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Analysis of a shrimp farming network during an outbreak of white spot disease in Rayong Province, Thailand

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ABSTRACT

This study used social network analysis with the aim of establishing the importance of units (nodes) of interest and to understand the network characteristics of shrimp farming during an epidemic of white spot disease (WSD) in the Rayong province of Thailand. A case–control study at the farm-level was carried out from October 2014 to May 2015. A total of 165 questionnaires from all active farms were used for data analysis. Among the active farms used in the sample, network data from 38 case-farms and 127 control-farms were analyzed, and risk factors were determined. We found that farm visitors and post-larvae (PL) provider companies are significant factors ($P < .05$). Given these findings, we recommend that farmers control WSD by obtaining PL only from reliable sources and regulating farm visits to prevent the spread of WSD. These measures can help farmers effectively reduce the risk of WSD occurrence and spread.

1. Introduction

White spot syndrome virus (WSSV) is the pathogen that causes white spot disease (WSD), which often occurs in shrimp farming. WSSV is a contagious virus that affects aquatic crustaceans including whiteleg shrimp (*Penaeus vannamei*) and black tiger shrimp (*Penaeus monodon*) (OIE, 2016). The virus spreads through hosts, which are often penaeid shrimp, as these shrimp are highly susceptible to WSSV. Infection causes a high mortality rate among affected shrimp (Nunan et al., 2001; OIE, 2016). Shrimp are commonly identified as being infected with the virus by a white spot that appears on the exoskeleton (OIE, 2016).

The first reported case of WSD was in Taiwan in 1992 (Chou et al., 1995). Today, the disease has spread to many parts of the world, specifically in Asia and the Americas (Flegel and Alday-Sanz, 1998; APHIS, 1999; Mcclennen, 2004; Walker and Mohan, 2009). Previous studies have determined that major risk factors associated with WSD include the introduction of infected water or an infected carrier into the farms (Rajendran et al., 1999; Flegel, 2006; Waikhom et al., 2006). This has indicated that the movement of feed, humans, or post-larvae (PL) shrimp can introduce the virus into farms. Studying the movement patterns of these entities during the disease outbreak can broaden our knowledge regarding how the disease enters into and spreads throughout a farm.

Many researchers have used social network analysis (SNA) to describe the pattern of infectious diseases in human and animal medicine (Ortiz-Pelaez et al., 2006; Poolkhet et al., 2013; Mulawa et al., 2016; Saldanha et al., 2016). In aquaculture, Green et al. (2009) showed that the SNA technique is useful for obtaining information that can broaden understanding of the behavior of network elements. This knowledge can facilitate the implementation of an effective surveillance system to monitor diseases among aquatic animals. Cañon Jones et al. (2010) also used SNA to analyze the causes of fin injury in salmon, finding that the aggressive behavior of Atlantic salmon during feeding time results in fin damage. Yatabe et al. (2015) described a network of live fish in Ireland, and found that the network presented small-world and scale-free characteristics, indicating a very dense network with dominance by some actors. These attributes are conducive to risk-based surveillance of infectious diseases in fish. Recently, Haak et al. (2017) used a network model to assess the possible transmission of diseases from a non-native snail species in the United States, and found that anthropogenic movement is leading to an increase in the non-native snail species *Bellamya chinensis*, which can transmit diseases to native species.

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In order to determine the possible source of infection, we use SNA to establish the importance of units (actors or nodes) of interest and to understand the network structure of shrimp farming during the occurrence of WSD in the Rayong province of Thailand. From the collected data, we can determine the disease pattern of WSD and thus better understand how WSD behaves. Moreover, this information will help the relevant authorities to develop and/or improve control measures for WSD in this context and other related areas.

2. Materials and methods

2.1. Study framework

For data collection, a case–control study at the farm-level was carried out from October 2014 to May 2015 to determine the risk of WSD in the Rayong province of Thailand. A total of 165 questionnaires from all active farms were used for data analysis. To obtain the data, 38 and 127 questionnaires were administered to 38 case-farms and 127 control-farms respectively. Case-farms were farms that demonstrated the following clinical signs of WSD: moribund shrimp or living shrimp with white spots on the exoskeleton, a decrease in food consumption, and a surge in mortality rate (OIE, 2016). Infection of the suspected shrimp was confirmed using WSSV strip-test kits (EnBiotech Laboratories, Japan; sensitivity = 34.7%, specificity = 100%). Control-farms were those that presented shrimps without the clinical signs of WSD and no evidence of other abnormal signs such as high mortality rate and/or decrease of feed consumption ratio until the end of the production cycle. For the farms where clinical signs of WSD in the shrimp were unclear or where there were some abnormal shrimp, classification as case-farms or control-farms was made using the results of WSSV strip-test kits and/or polymerase chain reaction methods (OIE, 2016). In accordance with our experience of WSD occurrence in Thailand, we assumed in this study that each farm was homogenous for WSD appearance or disappearance. For data analysis, based on dependency data, descriptive SNA and conditional logistic regression were used to find the important nodes and risk factors of WSD.

