Can the Flu Vaccine Provide Additional Protection Against SARS-CoV 2?

By Mehaghni Chaudhury

Purpose

We are examining whether or not there is a protein sequence overlap between SARS-CoV-2 and influenza. To do so, we will be comparing the protein sequences of novel coronavirus and other common coronaviruses with antigen-generating sequences of the influenza virus.



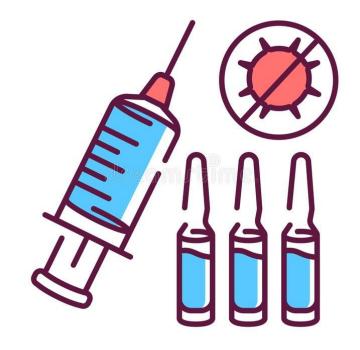
Background Information

• Influenza vaccine elicits blocking antibodies against hemagglutinin protein

- 1. The Influenza vaccine is an inactivated viral vaccine
- 2. The live attenuated virus elicits active immunity and produces blocking antibodies against hemagglutinin protein.
- 3. Hemagglutinin viral protein is required for cell adhesion of viral particles, thus facilitating viral cellular entry of influenza virus

Statement of the Problem

Due to the pending availability the the COVID-19 vaccine, can the flu vaccine provide additional protection against from COVID-19?



Hypothesis

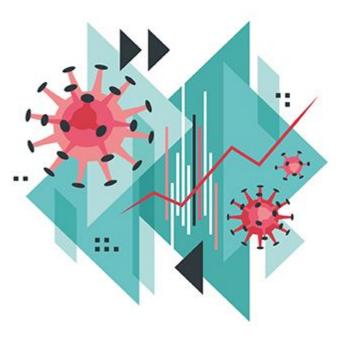
• Repurposing of influenza vaccine against SARS-CoV 2

I hypothesized that if there is peptide sequence overlap between hemagglutinin protein of influenza with surface glycoprotein or receptor protein of SARS-CoV2 novel coronavirus or any other proteins, then the blocking antibodies produced by influenza vaccination may offer additional protection against SARS-CoV 2 infection or SARS-CoV 2-Influenza infection



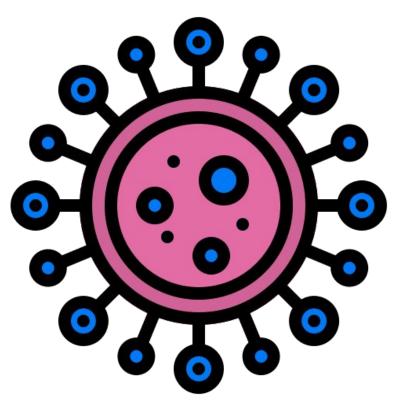
Variables

- Control pathogenic strains of influenza viruses and their key proteins
- Independent variable Whether the genomic sequences overlap
- Dependant variable Whether flu vaccine aides against COVID-19
- Constant protein sequences



Materials

- Genomic sequences of the flu and of COVID-19 (SARS-CoV-2)
- Different strains of COVID-19
- Different strains of influenza



Methods

- Methods of comparing protein sequences
- Protein sequences were obtained from NCBI protein
- NCBI BLAST were used for comparison of protein sequences
- Matching, if any were accessed after "blasting" the sequences

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. Learn more

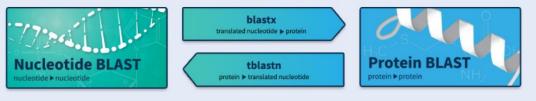
A new version BLAST+ (2.11.0) is here.

This version supports a new usage reporting service and a new multi-theading feature.

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B More BLAST news...

Web BLAST



BLAST Genomes



Standalone and API BLAST



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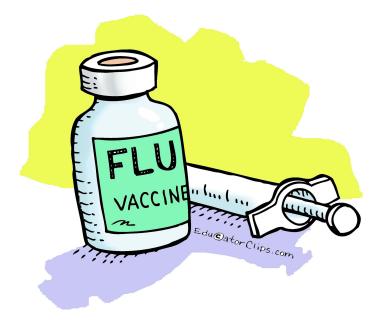
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- Examined proteins of the Influenza virus
- Mainly hemagglutinin of Influenza A was examined
- Hemagglutinin of other influenza strains covering both the northern and southern

hemisphere were examined.

• Further other influenza proteins like neuraminidases were additionally examined

- Protein sequences of SARS-CoV2 were used for comparison
- Surface glycoprotein
- 3 to 5 exonuclease
- Non Structural Protein(NSP)
- 2-0 ribose methyltransferase
- RNA dependent RNA Polymerase
- 3-C like Proteinases
- Membrane glycol protein
- Envelope protein
- Surface Glycoprotein
- Open reading frame(ORF)



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Results

• Upon repeated comparison by blasting, not enough similarity was found between any two protein sequences.

(Pictures of results continued on next slide)

Results (cont.)

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Conclusion

- There is minimum to no overlap in protein sequences of multiple proteins of SARS-CoV 2 with hemagglutinin or other proteins of major strength of Influenza A virus
- This indicated that influenza A virus and SARS-CoV 2 Virus are evolutionarily different
- Further detailed analysis are required to obtain more specific information whether shorter sequences of peptides overlap, we plan to use multiple sequence
- alignment tools like Clustal.
- However increasing epidemic intelligence is showing influenza A co infection alongside SAR-Cov 2 infection, whether
- Influenza A worsens the outcome of SARS-CoV 2 infection currently unknown.
- Nevertheless Influenza vaccination is highly protective as influenza is a major morbid and mortal illness across the globe.

