Emerging infectious diseases may spread across pig trade networks in Thailand once introduced: a network analysis approach

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REGULAR ARTICLES

Emerging infectious diseases may spread across pig trade networks in Thailand once introduced: a network analysis approach

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Abstract

In Thailand, pork is one of the most consumed meats nationwide. Pig farming is hence an important business in the country. However, 95% of the farms were considered smallholders raising only 50 pigs or less. With limited budgets and resources, the biosecurity level in these farms is relatively low. Pig movements have been previously identified as a risk factor in the spread of infectious diseases. Therefore, the present study aimed to explicitly analyze the pig movement network structure and assess its vulnerability to the spread of emerging diseases in Thailand. We used official electronic records of nationwide pig movements throughout the year 2021 to construct a directed weighted one-mode network. Degree centrality, degree distribution, connected components, network community, and modularity were measured to explore the network architectures and properties. In this network, 484,483 pig movements were captured. In which, 379,948 (78.42%) were moved toward slaughterhouses and hence excluded from further analyses. From the remaining links, we suggested that the pig movement network in Thailand was vulnerable to the spread of emerging infectious diseases. Within the network, we found a strongly connected component (SCC) connecting 1044 subdistricts (38.6% of the nodes), a giant weakly connected component (GWCC) covering 98.2% of the nodes (2654/2704), and inter-regional communities with overall network modularity of 0.68. The disease may rapidly spread throughout the country. A better understanding of the nationwide pig movement networks is helpful in tailoring control interventions to cope with the newly emerged diseases once introduced.

Keywords Animal movement · Community detection · Connected component · Network analysis · Trade network

Introduction

In Thailand, pork is one of the most consumed meats nationwide. In 2018, pork consumption was estimated at 10 kg per capita (FAO, 2016). Pig farming is hence an important business in the country. In total, 9,886,897 pig heads were notified in the database of the Department of Livestock Development (DLD) in 2015. These pigs were reared in 191,289 households, of which 95% were considered smallholders raising only 50 pigs or less (Department of livestock development, 2016). With limited budgets and resources, the biosecurity level in these farms is relatively low. Infectious diseases may attack the farms easily. Evidently, outbreaks of several infectious diseases were previously recorded in the Thai pig population. For instance, different lineages of porcine reproductive and respiratory syndrome viruses (PRRSV) have been separately introduced into Thai pig production systems on different occasions and remained co-circulated ever since (Tun et al., 2011). It is likely that other exotic pathogens, like African swine fever (ASF), may also behave like PRRSV.

As an example, ASF is caused by the only vector-borne DNA virus and transmitted by soft ticks, which belong to the genus *Ornithodoros* (Burrage, 2013; Galindo and Alonso, 2017). However, the virus can also spread by the means of direct contact through oral-nasal routes or

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ingestion of infected materials such as blood, feces, and urine (Dixon et al., 2019). Besides, the virus was observed as aerosol over a short distance (Olesen et al., 2017). These various routes of viral transmission make ASFV highly contagious once invading a naïve population. In January 2022, ASFV was first notified in Thailand (OIE, 2022). A better understanding of the nationwide pig movement networks is helpful in tailoring control interventions to cope with such newly emerged epidemics.

The movements of pig and pig products play an important role in the spread of emerging infectious diseases. A study in Europe indicated that the movements of wild boars and the trade of pigs and their products were important risk factors of the ASF transmission in the region (Taylor et al., 2020). A previous study constructed an epidemiological model and suggested that the ASFV was likely to be introduced from a free-range herd and spread across the pig trade network in France (Andraud et al., 2019). This indicates the vulnerability of the trade network to the spread of any emerging infectious diseases, not limited to only the ASF.

Network analysis is a branch of study emerging from social science. This approach has been recently becoming more popular in veterinary epidemiology. It has been used in the study of animal movement patterns in different species, for example, pig (Salines et al., 2017), goat (Chintrakulchai et al., 2017), cattle (Notsu et al., 2020), and chickens (Wiratsudakul et al., 2014). These studies intended to capture the key actors in the network and link with the risk of disease occurrences such as foot-and-mouth disease (Wiratsudakul and Sekiguchi, 2018), avian influenza (Sun et al., 2018), and African swine fever (Lichoti et al., 2016).

Therefore, the present study aimed to explicitly describe and analyze the pig movement network structure at subdistrict and provincial levels, as well as assess its vulnerability to the spread of emerging infectious diseases once introduced into Thailand.

Methods

Network analysis at the subdistrict level

We used official electronic records of pig movements in Thailand, from January 1 to December 31, 2021, to cross-sectionally illustrate how pigs were distributed across the country. Briefly, Thai DLD has designed an electronic system to capture all movements of livestock species including pigs. An online form must be filled out once animals are translocated between subdistricts and provinces. The subdistricts (a smaller administrative subunit of the province) of origin and destination are recorded in each transaction. These movement data are centrally stored in the DLD database. We filtered the pig movements and used them in our

analysis. In this study, we excluded all links toward slaughterhouses as these were dead-end.

