Community-wide transmission of a strain of *Mycobacterium tuberculosis* that causes reduced lung pathology in mice

Sally A. Cantrell, Lisa Pascopella, Jennifer Flood, Charles M. Crane, Lon V. Kendall and Lee W. Riley

Since 1992, *Mycobacterium tuberculosis* strain PG004 has been responsible for a large outbreak of tuberculosis in one northern Californian community. There are no epidemiological or host factors to explain this outbreak. PG004 was therefore analysed for biological characteristics that might explain its widespread distribution. BABL/c mice were infected intravenously with PG004, non-PG004 *M. tuberculosis* strains CCC20 and CCC23 isolated from patients in the same community, and the laboratory strain H37Rv. The susceptibility of PG004 to reactive nitrogen intermediates (RNIs) was compared with that of H37Rv. Because of the reported association of phenolic glycolipid production with mouse virulence, a junction sequence in the polyketide synthase gene cluster (*pks15/1*) was compared among strains. It was found that the most virulent strain, based on mouse mortality, was not the outbreak strain PG004, but the non-outbreak strain CCC20. This strain had an intact *pks15/1* sequence identical to that of another non-outbreak strain, CCC23, which caused death in only one out of ten mice in 300 days of follow-up. The outbreak strain PG004 had a frameshift mutation in the *pks15/1* sequence identical to the sequence of H37Rv, and it was no more resistant to RNIs than H37Rv. The most distinguishing feature of PG004 was its failure to produce well-organized, coalescing granulomas in mouse lungs. The lack of organized granulomas and reduced pathology may prevent restriction of PG004 in the lungs and allow it to spread into alveolar air spaces and escape the host to transmit to others. Humans with reduced lung pathology may remain undiagnosed and untreated in the community longer than those with severe disease. The over-representation of an *M. tuberculosis* strain in a community, therefore, may be more associated with strains that cause reduced rather than severe lung pathology.

INTRODUCTION

In 2000, a large outbreak of tuberculosis was described, caused by a strain of *Mycobacterium tuberculosis* referred to as PG004 due to its polymorphic GC-rich tandem repeat sequence (PGRS) genotype designation (Chin et al., 2000). Several other genotyping methods, including IS6110-based RFLP analysis and spoligotyping, were used to confirm that strain PG004 had been circulating in Contra Costa County in northern California, USA, since 1992. Between 1996 and 2000, 503 culture-confirmed tuberculosis patients were reported in the county. Of these, 117 (23%) were infected with PG004; 26 additional cases were found in surrounding San Francisco Bay Area counties, making the total size of the cluster of PG004 infections 143 cases. An epidemiological study of 73 patients in this cluster out of 221 tuberculosis patients from Contra Costa County in 1996–1997 found that factors significantly associated with the development of disease included the failure to identify contacts in a timely manner and diagnostic delays of source-case patients (Chin et al., 2000). However, these factors did not explain the large outbreak caused by a single strain of *M. tuberculosis*. It was postulated that PG004...
strain might have distinct biological characteristics that caused it to be overly represented in this community.

Similar suggestions have been made recently with M. tuberculosis strains associated with other large tuberculosis outbreaks. Strain CDC1551, which caused a large outbreak of tuberculosis in rural counties in Tennessee and Kentucky, USA, in 1994–1996 (Valway et al., 1998), was found to elicit a more vigorous cytokine response in mice compared with laboratory strains, as evidenced by a higher production of tumour necrosis factor alpha, interleukin 6 (IL-6) and IL-12 (Manca et al., 1999). This response was attributed to apolar lipids produced by this strain (Manca et al., 1999). Another strain (HN878), belonging to a widely distributed Beijing family clade, which caused a prison outbreak in Texas, USA (Sreevatsan et al., 1997), was found to express a highly biologically active lipid product, phenolic glycolipid (PGL), not detected in M. tuberculosis strain CDC1551 or the laboratory strains H37Rv and Erdman (Reed et al., 2004). This strain was ‘hyperlethal’ in mice (Reed et al., 2004).

Another widely disseminated strain, CB3.3, found in New York City in the 1990s, was found to be highly resistant to reactive nitrogen intermediates (RNIs) and hydrogen peroxide in vitro (Friedman et al., 1997). Both CB3.3 and CDC1551 strains were found to be relatively more resistant to RNIs and reactive oxygen intermediates (ROIs) in vitro than the laboratory strains of M. tuberculosis and most other clinical isolates (Firmani & Riley, 2002a, b; Friedman et al., 1997). More recently, a strain (CH) belonging to the East African–Indian lineage, which caused a large outbreak in Leicester, UK, was found to induce more anti-inflammatory IL-10 gene transcription in human monocyte-derived macrophages than strains CDC1551 and H37Rv (Newton et al., 2006).

