

Virus Surveillance of Bird Fecal Samples in New York City

Authors: Damely Abreu¹, Gisette Noriega¹

Mentor: Meagan McMahon²

¹ Manhattan Center for Science & Mathematics;

²Department of Microbiology, Icahn School of Medicine at Mount Sinai

Abstract

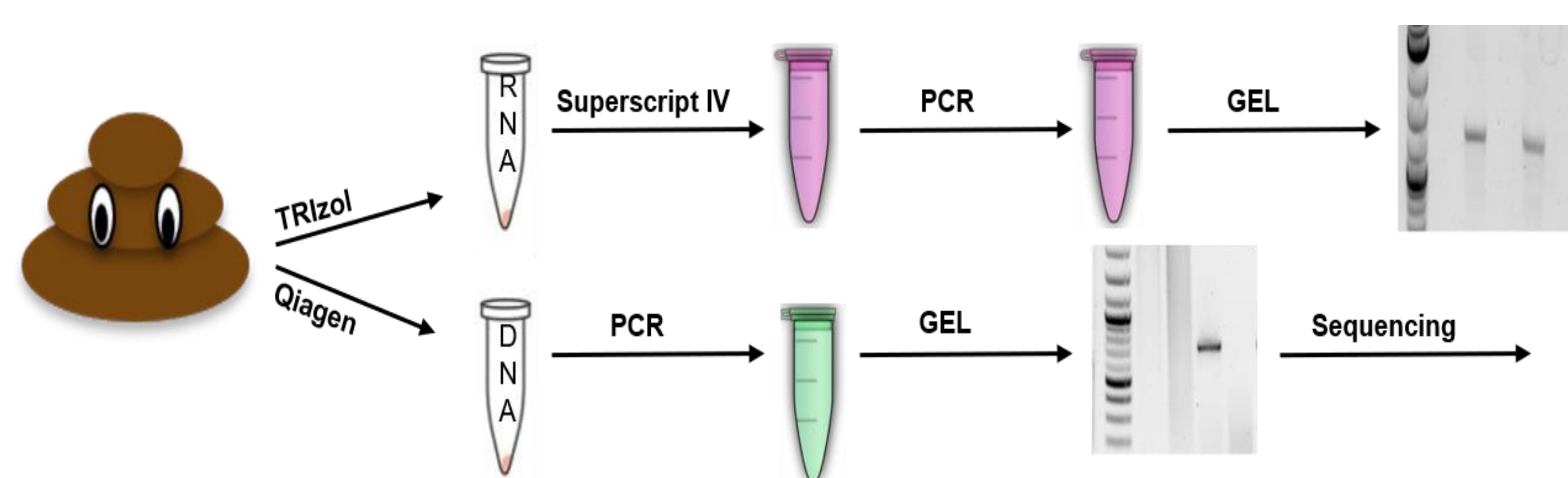
Wild birds are known to disseminate infectious particles that spread avian diseases. Bird-to-bird and bird-to-human transmissions of these diseases are more likely to occur in highly populated areas, such as New York City (NYC). To identify the prevalence of these diseases, we assessed the prevalence 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 enteric 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 presence 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 overserved birds. These sequences were then input into a phylogeny software. The circle next to the bird names represent the location where these birds were observed and matches the park colors on the map.