A directed weighted one-mode network was constructed. A node represents a subdistrict, in which the pigs were moved in and out. In this nationwide pig movement network, a total of 484,483 pig movement activities were identified throughout the year 2021. After excluding slaughterhouses, we had 104,535 remaining trade activities for further analysis. Ultimately, our network contained 2704 nodes (unique subdistricts) with 11,688 unique links (Fig. S1 of Supplementary Material 1). No missing data were found in our dataset as these were included in the obligatory fields of our electronic recording system. Additionally, the data are mandatorily requested following our legal requirements for the permission of animal movements. The node was weighted by the aggregated number of movements in and out of the subdistrict within the year 2021. Degree centrality was calculated for both subdistrict and provincial levels with the formula $D_i^W = \sum_{j \in \Pi(i)} W_{ij}$, where D_i^W denotes the weighted degree of node i, W is the frequency of pig movement between node i and node j, and node j is a contact member of node i ($\Pi(i)$). The power-law degree distribution, $P(k) \sim k^{-\gamma}$, was fitted to the degree distribution with maximum likelihood method to assess the scale-free properties of the network. The parameter $P(k)$ represents a fraction of nodes with k degree. The parameter γ indicates the degree exponent (Barabási et al., 2001; Barabasi, 2009) that lied between 2 and 3 (May, 2006). We assessed the presence of both weakly and strongly connected components. The network was divided into subgraphs based on a random walk algorithm to explore the emergence of the network community. Then, the network modularity was calculated.

Network analysis at the provincial level

To ease the visualization, we aggregated the pig movement network from the level of subdistrict to the provincial level. Weighted degree centrality was also aggregated accordingly. Additionally, we mapped the community at this level after the largest network community was detected.

All network analyses were performed with the functions equipped in package "igraph" version 1.2.7 (Csardi and Nepusz, 2006) in R version 4.1.2 (R core team, Vienna, Austria). All network parameters used in our study are defined in Table 1.

Results

Network analysis at the subdistrict level

The node distribution and the relevant weighted degree centralities are shown in Table 2. The region with the

Table 1 Definition of network parameters

Parameter	Definition	References
Weighted degree centrality	Number of nodes that are immediately connected to the focal node which is weighted with a certain quantifiable attribute. Here, we weighted the node with the aggregated number of movements in and out of that node during the study period	(Opsahl et al., 2010)
Weighted in-degree centrality	The weighted degree centrality in which only the incoming connections are counted	(Opsahl et al., 2010)
Weighted out-degree centrality	The weighted degree centrality in which only the outgoing connections are counted	(Opsahl et al., 2010)
Strongly connected components	A subset of a directed graph in which all the nodes are mutually reachable through directed links	(Kao et al., 2007; Passafaro et al., 2020)
Weakly connected components	A subset of a directed graph in which all the nodes are mutually reachable regardless of the direction of the links	(Kao et al., 2007; Passafaro et al., 2020)
Network community	A subgraph in which the nodes are densely grouped but sparsely connected to the outsiders	(Newman, 2016)
Network modularity	A fraction of links observed within communities minus those expected in a null model e.g., an equivalent randomly connected network	(Newman, 2006; Chen et al., 2018)

Table 2 Weighted degree centrality of the subdistricts, divided by regions in Thailand

Region	Number of subdistricts	Weighted degree centrality				
		Mean	Median	IQR	Min	Max
Central	555	72.3	17	4–60	1	1373
East	224	112.1	19.5	6–125	1	1425
North	309	68.91	15	3–57	1	1918
Northeast	965	72.4	11	3–43	1	4962
South	470	66.1	11	3–50	1	3093
West	181	104.5	23	5–89	1	1526

highest pig movement activities based on median weighted degree centrality was the west followed by east, central, north, northeast, and south, respectively. The node with the highest weighted degree centrality was identified in the northeastern region at Kham Ahuan subdistrict, Mueang district, Mukdahan province (Geocode: 490110) at 4962.

After assessing the power-law degree distribution, we found the degree exponent of 3.62 which was located outside the expected range. The network, hence, was not likely scale-free. The power-law fitted on the cumulative degree curve is shown in Fig. 1. In this network, a total of 1658 strongly connected components (SCC) were detected. In which, a large SCC connecting 38.6% of the nodes (1044/2704) was found. In contrast, a giant weakly connected component (GWCC) containing 2654 subdistricts (98.2% of the nodes) and 11,660 weighed connections were observed (Fig. 2). In total, 24 WCCs were identified. In the community detection, a total of 492 communities were captured, and the modularity was calculated at 0.68.

The largest community together with the two runners-up are illustrated in Fig. 3.

