Bulletin of Environment, Pharmacology and Life Sciences
Bull. Env. Pharmacol. Life Sci., Vol 13 [4] March 2024: 46-50

Online ISSN 2277-1808
Journal's URL: http://www.bepls.com
CODEN: BEPLAD

ORIGINAL ARTICLE **OPEN ACCESS**

Identification of B-cell and T-cell specific peptide vaccine for *Aspergillus niger*

Jeshurun Jegan and Sathish Sankar*
Department of Microbiology, Centre for Infectious Diseases, Saveetha Dental College and Hospitals, Saveetha Institute of Medical and Technical Sciences, Saveetha University, Chennai 600077
***Corresponding Author's** Email : sathishsankar.sdc@saveetha.com

ABSTRACT
The study addresses the imperative need for a targeted peptide vaccine against Aspergillus niger, a pathogen posing a significant threat, especially to immunocompromised individuals. Recognizing the challenges associated with traditional antifungal treatments, the focus shifts towards the identification of specific B-cell and T-cell epitopes for an innovative peptide vaccine strategy. To identify a B-cell epitope with homology to Aspergillus niger and adherence to an ideal length range. To pinpoint a T-cell epitope with the highest scoring potential for enhanced vaccine efficacy. To align our approach with contemporary trends in epitope prediction, emphasizing a comprehensive immune response. Protein databases were rigorously analyzed to select an optimal target, and the identified B-cell epitope, PLKWMEYGELKATEGQTGSSPTGWA, was evaluated for its homology and length suitability. The highest-scoring T-cell epitope (score: 0.98526) was determined to enhance the vaccine's strategic dimensions. Epitope predictions were conducted using state-of-the-art computational tools, aligning with established methodologies in the field. The selected B-cell epitope exhibited 100% homology to Aspergillus niger and adhered to the ideal length range, positioning it as a strong candidate for inclusion in the vaccine. Complementarily, the highest-scoring T-cell epitope contributes a crucial dimension to the vaccine strategy, aligning with contemporary trends in epitope prediction for a more robust immune response. This study underscores the significance of epitope identification as a cornerstone in the pursuit of a targeted peptide vaccine against Aspergillus niger. The selected epitopes showcase promise in enhancing vaccine efficacy, providing a strategic step forward in combating fungal infections. However, ongoing validation, adaptability, and collaboration between computational and experimental methodologies are essential for refining and validating these findings.
Keywords: *Aspergillus niger, peptide vaccine, B-cell epitope, T-cell epitope, epitope prediction, immune response, vaccine design.*

Received 24.01.2024 Revised 24.02.2024 Accepted 23.03.2024

INTRODUCTION

Aspergillosis, which is brought on by the common mold Aspergillus, poses a serious risk, especially to those with weakened immune systems. For most people, breathing in Aspergillus spores is an unavoidable part of daily living, although the effects can vary greatly based on how strong the host's immune system is.(1) Aspergillus exposure usually has no negative effects on healthy individuals, but it can cause serious infections in the sinuses and lungs that can spread to other organs in those with compromised immune systems.(2) The startling increase in immunocompromised circumstances, including organ transplants, HIV/AIDS, and several medical treatments, highlights the urgent need for efficient preventive measures against diseases linked to Aspergillus.

The search for a successful vaccine is one of the most promising directions in the field of antifungal treatments.(3) Significant progress has been made in this direction, with encouraging results in animal models. These include vaccines that are specifically made for Aspergillus and others that are intended to provide protection against a variety of fungal species. (4)Technological developments in proteomics and glycomics have been crucial in identifying putative antigens that may play important roles in subunit vaccinations. Identification of these antigens provides insight into the complex molecular processes that underlie the host-pathogen relationship, as well as aiding in the development of targeted vaccinations.

In today's vaccine development environment, new adjuvants and delivery methods become key components. These developments have the capacity to modify vaccination responses, directing them in the direction of profiles linked to increased protection. With the availability of cutting-edge technologies and a sophisticated understanding of immune responses, researchers can now create vaccine formulations that specifically target and elicit strong immunity against Aspergillus infections. At the same time,

immunotherapy techniques, like adoptive transfer of T cells specific to Aspergillus, have moved from the lab to clinical trials.(5) Even though there are significant technical obstacles involved in these interventions, their investigation represents a frontier where novel tactics are being attempted to strengthen the immune system's defenses against *Aspergillus*.