We studied PG004 to determine whether any of the biological characteristics previously found in other widespread M. tuberculosis strains were present in this Californian outbreak strain. Here, we report yet another phenotype associated with over-representation of a M. tuberculosis strain in the Californian community.

**RESULTS AND DISCUSSION**

**Mouse infection studies.** Pathogen-free 8-week-old female BALB/c mice obtained from Charles River (Wilmington, MA, USA) were challenged via the tail vein with approximately $10^5$ bacilli of each strain according to a previously reported procedure (Shimono et al., 2003). Briefly, groups of five mice were infected with each mycobacterial strain for bacterial lung infection and histology studies, and groups of ten mice were infected with each mycobacterial strain for survival studies. The mice were monitored for signs of disease and then sacrificed. Differences in mortality over time were assessed using Kaplan–Meier survival analysis. Animal experimentation guidelines were followed in all murine experiments, as approved by the University of California, Berkeley, Institutional Animal Care and Use Committee.

Groups of five mice were euthanized at 1, 42 and 120 days post-infection (p.i.). The lungs and spleens were removed, homogenized, diluted and inoculated onto 7H11 agar plates for c.f.u. enumeration according to the procedure reported by Dunn & North (1995).

Histology slides were prepared commercially and examined by a veterinary pathologist specializing in mouse pathology who was blind to the information about the strains used to infect the mice. The left lung was removed from two mice at 42 and 120 days p.i., and fixed in 10% buffered formalin, embedded in paraffin and processed. Sections were stained with haematoxylin and eosin for histological examination. At least two transverse sections of the upper third and lower third of the lung were examined for extent of damage, distribution of cell types, airway lesions and granuloma formation.

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**RNIs susceptibility test.** Several outbreak strains have been reported previously to be associated with increased resistance to RNIs (Firmani & Riley, 2002b; Friedman et al., 1997). Therefore, one PG004 strain was compared against H37Rv for susceptibility to RNIs. Single-cell suspensions were prepared as described by Grover et al. (1967) and isolates were tested for resistance to RNIs in acidified sodium nitrite (ASN) as reported previously (Firmani & Riley, 2002b). The c.f.u. recovery from ASN-exposed strains was compared with that of strains exposed to ASN-free 7H9 broth. Comparison of the mean c.f.u. recovery of each strain, performed in triplicate, was done using Student’s t-test, and a value of $P<0.05$ was considered significant.

**Comparison of the pks15/1 sequence.** The junction between the 3’ end of pks15 and the 5’ end of pks1 ampliﬁed by PCR, and the product was sequenced, according to a published method (Camacho et al., 2001). The sequences obtained from PG004, CCC20, CCC23 and H37Rv were aligned and compared visually.
Infected mice were monitored for up to 300 days. The survival of mice infected with the outbreak isolate was not significantly different from that of mice infected with H37Rv ($P>0.05$, Mantel–Haentzel test) (Fig. 1b). One non-outbreak strain (CCC23) caused death in only one out of ten mice during this period. This was the same strain that showed the lowest peak bacterial burden in lungs (Fig. 1a). Mice infected with this strain survived significantly longer than all other groups of mice ($P<0.0001$). The other non-outbreak-associated strain, CCC20, caused accelerated mortality in mice. All of the mice infected with this strain were dead by 182 days compared with $>250$ days in the mice infected with the other strains ($P<0.005$).

