HOMOLOGY MODELLING AND INSILICO ANALYSIS OF HEMAGGLUTININ PROTEIN FROM H1N1 INFLUENZA A VIRUS

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Abstract
World wide spread of H1NI Influenza A Virus has raised concerns. Modelling of Hemagglutinin protein of Influenza A virus (A/Sakai/1/2009(H1N1)) Hemagglutinin (HA) protein was done using Modeller 9V2. Modelled structure was submitted to protein model database and can be downloaded using accession number PM0075832. Further modelled protein structure was subjected to Insilco analysis using various Bioinformatics tools. Two anti-influenza drugs currently being used to treat infected patients are oseltamivir (Tamiflu) and zanamivir (Relenza), both of which target the neuraminidase enzyme of the virus. Reports of the emergence of drug resistance make the development of new anti-influenza molecules a priority. Hence, modelled structure of H1NI Hemagglutinin will be very useful for insilico analysis of potential Hemagglutinin inhibitors.
Keywords: H1N1, Hemagglutinin, Modelling, Insilico analysis.

Introduction

The **2009 flu pandemic** is a global outbreak of a new strain of **influenza A virus subtype H1N1**, identified in April 2009 and commonly referred to as **swine flu**, which infects and is transmitted between humans. It is thought to be a mutation—more specifically, a reassortment—of four known strains of influenza A virus subtype H1N1: one endemic in humans, one endemic in birds, and two endemic in pigs (swine). Swine influenza (also called swine flu, hog flu, and pig flu) is an infection of a host animal by any one of several specific types of microscopic organisms called "swine influenza virus". A June 10, 2009 update by the U.N.'s World Health Organization (WHO) states that "74 countries have officially reported 27,737 cases of influenza A (H1N1) infection, including 141 deaths".

WHO officially declared the outbreak to be a "pandemic" on June 11, but stressed that the new designation was a result of the global "spread of the virus," not its severity. The WHO stated the pandemic appears to have moderate severity in comparatively well-off countries, however it is prudent to anticipate a bleaker picture as the virus spreads to areas with limited resources, poor health care, and a high prevalence of underlying medical problems.The case fatality rate (CFR) of the pandemic strain is estimated at 0.4% (range 0.3%-1.5%)

A **swine influenza virus** (**SIV**) is any strain of the influenza family of viruses that is usually hosted by (is endemic in) pigs.[1] As of 2009, the known SIV strains are the influenza C virus and the subtypes of the influenza A virus known as H1N1, H1N2, H3N1, H3N2, and H2N3. Swine influenza is common in pigs in the United States (particularly in the midwest and occasionally in other states), Mexico, Canada, South America, Europe (including the United Kingdom, Sweden, and Italy), Kenya, and eastern Asia (namely China, Taiwan, and Japan).[1]

The 2009 swine flu outbreak in humans is due to a new strain of influenza A virus subtype H1N1 that contains genes closely related to swine influenza.[2] The origin of this new strain is unknown. However, the World Organization for Animal Health (OIE) reports that this strain has not been isolated in pigs.[3] This strain can be transmitted from human to human, and causes the normal symptoms of influenza.[6]Pigs can become infected with human influenza, and this appears to have happened during the 1918 flu pandemic and the 2009 swine flu outbreak.

Virus characteristics

The virus is a novel strain of influenza from which human populations have been neither vaccinated nor naturally immunized. The CDC, after examining virus samples from suspected cases in Mexico, matched the strain with those from cases in Texas and California, and found no known linkages to either to animals or one another. It was also determined that the strain contained genes from four different flu viruses: North American swine influenza; North American avian influenza; human influenza; and two swine influenza viruses typically found in Asia and Europe. Further analysis showed that several of the proteins of the virus are most similar to strains that cause mild symptoms in humans, leading virologist Wendy Barclay to suggest on May 1 that the virus was unlikely to cause severe symptoms for most people. Scientists in Winnipeg completed the first full genetic sequencing of the virus on 6 May 2009.

