Short Communications

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Unusual cluster of *Mycobacterium bovis* infection in cats

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BOVINE tuberculosis (TB) caused by *Mycobacterium bovis* is a major problem in British cattle. Furthermore, *M bovis* infection has been documented in many other mammals, with badgers acting as an important reservoir and vector of infection for cattle in the west of England and parts of Wales. However, with a few exceptions, the bovine TB epidemic in British cattle has not significantly affected companion animal populations, which are considered 'spillover' hosts (Shrikrishna and others 2009, Broughan and others 2013, Gunn-Moore and others 2013). In the seven years (2006/12) since *M bovis* infection in pet animals became notifiable to the AHVLA, fewer than 30 cats have been confirmed with *M bovis* each year in Great Britain (Broughan and others 2013, Defra 2013). The vast majority of these cases are sporadic and concentrated in regions of Great Britain where bovine TB is endemic, although a small number of multiple cases in single households have been reported (Monies and others 2000).

Between December 2012 and March 2013, seven laboratory-confirmed cases of feline *M bovis* infection were presented to one small animal veterinary clinic in Newbury, Berkshire, England. A further two suspected cases of *M bovis* infection were also identified in the same time-frame, but the cats died without further sampling and confirmation of the diagnosis by laboratory culture of the bacterium was not possible. All nine cats belonged to separate households and presented with different clinical pictures, although some common signs were seen. In three cases, one enlarged popliteal lymph node was the principal finding. In two of these, general malaise including anorexia was accompanied by a serosanguinous fluid discharge from the skin overlying the lymph node. Three other cats had a non-healing lesion on a foot (two forefeet and one hindfoot) consistent with having been bitten; most likely by rodents or another cat judging by the size of the lesions. Generalised lymphadenopathy with no other signs was described in another case, although one popliteal lymph node was much larger than other palpably enlarged nodes. One case was identified incidentally at a booster vaccination, presenting with an abdominal mass and a history of diarrhoea. Radiography of this cat and six of the other cases showed interstitial pneumonia. The ninth case was possibly a nosocomial infection presenting with a serosanguinous discharge from a swollen castration wound three weeks after the operation. *M bovis* was isolated in all seven confirmed cases from tissue samples – three biopsies of lymph node, lung removed postmortem, and three samples from non-healing wound tissue. Five cases were treated with antibiotic combinations of azithromycin with either marbofloxacin or rifampicin. All showed an apparent good response with marked diminishment of signs on chest radiographs taken one to three months following the beginning of treatment. For cases that were not treated, one died and the rest were euthanased. Only three of the five treated cats were known to have survived (one was euthanased and one disappeared). The presence or history of likely bite wounds in four cases, and popliteal lymph nodes potentially enlarged from a distal hindlimb inoculation in three others, offers a route of infection through biting for seven of the nine cases.

Geographically, the nine cats lived within a 5 km radius; six lived within a 250 m radius on a housing estate located adjacent to woodlands and approximately 250 m from a common, grazed with cattle from three different herds. Following the diagnosis of *M bovis* infection in the cats, tuberculin skin testing of the cattle on the common revealed a small number of test reactors infected with the same geno-

