

DISEASE SURVEILLANCE IN ARCTIC-BREEDING SHOREBIRDS

Biological Objectives

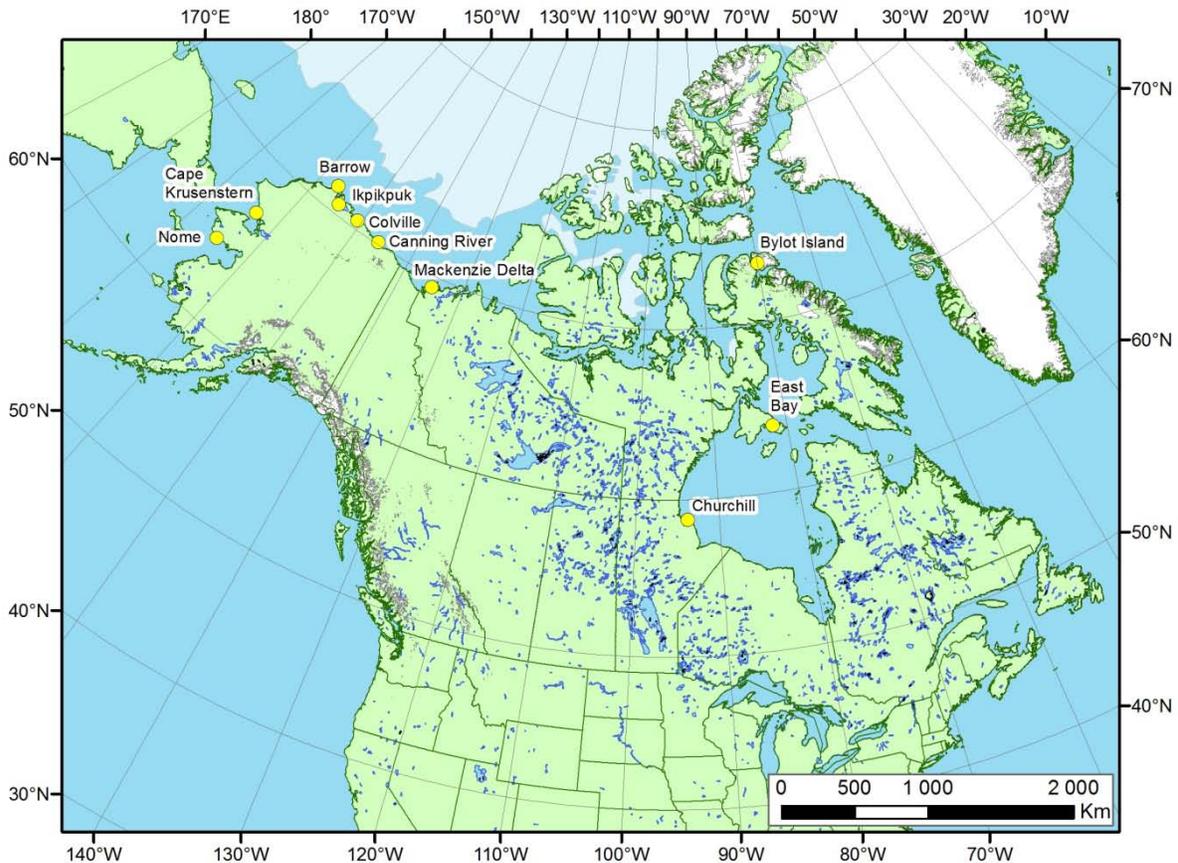
- To collect and archive a large number of plasma, red blood cell, RNA, and fecal samples from a variety of shorebird species sampled over a large geographic area in the Arctic.
- To assess shorebird blood samples for avian malaria, with a focus on several species that are sampled over a large geographic area.
- To assess shorebird fecal samples for the presence and quantity of fecal bacteria and opportunistic pathogens, with a focus on several species that occur at multiple sites.
- To correlate the migration pathways determined by light-level loggers of three subspecies of Dunlin that use different migration routes and wintering areas with the prevalence of pathogens.