Influenza A

Swine influenza is known to be caused by influenza A subtypes H1N1,[4] H1N2,[4] H3N1,[4] H3N2,[5] and H2N3.[5] In pigs, three influenza A virus subtypes (H1N1, H3N2, and H1N2) are the most common strains worldwide.[5] In the United States, the H1N1 subtype was exclusively prevalent among swine populations before 1998; however, since late August 1998, H3N2 subtypes have been isolated from pigs. As of 2004, H3N2 virus isolates in US swine and turkey stocks were triple reassortants, containing genes from human (HA, NA, and PB1), swine (NS, NP, and M), and avian (PB2 and PA) lineages. [7]

Virus origins

In early June, Oxford University's Department of Zoology, reported test results that "show that this strain has been circulating among pigs, possibly among multiple continents, for many years prior to its transmission to humans." The research team that worked on this report also believe that it was "derived from several viruses circulating in swine," and that the initial transmission to humans occurred several months before recognition of the outbreak. The team concluded that "despite widespread influenza surveillance in humans, the lack of systematic swine surveillance allowed for the undetected persistence and evolution of this potentially pandemic strain for many years."

According to the researchers, movement of live pigs between Eurasia and North America "seems to have facilitated the mixing of diverse swine influenza viruses, leading to the multiple reassortment events associated with the genesis of the (new H1N1) strain. [8]

Transmission of swine influenza virus from pigs to humans is not common and does not always cause human influenza, often only resulting in the production of antibodies in the blood. The meat of the animal poses no risk of transmitting the virus when properly cooked. If transmission does cause human influenza, it is called zoonotic swine flu. People who work with pigs, especially people with intense exposures, are at increased risk of catching swine flu. In the mid-20th century, identification of influenza subtypes became possible, which allows accurate diagnosis of transmission to humans. Since then, fifty confirmed transmissions have been recorded, Rarely, these strains of swine flu can pass from human to human. In humans, the symptoms of swine flu are similar to those of influenza and of influenza-like illness in general, namely chills, fever, sore throat, muscle pains, severe headache, coughing, weakness and general discomfort. [9]

Influenza hemagglutinin

Influenza **hemagglutinin** (HA) is a type of hemagglutinin found on the surface of the influenza viruses. It is an antigenic glycoprotein. It is responsible for binding the virus to the cell that is being infected.The name "hemagglutinin" comes from the protein's ability to cause red blood cells (erythrocytes) to clump together ("agglutinate") *in vitro*

Subtypes

There are at least 16 different HA antigens. These subtypes are labeled H1 through H16.

Functions and mechanisms of action

HA has two primary functions:

1. allowing the recognition of target vertebrate cells, accomplished through the binding of these cells' sialic acid-containing receptors, and
2. allowing the entry of the viral genome into the target cells by causing the fusion of host endosomal membrane with the viral membrane.

Mechanism

HA binds to the monosaccharide sialic acid which is present on the surface of its target cells. This causes the viral particles to stick to the cell's surface. The cell membrane then engulfs the virus and the portion of the membrane that encloses it pinches off to form a new membrane-bound compartment within the cell called an endosome, which contains the engulfed virus. The cell then attempts to begin digesting the contents of the endosome by acidifying its interior and transforming it into a lysosome. However, as soon as the pH within the endosome drops to about 6.0, the original folded structure of the HA molecule becomes unstable, causing it to partially unfold, and releasing a very hydrophobic portion of its peptide chain that was previously hidden within the protein. This so-called "fusion peptide" acts like a molecular grappling hook by inserting itself into the endosomal membrane and locking on. Then, when the rest of the HA molecule refolds into a new structure (which is more stable at the lower pH), it "retracts the grappling hook" and pulls the endosomal membrane right up next to the virus particle's own membrane, causing the two to fuse together. Once this has happened, the contents of the virus, including its RNA genome, are free to pour out into the cell's cytoplasm.

Treatment

Antiviral drugs

According to the CDC, antiviral drugs can be given to treat those who become severely ill. These antiviral drugs are prescription medicines (pills, liquid or an inhaler) and act against influenza viruses, including the 2009 pandemic virus. There are two such medications that are recommended for use against the 2009 H1N1 swine flu virus, oseltamivir (Tamiflu) and zanamivir (Relenza). [10] The CDC has noted that as the flu pandemic spreads, antiviral drugs such as oseltamivir (Tamiflu) and zanamivir (Relenza) might become in short supply. Therefore, the drugs would be given first to those people who have been hospitalized or are at high risk of complications. [11] The drugs work best if given within 2 days of becoming ill, but might be given later if illness became severe or to those at a high risk for complications.

