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Short communication

Spatial analysis of bovine cysticercosis in France in 2010

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ABSTRACT

Bovine cysticercosis is a zoonosis caused by the cestode *Taenia saginata* and involves cattle as the intermediate host and humans as the final host. This disease is both a public health issue and an economic concern for farmers. Cattle are infected after grazing on infected pasture. Humans are infected by the consumption of raw or under-cooked meat.

This study aimed to identify geographical areas where animals are infected by bovine cysticercosis so as to implement adequate control measures and to provide a risk-based meat inspection process for improving disease detection. Considering both the long period of cyst development in cattle muscle and the complexity of cattle movements, a spatial analysis of slaughtered cattle found to be harboring viable and degenerated cysts was a challenge. Detection of clusters of bovine cysticercosis cases was performed using a spatial scan statistic with a discrete Poisson model adjusted for a variable combining age and sex. The novelty of this approach was that it used an animal-herd level weighted analysis to take into account the uncertainty of the location where animals became infected.

This study included 4,557,593 (91.3%) cattle slaughtered in 2010 in France in 181 slaughterhouses. The meat inspection process enabled the detection of 6431 cattle harboring at least one bovine cysticercosis lesion and 603 harboring at least one viable cyst. Three significant clusters for cattle with all types of cysts were detected through the spatial analysis in north-western and eastern France. One significant cluster was detected in eastern France for cattle with viable cysts only.

The difference in location of the clusters detected, when considering only cattle harboring viable cysts or cattle harboring all types of cysts, proved the relevancy of this novel approach. We identified areas in France with a higher risk of bovine cysticercosis in which investigations could be performed to identify the risk factors that explained this spatial distribution. These risk factors could then be used to suggest control measures in these areas and to implement a reinforced meat inspection protocol so as to increase the efficiency of the current meat inspection process.

1. Introduction

Bovine cysticercosis is a zoonosis caused by the cestode *Taenia saginata*. The life cycle of this parasite involves humans as the definitive host and cattle as the intermediate host. Infected humans excrete tapeworm eggs in their feces that can infect pastures when sewage sludge is used for fertilization (Cabaret, Geerts, Madeline, Ballandonne, & Barbier, 2002; Dorny & Praet, 2007; Kyvsgaard, Ilsoe, Henriksen, & Nansen, 1990). Cattle can ingest eggs by grazing on these pastures and cysticerci can then develop in the cattle's muscles forming cysts. These cysts first go through a viable stage and then develop into a degenerated stage over a period of one to nine months (OIE, 2008). Humans can be infected through consumption of raw or under-cooked meat from carcasses harboring

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viable cysts (Scientific Committee on Veterinary Measures relating to Public Health, 2000).

Identifying the geographical areas where animals have become infected with bovine cysticercosis is crucial for implementing adequate control measures and providing a risk-based meat inspection procedure to improve disease detection. When an animal has been found to harbor cysts during post-mortem inspection (PMI) at the slaughterhouse, identifying the location where the infection took place is essential but presents a challenge. This is due to both the long development of the cysts in the animals' muscles and the complexity of cattle movements from one herd to another. In France, for instance, animals can be transferred into and out of anywhere from one to over 10 different herds (mean = 1.4) or operators (e.g. dealers) over their lifetime. Consequently the spatial representation of bovine cysticercosis cases is often imprecise, especially for cattle harboring degenerated cysts, which is the stage of the disease that is most commonly detected during PMI.

The objective of this study was to identify clusters of bovine cysticercosis cases while taking into account factors of uncertainty regarding the location where the animal became infected. To do this, we used an animal-herd level weighted analysis.

