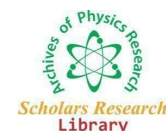




Extended Abstract

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Genus specific protein patterns of viruses

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In the generation of rising and re-emerging viral infections, diagnostics and its allied fields have a predominant function to play in combating the diseases. Enormous quantity of the molecular sequence data handy in the public domain has the practicable to contribute in a important way in the improvement of novel diagnostic tools. One of the perquisites for such a learn about is the identification of signature sequences i.e., small stretches of protein/nucleotide sequences that are special to a given family/genus/organism. There exist numerous resources in the public area archiving signature sequences of proteins based on sequence identity/ similarity. However, these resources do not take into account the taxonomic facts which has a extensive position to play in viral diagnostics. The present find out about is an effort to explicitly take into account the taxonomic information and thereby derive genus-specific signature sequences of viral proteins. The preliminary facts for obtaining patterns viz., multiple sequence alignment (MSA) is received from VirGen database. An in-house developed perl script is used to derive the patterns from the MSA. The patterns are then validated by using search against the non-redundant protein sequence database at NCBI, thereby enabling the computation of their sensitivity and specificity. Such a validation requires datasets pertaining to true-positives and true-negatives. True-positive dataset is acquired from the taxonomy database at NCBI by formulating an Entrez query such that the whole variety of species belonging to a given genus is retrieved. The true-negative dataset constituted of any protein sequence that belongs to genus different than the one in question. Of the 262 proteins belonging to 19 families (RNA viruses) in VirGen, patterns should be detected for 125 proteins, all of which actually uncommon true-positives and false-positive sequences. These patterns when mapped onto their corresponding 3D constructions (25 unique entries of Protein Data Bank) are located to be part of essential useful regions like energetic website and dimerization interface. The unique viral signature sequences/peptides consequently obtained have applications not only in detection assays and as therapeutics but also can serve as putative targets for viral vaccines. Viruses have induced some of the most dramatic and deadly sickness pandemics in human history. Before it was declared to be eradicated in 1980, smallpox, a rather contagious human disorder caused by means of the Variola virus, killed 300 to five hundred million humans international in the 20th century alone. The 1918–1919 “Spanish flu” pandemic infected roughly one-third of the world's human populace and brought on an estimated 50 to a hundred million deaths. In the past half century, deadly disorder outbreaks brought about through novel viruses of animal origin—Nipah virus in Malaysia, Hendra virus in Australia, hantavirus in the United States, Ebola virus in Africa, along with HIV (human immunodeficiency virus), various influenza subtypes, and the SARS (severe acute respiratory syndrome) and MERS (Middle East respiratory syndrome) coronaviruses—have underscored the urgency of grasp elements influencing viral disease emergence and spread. The world's modern main infectious killer, HIV, has prompted an estimated 36 million deaths since the first cases were pronounced in 1981. In 2012, more than two million people were newly contaminated with the virus, and 1.6 million died of HIV/AIDS. In 2009, a novel swine-origin H1N1 strain of influenza A hastily unfold to over 213 countries in the first declared pandemic of the 21st century. And now, on August 8, 2014, the World Health Organization (WHO) Director-General Margaret Chan declared the Ebola outbreak in West Africa a “public fitness emergency of worldwide concern,” triggering powers below the 2005 International Health Regulations (IHR). The IHR require countries to increase national preparedness capacities, such as the obligation to file internationally huge events, habits surveillance, and exercising public fitness powers, while balancing human rights and global trade.

Bottom Note: This work is partly presented at *International Conference on Biochemistry, Proteomics & Bioinformatics* May 16-17, 2018 Singapore.