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Project Abstract Summary

This Project Abstract Summary form must be submitted or the application will be considered incomplete. Ensure the Project Abstract field succinctly describes the project in plain language that the public can understand and use without the full proposal. Use 4,000 characters or less. Do not include personally identifiable, sensitive or proprietary information. Refer to Agency instructions for any additional Project Abstract field requirements. If the application is funded, your project abstract information (as submitted) will be made available to public websites and/or databases including USAspending.gov.

* Funding Opportunity Number

F-FWS-WSFR-24-002

CFDA(s)

15.628

* Applicant Name

University of Georgia Research Foundation, Inc.

* Descriptive Title of Applicant's Project

2024 MSCGP - Predicting risk and the long-term trajectory of highly pathogenic H5 avian influenza virus on North American nesting and wintering geese based on population immunity

* Project Abstract

Currently, there are more questions than answers regarding potential impacts and risks associated with highly pathogenic (HP) H5N1 influenza A virus (IAV). Since introduction into North America via wild birds late in 2021, HP H5N1 IAV infections and mortality in wildlife continue to be reported throughout North America. In addition to spreading rapidly across the continent and now, into South America, this virus has demonstrated an extremely broad host range that includes many wild mammal and bird species, most of which had not previously undergone IAV-associated disease or death. We know that HP H5N1 IAV has been detected in over 150 wild avian species and in many cases, including in Arctic-nesting geese, has led to alarming levels of morbidity and mortality. We know that HP H5N1 IAV has been confirmed in all U.S. states (except Hawaii) and in all Canadian territories and provinces. Finally, we know that HP H5N1 IAV has drastically changed the IAV landscape in North America, likely forever. The extent of potential population-level impacts, and risks to wildlife, domestic animal, and human health associated with HP H5N1 IAV, however, are still unknown.

Arctic-nesting geese, including snow geese (Anser caerulescens), Ross geese (Anser rossii), and greater white-fronted geese (Anser albifrons), comprise some of the most numerous waterfowl species in North America and represent important recreational and subsistence food resources. Additionally, many have proven to be highly susceptible to fatal HP H5N1 IAV disease. This susceptibility, coupled with their broad distribution and large population numbers, position Arctic-nesting geese as an excellent model system in which to start to better understand population immunity to IAV across different seasons, age cohorts, and species as a predictor of potential infection and mortality/morbidity associated with HP H5N1 IAV.

By linking retrospective and prospective virologic (evidence of active infection with IAV) and serologic (evidence of previous IAV exposure, and potential protection from future infection) data with specific Arctic-nesting geese species and age cohorts at multiple spatial and seasonal scales, we can start to unravel what the long-term effects of HP H5N1 IAV might be on North American geese, and other waterfowl species. Further, we will characterize IAV diversity in North American Arctic-nesting geese on their wintering grounds and explore species-related differences in pathology. The information gained from this proposed work will provide a data driven approach to not only inform managers and policy makers of the risk of HP H5N1 IAV infection and mortality/morbidity in Arctic-nesting geese, but also provide a predictable framework for public and hunter outreach related to

* Project Abstract (Continued from previous page)

risk (including potential hunter exposure to this virus). Although this research is focused on geese, the information generated will lend itself to a risk assessment approach that can easily be applied to other waterfowl and wild avian species affected by this virus.