2. Materials and methods

2.1. Data collection

A survey was conducted in France in 2010 by the French Ministry of Agriculture in all the cattle slaughterhouses throughout the country ($n = 221$). Each slaughterhouse was asked to register all the animals that were found at PMI to have at least one cysticercosis lesion, and to specify the stage of development of the cyst (viable or degenerated). PMI was performed according to current European legislation (European Parliament, 2004). Viable cysts were defined as fully transparent cysts with a visible scolex and degenerated cysts as cysts with cheesy (yellowish and smooth) or calcified (solid and perceptible when cysts were sliced) contents (Kyvsgaard et al., 1990; Minozzo, Gusso, de Castro, & Lago, 2002). Animals harboring both viable and degenerated cysts were accounted for identically to animals harboring only viable cysts. The objective was to take into account only the most recent infection with bovine cysticercosis for these animals.

The French National Cattle Register (BDNI) was used to extract the sex and age for each animal slaughtered in France in 2010, based on its ID. In keeping with zootechnical standards (Barbin et al., 2011) and EU regulation (European Parliament, 2007), the cattle were classified into six age groups: <8 months old, 8–24 months old, 2–3.5 years old, 3.5–5 years old, 5–10 years old and ≥10 years old. All animals that were slaughtered in one of the slaughterhouses that answered the survey were included in the study.

Data on each movement from birth to slaughter of an animal harboring at least one cyst was extracted from the BDNI. The location of each herd was determined by using the geographical coordinates of the *commune* (smallest French administrative area) where it was located (obtained through the National Geographic Institute of France website (http://www.data.gouv.fr/DataSet/30383083)). Animals with missing data regarding sex, age or *commune* coordinates were excluded from the study.

2.2. Animal-herd level weighting

A literature review was performed to establish a chronology of the development of cysts from the viable to the degenerative stage (Appendix A). The probability that an animal was infected during a given period k (expressed as a number of days prior to the date of slaughter) was then defined for cattle harboring at least one viable cyst and cattle harboring degenerated cysts (Table 1). For instance, the probability that an animal harboring viable cysts has been infected between 15 and 30 days prior to the date of slaughter was estimated at 0.1.

Table 1
Probability that an animal was infected a given number of days before the date of slaughter in cattle harboring only degenerated cysts and cattle harboring at least one viable cyst.

Period k	Degenerated cysts only		At least one viable cyst	
	Range of period k in number of days before slaughter $[b_{\text{inf } k}–b_{\text{sup } k}]$	Probability of infection during period k (Prob_k)	Range of period k in number of days before slaughter $[b_{\text{inf } k}–b_{\text{sup } k}]$	Probability of infection during period k (Prob_k)
1	[0–30]	0	[0–15]	0
2	[31–150]	0.1	[16–30]	0.1
3	[151–270]	0.2	[31–150]	0.7
4	[271–Age[a]]	0.7	[151–270]	0.2
5	–	–	[271–Age[a]]	0
		1		1

[a] Age of slaughtered animal (in number of days).

For each animal-herd combination (period of time an animal was present in herd j), a probability P_j that infection of the animal occurred in this same herd j (also known as the animal-herd weight) was calculated as the number of days spent during each period at risk of infection k while in herd j multiplied by the daily infection probability for the period, using the following formula:

$$P_j = \left| \begin{array}{l} \text{for } j \neq j_{\max} : \sum_{k=1}^{k_{\max}} [\text{Prob}_k/\text{Length}_k] \times Nb_{\text{day}_{kj}} \\ \text{for } j = j_{\max} : 1 - \sum_{j=1}^{j_{\max}-1} P_j \end{array} \right. \quad (1)$$

with

- j representing the order number associated with each herd: 1 for the last herd before slaughter, $j_{\max}$ for the herd of birth.
- k representing the period as defined in Table 1, $k_{\max}$ being 5 for viable cysts and 4 for degenerated cysts.
- Prob_k representing the probability that an animal was infected during the period k.
- Length_k representing the number of days in period k.
- $Nb_{\text{day}_{kj}}$ representing the number of days during period k that an animal was present in herd j as