Network analysis at the provincial level

Figure 4 demonstrates how pigs were spatially shipped between provinces in Thailand. The movement network covered all 77 provinces of the country. The highest overall movement and moving-in activities were observed in Nakhon Ratchasima province with the weighted degree centrality of 864 and 398, respectively. On the other hand, the largest out-degree centralities were found in Phatthalung provinces at 536. The top five provinces regarding weighted degree centrality values are depicted in Table 3.

At the provincial level, we mapped the largest community (Fig. 3A) to visualize the spatial distribution of the community across regions of Thailand (Fig. 5). This community covered 61.0% of the provinces (47/77) with 228 weighted connections.
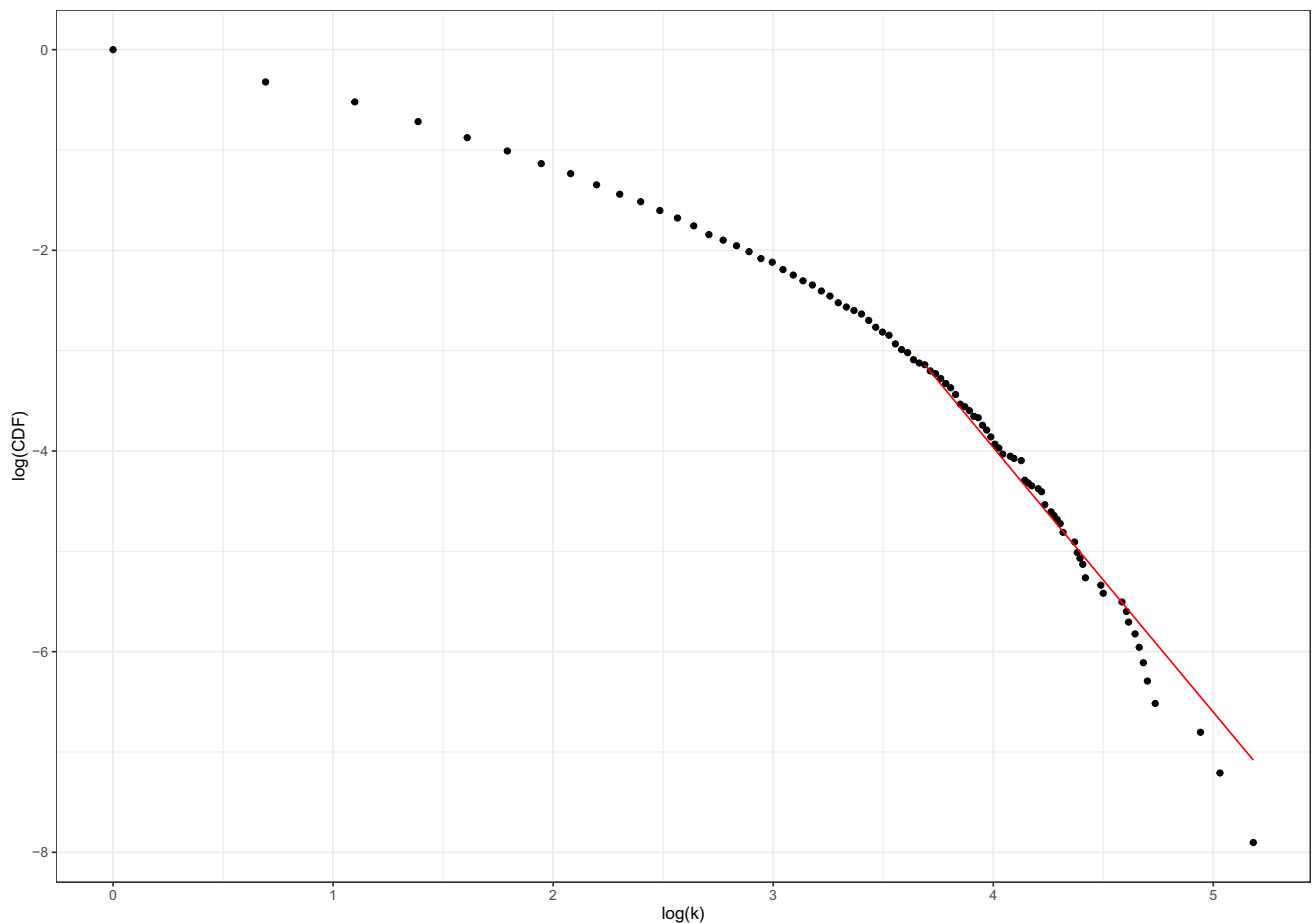
Fig. 1 The power-law (red line) is fitted on the cumulative distribution function (CDF) curve of the node degree at the subdistrict level

