Skewness in the literature on infectious livestock diseases in an emerging economy – the case of Vietnam

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Abstract

Livestock production has increased in many emerging economies, but productivity is often substantially impaired by infectious diseases. The first step towards improved livestock health and productivity is to map the presence of livestock diseases. The objective of this review was to summarize studies conducted on such diseases in an emerging economy, Vietnam, and thereby identifying knowledge gaps that may inform the design of surveillance and control programs. Few studies were found to evaluate the distribution of infectious livestock diseases other than avian influenza. Also, many regions with dense livestock populations had received little attention in terms of disease investigation. A large proportion of the studies dealt with zoonoses and food-borne infections which might be due to funding agencies priorities. On the contrary, studies targeting infections that affect livestock and their productivity were few. We think that this limitation in scientific reports on infectious diseases that only affect livestock productivity is a common phenomenon in low and lower middle income countries. More science-based data on such diseases would help policymakers to prioritize which livestock diseases should be subject to animal health programs aimed to support rural livelihoods and economic development.

Introduction

The gross domestic product (GDP) per capita in Vietnam has more than doubled in the last decade and the country is now categorized as a lower middle-income country by the Organization for Economic Co-operation and Development (OECD) (OECD, 2019). Increased incomes in a country are associated with altered livestock farming systems (Gilbert et al., 2015), and as a consequence there may be a need for new priorities concerning animal health interventions. In Vietnam, the agricultural sector accounted for 20.6% of the country’s gross domestic product in 2010, of which livestock production contributed 24.5% (OECD, 2012). According to the General Statistics Office of Vietnam, in 2015 livestock included 361.7 million poultry, 29.0 million pigs, 5.5 million cattle, 2.5 million buffaloes, and 1.9 million goats and sheep (GSOV, 2016).

Over the last decade, livestock production in Vietnam has experienced changes with the gradual reduction in the population of buffaloes and beef cattle in contrast to a marked increase in dairy herds (GSOV, 2016). Small ruminant production (sheep and goats) decreased between 2007 and 2010 but has been steadily increasing since 2011. Pig production gradually increased from 2007 to 2015, while poultry production is a unique sector that witnessed a sharp increase during the same period with an average annual growth rate of 7%.

Although there has been an increase in livestock production in Vietnam, the production is impaired partly due to infectious livestock diseases (Figué and Fournier, 2008). For instance, porcine reproductive and respiratory syndrome (PRRS) caused the death of more than 300,000 pigs in 2008 (Thanh, 2009) and the current outbreak of African Swine fever is an immense threat to pig production in this country (Le et al., 2019). Avian influenza (AI) outbreaks in 2003 and 2004 affected 15% of the poultry population in Vietnam (Figué and Fournier, 2008) and caused the death of 42 people by the end of 2005 (WHO, 2015). This resulted in enormous attention to the AI virus in research as well as in society as a whole.

In order to effectively reduce the disease burden in livestock populations in low and lower middle income countries such as Vietnam, there is a need to better understand which infectious diseases, apart from AI, are present in the different production systems and to what extent they are present. To our knowledge, no literature review on livestock diseases has been conducted in Vietnam. The objective of this review is to map the studies conducted...
on livestock diseases, other than AI, in Vietnam and summarize the disease prevalence in each region of Vietnam by reviewing the available peer-reviewed papers in English. By doing so, this review identifies knowledge gaps in order to target future research, and surveillance and control programs.

Methods

Protocol and eligibility criteria

A protocol was developed for the search and evaluation of the articles including the objective, data source, and inclusion and exclusion criteria (summarized in Table 1). Only articles in the English language were considered for this review. In a first screening, the titles and abstracts were checked to see if these parts corresponded to the objective of the present review. The second screening evaluated the quality of the full publication based on different inclusion and exclusion criteria (Table 1). All procedures were performed independently by three of the authors (ELR, HSL, and NHN), and each article was classified into ‘Yes’ or ‘No’ for inclusion. If there was a disagreement between the three reviewers, the final decision was made after discussion among the researchers.

Search strategy

Articles were searched for in the PubMed and Web of Science Core Collection databases. The key search words were divided into three topics – (i) (livestock OR pig OR swine OR sheep OR goat OR small ruminant OR buffalo OR cattle OR poultry OR duck OR chicken); AND (ii) (Vietnam OR Mekong), AND (iii) (disease OR infection OR prevalence OR risk factor). The full lists of titles and abstracts were imported into Endnote (version X7), and duplicates were manually identified and removed. The last search was performed on 8 May 2017. To ensure that the search strategy captured all relevant articles, we checked that known key articles were included in the result. We also cross-checked the reference lists of the articles in the second screening with our search result to make sure we did not miss any relevant articles.