$$Nb_{\text{day}_{kj}} = \begin{cases} 0 & \text{if } n_j - b_{\text{inf}_k} < 0 \text{ or } b_{\text{sup}_k} - n_{j-1} < 0 \\ b_{\text{sup}_k} - n_{j-1} & \text{if } n_j < b_{\text{sup}_k} < n_{j-1} \text{ and } b_{\text{inf}_k} < n_{j-1} \\ b_{\text{sup}_k} - b_{\text{inf}_k} & \text{if } n_j < b_{\text{sup}_k} < n_{j-1} \text{ and } n_j < b_{\text{inf}_k} < n_{j-1} \\ n_j - b_{\text{inf}_k} & \text{if } n_j < b_{\text{inf}_k} < n_{j-1} \text{ and } b_{\text{sup}_k} < n_j \end{cases}$$

- $b_{\text{inf } k}$ and $b_{\text{sup } k}$ being the lower and upper limit for period k expressed as a number of days before slaughter.
- n_j representing the number of days before slaughter corresponding to the entrance date into herd j and the exit date from herd $j + 1$.

Table 2
Description of animal-herd (number, proportion and distribution of weights) according to the herd order number for cattle harboring any type of cyst ($n = 6431$) and cattle harboring at least one viable cyst ($n = 603$).

Herd order number	All types of cysts		At least one viable cyst	
	Number of animal-herds (%)	Weight mean [min; max]	Number of animal-herds (%)	Weight mean [min; max]
1	6431 (69.75)	0.90 [0; 1]	603 (67.3)	0.97 [0; 1]
2	2133 (23.13)	0.25 [0; 1]	229 (25.56)	0.08 [0; 1]
3	472 (5.12)	0.24 [0; 0.98]	47 (5.25)	0.01 [0; 0.13]
4	109 (1.18)	0.20 [0; 0.69]	11 (1.23)	0 [0; 0]
5	42 (0.46)	0.16 [0; 0.65]	5 (0.56)	0 [0; 0]
6	17 (0.18)	0.16 [0; 0.42]	1 (0.11)	0 [0; 0]
7	8 (0.09)	0.09 [0.02; 0.24]		
8	5 (0.05)	0.11 [0.04; 0.22]		
9	2 (0.02)	0.05 [0.02; 0.07]		
10	1 (0.01)	0.19 [0.19; 0.19]		
Total	**9220 (100)**		**896 (100)**	

The sum of all animal-herd weights for each animal was equal to 1. The total number of cases was thus not modified, but divided into several animal-herd weights according to how sure we were that the animal was infected in each herd in which it spent time. For instance, an animal that spent time in three different herds was assigned three probabilities P_1, P_2 and P_3 (with $P_1 + P_2 + P_3 = 1$) representing the probability of being infested in one of these herds according to Equation (1) and the probabilities defined in Table 1.

2.3. Spatial analysis

Detection of clusters of bovine cysticercosis cases was performed using a spatial scan statistic with discrete Poisson model (Kulldorff, 1997) using SaTScan v9.9.1 (Kulldorf, 2009). The case population was defined as the sum of the animal-herd weights aggregated by *commune*, and the background population as the number of cattle slaughtered in 2010 aggregated by *commune* of the last farm in which they resided. A circular window was used for clustering and the maximum spatial cluster size was defined as 20% of the background population.

The model was adjusted for a variable combining age and sex because of the strong impact of this variable on bovine cysticercosis (Dupuy et al., 2014). Two separate analyses were performed respectively on cattle harboring at least one viable cyst and on cattle harboring cysts regardless of their level of development. Only clusters with more than one *commune* and a p-value under 0.05, indicating a significant difference between the observed and expected number of cases, were retained. These clusters were put on maps with the prevalence of cattle harboring cysts at the *département* (French administrative area) level as a background indicator. Apparent prevalence, i.e. the number of cattle harboring cysts divided by the number of cattle slaughtered, was presented as the number of cases per 100 cattle (%).

