Animal Health Research Reviews

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Review

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

Elisabeth Rajala[1], Hu Suk Lee[2], Nguyen Hoai Nam[3], Chu Thị Thanh Huong[3], Hoang Minh Son[3], Barbara Wieland[4] and Ulf Magnusson[1]

[1]Division of Reproduction, Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden; [2]International Livestock Research Institute, Hanoi, Vietnam; [3]Faculty of Veterinary Medicine, Vietnam National University of Agriculture, Hanoi, Vietnam and [4]International Livestock Research Institute, Addis Ababa, Ethiopia

Cite this article: Rajala E, Lee HS, Nam NH, Huong CTT, Son HM, Wieland B, Magnusson U (2021). Skewness in the literature on infectious livestock diseases in an emerging economy – the case of Vietnam. *Animal Health Research Reviews* **22**, 1–13. https://doi.org/10.1017/S1466252321000013

Received: 25 October 2019
Revised: 9 June 2020
Accepted: 6 January 2021
First published online: 10 May 2021

Key words:
Infectious diseases; livestock; prevalence

Author for correspondence:
Elisabeth Rajala, Division of Reproduction, Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden.
E-mail: Elisabeth.Rajala@slu.se

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 (Figuié 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 (Figuié 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

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	

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

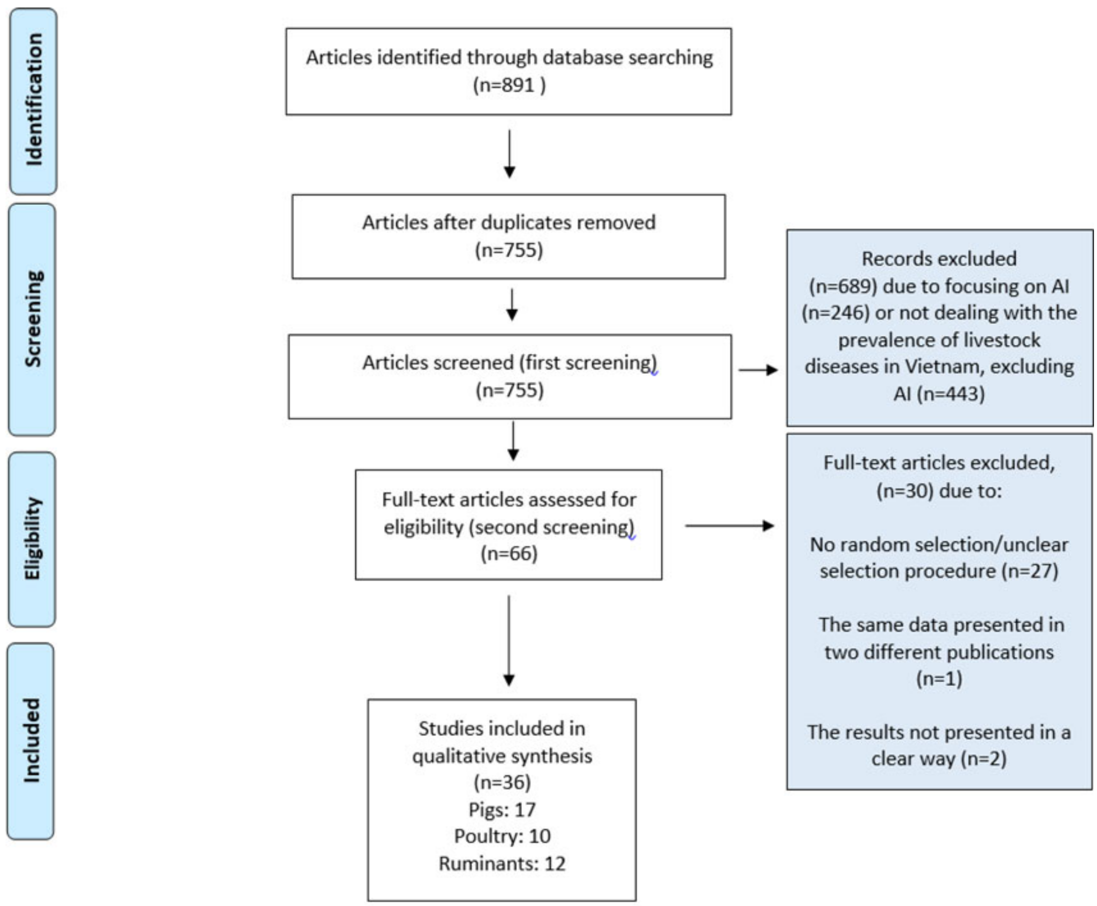

Fig. 1. Schematic flow diagram of the literature selection for the review on infectious livestock diseases in Vietnam (www.prisma-statement.org).

