Project Information

1R01AI110964-01

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Project Number: 1R01AI110964-01
Title: UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE
Contact PI / Project Leader: DASZAK, PETER
Awardee Organization: ECOHEALTH ALLIANCE, INC.

Abstract Text:

DESCRIPTION (provided by applicant): This project will examine the risk of future coronavirus (CoV) emergence from wildlife using in-depth field investigations across the human-wildlife interface in China, molecular characterization of novel CoVs and host receptor binding domain genes, mathematical models of transmission and evolution, and in vitro and in vivo laboratory studies of host range. Zoonotic CoVs are a significant threat to global health, as demonstrated with the emergence of pandemic severe acute respiratory syndrome coronavirus (SARS-CoV) in China in 2002, and the recent and ongoing emergence of Middle East Respiratory Syndrome (MERS-CoV). Bats appear to be the natural reservoir of these viruses, and hundreds of novel bat-CoVs have been discovered in the last two decades. Bats, and other wildlife species, are hunted, traded, butchered and consumed across Asia, creating a large scale human-wildlife interface, and high risk of future emergence of novel CoVs. This project aims to understand what factors increase the risk of the next CoV emerging in people by studying CoV diversity in a critical zoonotic reservoir (bats), at sites of high risk for emergence (wildlife markets) in an emerging disease hotspot (China). The three specific aims of this project are to: 1. Assess CoV spillover potential at high risk human-wildlife interfaces in China. This will include quantifying he nature and frequency of contact people have with bats and other wildlife; serological and molecular screening of people working in wet markets and highly exposed to wildlife; screening wild-caught and market sampled bats from 30+ species for CoVs using molecular assays; and genomic characterization and isolation of novel CoVs. 2. Develop predictive models of bat CoV emergence risk and host range. A combined modeling approach will include phylogenetic analyses of host receptors and novel CoV genes (including functional receptor binding domains); a fused ecological and evolutionary model to predict host-range and viral sharing; and mathematical matrix models to examine evolutionary and transmission dynamics. 3. Test predictions of CoV inter-species transmission. Predictive models of host range (i.e. emergence potential) will be tested experimentally using reverse genetics, pseudovirus and receptor binding assays, and virus infection experiments across a range of cell cultures from different species and humanized mice.

Public Health Relevance Statement:

PUBLIC HEALTH RELEVANCE: Most emerging human viruses come from wildlife, and these represent a significant threat to global public health and biosecurity - as demonstrated by the SARS coronavirus pandemic of 2002-03 and an ongoing SARS-like epidemic in the Middle East. This project seeks to understand what factors allow animal Coronaviruses to evolve and jump into the human population by studying virus diversity in a critical group of animals (bats), a sites of high risk for emergence (wildlife markets) in an emerging disease hotspot (China).

NIH Spending Category:

Biotechnology; Emerging Infectious Diseases; Genetics; Infectious Diseases

Project Terms:

Affect; Animals; Asia; Binding; Binding Sites; Biological Assay; biosecurity; Blood specimen; Cell Culture Techniques; Cell Line; Cells; Chimeric Proteins; China; Chiroptera; Clinical; Coronavirus; coronavirus receptor; Data; Dipeptidyl-Peptidase IV; Disease; Ecosystem; Epidemic; Evolution; Exposure to; field study; Frequencies; Future; Genbank; Genes; Genetic; Genetic Recombination; Genetic Variation; Genomics; global health; high risk; Human; human population study; Human Virus; improved; In Vitro; in vitro Assay; in vivo; Infection; interest; Interview; Investigation; Laboratory Study; Life; Mammals; Marketing; mathematical model; Middle East; Modeling; Molecular; Mus; mutant; Nature; novel; Occupational Exposure; pandemic disease; Pattern; Phylogenetic Analysis; Phylogeny; positional cloning; predictive modeling; Primates; Process; Property; Public Health; public health relevance; receptor; receptor binding; research study; respiratory; Risk; Rural; Sampling; SARS coronavirus; screening; Serological; Severe Acute Respiratory Syndrome; Site; Southeastern Asia; Syndrome; System; Testing; trait; transmission process; Viral; Virus; Virus Diseases; Work

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