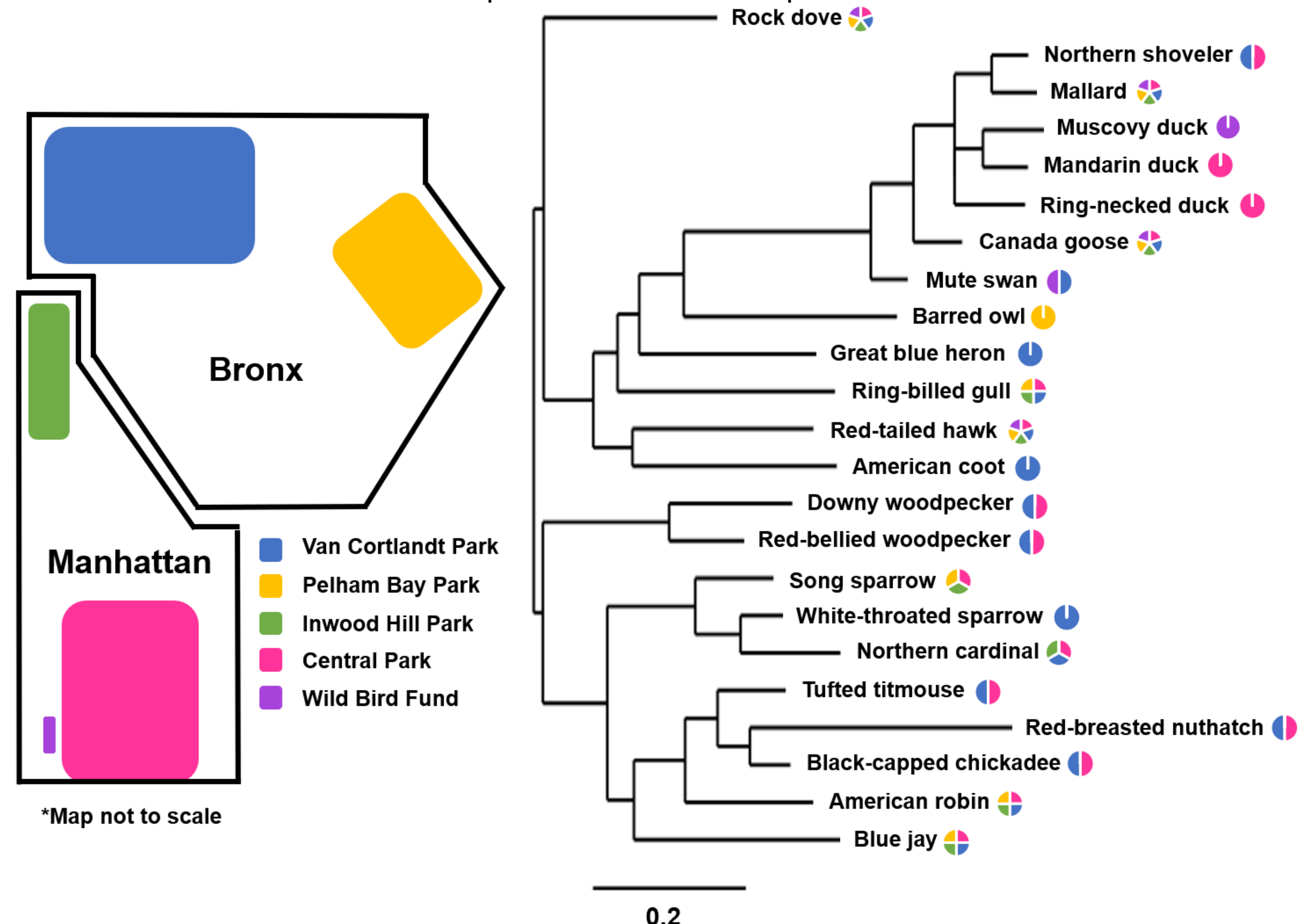
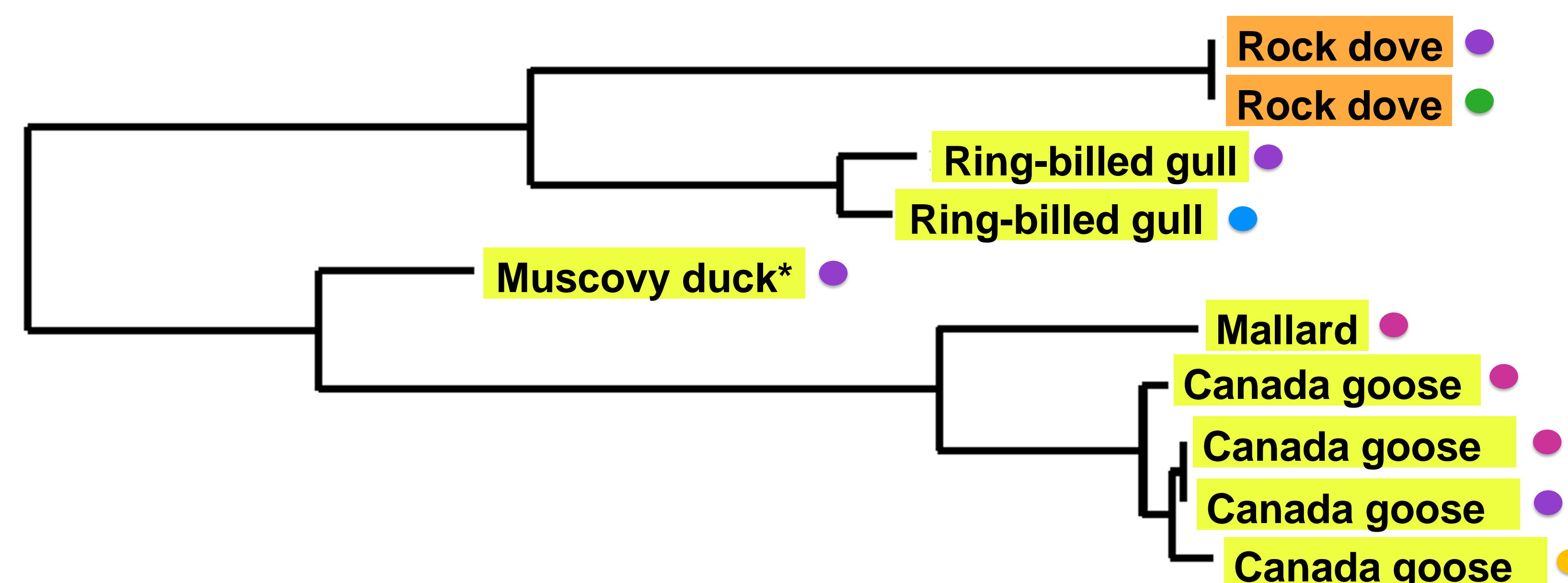