3. Results

3.1. Study population

In 2010, 4,997,846 cattle were slaughtered in France in 221 slaughterhouses. Among them 4,564,217 animals (91.3%) from 181 slaughterhouses participated in this study. Animals with missing data regarding sex, age ($n = 152$) or *commune* coordinates ($n = 6472$) were excluded. Finally, after the removal of animals with missing data, 4,557,593 (91.1%) cattle were included. Among these animals, PMI made it possible to identify 6431 cattle harboring at least one cysticercosis lesion and 603 harboring at least one viable cyst.

For cattle harboring at least one cysticercosis lesion, the number of farms where they lived from birth to slaughter ranged from 1 to 10 (Table 2). Among them, 66.8% did not move from birth to slaughter, 25.8% moved once, 5.6% twice and 1.8% more than twice.

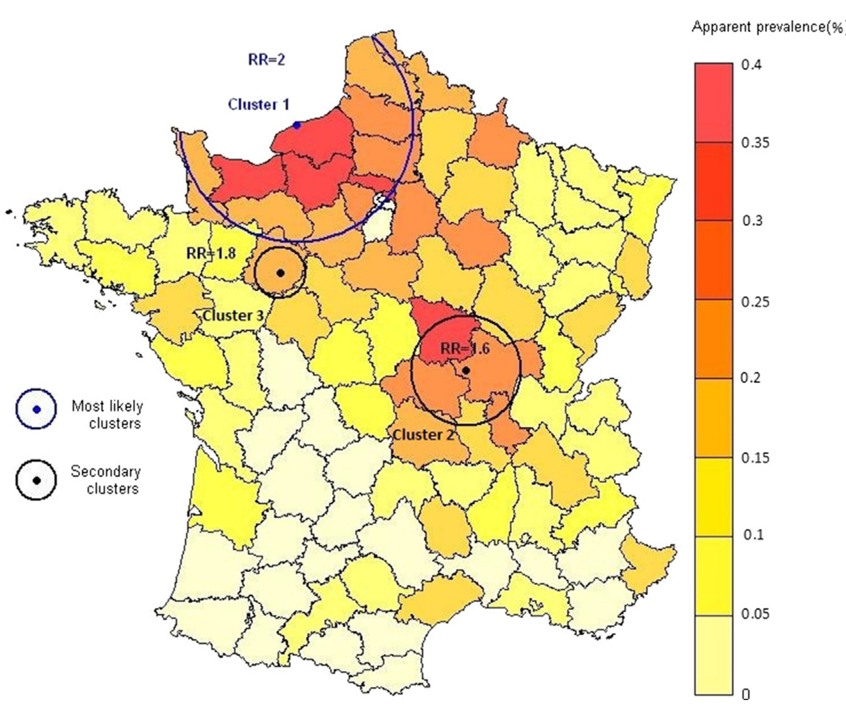

Fig. 1. Apparent prevalence (%) of bovine cysticercosis (with viable or degenerated cysts) and significant clusters of cattle harboring viable or degenerated cysts. Spatial analysis was performed after adjustment for Age and Sex. RR = relative risk.

Table 3
Description of significant clusters of cases of bovine cysticercosis.

Cluster number	Cluster radius (km)	Number of observed cases (%)	Number of expected cases	Relative risk (RR)	*P* value
All types of cysts					
1	172.1	2135 (33.2%)	1267.5	2.0	$1 \cdot 10^{-17}$
2	81.9	453 (7.0%)	292.0	1.6	$3.9 \cdot 10^{-12}$
3	38.4	123 (1.9%)	70.9	1.8	$4.5 \cdot 10^{-3}$
	Total	**6431 (100%)**			
Viable cysts					
1	210.5	203 (33.7%)	107.5	2.3	$8.7 \cdot 10^{-15}$
	Total	**603 (100%)**			

For cattle harboring at least one viable cyst, the number of farms where they lived from birth to slaughter ranged from 1 to 6 (Table 2). Among them, 62% did not move from birth to slaughter, 30.2% moved once, 6% twice and 1.8% more than twice.