MATERIALS AND METHODS

Influenza A virus (A/Sakai/1/2009(H1N1)) segment 6 Hemagglutinin (HA) sequence with accession number GQ267839 Submitted (16-JUN-2009) by Horikawa,H.,Kato Y., Oguchi,A. and Fujita,N of National Institute of Technology and Evaluation (NITE), Tokyo, Japan was selected for insilico analysis.

Sequence selected for analysis

>MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLCKLRGVAP
LHLGKCNIAGWILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTS
SWPNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIHHPSTSADQ
QSLYQNADAYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFA
MERNAGSGIIISDTPVHDCNTTCQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNVPSIQSRG
LFGAIAGFIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQKAIDEITNKVNSVIEKMNTQFTAVGK
EFNHLEKRIENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNG
CFEFYHKCDNTCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTVASSLVLVVSLGAI
SFWMCSNGSLQCRICI

Tool used for modelling of Hemagglutinin protein.

Modeller 9V2. Chain A, Structure Of H2 Japan Hemagglutinin with pdb id 2WRD which had 63% identity with target protein was used as template for comparative modeling.

Tools used for Hemagglutinin protein analysis

- Gor IV secondary structure prediction tool.
- Pep tool.

Details of protein properties calculated using Pep tool are as follows.

Number of Amino acids

The total number of amino acids comprising the current sequence.

Mean Amino Acid Weight (Daltons)

The average molecular weight of the amino acids comprising the current sequence. The mean amino acid weight is calculated simply as the molecular weight divided by the number of amino acids in the sequence.

Average Hydrophobicity

The average hydrophobicity (AH) is the sum of all hdrophobicity values for the given sequence divided by its sequence length. The hydrophobicity values from Kyte/Doolittle are used in this calculation.

Ratio of Hydrophilicity to Hydrophobicity

The ratio of hydrophobic to hydrophobic amino acids. RH=1.22 indicates an average protein ,RH>1.90 indicates a non-folding protein,RH<0.85 indicates an insoluble protein.

Percentage of hydrophilic Amino acids

The percentage of hydrophilic amino acids comprising the current sequence. For naturally occurring soluble proteins, the average percentage of hydrophilic amino acids is :47.56%.

Percentage of Hydrophobic Amino Acids

The percentage of hydrophilic amino acids comprising the current sequence. For naturally occurring soluble proteins, the average percentage of hydrophobic amino acids is 52.44 %.

Ratio of % Hydrophilic to hydrophobic.

This is an indicator of the protein sequence's propensity to fold into a globular structure in normal physiological conditions. RHP=0.91 indicates average protein. RHP>1.42 indicates a non-folding protein. RHP<0.77 indicates an insoluble protein.

Mean beta hydrophobic moment.

The mean beta hydrophobic moment is the sum of all beta hydrophobic moment values for the given sequence divided by its sequence length. The hydrophobic moment values from Cornette are used in this calculation.

Mean Helix Hydrophobic moment.

The mean helix hydrophobic moment is the sum of all helix hydrophobic moment values for the given sequence divided by its sequence length. The hydrophobic moment values from Cornette are used in this calculation.

Number of Basic Amino acids.

The sum total of Arginine(R) and Lysine (K) residues comprising the current sequence. Basic amino acids carry a net positive charge at physiological Ph (7.2)

Number of Acidic Amino acids.

The sum total of aspartic acid(D) and glutamic acid(E) residues comprising the current sequence. Acidic amino acids carry a net negative charge at physiological Ph (7.2).

Estimated Pi for protein

The pH at which the protein carries a net zero charge. Peptides and proteins at their isoelectric point tend to be somewhat insoluble.

Total Linear charge Density

The total number of charged amino acids (K,R,D, and E), plus the N- and C- terminal groups, divided by the total number of amino acids in the protein sequence. The total linear charge density is a measure of the potential solubility of a protein; values greater than about 0.2 are typically required for a protein to be soluble.

