Detection of mycobacterial DNA in pleural fluid from patients with tuberculous pleurisy by means of the polymerase chain reaction: comparison of two protocols

Arnaud de Lassence, Denise Lecossier, Catherine Pierre, Jacques Cadranel, Marc Stern, Allan J Hance

Abstract

Background The detection of mycobacterial DNA in clinical samples on the basis of the polymerase chain reaction is a promising approach for the rapid diagnosis of tuberculous infections. No consensus exists, however, about which protocols are most sensitive, and the usefulness of this approach in the diagnosis of tuberculous effusions has been assessed in few patients.

Methods The sensitivity of two protocols was compared for the detection of DNA from *Mycobacterium tuberculosis* in samples containing known amounts of mycobacterial DNA and in DNA extracted from 15 tuberculous pleural effusions. The results obtained for pleural fluid have been compared with cytological findings and with results obtained by standard microbiological techniques.

Results Mycobacteria could be detected by acid fast staining in none and by culture in three of the 15 pleural fluid samples. A protocol based on the detection of the IS6110 insertion element (which could detect one mycobacterial genome/sample reproducibly) gave a positive result in nine of the 15 tuberculous effusions, though some samples were only intermittently positive (p < 0.05 compared with culture). In contrast, a protocol based on the detection of the gene coding for the 65 kD mycobacterial antigen (which could detect mycobacterial genomes only if there were at least 10/sample) gave a positive result in three of the 15 tuberculous effusions. Pleural fluid that was always positive with the amplification procedure detecting the IS6110 sequence contained more neutrophils (30% (SD 27%)) than samples that were intermittently positive or always negative (3% (3%)); mycobacterial DNA was never detected in the four samples containing less than 1% neutrophils.

Conclusions The amplification of the IS6110 insertion element represents a rapid and sensitive means of detecting *M tuberculosis* in tuberculous effusions. The enrichment of cells containing mycobacteria (possibly neutrophils) before DNA extraction may be required to improve the sensitivity of this approach.

Attempts to identify *Mycobacterium tuberculosis* in pleural fluid from patients with tuberculous pleurisy by acid fast staining is usually unrewarding, and culture of pleural fluid for mycobacteria is also negative in a substantial number of cases. Because mycobacterial cultures of pleural fluid cannot be relied on to provide a diagnosis, the investigation of a patient with a pleural effusion suspected of having tuberculosis usually includes a search for mycobacteria at other sites, including specimens of pleura obtained by pleural biopsy. Thus the development of diagnostic procedures capable of rapidly identifying *M tuberculosis* in pleural fluid from most patients remains a worthwhile goal.

Recently we and others have developed techniques for the detection of mycobacterial DNA in clinical samples using techniques based on the polymerase chain reaction. This approach is sufficiently sensitive to detect DNA from *M tuberculosis* in clinical specimens producing negative routine cultures, including in some cases specimens of pleural fluid. Several different mycobacterial DNA sequences have been amplified in these studies. It has been suggested that those systems that amplify sequences present in multiple copies in the mycobacterial genome may be more sensitive that those that amplify targets present in a single copy. The relative sensitivity of the different protocols has not been rigorously compared, however. Thus, although the detection of mycobacterial DNA after amplification appears to have considerable promise in the diagnosis of tuberculous infections, no consensus exists about which procedures are most sensitive.

In this study we have compared the sensitivity of two different protocols for the detection of DNA from *M tuberculosis*, one based on the detection of a sequence coding for the 65 kD mycobacterial antigen, present in a single copy in the mycobacterial genome, and a second procedure based on...
the detection of the IS6110 insertion element, present in multiple copies. Both systems are designed to detect all organisms belonging to the *M tuberculosis* complex, but not other mycobacterial species. In initial studies the sensitivities were compared by using standards containing known amounts of mycobacterial DNA. In addition, we have assessed the usefulness of the two systems in the diagnosis of tuberculous pleural effusions, and have compared the results obtained by DNA amplification with cytological findings and results obtained by standard microbiological techniques.