Background

Migratory birds are excellent targets for disease surveillance because of their potential to spread disease globally. Although the recent focus of migratory bird surveillance has been to detect avian influenza, there are many other disease agents that may be equally dangerous. The prevalence of diseases in birds is likely to vary with many factors, including the regions of the world where they breed and winter, and at these locations, the specific habitats that they occupy. Another factor that may affect pathogen load is how and where species migrate. Long-distance migrants that use numerous stopovers may have larger pathogen loads because they are stressed from migrating and are being exposed to more pathogens than a species that travels shorter distances, avoids stopovers or does not aggregate at stopover sites. Because Arctic-breeding shorebirds migrate to southern latitudes to winter, use different habitats while migrating and wintering, and use different migratory routes, they are an especially good group of birds to investigate how disease prevalence varies with these factors.

Planning/Project Design

Obtaining samples from Arctic shorebirds that breed over large geographic areas and in remote locations is very challenging and costly. However, the creation of the Arctic Shorebird Demographics Network in 2010 has provided a unique opportunity to study a diverse array of shorebird species and obtain large numbers of samples from shorebirds in a way that was not previously possible. The Arctic Shorebird Demographics Network (the Network) is a geographically broad, multi-partner strategy, composed of representatives from the U.S. Fish and Wildlife Service, the U.S. Geological Survey, the Canadian Wildlife Service, Environment Canada Science and Technology Branch, academia, and non-governmental conservation organizations. Currently there are six Network sites in the U.S. and four in the Canadian Arctic (see map). The Network's 2011 field season also provided an excellent opportunity to investigate disease prevalence in three subspecies of Dunlin that were equipped with light-level loggers in the summer of 2010. We have the rare opportunity to examine how infection status may relate to prior movement rates and patterns. The Dunlin study allowed us to collect fecal and RNA samples from this species at the Izembek and Yukon Delta national wildlife refuges in southwestern Alaska (not shown on map).



Study locations for the Arctic Shorebird Demographics Network in North American Arctic, 2011. (map prepared by J.F. Lamarre)

Implementation

Initial disease surveillance included collecting samples to detect avian malaria, assessment of gut microbiota and its relationship to overall health of migratory birds, and immune gene expression. Detailed field protocols were developed and implemented during the 2011 field season. Personnel at eleven sites collected samples (481 plasma, 481 red blood cells, 585 RNA, and 630 fecal) from 12 species of shorebirds. 419 red blood cell samples were sent to Kansas State University; DNA was extracted from 200 and 188 of these were screened for haematozoans (*Plasmodium*, *Haemoproteus* and *Leucozytocoön*; i.e., avian malaria) using PCR techniques. Nine individuals belonging to five species and originating from three Network sites were found to have haematozoans present. Plasma samples have not been analyzed yet but will show whether a bird was previously exposed to avian malaria but no longer has the disease. 588 fecal samples were sent to the U.S. Environmental Protection Agency's office in Cincinnati, Ohio; DNA was extracted from these and the quality is good. DNA extracts will be used as "fecal libraries" and are now being prepped for processing using High-throughput Genetic Sequencing techniques to identify enteropathogenic bacteria (i.e., those that produce disease in the intestinal tract). No analysis has been conducted on the RNA samples to date, although these samples will be useful for the study of immune gene expression using molecular methods in the future. Light intensity data from 97 Dunlin (26 *arctica*, 54 *pacifica*, and 17 *hudsonia*) belonging to three subspecies are currently being analyzed to generate migration tracks; once completed these migration routes will be correlated with prevalence of disease.

Management

Based on the information gathered during this study, planning, biological objectives and implementation could be adapted as follows:

- Sample analysis will be used to assess disease vulnerability of particular species, and how vulnerability varies among breeding sites, migration corridors, and wintering areas.
- Additional samples will be collected by the Network where a given species or location indicates more detailed analyses are needed.
- Side projects that take advantage of this work will be initiated (e.g., DNA already extracted from fecal samples for the gut microbiota study will be used to assess foods eaten).

Accomplishments

Shorebird species in North America are facing serious population declines, but we do not know why. The Shorebird Research Group of the Americas identified major reasons why these declines may be occurring; one of the seven identified factors was disease or contaminant exposure. This project directly addresses this factor by collecting baseline data on disease prevalence (i.e., avian malaria), and susceptibility to disease (i.e. gut microbiota and immune gene expression). Obtaining a better understanding of the potential effects of disease at regulating shorebird populations will help determine the nature and extent of this problem. If problems are identified, this new knowledge will allow us to target conservation investment appropriately, rather than guessing where conservation funds can best be spent. This will ultimately lead to increased conservation success.