Multiplex polymerase chain reaction for the simultaneous detection of *Mycoplasma pneumoniae*, *Chlamydia pneumoniae*, and *Chlamydia psittaci* in respiratory samples

C Y W Tong, C Donnelly, G Harvey, M Sillis

Abstract

**Aims**—To develop a multiplex polymerase chain reaction (PCR) for the simultaneous detection of *Mycoplasma pneumoniae*, *Chlamydia pneumoniae*, and *Chlamydia psittaci* in respiratory samples.

**Methods**—Oligonucleotide primers for the amplification of the DNA of these three organisms were optimised for use in combination in the same reaction. PCR products were detected by hybridisation with pooled internal probes using an enzyme linked immunosorbent assay. Those with positive signals were further differentiated using species specific probes. Quality of DNA extraction and PCR inhibition were controlled by amplification of a human mitochondrial gene. A panel of 53 respiratory samples with known results was evaluated blindly. This was followed by a retrospective study on sputa collected from 244 patients with suspected community acquired pneumonia.

**Results**—The multiplex assay had a lower sensitivity than PCR with individual primers by about one log. The resultant sensitivity was considered acceptable for diagnostic use. Of the panel of 53 samples, nine of 11 *M pneumoniae*, 11 of 11 *C pneumoniae*, six of seven *C psittaci*, and 24 of 24 negative samples were correctly identified. Of the 244 patients with pneumonia, seven (2.9%) had detectable *M pneumoniae*, six (2.5%) had *C pneumoniae*, and one (0.4%) had *C psittaci*. The case notes from 11 patients were studied. The PCR finding was of possible significance in at least eight of these patients.

**Conclusions**—This multiplex PCR assay has the potential to be used as a diagnostic and epidemiological tool. Further prospective studies are needed to establish its clinical value.

Keywords: atypical pneumonia, polymerase chain reaction, *Mycoplasma pneumoniae*, *Chlamydia pneumoniae*, *Chlamydia psittaci*
The expected results included: *M. pneumoniae* (*n* = 11), *C. pneumoniae* (*n* = 11), *C. psittaci* (*n* = 7), and negative (*n* = 24). All the positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection. The positive samples of the panel contained a single organism with no double infection.

### HOSPITAL BASED STUDY

Sputum samples (*n* = 279) from 244 patients (mean age 60 years, range 5 to 95; 122 females and 122 males) with suspected community acquired pneumonia, received and stored by the department of medical microbiology of the Royal Liverpool University Hospital during the winter of 1996–1997, were studied retrospectively using the multiplex assay.

### SPECIMEN PREPARATION AND DNA EXTRACTION

An aliquot of each sputum sample was diluted 1 in 5 with phosphate buffered saline (PBS) and centrifuged for 10 minutes in a microfuge at 12,000 x g. Supernatant was discarded and the pellet was resuspended in 200 µl of PBS. DNA extraction was performed using the QIAamp blood kit (Qiagen) according to the blood and body fluid protocol recommended by the manufacturer. Briefly, the sample was digested with the supplied protease at 70°C for 10 minutes, precipitated in ethanol, and centrifuged through a spin column. The spin column with the bound DNA was washed and eluted in 200 µl of the supplied AE buffer. These were tested either immediately or stored at –20°C.

### POLYMERASE CHAIN REACTION AND PRODUCT DETECTION

The PCR primers for mycoplasma (P4A, P4B) and chlamydia (CP1, CP2) were described previously; they respectively amplify a 345 bp region of the P1 adhesin gene of *M. pneumoniae* and a 333 bp region of the major outer membrane protein gene of both *C. pneumoniae* and *C. psittaci*. The reverse primers P4B and CP2 were both biotinylated at the 5’ end to facilitate PCR product detection (Life Technologies). PCR reactions for mycoplasma and chlamydia were initiated evaluated separately using serial dilutions of culture materials. The reactions were subsequently combined. Optimisation of the multiplex assay was performed by testing different combinations of primer concentration and magnesium concentration using a fixed dilution of the culture materials at about 2 log above the detection threshold of the individual assays, to establish a combination with the most comparable result. The annealing temperature was set at 60°C as a compromise between the original individual PCRs (Touchdown PCR from 65°C to 55°C for chlamydia and 65°C for mycoplasma).

Apart from the annealing temperature, the condition of the optimised multiplex PCR assay was not significantly different from the individual assays and consisted of 10 µl of extracted DNA per reaction with 20 mM Tris HCl, pH 8.4, 50 mM KCl, 1.5 mM MgCl2, 200 µM of dNTP, 0.5 µM of each primer, and 0.6 units of Taq polymerase (Life Technologies) in a final volume of 50 µl.