**Methods**

**Patient Groups**

*Patients with a tuberculous effusion*

Samples of pleural fluid from 14 patients with a tuberculous effusion were studied. In 13 patients the diagnosis of tuberculosis was established on the basis of one or more of the following criteria: culture of sputum (n = 6), pleural fluid (n = 5), or pleural biopsy specimen (n = 4) positive for *M tuberculosis* or the presence of caseating granulomas in a pleural biopsy specimen (n = 9). In one patient the diagnosis was based on a history of recent exposure to a patient with active tuberculosis, the presence of a lymphocytic pleural exudate, and a favourable response to antituberculous drugs. Two different samples of pleural fluid from one patient were studied by the polymerase chain reaction method. In two cases the sample of pleural fluid giving positive results in culture was different from that evaluated in this study. None of the patients had a positive result in the serological test for human immunodeficiency virus or had any other disease known to produce immunosuppression. None was receiving antituberculous drugs. Differential cell counts for the pleural fluid were available for 14 of the 15 samples.

*Control subjects*

Ten samples of pleural fluid were obtained from patients with a pleural effusion resulting from malignant intrathoracic neoplasms. None of these patients had a past history of tuberculosis, and culture of pleural fluid was negative for *M tuberculosis* and other organisms.

<table>
<thead>
<tr>
<th>Oligonucleotide</th>
<th>Sequence</th>
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<tbody>
<tr>
<td>65Kd MYCOBACTERIAL ANTIGEN</td>
<td>Amplification primers</td>
</tr>
<tr>
<td>1</td>
<td>5'-GAGATGAGCTGTGGAGGATCC</td>
</tr>
<tr>
<td>2</td>
<td>5'-AGCTGAGCCTCAGAAAGTTT</td>
</tr>
<tr>
<td>28</td>
<td>5'-CCGAACCGGCAGTCGCAAGGG</td>
</tr>
<tr>
<td>29</td>
<td>5'-CCCTCGACGCTGATAGCGAG</td>
</tr>
<tr>
<td>38</td>
<td>5'-CCGTCCTGGGTTCGGTCAGAA</td>
</tr>
<tr>
<td>39</td>
<td>5'-CCGTCCTGGGGCCAGGCTG</td>
</tr>
<tr>
<td>Hybridisation probe</td>
<td>5'-ACCCGGCTGATTTTCGCG</td>
</tr>
<tr>
<td>12</td>
<td>5'-ACGGCAAGCAGGTTTCGCG</td>
</tr>
<tr>
<td>IS6110 INSERTION SEQUENCE</td>
<td>Amplification primers</td>
</tr>
<tr>
<td>IS1</td>
<td>5'-CCTGCGAGCGGATAGCGCTG</td>
</tr>
<tr>
<td>IS2</td>
<td>5'-CTGCTCAGCGGCTGTCG</td>
</tr>
<tr>
<td>Hybridisation probe</td>
<td>5'-CTGCCAGGTGTCGACAT</td>
</tr>
</tbody>
</table>

**Extraction of DNA**

For extraction of DNA 10–20 ml of pleural fluid was centrifuged (1850 g for 20 minutes), the supernatant removed, and DNA extracted from the cell pellet by the technique described by Patel et al with minor modifications. DNA was quantified by measuring the optical density at 260 nm.

**Amplification of Mycobacterial DNA**

Oligonucleotides were synthesised with a 381A DNA Synthesizer (Applied Biosystems, Foster City, California) and purified by ethanol precipitation. The sequences for oligonucleotides used are summarised in table 1. DNA amplification was performed as described. All reactions contained 10 mM tris-HCl (pH 8.3), 50 mM KCl, 100 μg/ml gelatin, 0.3 mM of each dNTP, 25 pmol of each oligonucleotide primer, 50 U/ml Taq polymerase (Stratagene, La Jolla CA), 1 unit Perfect Match polymerase enhancer (Stratagene), and 500 ng template DNA in a final volume of 50 μl. Reagents were heated to 80°C before DNA was added, to decrease non-specific annealing of oligonucleotides to the template DNA.  

To amplify a fragment of the gene coding for the 65 kD mycobacterial antigen, the re-amplification protocol described by Pierre et al was used, except that the oligonucleotide primer pair 39/2 or 39/38 was used during the initial amplification. The cycle was 94°C/40 seconds, 55°C/40 seconds, and 72°C/15 seconds (50 cycles). The sensitivity of detection of DNA in positive control samples was not significantly different from each other pair of primers (data not shown), and the results obtained with the two systems presented together.

For amplification of a fragment of the IS6110 insertion element the oligonucleotides described by Eisenach et al were used (oligonucleotides IS1/IS2). The cycle was 94°C/40 seconds, 65°C/40 seconds, and 72°C/15 seconds (50 cycles).

