National Wildlife Disease Program

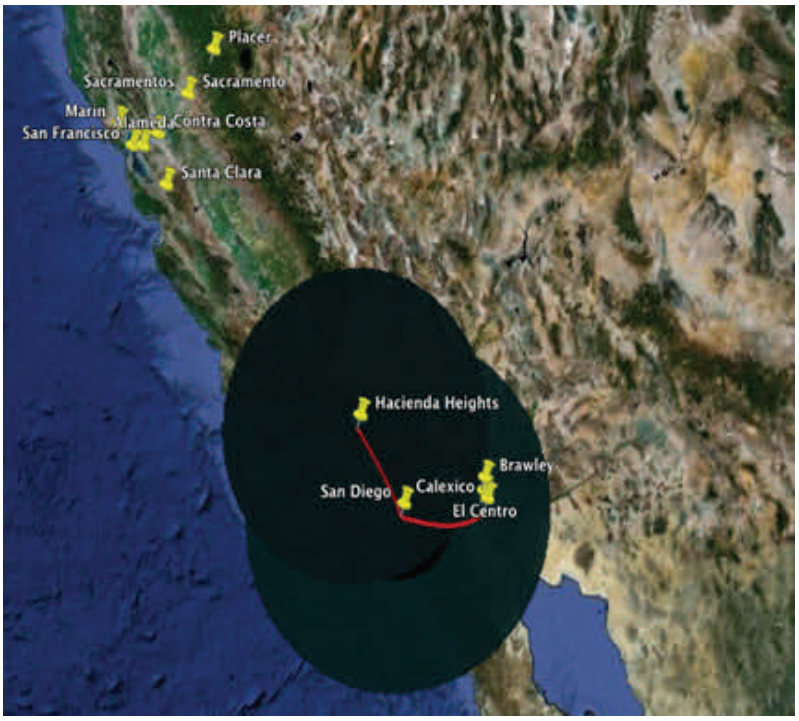
23 April 2012

Program Activity Report (PAR)

Comparison of Flu Viruses in Wildlife and Humans

The NWDP is collaborating with Arizona State University, The Mayo Clinic, and Colorado State University to determine relatedness of influenza A viruses circulating in wildlife and humans in the Southwest United States. The project, supported in part by a 2011 Arizona State-Mayo Clinic Seed Grant, is exploring the potential of using the health of wild animals as sentinels for zoonotic diseases in humans.

This study uses samples collected during wild bird surveillance activities and stored in the Wild Bird Tissue Archive established in 2006. Genetic material from influenza A matrix positive samples are being harvested by Colorado State University personnel using virus isolation and lysis techniques. Once harvested, extracted RNA is sent to Dr. Matthew Scotch, the project's lead researcher based at Arizona State University. Dr. Scotch performs reverse transcription and PCR to amplify the hemagglutinin (HA) segment of the genome. Cloning is then conducted using plasmid vectors transformed into competent E-coli cells. The plasmids are incubated overnight, extracted, and sequenced. The sequences are then assembled and the influenza subtype is determined by using NCBI BLAST (http://blast.ncbi.nlm.nih.gov/Blast.cgi). The avian sequences will be compared with the HA sequences of human cases using a variety of bioinformatics techniques. One approach is Dr. Scotch's bioinformatics tool *ZooPhy* (zoophy.wikispaces.asu.edu), which models the dispersion of influenza in avian species and humans across the Southwest United States.



An example from previous research of how the relatedness of viruses can be viewed with the ZooPhy tool created by Dr. Scotch, Arizona State University.

Thus far, 228 matrix positive samples have been harvested. Of those samples, seven viable viruses have been identified and genetic material sent to Arizona for genetic sequencing. Currently, the seven HA sequences have been completed and four of these have been published in GenBank with the following accession numbers: JN673246, JN864063, JN798212, and JN590044. The avian subtypes are: H8N4 (1), H4N6 (2), H11N9 (1), H3N8 (1), H6N1 (1). One sample is currently being sequenced but preliminary results suggest it is H3N8.

For more information contact Dennis Kohler.

Dennis.Kohler@aphis.usda.gov

The original artwork on this page was created by the National Wildlife Disease Program's Erika Kampe and Sarah Goff