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United States Department of Agriculture
Project Initiation

Project Data for Accession Number 1034300

Project Title

US-UK Collab: Avian influenza virus in cattle, a framework for forecasting transmission dynamics of zoonotic disease in livestock systems

Project Details

Sponsoring Institution National Institute of Food and Agriculture	**Project Status** ACTIVE
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Performing Department

(N/A)

Non Technical Summary

Infectious diseases are a major threat to the livestock industry. Disease outbreaks can be very difficult and expensive to control with livestock producers and the industry facing the highest financial and personal costs. The ongoing highly pathogenic avian influenza (HPAI) outbreak in US dairy cattle shows how rapidly infection can spread and the multiple challenges faced by the livestock industries in controlling disease. Diseases like HPAI that can infect multiple livestock species, wildlife, and humans are particularly challenging. Our goal is to build a toolset that can make national-scale projections about the likely spread of HPAI in livestock, wildlife, and humans, and how we can enact effective control. We will achieve this through five main objectives: 1) we will collect and combine data on the HPAI outbreak and livestock shipments; 2) we will determine the risk of HPAI being spread to livestock from wildlife and the environment; 3) we will develop models to make HPAI predictions in the US and the UK; 4) we will make predictions about the

future risk that HPAI poses to cattle farms and whether the biggest threats come from other cattle farms or from wildlife; 5) we will study the role of surveillance and control actions on reducing the spread and the risk of HPAI. By the end of the project, we will have the software, data and methods in place to understand and predict the spread and control of HPAI and similar infections. We will ensure our results meet the needs of the industry by working closely with the US Department of Agriculture, state veterinarians, and industry stakeholders. The findings of this project will help protect livestock producers, livestock industries, and US agriculture from the costs and consequences of current and future infectious disease outbreaks.

Animal Health Component

Animal Health Component: 100%

Research Effort Categories

Basic	10%
Applied	80%
Developmental	10%

Classification

Knowledge Area (KA)	Subject of Investigation (SOI)	Field of Science (FOS)	Percent
311	3910	1170	100%

Knowledge Area

[311] Animal Diseases

Subject Of Investigation

[3910] Cross-commodity research--multiple animal species

Field Of Science

[1170] Epidemiology

Keywords

highly pathogenic avian influenza, livestock-wildlife transmission, zoonotic disease in livestock

Goals / Objectives

Infectious diseases pose a major threat to intensive livestock industries, and responding to an outbreak is often expensive - with producers and the industry bearing the brunt. The 2024 emergence and spread of highly pathogenic avian influenza (HPAI) in US dairy cattle highlights the threat posed to livestock systems by infectious diseases and the difficulties of control. One of the major challenges for characterizing the transmission dynamics of a zoonotic livestock disease like HPAI is the transmission that occurs between livestock and wildlife. The role of transmission between domestic and wild animals in driving transmission at different scales is not well understood but has major implications for surveillance and response. Both the US and the UK have well established, robust livestock disease models that incorporate a wealth of information at different spatial scales.To understand the full transmission

