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Novel platform (wEB) to study flu virus evolution and predict vaccine efficacy

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Flu epidemics and potential pandemics pose great challenges to public health institutions, scientists and vaccine producers. Creating right vaccine composition for different parts of the world is not trivial and has been historically very problematic. This often resulted in decrease in vaccinations and reduced trust in public health officials. To improve future protection of population against flu we urgently need new methods for vaccine efficacy prediction and vaccine virus selection. Recently, novel bioinformatics platform based on electronic biology was successfully utilized for real-time monitoring of influenza A viruses as well as for prediction of vaccine efficacy in Australia and USA in 2017 and 2018. Here we present wEB platform and its usage in identifying functional biological changes in haemagglutinin protein of influenza A viruses and how this knowledge can be applied for vaccine design, prediction of future vaccine efficacy and real-time virus evolution monitoring.

Biography

Slobodan Paessler, is a Professor in the Department of Pathology and Director of Galveston National Laboratory Preclinical Studies Core. Dr. Paessler is a co-principle investigator on the Universal Influenza Vaccine project funded by an NIAID grant at Etubics Corporation. He serves as the Director of Animal Biosafety Level 3 for the Institute of Human Infections and Immunity. He has been Member of Scientific Advisory Board at Etubics Corporation since July 2015. He serves as a Member of the Center for Biodefense & Emerging Infectious Diseases. He received a Dr. Med Vet (D.V.M) at Ludwig-Maximilian University and a Ph.D in Experimental Pathology from UTMB.

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