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► To cite this version:

Céline Richomme, Maria-Laura Boschioli, Jean Hars, François Casabianca, Christian Ducrot. Bovine tuberculosis in livestock and wild boar on the mediterranean island, Corsica. *Journal of wildlife diseases*, 2010, 46 (2), pp.627-631. hal-02655308

HAL Id: hal-02655308

<https://hal.inrae.fr/hal-02655308>

Submitted on 29 May 2020

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Bovine Tuberculosis in Livestock and Wild Boar on the Mediterranean Island, Corsica

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ABSTRACT: The zoonotic agent of bovine tuberculosis (bTB), *Mycobacterium bovis*, can be transmitted between domestic and wild animals, threatening wildlife populations and control programs for bTB in cattle. In Corsica, a French Mediterranean island where domestic and wild species have close interactions, bTB cases have been reported in cattle, pigs, and wild boar. Moreover, genotypes of *M. bovis* found in wild and domestic animals from the same area were identical. These data strongly suggest that wild and domestic animals are associated in an epidemiologic bTB-transmission cycle. More investigations are needed, not only to understand the role played by each species in order to implement appropriate control measures, but also to assess the risk of transmission to humans.

Key words: Bovine tuberculosis, Corsica, epidemiology, wild boar, zoonosis.

Bovine tuberculosis (bTB) is a major disease with serious socioeconomic and public-health implications that is found throughout the world. Like most mammal species, human beings are susceptible to *Mycobacterium bovis*, the principal agent of bTB. In France, after health measures were introduced in the 1950s (mainly milk pasteurization), the incidence of *M. bovis* tuberculosis in humans decreased dramatically (Boulahbal et al., 1998); however, this pathogen is still a cause of human tuberculosis (Mignard et al., 2006). Cattle in France were declared bTB-free by the European Commission in 2001, although the disease still persists in some French regions (Anonymous, 2009). As in the United Kingdom, Spain, Italy, the United States, and New Zealand (Palmer, 2007), bTB in wildlife was recently demonstrated in Normandy (northern France), where

red deer (*Cervus elaphus*) and wild boar (*Sus scrofa*) may be responsible for spill-back transmission to cattle (Zanella et al., 2008a). In this article we report the bTB cases discovered in livestock and wildlife on the French Mediterranean island of Corsica (8,680 km², 42°00'N, 09°00'E) and discuss the epidemiologic and public-health concerns raised by these findings.

In Corsica, cattle (the natural domestic host and main source of *M. bovis*), and other *M. bovis*-susceptible species such as pigs, goats, and sheep (O'Reilly and Daborn, 1995) live in a pastoral, unfenced, mainly mountainous agroecosystem, composed of maquis (xerophilic vegetation) and nondeciduous forests. In 2005 agricultural data reported a total of 74,000 cattle, 37,000 pigs, 48,000 goats, and 149,000 sheep (Source: Agreste, French Ministry of Agriculture and Fishing, <http://agreste.agriculture.gouv.fr/en-region/corse/>); these animals were mainly free-range reared. The two main susceptible wild species in Corsica are the wild boar and the Corsican red deer (*Cervus elaphus corsicanus*). As in mainland France, wild boar populations have increased in the last decade (Klein et al., 2007). Around 20,000 wild boars are hunted each year in Corsica, suggesting a high population density. The habitat of the wild boar is mainly maquis and forest. Wild red deer became extinct on the island in the 1960s. Since 1985, animals from Sardinia, which are believed to be phylogenetically closely related to Corsican red deer, have been bred in fenced areas and reintroduced stepwise in mountainous forested areas. The animals

were first introduced in two areas in south-central and afterwards two areas in north-central Corsica (Fig. 1). The current population of wild red deer is about 200 animals (N. Kidjo, pers. comm.).

In the last two decades domestic outbreaks of bTB have been reported not only in cattle but also more recently in pigs (Table 1, Fig. 1). *Mycobacterium bovis* was isolated from all of these outbreaks. *Mycobacterium bovis* was first isolated from a wild boar in 1989 in the southeastern part of the island (Boschioli, unpubl.). Then, in the 2000s, nine cases from which *M. bovis* was isolated were reported (Table 2) in the same areas where bTB outbreaks also occurred in livestock (Fig. 1). No cases have been reported in goats, sheep, or red deer.

