Avian Influenza

Identifying High-risk Species

Our diverse, interdisciplinary team uses a suite of approaches to predict the risk of H5N1 influenza evolution through the host. These approaches will guide and focus our surveillance efforts for strains of concern.

Left: *The most critical mitigation for stopping the emergence of the highly pathogenic avian influenza into human populations in the pandemic form is to detect and control H5N1 in avian populations.*

Inset: *Jeanne Fair of Los Alamos National Laboratory measures the wing of a pigeon.*

Background

It is estimated that some 40 million Americans would become infected if an avian influenza (A/H5N1) pandemic emerged and over 700,000 people would need hospitalization. The most effective method to stop a pandemic in human populations is to detect and control it in avian populations. However, management of wild and domestic animal populations will require a better understanding of the determinants of host range and how this is changing in response to continual viral evolution. What is missing at the moment are critical data that would allow us to determine which avian species should be under surveillance.

Capabilities

To solve this surveillance problem, we are investigating the major host range determinant, the binding site for the virus sialic acid that varies between mammals and bird cell membrane. Our hypothesis is that the characterization of sialic acid of species in each order in the Class Aves can be used as a phylogenetic guide map to host range for influenza. That data will be compiled in a new sialic acid phylogenetic tree, allowing researchers to focus their surveillance efforts on particular strains of influenza.

Future Applications

Sialic acid types and quantities vary between species with a strong phylogenetic relationship. Understanding this relationship is key to deciding which species to survey in order to detect and contain an influenza outbreak.

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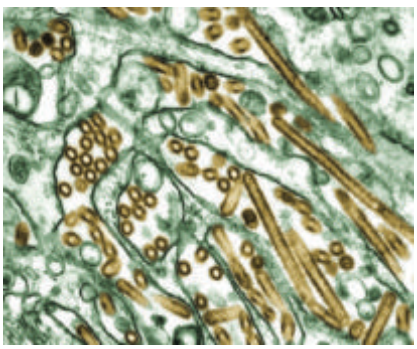

Right: Colorized transmission electron micrograph of Avian influenza A/H5N1 viruses (seen in gold) grown in MDCK cells (seen in green).