

Anti-MDR Pathogen Epitope Driven Broad Spectrum Peptide Vaccines

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Received: 03-December-2022; Manuscript No. mracs-23-85264; **Editor assigned:** 04-December-2022, Pre QC No. mracs-23-85264 (PQ); **Reviewed:** 12-December-2022, QC No. mracs-23-85264 (Q); **Revised:** 17-December-2022, Manuscript No. mracs-23-85264 (R); **Published:** 20-December-2022, doi: 10.4172/2572-5130.7.12.1000228

Editorial

A set of co-existing, multi-drug resistant nosocomial bacteria, including *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae*, have evolved and are now found around the world. High death rates among hospitalised patients are a result of the overuse of antibiotics, which has caused the rise of bacterial strains that are resistant to all antimicrobial drugs, including carbapenems and even the last-resort antibiotic, colistin. Although vaccination is a very effective and widely used method of lowering the prevalence of infectious diseases, little has been done to produce vaccines to prevent nosocomial infections. A broad range vaccination that offers protection not just against *A. baumannii* but also against the entire collection of co-existing nosocomial infections is the futuristic necessity in this direction.

The method of in silico vaccine prediction and development has undergone a revolution thanks to the accessibility of entire bacterial genome and proteome sequences. The availability of genomic sequences and functional characterization of several genes involved in virulence has significantly improved our understanding of the molecular basis of pathogenesis and provided a wealth of information that can be used to design new strategies for the development of effective vaccines, even though the proteomes of the pathogens contain a number of uncharacterized and putative proteins. By analysing bacterial proteomes in silico and facilitating in vivo confirmation, reverse vaccinology is a time-efficient method that can anticipate possible epitopes as vaccine candidates, improving the alternatives for treating diseases. Epitope-based techniques might be able to address the issue in some circumstances where natural immunogens fail to elicit the best response and the production of recombinant subunit vaccines becomes challenging. Epitopes are simple to create, formulate, and test in mouse models. The synthetic peptide vaccination is predicted to be more effective, safe, and long-lasting than traditional ones in the near future. In contrast to conventional vaccinations made of live, attenuated, or killed entire organisms or purified antigen, peptide vaccines can induce both antibodies and Cytotoxic T Lymphocytes (CTLs), making them a viable vaccine method to test against a variety of pathogens [1-3].

The fact that peptides are chosen after comprehensive in silico research utilising both sequence-based and structure-based screening approaches may be the reason for the efficacy of peptide vaccines. Synthetic peptides

offer particular benefits in terms of chemical characterization and manufacturing due to their well-defined chemical nature and tiny size. The traditional method for identifying T cell epitopes entails expensive and time-consuming experimental screening of overlapping peptides in the protein of interest. Nevertheless, the creation of numerous systems for epitope prediction has made it easier to forecast the most likely epitope possibilities and decreased the number of peptides chosen for experimental validation. It is possible to predict identical epitopes that are present in the majority of bacterial proteomes by choosing outer membrane proteins that are conserved across different bacterial genera. Epitope promiscuity, a key characteristic of epitope-driven vaccines, renders them more relevant immunogens in populations of genetically diverse species like humans. Consequently, it is possible to create the optimal peptide vaccine (peptope) by searching the entire collection of epitopes for the most conserved, surface-exposed ones that bind to the majority of HLA alleles. These synthetic peptide vaccines can either be utilised as such or coupled with metalloproteins like Keyhole Limpet Hemocyanin (KLH). The lipid core peptide vaccine delivery system, azide-alkyne cycloaddition with copper catalyst, thioether ligation, multi-epitope construct made by random polymerization of several acrylates modified B cell epitopes, and recombinant polyepitope conjugated to adjuvant moiety with the aid of intramammary ligation are some examples of synthetic techniques. When administered, the tailored peptide vaccine signals the host's immune system to produce immunisation memory cells. Peptope is a viable option for a vaccine, but clinical trials are required to establish its efficacy. The diminished side Effects have a cost. A significant advancement in the production of vaccinations against pathogens can be made possible by the liveness and enhanced stability of epitope driven peptide-based vaccines. Additionally, combining significant epitopes that are conserved across a number of nosocomial pathogens' proteomes can produce a vaccine candidate that exhibits promise for broad-spectrum immunity. By creating future epitope-driven vaccines, we anticipate a revolutionary shift in the range of available treatments [4,5].

References

1. Aguilar, Laura K., et al. "The spectrum of vaccine therapies for patients with glioblastoma multiforme." *Curr treat options oncol* 13.4 (2012): 437-450.
2. Zeigler, David F., et al. "Epitope targeting with self-assembled peptide vaccines." *npj Vaccines* 4.1 (2019): 1-8.
3. Wada, H., et al. "Development of a novel immunoproteasome digestion assay for synthetic long peptide vaccine design." *Plos one* 13.7 (2018): e0199249.
4. Almeida, Joao P.M., et al. "In vivo gold nanoparticle delivery of peptide vaccine induces anti-tumor immune response in prophylactic and therapeutic tumor models." *Small* 11.12 (2015): 1453-1459.
5. McMurphy, Julie A., et al. "A call to cellular & humoral arms: enlisting cognate T cell help to develop broad-spectrum vaccines against influenza A." *Hum Vaccines* 4.2 (2008): 148-157.