Student Post- Activity Assessment of Flu Fighters Activity

You will need to either submit your answers on a separate document (as there isn't enough space here) or edit this document. Questions should not just be yes, and no. Several sentences of well thought out answers are expected.

1. Based on what you have learned in the previous activity, review the alignment below

   a. Currently some young scientists are thinking about designing a vaccine that targets the 244 to 323 amino acid part of the protein. Do you agree that this would be a good area to target for a vaccine? Why or why not?

      ***Lower level**: The 244-323 segment shows differences between all three sequences at or around the same positions (260, 283, and 300/301). If those differences do not interfere with the binding of antibodies, then the target segment could be appropriate.*

      ***Upper level:** The answer above plus… Glutamic acid (E) is bulkier than Glycine (G), and that may play a role in which that segment of the protein is exposed for antibody recognition. Alternatively, the bulkier nature of the amino acid may interfere with the proper recognition of that segment by an antibody. More information would be required about the affinity of antibodies for that segment, or a portion of it to decide if it is a good idea to select it for a vaccine target.*

b. If you were choosing an area to target, just based on amino acid sequence, what area might you propose and why?

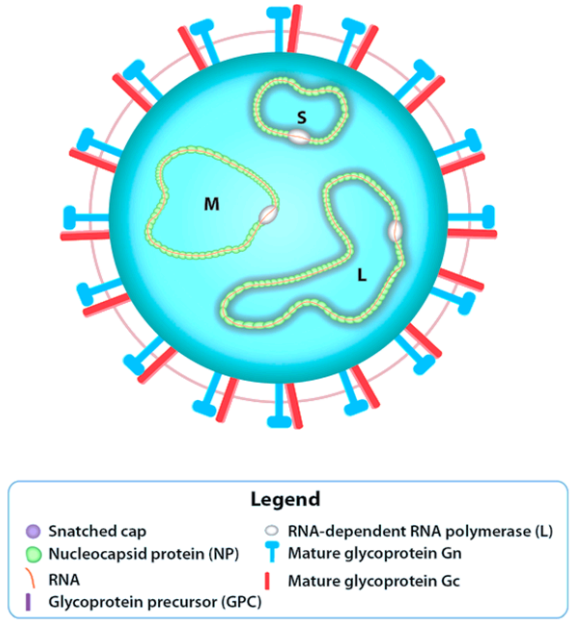
***Lower and Upper level**: Based only on amino acid sequence, any area between positions 84 and 237 would work since there are no differences between the proteins in those segments.*

c. Besides the amino acid sequence, what other factors should you consider when picking a part of a protein to design a vaccine against?

***Lower**: Besides amino acid sequences, the other factors that need to be considered is how immunogenic a particular region of the protein is.*

***Upper level:** Besides amino acid sequences, the other factors that need to be considered is how immunogenic a particular region of the protein is. How exposed to the binding of antibodies that particular region is and what is the affinity with which antibodies bind to that region. In addition, potential antigenic drift should be determined to see with which frequency a change in that region is to be expected, therefore affecting how antibodies recognize it.*

2. Crimean-Congo Hemorrhagic Fever Virus (CCHFV), a virus endemic to parts of Africa, Asia, and Europe, is initially transmitted to humans via a tick bite. Once a human becomes infected, person to person transmission can occur through infectious blood and other bodily fluids. Research has shown that the major cell types infected are monocytes and macrophages (immune cells), endothelial cells (cells lining blood vessels), and hepatocytes (liver cells). Infected individuals may experience mild, vague symptoms such as fever, fatigue, and vomiting, while others experience severe symptoms such as anemia, heart attack, or bleeding in the brain. Currently, there is no vaccine against CCHFV.



Modified from: Zivec et al. (2016) Molecular Insights into Crimean-Congo Hemorrhagic Fever Virus. Viruses 8, 106; doi:10.3390/v8040106

a. Explain how you would design a vaccine to CCHFV. In your response, explain what part of the virus you will target and the components of the immune system that you must trigger for effective immunity.

Lower level: *The best targets for a vaccine would be the proteins in the spikes, Gn and Gc.*

Upper Level*: The structure of the virus suggests that the best targets would be the proteins in the spikes (Gn, and Gc). However, more information would be needed to establish that either protein or both are immunogenic, and the potential rate of mutations of those proteins.*

b. Using the information we have learned about bioinformatics, describe which tools you could use during the development of your vaccine and how you would use those tools.

***Lower Level**: I could use GeneBank to find the sequences of the spike proteins, and COBALT to perform sequence alignments and analysis of differences.*

***Upper Level**: I could use GeneBank to find the sequences of the spike proteins, and COBALT to perform sequence alignments and analysis of differences. However, to look more closely at the proteins, I could also use other tools for molecular visualization, such as ICn3D. GeneBank would provide a list of sequences, in case there are sub variants of CCHFV, which I would then align using COBALT and look for any conserved regions, which would be the first choice of vaccine target.*