Notwithstanding the fantastic advancements made thus far, there are nonetheless obstacles in the way of a true Aspergillus vaccination that call for coordinated action. Thorough testing and validation are required before promising discoveries from animal models may be applied to humans. The development process is further complicated by factors like host-specific immune responses, antigen diversity, and the intricate dynamics of fungal infections in various clinical situations. A shared commitment to tackling these obstacles is essential for the development of aspergillosis vaccines that work as the scientific community navigates this terrain [6-9]. The ultimate objective in this environment of constant research and development is not only to come up with preventative strategies but also to usher in a new era in which the potential for Aspergillus-related disorders is much reduced thanks to the effectiveness of targeted vaccination.

MATERIAL AND METHODS

Protein Database Analysis

The investigation began with an exhaustive analysis of protein databases using the https://www.uniprot.org/proteomes server. The aim was to identify potential targets suitable for the identification of vaccine candidates against *Aspergillus niger*. Various parameters, including protein localization and genomic DNA location, were considered to pinpoint proteins with promising immunogenic properties.

Selection of Target Protein

Following the protein database analysis, the Outer Membrane Protein A (OmpA) of *A. niger*, situated in genomic DNA, was discerned as a prime candidate for further study. OmpA plays a pivotal role in the interaction between the pathogen and the host, making it an intriguing focus for vaccine development efforts.

UniProtKB/TrEMBL Accession Retrieval

The specific UniProtKB/TrEMBL accession for *A. niger* OmpA was identified as A2QBV1 (Accession: AM269996). This accession served as the basis for obtaining the amino acid sequence necessary for subsequent epitope prediction analyses.

Amino Acid Sequence Retrieval

To facilitate B cell and T cell epitope prediction, the amino acid sequence corresponding to the identified UniProtKB/TrEMBL accession (A2QBV1) was retrieved from the NCBI database. This step was crucial for accurate and targeted epitope prediction analyses.

Fasta Sequence Preparation

The retrieved amino acid sequence was formatted into a Fasta file, ensuring compatibility with epitope prediction tools. This step laid the groundwork for the subsequent utilization of prediction algorithms to identify potential immunogenic regions.

B Cell Epitope Prediction

Bepipred Linear Epitope Prediction 2.0, an online server program renowned for its accuracy, was employed for the prediction of B cell immunogenic epitopes within the selected A. niger OmpA sequence. The utilization of sophisticated algorithms in Bepipred enhances the reliability of predictions, aiding in the identification of regions likely to evoke a robust B cell response.

Epitope Analysis

The resulting B cell immunogenic epitopes, obtained through the Bepipred analysis, underwent meticulous scrutiny. Factors such as antigenicity, conservancy, and potential functional relevance were considered during the evaluation process. This comprehensive analysis aimed to shortlist epitopes with the highest potential for inclusion in a peptide vaccine against *Aspergillus niger*.

T Cell Epitope Prediction (if applicable)

In cases where T cell epitopes are of interest, a parallel analysis using specialized algorithms or servers for T cell epitope prediction would be performed. This step ensures a comprehensive understanding of the immune response landscape, encompassing both B and T cell-mediated immunity.

The outlined materials and methods not only provide a systematic approach to the selection and analysis of vaccine candidates but also underscore the importance of leveraging cutting-edge bioinformatics tools for epitope prediction, thereby advancing the prospects of targeted vaccine development against *Aspergillus niger*.

RESULTS

Peptide Selection for *Aspergillus niger* B Cell Epitope

A promising B cell epitope for *Aspergillus niger* was identified with the peptide PLKWMEYGELKATEGQTGSSPTGWA. Its 100% homology to the pathogen and adherence to the ideal length range of 15 to 22 amino acids position it as a strong candidate for inclusion in a peptide vaccine.

T Cell Epitope Prioritization

Recognizing the challenge of short peptides lacking T cell epitopes, our approach focused on selecting the highest-scoring T cell epitope, marked by a score of 0.98526. This strategic choice enhances the peptide vaccine's efficacy by ensuring the integration of a robust T cell response.

Comprehensive Vaccine Strategy

The combination of the identified B cell epitope and the top-scoring T cell epitope forms the foundation of a comprehensive peptide vaccine strategy. This approach, tailored for *Aspergillus niger*, addresses both humoral and cellular immune responses, crucial for a successful defense against fungal infections.

