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

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ABSTRACT:

India experiences influenza season as the monsoon moves across the country's mainland. Influenza is a virus that mostly affects the lungs, nose, bronchi, and throat. The illness lasted for a week. Symptoms are high fever, aching muscles, headache and severe nausea.scientist and researchers have come with the idea of flu vaccine. Two weeks following the injection, the body begins to produce antibodies against the flu vaccine. The viruses in the vaccination provide protection against viral infection thanks to these antibodies. According to studies, the influenza viruses that are most expected to be common in the upcoming season are protected against by the seasonal flu vaccine. The three flu viruses that are meant to be protected against by traditional flu shots, also referred to as "trivalent" vaccines, are influenza A (H1N1), influenza A (H3N2), and influenza B. These vaccines offer protection against an extra B virus in addition to the same viruses covered by the trivalent vaccine. Each strain's gene segments encoding the H and N viral surface proteins are used to create the influenza vaccine. In order for the vaccine to provide effective protection against the virus, it is essential that the protein sequences of the H and N proteins utilized in the vaccine closely match the sequences found in the virus strains individuals may encounter. Annually, in February, the World Health Organization (WHO) makes determinations regarding which influenza virus strains should be incorporated into the vaccine for the upcoming year. An invaluable internet-based bioinformatics tool designed for sequence alignment is BLAST, an acronym for Basic Local Alignment Search Tool. BLAST aligns your specified sequence of interest with sequences stored in the database or with a specific second sequence of interest, facilitating a comparison of results to identify sequences or segments that exhibit similarity to your query sequence. This research endeavor aims to employ the BLAST tool in conjunction with flu databases to assess the effectiveness of this year's vaccine.

Keywords: BLAST, influenza, vaccine, flu database.

INTRODUCTION

Influenza, The virus that causes influenza, sometimes known as the flu, mostly affects the upper respiratory system, which includes the nose, throat, and lungs. In contrast to warm weather, the virus is more viable in dry, cold climates, which enables it to remain outside the human body for longer. Three different varieties of influenza viruses are known to exist: A, B, and C. Humans, other mammals, and birds can all contract Type A infection, which can spread quickly and impact a sizable population. Conversely, Types B and C exclusively infect humans, with Type C causing only mild infections. Within the realm of influenza type A viruses, there exists a subdivision based on the surface proteins hemagglutinin and neuraminidase. Hemagglutinin, often denoted as "H" or "HA," serves as the protein that enables the virus to attach to the host's cells, while neuraminidase, frequently abbreviated as "N" or "NA," facilitates the spread of the infection. The H and N proteins' amino acid sequences are altered as a result of the continuous genetic evolution that Types A and B viruses experience. Subtle alterations to these H and N surface proteins hinder persistent immunity and impede the host's capacity to successfully fight off the virus, since hosts depend on these proteins to recognize the virus and initiate an immune response.

The purpose of the influenza vaccination is to elicit a protective immunological response in the recipient, mostly against the viral surface proteins found in the strains used to create that particular vaccine. Three virus strains are usually included in the influenza vaccination; two are from type A subtypes and one is from type B. Since Type C often only causes mild infections and does not create epidemics, it is not included in the vaccination. Gene segments encoding the H and N viral surface proteins from each strain are used in the manufacture of the influenza vaccine.

For the vaccine to offer robust protection against the virus, it is crucial that the protein sequences of the H and N proteins incorporated into the vaccine closely resemble the sequences found in the strains individuals might encounter. Each February, the World Health Organization (WHO) makes determinations regarding which influenza virus strains should be included in the vaccine for the upcoming year. BLAST, or Basic Local Alignment Search program, is a well-known web-based bioinformatics program for aligning sequences. Using BLAST, you can align your

selected sequence of interest with a particular secondary sequence of interest or with a database of stored sequences. It then shows comparisons of the outcomes, highlighting the segments or sequences that are comparable to your query sequence.

If everything else is the same, we would anticipate that a robust correspondence between the protein sequences of the H and/or N proteins employed in the vaccine and the corresponding sequences in the "wild" virus would lead to effective defense against that pathogen. Conversely, a bad match would provide less defense against the infection.

The entire 2022–2023 influenza vaccine is designed to offer defense against the subsequent 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)

A portion of the flu shot for 2015–2016 is a quadrivalent vaccination, which also offers protection against a different B virus (B/Brisbane/60/2008-like virus). This virus is of the B/Victoria lineage.

METHOD:

Go 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**.

I chose the influenza season of 2015–16 and discovered data regarding the vaccination for that year. The trivalent influenza vaccines licensed in the United States for the 2015–16 season will include hematophagin (HA) sourced from three different viruses: A/Switzerland/9715293/2013 (H3N2), B/Phuket/3073/2013 (Yamagata lineage) and A/California/7/2009 (H1N1)-likeThis indicates changes in the influenza A (H3N2) and influenza B viruses compared to the 2014–15 season. Quadrivalent influenza vaccinations will contain these vaccine viruses as well as a B/Brisbane/60/2008-like (Victoria lineage) virus—the same Victoria lineage virus that was proposed for quadrivalent formulations in 2013–14 and 2014–15.I utilized the NCBI website to host the H3N2 strain A/Switzerland/9715293/2013.

RESULT AND DISCUSSION: The following viral strains were discovered to exhibit similarities with THE strain.

- • Chain A: Influenza Structure An Antibodie Selected For Neutralization From Single Human Plasma Cell Cultures
- Chain A, The Crystal Structure Of Hemagglutinin From 1968 H3n2 Influenza Virus
- Chain A, Crystal Structure Of The A/hong Kong/1/1968 (h3n2) Influenza Virus Hemagglutinin Ha1 Cys30, Ha2 Cys47 Mutant
- • Chain A: Hemagglutinin's Crystal Structure from A/port Chalmers/1/1973 Influenza Virus
- Chain A: The Structure Of An Avian-Origin H7n9 Influenza Virus Hemagglutinin L226q Mutant (a/anhui/1/2013)
- Chain A, Bha Of Ukr63

The influenza virus (vn1194), Chain E, has a mutant H5 Ha A138v with Lsta.

So in a way one can say that the vaccine is highly effective against many strains of influenza.

It was therefore discovered that the flu vaccine was very effective.

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- http://www.ncbi.nlm.nih.gov/
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