Inter-Species Modeling for Spillback/Spillover Avoidance

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While scientific reaction to the COVID-19 pandemic has been swift, the risk of SARS-CoV-2 spilling back into native North American wildlife and feral domestic animals remains underexplored. Experimental infections of a variety of hosts, serological analyses of the cats in Wuhan, and cases of COVID-19 among tigers and lions in the Bronx Zoo, all have shown transmission back to wildlife and feral cats is highly probable. Tools are urgently needed to determine which of these animal populations are at greatest risk of establishing a native reservoir, and where the overlap with human populations is greatest. We propose to model the risk of spillover to animal populations and conversely the risk of future secondary spillover by combining models of molecular interaction between the virus and potential hosts, with multi-species Susceptible-Infectious-Recovered (SIR) models. Complementing decades of experience in vertebrate genomics (Dávalos) with expertise in epidemiology (Meliker), and spatial dynamics of wildlife disease (Mets), ours is the ideal team to quickly generate and test the necessary models to avert this risk. With a strong track record of external support, we anticipate being able to submit grants to the NIAID, as well as the joint NIH-NSF call for ecology and evolution of infectious disease.