

Development of a novel multiepitope vaccine against Gag polyprotein of *HTLV* using in silico approaches

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Abstract

Human T-cell Lymphotropic Virus (HTLV) is a retrovirus associated with various diseases, including adult T-cell leukemia/lymphoma, uveitis, dermatitis, polymyositis, arthritis, alveolitis, and Sjogren's syndrome. Despite its prevalence, especially in certain regions of the world, such as Japan, parts of Africa, and the Caribbean, there is a substantial gap in preventive measures such as vaccination. Therefore, the development of an effective vaccine against *HTLV* not only holds the promise of reducing the incidence of associated diseases but also aims to alleviate the economic burden on healthcare systems. For the first time, the present study employed in silico approaches to predict various epitopes to design a multiepitope vaccine against the *HTLV* Gag polyprotein. Our vaccine coverage analysis revealed that the vaccine construct was highly effective, making it a potential candidate for worldwide use. Furthermore, the vaccine construct was able to interact effectively with immune receptors such as TLRs. Molecular dynamic (MD) simulations revealed that the vaccine attained its stable conformation within the biological environment after a brief temporal interval, thereby indicating stabilized behavior in practical settings. Finally, the vaccine construct was also able to induce immune responses, such as the activation of B cells and T cells and increase antibody and cytokine responses. To the best of our knowledge, this is the first study that has focused on *HTLV* Gag epitopes to design a multiepitope vaccine in silico, which needs in-vitro/in-vivo experimental validation.

Keywords Human T-lymphotropic virus · Vaccine · Gag polyprotein · Immunoinformatics · Molecular dynamic simulation

Abbreviations

B cell	BCL
CTL	Cytotoxic T lymphocyte
Helper T lymphocyte	HTL
Human T-cell Lymphotropic Virus	HTLV
Interferon-gamma	IFN- γ
Interleukin	IL
Pan-HLA-DR-binding epitope	PADRE

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C-termini of the codon-optimized sequence for in silico cloning in the pGen 2.1 vector. For prokaryotic expression, the pET-30a (+) plasmid was used. The codon-optimized nucleotide sequence of the vaccine construct was cloned and inserted into the aforementioned vector via the BamHI and XhoI restriction enzymes in the SnapGene software program.

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1038/s41598-026-64039-0>.

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Data availability Data will be available upon request.

Declaration

Competing interests The authors declare no competing interests.

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