landscape, these national-scale models will be expanded to include wildlife and HPAI-specific data. Our goal is to build a modeling framework to forecast the transmission dynamics of national-scale outbreaks of zoonotic diseases in livestock, using HPAI as our template. This modeling framework will transform our previous models into robust predictors of HPAI spread and control - allowing us to quantify whether this novel infection can be eradicated from the US, prevented from establishing in the UK, and whether the costs of control are likely to be worth the benefits. Objective 1. Collection/Collation of Data Including Shipment Data and the Development of Multi-Year US Animal Movement Model. Robust mechanistic modeling requires high-quality data that accurately reflects the underlying processes. It is therefore vital that we collect and collate data on all aspects of the US and UK livestock industries that impinge on the likely dynamics. This is dominated by the need to update models of livestock movements across the USbut also includes historical data on premises sizes and composition to allow us to extrapolate changes into the near future, and economic drivers of movement and behavior, together with likely costs of infection and control measures. In this objective, we will collect interstate livestock shipment data from a subset of key states in the contiguous US. Those data will be used to update the US Animal Movement Model such that it can produce multi-year, national shipment predictions. The updated shipment model will be integrated into the US disease model to allow for robust predictions of long-distance transmission events. We will also collect data on HPAI infections, HPAI genetic sequences, economic impacts, and UK movement data.Objective 2. Quantify Wild Bird/Environmental/Wildlife Spillover Risk. For HPAI, understanding environmental and inter-species transmission is very important. However, little is known about the role wildlife and the environment play in transmission risk to livestock, which limits our ability to build mechanistic models that can be used for prediction. Sequence data, and the time-scaled phylogenetic trees that can be reconstructed from these data, remain important tools for understanding the spread of H5N1 and can inform mathematical model development. We will use the latest sequence data from public sources including GISAID and NCBI to infer the patterns of transmission and to better inform the spatial simulation models. We will use sequence data to better inform our modeling approach across different spatial scales, from within-farm to between-states.Objective 3. Adaptation of US and UK Models for HPAI Our team has already pioneered the development of mechanistic mathematical models that capture the spread of foot and mouth disease (FMD) in the US and UK. For the US approach, the US Disease Outbreak Simulation (USDOS) incorporates both the movement of livestock (taking infection from one farm to another) and the shorter-range transmission via other routes; this makes USDOS an ideal model for other livestock infections including HPAI. UK models of FMD have focused on short-range transmission, due to movement restrictions that are mandated in the UK, but there is complementary work from the team on bTB and generic infections where cattle movements play a vital role in transmission. Development of the US and UK models will require different approaches given the state of the underlying methodology. However, both the US and UK models require that there is the capability to handle transmission between livestock herds, wildlife, and the environment. This objective will produce transmission models for the spread of HPAI between livestock herds and between livestock and wildlife on the national scale for the UK and the US.Objective 4. Forecasting of Future HPAI Risk in Cattle Farms and Quantification of Relative Risk of Spillover vs Within-industry Spread. We will use the adapted models from Obj. 3 to perform spatial simulations of HPAI outbreaks in cattle premises in the US and the UK. We will use the models to explore a range of scenarios involving different demographic, ecological and epidemiological uncertainties, as well as providing projections at the short, medium and long term. This objective will provide bespoke spatial assessments of HPAI transmission in cattle farms in the US and UK. It will inform drivers of transmission and identification of likely infection hot spots (short-term); decisions regarding intervention policy against influenza in cattle (medium-term); an outlook on the likely range, persistence and impact of HPAI in cattle (long-term). These outputs will be continually refined to capture the changing nature of the HPAI outbreak in the US and possibly in the UK.Objective 5. Elucidating the role of Surveillance and Interventions at Controlling Spread and Risk of Zoonotic Spillover. This objective will focus upon the development of context-specific surveillance and intervention strategies, that in turn will inform the development of local and national policies in both the US and the UK. Throughout we will assess the burden of the disease within the cattle industry, the likely economic costs and the risk to public health at the zoonotic interface. Intervention policies may be hindered by lack of compliance with control measures, limited manpower and available resources to establish or sustain the practice, and the timeliness of the interventions. Additionally, the inherent uncertainty in the location of infection, which is highly dependent upon surveillance protocols, may also hamper

efficient deployment of controls. As such, it is important that we consider realizable (not idealized) control measures, in modeling frameworks that explicitly recognize both parameter uncertainties and imperfect knowledge of the presence of infection. By working closely with USDA, we will ensure that we consider implementable control strategies, avoiding unnecessary testing of measures that are effective in theory but cannot be introduced in practice. We will also consider the cost effectiveness of control measures which may be dependent upon the location, spatial extent of infection and time of year.