Discussion

The pig movement network covered all regions in Thailand (Fig. S1). Nevertheless, subdistricts involved were mainly identified in the northeastern region and the central plains (Table 2). At the provincial level, the high volume of pig movements involved different central provinces (Nakhon Pathom, Suphan Buri, and Lop Buri) and other provinces located in the northeast (Nakhon Ratchasima and Khon Kaen), the south (Phatthalung and Nakhon Si Thammarat), and the east (Prachin Buri) (Table 3; Fig. 4). Indeed, many provinces in the central region reached their reputation for pig producing capacity, as reflected by the weighted degree centrality. Undoubtedly, the prevalence of several swine diseases was remarkably high in the area, for examples, porcine reproductive and respiratory syndrome (Thanapongtharm et al., 2014; Jantafong et al., 2015; Olanratmanee et al., 2015), porcine epidemic diarrhea (Puranaveja et al., 2009; Temeeyasen et al., 2014; Cheun-Arom et al., 2015), and swine influenza (Nonthabenjawan et al., 2015). Therefore, any emerging infectious diseases are hard to be eradicated from this region once introduced.

At the subdistrict level, the highest degree centrality was found in a subdistrict located in a northeastern province, namely Mukdahan. The province is found along the border of Thailand and Laos PDR. Besides, Nakhon Ratchasima, the province with the highest overall weighted degree centrality, is also located in this region. Nakhon Ratchasima may act as a hub in the region supplying pigs to other provinces including Mukdahan and the pigs may be further shipped elsewhere, probably to other neighboring countries. Nonetheless, we only focused on the domestic movements of the pigs. A future study exploring the transboundary movements is highly recommended. The highest weighted out-degree centrality was observed in Phatthalung province, located in the south (Table 3; Fig. 4). Given that the province is located in the lower south, it may also act as another regional hub serving the pigs to other nearby provinces in this region. Holistically, the central plain was the national hub for pig production and the pigs were distributed through some regional hubs across the country. With limited manpower and resources, the implementation of disease prevention and control should be prioritized in these regional hubs as well as the movements across borders in these areas.
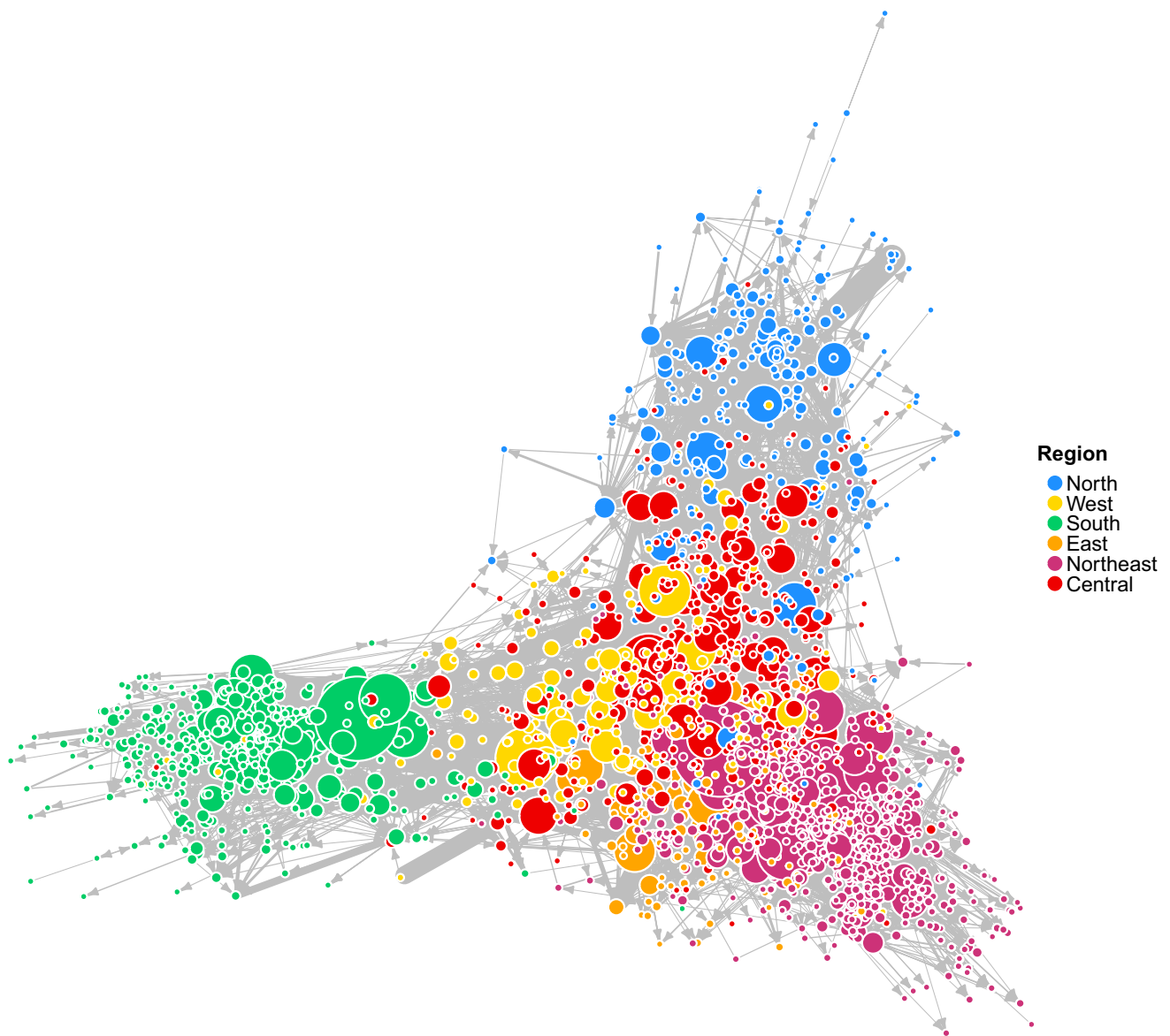
Fig. 2 A giant weakly connected component (GWCC) identified in the network (#node: 2654, #link: 11,660). The node size is proportionate to degree centrality, calculated from the number of connected subdistricts during the study period. The arrowhead represents the direction of animal movements. The width of the link shows the relative frequency of the movements between the subdistrict of origin and that of destination

