Despite control efforts, *Mycobacterium bovis* incidence among cattle remains high in parts of England, Wales, and Northern Ireland, attracting political and public health interest in potential spread from animals to humans. To determine incidence among humans and to identify associated factors, we conducted a retrospective cohort analysis of human *M. bovis* cases in England, Wales, and Northern Ireland during 2002–2014. We identified
After the 1960s, the number of human cases of tuberculosis (TB) caused by *Mycobacterium bovis* decreased significantly in England, Wales, and Northern Ireland, coinciding with widespread implementation of milk product pasteurization and national bovine TB control programs (1–3). During the past 2 decades in these 3 countries, an average of 30 cases of *M. bovis* in humans occurred annually; numbers decreased in the early 2000s before again increasing (4–6). During the same period, incidence of *M. bovis* in cattle herds in parts of England, Wales, and Northern Ireland increased substantially but has now plateaued (4,7–9).

*M. bovis* control (2,7,10,11) attracts political, public health, and media interest because of potential spread from animals to humans, effects on animal health and trade (1), and the role of wildlife in the transmission cycle (12). Highly visible interventions, including wildlife management to prevent transmission to livestock, are used to attempt to control *M. bovis* spread (6,9,10), thereby protecting human health.

Compared with other countries in western Europe, the rate of TB among humans in the United Kingdom is high: 9.6 cases/100,000 population (6,240 cases) in 2015 (13). Most TB cases occurred in those born abroad, who probably acquired infection before entering the United Kingdom. Although only 1.1% (42 cases) of culture-confirmed TB cases were caused by *M. bovis* (6), it remains a public health priority.

The drivers of the epidemiology of *M. tuberculosis* are well described (13–15). However, there is comparatively less information on the sources of *M. bovis* in humans, other than the recognized risks of unpasteurized milk consumption and close contact with infected cattle (1,3). We provide an update on the demographic characteristics of humans with *M. bovis* disease in England, Wales, and Northern Ireland (16). To address the gap in knowledge regarding lesser known sources of acquisition, we describe the demographic and clinical characteristics of humans with TB caused by *M. bovis* compared with *M. tuberculosis*. In addition, we describe potential human exposures that may indicate *M. bovis* acquisition and include a genotyping comparison of the causative organisms.

### Materials and Methods

#### Study Population and Definitions

Our retrospective cohort study included all human *M. bovis* patients in the descriptive analysis. To describe demographic and clinical characteristics associated with *M. bovis* disease, we compared all *M. bovis* notified patients with all *M. tuberculosis* notified patients. Potential exposures to risk factors associated with *M. bovis* acquisition were collected through a questionnaire and limited to *M. bovis* cases identified during 2006–2014, when the questionnaire return rate was high (>80%).

An *M. bovis* case was defined as a culture-confirmed human case of TB specified as *M. bovis* isolated during 2002–2014. A notified *M. bovis* case was an *M. bovis* case clinically notified to the Enhanced TB Surveillance system (ETS); a nonnotified *M. bovis* case was an *M. bovis* not reported clinically to ETS. An *M. tuberculosis* notified case was defined as a culture-confirmed human case of TB specified as *M. tuberculosis* isolated during 2002–2014 and clinically notified to ETS.

#### Data Collection

Results from culture-positive laboratory isolates were sent from *Mycobacterium* reference laboratories in England, Wales, and Northern Ireland to Public Health England. These results were matched with notified TB cases from ETS, used for statutory notification of TB, by use of a probabilistic matching method (17).

Data on demographics (age, sex, ethnicity, country of birth, time since UK entry, address, and occupation); clinical factors (site of disease and previous diagnosis); and social risk factors (current or past imprisonment, homelessness, drug and alcohol misuse) were obtained from ETS notifications. For nonnotified *M. bovis* cases, the only patient demographic information available was age, sex, and address; the disease site was inferred from specimen site. For analysis, we used the age groups 0–14, 15–44, 45–64, and ≥65 years and the ethnic groups white, black African, Indian subcontinent (Indian, Pakistani, and Bangladeshi grouped together), and other. After assignment to a geographic area of residence based on address, the place of residence was classified as rural or urban by using 2011 census classifications (18).