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 hemoprotozoan 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 hemoprotozoan parasites in cattle found *Babesia bovis* in 9%, *Trypanosoma theileiri* 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 hemoprotozoan 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).

Table 2. Investigated diseases among pigs in a review of infectious livestock diseases in Vietnam

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

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

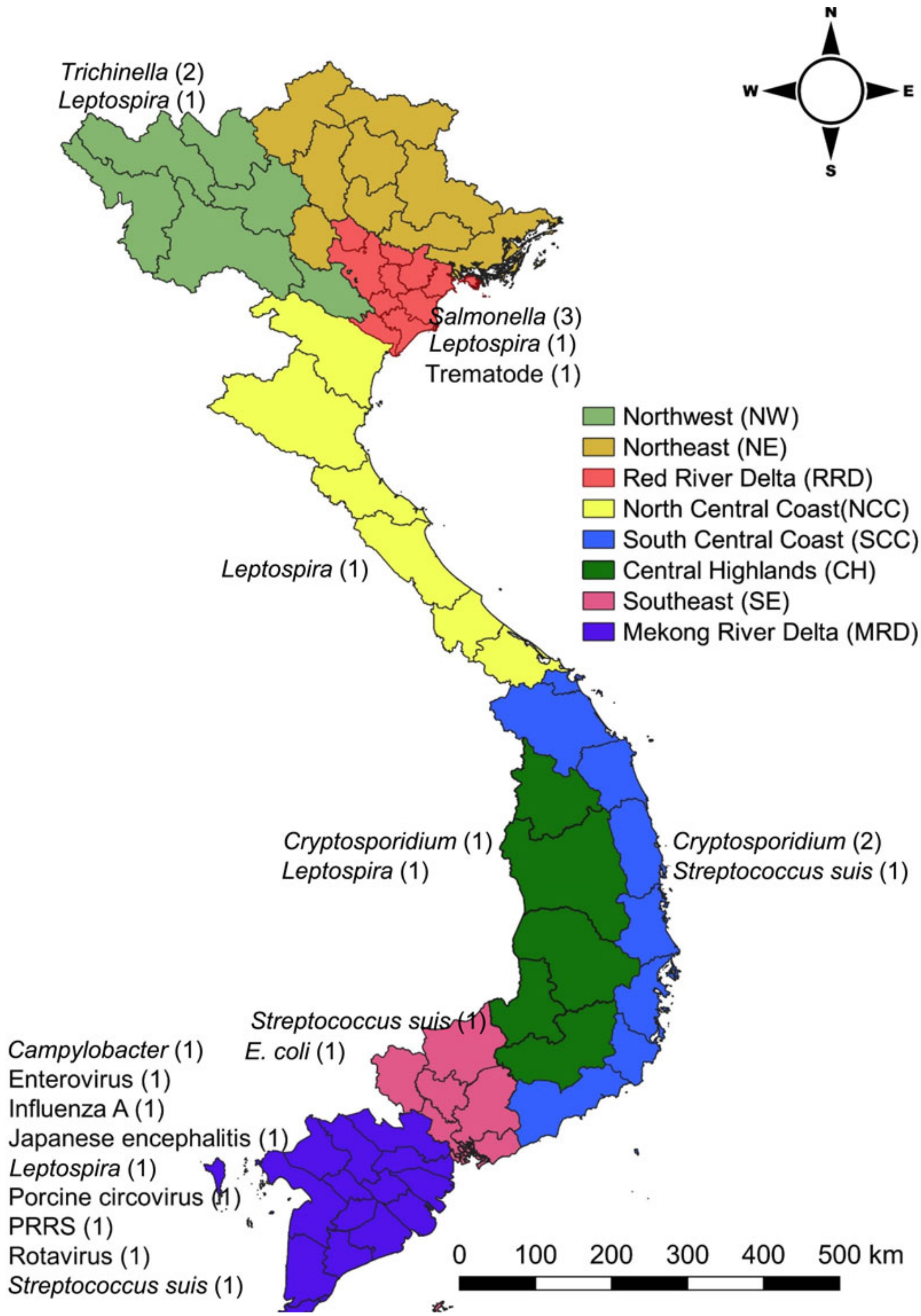

Fig. 2. Distribution of studied pathogens in pigs by region.