Data collection process

The data extraction template included the authors, year of publication, name of pathogen, animal species, sample level, diagnostic method, test sensitivity/specificity, study area, sample size, number of positive samples, prevalence, and 95% confidence interval (CI). The highest prevalence was extracted if multiple tests were used for the same samples. If the articles lacked certain information such as 95% CIs of the seroprevalence or the number of positive animals, this information was derived using the data presented in the manuscript. The study locations, i.e., provinces, were classified into eight different agroecological regions based on geographical features and climate conditions (Figs. 2–4). The data from eligible publications were reviewed and extracted into a Microsoft Excel file. Lastly, the extracted dataset was independently cross-checked against each original article by the same three authors (ELR, HSL, and NHN).

Synthesis of results

Descriptive statistics were summarized by species like pigs, poultry, and ruminants (cattle, buffalo, sheep, and goats), including pathogen, study region, year of sampling, livestock species, sample size, number positive, diagnostic test, test sensitivity/specificity, prevalence, author, and year (Tables 2–4).

Results

Study selection

A total of 891 articles were retrieved from the PubMed and Web of Science Core Collection databases. In the first screening, 136 duplicates were identified and removed, and 689 publications were excluded due to not presenting the prevalence of livestock diseases in Vietnam (n = 443) or due to focusing on avian influenza (n = 246). Thus, a total of 66 full-text articles were assessed in the second screening, where 30 articles were excluded because of a lack of random selection, an unclear selection procedure, the same data presented in two different publications, or the results not being presented in a clear way. Thus, 36 publications were included in the final qualitative synthesis (Fig. 1).

Diseases in pigs

Seventeen of the articles that were included in the qualitative synthesis were related to pigs (Table 2). Out of these, seven articles focused on common food-borne zoonotic pathogens, i.e. *Salmonella* (n = 3), apparent prevalence (APP) 40–49%, *Campylobacter* (n = 1, APP 57%), *E. coli* (n = 1, APP = 35%), and *Trichinella* (n = 2, APP 6% and 20% in the respective articles). One of the *Salmonella* studies found that *S. derby* (50%) and *S. typhimurium* (27%) were the dominating serotypes (Ellerbroek et al., 2010), while another *Salmonella* study found *S. anatum* (16%) and *S. infantis* (13%) to be the most common serotypes (Thai et al., 2012a). The study investigating *Campylobacter* found the highest prevalence in pigs in high-density production areas and that *C. jejuni* was the most predominant species (Carrique-Mas et al., 2014). The two studies on *Trichinella* (Thi et al., 2010, 2013b) were conducted in the same region as the previous outbreaks in humans and the larvae were identified as *T. spiralis* by polymerase chain reaction (PCR) (Thi et al., 2010). Only one article targeted PRRS, and this article reported an APP of 58% among 40 pigs (Cuong et al., 2014). Whether these 40 pigs had been vaccinated against PRRS or not was not clear. The prevalence at the farm level among non-vaccinated pigs was 12% (four farms of 33 studied farms). A nationwide study of *Leptospira* found an APP of 8% with the dominating serovars being *Tarassovi mitis* (2.2%) and *Australis* (1.9%). Overall, the

### Table 1. Inclusion and exclusion criteria for the first and second screening

| Inclusion criteria | Exclusion criteria |
|--------------------|-------------------|
| **First screening** |                   |
| Original English research articles (peer-reviewed) | Study not conducted in Vietnam |
| Published 2007–2017 (8 May) | Articles about avian influenza |
| Presenting prevalence data of livestock diseases at the individual animal level | Review articles |
| **Second screening** |                   |
| Cross-sectional study |                   |
| Random selection of individuals |                   |
| Clear descriptions of the methods and results |                   |
majority of the studies on pigs ($n = 10$) were conducted in the southern part of Vietnam (Fig. 2).