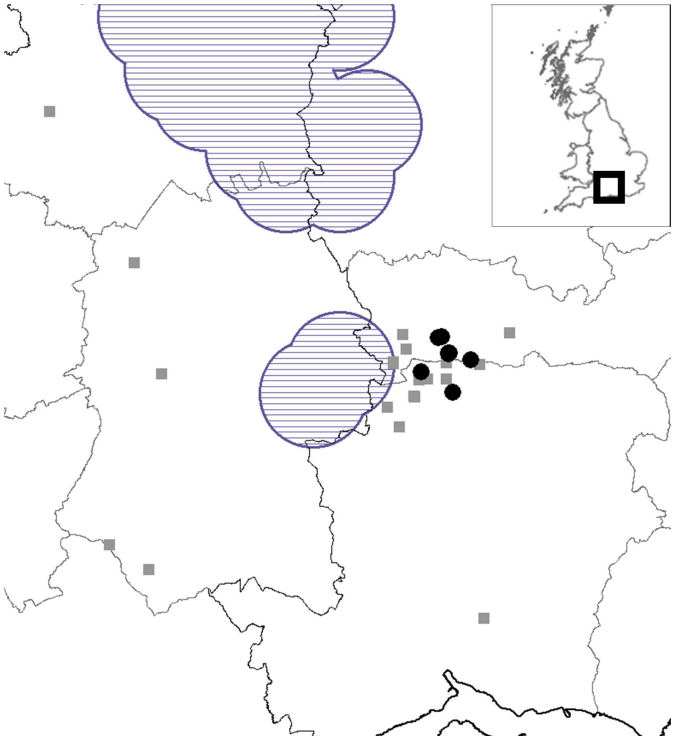

FIG 1: Geographical localisation of the seven confirmed (2012/13), two suspected (2012/13) and one identified from the spoligotype database (2011) cases of *Mycobacterium bovis*-infected cats in the Newbury area (filled circles). The two northern-most filled circles represent seven overlapping isolates. A selection of tuberculosis breakdowns caused by genotype 10:u in cattle and an alpaca are also shown (grey squares). The first isolation of 10:u was in a cow with tuberculous lesions detected during routine postmortem meat inspection (2008). The home range (a region where the genotype is commonly found in cattle) of the closely related genotype 10:a is shown (hatched). A home range consists of a series of 5 km squares considered 'in home range' if a confirmed breakdown of a particular genotype has been recorded in three or more years, in at least two unique holdings, in the last five years. A 10 km buffer is then applied to reduce the 'swiss cheese' effect. Inset: The area within the UK is shown

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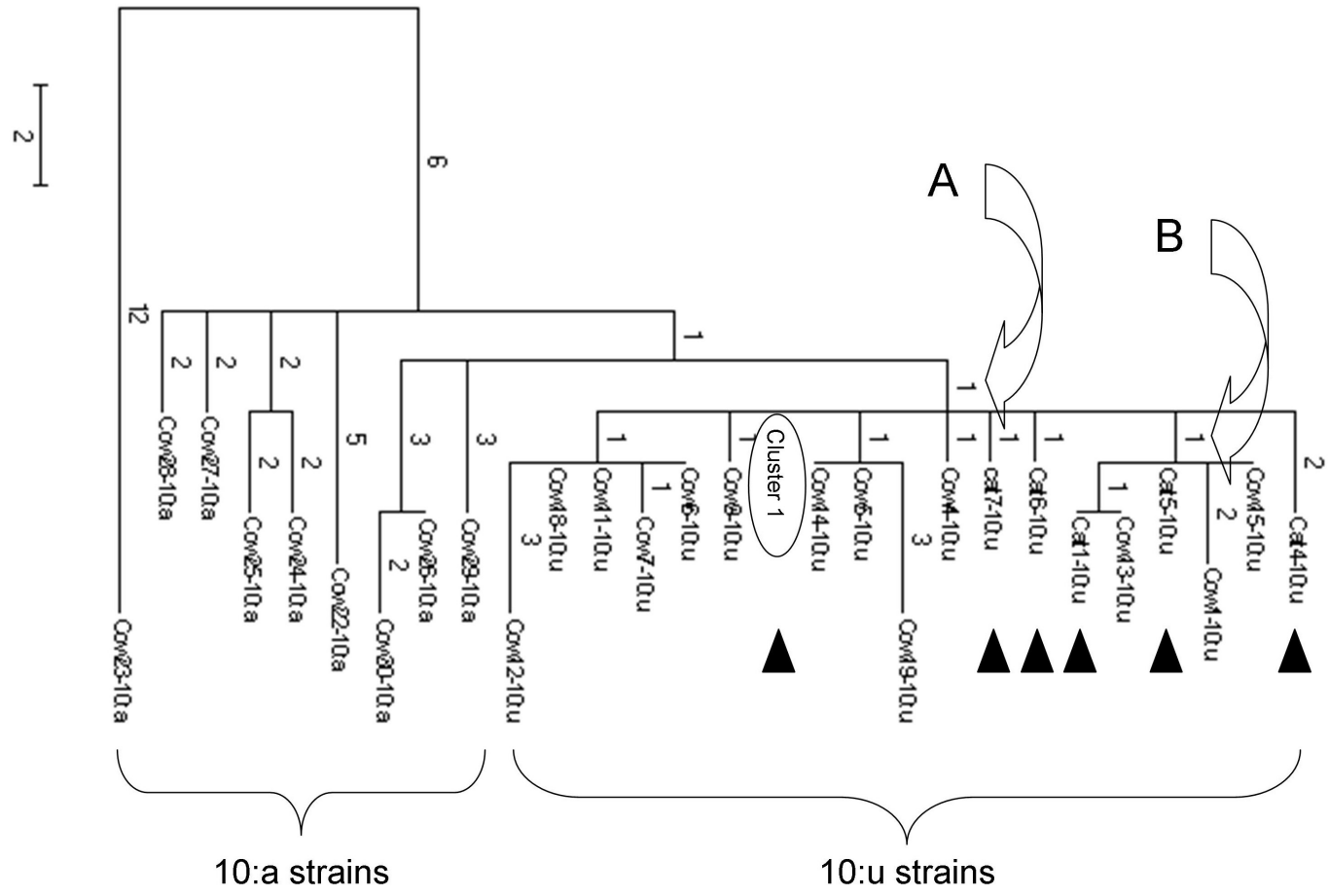