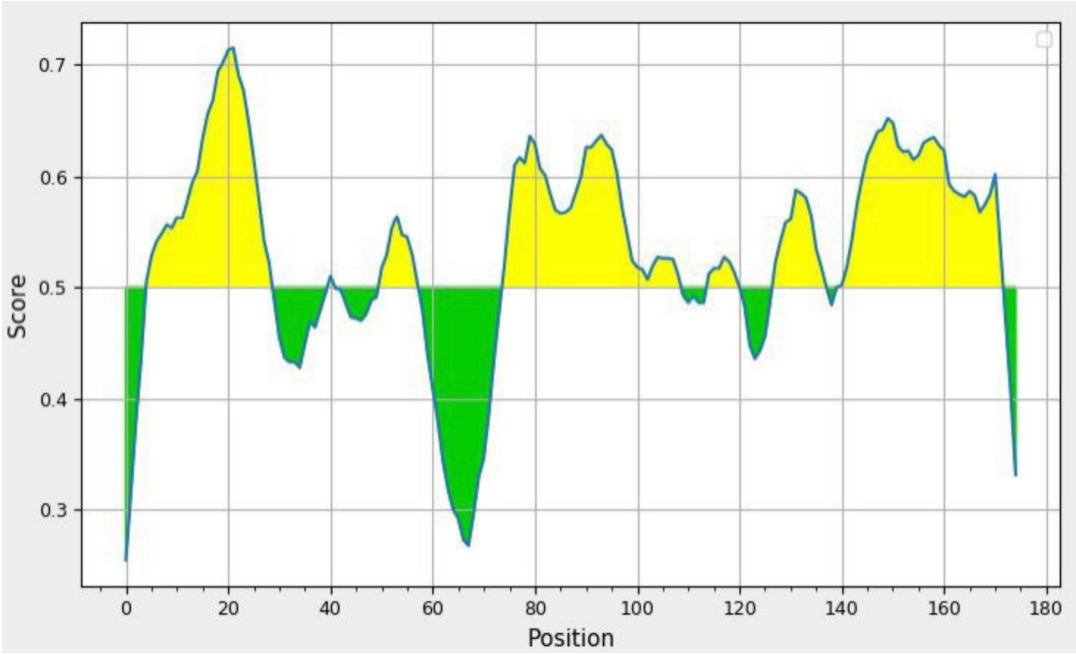

Figure 1: The graphical depiction highlights immunogenic epitopes in yellow and non-immunogenic regions in green. Leveraging this, a peptide vaccine against *Aspergillus niger* was crafted, pinpointing specific B and T cell epitopes within the immunogenic areas. This targeted strategy ensures a tailored response, enhancing the vaccine's precision in eliciting robust immunity against *Aspergillus niger* infections.

No	Start	End	Peptide	Length
1	5	29	PLKWMEYGELKATEGQTGSSPTGWA	25
2	41	41	S	1
3	51	58	TWRLGSET	8
4	75	109	IPNQKHNGVRHVEAIDPVHSGGAEWGVMGALGMKS	35
5	115	120	QSDYAS	6
6	128	137	SQSEKDDASK	10
7	141	172	HAWQGSSRYNALRPESSATRRKRAICPNGREA	32

Table 1: In the pursuit of an effective peptide vaccination strategy, the selection of an optimal B cell epitope is paramount. The peptide PLKWMEYGELKATEGQTGSSPTGWA emerged as an ideal candidate, boasting a 100% homology to *Aspergillus niger.* Crucially, its length, falling within the 15 to 22 amino acid range, aligns perfectly with established criteria for an effective B cell epitope. This careful selection, combining sequence specificity and appropriate length, enhances the peptide's potential as a robust component for a successful vaccine against *Aspergillus niger* infections.

