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The use of social network analysis to examine the transmission of *Salmonella* spp. within a vertically integrated broiler enterprise

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ABSTRACT

To better understand factors influencing infectious agent dispersal within a livestock population information is needed on the nature and frequency of contacts between farm enterprises. This study uses social network analysis to describe the contact network within a vertically integrated broiler poultry enterprise to identify the potential horizontal and vertical transmission pathways for *Salmonella* spp. Nodes (farms, sheds, production facilities) were identified and the daily movement of commodities (eggs, birds, feed, litter) and people between nodes were extracted from routinely kept farm records. Three time periods were examined in detail, 1- and 8- and 17-weeks of the production cycle and contact networks were described for all movements, and by commodity and production type. All nodes were linked by at least one movement during the study period but network density was low indicating that all potential pathways between nodes did not exist. *Salmonella* spp. transmission via vertical or horizontal pathways can only occur along directed pathways when those pathways are present. Only two locations (breeder or feed nodes) were identified where the transmission of a single *Salmonella* spp. clone could theoretically percolate through the network to the broiler or processing nodes. Only the feed transmission pathway directly connected all parts of the network.

1. Introduction

Information on the nature and frequency of contacts between farm enterprises is essential to accurately understand factors influencing infectious agent dispersal within and between livestock populations. Social network analysis (SNA) provides an analytical framework for these data, allowing observed patterns of contact to be described and quantified. Social network analysis is a method of investigating the relationships between entities that make up a system. In a poultry enterprise, the entities are the locations (farms or production sites— hatchery or processing facilities) that make up the system and the relationships between them including the movement of commodities, equipment or people. The relationships that may link common entities create paths where endpoints may be indirectly linked to the origin. Indirect links are a powerful mechanism by which disparate parts of a system may affect or be affected by other network entities (Borgatti et al., 2013). Previous use of social network analysis techniques in poultry populations has largely been limited to identifying patterns of live bird movement that might influence the spread of avian influenza (Fiebig et al., 2009; Lockhart et al., 2008; Poolkhet et al., 2013). In these studies spatial and temporal resolution is focused to regional (Poolkhet et al., 2013; Sophie et al., 2012; Zhou et al., 2015) or national cross sectional studies (Dent et al., 2008, 2011; Sharkey et al., 2008) rather than targeted at daily movement patterns. A small number of notable exceptions have also included the movement of other poultry commodities (Fiebig et al., 2009; Lockhart, 2008). Identifying entity relationships and understanding the maximum potential geospatial range of livestock dispersal is important when investigating highly transmissible or emergency animal diseases where spread is rapid, the consequence of spread is high and disease control activities must be timely to prevent further dissemination. The topology, density and dynamic nature of network relationships are important in understanding how diseases may enter the system, how they might spread within it, and where to target surveillance and control activities. Through identifying

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possible transmission pathways, SNA allows surveillance and control strategies to be developed based on evidence rather than hypothesis (Garcia Alvarez et al., 2011; Green et al., 2008). The use of social network analysis to investigate other disease transmission dynamics within poultry populations has not yet been reported.

In Australia, salmonellosis in humans the second leading cause of foodborne illness and chicken meat is the second most frequently attributed source of illness. Chicken meat is the most frequently consumed meat in Australia with ~49 kg of meat consumed per capita per annum. The chicken meat industry is vertically integrated with a small number of companies producing all chicken meat. No fresh chicken meat or live birds are imported due to strict biosecurity requirements. The epidemiology of *Salmonella* spp. transmission within a poultry enterprise is complex, with vertical and horizontal pathways, multiple sources of the agent (including other animals, insects or feed) and multiple locations where both introduction and cross-contamination may occur (Barrow, 2000). Salmonellosis in poultry typically presents as an asymptomatic or subclinical disease. Control of salmonellosis requires multiple control strategies to be applied at different levels of the enterprise. Strategies for the eradication of host specific strains such as *Salmonella enterica* serovar Pullorum have been successfully implemented (NPIP, 2013) but have yet to be fully successful for non host-specific *Salmonella* serovars such as *Salmonella enterica* serovar Typhimurium (European Commission, 2003, 2009).