2.2. Questionnaire and network components

The questionnaire was composed of open-ended and closed questions. The questions were reviewed by one epidemiologist and two aquaculture scientists for accuracy. The questions focused on production index, abnormal signs in shrimp, source and destination of possible movable vectors and carriers, and the presence of possible animal carrier and risk factors associated with WSD (MPEDA/NACA, 2003; OIE, 2016) during the production cycle. In this study, individual farms were designated as receiver nodes. Each of the PL provider companies (nominal data; 43 companies), sources of culture water (nominal data; canal-, ground-, river-, sea-, surface-water), feed provider companies (nominal data; 16 companies), visitor types (nominal data; aquaculture sales representative, feed vehicle drivers, fisheries, biologists, more than one type of visitor), and the presence of any birds, cats, crabs, dogs, or rats as possible animal carriers (binary data; not found, found) on the farm were designated as sender nodes. Ties, which indicate a relation between sender and receiver nodes, were defined as PL or feed delivery activities, introduction of water into the farm, visitors to the farm, or the presence of any animal carriers. In this study, it is possible that WSSV can spread through these connections.

2.3. Network properties and data analysis

Networks of shrimp farming were analyzed using a static, binary, non-valued, and non-symmetrized method (Hanneman and Riddle, 2005; Borgatti et al., 2013). Common statistical measures (Table 1) of descriptive network analysis were calculated using Ucinet6 (Analytical Technologies, USA). In this way, the centrality values were analyzed using a randomization unequal *t*-test with 1000 iterations using NCSS 11 (NCSS 11, 2016). The box-whisker plots of centrality values were presented by grouping case-farms and control-farms using R 3.3.2 (Core Team, 2016). For defined risk factors, each type of node (sender nodes or independent variables) connected to the farm (WSD status: dependent variables) was assigned both variables and analyzed their relationship by an asymptotic Pearson's chi-squared test using the R package “coin” (Hothorn et al., 2008). Factors with a significance level of 5% alpha error were selected and tested by conditional logistic regression with Breslow's method using NCSS 11. In this step, the proportion of case-farms to control-farms was 1:3 ($n = 38$ and $n = 114$, respectively). Thirteen of the farms in the control-farm group were randomly removed from the data to comply with the 1:3 proportion. This analysis was performed with 1000 iterations.

3. Results

3.1. General information

The 165 interviewees were either farm owners (132, 80.00%) or managers (33, 20.00%) who lived in Rayong province. Most of the interviewees were men (n = 153, 92.72%). Almost all farms (n = 163, 98.79%) raised only the shrimp species *P. vannamei*, while two farms (1.21%) raised only the shrimp species *P. monodon*. The median number of active ponds was three (minimum = 1, maximum = 18). The average shrimp stocking rate was 72 units/m^2 (SD = 25.28).

PL were sent to farms from 43 hatcheries located in various provinces. PL were sent mostly from Trad (n = 76, 46.06%), Chachoengsao (n = 53, 32.12%), and Chonburi (n = 34, 20.61%). A few hatchery sources were located in Chumphon, Rayong, and Songkla. The average stage of PL was 12 (minimum = 10, maximum = 18). As their source of culture water, farmers used river-water (69, 41.82%), canal-water (58, 35.15%), and seawater (36, 21.82%). Only two farms used ground- or surface-water.

Sixteen companies provided feed to the shrimp farms during the study. Most of the feed companies delivered their products to the farms by truck through a local agency in Rayong or in neighboring provinces such as Chanthaburi. Only one company delivered their product by motorcycle through a local agency in Rayong province. In this way, feed delivery-vehicle drivers visited the farms during the delivery period (115 times). Other visits to the farms were by aquaculture sales representatives (83 times), and Department of Fisheries staff and private sector fishery biologists (127 times). There were only 32 farms (19.39%) that had no visitors during the study.

Regarding the presence of possible disease carriers in farms, 104 (63.03%) farms reported sightings of birds such as cormorant, egret, kingfisher, sparrow, or teal. The presence of domestic animals such as dogs or cats was reported in 112 (67.88%) and 23 (13.94%) farms, respectively. Rats were reported to appear in only 18 (10.91%) farms, while crabs (usually Thai vinegar crabs) were reported to appear in 88 (53.33%) farms.

3.2. Network analysis

3.2.1. Descriptive network analysis

The data from the 165 questionnaires shows the network as having 235 nodes and 1142 ties (78 nodes and 273 ties for case-farms, 185 nodes and 869 ties for control-farms). Table 2 shows that the means of indegree and outdegree centrality for all nodes were 0.011 (SD = 0.008) and 0.010 (SD = 0.040), respectively. In this way, only the indegree centrality of case-farm networks was greater than that of control-farm networks with statistical significance ($P < .05$). The means of in- and out-closeness centrality for all nodes were 0.505 (SD = 0.004) and 0.506 (SD = 0.025), respectively. Moreover, only in-closeness centrality of case-farm networks was greater than control-farm networks with statistical significance. The mean of proximal