**Histopathology**

Lung pathology caused by each of the *M. tuberculosis* strains was examined histologically at 42 and 120 days p.i. (Fig. 2). At day 42, the laboratory strain H37Rv produced a moderate to severe granulomatous pneumonia characterized by large multifocal to coalescing granulomas affecting 25–75% of the lung parenchyma (Fig. 2; Table 1). The lungs of mice infected with the outbreak strain PG004 showed mild granulomatous pneumonia with scattered foci of small- to moderate-sized granulomas affecting less than 25% of the lung parenchyma. Granulomas were composed of epithelioid and alveolar macrophages and a few lymphocytes and neutrophils. Many of the air spaces were preserved. At 42 days, lung sections of mice infected with the non-outbreak strain CCC20 had moderate granulomatous pneumonia affecting more than 75% of the lung (Fig. 2). Compared with day 42, the granulomas were composed of a denser cellular infiltrate of alveolar macrophages with few neutrophils scattered throughout the granulomas. The lymphocytic infiltrates around and within the granulomas were also denser than those at day 42. The outbreak strain PG004 produced moderate, rarely coalescing granulomatous pneumonia affecting 25–75% of the lung. Granulomas were composed of epithelioid macrophages with infiltrates of lymphocytes and neutrophils. There were foci of necrosis within the granulomas and cholesterol cleft formation that were not seen at day 42. Mice infected with strain CCC20 had severe granulomatous pneumonia affecting nearly 100% of the lung parenchyma. Granulomas were coalescing and composed of epithelioid macrophages with cellular necrosis and cholesterol cleft formation. At day 120, lungs infected with strain CCC20 had severe granulomatous pneumonia affecting more than 75% of the lung parenchyma. Granulomas were similar to those found at day 42; however, the lymphocytic infiltrates adjacent to and within granulomas were denser and cholesterol cleft formation was present.

**RNI susceptibility**

After exposure to 3 mM ASN, PG004 showed 56% survival (as determined by comparison of c.f.u. recovery) and H37Rv showed 76% survival compared with the respective ASN-unexposed control strains ($P>0.1$); exposure to a 6 mM concentration of ASN produced 3% survival in the PG004 strain and 11% survival in H37Rv ($P>0.2$).

**pk{}s15/1 gene sequence**

The junction sequence of the polyketide synthase gene cluster *pk{}s15/1* was aligned for strains PG004, CCC20,
CCC23 and H37Rv (Fig. 3). Their sequences were compared with the published corresponding sequence of HN878, a strain reported to express PGL. The outbreak strain PG004 had the same sequence found in the laboratory strain H37Rv, whilst the two non-outbreak strains from the same community in California shared the same sequence found in HN878, with a 7 bp insertion.

Molecular epidemiology studies have shown that certain *M. tuberculosis* strains are over-represented in some communities. Whilst some of this over-representation can be explained by epidemiological or host-related factors, often there is no obvious explanation, and hence biological reasons for their enhanced transmissibility are sought. By definition, all human clinical isolates of *M. tuberculosis* are virulent; thus, the ability of a strain to cause active disease in a human host per se is not an explanation for its transmissibility.

Strain CDC1551, which caused an outbreak of tuberculosis and tuberculin skin test conversions in Tennessee and Kentucky, was initially found to be more virulent in mice than laboratory strains (Valway et al., 1998). However, subsequent studies have shown that, rather than being more virulent than H37Rv or Erdman, it induced a more vigorous pro-inflammatory cytokine response (Manca et al., 1999). Apolar lipid fractions from CDC1551 induced higher levels of tumour necrosis factor alpha, IL-6 and IL12 by monocytes than those from the other strains.

Another outbreak strain (HN878) reported from a prison outbreak in Texas was found to express PGL, which had an inhibitory effect on the release of pro-inflammatory cytokines by macrophages (Reed et al., 2004). The strain that expressed this lipid product belonged to a subset of the internationally widespread Beijing family. All strains belonging to this family share an identical *pks15/1* gene sequence, which is expressed as a single open reading frame (Camacho et al., 2001; Reed et al., 2004). Strains H37Rv, Erdman and CDC1551 have a natural frameshift mutation at this locus and they do not produce PGL. An extra 7 bp

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**Fig. 2.** Lung histology at 42 and 120 days p.i. for mice infected with strain PG004, CCC20, CCC23 or H37Rv. Lungs were stained with haematoxylin and eosin. Magnification ×12.5 (first and second columns) and ×100 (third and fourth columns).
sequence in *pks15/1* found in HN878 and some other clinical strains corrects the frameshift mutation, which generates a single *pks15/1* open reading frame and restores PGL production (Camacho *et al.*, 2001). It should be noted that an intact *pks15/1* sequence does not necessarily correlate with PGL production (Camacho *et al.*, 2001).

