Bioinformatic Analysis of Conformational Epitope Peptide Sequences for the Effective Diagnosis of Sudan Ebola Virus Disease

S.A. Omerigwe[1], J.A. Oluwasegun[8], E.O. Aro[2], M.A. Ockiya[5], A.O. Jimoh[3,9], O.J. Olaoye[4], O.S. Ajasa[6], C.U. Nwaigwe[7], P.T. Adedokun[8], D.A. Adediran[8], E.K. Oladipo[8]

[1] University of Strathclyde, Glasgow, United Kingdom. [2] Medical Laboratory, University College Hospital, Ibadan. [3] Institute of Infectious Disease and Molecular Medicine, University of Cape Town, Cape Town, South Africa. [4] Genetic Resource Center, IITA Ibadan. [5] Department of Animal Science, Niger Delta University, Wilberforce Island, Bayelsa State, Nigeria. [6] GHIDI Department of Molecular Biology and Genomic, Nasarawa State University, Keffi. [7] Faculty of Veterinary Medicine, University of Nigeria, Nsukka. [8] Genomics unit, Helix Biogen Institute, Ogbomoso, Oyo State, Nigeria, [9] National Biotechnology Research and Development Agency, Abuja, Nigeria.

Introduction

Ebola Virus disease is perceived as a recurring menace due to the mutation and discovery of newer strains less than a decade after its most devastating outbreak or greatest outburst occurring between 2013 and 2016 [1-4]. EVD previously known as Ebola haemorrhagic fever no doubt is an acute infectious disease associated by means of high levels of mortality and transmissibility [1].

EVD as a viral threat, requires accurate and rapid detection to allow for prompt therapeutic intervention in order to obviate transmission and imminent repercussions on public health, hence allowing room for higher chances of survival [5-7]. However, the incubation period ranges from 2 to 21 days depending on the route of infection. This typically takes 6 to 10 days in most instances and 10 to 14 days for the Zaire strain, manifesting symptoms with nonspecific febrile [8,9].

Pathogenesis and host immune response to EVD attributes the levels of severity exhibited with a pattern common to most filovirus infections. Slightly above fifty percent (50%) of cases display haemorrhagic abnormalities manifested as bleeding also presenting conjunctiva at death with haematemesis and bloody stool a common phenomenon [8].

Objective

To evaluate EVD strains using immunoinformatic tools for the analysis of multi-epitope peptide sequences, aiming to identify potential epitopes that can be used in the development of diagnostic assays.

To develop and validate lateral flow test kits based on the identified epitopes, enabling rapid point-of-care detection of EVD infection to facilitate timely treatment decisions.

Methods: Process Diagram and Outcomes

Table 4: Peptides of high binding affinity across accession numbers and their interleukin inducer.

Accession Number	IL4 Inducers	IL10 Inducers	IL4 & IL10 Inducers
MK952150.1	PEGETTLPSQNSTEG	GEWAFWENKKNLSEQ	GEWAFWENKKNLSEQ
U28134.1	TATIIGTNGNNMQIS	GEWAFWENKKNLSEQ	GEWAFWENKKNLSEQ
FJ968794.1	YYATSYLEYEIENF	TTKGRISDRATRKY	TTKGRISDRATRKY
MH121163.1	EYEIENFGAQHSTTL	QFLFQLNDTIHLHQQ	GEWAFWENKKNLSEQ
KR063670.1	DIGEWAFWENKKNLS	LGSLGLRKRSRRQTN	GEWAFWENKKNLSEQ
JN638998.1	DIGEWAFWENKKNLS	ILGSLGLRKRSRRQT	GEWAFWENKKNLSEQ

Table 5: High binding peptides selected and classified based on interleukin inducers they promote.

Selected HTL Peptides and Interleukin Inducers		
IL4	IL10	IL4 & IL10
PEGETTLPSQNSTEG	QFLFQLNDTIHLHQQ	GEWAFWENKKNLSEQ
TATIIGTNGNNMQIS	LGSLGLRKRSRRQTN	TTKGRISDRATRKY
YYATSYLEYEIENF	ILGSLGLRKRSRRQT	
EYEIENFGAQHSTTL		
DIGEWAFWENKKNLS		

