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Contact tracing for the control of infectious disease epidemics: Chronic Wasting Disease in deer farms

Chris Rorres^{a,*}, Maria Romano^b, Jennifer A. Miller^c, Jana M. Mossey^d, Tony H. Grubestic^e, David E. Zellner^f, Gary Smith^a

^a Section of Epidemiology and Public Health, School of Veterinary Medicine, University of Pennsylvania, Kennett Square, PA, 19348, United States

^b Department of Epidemiology and Biostatistics, Drexel University School of Public Health, Bellet Building, 6th Floor, 1505 Race Street, Philadelphia, PA, 19102, United States

^c Department of Geography and the Environment, 1 University Station A3100, The University of Texas at Austin, Austin, TX, 78712, United States

^d Department of Epidemiology and Biostatistics, School of Public Health, Drexel University, Nesbitt Hall, 3215 Market Street, Philadelphia, PA, 19104, United States

^e Center for Spatial Reasoning & Policy Analytics, College of Public Service and Community Solutions, Arizona State University, Phoenix, AZ, 85004, United States

^f Bureau of Animal Health and Diagnostic Services, Pennsylvania Department of Agriculture, 2301 North Cameron Street, Harrisburg, PA, 17110, United States

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ABSTRACT

Contact tracing is a crucial component of the control of many infectious diseases, but is an arduous and time consuming process. Procedures that increase the efficiency of contact tracing increase the chance that effective controls can be implemented sooner and thus reduce the magnitude of the epidemic. We illustrate a procedure using Graph Theory in the context of infectious disease epidemics of farmed animals in which the epidemics are driven mainly by the shipment of animals between farms. Specifically, we created a directed graph of the recorded shipments of deer between deer farms in Pennsylvania over a timeframe and asked how the properties of the graph could be exploited to make contact tracing more efficient should Chronic Wasting Disease (a prion disease of deer) be discovered in one of the farms. We show that the presence of a large strongly connected component in the graph has a significant impact on the number of contacts that can arise.

1. Introduction

Epidemiologic contact tracing is an arduous and time-consuming process, but is important because timely interventions are well known to reduce the size and spatial scale of infectious disease epidemics. Methods that increase the efficiency with which contacts can be identified increase the likelihood that effective controls can be implemented sooner and thus reduce the magnitude of the epidemic. The 2013–2015 Ebola epidemic in West Africa demonstrated the danger of committing too few resources to contact tracing soon enough to be maximally effective (Auci, 2014).

Contact tracing is not limited to infectious disease epidemics in human populations; it is extensively used during infectious disease outbreaks of farmed animals. When an animal epidemic threatens a community of farms – and that epidemic is driven largely by the transport of animals between farms – some sense of the resources required for contact tracing together with concrete information on where surveillance should be focused can be gained by understanding the properties of the transport network. This will increase the efficacy of

the control effort by ensuring timely investigation or quarantine of at-risk farms. Allocating resources sufficient to the task is crucial to successful contact tracing

The rapid and frequent movement of animals between farms has become a prominent characteristic of modern animal agriculture throughout the world. Infected animals that are not obviously sick at the time of shipment can infect other animals on farms that are hundreds of miles distant from the source farm and these newly infected farms present a risk to other susceptible farms if they too ship stock out. Contact tracing in animal agriculture is used to trace where an infection may have come from and where it might have gone. Farms identified as contacts will undergo a voluntary or mandatory quarantine (depending on the disease) and will be monitored until declared disease free.

Recent experience of Foot and Mouth Disease and Highly Pathogenic Avian Influenza epidemics has heightened interest in—and demonstrated the utility of—using network theory to optimize strategies for surveillance and control (Rivas et al., 2012; Kao et al., 2006; Ortiz-Pelaez et al., 2006) of infectious disease epidemics in farmed animals. But most of this work has been carried out in regions where

* Corresponding author.

E-mail addresses: rorres@comcast.net, rorres@cs.drexel.edu (C. Rorres), maria.g.romano@aphis.usda.gov (M. Romano), jennifer.miller@austin.utexas.edu (J.A. Miller), jm55@drexel.edu (J.M. Mossey), grubestic@asu.edu (T.H. Grubestic), dzellner@pa.gov (D.E. Zellner), garys@vet.upenn.edu (G. Smith).

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animal movements are monitored and the location and nature of agricultural enterprises a matter of public record. The USA does not have a compulsory, national animal identification system that could track animal movement. This has necessitated the creation of synthetic farm maps and animal movement networks (Buhnerkempe et al., 2014; Bruhn et al., 2012).

Tracing contact farms is simplified by the voluntary registration of farm addresses (and production details) in spatial databases like the United States Animal Health Emergency Reporting Diagnostic System database (USAHerds). In particular, the Pennsylvania USAHerds database on the location, nature and movement between deer farms is almost unique in the USA in terms of its comprehensiveness. We used this database to create a network showing the pattern of movement of captive deer between farms in the Commonwealth of Pennsylvania. We were interested in how contact-tracing procedures could be made more efficient by a clearer understanding of this pattern of movement—and we used Chronic Wasting Disease as our example.

