



Surveillance and molecular epidemiology of especially dangerous respiratory viruses in commercial and backyard poultry and migratory waterfowl

Mission Area:

Understanding Pathogen Dynamics and Creating Sustainable Interventions

Type: Hypothesis-Driven Research

Region: Asia

Countries: India

Status: Ongoing

Overview

Emerging and re-emerging respiratory diseases in poultry, especially velogenic viscerotropic Newcastle disease (vNDV) and highly pathogenic avian influenza (HPAI), present a major threat to animal and public health worldwide, especially in rapidly developing nations such as India. The core viral pathogens of human and animal concern involved in Respiratory Disease Complex of poultry have not been studied. The overall goal of this project is to discover novel viruses and enable the development of genomics based strain-typing capability of EDP and emerging viral pathogens from avian sources in academic research settings in India. Molecular epidemiologic analysis and comparative metagenomics investigation of respiratory viromes of domestic poultry and migratory birds, using a comprehensive and statistically robust stratified random sampling approach, will provide a strong foundation for the development of evidence-based approaches for implementing sustainable measures to control EDP; and help generate data and tools, build sustainable capabilities, and enhance domestic and international academic partnerships critical to characterizing the zoonotic pathogens associated with domestic poultry and waterfowl in India.

Objectives / Goals

The primary objective of this study is to map and compare the respiratory viromes of commercial chickens, backyard poultry, and migratory birds in three states of India representing different geographical and ecological regions and assess the risk posed by especially dangerous pathogens. This work is testing three hypotheses: Hypothesis 1. The respiratory tract viromes from commercial and backyard flocks (herein referred to as domestic poultry) and waterfowl in Haryana, Odisha and Kerala are a potential source of especially dangerous pathogens (EDP); Hypothesis 2. Molecular genotyping approaches will identify host- and region-specific fingerprint profiles of select agents including vNDV and



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HPAI; Hypothesis 3. Next generation sequencing will help identify nucleic acid signatures of novel / emerging viruses in domestic poultry and waterfowl.

Technical Approach

We have assembled a multidisciplinary team of scientists from India and the U.S. to execute this program. To obtain representative and statistically robust estimates of the burden of “especially dangerous pathogens” circulating in domestic poultry and wild birds in India, we are completing a comprehensive survey of these three types of birds in three different Indian states (Haryana, Kerala and Odisha) in northern, southern, and eastern parts of the country, respectively. These locations were chosen because of: (i) the diversity and density of wild birds and domestic poultry available with a history of intermingling; (ii) the select agent burden in the avian respiratory tract in India remains unknown; and (iii) there is recent history of outbreaks of severe respiratory diseases including vNDV and HPAI in these areas. The stratified sampling plan will cover the whole state and each state will be divided into three regions.

Partners

Funders:

- Defense Threat Reduction Agency (DTRA) - Cooperative Biological Engagement Program (CBEP)

Implementation / Scientific:

- Lala Lajpat Rai University of Veterinary and Animal Sciences (LUVAS) Haryana, India
- Kerala Veterinary and Animal Sciences University (KVASU) Kerala, India
- Orissa University of Agriculture & Technology (OUAT) Odisha, India
- University of Minnesota, USA