

ITAP Animal Pathogens Sub-Committee Meeting

Federal Interagency Committee on Invasive Terrestrial Animals and Diseases (ITAP)

February 2, 2016; 1-2:30 PM ET
USDA George Washington Carver Center
5601 Sunnyside Avenue, Beltsville, MD
Conference Room 4-2240

Presentation Abstracts

Ensemble species distribution models and maps to evaluate risk of invasion into the United States by a rabies vector species

Mark A. Hayes · Antoinette J. Piaggio

M. A. Hayes, Cherokee Nation Technologies, U.S. Geological Survey Fort Collins Science Center, Fort Collins, Colorado 80526 USA; hayesm@usgs.gov

A. J. Piaggio: National Wildlife Research Center, U.S. Department of Agriculture, Fort Collins, Colorado 80521 USA

Common Vampire bats (“Vampire bats”, *Desmodus rotundus*) occur throughout much of South America to northern México. These bats feed on the blood of mammals and transmit rabies virus to livestock, causing impacts to agricultural economies. Vampire bats have not been documented in the United States in recent history, but have recently been documented within 50 km of the U.S. state of Texas. We used species distribution modeling (SDM) to map the potential distribution of Vampire bats in North America under current and future climate change scenarios. We used 7,094 Vampire bat records from North America including over 600 new records (77 unique locations) from the northeastern portion of their Mexican range. We analyzed and mapped the potential distribution of this species using 5 approaches to species distribution modeling: logistic regression, multivariate adaptive regression splines, boosted regression trees, random forest, and maximum entropy. We then extrapolated these models into future climate scenarios for year 2070 to generate hypotheses about future distribution in North America. Some of our SDM models support the hypothesis that suitable habitat for Vampire bats may currently exist in parts of the México–US borderlands, including extreme southern portions of Texas, as well as in southern Florida and Cuba. However, this analysis also suggests that extensive expansion into the south-eastern and south-western U.S over the coming ~60 years is unlikely. Our results demonstrate how species distribution models and maps can help generate well-justified hypotheses about animal invasions within the context of wildlife disease ecology.

Addressing the threat of *Batrachochytrium salamandrivorans* to US salamanders

Katherine Richgels, U.S. Geological Survey National Wildlife Health Center, Madison, Wisconsin 53711 USA; krichgels@usgs.gov

Batrachochytrium salamandrivorans (Bsal) is a fungal pathogen that has caused declines in Northern European salamanders. As an emerging and invasive disease, salamander chytridiomycosis is a concern to wildlife managers and decision makers worldwide. The USGS National Wildlife Health Center has conducted several research projects that aim to provide information to policy makers and managers about the risks of Bsal to US species. Archived salamander specimens at the NWHC from amphibian die-offs around the country over the past 20 years were negative for Bsal. Though while not exhaustive, these preliminary results suggest that Bsal may not yet be in the US. We also developed a risk assessment to determine the likelihood that Bsal would be imported to the US through the pet trade and what the consequences of establishment of Bsal in the US might mean for native salamander species. We found that while there are considerable uncertainties, enough information exists to suggest that Bsal would be both likely to be introduced and cause potentially severe consequences for native salamanders. Our risk assessment was recently used by the USFWS to reach a decision to list 201 salamanders as injurious using the Lacey Act to reduce the risk of Bsal importation into the US.

Richgels, K.L., Russell, R.E., Adams, M.J., White, C.L. and Grant, E.H.C., 2016. [Spatial variation in risk and consequence of *Batrachochytrium salamandrivorans* introduction in the USA](#). *Royal Society Open Science*,3(2), p.150616.