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[b]	268	115	Culture[c]	N/A	43	29–50	Thai *et al.* (2012a)
Salmonella	RRD, SE, MRD	2011	Chicken[b]	1000	459	Culture[c]	N/A	46	43–49	Ta *et al.* (2012)
Salmonella	RRD, SE, NE, CH	2011	Chicken[b]	300	146	Culture[c]	N/A	49	43–54	Ta *et al.* (2014)
Campylobacter	MRD	2012	Chicken[d]	100	24	Culture[c]	N/A	24	16–34	Carrique-Mas *et al.* (2014)
Campylobacter	MRD	2012	Duck[d]	83	15	Culture[c]	N/A	18	10–28	Carrique-Mas *et al.* (2014)
Campylobacter	SE	2005–2006	Chicken[b]	150	23	Culture[c]	N/A	15	10–22	Garin *et al.* (2012)
E. coli	SE	2012–2014	Chicken[b]	82	76	Culture[c]	N/A	93	85–97	Nguyen *et al.* (2016a, b)
Cryptosporidium	SCC	2011	Ostrich[d]	464	110	Ziehl-Neelsen[c]	N/A	24	20–28	Nguyen *et al.* (2013b)
Toxoplasma	SE, MRD	2003	Chicken[b]	330	80	Agglutination[e]	N/A	24	20–29	Dubey *et al.* (2008)
Histomonas	SCC, SE	2012–2013	Chicken[b]	194	49	PCR[c]	N/A	25	19–32	Nguyen *et al.* (2015)
Liver fluke	SCC	2013–2015	Duck[b]	178	61	Macroscopic examination[c]	N/A	34	27–42	Dao *et al.* (2016)

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.
[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 diagnostics (identification of antibodies).

