**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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| Chain A, Structure Of Influenza A Neutralizing Antibody Selected From Cultures Of Single Human Plasma Cells In Complex With Human H3 Influenza Haemagglutinin |
| Chain A, Refinement Of The Influenza Virus Hemagglutinin By Simulated Annealing |
| Chain A, Crystal Structure Of A Influenza A Virus (AAICHI21968 H3N2) Hemagglutinin In C2 Space Group |
| Chain A, Refinement Of The Influenza Virus Hemagglutinin By Simulated Annealing |
| Chain A, Influenza Virus Hemagglutinin |
| Chain A, Refinement Of The Influenza Virus Hemagglutinin By Simulated Annealing |
| Chain A, Binding Of Influenza Virus Hemagglutinin To Analogs Of Its Cell- Surface Receptor, Sialic Acid: Analysis By Proton Nuclear Magnetic Resonance Spectroscopy And X-Ray Crystallography |
| Chain A, Hemagglutinin Precursor Ha0 |
| Chain A, A New Conserved Neutralizing Epitope At The Globular Head Of Hemagglutinin In H3n2 Influenza Viruses |
| Chain A, Structure Of Influenza Haemagglutinin In Complex With An Inhibitor Of Membrane Fusion |
| Chain A, The Crystal Structure Of Hemagglutinin From 1968 H3n2 Influenza Virus |
| Chain A, Crystal Structure Of A Neutralizing Human Monoclonal Antibody With 1968 H3 Ha |
| Chain A, Crystal Structure Of Broadly Neutralizing Antibody Cr8020 Bound To The Influenza A H3 Hemagglutinin |
| Chain A, Crystal Structure Of The A/hong Kong/1/1968 (h3n2) Influenza Virus Hemagglutinin Ha1 Cys30, Ha2 Cys47 Mutant |
| Chain A, Bha Of Ukr63 |
| Chain A, The Crystal Structure Of Hemagglutinin From A/port Chalmers/1/1973 Influenza Virus |
| Chain A, The Crystal Structure Of Hemagglutinin From A H3n8 Influenza Virus Isolated From New England Harbor Seals |
| Chain A, Crystal Structure Of Heterosubtypic Fab S1391 IN COMPLEX WITH Influenza A H3 Hemagglutinin |
| Chain A, Crystal Structure Of Broadly Neutralizing Antibody F045-092 In Complex With A/victoria/3/1975 (h3n2) Influenza Hemagglutinin |
| Chain A, Structure Of The A\_equine\_newmarket\_2\_93 H3 Haemagglutinin In Complex With 6so4-3sln |
| Chain A, Structure Of The A\_equine\_newmarket\_2\_93 H3 Haemagglutinin |
| Chain A, Structure Of The A\_equine\_richmond\_07 H3 Haemagglutinin Mutant Ser30thr |
| Chain A, Structure Of The A\_equine\_richmond\_07 H3 Haemagglutinin |
| Chain C, Influenza Virus Hemagglutinin, (Escape) Mutant With Thr 131 Replaced By Ile, Complexed With A Neutralizing Antibody |
| Chain A, Structure Of The A\_canine\_colorado\_17864\_06 H3 Haemagglutinin Ser30thr Mutant |
| Chain A, Structure Of The A\_canine\_colorado\_17864\_06 H3 Haemagglutinin Met29ile Mutant |
| Chain A, Structure Of The A\_canine\_colorado\_17864\_06 H3 Haemagglutinin |
| Chain C, Influenza Virus Hemagglutinin Complexed With A Neutralizing Antibody |
| Chain C, Influenza Virus Hemagglutinin, Mutant With Thr 155 Replaced By Ile, Complexed With A Neutralizing Antibody |
| Chain A, Haemagglutinin Of 2004 Human H3n2 Virus |
| Chain A, Haemagglutinin Of 2005 Human H3n2 Virus |
| Chain A, The Crystal Structure Of Hemagglutinin Of Influenza Virus A/victoria/361/2011 |
| Chain A, Crystal Structure Of Broadly Neutralizing Antibody C05 Bound To H3 Influenza Hemagglutinin, Ha1 Subunit |
