

Letters to the Editor

Mycobacterium microti: More Widespread than Previously Thought

Mycobacterium microti typically causes disease in voles, wood mice, and shrews (6). Only rarely has this bacterium been isolated from other animals, among which are a llama, cats, pigs, a rock hyrax, and a ferret (2, 4, 5). Recently, *M. microti* isolates from different sources were characterized by using novel genetic markers (5), and this study for the first time disclosed four cases of *M. microti* infections in humans in The Netherlands. Here we describe the finding of additional *M. microti* infections in animals and a human in the United Kingdom (UK) that were identified by spoligotyping (3).

In the framework of a European Union project on the development of novel standardized methodology for the identification of and nomenclature for *Mycobacterium bovis*, spoli-

M. microti isolate from a llama (5) (Table 1). Six of these strains were from a study including 19 isolates from cats previously described as an undefined subgroup of the *M. tuberculosis* complex by Gunn-Moore et al. (1). In that study the authors occasionally observed acid-fast bacilli with hooked or looped forms, which are characteristic of *M. microti* (5). Because the sources of infection may have been prey related due to the avid hunting behavior of the respective cats, the authors speculated that this type of strain originated from wild prey animals, such as small rodents.

Only three spoligotypes were found among the 12 previously described *M. microti* strains (5), indicating that these spoligotypes are characteristic of *M. microti*. The finding of isolates

TABLE 1. Spoligotype patterns and information on the isolates described in this study^a

Type of pattern	Spoligotype	Laboratory	Source ^b
Vole■■..... ^c	RIVM	Vole (5), human (4), ferret (1), pig (1)
■■.....	CVL	Cat (1)
	..■.....■■.....	CVL	Badger (1), cat (1), cow (1)
Llama	..■■■■.....■■■■.....■■..... ^c	RIVM	Llama (1)
	..■■■■.....■■.....■■.....	CVL	Cat (5), human (1)
	..■■■■.....■■■■.....■.....	CVL	Cat (1)

^a The spoligotypes from the RIVM represent 12 recently characterized *M. microti* strains (5). The remaining spoligotypes were of 11 previously uncharacterized *M. tuberculosis* complex strains whose patterns are in the CVL database.

^b Numbers in parentheses indicate the number of isolates.

^c Spoligotype present in the database.

gotype patterns of *Mycobacterium tuberculosis* complex strains from the Central Veterinary Laboratory (CVL), UK, were compared to the ones in an international database of spoligotype patterns at the National Institute of Public Health and the Environment (RIVM) in The Netherlands. This database also contains the previously described spoligotype patterns of *M. microti* strains (5). Surprisingly, the patterns of 11 *M. tuberculosis* complex isolates from the CVL database were identical or highly similar to the spoligotypes of *M. microti* isolates (Table 1). The majority of these were from cats from the south of England (Kent and Sussex) and were sent to the CVL by the Public Health Laboratory Service, Cardiff, Wales, for further investigation on the basis that they had been found to have characteristics between those of *M. bovis* and *M. tuberculosis*.

Analysis of spoligotyping patterns revealed that one cat isolate had a spoligotype identical to that of the characteristic vole type, as established in the previous study with vole isolates from the UK (5) (Table 1). In addition, three strains exhibited a novel spoligotype that resembled the characteristic vole pattern. These strains hybridized with one additional spacer, spacer 4. These strains were obtained from a cat, a cow, and a badger. The cow and the badger originated from the Gloucestershire and Cornwall regions of England, respectively.

Furthermore, the spoligotypes of seven isolates identified in the CVL database originating from six cats and a human were almost identical to the spoligotype of a previously described

from animals and a human with identical or nearly identical spoligotypes within the CVL database suggests that these isolates represent *M. microti*.

Due to the fastidious nature of *M. microti* and the difficulties in characterizing this bacterial species by traditional methods (4), the prevalence, geographical distribution, and host range of this organism may have been underestimated. Our study suggests that *M. microti* is more widespread among different hosts than previously thought.

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