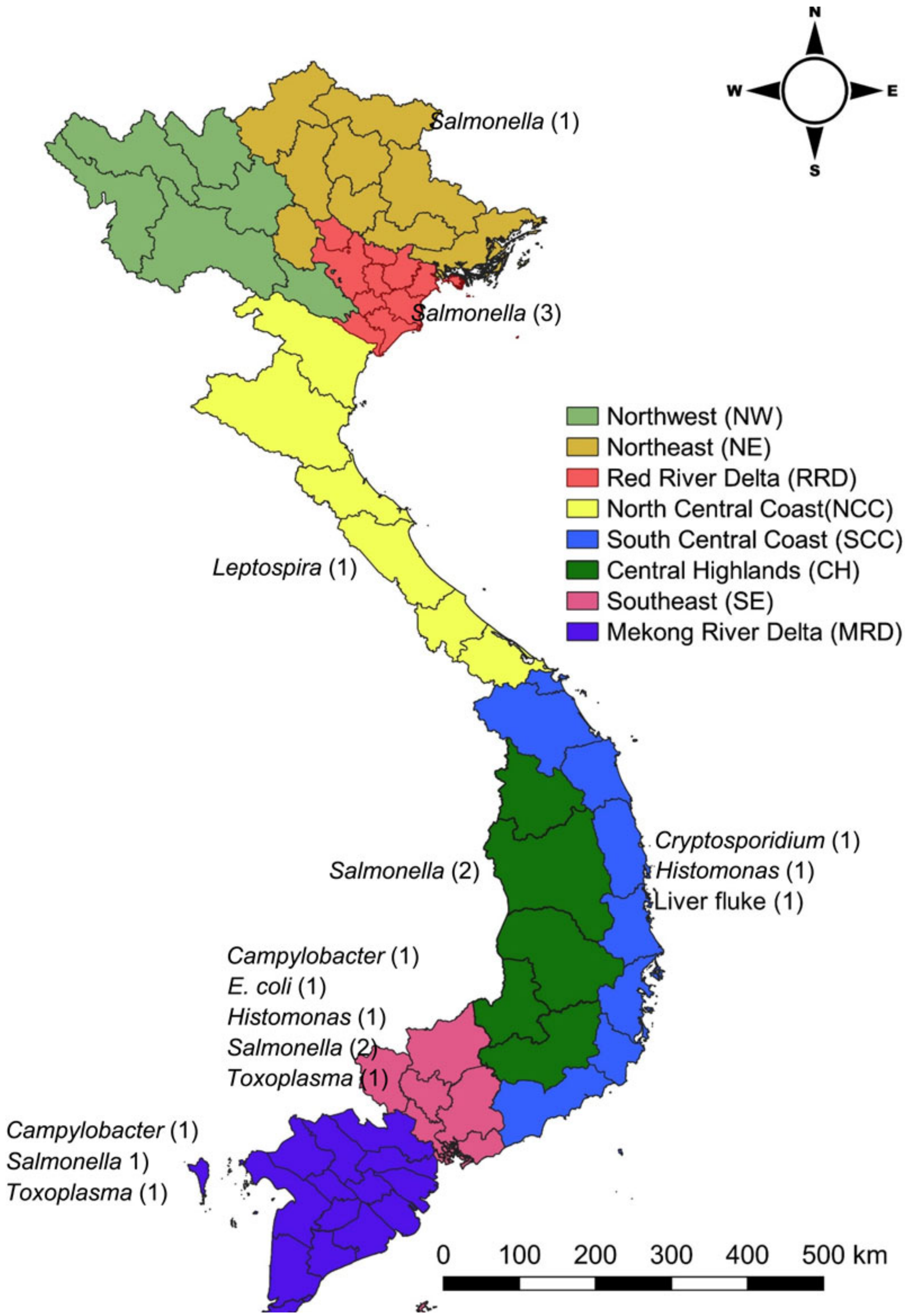

Fig. 3. Distribution of studied pathogens in poultry by region.

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,

Table 4. Investigated diseases among ruminants 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)
Hemoprotozoa	NCC	2010	Cattle[b]	94	13	PCR[c]	N/A	14	8–22	Khukhuu *et al.* (2011)
Hemoprotozoa	NCC	2010	Buffalo[b]	43	11	PCR[c]	N/A	26	14–41	Khukhuu *et al.* (2011)
Hemoprotozoa	NCC	2010	Sheep[b]	21	1	PCR[c]	N/A	5	0–24	Khukhuu *et al.* (2011)
Hemoprotozoa	NCC	2010	Goat[b]	21	0	PCR[c]	N/A	0	0–16	Khukhuu *et al.* (2011)
Hemoprotozoa	RRD	2006	Cattle[b]	239	129	ELISA[d]	N/A	54	47–60	Geurden *et al.* (2008)
Hemoprotozoa	RRD, NCC	2011	Cattle[b]	202	18	PCR[c]	N/A	9	5–14	Sivakumar *et al.* (2013)
Hemoprotozoa	NCC	2011	Buffalo[b]	43	4	PCR[c]	N/A	9	3–22	Sivakumar *et al.* (2013)
Hemoprotozoa	RRD, NCC	2011	Sheep[b]	51	0	PCRe	N/A	0	0–7	Sivakumar *et al.* (2013)
Hemoprotozoa	RRD, NCC	2011	Goat[b]	127	1	PCR[c]	N/A	1	0–4	Sivakumar *et al.* (2013)
Hemoprotozoa	NE	2010	Buffalo[b]	585	131	Agglutination[d]	N/A	22	19–26	Nguyen *et al.* (2013c)
Hemoprotozoa	NW, NE	2012–2013	Buffalo[b]	484	131	ELISA[d]	0,8/1,0	27	23–31	Nguyen *et al.* (2014)
Salmonella	RRD	2009	Cattle[e]	158	63	Culture[c]	N/A	40	32–48	Thai *et al.* (2012b)
E. coli	SE	2012–2014	Cattle[e]	74	18	Culture[c]	N/A	24	15–36	Nguyen *et al.* (2016a, b)
E. coli	SCC	2004–2005	Buffalo[b]	237	64	Culture[c]	N/A	27	21–33	Vu-Khac and Cornick (2008)
E. coli	SCC	2004–2005	Cattle[b]	126	29	Culture[c]	N/A	23	16–31	Vu-Khac and Cornick (2008)
E. coli	SCC	2004–2005	Goat[b]	205	79	Culture[c]	N/A	39	32–46	Vu-Khac and Cornick (2008)
Fasciola	SCC	2008	Cattle[b]	400	289	ELISA[d]	N/A	72	68–77	Nguyen *et al.* (2011)
Fasciola	SCC	2008–2009	Cattle[b]	1075	487	Sedimentation[c]	N/A	45	42–48	Nguyen *et al.* (2012a)
Cryptosporidium	CH	2011	Cattle[b]	232	44	Ziehl-Neelsen[c]	N/A	19	14–25	Nguyen *et al.* (2012b)
Giardia	RRD	2006	Cattle[b]	68	34	Immuno-fluorescence[d]	N/A	50	38–62	Geurden *et al.* (2008)
Giardia	SCC, CH	2014–2015	Cattle[b]	412	57	Flotation[c]	N/A	14	11–18	Nguyen *et al.* (2016a, b)
Neospora	RRD	2006	Cattle[b]	254	76	ELISA[d]	N/A	30	24–36	Geurden *et al.* (2008)
Anaplasma	RRD	2006	Cattle[b]	239	67	ELISA[d]	N/A	28	22–34	Geurden *et al.* (2008)
Common mastitis pathogens	SE	N/A	Cattle[b]	115	69	Culture[c]	N/A	60	50–69	Ostensson *et al.* (2013)