After identification of an *M. bovis* case (based on phenotypic, PCR, and genotypic methods [19,20]), a questionnaire (online Technical Appendix, https://wwwnc.cdc.gov/EID/article/23/3/16-1408-Techapp1.pdf) (21) was issued to collect information on potential recognized current or past *M. bovis* exposures. These exposures were contact with a human TB patient, travel (for ≥2 weeks) to or residence in a country with high TB incidence (defined as having an estimated rate of ≥40 cases/100,000 population during 2002–2014), consumption of unpasteurized milk product,
occupational contact with animals, physical contact with wild (nondomestic) animals, and physical contact with any animal with TB (including pets).

**M. bovis Trend Analysis**

We calculated incidence rates per 100,000 population by using mid-year population estimates produced by the UK Office for National Statistics (22). We used Poisson regression to calculate the incidence rate ratio to assess the trend in *M. bovis* incidence over time. We used a nonparametric test for trend across ordered groups to assess the age trend of *M. bovis* patients and the $\chi^2$ test for trend to assess the proportion of *M. bovis* among culture-confirmed TB cases.

**Factors Associated with *M. bovis* Disease and *M. tuberculosis* Disease**

Demographic and clinical characteristics for *M. bovis* notified patients were compared with those of *M. tuberculosis* notified patients by using univariable and multivariable logistic regression to calculate odds ratios to identify factors associated with *M. bovis* disease. A forward stepwise multivariable logistic regression model was used, including sex and all variables with a p value <0.2 in univariable analysis; likelihood ratios were assessed after each stepwise addition to the model. In addition, we conducted a stratified analysis based on place of birth (UK-born/non–UK-born). A p value of <0.05 was considered statistically significant. We tested interactions between biologically and statistically plausible variables in the model by using likelihood ratios. All analyses were conducted by using Stata 13.1 (StataCorp LLC, College Station, TX, USA).

**Exposures to Risk Factors Associated with *M. bovis* Disease**

To identify frequent exposure to risk factors among the cohort, we used case exposure history, as collected through the questionnaire (online Technical Appendix), for descriptive analysis. In addition to obtaining questionnaire information about contact with another human TB patient, for culture-positive isolates identified during 2010–2014, we also obtained 24-loci mycobacterial interspersed repetitive unit–variable tandem repeat (MIRU-VNTR) strain typing results (20) from Mycobacterium reference laboratories. This information enabled us to identify strain type clusters, defined as $\geq$2 human TB cases with indistinguishable MIRU-VNTR profiles (or with an indistinguishable profiles but with 1 case only typed to 23 loci), Clustered cases were further investigated to identify possible epidemiologic links, the identification of which suggest recent human-to-human transmission (23).

**Results**

**Demographics of *M. bovis* Patients**

For 2002–2014, we identified 357 culture-confirmed cases of *M. bovis* disease in humans. During this time, the proportion of all culture-confirmed TB cases speciated as *M. bovis* increased from 0.4% to 0.9% (p<0.001). Annual case numbers ranged from 17 in 2002 to 35 in 2014, and the incidence rate fluctuated between 0.03 and 0.06 cases/100,000 population (Figure 1); the incidence rate ratio per year was 1.04 (95% CI 1.01–1.07). Overall, 92.2% (329/357) of *M. bovis* cases were notified to ETS; since 2011, all identified cases have been notified.

Among 297 *M. bovis* patients for whom place of birth was recorded, 214 (72.1%) were born in the United Kingdom. The most frequent countries of birth for the others were Nigeria (18 patients), Morocco (9 patients), and India (8 patients). The age distribution differed significantly between those born and not born in the United Kingdom (p<0.001) (Table 1). The median age of UK-born patients fluctuated over time, from 71 years (interquartile range 60–76)
in 2002 to 53 years (interquartile range 35–79) in 2014 (p = 0.099), as did the proportion of cases by age group (Figure 2). Only 6 M. bovis cases in patients <15 years of age were reported (all 11–14 years of age).

