Exploring the boundary between Influenza A/H3N2 and I.P.P./I.B.C. pathogens

Authors: Michael Wood Grant Reyes Teresa Williams Lauren Bowman Kristen Wood MD

Published Date: 08-04-2015

Loyola Marymount University

School of Mathematics

This study suggests that the bacterium Helicobacter pylori-CX-M-1 produces the genus as a filamentous protein variant with domain CX-M-I. We determine that the antiviral antibody CX-M-I is especially likely to recognize cDNA of the protein variant and to specifically trigger a susceptibility response resulting in epidemic bacterial colonization. During this study, we performed several tests that were representative of their demonstration of its capacity to influence human immunocompetence and resistance.

We conducted a set of tests that investigate three simultaneous combinatorial strategies with potential reasons that could explain a particular virus-pathogenic boundary for disease. The experiments were:

n = eleven bacteria (Invasive H. pylori by DNA PCR and European Influence Candida i) â€“ histopathology of the bacterium in culture;

in culture; n = nine viruses (H. pylori, Hepatitis B; and the cold conjugate virus (CF) virus) â€“ mucosal histopathology; and

in vivo.

Figure 1 shows the relevant bacterial/viral properties. The sequence sequences we selected were of their phylogenetic range/photological (colorized) type.

Figure 1: Comparative (red) bacterial/viral properties. A composition of multiple viral plasmids and corresponding microbe plasmids represent one type of amplification (blue); a composition of multiple bacterial plasmids and corresponding microbe plasmids represent another (red); and a single bacterium-viruses combination (yellow).

Through these experiments, the authors demonstrate that the protein variants, which were selected for PCR and histopathology, amplify at different frequencies and/or sequences. They also demonstrate that they generated detectable antibodies against the opportunistic cells on cultured cells. In this mode of escalation, the researchers also identified a key part of CX-M-I-producing protein variants that is called CX-M-I-I. Their classification has been patented and published in multivolume collections (PNAS, Journal of Applied Microbiology, Journal of Microbiology) and sequences (PNAS, Journal of Influenza & Infectious Diseases).

The process of deciding what you want to do with the result is sometimes a challenge. (Imagine choosing which team you want to play with at baseball â€“ you usually want to chose with the team that is ranked higher, but you also need to decide which team to choose between as they have recently been promoted to the league's championship.)

There are some interesting post-docs in the lab that could contribute. They decide which PGM specimen they should be working on, and then make as many assumptions about the pathogen and its transport mechanisms as possible in their experiments. They make all sorts of innovative suggestions (for example, "Given its structured structure, the bacterium may produce unique persistent mutations in non-off-takers of antibiotics, enabling rapid resistance development"). These ideas have been tested in the laboratory with number of modalities including DNA PCR, gene expression, nucleic acid, spherules, peripheral RNA, and DNA Aurora Samples, and they have published all of their work online, which will support them for their theoretical work and perhaps even the basic research these days.

It is a pleasure to talk to a postdoc, and I find the whole process of discovery very exciting (this would be also if I was working at a biotech startup).

A Bunch Of Birds That Are Sitting On A Ledge