

In Silico Analysis of Hemagglutinin, Neuraminidase, and Matrix Protein- A Comparative Study on Different Strains of H5n1 Virus

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Pandemic influenza virus has its origins in avian influenza viruses. The highly pathogenic avian influenza virus subtype H5N1 is already panzootic in poultry, with attendant economic consequences. It continues to cross species barriers to infect humans and other mammals, often with fatal outcomes. Therefore, H5N1 virus has rightly received attention as a potential pandemic threat. The proteins, matrix protein (MP), neuraminidase (NA) and hemagglutinin (HA) of influenza A virus (Bird flu virus) sub-type A/Hatay/2004/ (H5N1) from chicken were selected for this study. The *in silico*

analysis predicted that HA of influenza A virus is highly sensitive to mutations and hence it is significant for its pathogenic nature. None of the mutations was detected as an important change except in NA where K332R was at a PKC phosphorylation site. Analysis of the sequence comparison showed that the maximum numbers of mutation were observed in HA. These mutations are significant as they are involved in change in polarity or hydrophobicity as well as in propensity of each amino acid residue to stabilize the secondary structure.