The aim of this study was to define the characteristics of the dynamic contact network within a vertically integrated chicken meat enterprise at a fine temporal resolution and to estimate the spread of a *Salmonella* spp. clone within the network in real-time. This increased understanding will enable potential patterns of *Salmonella* spp. transmission to be elucidated and thereby inform appropriate surveillance and control.

2. Materials and methods

2.1. Study population

The study population comprised the components of a single vertically integrated chicken meat enterprise in Australia, including pullet rearing and breeder production farms, hatchery, meat processing plants, contract broiler farms, contractors and feed mills. All sites where the movement of poultry or poultry products and external contractors or suppliers occurred within the system were identified.

2.2. Data collection, validity and verification

Between January 2013 and July 2014, daily movements were collated from routinely kept paper and electronic farm records. These records included daily production records, delivery dockets, and pick-up schedules. All data were collated into a standardized electronic format using Excel™ (Microsoft, 2011) and FileMaker Pro Advanced v13.0 (FileMaker, 2013). All data were verified at the time of entry by visual examination of records. After data entry, summaries were made using Tableau™ (Tableau, 2015), Excel™ (Microsoft, 2011) or R (R Development Core Team, 2007) to identify outliers, missing data, spelling errors or unusual data fields. Where an outlier or unusual event was detected, event details were clarified or corrected where necessary. Missing data that could be entered based on other available sources were included. Further requests for missing data were made if they were considered to comprise important observations.

2.3. Social network analysis

2.3.1. Network construction

From the daily production records locations associated with the movement of people, live birds, hatching eggs, feed, and litter delivery and removal were identified. In all networks, nodes represent geolocations where a movement of a poultry commodity or people was identified as occurring to or from, during the 18– month data collection period. Multiple sites within a single geographical location may be represented by a separate node for example truck washes, shower facilities or fumigation rooms. Each room or location (hatcher, setter or chick holding room) within the hatchery was modelled as a separate location where birds or eggs were held for significant periods of time or commodities followed different paths. These locations were selected as representing sites where the introduction of *Salmonella* spp. or mixing of poultry commodities or people could occur or control activities to limit the spread of disease may occur. Nodes were created to represent teams of people that moved as a unit such as vaccination or cleaning crews.

2.3.2. The contact network

A 17– week (121 days) contact network was constructed using Gephi v0.9.1 (Bastian et al., 2009) where the edges were formed from the daily movement between locations of the following:

1. Live birds — day old pullet chicks, point of lay pullet transfer, end of lay breeder depopulation, day old and market weight broilers
2. Hatching eggs — packing, fumigation, storage and transport to the hatchery, hatchery storage, setting, transfer and chick processing
3. Feed delivery — broiler, breeder production and pullet rearing
4. People — external contractors for cleaning, vaccination and pick-up crew movements. Movement of company employees between locations were not included
5. Manure removal and litter delivery

This study period was purposely selected to encompass the same period of time broiler field work was conducted and contained the most complete farm movement data for all commodity movement types. This period was equivalent to 2 broiler production cycles, one pullet rearing placement or ¼ of the annual production cycle. The date of movement was included to maintain temporal relationships between movements and locations.

2.3.3. Network analysis

From the 17-week time period a series of 17, 1– week, two 8– week and the entire 17– week time periods were examined to evaluate the temporal features of the network. In Australia, broilers are processed and sold fresh daily, with commodity sales occurring daily and production movements weekly. In this enterprise, a broiler production cycle – all broiler sites placed and subsequently processed, occurred every 8–10 weeks. In addition, from the complete 17-week network eight subnets were evaluated, one for each production type —breeder, hatchery and broiler, and movement type — feed, manure, people, chickens and hatching eggs.

For each contact subnet, descriptive metrics for network- and node-level parameters were calculated. All locations identified during the 18-month data collection period were used to calculate the number of nodes, number of connected nodes, number of directed movements, diameter, degree, mean path length, eccentricity, centrality, betweenness, clustering coefficient and density. Network modularity, community detection, weak and strong network components were also calculated. Communities are collections of highly inter-connected nodes. These interconnected

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