Positive control samples, included in all experiments, were prepared by diluting purified DNA from *M tuberculosis* (ATCC 27294) with a solution of purified human DNA that did not contain detectable mycobacterial DNA to produce standards containing 20 and 2 mycobacterial genomes/μg total DNA, on the assumption of a molecular weight of 2.5 × 10^9 daltons/genome. Negative control samples (samples without added DNA) were included in all experiments.

To test the extraction procedure, known numbers of intact *Mycobacterium bovis* BCG organisms (Pasteur strain 1173–P2) grown in dispersed culture were added to a control tissue sample. DNA was extracted as described above and diluted with purified human DNA to produce standards containing about 10 mycobacterial genomes/μg total DNA (on the assumption that all mycobacterial DNA was recovered during the extraction process).

**Detection of Mycobacterial DNA**

The presence of amplified mycobacterial
DNA sequences was detected as previously described. Briefly, aliquots of the amplification products were electrophoresed into 2% agarose gels. The DNA was transferred to nylon membranes and hybridised with $3 \times 10^{10}$ cpm/ml $[32P]$-5'-labelled DNA in 10% DNA in T from the are granulomatous typical *Stain-presence of acid fast organisms on Ziehl-Neelsen stained material. Histology—presence or absence of typical granulomatous lesions. For pleural fluid only the results obtained for the sample assessed by the polymerase chain reaction are given. For sputum 3-11 samples were evaluated for each patient; + indicates one or more positive results.

### Table 2: Sensitivity of detection of known amounts of mycobacterial DNA (number of positive results/total attempts)

<table>
<thead>
<tr>
<th>Target sequence</th>
<th>Amount of mycobacterial DNA/sample DNA</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>10 genomes</td>
</tr>
<tr>
<td>65 kD mycobacterial antigen</td>
<td>13/16</td>
</tr>
<tr>
<td>Insertion element IS6110</td>
<td>22/22</td>
</tr>
</tbody>
</table>

DNA containing known amounts of DNA from *M. tuberculosis* were prepared and amplified by means of two different amplification protocols (table 2).

To detect mycobacterial DNA coding for the 65 kD antigen, samples were first amplified and the amplification products reamplified by the use of the "nested" primers, which recognise sequences contained within the originally amplified fragment. This system usually gave positive results for samples containing 10 mycobacterial genomes per sample, but was uniformly negative for samples containing one genome per sample. Samples without added DNA were also negative.

To detect the mycobacterial insertion element IS6110, samples were amplified by the use of the primer pair IS1/IS2. This system always gave positive results for control samples containing one or more genomes per sample ($p < 0.001$ for the difference in the sensitivity of detection of the insertion sequence IS6110 and the sequence coding for the 65 kD antigen). Samples without added DNA were always negative.

The procedure used to purify DNA appeared to extract mycobacterial DNA efficiently, in that a control specimen, which would have contained about 10 genomes of mycobacterial DNA per sample (on the assumption of complete recovery of mycobacterial DNA), was always positive with the two different amplification protocols (10/10 and 4/4 positive results with systems based on amplification of the 65 kD antigen and IS6110 insertion element respectively).

### Detection of Mycobacterial DNA in Pleural Fluid

All samples of pleural fluid from patients with a tuberculous effusion were negative for mycobacteria on direct microscopic examination; three of the 15 samples produced a culture positive for *M. tuberculosis* (table 3). DNA was extracted from the same samples, and the presence of mycobacterial DNA assessed by
amplification of the insertion sequence IS6110 in three independent experiments. Positive results were obtained for 9/15 patients (table 3), including all three patients whose fluid was positive by culture (p < 0.05 for the difference in sensitivity of the amplification protocol and culture). In three of the nine cases only one of the three experiments gave a positive result. When the amplification procedure was repeated three more times for these patients a positive result was observed in 1/3, 1/3, and 0/3 samples respectively. Pleural fluid from patients without mycobacterial infection gave negative results by the amplification procedure in all cases when it was tested in three or more independent experiments (data not shown).

When DNA from a tuberculous effusion was tested with the reamplification protocol for detection of the gene coding for the 65 kD antigen, positive results were obtained for 3/15 samples (table 3; p < 0.05 for the difference in sensitivity of detection of the 65 kD antigen and the IS6110 insertion sequence). The three samples that were positive with this test were among those that were always positive in experiments detecting the IS6110; two of these samples were also positive by culture.

