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Bioinformatic analysis of the 2009-2010 pandemic H1N1 influenza virus

The purpose of this research is to determine whether the processes that dominated the mutational evolution of the 2009-2010 pandemic influenza H1N1 virus (pH1N1) were either random or non-random. An analysis of pH1N1 viral sequences from the NCBI-NIH Influenza Virus Resource will be presented. The analysis is based upon the molecular bioinformatics of viral subsets sorted according to a reference nucleotide position of maximum information entropy. The ordinary differential equations used in these studies can be solved by analytical, non-numerical methods. The results of this analysis revealed the presence of non-random, intergenic biological forces acting at the nucleotide level of viral organization. Evidence will be presented that these organizational and evolutionary forces may be of epidemiological and clinical significance.

Biography

Joel K Weltman attended the Bronx HS of Science (1946-1950), New York University (BA, 1954), State University of NY-Downstate Medical Center (MD, 1958) and the University of Colorado (PhD, Microbiology/Immunology, 1963), with Post-Doctoral Fellowships at the Weizmann Institute of Science and at Rockefeller University. He served a Rotating Internship at Indiana University Medical Center and is certified by American Board of Allergy and Immunology with a Special Qualification in Diagnostic Laboratory Immunology. He practiced clinical allergy/immunology from 1979 to 2004 and is Past-President both of the New England and of the Rhode Island Societies of Allergy. Since 1966 he has been at Brown University where he is Clinical Professor Emeritus of Medicine at the Alpert/Brown University School of Medicine. He has published 58 peer reviewed scientific articles and holds six patents from the USPTO and one foreign patent (Belgium). Dr. Weltman's current research interest is the molecular bioinformatics of the influenza virus.

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