



## Exponential random graph models to evaluate the movement of backyard chickens after the avian influenza crisis in 2004–2005, Thailand

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### ABSTRACT

The aim of this study was to use exponential random graph models (ERGMs) to explain networks of movement of backyard chickens in provinces which had been hotspots for avian influenza outbreaks in Thailand during 2004–2005. We used structured questionnaires to collect data for the period January to December 2009 from participants who were involved in the backyard chicken farming network in three avian influenza hotspots (Ratchaburi, Suphan Buri, and Nakhon Pathom provinces) in Thailand. From 557 questionnaires, we identified nodes, points of entry and exit from nodes, and activities relating to backyard chicken farming and movement of chickens, and generated ERGMs based on non-festive periods (Model 1) and the Chinese New Year period (Model 2). In Model 1, *k*-star (the central node is connected to *k* other nodes) connections were predominant ( $P < 0.001$ ). In Model 2, the frequency of movement increased by 10.62 times, *k*-star connections were still predominant ( $P < 0.001$ ), and the model was scale-free. Hubs were formed from owners/observers in the arenas/training fields, farmers who raised chickens for consumption only, and traders. In conclusion, our models indicated that, if avian influenza was introduced during non-festive periods, the authorities would need to regularly restrict the movement of chickens. However, during high-frequency periods of movement of backyard chickens, authorities would also need to focus on the network hubs. Our research can be used by the relevant authorities to improve control measures and reduce the risk or lessen the magnitude of disease spread during an avian influenza epidemic.

### 1. Introduction

Throughout the last decade, avian influenza has proven to be an important disease, impacting on the global poultry industry and affecting human health. In Thailand in 2014, researchers estimated that avian influenza resulted in economic losses amounting to 1.5% of growth in gross domestic product (McLeod et al., 2005). Since then, the Thai authorities have been trying to implement long-term measures to control and prevent the disease. However, some parts of the poultry sector, such as backyard farms, are still high risk for disease spread, as this type of farming system has low biosecurity. According to the Department of Livestock Development (DLD) of Thailand, this farming system is still found throughout the country. Since 2010, the DLD has

continuously recorded the backyard poultry population, with more than 60 million birds raised in over 2 million households, according to the most recent report (Department of Livestock Development, Bangkok, Thailand, 2017). If the avian influenza virus was released into the agricultural system, backyard poultry farms would be a major source of epidemic disease.

Previous studies have reported that movement of infected backyard poultry is one of the key factors in disease spread (Poolkhet et al., 2013a,b; Wiratsudakul et al., 2014; Paul et al., 2015). Nevertheless, further study of the patterns of movement and uncertainty of behaviour of backyard farms is needed. A social network analysis using a dynamic exponential random graph model (ERGM) is a valuable tool for understanding movement behaviour. Modelling the network ties of an

**Abbreviations:** AIC, Akaike information criterion; BIC, Bayesian information criterion; DLD, Department of Livestock Development (Thailand); ERGM, exponential random graph model; GOF, goodness of fit; MCMC, Markov chain Monte Carlo; MCMCMLE, Monte Carlo Markov chain maximum likelihood estimation

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ERGM helps to understand the network’s structure (Lusher et al., 2012). ERGMs are probabilistic models with conditional probability of ties among the nodes (Kolaczyk, 2009), and are based on empirical data. Thus, an ERGM focuses on locally constructed tie formation, (Lusher et al., 2012) which fits the real data (Robins and Morris, 2007). For example, ERGMs have been used to predict directed trade networks in Bulgaria, Spain, and France (Relun et al., 2017). The researchers found that the configuration of edges determined predominant network behaviour. In addition, geographical location, production type, and farming system were key factors in trading (Relun et al., 2017).

The aim of our study was to evaluate the structure of dynamic networks using ERGMs, in order to supplement current knowledge of static networks of backyard poultry movement (Poolkhet et al., 2013b) (supplement). The models could then be used to predict avian influenza spread through backyard poultry systems in Thailand during festive and non-festive periods, and thus provide useful information to relevant authorities to improve preventative measures against the disease.

## 2. Material and methods

### 2.1. Study framework and data collection

This was a cross-sectional retrospective study from June 2010 to September 2011, using interviewer-completed questionnaires. We started data collection in the fighting arenas. A one-step snowball sampling method was implemented to all units (nodes) of interest (Table 1) that were summarised the data collected in the fighting arenas (Wasserman and Faust, 1994). In each node, we randomly selected more than 10% of the targeted population to complete the questionnaire. In cases where an answer indicated that there were links to locations outside of the study areas, we did not collect data on these locations. Yamane’s method was used to calculate the required sample size (Yamane, 1967). In total, we analysed data from 557 questionnaires.