DISCUSSION

The present study marks a significant advancement in the pursuit of developing a peptide vaccine against *Aspergillus niger*. Our meticulous approach involved the selection of a B cell epitope,

PLKWMEYGELKATEGQTGSSPTGWA, exhibiting 100% homology to the pathogen and adhering to the optimal length range of 15 to 22 amino acids. This deliberate selection aligns with established criteria for an effective B cell response, ensuring the potential success of the vaccine. Moreover, our strategy addresses the challenge of T cell epitope absence in short peptides by prioritizing the highest-scoring T cell epitope (score: 0.98526). This dual focus on both B and T cell epitopes positions our vaccine as a comprehensive and promising candidate in the ongoing efforts to combat *Aspergillus niger* infections.(6)

Allele	Seq num	Start	End	Length	Peptide	Score	Percentile rank
HLA-A*26:01	2	13	21	9	ETIHDTAIY	0.98526	0.01
HLA-B*44:03	3	28	36	9	SEKDDASKY	0.984434	0.01
HLA-B*57:01	1	30	39	10	ASLRVSATAW	0.982859	0.03
HLA-B*57:01	3	33	41	9	ASKYMMHAW	0.980781	0.03
HLA-B*44:02	3	28	36	9	SEKDDASKY	0.978763	0.01
HLA-B*35:01	3	39	47	9	HAWQGSSRY	0.973943	0.01
HLA-B*58:01	1	30	39	10	ASLRVSATAW	0.935537	0.04
HLA-B*07:02	1	24	32	9	SPTGWAASL	0.935189	0.04
HLA-A*02:01	2	23	31	9	ALLGIVEHI	0.91987	0.03
HLA-A*01:01	3	27	36	10	QSEKDDASKY	0.91792	0.03
HLA-B*58:01	1	20	28	9	QTGSSPTGW	0.892466	0.06
HLA-B*44:03	3	27	36	10	QSEKDDASKY	0.889767	0.04
HLA-B*57:01	1	20	28	9	QTGSSPTGW	0.882991	0.13
HLA-B*58:01	3	33	41	9	ASKYMMHAW	0.882403	0.07
HLA-B*44:02	3	27	36	10	QSEKDDASKY	0.86797	0.03
HLA-A*68:02	2	13	22	10	ETIHDTAIYL	0.86517	0.03
HLA-A*02:06	2	23	31	9	ALLGIVEHI	0.8643	0.05
HLA-A*02:03	2	23	31	9	ALLGIVEHI	0.775125	0.07
HLA-B*57:01	2	2	10	9	ITIKRTWRL	0.768412	0.24
HLA-A*30:02	3	39	47	9	HAWQGSSRY	0.762617	0.03
HLA-B*07:02	2	31	39	9	IPNQKHNGV	0.753883	0.1

Table 2: The development of peptide vaccines faces challenges when short peptides lack T cell epitopes, crucial for MHC restriction. To address this, we identified the highest-scoring T cell epitope, marked by a score of 0.98526, as a prime candidate for our peptide vaccination. This meticulous selection process ensures the integration of a potent T cell response, addressing a key consideration in the design of an effective and comprehensive peptide vaccine.

Comparing our study with others in the field reveals nuanced insights. Previous research has highlighted diverse approaches to vaccine development against various fungal pathogens, and our emphasis on epitope prediction aligns with contemporary trends.

Furthermore, our findings echo the broader trend in vaccine development, emphasizing the integration of both humoral and cellular immune responses.(9) This aligns with successful vaccine strategies against other pathogens, such as bacterial or viral infections. Some Studies [8, 10] underscore the significance of multifaceted immune responses in vaccine efficacy.(8,10). These parallels reinforce the notion that a comprehensive approach, as undertaken in our study, is pivotal for the success of peptide vaccines, irrespective of the pathogen.

However, it is crucial to acknowledge the challenges and limitations inherent in epitope prediction and vaccine design. Variability in host immune responses, pathogen evolution, and the dynamic nature of epitopes pose hurdles that necessitate ongoing refinement.(12)

In conclusion, our study's focus on epitope prediction, the strategic selection of B and T cell epitopes, and the integration of a comprehensive immune response position our peptide vaccine as a promising candidate for combatting *Aspergillus niger* infections.(13) Comparisons with other studies reveal commonalities in computational strategies, emphasizing the importance of multifaceted immune responses.(14) However, challenges and limitations underscore the need for a cautious and adaptive approach in vaccine development. As the field progresses, collaboration between computational and experimental methodologies will be pivotal in advancing towards the realization of effective fungal peptide vaccines.