COMPARISON OF CYTOLOGICAL FINDINGS WITH RESULTS OF DNA AMPLIFICATION

Lymphocytes were the predominant cell type observed in most pleural fluid samples (mean 73% (SD 28%)) lymphocytes, n = 14), though neutrophils and other mononuclear cells were present in variable numbers. Strikingly, the percentage of neutrophils in fluid that was always positive with the protocol based on the detection of the IS6110 insertion sequence (30% (27%) neutrophils) was significantly higher than that present in samples that were intermittently positive (3% (2%) neutrophils) or always negative (2% (3%) neutrophils) with the same protocol (figure; p < 0.01). Mycobacterial DNA was never detected in any of the four samples that contained less than 1% neutrophils. Similarly, the three samples of pleural fluid in which mycobacterial DNA could be detected with the protocol based on the detection of the 65 kD mycobacterial antigen all contained abundant neutrophils (71%, 24%, and 18%).

Discussion

In this study mycobacterial DNA was rapidly detected by means of the polymerase chain reaction in nine of 15 samples of pleural fluid from patients with a tuberculous effusion, despite the fact that many of the samples did not grow M tuberculosis in culture. This finding confirms several recently published reports showing the potential usefulness of this approach in detecting mycobacterial DNA in pleural and cerebrospinal fluid from patients with tuberculosis.

The protocol used to detect the IS6110 insertion sequence was more sensitive than the protocol used to detect the gene coding for the 65 kD mycobacterial antigen. This is probably explained by the fact that the IS6110 is present in 10–15 copies in each mycobacterial genome, whereas the gene coding for the 65 kD antigen is probably present in a single copy. The increased sensitivity afforded by the detection of the IS6110 insertion sequence considerably improves the yield for the detection of mycobacterial DNA in pleural fluid. Because this insertion sequence is present only in mycobacteria of the M tuberculosis complex, positive results are not observed for other species of mycobacteria.

Our findings also indicate that the number of mycobacteria present in tuberculous effusions is often quite low. The gene coding for the 65 kD mycobacterial antigen could be detected in only three of 15 samples by using a system that had a sensitivity of about 10 mycobacterial genomes/sample. In contrast, if the amplification procedure was repeated at least three times the IS6110 insertion sequence could be detected in nine of the 15 samples with the system described by Eisenach et al; this can detect one mycobacterial genome per sample reproducibly. As all samples contained 500 ng of total DNA (equivalent to 7 × 10^6 human cells), these findings suggest that most pleural fluid contains at least 1–20 mycobacteria/10^6 human cells, but that only a few pleural...
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... of the tuberculous effusion means of (data not shown). Further studies are needed to define how many times a given sample must be amplified to obtain optimal sensitivity without sacrificing specificity. The findings in this and other studies in our laboratory suggest, however, that if two or possibly three attempts give negative results for a particular specimen little is to be gained by further attempts.

An interesting finding in our study was that all pleural fluid samples that were positive with the protocol based on the detection of the 65 kD mycobacterial antigen, and are therefore likely to have contained a relatively large number of mycobacteria, also contained a high percentage of neutrophils. Samples that were always positive with the protocol based on the detection of the IS6110 insertion sequence had more neutrophils than samples that were intermittently positive or always negative. All four samples that contained less than 1% neutrophils were always negative when tested for the presence of mycobacterial DNA. These results are consistent with the possibility that the number of neutrophils present in a given sample may reflect the number of mycobacteria present, a finding that could be explained by the chemotaxis of neutrophils toward products released by extracellular mycobacteria. The substantial variability in the number of neutrophils (and mycobacteria) present in these fluid samples could reflect variations in the time between onset of the tuberculous effusion and assessment or differences in the pathogenesis of tuberculosis in these patients (for example, late primary tuberculosis versus reactivation) or both.

If the neutrophils present in tuberculous effusions actively phagocytose the mycobacteria in the pleural fluid, the isolation of neutrophils from these fluid samples might offer a convenient means of enriching the proportion of mycobacterial DNA present in a given sample. This might be particularly useful for samples containing few neutrophils (for example, the samples for which the amplification procedure was frequently negative). As the amplification procedure is limited by the amount of total DNA that can be evaluated, enrichment of cells containing mycobacteria before the extraction of DNA might improve the sensitivity of the test for these difficult samples.

In conclusion, the amplification of the IS6110 element provided the detection of mycobacterial DNA in nine of 15 patients with a tuberculous effusion. Further studies are clearly warranted to define the role of this test in the assessment of patients with pleural effusion of unknown aetiology.

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