Virus Surveillance of Bird Fecal Samples in New York City

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Abstract
Wild birds are known to disseminate infectious particles that spread avian diseases. Bird-to-bird and bird-to-human transmissions of these diseases are more likely to occur in highly populated areas, such as New York City (NYC). To identify the prevalence of these diseases, we assessed the prevalence of Avian Influenza virus (AIV) and Newcastle Disease virus (NDV) in bird fecal samples collected from NYC parks. The presence of these viruses were determined through polymerase chain reaction (PCR) using virus specific primers. All but one sample was negative, indicating that AIV or NDV levels are low in NYC. We also used DNA barcoding to identify species who are known hosts of these viruses. It is important to perform surveillance and species identification to prepare for a possible epidemic and identify the species of birds that may be harmful to humans and other birds.

Introduction
RNA viruses, such as AIV and NDV, are commonly known to infect birds. These diseases are threatening to bird populations causing respiratory problems, fever, and a swollen head and neck. NDV also causes infections in the energetic nervous system in poultry, and significant morbidity and mortality in poultry (Dhama, 2013). These viruses are transmitted from bird-to-bird and from birds-to-humans through the inhalation of disseminated bird feces, residents living near infected birds risk infections. Symptoms include fever, cough, muscle pain, and respiratory issues. A study assessing the prevalence of AIV and NDV in NYC birds would help to better prepare for a possible avian disease outbreak, as well as increase the knowledge surrounding avian diseases.

Methods
Fig 1. Methodology for virus detection and DNA barcoding of bird fecal samples.

Results
Fig 2. Sampling collection sites and birds observed during sampling. The sampling sites are depicted in the map. The phylogenetic tree was created by downloading the cytochrome c oxidase (COI) gene DNA sequences from NCBI of all the overeased birds. These sequences were then input into a phylogeny software. The circle next to the bird names represent the location were these birds were observed and matches the park colors on the map.

Fig 3. Virus surveillance and DNA barcoding of NYC bird fecal samples. Forty-one fecal samples were collected from the parks depicted in Fig 2. In total, 10 samples were identified using DNA barcoding. The colored circles next to the bird name represent where the sample was collected. The identified bird species are also highlighted based on whether their species is known to be natural reservoirs for NDV (orange) or both NDV and AIV (yellow).

Discussion
• Even though birds are natural reservoirs for AIV and NDV, only the Muscovy Duck had detectable NDV, coinciding with detection levels in similar studies (Fig 4).
• Only 3% of our DNA samples amplified and 24.4% were successfully identified using DNA barcoding. This maybe due to sample degradation.
• Our results indicate that the prevalence of AIV or NDV is low, but birds that are reservoirs for these viruses are highly prevalent in NYC.
• By increasing our sample size and sampling time frame, we could better determine the prevalence of these viruses in NYC bird populations and the effect they may have on human health.

Fig 4. Frequency of NDV and AIV in birds. Surveillance results from similar studies were compiled to determine the average percent of detected virus. This average was used to compare our results to previous studies to determine whether our results are common. The colored portion represents positive results, while the rest are negative.

References

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