



Estimating the potential for disease spread in horses associated with an equestrian show in Ontario, Canada using an agent-based model



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ABSTRACT

Participation in equestrian shows provides opportunities for contact between horses, increasing the risk of disease introduction and spread within the population. The magnitude of a potential outbreak, and the impact of disease prevention and control strategies, can be estimated using simulation modeling. The objectives of this study were to (1) examine the potential spread of equine influenza in a network of horses associated with a 2-day equestrian show in Ontario, Canada; and (2) determine the effectiveness of several interventions during a simulated outbreak. A discrete-event, continuous-time, stochastic agent-based simulation model was constructed to represent horses associated with the show, including those in attendance at the show, and those that were not in attendance but co-boarded with attending horses at their home facilities. At the beginning of each simulation run, one random horse in attendance at the show was infected with equine influenza. In the absence of interventions, the median attack rate was 0.029 (IQR: 0.016–0.056; mean: 0.043; 95% CI: 0.040–0.044) and the average outbreak duration was 19.58 days (95% CI: 19.31–19.85). The most effective intervention was the implementation of either a 5-day or 14-day quarantine period, which both resulted in the same median attack rate of 0.0026 (IQR: 0.0013–0.0039), although the mean attack rates differed (mean: 0.0043, 95% CI: 0.0039–0.0046; and mean: 0.0029, 95% CI: 0.0028–0.0029; respectively). In instances where implementing either a 5-day or 14-day quarantine period would not be feasible, quarantine for shorter time periods was effective when combined with targeted increases in initial facility-level vaccine coverage. The combined implementation of a 2-day quarantine period and an increased vaccine coverage of 75% in facilities with four or more owners resulted in a median attack rate of 0.013 (IQR: 0.0052–0.026; mean: 0.022; 95% CI: 0.020–0.024). This study demonstrates a relative comparison of intervention effectiveness during a simulated outbreak of equine influenza in a population of horses associated with an equestrian show. The results have the potential to inform and improve the current strategies used to prevent the introduction and spread of disease within the equine population.

1. Introduction

The nature of equestrian sport and competition events brings horses from different boarding facilities into contact with each other. The mixing of horses at facilities which are unique to them provides opportunities for the potential introduction and spread of infectious diseases. There are several examples of large disease outbreaks that have been associated with horses attending equestrian shows (Morley et al., 2000; Satou and Nishiura, 2006; Traub-Dargatz et al., 2013). In 2007, equine influenza was diagnosed in a horse at a boarding centre in Australia, and the pathogen was subsequently spread throughout the country as horses travelled to attend equestrian shows and events (Moloney, 2011; Wong, 2011). In 2011, an outbreak of equine herpesvirus occurred after horses attended a national event, resulting in

subsequent spread in the USA and Western Canada (Traub-Dargatz et al., 2013). In 2016, an outbreak of equine influenza occurred in Atlantic Canada after horses attended various equestrian events during the fall fair season (MacPhee, 2016). While these examples provide insight into outbreaks linked to equine shows and events, the literature reports are biased towards outbreaks that have spread widely or which exhibited significant morbidity and/or mortality. Therefore, it is likely that there are also occurrences of smaller outbreaks that are not captured in the peer-reviewed literature, but might be of importance to horse owners or event organizers as they highlight the need for increased awareness of the risk of disease spread.

Retrospective analyses of outbreaks are beneficial to understand risk factors associated with disease spread for the development of disease control strategies (Firestone et al., 2011; Traub-Dargatz et al., 2013)

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and to improve outbreak preparedness (Garner et al., 2011b; Lewis et al., 2015). However, developing a more refined understanding of potential disease spread prior to an outbreak can lend support to disease management plans both before and after an equine event. Simulation models are tools that can incorporate known disease dynamics and underlying contact patterns to describe a potential outbreak in a population (McNab et al., 2011). Models can also be used to evaluate the effectiveness of disease interventions which may not be practical to test in the population of interest (Mishra et al., 2011). Models have been previously used in equine populations to understand disease dynamics (Glass et al., 2002; Satou and Nishiura, 2006; Daly et al., 2013), to characterize transmission of viral equine pathogens (Park et al., 2009; Hughes et al., 2012), and to evaluate equine disease control strategies (de la Rua-Domenech et al., 2000; Park et al., 2003; Baguelin et al., 2010; Garner et al., 2011a; Perkins et al., 2011; Rosanowski et al., 2016).

The objectives of this study were to (1) use an agent-based model to examine the potential for disease spread in a network of horses associated with a 2-day equestrian show in Ontario, Canada; and (2) evaluate interventions to determine their effectiveness in minimizing the extent of a simulated outbreak. Agent-based models allow for the description of autonomous “agents” in a population, which can include individual animals or locations. Agent-based models have been previously used to explore within-herd disease dynamics (Jiang et al., 2012; Robins et al., 2015), evaluate disease surveillance and control strategies (Lewis et al., 2015; Arruda et al., 2016, 2017), and describe interactions between animals, humans, and the environment (Chen et al., 2013; Havas et al., 2014). In this current study, an agent-based model was selected because it could describe a high degree of individual-level heterogeneity in the population, including variability in susceptibility, infectiousness, and contact patterns (Lanzas and Chen, 2015).