Genotypes were determined for all *M. bovis* strains. A description of each of the strains analyzed by species, year, and site is provided in Tables 1 and 2. Spoligotyping, the most widely used genotyping method for *M. bovis*, is based on the characterization of the direct repeat (DR) region of the *Mycobacterium tuberculosis* complex (Kamerbeek et al., 1997). The technique was used in this study to distinguish between two spoligotypes circulating in both domestic and wild animals: 1) The SB0120 (Mbovis.org database nomenclature), or BCG-like strain, prevalent in mainland France; and, 2) SB0840, specifically found in Corsica (Haddad et al., 2001). MIRU-VNTR typing (Skuce et al., 2005), a more discriminating genotyping method, which allows the discrimination of strains of widely represented spoligotypes such as SB0120, was also used (Zanella et al., 2008a; Tables 1 and 2). The loci ETRA, ETRB, ETRC, and QUB11a and 11b, which in our view provide the best discrimination for *M. bovis* (Zanella et al., 2008a), were characterized. SB0120 strains had a unique MIRU-VNTR profile, as did the SB0840 strains, confirming the existence of two circulating strains on the island; strains isolated from wildlife are identical to those

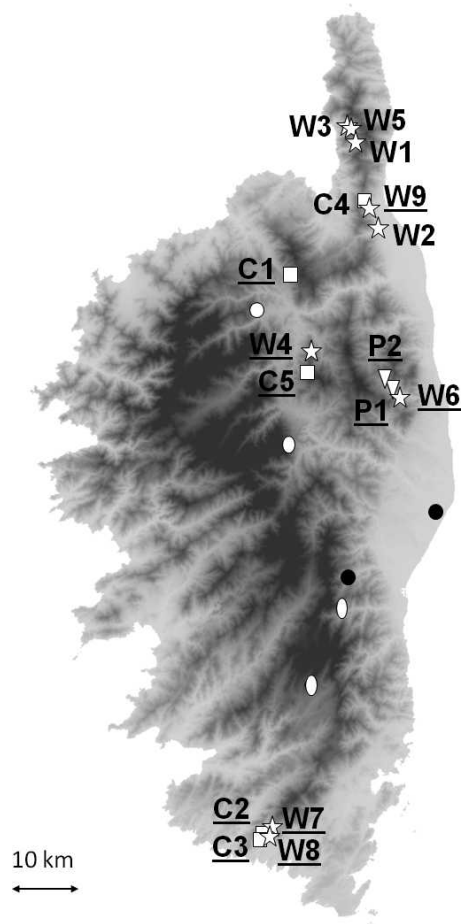


FIGURE 1. Location of outbreaks of bovine tuberculosis in cattle (white squares) and pigs (white triangles), and cases in wild boar (white stars). Geocode numbers refer to Tables 1 and 2. Underlined geocodes=spoligotype SB0840-VNTR pattern 7-5-5-8-2 (Corsican strain). Others=spoligotype SB0120-VNTR pattern 4-5-5-11-4 (BCG-like strain). Location of red deer populations: white ellipses = reintroduced populations; black circles = fenced-reared populations. Cartography: MNT-IGN source.

isolated from domestic outbreaks in the same area (Fig. 1).

Our study disclosed the similarity of strains among different host species in the same sampling sites. These results support the hypothesis that bTB is transmitted between domestic and wild animals in Corsica. Similar findings have been described in other Mediterranean ecosystems including Spain (Aranaz et al., 2004),

TABLE 1. Strains of *Mycobacterium bovis* isolated from livestock in Corsica, France. MIRU-VNTR allele profiles correspond in order to loci ETRA, ETRB, ETRC, QUB11a, and QUB11b.

Site	Year	Species	Spoligotype	MIRU-VNTR profile	Geocode ^a
Pietralba	1997	Cattle	SB0840	7-5-5-8-2	C1
Sartène	2006	Cattle	SB0840	7-5-5-8-2	C2
Sartène	2007	Cattle	SB0840	7-5-5-8-2	C3
Furiani	2008	Cattle	SB0120	4-5-5-11-4	C4
Tralonca	2008	Cattle	SB0840	7-5-5-8-2	C5
Novale	2006	Pig	SB0840	7-5-5-8-2	P1
Pietricaggio	2007	Pig	SB0840	7-5-5-8-2	P2

^a Code refers to Figure 1.

mainland Italy (Serraino et al., 1999) and Sardinia, an Italian Mediterranean island near Corsica (Zanetti et al., 2008).

In Corsica, a large portion of cattle are free-ranging, which hinders the application of screening tests such as the skin test. In some parts of the island, there are also feral cattle that do not belong to identified herds and behave like wild animals. Feral animals are not submitted to the screening tests or the health control or inspection applied to the rest of the cattle on the island under the national bTB eradication program (Reviriego Gordejo and Vermeersch, 2006). Finally, because recently

introduced quartering sites on the island are not used systematically, cattle carcasses are often left in the environment. Infected carcasses, in which *M. bovis* can survive for long periods (Biet et al., 2005), may be responsible for interspecific transmission, especially to scavengers. Thoracic and mesenteric lesions observed in infected wild boar (Table 2) suggest that they acquire the infection through ingestion (Pollock and Neill, 2002). Under these circumstances, it is likely that cattle, especially feral, play a major role in maintaining bTB and represent a source of contamination to wildlife. Nevertheless,

TABLE 2. Strains of *Mycobacterium bovis* isolated from wild boar in Corsica, France.