Polar Area of Extended chain (Angs^ 2)

The summation of polar surface area (ASAp) for each of the amino acids comprising the current sequence, assuming an extended structure (in square angstroms). ASAp values are attributed to unchanged nitrogen, oxygen and sulphur atoms, which are considered to be polar.

Non-Polar Area of Extended chain (Angs^ 2)

The summation of the non-polar surface area (ASAp) for each of the amino acids comprising the current sequence, assuming an extended structure (in square angstroms). ASAnp values are attributed to carbon atoms, which are considered to be non-polar.

Total Area of Extended chain (Angs^2)

The summation of charged, polar and non-polar accessible surface area for each of the amino acids comprising the current sequence (In square Angstroms).

Polar ASA of Folded Protein (Angs^2)

The polar accessible surface area for the amino acids comprising the current sequence, assuming the protein folds into globular structure (in square Angstroms).

Non-Polar ASA of Folded Protein (Angs^2)

The non-polar accessible surface area for the amino acids comprising the current sequence, assuming the protein folds into globular structure (in square Angstroms).

ASA of folded protein (Angs^2)

The total accessible surface area for the amino acids comprising the current sequence, assuming the protein folds into a globular structure.

Ratio of Folded to Extended Area

The value for the estimated accessible surface area of an assumed globular folded protein to that of the extended chain.

Buried Polar Area of Folded Protein (Angs^2)

The total polar area of the folded protein that is not accessible to solvent, assuming a globular protein structure (in square Angstroms). The ABP is assumed to be 35% of the total buried surface area.

Buried Non-Polar Area of Folded Protein (Angs^2)

The total Non-polar area of the folded protein that is not accessible to solvent, assuming a globular protein structure (in square Angstroms). The ABN is assumed to be 61% of the total buried surface area.

Buried Charge Area of Folded protein

The total charged area of the folded protein that is not accessible to solvent, assuming a globular protein structure (in square Angstroms). The ABC is assumed to be 4% of the total buried surface area.

Total Buried surface (Angs^2)

The total charged area of the folded protein that is not accessible to solvent, assuming a globular protein structure (in square Angstroms). The AB is defined as the total area of the extended chain minus the accessible surface area of the folded protein.

Number of Buried Amino Acids

The number of amino acids that have less than 5% surface area accessible to solvent, assuming the protein forms a globular structure. Average NB% for small proteins (<100aa): 15% Average NB% for small proteins (>100aa):32%

Packing Volume (est) (Angs^3)

This value is a rough estimate of the packing volume (in cubic Angstroms) calculated from the molecular weight of the current sequence. Estimated packing volume(VPe) is defined as 1.245*molecular weight. This value assumes the protein forms a globular , spherical structure.

Interior Volume of Protein (Angs^3)

The volume occupied by the fraction of amino acids estimated to be hidden from the solvent (in cubic Angstroms).

Exterior Volume of Protein (Angs^3)

The volume occupied by the fraction of amino acids estimated to be accessible to the solvent (in cubic Angstroms).

Partial Specific volume (ml/g)

The sum of the partial specific volumes multiplied by the weight percent, for each of the individual amino acids comprising the protein sequence. PSVs may be useful in determining a protein's retention time during size-exclusion chromatography, or in ultra-centrifugation studies.

Fisher Volume Ratio (act)

If FVR(act) >FVR(idealized) the molecule likely forms soluble monomer. If FVR(act) >> FVRRatio(idealized) the molecule likely doesn't fold into compact structure. If FVR(act) < FVR(idealized) the molecule likely aggregates.

Fisher Volume Ratio (idealized)

If FVR(act) >FVR(idealized) the molecule likely forms soluble monomer. If FVR(act) >> FVRRatio(idealized) the molecule likely doesn't fold into compact structure. If FVR(act) < FVR(idealized) the molecule likely aggregates.

Protein Solublilty

A relative measure of a protein's solubility based on hydrophobicity and acharge data. Solublity=1.6 indicates an average protein. Solubilty < 1.1 indicates an insoluble protein.

Est. Radius of Folded Protein (Angs)

The estimated radius, in Angstroms, for the current sequence, assuming it folds into a globular protein. The radius is defined as the cube root of the number of amino acids comprising the sequence multiplied by the average distance between adjacent amino acid c-alpha atoms (3.875 Angstroms).