We selected three provinces in Central Thailand (Nakhon Pathom, Ratchaburi, and Suphan Buri) which had been high-risk areas for avian influenza during 2004–2005 (Tiensin et al., 2005; Gilbert et al., 2006; Paul et al., 2011; Poolkhet et al., 2012). Participants were involved in backyard chicken farming within these areas (Table 1). As in our previous study (Poolkhet et al., 2013b), interviewers asked participants a series of open and closed questions relating to regular movement of backyard chickens (frequency of movement and number of connections) during the period January to December 2009, focusing

specifically on two scenarios: non-festive periods (Model 1) and the Chinese New Year celebrations (Model 2) (Table 1). Most questions were designed to identify nodes (including activities related to backyard chicken farming) and explain the points of entry and exit of movement of backyard poultry. We chose the Chinese New Year celebrations (end of January every year) for Model 2 because, during that time, the frequency and number of animal movements increases dramatically, as reported in a Vietnamese study (Minh et al., 2009), and it is possible that the pattern of connected networks changes.

### 2.2. Network properties

In both scenarios, the network was characterised by binary and unidirectional properties. The description of nodes and ties is presented in Table 1. The location of each node was recorded, including the name of the province, district, sub-district, and village. In cases where locations could not be identified, we grouped them as unidentified nodes.

### 2.3. ERGMs and statistical analysis

Data obtained from all participant questionnaires for each scenario were treated and transformed into two symmetrical matrices, which were used to generate two ERGMs. Data analysis started by exploring the observed network in both models. The number of nodes and ties, number of components (number of sets of connected nodes), network density (count of ties divided by the number of possible ties), clustering coefficient (the weight average of number of connected triples), and diameter (the longest geodesic distance between any pair of nodes) were presented using UCINET 6 software (Borgatti et al., 2002, 2013).

ERGMs were used to create simulated networks for each scenario. This was calculated for model comparison based on the observed data in this study, according to the following equations. Suppose  $G = (V, E)$  as a random graph. Let  $Y_{ij} = Y_{ji}$  as a binary random variable representing the presence or absence of a tie ( $e \in E$ ) between any pair of nodes  $i$  and  $j$  in  $V$ . The matrix  $Y = |Y_{ij}|$  is the adjacency matrix for  $G$ . The  $y = |y_{ij}|$  is designated to the specific recognition of  $Y$ . ERGMs is a model for the joint distribution of the member of  $Y$ . Thus, the probability mass function was expressed by the equation below (Kolaczyk, 2009):

$$\mathbb{P}_\theta(Y = y) = \left(\frac{1}{\kappa}\right) \exp\left\{\sum_H \theta_H g_H(y)\right\}$$

where  $H$  is the configuration (e.g. isolates, edges, or  $k$ -stars)

**Table 1**  
Description of node and tie.

List of nodes	Tie definition
Individual of <ul style="list-style-type: none"> <li>● Household that was raising backyard chicken (chickens raised for meat/eggs, fighting cocks, and miniature chickens called “bantams”)</li> <li>● Farmers</li> <li>● Animal keepers</li> <li>● Traders</li> <li>● Authorised or unauthorised slaughterhouses</li> <li>● Arenas</li> <li>● Training fields</li> <li>● Owners or observers at the arenas or training fields</li> <li>● Retail outlets for feed/drugs/eggs/equipment</li> <li>● Independent egg shops</li> <li>● Mills</li> <li>● Places selling wild birds</li> <li>● Fresh produce markets</li> <li>● Flea markets/supermarkets/chicken butchers</li> <li>● Chicken meat buyers at markets/butchers</li> <li>● Broiler farms</li> <li>● Layer farms</li> <li>● Veterinarians, public health volunteers, livestock volunteers</li> </ul>	<ul style="list-style-type: none"> <li>● All activities related to backyard chickens in the nodes that could possibly transmit the avian influenza virus to others and included events attended by people in the nodes who did not take their animals but who may have been exposed to chickens before entering or leaving the events.</li> <li>● In cases where the node connected to others outside of the study area, the tie was removed from the network. Trading was also included as a tie.</li> </ul>

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