For all 3 countries, the highest proportion of M. bovis patients resided in London, England (18.5%; 66/357), followed by the South West (15.4%; 55) and West Midlands regions of England (13.2%; 47) (Figure 3, panel A). However, the incidence rate was highest in Northern Ireland (0.11 cases/100,000 population), followed by the South West (0.08/100,000) and West Midlands (0.07/100,000) regions. The highest proportion (71.9%; 41/57) of M. bovis patients not born in the United Kingdom lived in London. In comparison, 85.1% (40/47) and 82.1% (32/39) of patients from the South West and West Midlands, respectively, were born in the United Kingdom.

### Comparison between Notified M. bovis and M. tuberculosis Patients

Univariable analysis showed that, when compared with M. tuberculosis notified patients, M. bovis notified patients were more likely to be ≥45 years of age, born in the United Kingdom, of an ethnic group other than that of the Indian subcontinent, live in a rural area, and work in agricultural or animal-related occupations. M. bovis patients were less likely than M. tuberculosis patients to have pulmonary disease. Multivariable analysis showed that the same factors, other than age, were independently associated with M. bovis; only those ≥65 years of age were more likely to have M. bovis disease. The strongest risk factor for M. bovis disease was working in an agricultural or animal-related occupation (adjusted odds ratio 29.5, 95% CI 16.9–51.6; Table 2). The model showed no interactions between explanatory variables. Analysis stratifying by place of birth (UK-born vs. non–UK-born) indicated that the same variables were significant.

### M. bovis Patient Exposure to Risk Factors

Of the 272 M. bovis patients identified during 2006–2014, exposure questionnaires were completed for 241 (88.6%). Of these, 179 (74.3%) reported exposure to at least 1 risk factor for M. bovis acquisition; 78 (43.6%) reported 1 exposure, 57 (31.8%) 2 exposures, 28 (15.6%) 3 exposures, and 16 (9.9%) 4 exposures. For 6 patients, no exposure was known; for the remaining 56 patients, data were missing for ≥1 risk factor and the patients could not be classified as not having been exposed to a risk factor.

The most frequently reported exposure was consumption of unpasteurized milk products (65.7%; 109/166; Table 3); proportions reporting this factor were

### Table 1. Characteristics of patients with Mycobacterium bovis disease, England, Wales, and Northern Ireland, 2002–2014

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>All patients, no. (%)</th>
<th>UK-born patients, no. (%)</th>
<th>Non–UK-born patients, no. (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age group, y</td>
<td>n = 357‡</td>
<td>n = 214§</td>
<td>n = 83¶</td>
</tr>
<tr>
<td>0–14</td>
<td>6 (1.7)</td>
<td>4 (1.9)</td>
<td>2 (2.4)</td>
</tr>
<tr>
<td>15–44</td>
<td>106 (29.7)</td>
<td>39 (18.2)</td>
<td>54 (65.1)</td>
</tr>
<tr>
<td>45–64</td>
<td>70 (19.6)</td>
<td>45 (21.0)</td>
<td>12 (14.5)</td>
</tr>
<tr>
<td>≥65</td>
<td>175 (49.0)</td>
<td>126 (58.9)</td>
<td>15 (18.1)</td>
</tr>
<tr>
<td>Male sex</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>White</td>
<td>230 (73.0)</td>
<td>199 (93.9)</td>
<td>15 (18.5)</td>
</tr>
<tr>
<td>Black African</td>
<td>37 (11.8)</td>
<td>2 (0.9)</td>
<td>35 (43.2)</td>
</tr>
<tr>
<td>Indian subcontinent</td>
<td>16 (5.1)</td>
<td>3 (1.4)</td>
<td>9 (11.1)</td>
</tr>
<tr>
<td>Other</td>
<td>32 (10.2)</td>
<td>8 (3.8)</td>
<td>22 (27.2)</td>
</tr>
<tr>
<td>Time since entered United Kingdom, y</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;2</td>
<td>NA</td>
<td>NA</td>
<td>10 (14.7)</td>
</tr>
<tr>
<td>2–5</td>
<td>NA</td>
<td>NA</td>
<td>17 (25.0)</td>
</tr>
<tr>
<td>6–10</td>
<td>NA</td>
<td>NA</td>
<td>20 (29.4)</td>
</tr>
<tr>
<td>&gt;10</td>
<td>NA</td>
<td>NA</td>
<td>21 (30.9)</td>
</tr>
<tr>
<td>Place of residence</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rural</td>
<td>86 (24.9)</td>
<td>62 (29.0)</td>
<td>9 (10.8)</td>
</tr>
<tr>
<td>Urban</td>
<td>259 (75.1)</td>
<td>152 (71.0)</td>
<td>74 (89.2)</td>
</tr>
<tr>
<td>Pulmonary TB#</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>199 (56.9)</td>
<td>131 (61.5)</td>
<td>38 (45.8)</td>
</tr>
<tr>
<td>No</td>
<td>151 (43.2)</td>
<td>82 (38.5)</td>
<td>45 (54.2)</td>
</tr>
<tr>
<td>≥1 social risk factor**</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>12 (7.9)</td>
<td>6 (5.9)</td>
<td>5 (11.1)</td>
</tr>
<tr>
<td>No</td>
<td>17 (6.1)</td>
<td>13 (6.7)</td>
<td>5 (5.4)</td>
</tr>
</tbody>
</table>