For the purpose of this study, we used equine influenza as a case study. Equine influenza is a respiratory disease caused by a highly contagious influenza A virus (Timoney, 1996). Equine influenza can be transmitted between horses through direct contact with respiratory droplets, and indirect transmission can occur through contact with fomites such as contaminated equipment (Landolt, 2014). Additionally, the natural history of equine influenza has been well-characterized through various challenge studies (Mumford et al., 1988; Newton et al., 2000; Park et al., 2004) and field observations (Cullinane et al., 2001; Newton et al., 2006; Gildea et al., 2013), making it an ideal candidate to use in our simulation.

2. Materials and methods

2.1. Study population

The study population consisted of horses associated with a two-day provincial-level sanctioned dressage show in southwestern Ontario, Canada in 2014 (Equestrian Canada, 2016). Data collection and descriptive characteristics of the study population have been previously described (Spence et al., 2017). To summarize, data on horse age, sex, vaccination status, and home facilities were collected from horse owners at the show using a questionnaire. There were 69 horses attending the show (referred to as “attending horses”), and questionnaire responses were received for 55 of the 69 horses (79.7% questionnaire response rate) (Spence et al., 2017). In the current study, horses that attended the show but whose owners did not complete the questionnaire (14/69 horses) were excluded from the population due to the absence of information on their potential contacts. From the questionnaire responses, an additional 710 horses (referred to as “non-attending horses”) were identified as residing at the 38 home facilities of the attending horses (Spence et al., 2017). The model was developed to replicate the observed contact network of the 765 horses (55 attending horses and 710 non-attending horses) (Spence et al., 2017).

2.2. Model description

A discrete-event, continuous-time, stochastic agent-based simulation model was constructed using AnyLogic 7.3.6 (XJ Technologies, St. Petersburg, Russia). AnyLogic is a Java-based simulation tool that supports multiple types of mathematical and simulation modeling (<https://www.anylogic.com>). The structure of AnyLogic is based on stock-and-flow diagrams and object-oriented language that governs how agents within a specified environment will behave. AnyLogic uses a continuous-time discrete-event scheduler, where model processes and agent interactions can be executed at any time as defined by the modeler. A copy of the model can be obtained from the corresponding author upon request.

The model described two types of agents: horses and locations. Horses were individual-level agents described by associated state variables, including their identification number, vaccination status, and disease status. Locations were represented as aggregating “collective agents”, which defined the connections between individual horses within a location at a given time. Locations included 38 home facilities (which housed both attending horses and non-attending horses) and 3 boarding locations at the competition venue (which housed only attending horses). The competition venue was comprised of three distinct areas where attending horses could be located: stabling barn #1 (SB1), stabling barn #2 (SB2), and the daily ship-ins (SI), located in a field at the venue.

2.3. Process overview

The model proceeded in daily time units and was run for 90 days. Horses executed a specific sequence of discrete-event processes that defined their individual contacts based on their associated location. At the beginning of the simulation (time $(t) = 0.0$), horses were located in their respective home facilities. One day later ($t = 1.0$), the attending horses travelled to the competition venue and were assigned to their boarding location, and therefore had a different group of horse contacts. There were 15 horses boarded in SB1, 20 horses boarded in SB2, and 20 horses in SI (Spence et al., 2017). Attending horses returned to their home facilities after two days ($t = 3.0$). This movement pattern describes a dynamic network where contact between horses occurs when they are present in the same location and contact ends once they are no longer in the same location. We assumed that all horses remained in their respective location (SB1, SB2, SI) at the competition venue for the entire duration of the show, and that all horses boarded at the individual home facilities remained in their location for the duration of the model simulation. The input data used to assign horses to their locations, and a schematic diagram that describes the horse contact patterns within each location, are provided as supplementary materials (Table S1 and Fig. S1).

2.4. Equine influenza infection

At the beginning of the simulation, one horse that was attending the show was randomly “infected” with a disease that exhibited the same natural history characteristics as equine influenza (Fig. 1). An attending horse was the index case in all simulation runs, as we assumed that this scenario represented the highest risk for continued spread within the larger population. The process of disease initialization (i.e. the infection of a randomly chosen attending horse) was stochastic, as a random seed was used for each simulation run.

The equine influenza disease process followed a susceptible-exposed-infectious-recovered (SEIR) design, while considering the differences in the natural history of the disease between unvaccinated and vaccinated horses (Fig. 1). Susceptible horses were assumed to have no immunity to equine influenza either as a result of vaccination or natural infection. We assumed that homogeneous mixing occurred within a location, so that all horses in the same location had an equal probability

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