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.
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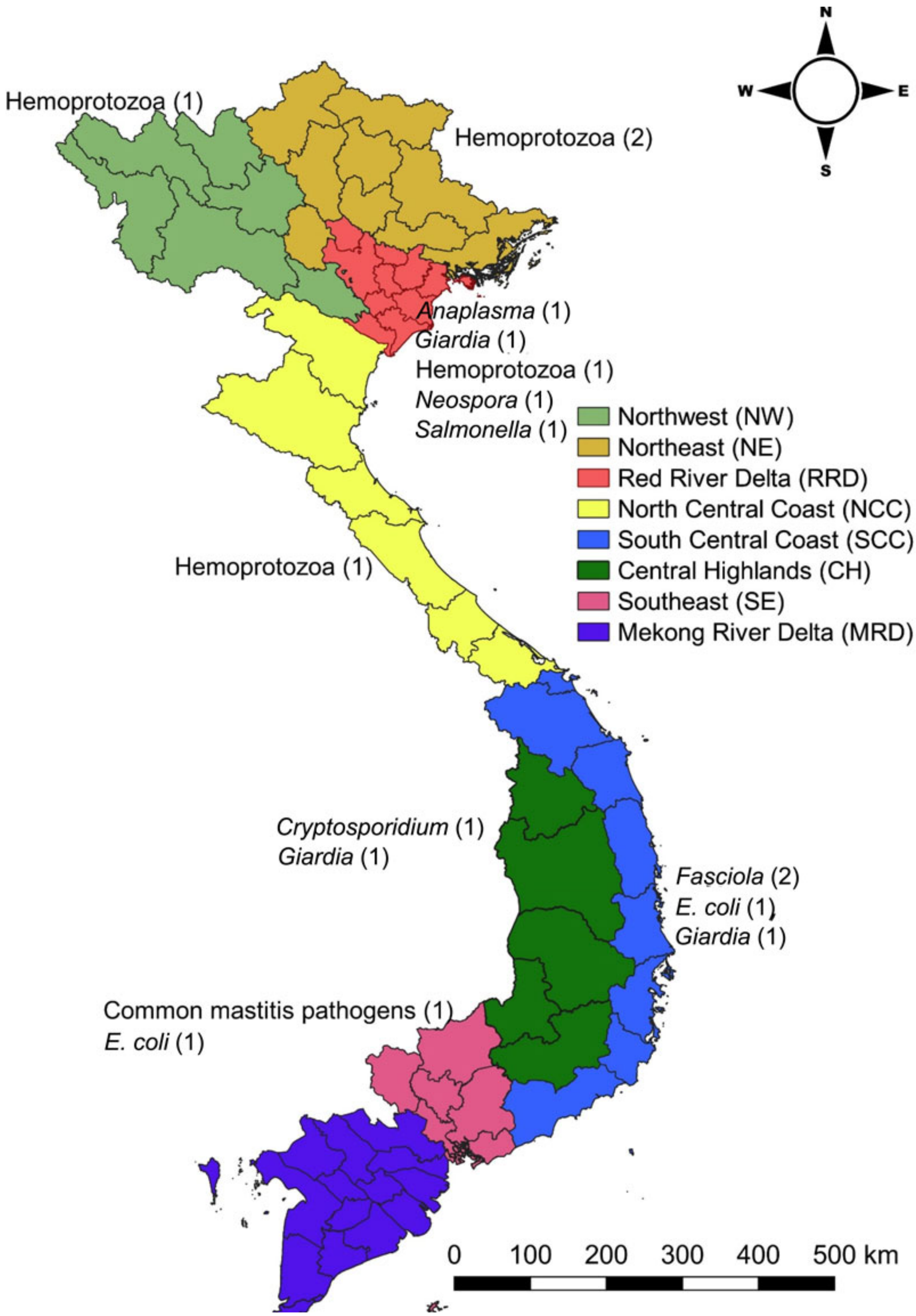

Fig. 4. Distribution of studied pathogens in ruminants by region.

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 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 hemoprotozoan 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 hemoprotozoan 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 fasciolis, 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). That 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.

Acknowledgments. The authors would like to thank the SIDA-funded program AgriFoSe2030 for financial support.

Consent for publication. Not applicable.

Conflict of interest. The authors declare that they have no competing interests.

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