*§Median age (IQR) 58 (36–77) y.
**Data only available from 2010 on.
similar among those born in the United Kingdom and those born elsewhere. Among those for whom the most recent consumption of unpasteurized milk product was known, most (85.9%, 55/64) had consumed the product >5 years before TB diagnosis; 42.2% (27/64) were >50 years of age before diagnosis. No change in the age distribution of patients consuming unpasteurized milk was identified over time; most (56.0%, 61/109) were >65 years of age.

Contact with a human TB patient was reported by 18.2% (33/181), but for most, recorded information was insufficient to identify the contact, particularly if the contact was not recent. Where known, 80.8% (21/26) of contacts occurred >5 years before TB diagnosis. From 24-loci MIRU-VNTR strain typing data available during 2010–2014, a total of 48.7% (57/117) of patients (of which 46 were born in the United Kingdom and 9 were not) were in 15 M. bovis strain type clusters. One cluster contained exclusively patients not born in the United Kingdom and 7 exclusively born in the United Kingdom; 2 of the latter clusters contained the only epidemiologically linked human patients, each with a pair of household contacts.

Recent acquisition of infection cannot be directly measured, but the rate of M. bovis disease among children, along with their exposures, can provide an indirect indicator of recent acquisition. Exposure information was available for 5/6 M. bovis patients <15 years of age and suggested potential overseas acquisition; 5 had traveled to a country where TB incidence was high, 1 of whom had consumed unpasteurized milk while abroad. For 1 child not born in the United Kingdom, a questionnaire response was not obtained.

Overall, among those for whom location of exposure was known, 59.1% (97/164) of patients were exposed to ≥1 risk factor in the United Kingdom (Table 3). Among those not born in the United Kingdom, 18.0% (9/50) were known to have been exposed to a risk factor while in the United Kingdom, but 4 of the 9 also were exposed outside the United Kingdom.

Discussion

Our findings confirm that M. bovis disease remains rare among humans in England, Wales, and Northern Ireland. Over the study period, the annual rate of M. bovis disease and the proportion of culture-confirmed TB cases with M. bovis identified as the cause displayed a small but statistically significant increase; annual case numbers for the past 10 years were similar to those for the early 1990s (4). Although speciation has improved from the use of strain typing results (19,20), this improvement is unlikely to account for all of the increase identified. Although the previous study by Jalava et al. (4) and our study overlap by 2 years, our results benefit from improved matching (17) between case notification and culture results from 2002 on, thereby providing improved accuracy for reporting annual case numbers.

