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Short communication

Spatial analysis of bovine cysticercosis in France in 2010

Céline Dupuy [a, b], Claire Morlot [c], Pierre Demont [d], Marie-Pierre Callait-Cardinal [d, e, f], Christian Ducrot [b], Didier Calavas [a], Emilie Gay [a, *]

[a] Epidemiology Unit, French Agency for Food, Environmental and Occupational Health & Safety (ANSES), 31 Avenue Tony Garnier, F-69364 Lyon, Cedex 07, France
[b] Unité d'épidémiologie animale, UR346, INRA, F-63122 St Genès Champanelle, France
[c] Direction générale de l'Alimentation, 251 rue de Vaugirard, F-75732 Paris Cedex 15, France
[d] VetAgroSup Campus Vétérinaire, 1 avenue Bourgelat, F-69280 Marcy l'Etoile, France
[e] Université de Lyon, F-69000 Lyon, France
[f] Université Lyon 1, CNRS, UMR5558, Laboratoire de Biométrie et Biologie Evolutive, Bâtiment Mendel, 43 Bd du 11 novembre 1918, F-69622 Villeurbanne, France

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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

* Corresponding author. Tel.: +33 (0)4 78 61 44 17; fax: +33 (0)4 78 61 91 45.
E-mail address: emilie.gay@anses.fr (E. Gay).

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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 $[b_{\inf\ k}–b_{\sup\ k}]$	Probability of infection during period k (Prob_k)	Range of period k in number of days before slaughter $[b_{\inf\ k}–b_{\sup\ k}]$	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

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

- $b_{\inf\ k}$ and $b_{\sup\ k}$ 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 $j + 1$.