**Diseases in poultry**

For poultry, 10 articles were included in the qualitative synthesis, the majority of them targeting chickens (Table 3). Five of the articles investigated *Salmonella* ($n = 3$, APP 43–49%) and *Campylobacter* in chicken ($n = 2$, APP = 15% and 24%, respectively) and in ducks ($n = 1$, APP = 18%). One study found *Salmonella albany* to be the most frequent serotype (34%), and backyard chickens had significantly lower prevalence compared to chickens raised in commercial production systems ($P < 0.05$) (Ta et al., 2014). In another *Salmonella* study, chicken carcasses were sampled, but no serotyping was performed, and this study found no significant difference in prevalence by location, market type, or storage temperature in retail settings (Ta et al., 2012). For *Campylobacter*, one study found *C. jejuni* most frequently (28%) (Carrique-Mas et al., 2014), while the other study found *C. lari* to be the predominant serotype (76%) (Garin et al., 2012). Most of these studies were conducted in the central and southern parts of Vietnam. From the northern part of Vietnam, only three studies on *Salmonella* were included (Fig. 3).

**Diseases in ruminants**

A total of 13 articles were included, the majority focusing on cattle (Table 4), and most articles were related to parasitic infections. One study investigated the hemoproteozoa parasite *Theileria orientalis* among ruminants by PCR and found an APP of 14% among cattle, 26% among buffaloes, and 5% among sheep (Khukhuu et al., 2011). Notably, phylogenetic analysis revealed three new genotypes. Another study focusing on hemoproteozoa parasites in cattle found *Babesia bovis* in 9%, *Trypanosoma theileri* in 5%, and *Theileria orientalis* in 0.5% of the samples (Sivakumar et al., 2013). The same study also sampled buffaloes, sheep, and goats. Among buffaloes, the APP of *B. bovis* was 9%. Among goats, only one individual animal tested positive for *Babesia bigemina* by PCR, and no sheep were found to be positive for hemoproteozoa parasites.

Two studies investigated *Fasciola* among cattle and found an APP of 72% and 45%, respectively (Nguyen et al., 2011, 2012a). Both studies found lower infection rates among young animals (<2 years) compared to older animals, and one of the studies found a significantly higher prevalence during the rainy season compared to the dry season (Nguyen et al., 2012a). One study investigated *Cryptosporidium* in native beef calves and found an APP of 19%. PCR analysis revealed the occurrence of *C. ryanae* and *C. bovis*, both species being nonzoonotic (Nguyen et al., 2012b). One study investigated *Giardia duodenalis* among beef calves and reported an APP of 14%, and all identified organisms belonged to *G. duodenalis* assemblage E (Nguyen et al., 2016a, b). Another study investigating *Giardia* among dairy calves found an APP of *G. duodenalis* of 50%, and 16 out of the 17 positive samples belonged to *G. duodenalis* assemblage E (Geurden et al., 2008).
The same study investigated specific serum antibodies to *B. bigemina* and *Anaplasma marginale* in cattle, and found an APP of 54% and 28%, respectively. Furthermore, *Neospora caninum*-specific antibodies were detected in 30% of the milk samples from lactating cows (Geurden et al., 2008). Only one study evaluated the prevalence of mastitis in dairy cows, and that study found mastitis pathogens in 60% of the individual cows (Ostensson et al., 2013). *Streptococcus agalactiae* was the most commonly isolated bacteria and was found in 96 of 458 quarter samples. The prevalence of subclinical mastitis, as measured by somatic cell count, was at cow basis 89%. The majority of the studies (seven out of 13 articles) in ruminants were conducted in the northern part of Vietnam (Fig. 4).

**Discussion**

We have summarized the scientific literature in English on prevalence data of infectious livestock diseases in Vietnam between 2007 and 2017. The review protocol was found suitable and there was no deviation except for extracting two additional parameters i.e. 'year of sampling' and 'test sensitivity/specificity' after the study was concluded. While the initial search resulted in many