Thermocyclers with heated lids (Perkin Elmer 2400 or 9600) were used and the programme consisted of an initial denaturation at 94°C for five minutes, followed by 40 cycles of 94°C for 30 seconds, 60°C for 30 seconds, and 72°C for 30 seconds, with a final extension at 72°C for 10 minutes. Internal probes were designed for PCR product detection as follows: (1) an *M. pneumoniae* specific probe (P4P: 5’ GACCTTTCTGAAGGACGCGCCGAAAG-ATGA); (2) a *C. pneumoniae* specific probe (CPDP: 5’ AAACCTACTACTGCGGATA); and (3) a common probe for both *C. pneumoniae* and *C. psittaci* (CPCP: 5’ TTATATATTGTAGGACWATRGGAGG).

Each probe was labelled at the 3’ end with digoxigenin using a commercial oligonucleotide 3’ end labelling kit (Boehringer Mannheim).

The PCR products were denatured with an equal volume of 1.6% NaOH and 1 mM EDTA at room temperature for 20 minutes. Then 10 µl of the denatured PCR product was mixed with 100 µl of hybridisation buffer (Boehringer Mannheim) and 1 pmol of each probe

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**Table 1 Test results of the positive members of the evaluation panel**

<table>
<thead>
<tr>
<th>Samples</th>
<th>Culture</th>
<th>Serology</th>
<th>Previous PCR</th>
<th>Multiplex PCR</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>NA</td>
<td>Neg</td>
<td>Pos</td>
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<tr>
<td>11</td>
<td>NA</td>
<td>Pos</td>
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</table>

NA, test or sample not available; NT, not tested.

<table>
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in a streptavidin coated microtitre plate (Lab-systems), and hybridised at 40°C for one hour. The plate was washed five times with 25 mM Tris HCl pH 7.5, 0.15 M NaCl, 2 mM MgCl2, and 0.1% Tween 20. Antidigoxigenin peroxidase conjugate (Boehringer Mannheim) was added to each well (75 mU in PBS 1% skimmed milk) and the plate was incubated at 37°C for 30 minutes, followed by a ×5 wash with PBS 0.1% Tween 20; 100 µl of 3,3',5,5' tetramethylbenzidine (Sigma) was used as the substrate. This reaction was stopped with 0.5 M sulphuric acid after 10 minutes. The optical density (OD) was read at 450 nm. A pool of the three probes was used in the initial screening, and any positive signal was confirmed and differentiated using the individual probe: a positive signal with P4P indicates the presence of *M pneumoniae*, a positive signal with both CPCP and CPDP indicates the presence of *C pneumoniae*, whereas a positive signal with CPCP only indicates the presence of *C psittaci*.

Quality of the samples and amplification inhibitors was controlled with a human mitochondrial DNA PCR, using previously described primers (H6A, H6B), in a separate reaction but using the same format as the multiplex assay. PCR product from the human DNA amplification was similarly detected using the human probe H6P (5' CATCCG-TATTACGCATTACGGAGTATCAA) in a separate reaction. Samples that showed negative results in both the multiplex assay and the human DNA assay were repeated at 1 in 20 dilution to overcome possible PCR inhibition.

**DETERMINATION OF CUTOFF, SENSITIVITY, AND SPECIFICITY**

Using the results of serial dilutions of a strain of *C pneumoniae* (IOL 207) and *M pneumoniae* (NCTC 10119) and a panel of known positive and negative materials, it was decided to set a provisional cutoff at the OD reading of 0.4 with a “grey zone” of 0.1 on either side. The validity of this cutoff was further determined in a subsequent survey of hospital samples. Sensitivity was correlated by comparing *C pneumoniae* elementary body count using direct immunofluorescence (DIF) and colony forming unit (CFU) count of *M pneumoniae*. Sensitivity and specificity were further evaluated by blindly testing the panel of 53 samples with known positive and negative results.

**Results**

**SERIAL DILUTIONS OF CULTURE**

Using the arbitrary cutoff of 0.4, the chlamydia PCR was positive with individual primers up to a dilution of 10⁻⁶ and the multiplex assay, 10⁻⁵. By comparing with elementary body count by DIF, the multiplex PCR had a detection limit of within 10 elementary bodies per reaction. The mycoplasma PCR was positive with individual primers up to the dilution of 10⁻¹⁰ and the multiplex assay, 10⁻⁹. By comparing with CFU count, the multiplex PCR had a detection limit of between 10 and 20 CFU per reaction. Overall, the sensitivity of each PCR dropped by 1 log when the assays were combined (fig 1). However, the resultant reaction still had a detection limit of within 10–20 organisms and is therefore considered acceptable as a diagnostic test, but this has still to be clinically evaluated.

