

Mycobacterium caprae Infection in Livestock and Wildlife, Spain

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Mycobacterium caprae is a pathogen that can infect animals and humans. To better understand the epidemiology of *M. caprae*, we spoligotyped 791 animal isolates. Results suggest infection is widespread in Spain, affecting 6 domestic and wild animal species. The epidemiology is driven by infections in caprids, although the organism has emerged in cattle.

Mycobacterium caprae is a cluster within the *M. tuberculosis* complex (online Technical Appendix, www.cdc.gov/EID/content/17/3/532-Techapp.pdf). This pathogen has been recognized mainly in central Europe, where it has been occasionally isolated from tuberculous lesions from cattle (1–5), pigs (4), red deer (*Cervus elaphus*) (4,5), and wild boars (*Sus scrofa*) (3). Its isolation from humans has also been described (3,6); often, a contact with livestock has been suggested as a likely means of transmission (5). To our knowledge, this pathogen has never been isolated outside continental Europe, except from a European patient in Australia (7) and a cow in Algeria (8).

The combination of disease tracing and molecular typing is needed to understand the epidemiology of tuberculosis. This report describes the molecular epidemiology of *M. caprae* infection in Spain compared with other countries. We characterized *M. caprae* isolates from goats and other domestic and wild animals by

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spoligotyping (9). The relative contribution of each animal and its role in animal tuberculosis are discussed.

The Study

This study included 791 *M. caprae* isolates from domestic goats (*Capra aegagrus hircus*, n = 542), sheep (*Ovis aries*, n = 2), cattle (*Bos taurus*, n = 229), domestic pigs (*S. scrofa domestica*, n = 2), wild boars (*S. scrofa*, n = 14), red deer (*Cervus elaphus*, n = 1), and a fox (*Vulpes vulpes*, n = 1). The samples originated from skin test-positive animals identified within the national or regional eradication programs, from abattoir surveillance, and from postmortem inspections of wildlife, and were collected from 1992 through June 2009 in different geographic areas in Spain (Figure 1). Spoligotyping was performed as described (9), and authoritative names for spoligotype

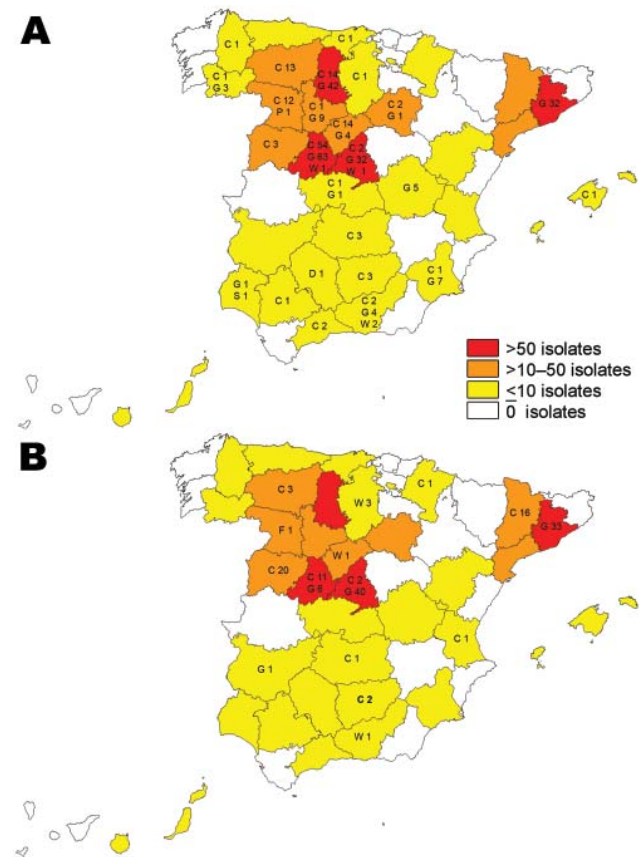


Figure 1. Map of Spain showing the distribution of the 2 most frequent *Mycobacterium caprae* spoligotypes and affected animals: C, cattle; D, red deer; F, fox; G, goats; S, sheep; P, pigs; WB, wild boar. A) Spoligotype SB0157. B) Spoligotype SB0416.

¹A list of members of The Spanish Network on Surveillance and Monitoring of Animal Tuberculosis can be found in the online Technical Appendix (www.cdc.gov/EID/content/17/3/532-Techapp.pdf).