| Chain A, Crystal Structure Of Fab 39.29 In Complex With Influenza Hemagglutinin A/perth/16/2009 (h3n2) |
| Chain A, Crystal Structure Of Broadly Neutralizing Antibody F045-092 In Complex With A/victoria/361/2011 (h3n2) Influenza Hemagglutinin |
| Chain A, The Crystal Structure Of Hemagglutinin Ha1 Domain From Influenza Virus A/perth/142/2007(h3n2) |
| Chain A, Structure And Receptor Binding Preferences Of Recombinant Human A(h3n2) Virus Hemagglutinins |
| Chain A, Structure Of Influenza Haemagglutinin In Complex With An Inhibitor Of Membrane Fusion |
| Chain A, Structure Of The A\_mallard\_sweden\_51\_2002 H10 Avian Haemmaglutinin In Complex With Avian Receptor Analog Lsta |
| Chain A, Structure Of The A\_mallard\_sweden\_51\_2002 H10 Avian Haemmaglutinin |
| Chain A, Structure Of H10 From Human-infecting H10n8 |
| Chain A, Human-infecting H10n8 Influenza Virus Retains Strong Preference For Avian-type Receptors |
| Chain A, Haemagglutinin Of H10n8 Influenza Virus Isolated From Humans In Complex With Human Receptor Analogue 6'sln |
| Chain A, The Crystal Structure Of Hemagglutinin From A/jiangxi-donghu/346/2013 Influenza Virus |
| Chain A, The Crystal Structure Of Hemagglutinin From A/green-winged Teal/texas/y171/2006 Influenza Virus |
| Chain A, H7 Haemagglutinin |
| Chain A, Structure Of The Hemagglutinin From A Highly Pathogenic H7n7 Influenza Virus |
| Chain A, Structure Of Medi8852 Fab Fragment In Complex With H7 Ha |
| Chain A, Crystal Structure Of An H7n3 Avian Influenza Virus Haemagglutinin |
| Chain A, The Structure Of Hemagglutinin From Avian-origin H7n9 Influenza Virus |
| Chain A, Human H7n9 Influenza Virus Haemagglutinin In Complex With Human Receptor Analogue Lstc |
| Chain A, Crystal Structure Of Fab H7.167 In Complex With Influenza Virus Hemagglutinin From A/shanghai/02/2013 (h7n9) |
| Chain A, The Crystal Structure Of Hemagglutinin From A H7n9 Influenza Virus (a/shanghai/2/2013) In Complex With Lstb |
| Chain A, Crystal Structure Of Broadly Neutralizing Antibody Cr9114 Bound To H7 Influenza Hemagglutinin |
| Chain A, The Structure Of Hemagglutinin L226q Mutant From A Avian-origin H7n9 Influenza Virus (a/anhui/1/2013) |
| Chain A, Crystal Structure Of A H7 Influenza Virus Hemagglutinin |
| Chain A, Crystal Structure Of The Haemagglutinin (with Asn-133 Glycosylation) From An H7n9 Influenza Virus Isolated From Humans |
| Chain A, Crystal Structure Of The "avianized" 1918 Influenza Virus Hemagglutinin |
| Chain A, The Structure Of Hemagglutinin From Avian-origin H7n9 Influenza Virus (a/shanghai/1/2013) |
| Chain A, The Crystal Structure Of Hemagglutinin Form A H7n9 Influenza Virus (a/shanghai/1/2013) In Complex With Lstb |
| Chain H, 1930 Swine H1 Hemagglutinin Complexed With Lsta |
| Chain H, 1930 H1 Hemagglutinin In Complex With Lstc |
| Chain H, Structure Of H1 Duck Albert Hemagglutinin With Human Receptor |
| Chain A, Crystal Structure Of Fab Cr6261 In Complex With The 1918 H1n1 Influenza Virus Hemagglutinin |
| Chain A, Crystal Sructure Of The 1918 Human H1 Hemagglutinin Precursor (Ha0) |
| Chain A, Crystal Structure Of 1918 Pandemic Influenza Virus Hemagglutinin Mutant D225g |
