Michael W. Deem
Bioengineering and Physics & Astronomy, Rice University |
Houston, TX
mwdeem@rice.edu

Evolution in the bacterial, archaeal, and jawed vertebrate immune systems

The influenza virus has a high evolution rate, which makes designing the annual flu vaccine challenging. A mismatch between the strain in the vaccine and the strain infecting the public leads to a less effective vaccine and broader infection in the population. A precise measure of how different the immune system perceives the vaccine and virus to be enables a better design of the flu shot. I will discuss a method to predict vaccine efficacy that we have developed. Data show that this method is at least as predictive as, and sometimes more so than, animal model studies. Interestingly, the immune system typically recognizes the H1N1 strain of the flu to a greater degree than the H3N2 strain, leading to better flu shots for H1N1 than H3N2. The evolution rate of H1N1 is also greater than that of H3N2, presumably due to greater pressure on the virus to evolve.

Dengue virus (DENV) infections result in an estimated 50 to 100 million cases annually. Since DENV is comprised of four related serotypes, an ideal vaccine would provide the basis for a simultaneous and balanced attack against all four viral variants. I will describe a theory of the immune response to DENV vaccines. I will use this theory to explain limitations in the vaccine for dengue fever and to suggest a transport-inspired amelioration of these limitations.

Clustered regularly interspaced short palindromic repeats (CRISPR) in bacterial and archaeal DNA have recently been shown to be a new type of anti-viral immune system in these organisms. I will discuss the diversity of spacers in CRISPR under selective pressure. I will propose a population dynamics model that explains the biological observation that the leader-proximal end of CRISPR is more diversified and the leader-distal end of CRISPR is more conserved. I will show this result to be in agreement with recent experiments. The results show that the CRISPR spacer structure is influenced by and provides a record of the viral challenges that bacteria face.