Computational Screening of Bird Flu Viral Strains to Find Conserved Epitopes for Vaccine Development

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Abstract:

Avian Influenza virus (AIV) is a common cause of bird flu in poultry and many other avian and mammalian species. It belongs to the family Orthomyxoviridae. It is an enveloped RNA virus with 8 negative-sense RNA strands which encode 11 different viral proteins. Avian Influenza (AI) is one of the leading disease-causing agents in the world, especially in the last 15 years. A number of outbreaks are reported throughout the world including Pakistan. Genetic shifting and drifting are the phenomena behind the emergence of new strains of AI. The high rate of mutation not only leads the virus to move from low pathogenic to highly pathogenic but also makes it capable of zoonotic behavior. The emergence of new strains is the major reason behind the failure of existing vaccines. Therefore, AI needs continuous surveillance from the field through modern and state-of-the-art computational biology and molecular biology techniques. By keeping all these aspects in view the present study is designed and computational analysis of major strains of AIV was done. All standard bioinformatics tools like Blast, Aligner, and antigenic epitope determining tool, etc. were used. First of all the conserved sequences were found from different strains of the virus against single protein like Haemagglutinin, Neuraminidase, Nucleoprotein, and Nonstructural proteins and later antigenic epitopes were tried to be found by using epitope determining tools. A number of epitopes are highlighted through this study and these epitopes are potential candidates for monovalent or multivalent subunit or DNA vaccines.