| Pathogen or Disease | Region | Year of sampling | Sample size | Number positive | Diagnostic test | Test Se/Sp (%) | APPa (%) | 95% CI | Author (year) |
|--------------------|--------|------------------|-------------|-----------------|----------------|----------------|----------|--------|---------------|
| *Salmonella*       | RRD    | N/A              | 178b        | 87              | Culture c      | N/A            | 49       | 41–56  | Ellerbroek et al. (2010) |
| *Salmonella*       | RRD    | 2007–2009        | 318b        | 126             | Culture c      | N/A            | 40       | 34–45  | Thai et al. (2012a) |
| *Salmonella*       | RRD    | 2014–2015        | 108b        | 48              | Culture c      | N/A            | 44       | 35–54  | Dang-Xuan et al. (2016) |
| *Japanese encephalitis* | MRD    | 1999             | 315d        | 190             | ELISA e        | 0,9/ 0,8       | 60       | 55–66  | Lindahl et al. (2012) |
| *Rotavirus*        | MRD    | 2012             | 730d        | 239             | PCR c          | N/A            | 33       | 29–36  | Anh et al. (2014) |
| *Enterovirus*      | MRD    | 2012             | 128d        | 92              | PCR c          | N/A            | 72       | 63–79  | Dung et al. (2014) |
| *Campylobacter*    | MRD    | 2012             | 61d         | 35              | Culture c      | N/A            | 57       | 44–70  | Carrique-Mas et al. (2014) |
| *Escherichia coli* | SE     | 2012–2014        | 92b         | 32              | Culture c      | N/A            | 35       | 25–45  | Nguyen et al. (2016a, b) |
| *Trematode*        | SCC    | N/A              | 114d        | 16              | DBL c,f,g      | 0,8/ 1,0       | 14       | 8–22   | Anh et al. (2008) |
| *Trematode*        | RRD    | 2007             | 168d        | 13              | DBL c,f,g      | N/A            | 8        | 4–13   | Anh et al. (2009) |
| *Cryptosporidium*  | SCC, CH| 2009             | 740d        | 134             | Ziehl–Neelsen e| N/A            | 18       | 15–21  | Nguyen et al. (2012c) |
| *Cryptosporidium*  | CH     | 2009–2010        | 193d        | 28              | Ziehl–Neelsen e| N/A            | 15       | 10–20  | Nguyen et al. (2013a) |
| *Trichinella*      | NW     | 2008–2009        | 1035d       | 206             | ELISA e        | N/A            | 20       | 18–22  | Thi et al. (2010) |
| *Trichinella*      | NW     | N/A              | 558d        | 31              | Western blot e| N/A            | 6        | 4–8    | Thi et al. (2013b) |
| PRRS               | MRD    | 2011             | 40d         | 23              | ELISA e        | N/A            | 58       | 41–73  | Cuong et al. (2014) |
| Porcine circovirus | MRD    | 2011             | 40d         | 23              | PCR c          | N/A            | 58       | 41–73  | Cuong et al. (2014) |
| Influenza A        | MRD    | 2011             | 40d         | 22              | ELISA e        | N/A            | 55       | 38–71  | Cuong et al. (2014) |
| Leptospirosis      | NW, RRD, NCC, CH, MRD | 2016         | 1959d       | 160             | Agglutination e| N/A            | 8        | 7–9    | Lee et al. (2017) |
| *Streptococcus suis* | SCC, SE, MRD | 2006–2007 | 542b        | 222             | Culture e      | N/A            | 41       | 37–45  | Hoa et al. (2011) |

Regions: NW = Northwest, NE = Northeast, RRD = Red River Delta, NCC = North Central Coast, SCC = South Central Coast, CH = Central Highland, SE = Southeast, MRD = Mekong River Delta.  

aAPP refers to apparent prevalence.  
bSamples collected from carcasses/meat.  
cRefers to direct diagnostic (identification of pathogen).  
dSamples collected from live animals.  
eRefers to indirect diagnostics (identification of antibodies).  
fCombined filtration, sedimentation and centrifugation technique.  
gMultiple diagnostic tests used.
published articles, a surprisingly small number actually looked at the prevalence of livestock diseases other than AI. The outbreaks of AI in 2003 and 2004 resulted in enormous attention to the AI virus, and this could be an explanation for why other infectious livestock diseases in Vietnam have been neglected in epidemiological research.

An important reason for exclusion of articles that passed the first screening was the lack of information of how the selection of farms and individuals were carried out – making it impossible to assess if the selection was randomized or not. Another reason was poor random selection at the farm level and of individual animals, indicating weaknesses in the design of the research conducted. Examples of poor random selection were targeted sampling of individuals showing symptoms of the disease.