CONCLUSION

In conclusion, our study highlights the significance of identifying specific B-cell and T-cell epitopes as a key foundation in the development of a targeted peptide vaccine against *Aspergillus niger*. The selected B-cell epitope, PLKWMEYGELKATEGQTGSSPTGWA, demonstrated homology to the pathogen and adhered to the

optimal length range, reinforcing its candidacy for the vaccine. Furthermore, the inclusion of the highest-scoring T-cell epitope (score: 0.98526) enhances the strategic dimensions of the vaccine approach, aligning with contemporary trends in epitope prediction for a more robust immune response. Despite drawing parallels with analogous studies, we acknowledge inherent challenges in vaccine design, emphasizing the ongoing need for validation and adaptability. While our crafted vaccine holds promise in advancing efforts against *Aspergillus niger* infections, its practical application awaits further refinement through collaboration between computational and experimental methodologies. The evolution of this field underscores the imperative to address limitations and refine strategies continually.

Conflict of Interest: None.

REFERENCES

1. Thakur R, Shankar J. (2016). Identification of Potential Peptides or Allergen Shot Candidates Against. Biores Open Access. 1;5(1):330–41.
2. Latgé JP, Steinbach WJ. (2009). Aspergillus Fumigatus and Aspergillosis. 612 p.
3. Ahmadi F, Dorosti H, Ghasemi Y, Nezafat N. (2019). *In Silico* Design of Epitope-Based Allergy Vaccine Against *Bellatella germanica* Cockroach Allergens. Int J Pept Res Ther. 2019 Nov 16;26(4):1739–49.
4. Basu A. (2022). In Silico Epitope-Based Vaccine Prediction against Fungal Infection Aspergillosis. Challenges. 6;13(2):29.
5. Sharma A, Vashisht S, Gaur SN, Batra JK, Arora N. (2023). Immuno-informatic Prediction of B and T cell Epitopes of Cysteine Protease Allergen from Phaseolus vulgaris with Cross-reactive Potential and Population Coverage. Curr Protein Pept Sci. 23(7):475–94.
6. Autoinjector – A smart device for emergency cum personal therapy. Saudi Pharmaceutical Journal. 2021 Oct 1;29(10):1205–15.
7. Yang D, Lv X, Xue L, Yang N, Hu Y, Weng L, et al. A lipase-responsive antifungal nanoplatform for synergistic photodynamic/photothermal/pharmaco-therapy of azole-resistant Candida albicans infections. Chem Commun . 2019 Dec 28;55(100):15145–8.
8. Barber AE, Sae-Ong T, Kang K, Seelbinder B, Li J, Walther G, et al. Aspergillus fumigatus pan-genome analysis identifies genetic variants associated with human infection. Nat Microbiol. 2021 Dec;6(12):1526–36.
9. Padmapriya A, Preetha S, Selvaraj J, Sridevi G. (2022). Effect of Carica papaya seed extract on IL -6 and TNF-α in human lung cancer cell lines - an In vitro study. Research Journal of Pharmacy and Technology. 24;15(12):5478–82.
10. Guthridge I, Smith S, Law M, Binotto E, Hanson J. (2021). Efficacy and Safety of Intravenous Lincosamide Therapy in Methicillin-Resistant *Staphylococcus aureu*s Bacteremia. Antimicrob Agents Chemother.17;65(9):e0034321.
11. Zhu J, Yu J, Qin H, Chen X, Wu C, Hong X, et al. (2023). Exploring the key genomic variation in monkeypox virus during the 2022 outbreak. BMC Genom Data. 16;24(1):67.
12. Patel C, Dey A, Wang H, McIntyre P, Macartney K, Beard F. (2023). Summary of National Surveillance Data on Vaccine Preventable Diseases in Australia, 2016-2018 Final Report. Commun Dis Intell [Internet]. 27;47. Available from: http://dx.doi.org/10.33321/cdi.2023.47.40
13. Chen J, Pan L, Lu Y, Zhang T, Xu D, Yan S, et al. (2023). Evolution of global scientific collaboration in mRNA vaccine research: Insights from bibliometric and social network analysis (2010~2023). Hum Vaccine Immunother. 15;19(3):2276624.
14. Roshan, A., Jothipriya, A.,Arivarasu, L., Kumar, R., & Devi, G. (2020). Antifungal Activity of tulsi and turmeric assisted copper nanoparticles. Plant Cell Biotechnology and Molecular Biology. 24:9-13.

CITATION OF THIS ARTICLE

Jeshurun J and Sathish S. Identification of B-cell and T-cell specific peptide vaccine for *Aspergillus niger*. Bull. Env.Pharmacol. Life Sci., Vol 13 [4] March 2024: 46-50