The prevalence at the *département* level of cattle harboring at least one cyst and cattle harboring at least one viable cyst ranged respectively from 0 to 0.390% (mean = 0.13%) and from 0 to 0.112% (mean = 0.014%). At the national level, prevalence for all types of cysts and viable cysts was 0.142% [0.142–0.143] and 0.013% [0.013–0.014] respectively.

The highest animal-herd weights were mainly attributed to the last herd before slaughter (herd number order equal to 1) for both all types of cysts and for viable cysts only, with a mean weight for these herds of 0.90 and 0.97 respectively (Table 2). For viable cysts, weights were all null for herd number orders higher than 3, whereas for all types of cysts the mean weight was never lower than 0.05 (Table 2).

3.2. Spatial analysis

A spatial analysis for the detection of clusters of cattle with all types of cysts made it possible to detect three significant clusters (relative risk (RR) ranging from 1.6 to 2) in north-western and eastern France (Fig. 1, Table 3). Among the cases in clusters 1–3, the proportion of animals harboring viable cysts was 5.6%, 9.3% and 5.1% respectively.

A spatial analysis for the detection of clusters of cattle with viable cysts made it possible to detect one significant cluster (RR = 2.3) located in eastern France (Fig. 2, Table 3).

For all the clusters detected with either all types of cysts or only viable cysts, more than 95% of the animal-herds had a herd-order number lower than or equal to 3.

4. Discussion

This study enabled the detection of clusters of cattle harboring cysts while taking into account the uncertainty regarding the location where the animals may have been infected. Three clusters were detected for cattle harboring all types of cysts and one for cattle harboring only viable cysts. The RRs were low, highlighting that there are no clearly identified areas of infection in France. Nevertheless, these clusters pinpointed areas with higher risk. Investigations in these areas could be performed to identify herd-level risk factors, or pasture management or climatic factors that might explain this spatial distribution. These risk factors could then be used to suggest control measures in these areas and to implement a reinforced meat inspection protocol so as to increase the efficiency of the current meat inspection procedure.

The originality of this spatial analysis was that it took into account the uncertainty regarding the location of cattle infection using an animal-herd weighted analysis. This involved establishing rules for weight attribution based on how certain we were that a given herd was the location in which the animal became infected. These rules were based on a literature review of the development of cysts from the viable to the degenerated stage and discussions with experts in bovine cysticercosis. These rules could be updated if new knowledge was obtained on the dynamics of cyst development from the viable to degenerated stage.