| Chain H, Structure Of H1 1918 Hemagglutinin With Human Receptor |
| Chain A, Crystal Structure Of H5 Hemagglutinin Mutant (n224k, Q226l, N158d And L133a Deletion) From The Influenza Virus A/chicken/vietnam/ncvd- 093/2008 (h5n1) |
| Chain A, Crystal Structure Of A Complex Formed Between Fld194 Fab And Transmissible Mutant H5 Haemagglutinin |
| Chain A, Crystal Structure Of The Haemagglutinin From A Transmissible Mutant H5 Influenza Virus |
| Chain A, Crystal Structure Of H5 Hemagglutinin Mutant (n158d, N224k And Q226l) From The Influenza Virus A/viet Nam/1203/2004 (h5n1) |
| Chain A, Crystal Structure Of H5 (vn1194) Asn186lys/gly143arg Mutant Haemagglutinin |
| Chain A, Crystal Structure Of H5 (vn1194) Influenza Haemagglutinin |
| Chain A, H5 (vn1194) Asn186lys Mutant Haemagglutinin In Complex With Avian Receptor Analogue 3'sln |
| Chain A, Crystal Structure Of H5 (vn1194) Gln196arg Mutant Haemagglutinin |
| Chain H, 1918 H1 Hemagglutinin |
| Chain A, Crystal Structure Of Fab H5m9 In Complex With Influenza Virus Hemagglutinin From A/goose/guangdong/1/96 (h5n1) |
| Chain A, Crystal Structure Of H5 Hemagglutinin Q226l Mutant From The Influenza Virus A/duck/egypt/10185ss/2010 (h5n1) |
| Chain A, Crystal Structure Of Aerosol Transmissible Influenza H5 Hemagglutinin Mutant (n158d, N224k, Q226l And T318i) From The Influenza Virus A/viet Nam/1203/2004 (h5n1) |
| Chain A, Crystal Structure Of H5 (vn1194) Ser227asn/gln196arg Gln196arg Mutant Haemagglutinin |
| Chain A, Crystal Structure Of The Hemagglutinin From A H1n1pdm A/washington/5/2011 Virus |
| Chain E, Influenza Virus (vn1194) H5 Ha With Lstc |
| Chain A, Crystal Structure Of H5 (tyty) Del133/ile155thr Mutant Haemagglutinin |
| Chain H, 1930 Swine H1 Hemagglutinin |
| Chain A, Crystal Structure Of A H5n1 Influenza Virus Hemagglutinin |
| Chain A, Crystal Structure Of Influenza Hemagglutinin (H5) In Complex With A Broadly Neutralizing Antibody F10 |
| Chain A, Crystal Structure Of H5n1 Influenza Virus Hemagglutinin, Strain 437-10 |
| Chain A, Influenza Hemagglutinin In Complex With A Neutralizing Antibody |
| Chain A, Structures Of Monomeric Hemagglutinin And Its Complex With An Fab Fragment Of A Neutralizing Antibody That Binds To H1 Subtype Influenza Viruses: Molecular Basis Of Infectivity Of 2009 Pandemic H1n1 Influenza A Viruses |
| Chain A, Structures Of Monomeric Hemagglutinin And Its Complex With An Fab Fragment Of A Neutralizing Antibody That Binds To H1 Subtype Influenza Viruses: Molecular Basis Of Infectivity Of 2009 Pandemic H1n1 Influenza A Viruses |
| Chain E, Influenza Virus (vn1194) H5 Ha A138v Mutant With Lsta |
| Chain A, Crystal Structure Of H1n1pdm Hemagglutinin |
| Chain A, Influenza Virus (Vn1194) H5 Ha |
| Chain E, Influenza Virus (vn1194) H5 Ha With Lsta |
| Chain A, Crystal Structure Of The Hemagglutinin Of Ferret-transmissible H5n1 Virus |
| Chain A, Structure Of A/egypt/n03072/2010 H5 Ha |
| Chain A, Structure Of Avian H5 Haemagglutinin Complexed With Lsta Receptro Analog |
| Chain A, Crystal Structure Of H5n1 Influenza Virus Hemagglutinin, Strain Yu562 . |
| Chain A, The Hemagglutinin Structure |

Therefore the flu vaccine was found to be highly effective.

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