Research Update: UCLA - IBP Feather Collection Projects

The UCLA Center for Tropical Research (CTR) feather collection has passed the 100,000 sample mark! Thank you all so much for your contributions. The collection has proven to be a valuable resource not only for CTR researchers but also for other US and international institutions.

Migratory Connectivity

Over the last thirty years, scientists and birdwatchers alike have noted precipitous population declines in many species of migratory songbirds. However, the transitory nature of migratory birds makes it difficult to pinpoint the exact cause of such declines. As a consequence, developing effective management strategies remains elusive. Some propose that habitat loss on the tropical wintering grounds has led to increased over-wintering mortality, while other researchers suggest that habitat degradation on the temperate breeding grounds may negatively influence reproductive success. Songbirds are also undoubtedly affected by disturbances along the migratory pathway. A central problem in understanding the cause(s) of declines is the inability to relate specific breeding and wintering populations and the migratory routes that connect them. Historically, efforts to correlate breeding, wintering, and migratory populations have relied on large-scale banding programs. However, these efforts have generally been of limited success, as recaptures of banded birds, especially on their wintering grounds, are rare.

In order to complement large-scale banding efforts, the Center for Tropical Research (CTR), UCLA and its collaborators have been developing biological markers to track migratory movements of birds. Our biological tags use genetic and isotopic information from a single feather sample to track where an individual was born, and where it has molted its feathers. As a consequence, a feather collected at one stage of the migratory cycle can be used to make essential links between where that bird may be going and/or where it came from. Unlike extrinsic tracking devices (radio transmitters, bird bands, and data loggers), genetic and isotopic markers can also help identify the appropriate spatial scales for understanding population trends. Until recently, the spatial scale for identifying where particular breeding populations spend the non-breeding seasons was too coarse to detect drivers of local population dynamics. However, recent advances in genetic, isotopic, and statistical methods will allow us to define populations at much finer spatial scales than before. These approaches will make a significant contribution to conservation strategies for threatened or endangered songbirds.

West Nile Virus

Another potential cause of population decline in migratory songbirds is disease. An ongoing component of our migratory work examines the spatial and temporal patterns of West Nile virus (WNV) in Neotropical passerines and contrasts samples from pre- and

post-WNV occurrence to determine whether particular species have experienced population declines. Based on the prevalence across selected species, we can also determine whether particular taxa are acting as species-equivalents of WNV "superspreaders". During the last year, we have been able to model the distribution of positive WNV occurrence in vectors (mosquitoes) over the northeastern part of the United States using ground-based and satellite-based environmental data layers and the Maximum Entropy Model (Maxent) distribution model. We used vectors in this analysis because presence data was already collected and readily available. We can screen feathers for genetic evidence for the presence of West Nile virus, then apply these same modeling methods to migratory bird positives. From this analysis, temperature and precipitation were both determined to be important correlates of high incidence, and several hotspots of incidence were revealed, occurring primarily in areas where high levels of urbanization may facilitate disease transmission between vectors and hosts. Using this information, we modeled how the distribution of WNV might change under a variety of climate change scenarios. The future incidence of WNV shifted in a consistent manner, revealing a northward shift in the distribution of West Nile virus within the Northeastern region of North America, expected as temperatures increase and mosquito vectors are able to increase their distributions. Finally, we will explore the anthropogenic stressors associated with the presence of WNV and identify the possible correlates between geographical WNV hotspots and areas where anthropogenic activity has altered the environment.