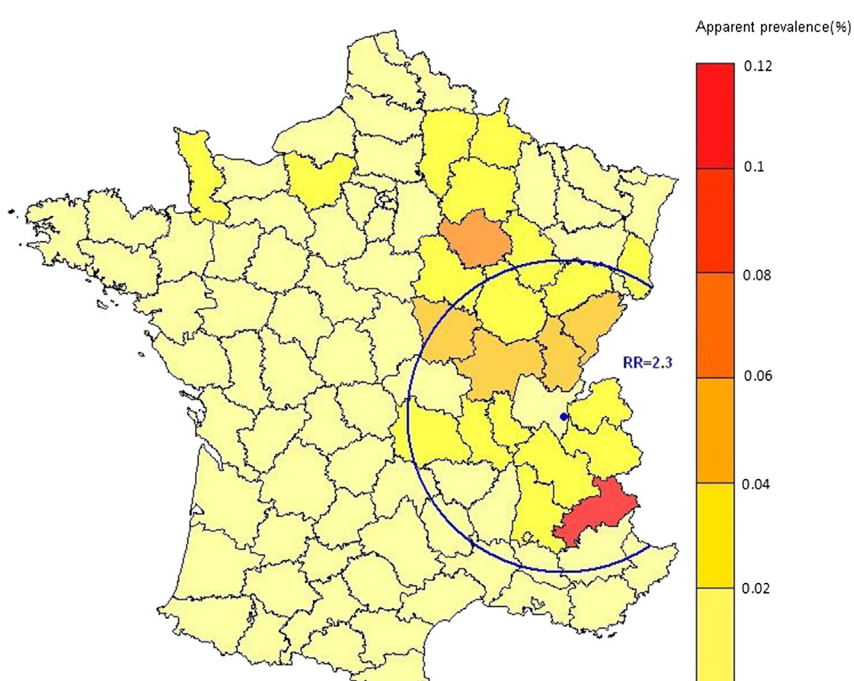

Fig. 2. Apparent prevalence (%) of bovine cysticercosis (with viable cysts) and significant clusters of cattle harboring viable cysts. Spatial analysis was performed after adjustment for Age and Sex. RR = relative risk.

Using the animal-herd level of analysis, it was possible to take into account, in a single spatial analysis, all the cattle harboring cysts regardless of the level of cyst development. As degenerated cysts are the main cysticercosis lesions detected during meat inspection, using only cattle harboring viable cysts for spatial analysis of bovine cysticercosis is restrictive. The different locations of the clusters detected when considering only cattle harboring viable cysts (Fig. 2) or cattle harboring all types of cysts (Fig. 1) proved the relevancy of this method. This novel approach could be used to pinpoint herds with a high risk of infection in order to the identify herd-level risk factors through dedicated investigation and then implement relevant control measures.

Ten percent of the cattle in cluster 2 (cattle with all type of cysts) harbored viable cysts. This cluster was included in the cluster detected during the spatial analysis with cattle harboring only viable cysts. The radius of cluster 2 was however 2.5 times smaller. The proportion of cattle harboring viable cysts in clusters detected during the spatial analysis with cattle harboring all types of cysts could be used as an indicator that the cluster was recent. A cluster in which cattle harboring viable cysts continue to be found is a location in which bovine cysticercosis infection is recent.

5. Conclusion

This study used bovine cysticercosis data from a nearly exhaustive survey conducted in all the cattle slaughterhouses of France.

Results highlighted the usefulness of an animal-herd level spatial analysis in accounting for uncertainty with regard to the location where cattle became infected. Such a method could be used for other diseases, such as tuberculosis or liver fluke, which also have variable time lags between infection and detection.

Performing a similar type of spatial analysis after implementation of control measures, for instance increasing the control of sewage sludge in areas identified as of higher risk could be a useful tool for assessing the effectiveness of these measures.

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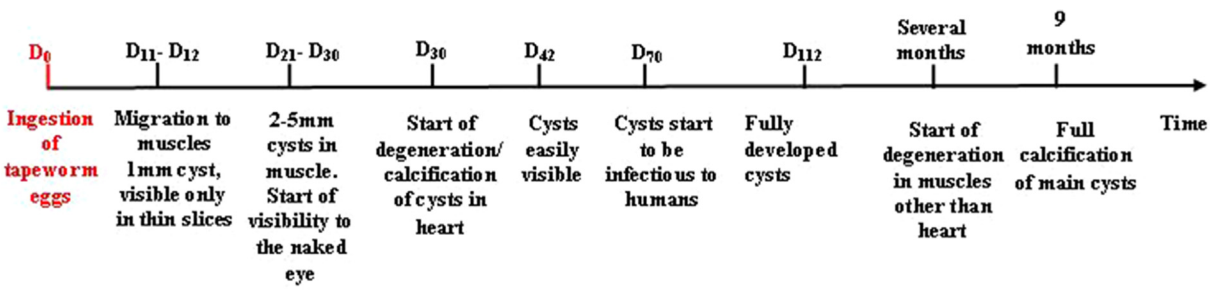
Appendix A

Chronology of the development of cysticercosis cysts from ingestion of tapeworm eggs to calcification. D = Day. From (Allan et al., 2005; Morlot, 2011; Ogunremi & Benjamin, 2010; OIE, 2008).



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