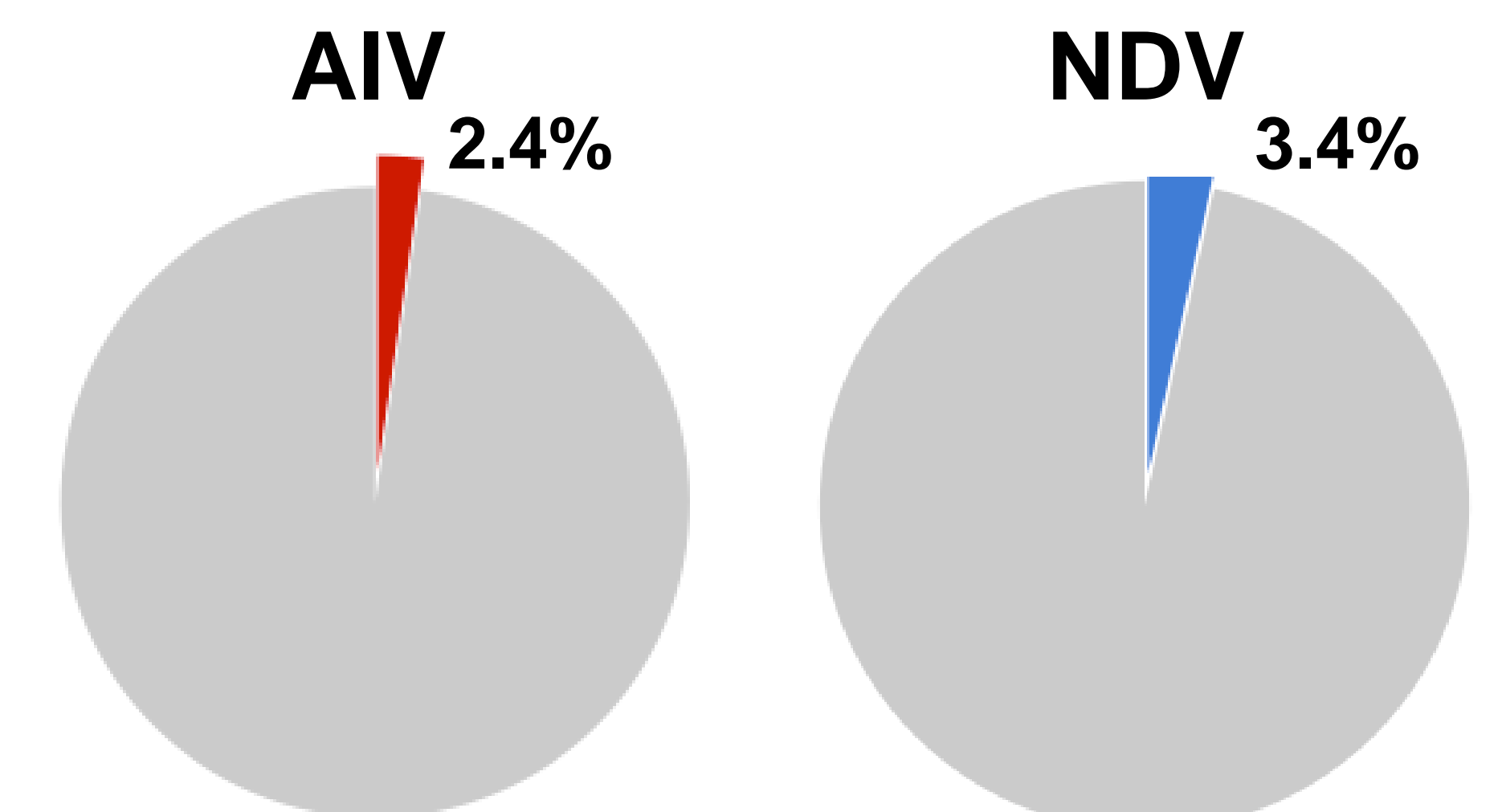
Fig 3. Virus surveillance and DNA barcoding of NYC bird fecal samples. Forty-one fecal samples were collected from the parks depicted in Fig 2. In total, 10 samples were identified using DNA barcoding. The colored circles next to the bird name represent where the sample was collected. The identified 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 39% 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