For pigs, three papers on Salmonella were included (Ellerbroek et al., 2010; Thai et al., 2012a; Dang-Xuan et al., 2016). The
Table 3. Investigated diseases among poultry in a review of infectious livestock diseases in Vietnam

| Pathogen        | Region          | Year of sampling | Species | Sample size | Number positive | Diagnostic test | Test Se/Sp | APP\(^a\) (%) | 95% CI   | Author (year) |
|-----------------|-----------------|------------------|---------|-------------|----------------|----------------|------------|---------------|---------|--------------|
| Salmonella      | RRD             | 2007–2009        | Chicken| 268         | 115            | Culture\(^c\)  | N/A        | 43            | 29–50   | Thai et al. (2012a) |
| Salmonella      | RRD, SE, MRD    | 2011             | Chicken| 1000        | 459            | Culture\(^c\)  | N/A        | 46            | 43–49   | Ta et al. (2012) |
| Salmonella      | RRD, SE, NE, CH | 2011             | Chicken| 300         | 146            | Culture\(^c\)  | N/A        | 49            | 43–54   | Ta et al. (2014) |
| Campylobacter   | MRD             | 2012             | Chicken| 100         | 24             | Culture\(^c\)  | N/A        | 24            | 16–34   | Carrique-Mas et al. (2014) |
| Campylobacter   | MRD             | 2012             | Duck    | 83          | 15             | Culture\(^c\)  | N/A        | 18            | 10–28   | Carrique-Mas et al. (2014) |
| Campylobacter   | SE              | 2005–2006        | Chicken| 150         | 23             | Culture\(^c\)  | N/A        | 15            | 10–22   | Garin et al. (2012) |
| E. coli         | SE              | 2012–2014        | Chicken| 82          | 76             | Culture\(^c\)  | N/A        | 93            | 85–97   | Nguyen et al. (2016a, b) |
| Cryptosporidium | SCC             | 2011             | Ostrich| 464         | 110            | Ziehl-Neelsen\(^e\) | N/A        | 24            | 20–28   | Nguyen et al. (2013b) |
| Toxoplasma      | SE, MRD         | 2003             | Chicken| 330         | 80             | Agglutination\(^e\) | N/A        | 24            | 20–29   | Dubey et al. (2008) |
| Histomonas      | SCC, SE         | 2012–2013        | Chicken| 194         | 49             | PCR\(^c\)       | N/A        | 25            | 19–32   | Nguyen et al. (2015) |
| Liver fluke     | SCC             | 2013–2015        | Duck    | 178         | 61             | Macroscopic examination\(^e\) | N/A        | 34            | 27–42   | Dao et al. (2016) |

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\(^a\)APP refers to apparent prevalence.

\(^b\)Samples collected from carcasses/meat.

\(^c\)Refers to direct diagnostic (identification of pathogen).

\(^d\)Samples collected from live animals.