We identified, unlike previous studies (4,5), that although the number of M. bovis patients not born in the United Kingdom remained low and fluctuated over time, the annual number of cases in this group increased slightly over time. Our finding may be confounded by better recording of place of birth but is not unexpected given the increase during this period in the overall number of TB patients not born in the United Kingdom (13). Similar to previous findings (5), our findings indicate that most M. bovis patients not born in the United Kingdom lived in urban areas, specifically London. These patients originated mostly from low-income countries where TB incidence is high and therefore are at higher risk for human-to-human transmission and animal-to-human transmission because of limited
detection of *M. bovis* in animals and less frequent milk pasteurization (24). Thus, infection was probably acquired before arrival in the United Kingdom and less likely to be related to exposure to risk factors while in the United Kingdom. Unfortunately, speciation is not routinely conducted in many high TB burden, low-income countries (16), so it is difficult to identify in which countries incidence of *M. bovis* is high and whether the trends in country of birth for *M. bovis* patients not born in the United Kingdom reflect the global incidence of the disease (24,25).

We identified a decrease over time in the proportion of UK-born patients ≥65 years of age and a decrease in the median age, although neither was statistically significant. Previously, most cases in UK-born patients were the result of reactivation of infection acquired before the large rollout of pasteurization (by the 1960s) (4), when *M. bovis* incidence was higher. Given the length of time that widespread pasteurization has been in place, progressively fewer cases among the older population are expected as the cohort exposed before pasteurization decreases. It was unexpected that, despite this decrease, the number of *M. bovis* cases occurring in the UK-born population did not reduce over the study period. Instead, the number and proportion of younger UK-born patients increased slightly. Numbers remain small, and it is not possible to yet detect any change in exposures; however, in recent years, the media have reported increased public demand for unpasteurized milk, which, if contaminated, could result in more human infections.

No data are available to quantify unpasteurized milk production or consumption within England, Wales, and Northern Ireland. However, results from a 2012 survey of adult consumer attitudes about unpasteurized milk (26) showed that 33% of respondents had consumed unpasteurized milk but only 3% currently consumed unpasteurized milk. Although the proportion who had ever consumed unpasteurized milk was highest among older age groups (18–24 years, 31%; 25–44 years, 28%; 45–64 years, 38%; ≥65 years, 40%), the proportion of current consumers was higher among younger age groups (18–24 years, 7%; 25–44 years, 4%; 45–64, 1%; ≥65, 1%). It is possible that increased consumption of unpasteurized milk, as reported by the media, is contributing to the small increase in *M. bovis* cases and may contribute to a change in demographics of patients over time. Although we do not have evidence to confirm, this hypothesis could be explored further through a formal observation study. The time between unpasteurized milk consumption and onset of TB disease among the *M. bovis* patients in our cohort emphasizes that the effects of current unpasteurized milk consumption may not be observed for many years.

The results of combining routine 24-loci MIRU-VNTR typing of *M. bovis* from humans with epidemiologic data provide evidence of only occasional human-to-human *M. bovis* transmission; despite extensive follow-up of the 57 clustered cases, only 2 instances of 2 cases being epidemiologically linked were found. Only 1 prior occurrence of MIRU-VNTR–confirmed (using 15-loci typing) human-to-human transmission of *M. bovis* in the United Kingdom has been documented (5,27); it occurred before the rollout of routine prospective 24-loci MIRU-VNTR
typing. There are also a few examples of human-to-human *M. bovis* transmission in countries other than those included in this study (28,29), suggesting that such transmission is rarely identified. Overall, the proportion of clustering in this study (32), suggesting that such transmission should continue to be monitored and thoroughly investigated to ensure that lesser known exposures are not missed.

A high proportion of UK-born patients lived in rural areas, especially across the South West and Midlands of England, where *M. bovis* is more common in neighboring Mexico (39,40). In comparison with studies from the United States found that being foreign born (in particular, being of Hispanic ethnicity) and younger were independently associated with *M. bovis* when compared with *M. tuberculosis* (35,36). The difference in demographic characteristics of *M. bovis* patients in the United States and in England, Wales, and Northern Ireland may be explained by the fact that *M. bovis* in cattle or wildlife is not frequently reported in the United States (37,38) but is more common in neighboring Mexico (39,40). Thus, the epidemiology of human *M. bovis* in England, Wales, and Northern Ireland continues to be driven by the past and, to some extent, present prevalence of disease in cattle. Given advances in molecular techniques,
improved understanding of animal-to-human transmission will require linking the genotyping results from animals with *M. bovis* infection in England, Wales, and Northern Ireland with data from humans.