RMS End to End Dist. of Ext. chain (Angs)

The root-mean-square(RMS) distance, from N-C-terminus, for the protein sequence assuming an extended structure. The RMS distance is in Angstroms.

Radius of Gyration of Ext. Chain (Angs)

The root-mean-square (RMS) radius of the unfolded, extended protein chain from its center of gravity.

Solv. Free Energy of Folding (Kcal/mol)

The estimated Gibbs free energy difference (in Kcal/mol) between the extended, unfolded chain and an assumed globular, folded protein. Negative SFEs correspond to a stabilizing solvent effect upon folding of the extended chain into the globular form.

RESULTS AND DISCUSSION

MODELLER was used for homology or comparative modeling of protein three-dimensional structures .Alignment of a sequence to be modeled is provided with known related structures and MODELLER automatically calculates a model containing all non-hydrogen atoms. MODELLER implements comparative protein structure modeling by satisfaction of spatial restraints ,and can perform many additional tasks, including de novo modeling of loops in protein structures, optimization of various models of protein structure with respect to a flexibly defined objective function, multiple alignment of protein sequences and/or structures, clustering, searching of sequence databases, comparison of protein structures, etc.

Modelled structure was submitted to protein model database which is a repository for three dimensional protein models obtained by structure prediction methods. Submitted, Modelled H1N1 Hemagglutinin protein can be downloaded from PMDB using accession number PM0075832**.**

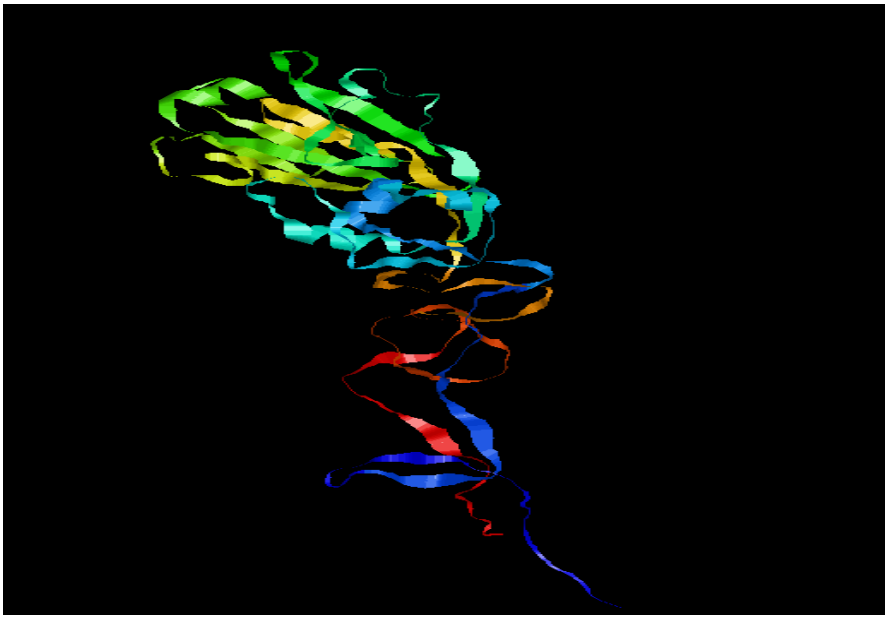

Fig 1: Structure of modelled Hemagglutinin protein of H1N1 Influenza virus.

