Toward better infectious disease control: A breeding ground for H3N2 and H1N1 viruses

Authors: Christopher Robinson Sydney Garza Sean Marquez Michael Pruitt Dr. Marvin Clark

Published Date: 08-03-2017

University of California-San Francisco

School of Mathematics

Influenza A (H3N2) and Influenza A/H1N1 viruses, which closely resemble each other, evolve their immune and developmental pathways in parallel. However, there is one sole and uncoordinated group in which the development of the influenza A/H3N2 and/or H1N1 viruses proceeds more slowly and accumulates, leading to better emergence of H3N2 and H1N1 (or A/H3N2/A) viruses. If this variation of timing of emergence, called real time variability, should become a route for evolution of the viruses, then it could represent a route to better virus selection and put global health at risk.

Using a novel approach to understand the evolution of influenza A viruses (or A/H3N2/A), Ana Mena, Laura Garci-a, Virginia Plasencia, Olga Hidalgo, Jos- Ignacio Ayestar-n, Sebasti-n Alberti, Nuria Borrell, Jos- L. P-rez, Antonio Oliver, and JosÃ© Oliver, "DemographiaH3-1s:: Sorting particles between H3N2 and H1N1/A strains: A meta-analysis of uncoordinated evolution with real time variability" in the recent issue of the highly prestigious Proceedings of the National Academy of Sciences.

A Close Up Of A Red And White Fire Hydrant