Globally, zoonotic TB should be tackled, and the needs of those affected by *M. bovis* disease, namely those in animal-related occupations and those consuming unpasteurized milk from infected animals, should be addressed. The implementation of methods to identify *M. bovis* where culture is not possible have been highlighted as essential (16,41,42). Although findings from England, Wales, and Northern Ireland cannot be extrapolated even to other high-income countries, much less to high TB burden, low-income countries, our study does illustrate the value of monitoring *M. bovis* disease and the data required to do so.

Our study does have some limitations. The exposure questionnaires return rate was 89%, and some responses were missing, which could lead to some error in the estimation of exposures; in addition, nonresponders were more likely to be urban dwellers. Our comparison of *M. bovis* and *M. tuberculosis* patients was limited because exposure questionnaire information was only collected for *M. bovis* patients; therefore, animal-related exposures, travel to countries with high TB incidence, and contact with human TB patients could not be included in the analysis. In addition, patients not born in the United Kingdom, most of whom belong to Indian subcontinent ethnic groups, are more likely missed in analysis because a higher proportion have exclusively extrapulmonary disease (43), for which culture confirmation is lower. Approximately 60% of TB cases in England, Wales, and Northern Ireland are culture confirmed; therefore, the estimated *M. bovis* incidence presented in this article is probably an underestimate. The proportion of TB cases culture confirmed over time has remained relatively stable (44), so underascertainment should not affect changes in the number or proportion of TB cases caused by *M. bovis*.

In conclusion, we found that *M. bovis* disease continues to account for a small number and low proportion of total TB cases in England, Wales, and Northern Ireland. The proportion of culture-confirmed TB cases caused by *M. bovis* has increased slightly, and the age of UK-born patients has decreased. The reasons are not fully understood, and trends should continue to be monitored. For most patients, exposure to risk factors for *M. bovis* acquisition (e.g., unpasteurized milk consumption, farm work, or contact with a human TB patient) were known. The current control measures in place to prevent animal-to-human spread seem to be effective; such spread occurs in a few isolated incidents and sporadic events. However, to increase understanding of *M. bovis* transmission in England, Wales, and Northern Ireland, we recommend strengthening collaboration between animal and human health, including linking genotyping results.

**Acknowledgments**

We thank Ross Harris for his support and guidance on statistical analysis and Adam Brouwer and Maria O’Hagan for providing data on herds with TB outbreaks, shown in Figure 3, panel B.

Ms. Davidson is an epidemiologist in the Centre of Infectious Disease Surveillance and Control at Public Health England, based in London. Her main research interests cover various aspects of TB epidemiology within the United Kingdom.

**References**


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Epidemiology of *Mycobacterium bovis* Disease in Humans in England, Wales, and Northern Ireland, 2002–2014

Technical Appendix

*Mycobacterium bovis* questionnaire, England, Wales, and Northern Ireland

The questionnaire was introduced in 1993 to collect basis demographic, clinical and exposure information for *M. bovis* cases before the current Enhanced Tuberculosis Surveillance system (ETS) was implemented to collect demographic and clinical data for all TB cases in 1999.

Since this time the questionnaire has undergone slight revisions. In 2004, travel history was added to the questionnaire. In 2012, much of the demographic and clinical information was removed as this was by then available through ETS. Additionally, tickbox options were added to categorise the setting in which contact with a human case of TB occurred. In 2015, the collection of details on unpasterised milk product consumption were expanded to include the type of product (milk, cheese, yogurt) and the animal which the product came from. Additionally, a tickbox to specific if the patient was a livestock farmer was added (previously only worked in an abattoir, as a vet, with animals in another capacity was collected) and a question to ask about contact with farm animals.