PROTEIN STRUCTURE ANALYSIS

Secondary structure prediction of modelled Hemagglutinin virulence protein was carried out using GOR IV SECONDARY STRUCTURE PREDICTION tool (Figure 2). Amino acid frequency plot (Figure 3),Plot of charge vs pH (Figure 4), Beta staircase model (Figure 5) and molecular properties calculation (Table 1) of Hemagglutinin protein of H1N1 Influenza virus was obtained using pep tool a comprehensive protein analysis software.

```
      10        20        30        40        50        60        70
       |        |         |         |         |         |         |
MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLCKLRGVAPL
HLG
ccceeeeehhhhccccccceeeecccccccccceeeeeecccceeeeeeehhhhhccccceeeeccceecccccc
KCNIAGWILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSW
ccceeeeeecccccceecccccceeeeeecccccccccccccchhhhhhhhcccccccceeeecccccc
PNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIHHPSTSADQQS
LYQ
cccccccceeeecccccceeeeeeeeeecccccccccceeecccccceeeeeeeecccccchhhhhhh
NADAYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERN
AGS
cccceeeecccccccccchhhhchhhhhhcceeeeeeeeeccccceeeecccchhhhhhhhhhhcccc
GIIISDTPVHDCNTTCQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNVPSIQSRGLFGAI
ceeeeecccccccccccccccccccccccccceeecccccccccchhhhcccccccccccchhhhe
AGFIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQKAIDEITNKVNSVIEKMNTQFTAVGKEFNH
LEKR
eeeecccceeeeeeeeecccccccchhhhhhhhhhhhhhhhhhhhchhhhhhchhhhhhhhhhhhhhhh
IENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKC
DN
hhhhcccccceeehhhhhhhhhhhhhhhcccccccccchhhhhhhhhhhhhhcccccccceeeeeecccc
TCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTVASSLVLVVSLGAISFWMCSNGSL
eeeeecccccccccchhhhhhhhhhhcccccccchhhhhhhhhcccccceeeeeeecceeeeeecccee
QCRICI
ccceec
Sequence length :   566
GOR4 :
  Alpha helix     (Hh) :   146 is  25.80%
  3₁₀ helix       (Gg) :     0 is   0.00%
  Pi helix        (Ii) :     0 is   0.00%
```

Beta bridge (Bb) : 0 is 0.00%
Extended strand (Ee) : 142 is 25.09%
Beta turn (Tt) : 0 is 0.00%
Bend region (Ss) : 0 is 0.00%
Random coil (Cc) : 278 is 49.12%
Ambigous states (?) : 0 is 0.00%
Other states : 0 is 0.00%

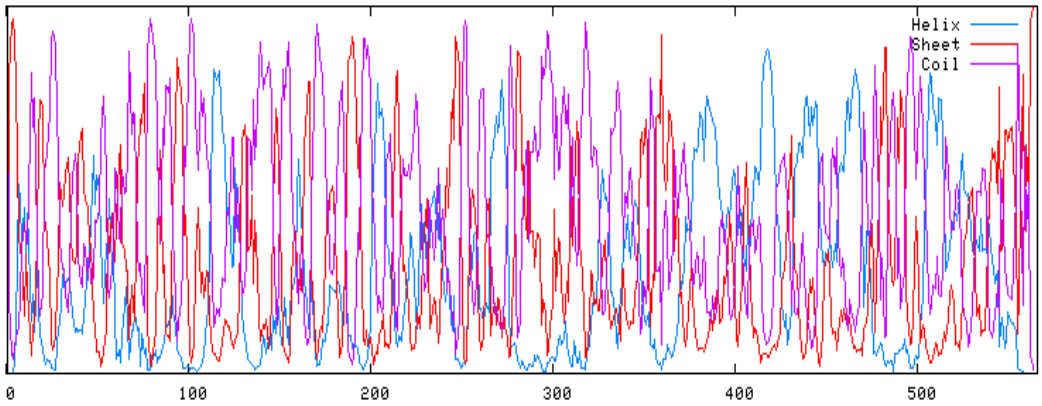

Figure 2: GOR IV secondary structure prediction of Hemagglutinin protein of H1N1 Influenza virus.

