's evolution emphasizes how important it is to address constraints and continuously improve tactics.

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