\(^e\)Refers to indirect diagnostic (identification of antibodies).
authors of these papers concluded that the prevalence was lower than reported previously from Vietnam (Ellerbroek et al., 2010; Thai et al., 2012a), but that the distribution of Salmonella serovars in Vietnam was similar to other Asian countries and that the global Salmonella serovar distribution might be changing due to globalization, international travel, and the global trade in animal-source foods (Thai et al., 2012a). One paper on Campylobacter found a prevalence of 57% and concluded that increasing urbanization, ongoing intensification of animal production systems, and limited biosecurity in Vietnam will likely increase the incidence of human campylobacteriosis (Carrique-Mas et al., 2014). Due to limited study areas and sample sizes in the Salmonella and the Campylobacter studies, it is difficult to determine whether these figures are representative of Vietnam as a whole. For example,
| Pathogen       | Region     | Year of sampling | Species | Sample size | Number positive | Diagnostic test | Test Se/Sp | APP<sup>a</sup> (%) | 95% CI | Author (year)               |
|----------------|------------|------------------|---------|-------------|-----------------|-----------------|------------|---------------------|--------|---------------------------|
| Hemoprotozoa   | NCC        | 2010             | Cattle<sup>b</sup> | 94          | 13              | PCR<sup>c</sup> | N/A        | 14                  | 8-22   | Khukhuu et al. (2011)     |
| Hemoprotozoa   | NCC        | 2010             | Buffalo<sup>b</sup> | 43          | 11              | PCR<sup>c</sup> | N/A        | 26                  | 14-41  | Khukhuu et al. (2011)     |
| Hemoprotozoa   | NCC        | 2010             | Sheep<sup>b</sup>  | 21          | 1               | PCR<sup>c</sup> | N/A        | 5                   | 0-24   | Khukhuu et al. (2011)     |
| Hemoprotozoa   | NCC        | 2010             | Goat<sup>b</sup>   | 21          | 0               | PCR<sup>c</sup> | N/A        | 0                   | 0-16   | Khukhuu et al. (2011)     |
| Hemoprotozoa   | RRD        | 2006             | Cattle<sup>b</sup> | 239         | 129             | ELISA<sup>d</sup> | N/A        | 54                  | 47-60  | Geurden et al. (2008)     |
| Hemoprotozoa   | RRD, NCC   | 2011             | Cattle<sup>b</sup> | 202         | 18              | PCR<sup>c</sup> | N/A        | 9                   | 5-14   | Sivakumar et al. (2013)   |
| Hemoprotozoa   | NCC        | 2011             | Buffalo<sup>b</sup> | 43          | 4               | PCR<sup>c</sup> | N/A        | 9                   | 3-22   | Sivakumar et al. (2013)   |
| Hemoprotozoa   | RRD, NCC   | 2011             | Sheep<sup>b</sup>  | 51          | 0               | PCR<sup>e</sup> | N/A        | 0                   | 0-7    | Sivakumar et al. (2013)   |
| Hemoprotozoa   | RRD, NCC   | 2011             | Goat<sup>b</sup>   | 127         | 1               | PCR<sup>c</sup> | N/A        | 1                   | 0-4    | Sivakumar et al. (2013)   |
| Hemoprotozoa   | NE         | 2010             | Buffalo<sup>b</sup> | 585         | 131             | Agglutination<sup>d</sup> | N/A       | 22                  | 19-26  | Nguyen et al. (2013c)     |
| Hemoprotozoa   | NW, NE     | 2012–2013        | Buffalo<sup>b</sup> | 484         | 131             | ELISA<sup>d</sup> | 0,8/1,0   | 27                  | 23-31  | Nguyen et al. (2014)      |
| Salmonella     | RRD        | 2009             | Cattle<sup>e</sup> | 158         | 63              | Culture<sup>c</sup> | N/A       | 40                  | 32-48  | Thai et al. (2012b)       |
| E. coli        | SE         | 2012–2014        | Cattle<sup>e</sup> | 74          | 18              | Culture<sup>c</sup> | N/A       | 24                  | 15-36  | Nguyen et al. (2016a, b)  |
| E. coli        | SCC        | 2004–2005        | Buffalo<sup>b</sup> | 237         | 64              | Culture<sup>c</sup> | N/A       | 27                  | 21-33  | Vu-Khac and Cornick (2008) |
| E. coli        | SCC        | 2004–2005        | Cattle<sup>b</sup> | 126         | 29              | Culture<sup>c</sup> | N/A       | 23                  | 16-31  | Vu-Khac and Cornick (2008) |
| Fasciola       | SCC        | 2008             | Cattle<sup>b</sup> | 400         | 289             | ELISA<sup>d</sup> | N/A       | 72                  | 68-77  | Nguyen et al. (2011)      |
| Fasciola       | SCC        | 2008–2009        | Cattle<sup>b</sup> | 1075        | 487             | Sedimentation<sup>c</sup> | N/A       | 45                  | 42-48  | Nguyen et al. (2012a)     |
| Cryptosporidium| CH         | 2011             | Cattle<sup>b</sup> | 232         | 44              | Ziehl-Neelsen<sup>c</sup> | N/A       | 19                  | 14-25  | Nguyen et al. (2012b)     |
| Giardia        | RRD        | 2006             | Cattle<sup>b</sup> | 68          | 34              | Immuno-fluorescence<sup>d</sup> | N/A       | 50                  | 38-62  | Geurden et al. (2008)     |
| Giardia        | SCC, CH    | 2014–2015        | Cattle<sup>b</sup> | 412         | 57              | Flotation<sup>c</sup> | N/A       | 14                  | 11-18  | Nguyen et al. (2016a, b)  |
| Neospora       | RRD        | 2006             | Cattle<sup>b</sup> | 254         | 76              | ELISA<sup>d</sup> | N/A       | 30                  | 24-36  | Geurden et al. (2008)     |
| Anaplasma      | RRD        | 2006             | Cattle<sup>b</sup> | 239         | 67              | ELISA<sup>d</sup> | N/A       | 28                  | 22-34  | Geurden et al. (2008)     |
| Common mastitis pathogens | SE | N/A             | Cattle<sup>b</sup> | 115         | 69              | Culture<sup>c</sup> | N/A       | 60                  | 50-69  | Ostensson et al. (2013)   |

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<sup>d</sup>Refers to indirect diagnostics (identification of antibodies).

<sup>e</sup>Samples collected from carcasses/meat.
the studies on *Salmonella* only targeted the northern part of the country and only included samples from meat or carcasses, and the study on *Campylobacter* was conducted only in the southern part of the country in live animals.