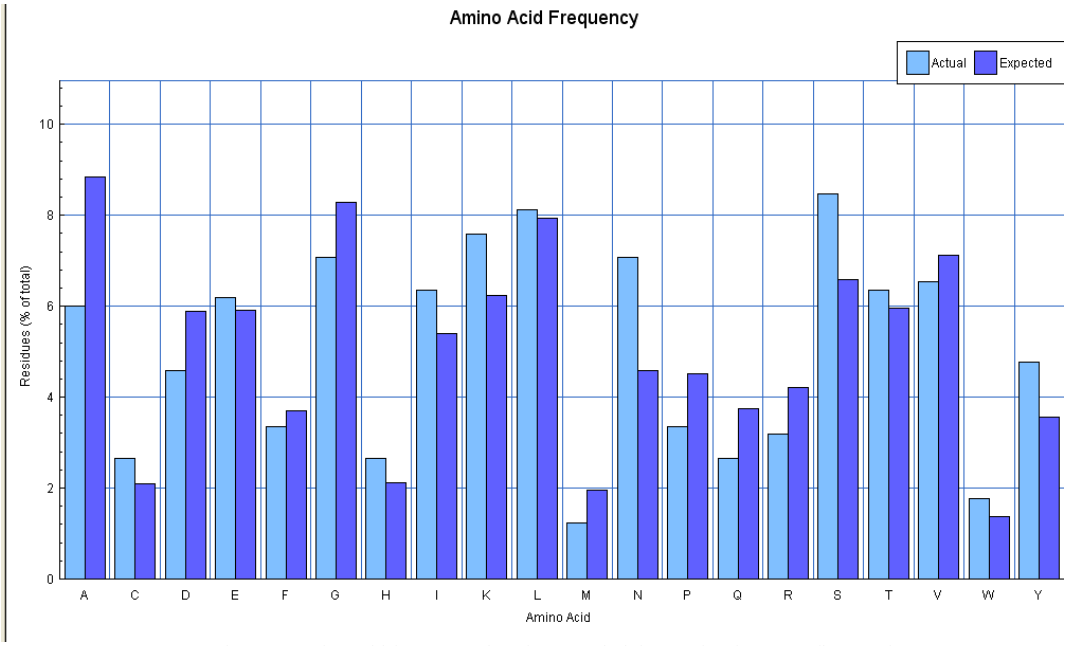

Figure 3: Amino acid frequency plot of Hemagglutinin protein of H1N1 Influenza virus.

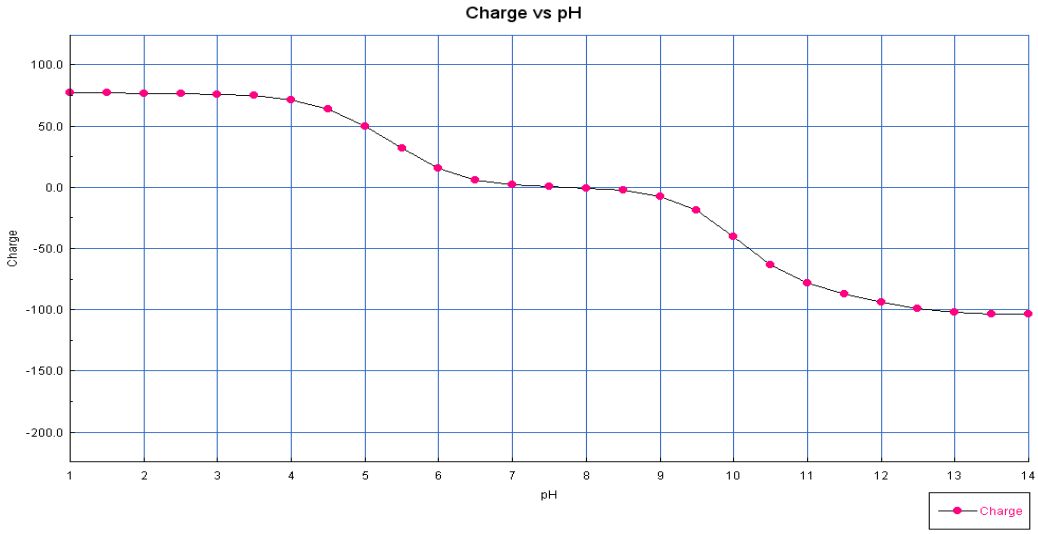

Figure 4:Plot of charge vs pH

The beta staircase Model

The beta staircase graphically displays (Figure 5) the disposition of amino acid side chains about an assumed alpha helix. The view is always along the central axis of the helix from N to C-terminus. The helical wheel is an effective method for displaying the symmetry of hydrophobic/hydrophilic side chains of BBI C-II. It is useful for observing how the amino acids are positional in relation to one another.[12]

