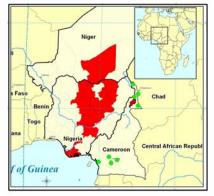
Bird Flu Research at the Center for Tropical Research by John Pollinger, CTR Associate Director

Evaluating Transmission Pathways of Avian Influenza (H5N1) by Domestic and Wild Birds in Central Africa

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The discovery of avian influenza subtype H5N1 in Central Africa in January 2006 presents serious threats to human health and warrants widespread surveillance of African migratory and resident landbirds. The African continent sustains a high diversity of migratory and non-migratory bird species, many of which live in close association with humans, swine, and poultry. It is also a continent battling HIV/AIDS and other infectious diseases, where there is poor or no public health infrastructure. As a consequence, an unchecked outbreak of avian influenza would potentially be catastrophic.

(Left: Central Africa H5N1 outbreak sites for birds indicated in red)

Long distance migratory birds have received considerable attention as important vectors of the H5N1 virus between countries and there is little question that infected migratory birds, particularly waterfowl, have carried influenza virus vast distances. Many questions remain about the role of migratory and resident species of birds in the transmission of H5N1. Of serious concern is the possibility that some migratory species may carry the virus but show no signs of disease. Such an instance, reported in healthy ducks in southern China between 1999 and 2002, is now thought to have led to ongoing outbreaks of H5N1 in Southeast Asia. Another concern is the role of resident passerines (perching birds and most songbirds) that are associated with agriculture and have been shown to be carriers.



African rainforest cattle egrets

The Center for Tropical Research was awarded a National Science Foundation (NSF) Ecology of Infectious Disease (EID) grant on "*Effects of Deforestation on the Prevalence of Blood-borne Pathogens in African Rainforest Birds*" in 2004. UCLA and its collaborative partners, San Francisco State University and Vilnius University, Lithuania, have been investigating the prevalence and evolutionary relationships of blood-borne diseases in populations of avian hosts that range from small to large, located in disturbed to pristine habitats, and across a variety of environmental gradients in Central Africa. At the time of the

H5N1 avian influenza outbreak, CTR had experienced researchers working in Cameroon and Uganda with an established research and logistics infrastructure and we were able to expand our current research in Cameroon to monitor the progress of the outbreak and to test hypotheses regarding transmission of avian influenza in domestic, migratory, and resident birds.

Initially, in mid-December 2005, after outbreaks of H5N1 in Central Europe, a collaboration was initiated between UCLA's Center for Tropical Research and the Walter Reed Johns Hopkins Cameroon Program to monitor H5N1 in Cameroon. Cameroon lies along the major migratory flyways between Africa and both Europe and Asia. The goal of this preliminary research effort was to: 1) identify important migratory bird wintering sites, with a focus on migratory waterbirds, 2) identify logistical challenges and test research methods to inform planning efforts, and 3) gather preliminary samples that would serve as baseline data in the event of an H5N1 introduction in Cameroon.

In mid-January 2006, shortly after research teams arrived in Cameroon, a major H5N1 outbreak was reported in central Nigeria. From previous waterbird surveys and BirdLife International's list of Important Bird Areas, we identified the Douala estuary and the Logone river floodplain (including Lake Maga, Lake Chad, and several large lakes) as potential locations for high concentrations of overwintering migratory waterbirds. From mid-February to present, we have visited and sampled birds at these sites in addition to sampling for H5N1 in conjunction with our ongoing research program studying disease in managed landscapes.

Over the course of this work, we have collected over 650 cloacal swab samples (samples from the common opening in birds through which the intestinal, urinary, and reproductive tracts empty) and fecal samples from 86 species, including 98 samples from 12 long-distance migratory species. These samples are now being tested at Los Alamos National Laboratory (LANL) for the presence/absence of H5N1 and other avian infleunza subtypes. LANL is UCLA's partner in the new High Speed, High Volume Laboratory Network for Infectious Diseases being built at UCLA and funded by the Department of Defense and the State of California.

Shortly after completing our initial visit to northern Cameroon, H5N1 was confirmed in domestic ducks in Maroua, a major city in the far north province of Cameroon. The outbreak took place near a livestock and poultry market in Maroua, close to bodies of water that could potentially be used by migratory waterbirds.

CTR was recently awarded additional funds from NSF to continue our sampling efforts and to establish a more systematic monitoring program that will allow us to examine the role of wild birds in H5N1 transmission. Our objectives include: 1) developing a systematic monitoring program, 2) broadening the existing geographic and taxonomic scope of H5N1 sampling in Cameroon, 3) monitoring the prevalence and persistence of H5N1 in wild and domestic birds near the initial outbreak site in Cameroon, 4) evaluating the potential for resident wild birds to act as reservoirs and regional vectors for avian influenza, 5) testing alternative hypotheses for the introduction and spread of H5N1 in Cameroon, and 6) training Cameroonian scientists to improve the government's capacity to monitor H5N1 avian influenza outbreaks.