**Use of bioinformatics tools to determine the efficiency of flu vaccine.**

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**ABSTRACT:**

As the monsoon advances further into the Indian mainland, the bulk of the country, barring the far north, is staring at the onset of influenza season. 

Influenza is a viral infection that affects mainly the nose, throat, bronchi and, occasionally, lungs. Infection usually lasts for about a week, and is characterized by sudden onset of high fever, aching muscles, headache and severe malaise. An annual seasonal flu vaccine (either the flu shot or the nasal spray flu vaccine) is the best way to reduce the chances that you will get seasonal flu and spread it to others. Flu vaccines cause antibodies to develop in the body about two weeks after vaccination. These antibodies provide protection against infection with the viruses that are in the vaccine. The seasonal flu vaccine protects against the influenza viruses that research indicates will be most common during the upcoming season. Traditional flu vaccines (called "trivalent" vaccines) are made to protect against three flu viruses; an influenza A (H1N1) virus, an influenza A (H3N2) virus, and an influenza B virus. There are also flu vaccines made to protect against four flu viruses (called "quadrivalent" vaccines). These vaccines protect against the same viruses as the trivalent vaccine and an additional B virus. To make the influenza vaccine, gene fragments that encode the H and N viral surface proteins are used from each strain. For the vaccine to give a person good protection against the virus, the **protein sequences** for the H and N proteins that are used in the vaccine should closely match the sequences in the strains the person may be exposed to. Every February, the World Health Organization (WHO), based on the analysis of various laboratories across the globe, will decide what influenza virus strains to include in the vaccine for the new year. A powerful Internet-based bioinformatics tool for aligning sequences is **BLAST**, which stands for Basic Local Alignment Search Tool. It aligns your query sequence of interest to a collection of sequences stored in the database, or to a specific second sequence you are interested in. It compares the results, telling you which sequences or segments are similar to your query sequence. This research aims to use blast tool along with flu databases to find out whether this year vaccine is effective or not.

**Keywords**: BLAST, influenza, vaccine, flu database.

**INTRODUCTION**

**Influenza**, commonly known as the flu, is caused by a **virus** that attacks the upper respiratory tract (i.e., the nose, the throat and the lungs). Cold and dry weather allows the virus to survive longer outside the body than in warm weather. There are three **types of influenza virus**: A, B and C. Type A can infect humans, other mammals and birds and can spread fast and affect many people. Types B and C affect only humans and type C causes only a mild infection. Influenza type A viruses are sub-typed into two categories based on proteins, specifically the proteins *hemagglutinin* and *neuraminidase*, on the surface of the virus. The virus uses the hemagglutinin protein (often abbreviated "H" or "HA") to latch on to the host's cell and uses the neuramidase protein (often abbreviated "N" or "NA") to spread the infection. Types A and B viruses continually evolve genetically, with changes being made to the *amino acid sequence* of the H and N proteins. Since hosts recognize the H and N **surface proteins** to identify and attack the virus, by changing these proteins a little bit the virus prevents the hosts from enjoying any prolonged protection against the virus.

When a person is vaccinated with the influenza **vaccine**, it should stimulate a protective immune response, particularly against the viral surface proteins in the viral strains used to make the specific vaccine. The influenza vaccine typically contains three **virus strains**, two are subtypes of type A and one is of type B. Type C is not included in the vaccine because it only causes a mild illness and does not lead to **epidemics**. To make the influenza vaccine, gene fragments that encode the H and N viral surface proteins are used from each strain. For the vaccine to give a person good protection against the virus, the **protein sequences** for the H and N proteins that are used in the vaccine should closely match the sequences in the strains the person may be exposed to. Every February, the World Health Organization (WHO), based on the analysis of various laboratories across the globe, will decide what influenza virus strains to include in the vaccine for the new year. A powerful Internet-based bioinformatics tool for aligning sequences is **BLAST**, which stands for Basic Local Alignment Search Tool. It aligns your query sequence of interest to a collection of sequences stored in the database, or to a specific second sequence you are interested in. It compares the results, telling you which sequences or segments are similar to your query sequence.

All else being equal, we would expect that a strong match between the protein sequences for the H and/or N proteins used in the vaccine virus and the corresponding sequences in the "wild" virus to result in good protection against that virus. On the other hand, a poor match would result in weak protection against the virus.

All of the 2022-23 influenza vaccine is made to protect against the following three viruses:

* an A/California/7/2009 (H1N1)pdm09-like virus
* an A/Switzerland/9715293/2013 (H3N2)-like virus
* a B/Phuket/3073/2013-like virus. (This is a B/Yamagata lineage virus)

Some of the 2015-2016 flu vaccine is quadrivalent vaccine and also protects against an additional B virus (B/Brisbane/60/2008-like virus). This is a B/Victoria lineage virus.

**METHOD:**

Gone to the Flu Activity & Surveillance webpage at The U.S. Centers for Disease Control and Prevention (CDC) website**: http://www.cdc.gov/flu/weekly/fluactivitysurv.htm**.

Selected the influenza season 2015-16,found information about the 2015–2016 vaccine. For 2015–16, U.S.-licensed trivalent influenza vaccines will contain hemagglutinin (HA) derived from an A/California/7/2009 (H1N1)-like virus, an A/Switzerland/9715293/2013 (H3N2)-like virus, and a B/Phuket/3073/2013-like (Yamagata lineage) virus. This represents changes in the influenza A (H3N2) virus and the influenza B virus as compared with the 2014–15 season. Quadrivalent influenza vaccines will contain these vaccine viruses, and a B/Brisbane/60/2008-like (Victoria lineage) virus, which is the same Victoria lineage virus recommended for quadrivalent formulations in 2013–14 and 2014–15 .Taken the strain A/Switzerland/9715293/2013 (H3N2) virus and blast it at NCBI site.

**RESULT AND DISCUSSION:** THE strain was found to show similarity with the following viral strains.

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Therefore the flu vaccine was found to be highly effective.

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