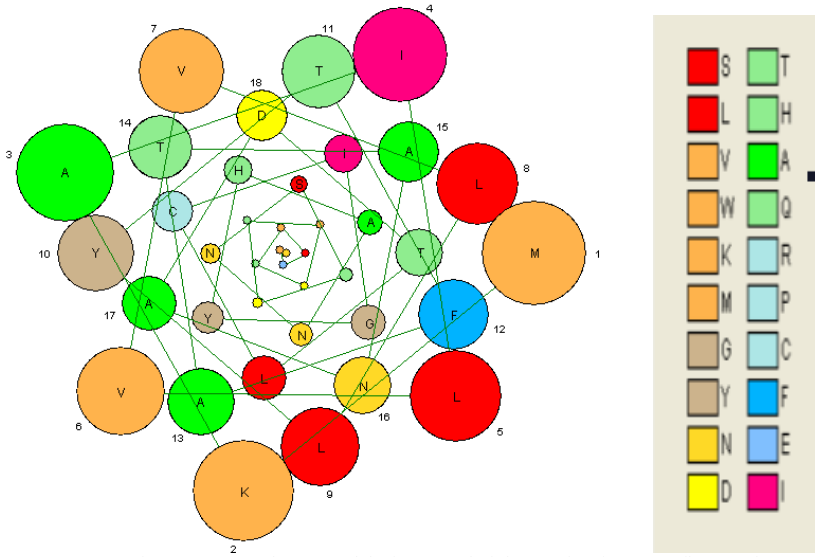

Figure 5: Beta staircase model of Hemagglutinin protein of H1N1 Influenza virus.

Molecular weight (Daltons)	63235.766
Number of Amino acids	566
Mean amino acid weight(Daltons)	111.724
Average hydrophobicity	-0.352297
Ratio of hydrophilicity to hydrophobicity	1.30332
Percentage of Hydrophilic Amino acids	52.1201
Percentage of Hydrophobic Amino acids	47.8799
Ratio of % hydrophilic to hydrophobic	1.08856
Mean Beta hydrophobic moment	0.194799
Mean helix Hydrophobic Moment	0.183592
Number of Basic Amino acids	61
Number of acidic Amino acids	61
Total linear charge density	0.0912951
Estimated Pi for protein	7.7
Polar area of extended chain (Angs^2)	37415.2
Non Polar area of extended chain (Angs^2)	62374.3
Total area of extended chain (Angs^2)	99789.5
Polar ASA of Folded Protein (Angs^2)	8122.61
Non Polar ASA of Folded Protein (Angs^2)	11778.3
ASA of Folded Protein (Angs^2)	19900.9
Ratio of folded to extended area	0.212654
Buried polar area of folded protein (Angs^2)	25706.9
Buried non polar area of folded protein (Angs^2)	44803.4
Buried Charge Area of FP	2937.93
Total Buried Surface (Angs^2	73448.2
Number of Buried Amino Acids	246
Packing Volume (est) (Angs^3)	76922.4
Packing Volume (act) (Angs^3)	74989.3
Interior Volume of Protein (Angs^3)	54267.9
Exterior Volume of Protein (Angs^3)	20721.4
Partial Specific Volume (ml/g)	0.723131
Fisher Volume Ration (act)	0.381835
Fisher Volume Ratio (idealized)	0.491642
Protein Solubility	1.52099
Est. Radius of Folded Protein (Angs)	32.0536
RSM End to End Dist. Of Ext. Chain(Angs)	249.52
Radius of Gyration of Ext. Chain (Angs)	101.866
Solvent Free Energy of Folding (kcal/mol)	-544.32

Table 1: Molecular properties calculation (Table 1) of Hemagglutinin protein of H1N1 Influenza virus.

CONCLUSION

Novel H1N1 (Referred to as “Swine flu” early on) is a new influenza virus causing illness in people. This new virus was first detected in people in the united states in April 2009. A June 10, 2009 update by the U.N.'s World Health Organization (WHO) states that 74 countries have officially reported 27,737 cases of influenza A (H1N1) infection, including 141 deaths. Two anti-influenza drugs currently being used to treat infected patients are oseltamivir (Tamiflu) and zanamivir (Relenza), both of which target the Neraminidase enzyme of the virus. Reports of the emergence of drug resistance make the development of new anti-influenza molecules a priority. This project aimed at designing structure of Hemagglutinin of H1N1 which will be useful for designing novel Hemagglutinin inhibitors which will help to combat H1N1 Pandemic.

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