FIG 2: Whole genome sequencing phylogenetic relationship of genotype 10:u isolates from cattle, an alpaca and eight cats and a selection of 10:a isolates from cattle (neighbour joining tree of all single nucleotide polymorphisms [SNPs], scale bar represents 2 SNPs). Heat-killed cultures were sequenced using a MiSeq sequencer (Illumina) and reads were mapped onto reference strain AF2122. The average coverage ranged from 10.7 to 103.2. Cat isolates are indicated by filled triangles and the single SNP present in all 10:u strains is indicated (A). The isolate 'Cluster1' (circled) represents six cattle, an alpaca and three cat strains with identical whole genome sequence. The single informative SNP, which marks a separate cluster containing both cattle and cat isolates is marked (B). If cat-to-cattle transmission is discounted then the simplest explanation for the two phylogenetic clusters that contain both cat and cattle isolates is that at least two separate transmissions from local wildlife/cattle have occurred into Newbury cats

type as the cats. Direct contact of cats with these cattle was unlikely considering the cats' roaming ranges. We suggest that the most likely source of infection for at least some of the cats is infected wildlife – probably rodents and/or badgers. Cat-to-cat transmission cannot be ruled out and could explain the tight spatiotemporal clustering of cases. Apart from one case mentioned, the veterinary practice could be ruled out as the source of infection for these cats because all were first presentations with little history of previous visits.

All *M bovis* isolates from the culture-confirmed feline cases were of the 10:u genotype, previously identified in Great Britain in another cat (2011), an alpaca (2010) and 21 cattle herd breakdowns (Fig 1). All eight 10:u feline isolates and a selection of 10:u isolates from cattle and an alpaca were whole genome sequenced (WGS), as well as representative isolates of the closely related genotype, 10:a (Fig 2). Strains of 10:a in Great Britain represent 3.5 per cent of cattle isolates and are the closest *M bovis* home range to Newbury (Fig 1). The isolates of 10:u from the cats are very similar in WGS, although two clusters can be separated by an informative mutation (Fig 2). These two clusters are also found in *M bovis* isolates from local cattle. Although these data can be interpreted in a number of ways, the simplest explanation is that the two clusters of 10:u isolates in cats represent two separate transmissions from the local bovine TB population into these cats. That is, the informative WGS polymorphism in Newbury cats merely reflects the polymorphism found in the local cattle/wildlife population.

The detection of this unusual cluster of tuberculous disease in cats associated with *M bovis* infection does not alter the current view that these animals represent occasional spillover hosts of the bacterium and play a limited role in the epidemiology of bovine TB in Great Britain. Nevertheless, *M bovis* infections in cats can cause a serious chronic disease that, if not quickly diagnosed, can pose a very low risk of infection to human contacts and other animals (Public Health England 2014).

Given the lack of validated antemortem diagnostic assays for feline TB infection, the similar clinical and pathological presentations caused by different mycobacteria, and the implications for prognosis and case management, identification of the causative organism by culture remains the 'gold standard' diagnostic technique for bovine TB in cats. Practitioners faced with a suspected case of feline mycobacterial infection should submit fresh tissue samples from the affected animal for culture to a specialist laboratory such as AHVLA – Weybridge.

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All authors were involved in the study design. TR carried out the field epidemiological investigation. CO'C provided an overview of feline infection by bovine TB in Great Britain. RdlR supplied an update of current policy implications and advice. NHS and JN-G genotyped and WGS the isolates. All authors contributed to the writing of the manuscript.

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Competing interests
No competing interests recorded.

References
BROUGHAN, J. M., DOWNS, S. H., CRAWSHAW, T. R., UPTON, P. A., BREWER, J. & CLIFTON-HADLEY, R. S. (2013) *Mycobacterium bovis* infections in domesticated non-bovine mammalian species. Part 1: review of epidemiology and laboratory submissions in Great Britain 2004-2010. *Veterinary Journal* **198,** 339-345

DEFRA (2013) Incidents of *M bovis* infection in non-bovine domestic animals and wild deer in GB confirmed by laboratory culture. www.gov.uk/government/uploads/system/uploads/attachment_data/file/232602/bovinetb-otherspecies-27aug13.xls. Accessed December 13, 2013

GUNN-MOORE, D. A., GAUNT, C. & SHAW, D. J. (2013). Incidence of mycobacterial infections in cats in Great Britain: estimate from feline tissue samples submitted to diagnostic laboratories. *Transboundary and Emerging Diseases* **60,** 338-344

MONIES, R. J., CRANWELL, M. P., PALMER, N., INWALD, J., HEWINSON, R. G. & RULE, B. (2000) Bovine tuberculosis in domestic cats. *Veterinary Record* **146,** 407-408

PUBLIC HEALTH ENGLAND (2014) *Mycobacterium bovis* and cat to human transmission in the UK. Health Protection Report 8(12). Advance Access Report, published March 27, 2014

SHRIKRISHNA, D., DE LA RUA-DOMENECH, R., SMITH, N. H., COLLOFF, A. & COUTTS, I. (2009) Human and canine pulmonary *Mycobacterium bovis* infection in the same household: re-emergence of an old zoonotic threat? *Thorax* **64,** 89-91