Focusing on the network structure, the trade network was vulnerable to the spread of infectious diseases. Even though the scale-free characteristics were not observed (Fig. 1), we found a large SCC and a GWCC in the network (Fig. 2). A scale-free network is characterized by a disproportionate fraction of high degree centrality nodes and a flat tail degree distribution. The scale-free properties were observed in various complex networks such as World Wide Web (WWW), protein interactions, and social connections (Barabasi, 2009). Epidemiologically, super spreaders may arise from those highly connected nodes (Liu and Zhang,

2011). This network structure was found to facilitate the spread of many viral diseases, for example, HIV/AIDS (Schneeberger et al., 2004) and avian influenza (Small et al., 2007). Within the network, even low virulent pathogens can rapidly spread (Barabasi, 2009). Thus, it is worth assessing in any large-scale network. However, the vulnerability of this nationwide pig movement network was evidenced by the occurrence of GCCs. Such network subgraph was found in some other animal movement networks, for instance, a cattle trade network in Cambodia (Poolkhet et al., 2016), live bird market connections in Mali (Molia et al., 2016),
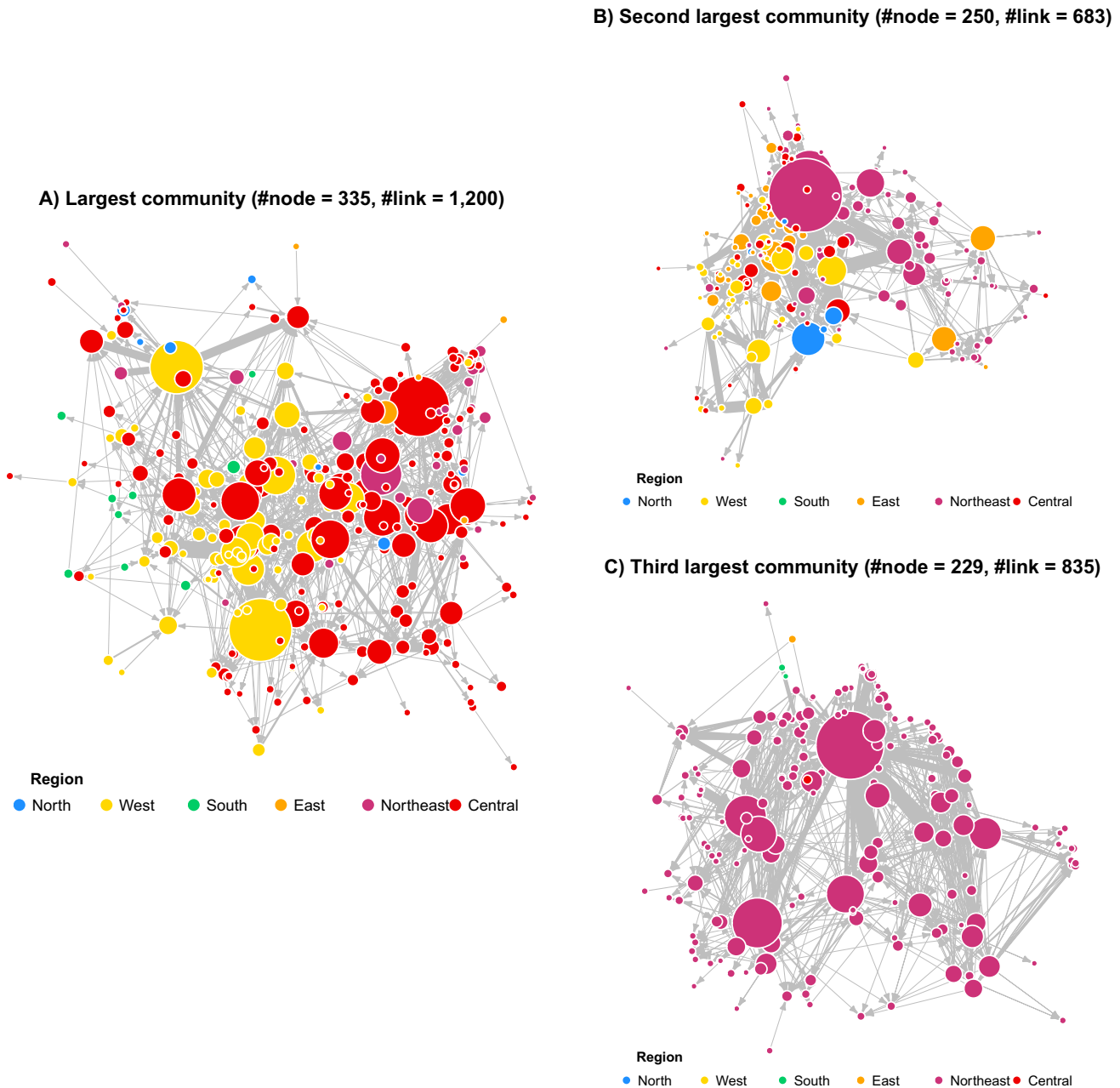
B) Second largest community (#node = 250, #link = 683)