1.1. Deer farms in Pennsylvania

The deer industry in Pennsylvania depends upon a complex network of interstate and intrastate deer movement, and, together with hunting activities in the Commonwealth, contributes over \$100 million annually to Pennsylvania's economy (Pennsylvania Deer Farmers Association, 2007). Pennsylvania has over 1000 deer farms (breeding premises, hobby premises, shooting preserves and zoos and menageries) housing a variety of species: white-tailed deer, moose, elk, red deer, elk/red hybrid, sika deer, mule deer, and mule deer hybrid. We shall use the word “deer” to generically refer to all of these species and the word “farm” to refer to the various types of premises containing them.

1.2. Chronic Wasting Disease

Chronic Wasting Disease is a transmissible prion disease of free-ranging and captive deer (Centers For Disease Control And Prevention (CDC), 2017). In the United States, Chronic Wasting Disease was first noticed in 1967 in Colorado and has since spread eastwards as far as Pennsylvania. It has damaged the economy of many affected states. It affects both free-ranging and captive deer, and, like all prion diseases, it has a long incubation period—the time between infection and signs of disease is 18 months to 2 years (National Wildlife Health Center, 2017). It can be horizontally transmitted among deer either by direct (nose to nose) contact with infected animals, or by the ingestion of herbage or soil contaminated with the feces, urine or saliva of infected animals (Nalls et al., 2013). Infected free-ranging deer could transmit the disease to captive deer along fence lines and, given the continual shipment of deer between farms, an undetected introduction could rapidly spread to a great many farms, especially if several infected animals from a single affected farm were moved to several other farms in a single truck shipment.

1.3. The control of Chronic Wasting Disease in Pennsylvania

All farms housing susceptible farmed or captive deer in Pennsylvania must participate in the Pennsylvania Chronic Wasting Disease Program (Pennsylvania Department Of Agriculture, 2017). Even in the absence of detected Chronic Wasting Disease all deer farms must participate in annual Chronic Wasting Disease surveillance and inspection activities and must report all shipments into and out of the farm. It is these shipments that are recorded in the USAHerds database. Only that subset of herds that are deemed to have satisfied the requirements of “certification” under the program can import deer from other states and even then only after having obtained permits in advance to ensure the deer are being imported from areas presumed free of Chronic Wasting Disease. Herds that are not certified may not import or export deer across state lines. Following the detection of deer with

Chronic Wasting Disease in Pennsylvania in the fall of 2012, the Commonwealth created Disease Management Areas around the affected, quarantined farms, and increased surveillance with those areas to determine the extent of the outbreak (Pennsylvania Game Commission, 2017).

2. Data collection

Data consisted of 77,171 deer records on the location of deer farms, deer birth and deaths, and deer arrivals and departures from farms compiled from the Pennsylvania USAHerds database. The records begin in 1997, but because of certain uncertainties associated with the earlier portion of the database, we began our data set with October 14, 2003. The data provided to us ran to June 19, 2011, resulting in a derived dataset of duration 7.68 years.

With such a large data base, inevitably there were duplicate or ambiguous entries. For example, each of the 77,171 events was associated with a farm identified in three different ways: its address, premises ID, and latitude/longitude. But there were 1098 different addresses, 1139 different premises IDs, and 1125 different latitude/longitude pairs. By examining the intersection of these different identifiers we were able to extract 1090 unique farms, which we numbered 1–1090 in an arbitrary order. The majority (74.3%) of these farms had 20 or fewer deer.

All captive deer in Pennsylvania have a unique identifier so it was possible to record the movements of individual animals. For each shipment, the date of shipment and the origin or destination of the shipment were recorded. We focused on within-state shipments only. We assumed the permitting system was sufficient to prevent the importation of infected deer from out-of-state farms and, given our focus on Pennsylvania, we ignored shipments to other states. Our main assumption was that Chronic Wasting Disease would be introduced into a Pennsylvania deer by free-ranging deer and that the scale of shipments subsequently was so large that we could ignore all subsequent introductions.

Of the 77,171 individual deer records in the database, 40,650 were individual births or deaths of deer and so did not involve deer movement. The movement data were contained in the remaining 36,521 events, which were recorded as departures or arrivals of individual deer from or to specific farms on specific days. From these 36,521 movement events we ascertained 5269 individual deer transfers by finding deer that departed one farm and arrived at a different farm within 24 h during the 7.68-year period. These 5269 individual deer transfers took place among 1474 distinct ordered pairs of farms, an average of 3.6 deer transfers over the timeframe. These transfers, however, may have been over several individual shipments at different times.

We shall say that farm i is *connected* to farm j if the ordered pair (i, j) is among these 1474 ordered pairs of farms. Thus farm i is connected to farm j if at least one deer was transferred from farm i to farm j within 24 h during the 7.68-year period. There may, in fact, have been many deer transferred between two connected farms on different occasions in the same direction, but in our contact investigation we are interested in whether or not there was at least one deer transferred. There were 12 pairs of farms in which at least one deer was transferred between the two farms in both directions (usually a different deer on different days).

There were only 681 different connected farm among the 1090 farms; the remaining 409 farms had no recorded deer transfers from or to other farms during the 7.68-year period. Approximately 69% of all shipments were 50 miles or less, although some deer travelled up to 300 miles across the entire state.

It is a matter of common experience that the first farm in which a disease is detected, which we shall call the “first-case farm”, is rarely the index farm: the farm where the disease originated. Thus it is as important to try to identify which other farms have *already been infected* as it is to identify the farms that could be infected in the future by a first-case farm.

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