Project Methods

Objective 1: All data collection efforts will follow strict data protocols that have been thoroughly vetted by our research team through past data collection activities. The data collection activities will be evaluated by quality control checks, adherence to the data protocols, and the successful use of those data for informing the development of our mathematical models (Obj. 3).US shipment data collection.A sample of 30% of the swine Interstate Certificates of Veterinary Inspection, and swine health plan agreement records from two recent years will be collected from a sample of 15 states that are important in the shipment network. The shipment data will be collated and cleaned following standard protocols published by this research team. The efforts from the compilation of the multi-year, multi-state shipment database will be shared with USDA, and each participating state will receive a state-specific cleaned dataset. We will analyze the multi-year, multi-state database using network statistics and a comparative analysis with 2010-2011 shipment data. These analyses will be used to inform the development and data incorporation of multi-year USAMM.Multi-year US Animal Movement Model (USAMM). We will incorporate a conditional autoregressive model structure into multi-year USAMM, such that when shipment data are sparse for a geographical area, statistical strength can be borrowed from nearby locations to improve the predictions. The updated USAMM model will be incorporated into the US Disease Outbreak Simulation (USDOS). Multi-year USAMM will be evaluated by validation analyses which will assess the ability of the model to make robust multi-year shipment predictions. The efforts from this objective will be updated multi-year swine shipment network predictions that will be published in a scientific journal and shared with the USDA.Additional data. We will work with USDA and state veterinary services to access data on HPAI infections. This infection data set will be used to parameterize the models (Obj. 3). US premises size and location data will be predicted by the Farm Location and Agricultural Production Simulator, which disaggregates data from the US Census of Agriculture, and will be updated using the most recent census. Genetic sequence data are readily accessible through GISAID and NCBI. Finally, economic data will be derived from several sources including primary analyses and secondary literature. These data collection efforts will produce data-informed parameters for modeling HPAI and will be evaluated through the modeling predictions and sensitivity analysis.Objective 2: Using tested methods and developing new methodology, we will use sequence data to better quantify the mechanistic processes that underpin transmission - in particular the spread between livestock and wildlife. Sequence data from infected farms will be analyzed and used to build phylogenetic trees to gain a better understanding of the within-farm dynamics. The trees will let us differentiate between single or multiple sources of invasion, and between slow long chains of infection or explosive outbreaks within farms. By examining the 'distance' between sequences collected over local scales we can ascertain transmission patterns between farms, and between cattle and the local environment and wildlife. The trees will provide a direct measure of transmission patterns that can inform our models. We will also use machine learning methods to look for relationships between genetic distances and the local environment. Identifying factors that correlate with genetic distance will suggest additional elements that impact transmission and may need to be included in models. Sequence data can also be used to suggest longer-range movements of infection between farms and other samples, which is likely to be key to the persistence of HPAI, allowing infection to jump to new susceptible areas. Throughout we will look for correlations between such identified long-range jumps and patterns of livestock movements or wild bird migration pathways, helping to identify which mechanisms are likely to be the most important for transmission to new areas. The efforts from Obj. 2 will be published in a scientific journal and will act as a template for how large-scale simulation models can be informed by sequence data. This objective will be evaluated by the successful completion of analyses at different spatial scales and the incorporation of those results to our models (Obj. 3).Objective 3: The development of the US model will include the integration of a robust, dynamic model for within-herd transmission based on the best available data. The US within-herd model will inform the development

of the within-herd component of the UK model. Both models will be updated includinga mechanism to capture transmission between cattle and wildlife, and other domestic hosts (poultry and swine) in any direction. Wildlife transmission will be added to the two modeling frameworks as new transmission mechanisms. The efforts from this objective will be published transmission models for the spread of HPAI between livestock and wildlife on the national scale for the UK and the US. The evaluation of these models will be done by how well the full models capture all the elements of data available. Throughout, we will holistically compare our model output against all available data. Objective 4: Working with the US and UK models in parallel, we will consider the likely dynamics and impact of HPAI on the livestock industry. Throughout we will generate projections under the null assumption that there is no change to local or national interventions, nor any changes to producer behavior. Short-term projections, which will be simulations over short timescales, will be used to calibrate the model, understand the main transmission processes and determine the locations with the highest probability of infection. Medium-term projections will be simulations covering a 3-6-month period and will be done to inform policy planning purposes. Finally long-term projections will be done to look at the long-term behavior of HPAI in livestock. The efforts from objective will provide bespoke spatial assessments of HPAI transmission in cattle farms in the US and UK, which will be published and used in visualization tools and reports to stakeholders. The results will be continually evaluated and refined to capture the changing nature of the HPAI outbreak.Objective 5: Our models will be modified to incorporate active surveillance and control strategies. For the US model, we will work closely with USDA to ensure that we consider region-specific capabilities to implement interventions and include the likely degree of compliance. The models will be used to analyze the impact of single and combined control measures, generating projections for the reduction in prevalence within different sectors of the cattle industry, and the likelihood of transmission from cattle to humans. We will also explore adaptive management intervention strategies and how implementing these may change the effectiveness of response. The results of these simulations will be evaluated using a cost effectiveness analysis, which will consider the direct and indirect costs associated with an outbreak. The efforts from Obj. 5 will provide evidence for policy makers regarding the effectiveness of intervention strategies and our cost effectiveness analysis will allow for a robust investigation of the value of each intervention policy in terms of reducing the impact upon the livestock industry as well as mitigating the risk of human cases occurring in the future. These results will be published in scientific journals and used to build visualization tools and reports for stakeholders.