A) Largest community (#node = 335, #link = 1,200)

Region
● North   ● West   ● South   ● East   ● Northeast ● Central

C) Third largest community (#node = 229, #link = 835)

Region
● North   ● West   ● South   ● East   ● Northeast ● Central

Fig. 3 The top-three largest communities (**A–C**). The node size is proportionate to degree centrality, calculated from the number of connected subdistricts during the study period. The arrowhead represents the direction of animal movements. The width of the link shows the relative frequency of the movements between the subdistrict of origin and that of destination

and ostrich production system in South Africa (Moore et al., 2014). The size of a GWCC was previously employed to estimate the upper bound of maximal epidemic size (Kiss et al., 2006; Dubé et al., 2008). Provided that our GWCC covered most of the nodes present in the network, infectious diseases may spread rapidly throughout the trade chain causing dramatic nationwide outbreaks. Early detection is crucially important for preventing the emergence of exotic diseases in such a vulnerable network. Advanced technology

such as artificial intelligence should be integrated to accelerate the disease detection process (Oeschger et al., 2021).

Fig. 4 Spatial distribution of the pig movement network in Thailand ▶ at the provincial level. The node size is proportionate to weighted degree centrality, calculated from the aggregated number of movements in and out of the province during the study period. The arrowhead represents the direction of animal movements. The width of the link shows the relative frequency of the movements between the province of origin and that of destination
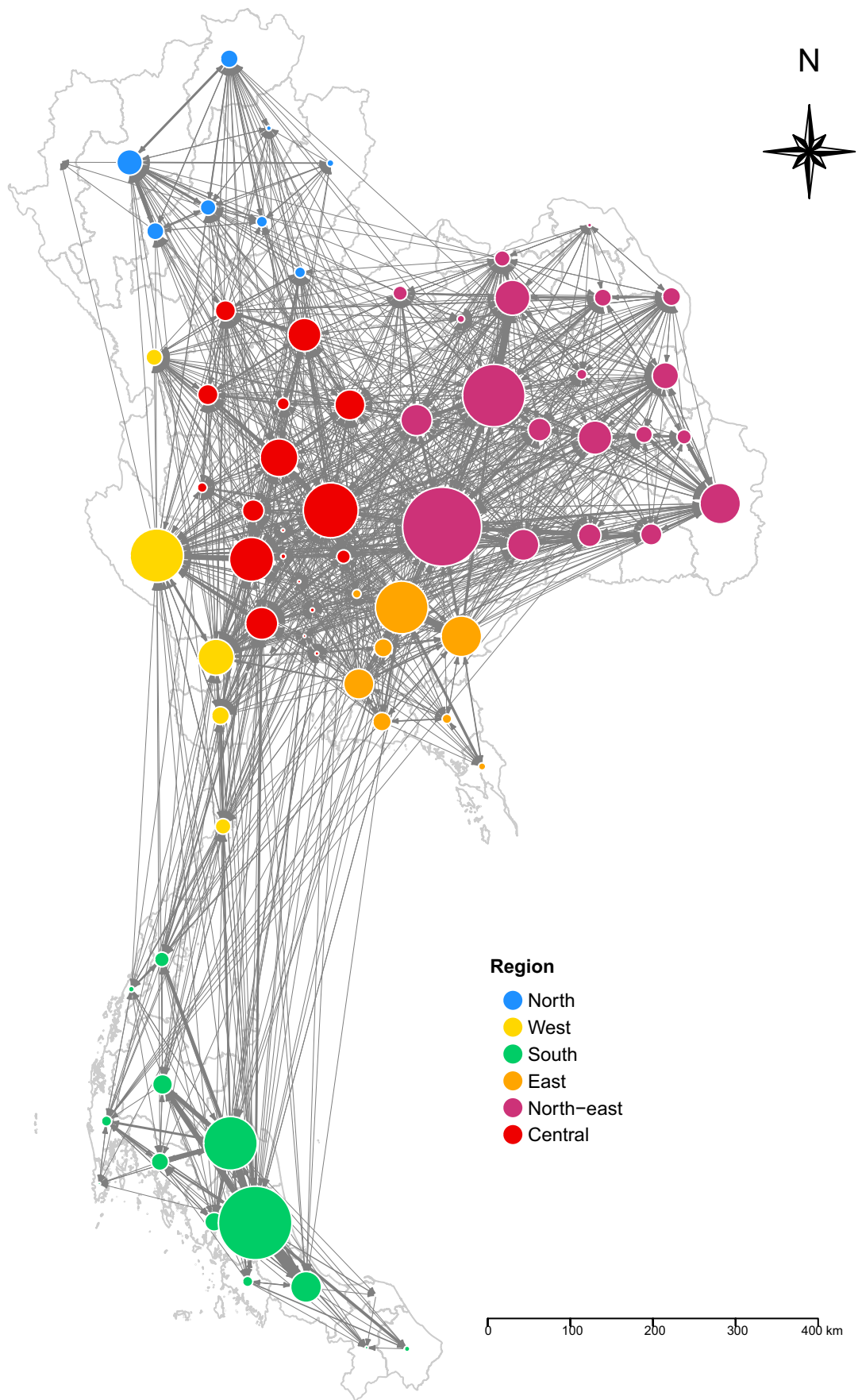
Table 3 The top five provinces for weighted degree centralities