The current exposure data collected are as follows:
**CASE BACKGROUND INFORMATION**

Please provide details of, if the patient is immunosuppressed, or on immunosuppressive therapy:

Please provide any other relevant clinical details:

---

**CONTACTS OF OTHER HUMAN CASES (DETAILS)**

Has the patient ever spent any time in contact with any known (human) cases of tuberculosis?

Yes [ ] No [ ] Unknown [ ] If yes, ETS/LTBR ID: ____________________

If yes, please provide details:

<table>
<thead>
<tr>
<th>Date</th>
<th>Exposure setting</th>
<th>Details</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Household</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Health care</td>
<td>Hospital [ ] Other [ ]</td>
</tr>
<tr>
<td></td>
<td>Education</td>
<td>Nursery [ ] Primary [ ] Secondary [ ] Tertiary [ ]</td>
</tr>
<tr>
<td></td>
<td>Detention</td>
<td>Prison [ ] Immigration [ ]</td>
</tr>
<tr>
<td></td>
<td>Homeless Hostel</td>
<td>Residential Hostel [ ] Night shelter [ ] Other [ ]</td>
</tr>
<tr>
<td></td>
<td>Other congregate settings</td>
<td>Elderly residential [ ] Nursing home [ ] Pub [ ]</td>
</tr>
<tr>
<td></td>
<td>Travel</td>
<td>Air [ ] Bus [ ] Train [ ] Ship [ ]</td>
</tr>
<tr>
<td></td>
<td>Workplace</td>
<td>Other [ ]</td>
</tr>
</tbody>
</table>

---

**UNPASTEURISED MILK PRODUCT CONSUMPTION**

Has the patient ever consumed unpasteurised milk products?  Yes [ ] No [ ] Unknown [ ]

If yes, please provide details: Milk [ ] Cheese [ ] Yogurt [ ]

Which animal(s) was milk product obtained from:

With what frequency? Once [ ] Occasionally [ ] Often/regularly [ ] Most recent year of consumption: ________________

Where did the patient obtain the unpasteurised milk products?  UK [ ] Outside of UK [ ]

If in the UK: Own farm [ ] Local farm [ ] Other [ ] And please specify the county: ________________

If outside UK, please specify the country: ________________

Other details: ________________
**TRAVEL HISTORY**

Has the patient travelled or lived outside the UK for more than one month?  Yes ☐ No ☐ Unknown ☐

(to a country with high TB prevalence where human-to-human *M. bovis*
transmission may occur i.e. the Indian Subcontinent or Sub-Saharan Africa)

If yes, please provide details:

<table>
<thead>
<tr>
<th>Country</th>
<th>Year of last visit</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**OCCUPATIONAL DETAILS / ANIMAL CONTACT**

Has the patient ever worked: *(include voluntary work, e.g. for animal welfare charities)* - tick all relevant

in an abattoir ☐ as, or with a vet ☐ as, or with a livestock farmer ☐ with animals in another capacity ☐

Has the patient ever: - tick all relevant

Had physical contact with wild animals:  Yes ☐ No ☐ Unknown ☐

Had physical contact with farm animals:  Yes ☐ No ☐ Unknown ☐

Had other relevant contact (excluding pets) with an animal:  Yes ☐ No ☐ Unknown ☐

**FURTHER DETAILS OF OCCUPATIONAL / ANIMAL EXPOSURE**

If YES to any of the above please provide details:

<table>
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<tr>
<th>Animal</th>
<th>Year of most recent contact</th>
<th>Duration (years)</th>
<th>Country (or if in UK county)</th>
<th>Details</th>
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**CONTACT WITH ANIMALS WITH TB**

Has the patient ever: had a pet [ ] Did the pet have: suspected TB [ ] confirmed TB [ ]

Has the patient had any contact with farm animals/wild animals with a positive TB test?

Yes [ ] No [ ] Unknown [ ] If yes (or pet had TB), please provide details:

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If the patient has had contact with TB positive farm animals,

Were visible lesions present in carcass? Yes [ ] No [ ] Unknown [ ]

Were udder lesions present? Yes [ ] No [ ] Unknown [ ]

Herd type: ______________ Herd size: ____________

Please provide any **other information** you think may be relevant to this illness:

____________________________________
____________________________________
____________________________________