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Poster presentation

Function prediction of a newly extracted protein from a newly extracted lassa virus gene

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Clinical background

Lassa virus has been the cause of mortality and morbidity in Ekpoma Nigeria. Lassa virus infection has existed over the years in epidemic form without any hope of vaccines and high cost of drugs have not offered any hope to the people in this locality. Ribavirin which is the drug of choice against the virus is usually beyond the reach of the people.

Materials and methods

A new strain of the virus with a new gene sequence was recently extracted which was between 85% and 45% similar to other viruses using the blast and wu-blast tools with matrix set at PAM50, PAM100 and blosum62. Sequence alignment was done using the blastp and blitz. This we did because protein of similar sequence will have similar function. The translate tool at expasy was used to determine the open reading frames of the sequence. The hydrophobicity of the protein was also determined at expasy using the protscale. As well as TMPRED, PHDhtm, PSIPRED, TMbase and signal P. The protein thread prediction was carried out using the phrye (3D PSSM)tool at expasy. We search through the coils, prints, block, Pfam and interpro.

Results

The sequence alignment at blastp gave significant hits of up between 85% and 45%. The proscan toll revealed that the protein has conserved regions with similarity percentage of 100% in N-glycosylation, kinase carbon hydrate phosphorylation and myristoylation sites. There were two major transmembrane helices, two major alpha helices. The signal P reveals the presence of the protein in the cell. There were no significant hits with the prints, block and coils while the protein was confirmed to be an Arena virus glycoprotein in the envelope. There was a 25% similarity with the thread prediction using the phrye 3D prediction tool. See Figures 1 and 2.

Conclusion

This means that if the virulence part of the protein is removed, it could be used as an antigen and used to vaccinate against other Lassa virus strains. Even the less virulence viruses could be easily manipulated to remove virulence and used as antigens.

Using the scale alpha-helix/Levitt, the individual values for the 20 amino acids are:

Ala: 1.290 Arg: 0.960 Asn: 0.900 Asp: 1.040 Cys: 1.110 Gln: 1.270

Glu: 1.440 Gly: 0.560 His: 1.220 Ile: 0.970 Leu: 1.300 Lys: 1.230

Met: 1.470 Phe: 1.070 Pro: 0.520 Ser: 0.820 Thr: 0.820 Trp: 0.990

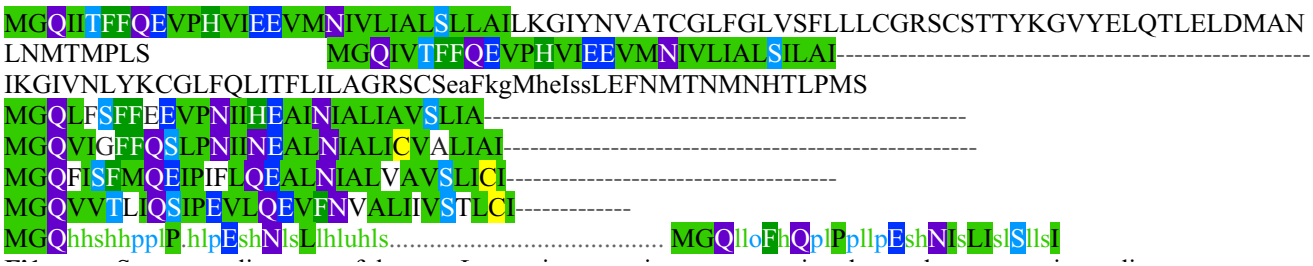

Figure 1
Sequence alignment of the new Lassa virus protein sequence using the prodom at protein predict server.

Tyr: 0.720 Val: 0.910 Asx: 0.970 Glx: 1.355 Xaa: 1.031

Using the scale Hydrophobicity. OMH/Sweet et al., the individual values for the 20 amino acids are:

Ala: -0.400 Arg: -0.590 Asn: -0.920 Asp: -1.310 Cys: 0.170 Gln: -0.910

Glu: -1.220 Gly: -0.670 His: -0.640 Ile: 1.250 Leu: 1.220 Lys: -0.670

Met: 1.020 Phe: 1.920 Pro: -0.490 Ser: -0.550 Thr: -0.280 Trp: 0.500

Tyr: 1.670 Val: 0.910 Asx: -1.115 Glx: -1.065 Xaa: 0.000

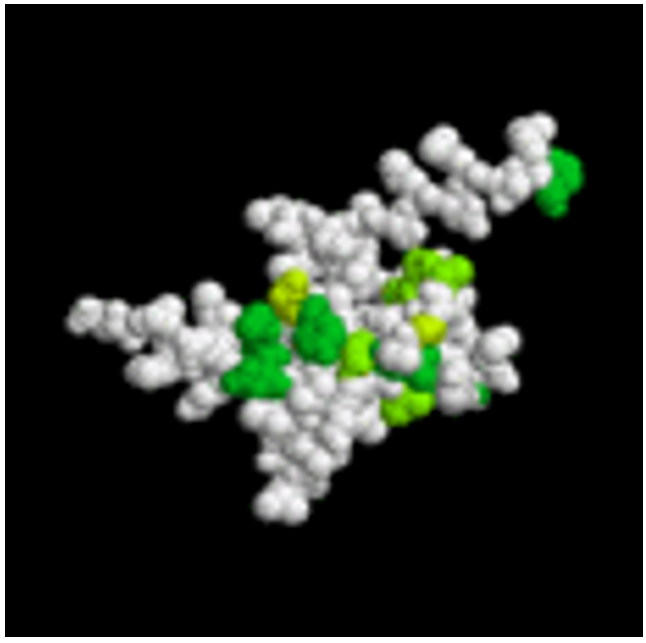

Figure 2
The predicted 3D structure of the protein from the newly isolated Lassa virus gene.

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