Site	Year	Site of gross lesions	Spoligotype	MIRU-VNTR	Geocode ^a
Olmeta du Cap ^b	2003	No data	SB0120	4-5-5-11-4	W1
Biguglia ^b	2003	No data	SB0120	4-5-5-11-4	W2
Olcani ^b	2003	No data	SB0120	4-5-5-11-4	W3
Aiti ^b	2003	No data	SB0840	7-5-5-8-2	W4
Olcani ^c	2006	Thoracic and mesenteric lymph nodes	SB0120	4-5-5-11-4	W5
Pietra-di-Verde ^d	2007	Lymph nodes in the head, liver	SB0840	7-5-5-8-2	W6
Sartène ^d	2007	Lymph nodes in the head, lung, liver	SB0840	7-5-5-8-2	W7
Sartène ^d	2007	Lymph nodes in the head, mesenteric lymph nodes	SB0840	7-5-5-8-2	W8
Furiani ^e	2008	Thoracic and mesenteric lymph nodes	SB0840	7-5-5-8-2	W9

^a Code refers to Figure 1.

^b Sanitation survey conducted on the northern *département* by the French National Hunting Office, the local hunting federation and the Veterinary Services (bacterial analysis only conducted on lymph nodes in the head; 99 individuals sampled).

^c Dying animal discovered in very poor body condition, shot by hunters and taken to the Departmental Veterinarian Laboratory for postmortem examination.

^d Trichinellosis surveillance program conducted 2006–2008 on the entire island by the French National Institute for Agricultural Research, the French Food Safety Agency, and the Veterinary Services.

^e Animal found dead in April 2008 in a private garden near the main city of the northern *département*, brought to the Departmental Veterinary Laboratory for postmortem examination.

our current data do not allow us to determine the exact transmission pathways between wild and domestic hosts.

Depending on the ecologic and epidemiologic situation, wild boar may be only spillover hosts as defined by Haydon et al. (2002). Infection may occur only sporadically or persist within the wild boar population in the presence of another source of infection in the ecosystem, as was observed in Italy (Serraino et al., 1999), New Zealand (Coleman and Cooke, 2001), and possibly the Brotonne forest, France (Zanella et al., 2008b). In other situations, the infection may be self-sustaining within the wild boar population in the absence of cattle or other ungulates, as was demonstrated in Spain (Vicente et al., 2006, Naranjo et al., 2008), where the wild boar is considered a reservoir of *M. bovis* due to large or highly concentrated populations resulting from artificial feeding (Haydon et al., 2002). Our findings are not sufficient to elucidate the role of wild boar in the transmission of bTB in Corsica. However, because of high population densities and local hunting practices we believe that the wild boar could be or may become a maintenance host (Haydon et al., 2002) of *M. bovis* on the island. Indeed, leaving game offal in the environment after quartering is an especially high-risk hunting practice that should be avoided to prevent bTB transmission. Although no cases in wild red deer have been reported, their increasing population and high susceptibility to *M. bovis* (Zanella et al., 2008a) makes this species a potential reservoir or spillover host. The composition of a multiple-host community influencing the establishment and prevalence of diseases should be considered when analyzing the role of each susceptible cohabitating population (Holt et al., 2003).

Creation and maintenance of wild reservoirs of tuberculosis and spillback transmission from wildlife to domestic herds would represent an additional threat to the bTB control program in Corsica and to human health. To better understand the

epidemiology of *M. bovis* and define the feasibility of controlling this pathogen on the island, more data must be collected and current surveillance in both livestock and wildlife must be optimized. The current method for investigating tuberculosis in wildlife is by looking for *M. bovis* in cephalic or respiratory lymph nodes or in infected organs after postmortem inspection. Significant efforts are needed to teach hunters how to recognize and sample the appropriate lesions on game carcasses for further analysis in the laboratory. However, because the presence of *M. bovis* is not always correlated with lesions in wild boar, bovine tuberculosis can be underestimated (Zanella et al., 2008b). The validation of serologic methods in wildlife may offer a new means of investigation (Aurtenetxe et al., 2008).

Transmission of *M. bovis* from animals to humans may occur via infectious aerosols while handling carcasses with lesions (Neill et al., 1989). In Corsica, farmers and hunters are considered to be at-risk populations to whom preventive practices relating to carcass handling and management should be promulgated.

We thank the Corsican Hunters' Federations and Veterinary Services for their collaboration, the Savoie and Gard Regional Veterinary Laboratories for bacterial analysis, O. Maestrini for his helpful work in the field, and Emmanuelle Gilot-Fromont and Victoria Boschiroli for valuable comments on the manuscript.

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Submitted for publication 27 February 2009.