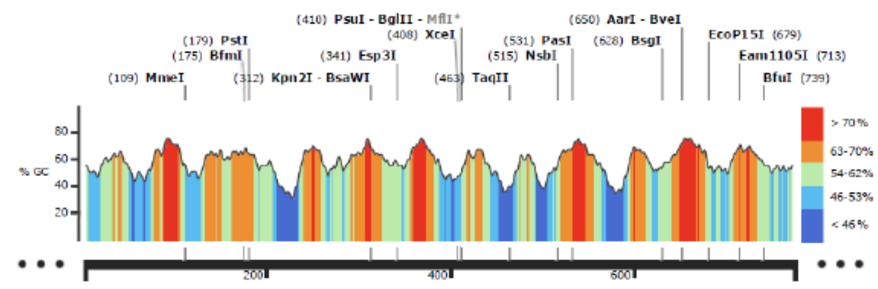
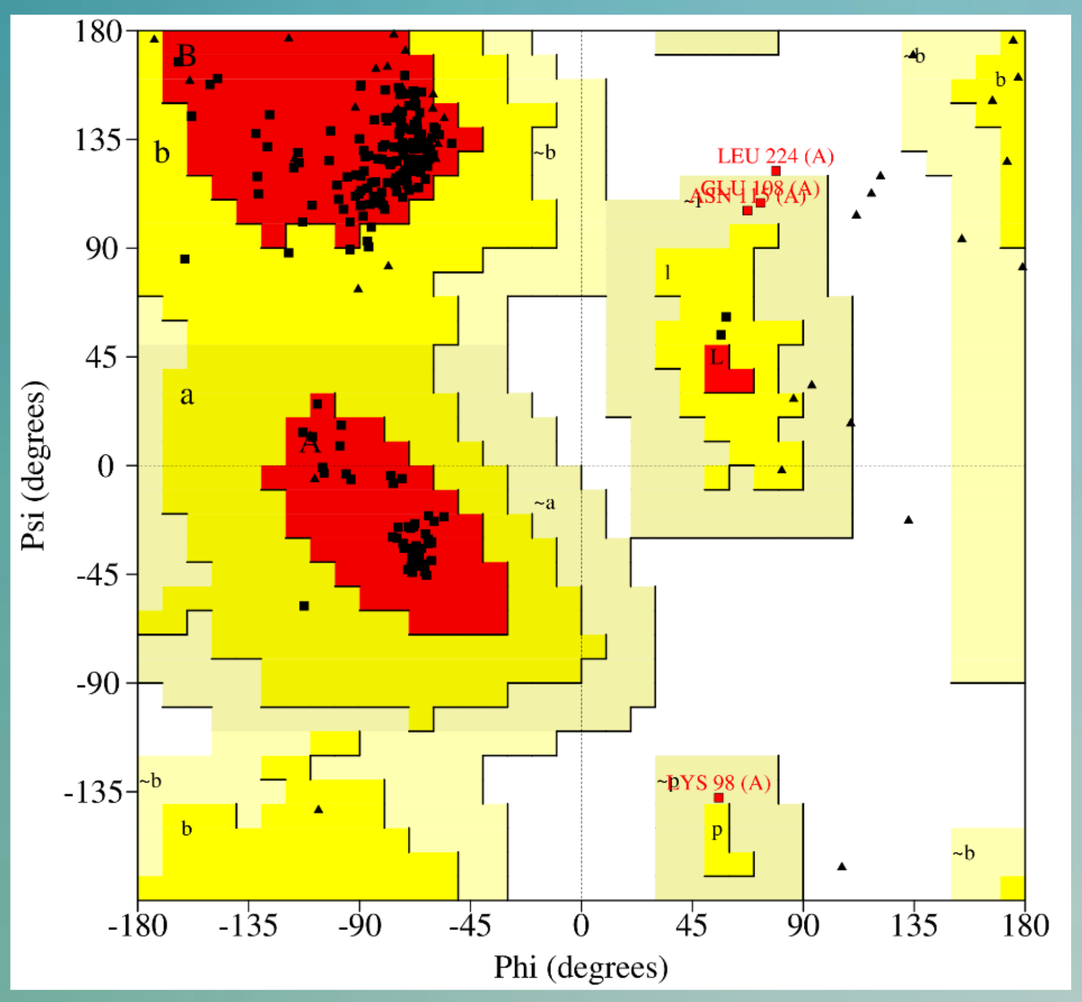


Figure 3: Optimised codon showing guanine-cytosine levels at slightly 60% in design fragment to be used for vector pTZ19R cloning.

Results



Ramachandran's plot showing 172 residues in most favoured region representing 93.0% of total residues [43-45].

Conclusion

- The construct demonstrates significant potential for rapid and accurate detection of Ebola Virus Disease (EVD), highlighting the promise of epitope-based diagnostics despite current limitations in global research and lateral flow test (LFT) applications.
- The conformational analysis of the epitope peptides, as evidenced by the Ramachandran plot, provides valuable insights into the structural integrity and functional suitability of the peptides, supporting their use in effective point-of-care diagnostic tools for EVD.
- With 93% of regions showing high conformational freedom and only 0.5% in disallowed regions, the epitope peptides exhibit a protein structure highly conducive to the rapid and reliable diagnosis of EVD, underscoring the future potential of such diagnostic approaches.

For References, Abstract & Full Article: Scan the QR Code

Full Article & References