



Epidemiological modelling for the assessment of bovine tuberculosis surveillance in the dairy farm network in Emilia-Romagna (Italy)



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ABSTRACT

Assessing the performance of a surveillance system for infectious diseases of domestic animals is a challenging task for health authorities. Therefore, it is important to assess what strategy is the most effective in identifying the onset of an epidemic and in minimizing the number of infected farms.

The aim of the present work was to evaluate the performance of the bovine tuberculosis (bTB) surveillance system in the network of dairy farms in the Emilia-Romagna (ER) Region, Italy. A bTB-free Region since 2007, ER implements an integrated surveillance strategy based on three components, namely routine on-farm tuberculin skin-testing performed every 3 years, tuberculin skin-testing of cattle exchanged between farms, and *post-mortem* inspection at slaughterhouses. We assessed the effectiveness of surveillance by means of a stochastic network model of both within-farm and between-farm bTB dynamics calibrated on data available for ER dairy farms. Epidemic dynamics were simulated for five scenarios: the current ER surveillance system, a no surveillance scenario that we used as the benchmark to characterize epidemic dynamics, three additional scenarios in which one of the surveillance components was removed at a time so as to outline its significance in detecting the infection. For each scenario we ran Monte Carlo simulations of bTB epidemics following the random introduction of an infected individual in the network. System performances were assessed through the comparative analysis of a number of statistics, including the time required for epidemic detection and the total number of infected farms during the epidemic.

Our analysis showed that slaughterhouse inspection is the most effective surveillance component in reducing the time for disease detection, while routine surveillance in reducing the number of multi-farms epidemics. On the other hand, testing exchanged cattle improved the performance of the surveillance system only marginally.

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1. Introduction

Bovine tuberculosis (bTB) caused by *Mycobacterium bovis* is among the major disease threats to farm animals worldwide (Skuce et al., 2012). bTB is a chronic disease characterized by a variable and generally long incubation period, and its aetiological agent has an exceptionally wide range of hosts, including humans, domestic

and wild animals, as well as high persistence in the environment (Morris et al., 1994). Besides its direct impact to the cattle industry, bTB is a zoonotic disease of great concern. For these reasons, regulatory restrictions are in place to prevent the trade of infected animals and their products within and between countries and to reduce the risk of spillover from the animal to the human compartment. Most countries and transnational areas (such as the European Union) with a thriving cattle industry have developed surveillance systems to prevent bTB outbreaks (Cousins, 2001). Despite the control efforts, bTB is still endemic in many countries, both developed and developing (World Organization for Animal Health, 2008) and

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its eradication has proved to be very challenging (Fitzgerald and Kaneene, 2013; Independent Scientific Group, 2007). Therefore, it is essential to develop surveillance strategies that allow for a rapid detection of infected animals both in endemic and bTB-free areas.

The organization and the components needed for an effective surveillance system in a given territory depend on bTB epidemiology, which is largely determined by the characteristics of the farming system in place. How these factors may interplay to determine the risk of outbreaks in the specific case of bTB has been well documented in the UK and Ireland, where the rising incidence of the infection in the last 20 years has caused significant economic losses (Abernethy et al., 2013; Reynolds, 2006). The direct costs of bTB for UK taxpayers in 2009 were estimated in around £63M (about 95M USD) and over 25,000 cattle were culled (Johnston et al., 2011). Outdoor farming, a common breeding system in the UK and Ireland, favours contacts between animals of different herds, one of the pathways for bTB transmission. In addition, this farming system exposes cattle to the possibly infected wildlife, such as the European badger (*Meles meles*) whose population is endemically infected by *M. bovis* in large areas of the British isles (Cheeseman et al., 1989; Griffin et al., 2005; Morris et al., 1994). Another factor associated with recurrent bTB outbreaks in the UK is between-farm movement of live animals (Johnston et al., 2011; Reilly and Courtenay, 2007). Therefore, preventing contacts between cattle of different herds and between cattle and wildlife are considered effective measures to control bTB risk in the UK and Ireland (Johnston et al., 2011; Phillips et al., 2003; Reilly and Courtenay, 2007).

In countries where indoor farming is the most common breeding practice, such as Italy, bTB transmission rarely occurs through contacts with infected wildlife. A study on bTB risk factors in Northern Italy showed that the main risk factor for bTB breakdown was cattle movement between farms (Marangon et al., 1998). bTB is still endemic, though at very low prevalence, in some Italian regions while it has been eradicated in others.