Cheung, Peter P, et al. "Identifying the Species-Origin of Faecal Droppings Used for Avian Influenza Virus Surveillance in Wild-Birds." *Journal of Clinical Virology : the Official Publication of the Pan American Society for Clinical Virology*, U.S. National Library of Medicine, Sept. 2009.

Dhama, K., A.K. Verma, S. Rajagunalan, A. Kumar, R. Tiwari, S. Chakraborty and R. Kumar, 2013. *Listeria monocytogenes* infection in poultry and its public health importance with special reference to food borne zoonoses. *Pak. J. Biol. Sci.*, 16: 301-308.

Hsieh, Ying-Hen, et al. "Quantification of Bird-to-Bird and Bird-to-Human Infections during 2013 Novel H7N9 Avian Influenza Outbreak in China." *PLOS ONE*, Public Library of Science, 5 Dec. 2014.

Lee, D H, et al. "DNA Barcoding Techniques for Avian Influenza Virus Surveillance in Migratory Bird Habitats." *Journal of Wildlife Diseases.*, U.S. National Library of Medicine

Acknowledgments

The authors would like to acknowledge the following organizations for the manufacture and characterization of the experiment: Urban Barcode Research Program at the Cold Spring Harbor Laboratory, and Department of Microbiology, Icahn School of Medicine at Mount Sinai.