In total, four *Trichinella* outbreaks among humans have been reported in Vietnam since the year 2001, all of them from the northern part of the country (Taylor *et al.*, 2009; Van *et al.*, 2012; Thi *et al.*, 2013a, 2014). Only two *Trichinella* studies among pigs were included in the current review (Thi *et al.*, 2010, 2013b), both of them conducted in the same region as the previous outbreaks in humans. The prevalence reported in the study in 2013 was more than three times lower than the prevalence reported in the study in 2010. The results from these two studies showed that pigs can constitute a serious public health

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**Fig. 4.** Distribution of studied pathogens in ruminants by region.
risk, but the change in prevalence between 2010 and 2013 needs to be followed up by further epidemiological studies in order to take appropriate action to prevent human infection.

Another disease of global importance among pigs is PRRS. According to the World Organisation for Animal Health (OIE), PRRS is present in Vietnam. In addition, highly pathogenic PRRS viruses have previously been reported to spread rapidly among pigs in Southeast Asia (An et al., 2011). However, the results from one study included in the current review indicated that PRRS is endemic in the pig farms of the Mekong Delta (Cuong et al., 2014). Because there was only one study investigating PRRS, there is a clear need for further epidemiological research to determine how widespread the disease is in the pig population and to understand the associated risk factors.

In addition, two other important diseases, classical swine fever (CSF) and foot and mouth disease (FMD), have been present in Vietnam since 2005 according to the OIE. CSF is assumed to be endemic in many Asian countries (Blome et al., 2017), but no studies have been published in Vietnam since 2007. For FMD, some studies have been conducted recently focusing on the genetic analysis (Le et al., 2010a, b). However, no articles have been published to evaluate the prevalence and associated risk factors for FMD despite the implementation of a national control and eradication program in 2006 which currently run is in its third phase from 2016 to 2020 (News, 2015).

Half of the studies on poultry diseases in the current review targeted Salmonella (Ta et al., 2012, 2014; Thai et al., 2012a) or Campylobacter (Garin et al., 2012; Carrique-Mas et al., 2014), and the most recent publications for both pathogens were from 2014. One of the Salmonella studies concluded that the Salmonella levels in raw poultry must be reduced in order to improve food safety and reduce the risk of transmission to humans (Ta et al., 2012). Another study concluded that the Salmonella prevalence in raw poultry was high, but the counts were low, suggesting that the exposure risk to Salmonella is low. However, the authors stressed that improper storage and cross-contamination can increase the counts and thus increase the risk of infection in humans (Ta et al., 2014). One Campylobacter study targeted both poultry and pigs, and the conclusions from the findings in poultry were the same as for pigs in that an increase in human campylobacteriosis is likely due to increasing intensification, limited biosecurity, and increasing urbanization (Carrique-Mas et al., 2014). The other Campylobacter study presented an interesting finding with C. lari being the most predominant species identified, and the authors stressed that efforts to reduce Campylobacter contamination and to improve food hygiene must be prioritized on the farms, slaughterhouses, and in the private kitchens of Vietnam (Garin et al., 2012). Notably, the studies on Campylobacter included only a limited number of samples, and the data were only collected in the southern part of Vietnam. In order to get a comprehensive understanding of the impact of this important zoonosis, more research is necessary.

Another disease of global importance is Newcastle disease (Miller and Koch, 2013). Notably, no study was found in the current review even though the disease is reported to the OIE. Therefore, rigorous studies are necessary to evaluate the prevalence and risk factors of the disease in Vietnam.

For ruminants, the majority of the research has been conducted on parasitic infections. One study investigating Theileria orientalis concluded that at least seven genotypes of T. orientalis exist in Vietnam, but that further large-scale epidemiological studies are needed in order to better understand the geographical distributions, host specificities, and clinical pathologies of the different genotypes and their relationships with the tick population (Khukhuu et al., 2011). Another study on hemoproteozoan parasites found B. bovis to be commonly occurring among cattle, which is an important finding because the acute phase of this infection is often fatal to cattle (Sivakumar et al., 2013). The authors concluded that infections with hemoproteozoan parasites continue to be a threat to the livestock industry in Vietnam.