Among the latter, Emilia-Romagna (ER), located on the right side of the river Po valley (Northern Italy), has been declared officially free from bovine tuberculosis (UE Decision n° 2007/174/CE). This Region has an important food-farming industry characterized by an intensive dairy production, and is the region of origin of Parmigiano-Reggiano cheese. According to the latest official statistics (Italian National Statistics Institute, 2010), about 550,000 cattle are reared in 7343 farms in ER. As an epidemic of bTB in this Region would have severe economic consequences, the regional health authorities have implemented, in compliance with EU regulations (UE Decision 2002/677/CE), an integrated surveillance system to prevent bTB re-emergence in dairy cattle (Regional decision GPG/2010/1049). The system is based on three detection methods, namely: (i) periodic routine skin-test on all animals aged over 24 months (RS); (ii) systematic skin-test on all exchanged cattle (ECT) at the destination farm; and (iii) inspection for bTB lesions of all slaughtered animals (SI). While ER Region has managed to remain bTB-free so far, the effectiveness of the integrated surveillance system (and its individual components) in the case of re-introduction of the infection has never been assessed.

The goal of this work is to quantitatively assess the performance of the current surveillance system and its individual components in terms of (i) time needed to detect a prospective newly introduced bTB epidemic in the dairy farms of ER, and (ii) the magnitude of the epidemic, in terms of number of farms infected before the detection of the epidemic.

Since ER has been free from bTB for many years, no empirical data on the epidemiological dynamics of the infection is available. Therefore, in order to test the performance of the three surveillance methods currently in place in the Region, we developed an individual-based epidemic model capable of simulating the spread

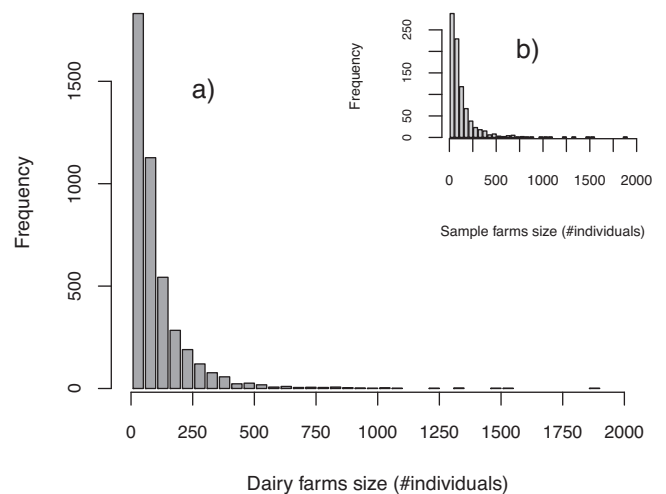


Fig. 1. Distribution of Emilia-Romagna dairy farms size. Every bar corresponds to a size interval of 50 individuals (0–50, 51–100, etc.). (a) All dairy farms size distribution (Min = 1, Median = 63, Mean = 101.9, Max = 1889); (b) sampled dairy farms size distribution (Min = 1, Median = 74, Mean = 126.6, Max = 1889).

of bTB in the regional network of dairy farms following the random introduction of infected animals in the system.

Considering that the rearing system in place in ER and that the components of bTB surveillance described above are largely widespread in several developed countries, our findings can be applicable to many farming and surveillance systems worldwide.

2. Materials and methods

To assess the performance of the current surveillance system and each of its components, we built a data-driven, stochastic network model that simulates both within-farm and between-farm bTB dynamics. We assumed that the contribution of transmission routes other than cattle exchanges – such as airborne transmission or transmission mediated by wildlife or fomites – was negligible within the regional system of industrial indoor farms. Thus, we considered cattle exchanges as the only transmission route for bTB among dairy farms.

Since bTB is a chronic disease characterized by slow transmission dynamics (see Augusto et al., 2011; Huang et al., 2013; Brooks-Pollock et al., 2014) the assumption of endemic equilibrium within a given farm is unrealistic. Then, we explicitly accounted for within-farm disease dynamics describing how epidemics evolve inside farms following the introduction of infected animals.

We represented the system of cattle exchanges of ER as a contact network where nodes represent farms and directional edges represent between-farm animal movements. We reproduced the network of 4353 dairy farms and 20 intermediary trader farms (ITF) by using information from the cattle movement dataset as described hereafter.

All statistical analyses and model simulations were performed using the software R with “MASS”, “triangle” and “poilog” packages (<http://www.r-project.com>).

2.1. Cattle trade movement data

Cattle movement data were provided by the Italian National Bovine database. At the end of 2010, 4353 dairy farms and 20 intermediary trader farms (ITF) were in operation in ER. For all of them we collected the farm size, i.e. number of animals per farm (Fig. 1). For all the ITF and a subset of 837 dairy farms we also collected individual records of every cattle movement, incoming and outgoing, over a 100-week time span (from the beginning of February

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