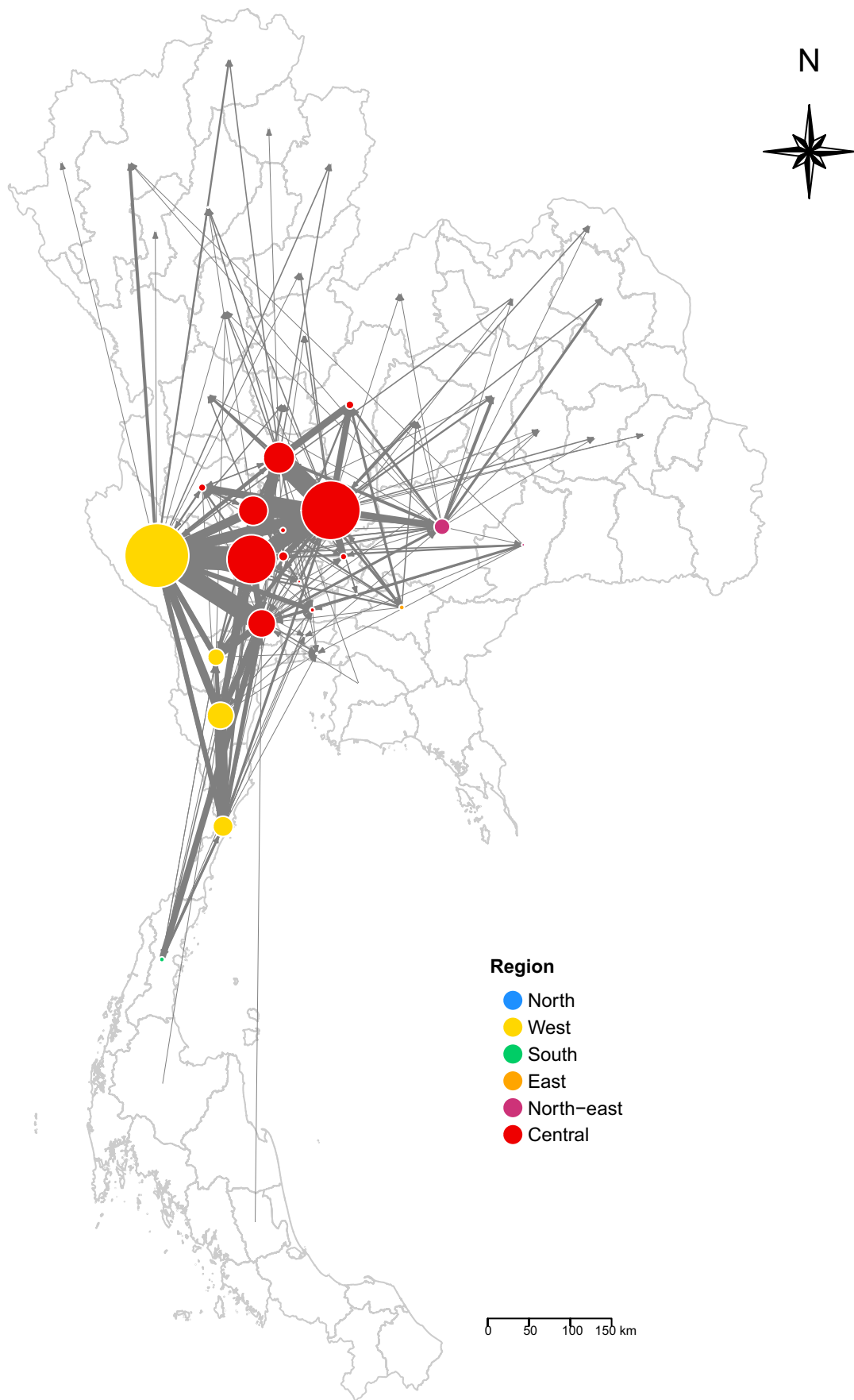| Province	Weighted all-degree centrality	Province	Weighted in-degree centrality	Province	Weighted out-degree centrality
Nakhon Ratchasima	864	Nakhon Ratchasima	398	Phatthalung	536
Phatthalung	805	Khon Kaen	336	Nakhon Ratchasima	466
Khon Kaen	684	Suphan Buri	318	Prachin Buri	459
Lop Buri	601	Nakhon Pathom	271	Nakhon Si Thammarat	438
Nakhon Si Thammarat	587	Phatthalung	269	Lop Buri	405