More recently, Newton *et al.* (2006) described yet another phenotype associated with a strain (CH) of *M. tuberculosis* that caused a large outbreak among school children in Leicester, UK, in 2001. Strain CH belongs to the so-called East African–Indian lineage of *M. tuberculosis* and was shown to induce more IL-10 gene transcription than strain H37Rv or CDC1551 in human monocyte-derived macrophages. It was also more susceptible to hydrogen peroxide but not to nitric oxide than the other strains. It has a deletion affecting *Rv1519*, the function of which is unknown. The authors suggested that its anti-inflammatory effect on macrophages contributes to its persistence in the community and its potential for causing outbreaks (Newton *et al.*, 2006).

Resistance to RNIs and ROIs has been shown to be associated with the outbreak strain CB3.3 from New York.

**Table 1.** Histopathological examination of infected mouse lung sections

<table>
<thead>
<tr>
<th><em>M. tuberculosis</em> strain</th>
<th>Lung parenchyma lesion (%)</th>
<th>Granuloma distribution</th>
<th>Cell types (macrophages/neutrophils/lymphocyte distribution)</th>
<th>Necrosis/cholesterol cleft</th>
<th>Alveolar air spaces</th>
</tr>
</thead>
<tbody>
<tr>
<td>42 days p.i.</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PG004</td>
<td>&lt;25</td>
<td>Scattered foci</td>
<td>Alveolar and epithelioid macrophages, few lymphocytes</td>
<td>None</td>
<td>Mostly preserved</td>
</tr>
<tr>
<td>CCC20</td>
<td>25–75</td>
<td>Multifocal, nodular</td>
<td>Alveolar and a few epithelioid macrophages, neutrophils present, few lymphocytes</td>
<td>None</td>
<td>Filled with inflammatory cells</td>
</tr>
<tr>
<td>CCC23</td>
<td>&lt;25</td>
<td>Small multifocal</td>
<td>Alveolar and epithelioid macrophages, few lymphocytes</td>
<td>None</td>
<td>Preserved</td>
</tr>
<tr>
<td>H37Rv</td>
<td>25–75</td>
<td>Multifocal, coalescing</td>
<td>Alveolar and epithelioid macrophages, dense lymphocytes</td>
<td>None</td>
<td>Filled with inflammatory cells</td>
</tr>
<tr>
<td>120 days p.i.</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PG004</td>
<td>25–75</td>
<td>Moderate, rarely coalescing</td>
<td>Epithelioid macrophages, neutrophils and lymphocytes present</td>
<td>Present, cholesterol cleft seen</td>
<td>Some spaces filled with inflammatory cells</td>
</tr>
<tr>
<td>CCC20</td>
<td>Nearly 100, severe granulomatous pneumonia</td>
<td>Large, coalescing</td>
<td>Epithelioid macrophages, neutrophils present, dense lymphocytes</td>
<td>Present, cholesterol cleft seen</td>
<td>Mostly filled with inflammatory cells</td>
</tr>
<tr>
<td>CCC23</td>
<td>&lt;25</td>
<td>Moderate, multifocal</td>
<td>Dense epithelioid macrophages and lymphocytes</td>
<td>Absent, cholesterol cleft seen</td>
<td>Largely preserved</td>
</tr>
<tr>
<td>H37Rv</td>
<td>&gt;75, severe granulomatous pneumonia</td>
<td>Large, coalescing</td>
<td>Dense, mostly alveolar macrophages, neutrophils scattered, dense lymphocytes</td>
<td>Present, cholesterol cleft seen</td>
<td>Mostly filled with inflammatory cells</td>
</tr>
</tbody>
</table>

**Fig. 3.** Sequence alignment of the *pks15/1* junction locus. Strain CCC20, which was the most virulent in mice, had the same sequence as strain CCC23, which caused the least number of murine deaths; both were non-outbreak strains. This sequence was identical to that of the Beijing clade HN878, which caused an outbreak in Texas (Sreevatsan *et al.*, 1997). The Contra Costa County outbreak strain, PG004, had a *pks15/1* sequence identical to that of H37Rv.
City (Friedman et al., 1997). However, strain RJ2E, which is more commonly distributed in Rio de Janeiro, Brazil, was no more resistant to RNIs and ROIs than the laboratory strains (Firmani & Riley, 2002b). In this study, strain PG004 from California did not exhibit resistance to RNIs when compared with H37Rv.

Here, we examined three clinical M. tuberculosis isolates from patients residing in the same community. The three strains examined (PG004, CCC20 and CCC23) were distinct by IS6110 RFLP pattern, PGRS and spoligotyping. Interestingly, all of the clinical isolates examined showed a distinct pattern of infection in mice. Strain CCC23, which was isolated only once in northern California among more than 2000 culture-confirmed cases, caused only one death among ten mice infected after 300 days, whilst another non-outbreak strain, CCC20, also seen only once in the same community, caused death in all mice after only 182 days. Although the latter did not attain a high bacterial burden compared with the other isolates, it caused more extensive lung damage and a faster time to death in mice.