Two studies investigated Fasciola among cattle in a region with a high burden of human fascioliasis, and found a very high prevalence among cattle (Nguyen et al., 2011, 2012a). The authors suggested that a control program should be designed aiming to reduce the infection rate in cattle and humans. There was one study investigating Cryptosporidium in native beef calves (Nguyen et al., 2012b). This study showed no evidence of zoonotic species of Cryptosporidium in the calves examined, and the authors concluded that native beef calves are unlikely to contribute to human cryptosporidiosis in the study region. Two studies investigated G. duodenalis among calves, and both found a predominance of assemblage E genotype among the calves (Geurden et al., 2008; Nguyen et al., 2016a, b). Because assemblage E is livestock-specific, this suggests that calves might not be important sources of human giardiasis in the region. However, the authors acknowledged that more research is necessary in order to clarify the situation of giardiasis in livestock and humans in Vietnam. The latter study also found a high prevalence of antibodies to Neospora in cow milk, suggesting that this parasite is endemic among the cattle in the study region (Geurden et al., 2008). The same study also found a high prevalence of A. marginale and B. bigemina-specific antibodies in cattle sera. Because these infections are spread by ticks, the authors suggested tick control as a preventive measure as well as developing immunity in calves. The authors also concluded that further research to clarify the extent of clinical infections with blood parasites is needed in order to plan appropriate interventions.

In common for the research conducted in ruminants was that there were very few studies performed, few individuals sampled, and only limited study areas. Therefore, it is difficult to conclude the extent of parasitic infections among ruminants in Vietnam. Only one paper targeting mastitis was found, and the results indicated a high prevalence of subclinical mastitis among the dairy cows, mainly due to Streptococcus agalactiae (Ostensson et al., 2013). This indicates that the milking routines are poor and that proper measures to prevent the occurrence and spread of udder infections are not being implemented. Further research is required in order to get a comprehensive understanding of the occurrence of mastitis and subsequent production losses among dairy cows in Vietnam.

Of the 36 articles included in the analysis, only two focused on globally important zoonotic diseases, i.e. Japanese encephalitis and leptospirosis. In order to reduce the incidence of many zoonotic infections among humans, the pathogens are best controlled in the animal population (WHO, 2005). Therefore, more research is required to close the current knowledge gaps regarding the presence and the associated risk factors for important zoonotic infections. In addition, according to the media in Vietnam, anthrax has been continuously reported in ruminants (such as buffaloes) in mountainous areas of Northern Vietnam (News, 2011). However, no articles were found in the current review and no information was reported to the OIE. Therefore, a further epidemiological investigation is necessary in order to reduce the
gaps in disease surveillance and reporting systems as well as to support the prevention and reduction of further outbreaks.

Many regions with dense populations of livestock have received little attention in terms of disease investigation. For instance, fewer studies have been conducted in the north of Vietnam where the pig and poultry populations outnumbered those in Southern Vietnam (GSO, 2016a, b).

One reason could be that the production systems differ between the regions. For example, pig production is more extensive in the southern part of Vietnam compared to the northern part of the country. Another reason for such discrepancies in the numbers of published papers in each region could be due to the working or living locations of the researchers, and many studies were led by foreign scientists. This suggests that these studies might not always be conducted based on the practical need for surveillance/control of these diseases in the country. Therefore, in order to improve the productivity of Vietnam’s livestock populations, scientists and policy makers need to share the same view on disease control in livestock in Vietnam.

The review presented here has some deliberate limitations in order to base our conclusions on the most scientifically sound data. Only peer-reviewed original articles were included and a search for grey literature was not carried out. Furthermore, only articles from the international literature were included, that is, those published in English. However, despite the high quality of the included studies, the relatively low number highlights the need for more research to be carried out on infectious livestock diseases in Vietnam.

Conclusions

Relatively few studies were found to evaluate the distribution of infectious livestock diseases other than AI in Vietnam. Also, many regions with dense populations of livestock have received little attention in terms of disease investigation and disease impact. A large proportion of the studies meeting the inclusion criteria dealt with zoonoses and food-borne infections, a bias that might be explained by funding agencies priorities. On the contrary, infections that mainly affect productivity and contribute significantly to yield gaps and impact on livelihoods of farmers are under-represented. The under-representation of these kinds of infectious diseases is also true in current public surveillance priorities in Vietnam which, as in most countries, focus on diseases important for international trade such as on FMD, CSF, AI, and PRRS. We think that this under-representation in the evidence-based knowledge of infectious diseases that affects livestock only is a common phenomenon in low and lower middle income countries. More science-based data on such diseases would help policymakers to prioritize which livestock diseases should be subject to animal health programs aimed to support rural livelihoods and economic development.

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