Active surveillance, for example, the use of sentinel animals, should be consecutively carried out (Oeschger et al., 2021). Additionally, relevant contingency plans should be promptly implemented once a foreign disease is detected.

Interestingly, several communities were detected with relatively high modularity (Clauset et al., 2004). Hence, it indicates that the pig trade network was densely connected within the groups but sparsely linked between different communities (Newman, 2006). It was suggested from previous studies that the emergence of multiple communities in the network may interrupt inter-community disease spread (Lentz et al., 2011; Rautureau et al., 2012). Nonetheless, those studies were performed at the farm level. However, the pathogens may diffuse relatively fast within each intra-community network (Nigsch et al., 2013), as the nodes in such communities were firmly connected. In our pig movement network, around one-third of the nodes were included in the three largest communities (Fig. 3). Consequently, emerging infectious diseases may rapidly spread within these prominent subgraphs and then reach out to other surrounding minor communities. In addition, a large inter-regional community covering over 60% of Thai provinces was observed as depicted in Fig. 5. This community architecture pointed out that the virus was likely to disseminate across different regions. An emerging pathogen may firstly circulate within a particular region and the transregional propagation occurs afterward. Considering overall network characteristics, the Thai pig trade network was, to some extent, vulnerable to the spread of infectious diseases, particularly the highly contagious ones. The pig movement across regions should be seriously monitored. Once a new disease is detected in one region, other regions should be instantly informed, and preparedness should be promptly implemented as the disease may spread distantly through the network community.

We did face some potential limitations. First, the resolution of our pig movement data ends at the subdistrict level. In Thailand, the highest level of the administrative system is the province. Each province is then subdivided into districts, subdistricts, and villages, respectively. The movement data at village and farm levels are not currently available. This is indeed an inevitable limitation we faced. The weakness of this system was also pointed out in a previous study (Noopataya et al., 2015). Thai veterinary authorities should reconstruct the procedures to include filtration in the village or farm levels if possible. Second, the local transmission was not considered in our model. We exclusively focused on how diseases spread along with the contact network which is regarded as remote transmission. Third, we preliminarily worked in the spatial dimension of the pig movement network. A future study exploring how the network changed over time is recommended. Finally, we excluded almost 80% of the original pig movement data as these moved directly to the slaughterhouses. However, these premises may pose the risk to some extent. A more elaborate modeling network classifying the risk of pig movement and relevant actors in different levels is suggested.

In conclusion, we suggested that the pig movement network in Thailand was vulnerable to the spread of emerging infectious diseases, as evidenced by a GWCC, and the inter-regional communities found in the network. The disease may rapidly spread throughout the country once introduced.

Fig. 5 Spatial distribution of the largest community at the provincial ▶ level (#node: 47, #link: 228). The node size is proportionate to the number of contacts each province has. The arrowhead represents the direction of animal movements. The width of the link shows the relative frequency of the movements between the province of origin and that of destination

Declarations

Ethics approval The study was completely based on secondary electronic data and computer simulations. No humans or animals are involved. Thus, ethical approval was not required. However, our study was approved by the Department of Livestock Development, Thailand.

Consent for publication Not applicable.

Conflict of interests The authors declare no competing interests.

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