Interestingly, in our study, the isolates associated with the outbreak (PG004) did not grow any faster or attain a higher bacterial burden than isolates seen only once during the study period or than strain H37Rv. These observations suggest that the ability of M. tuberculosis to cause outbreaks is not necessarily correlated with its rate of growth in a host or the ability to cause severe disease or death in the mouse model.

PG004 was found to have the same frameshift mutation in the pks15/1 locus as that found in strains H37Rv, Erdman and CDC1551 (Fig. 3). Interestingly, the most virulent (CCC20) and least virulent (CCC23) strain in mice each shared the same pks15/1 sequence found in HN878 (also known as strain 210) (Fig. 3). Hence, in this study, pks15/1 locus sequence differences did not correlate with mouse lung lesions and cannot explain the outbreak caused by PG004 in Contra Costa County. This finding is consistent with a recent report from Thailand that showed that an intact pks15/1 sequence is found among many non-Beijing family clinical M. tuberculosis strains isolated in similar proportions (>80%) from patients with severe manifestations of tuberculosis such as tuberculosis meningitis, as well as from those with lung disease (Chaiprasert et al., 2006).

The most striking feature of PG004 was the histopathological changes it produced in the mouse lung: the granulomas were composed of pro-inflammatory cells that rarely coalesced. Alveolar air spaces in mice infected with the outbreak strain were visible even after 120 days of infection, and yet mice infected with CCC20, the non-outbreak strain, showed no visible air spaces, despite having the same bacterial burden (Fig. 2). Mice infected with the other non-outbreak strain (CCC23) had preserved air spaces, but the granulomas were densely packed with lymphocytes and had a lower bacterial burden after the same duration of infection (Fig. 1a). The dense infiltration of inflammatory cells and coalesced granulomas may restrict tissue spread of the tubercle bacilli and thus prevent their entry into the alveolar air space. Reduced lymphocyte infiltration observed in mice infected with the outbreak strain may preclude effective containment of the viable bacilli inside granulomas, allowing the bacilli to enter the alveolar air space to escape the host and infect others. Whilst acknowledging that this observation made in a mouse model may not apply to the human disease, this differential host response elicited by PG004 may explain its over-representation in the Californian community.

It is often noted that patients with a cavitary lung lesion or granulomas that erode into bronchial trees transmit M. tuberculosis at a higher frequency than those without these lesions. This may be true, but such patients, due to the severity of their disease, are also more likely to be recognized, diagnosed and initiated on treatment sooner than those with less severe disease. Those with indolent, less severe disease are likely to remain undetected in the community for longer and have a greater opportunity to transmit their infection to their close contacts. This could potentially explain the over-representation of PG004 in one Californian community.

The above observation for PG004 could also explain the spread of strains such as HN878. This strain, although hypervirulent in mice, was reduced in its ability to elicit a strong T helper (Th1)-type immune response in mice (Reed et al., 2004). Although not tested in mice, another large outbreak strain, CH, from the UK was found to induce an enhanced anti-inflammatory cytokine response in macrophages (Newton et al., 2006). A reduced Th1-type immune response would affect the cell-mediated immune response and might preclude bacterial clearance and restriction of bacterial spread, which could lead to the strain’s enhanced transmission to other hosts. A reduced Th1 response has also been shown to be associated with a hypervirulent phenotype in a mutant M. tuberculosis strain disrupted in its mce1 operon (Shimono et al., 2003). The mce1 mutant was found to be unable to establish a tightly organized granuloma in mouse lungs and was reduced in its ability to elicit pro-inflammatory cytokines in murine macrophages infected ex vivo (Shimono et al., 2003).

Thus, a M. tuberculosis strain associated with one of the largest tuberculosis outbreaks in the USA was found to elicit a distinct lung pathology in mice. Whether this phenotype observed in mice is related to its ability to cause an outbreak in a human community is not clearly established, but this phenotype appears to be a distinct biological property of a clinical M. tuberculosis isolate that to the best of our knowledge has not been described previously. Bacterial factors that elicit this pathology are not known, but the identification of such factors may lead to a better understanding of tuberculosis transmission in general.

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REFERENCES