Table 2. Variable number tandem repeat analysis of isolates from 10 farms that presented mixed *Mycobacterium caprae* infection (different spoligotype patterns), Spain, 1992–2009*

Farm	Animal	Spoligotype	No. alleles at locus							
			ETR-A	ETR-B	ETR-D	QUB3232	QUB 11a	QUB 11b	MIRU 26	MIRU 31
1	Goat	SB0416	4	4	4	8	7	2	5	2
		SB0866	5	3	3	8	7	4	2	4
2	Goat	SB0416	4	3	4	8	7	2	4	2
		SB0157	4	3	4	8	7	2	4	2
3	Goat	SB0416	4	5	5	7	6	4	5	5
		SB0415	5	1	3	8	7	3	5	5
4	Cattle	SB0157	3	3	4	8	7	2	5	2
		SB1081	3	3	4	8	7	2	5	2
5	Cattle	SB0157	4	3	4	3	7	2	5	2
		SB1081	4	3	4	3	7	2	5	2
6	Goat	SB0157	4	3	4	8	7	2	5	2
		SB1078	4	3	4	8	7	2	5	2
7	Goat	SB1084	5	1	3	9	5†	3	5	4
		SB1889	5	1	3	9	5†	3	5	4
8	Cattle	SB0157	4	3	4	8	7	2	5	2
		SB1081	4	3	4	8	7	2	5	2
9	Cattle	SB0416	5	3	3	8	6	4	2	3
		SB0157	4	3	4	8	7	2	5	2
10	Goat	SB0973	4	3	–	–	–	–	–	–
		SB0157	4	3	4	9	–	2	5	–

*–, no amplification.

†Gel band of ≈1,800 bp. Sequencing showed that insertion sequence IS6110 is inserted within the third repetition of QUB11a.

disseminated tuberculous lesions that it produces and its fast transmission within a herd. Second, caprine herds have not been included in the national eradication campaign (except when coexisting with cattle or as part of some regional programs). Therefore, *M. caprae* infection can spread easily through animal movements, such as purchase for replacement or genetic improvement.

The emergence of this pathogen in cattle has been observed. Cattle were involved in 106 outbreaks (53.3%) during the study period. Since 2004, cattle from 2,218 herds identified in the eradication program have been inspected by bacteriology. The number of cattle properties infected with *M. caprae* represented 0.85%–6.67% of the total number of herds diagnosed with bovine tuberculosis. Temporal trend of *M. caprae* isolates cultured over time was assessed by using the software WINPEPI 9.4 (13). The proportion of *M. caprae* isolated from bovine samples has increased consistently during 2004–2009, showing a significant positive trend ($p = 0.009$, by Mantel trend test) (Figure 2). We observed more *M. caprae* infections in cattle in regions with a high goat density. However, an analysis of the type of farm production shows that 86.7% of *M. caprae*-infected cattle have been raised in farms without any contact with small ruminants. This fact indicates recirculation of the pathogen within and between cattle herds. In countries that are virtually free of animal tuberculosis such as Germany, Austria, and the Czech Republic, a large number of cases in cattle and red deer are caused by *M. caprae*.

Identification of isolates from human patients has shown *M. caprae* as a human pathogen (3,6,14). A recent study suggests that *M. caprae* causes 0.3% of the cases of human tuberculosis in Spain, with SB0157 also being the most dominant spoligotype (14). The role of the pathogen as a public health risk is highlighted by lesions that can

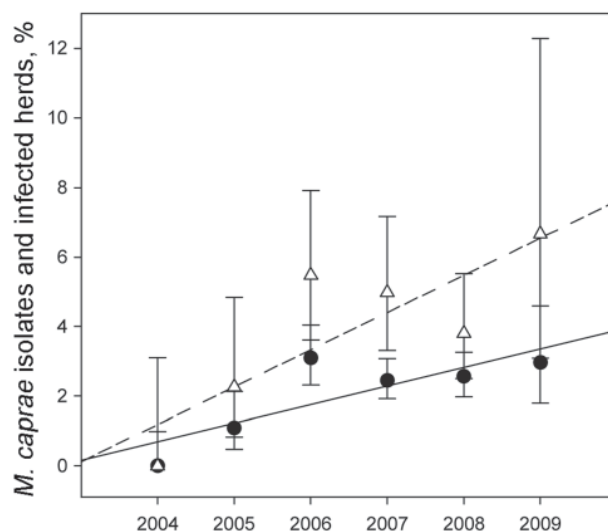


Figure 2. Proportion and regression lines of *Mycobacterium caprae* isolates (black dots, continuous line) and *M. caprae*-infected herds (white triangles, dashed lines) of the total number of *M. tuberculosis* complex isolates and *M. tuberculosis* complex-infected herds identified in cattle during 2004–2009. Error bars indicate 95% confidence intervals.

also be found in the mammary glands of infected goats; thus, consumption of unpasteurized dairy products remains a concern (15).

Conclusions

Compelling evidence indicates that *M. caprae* poses a serious health risk not only for goats, but also for other domestic and wild animal species and humans. Our results indicate that *M. caprae* infection is widespread in Spain and that the epidemiology is driven by caprine infections. Considering the role of *M. caprae* in animal tuberculosis, relevant legislation should be considered to address the infection as was done for *M. bovis*.

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