**PANEL OF KNOWN POSITIVE AND NEGATIVE SAMPLES**

Of the 11 expected *M pneumoniae* samples, eight were correctly identified by the initial multiplex assay. One sample had no detectable human DNA and was retested after 1:20 dilution; both *M pneumoniae* and human DNA became detectable after dilution. The two samples missed by the multiplex assay when retested using individual primers also gave negative results, suggesting that the amount of DNA in the sample was below detection limit.
Of the 11 expected *C pneumoniae* samples, 10 were correctly identified by the initial multiplex assay. The remaining sample had no detectable human DNA. Both *C pneumoniae* and human DNA became detectable after dilution.

Of the seven expected *C psittaci* samples, five were correctly identified by the initial multiplex assay; the two remaining samples both had undetectable human DNA and were retested after dilution: one had detectable *C psittaci* DNA after dilution but the other sample remained negative for both *C psittaci* and human DNA, suggesting either a failure of DNA extraction or a high level of PCR inhibition.

All 24 negative samples were correctly identified as negative by the multiplex assay, with no inhibition and no cross reaction with other mycoplasma species observed. On the basis of the results of this panel of samples and with adjustment for inhibition control by dilution, the sensitivity of the multiplex assay for *M pneumoniae*, *C pneumoniae*, and *C psittaci* were 82% (9/11), 100% (11/11), and 86% (6/7) respectively, and the specificity was 100% (24/24). Overall, four of 53 samples (7.5%) had negative human DNA PCR and required retesting by dilution.

**HOSPITAL BASED STUDY**

The OD readings of the 279 samples (from 244 patients) from the retrospective hospital based study were plotted for distribution analysis and to determine the suitability of the chosen cutoff. The provisional cutoff value of 0.4 clearly distinguished between two groups of samples (fig 2) and therefore was formally adopted as the cutoff for the multiplex assay.

Three samples that had the original OD within the grey zone were repeated: two were negative and one was clearly positive on repeat, suggesting that the initial results could have been caused by a technical error. Of the 279 samples, nine (3.2%) had negative human DNA PCR and were therefore retested after dilution. All had detectable human DNA after dilution but remained negative by the multiplex assay and were considered negative. In all, eight sputa from seven patients were positive for *M pneumoniae* (7/244 = 2.9%); six sputa from six patients were positive for *C pneumoniae* (6/244 = 2.5%), and one patient was positive for *C psittaci* (1/244 = 0.4%).

Only 36 of 244 patients had an acute blood sample sent for investigation and none had a convalescent sample. Of the 14 positive patients, only two had an acute blood sample sent for investigation. All of the acute blood samples had negative serological results for *M pneumoniae* (Serodia-mycoII, Fujirebio) and chlamydia (microimmunofluorescence, IO International).

To study the likelihood of atypical infection, the case notes of 11 patients were retrieved and studied (table 2). Three sets of case notes could not be retrieved. Most of these 11 patients were elderly (seven were over 60 years old) and had predisposing conditions such as chronic obstructive pulmonary disease or steroid treatment (nine patients). Chest radiography was done in seven and radiological evidence of pneumonia was identified in six. On the basis of bacterial culture and response to antibiotics, the multiplex PCR result was considered significant in four of these 11 patients (three *M pneumoniae* and one *C pneumoniae*). In a further four patients, other significant bacterial pathogens were isolated, but on the basis of the response to the prescribed antibiotics, the role of either *M pneumoniae* (n = 2) or *C pneumoniae* (n = 2) could not be excluded. Two young patients (Nos 9 and 10) with no underlying illness had *C pneumoniae* DNA detected in sputum, but both responded to antibiotics not suitable for treatment of chlamydia. Though the PCR results in these two cases may seem irrelevant, they may simply indicate that in the
Table 2  Clinical and radiological features, bacterial culture results, and treatment responses of the 11 patients who had a positive multiplex PCR result

<table>
<thead>
<tr>
<th>Patient</th>
<th>Age (years)</th>
<th>Presenting symptoms</th>
<th>Radiological evidence of pneumonia</th>
<th>Bacterial culture results</th>
<th>Initial antibiotic treatment</th>
<th>Response to initial treatment</th>
<th>Further treatment (with clinical success)</th>
<th>Multiplex PCR results</th>
<th>Relevance and significance of PCR result</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>65</td>
<td>Metastatic carcinoma, COPD COPD</td>
<td>Cough, green sputum</td>
<td>No*</td>
<td>Normal flora</td>
<td>Co-amoxiclav</td>
<td>No</td>
<td>Erythromycin</td>
<td>M pneumoniae</td>
</tr>
<tr>
<td>2</td>
<td>66</td>
<td>Renal failure, steroids COPD COPD</td>
<td>Cough, SOB</td>
<td>NA</td>
<td>B catarhalis, S pneumoniae, H influenzae</td>
<td>Amoxycillin, erythromycin</td>
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<td>None</td>
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<td>None</td>
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<td>Cough, purulent sputum</td>
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<td>Normal flora</td>
<td>Co-amoxiclav</td>
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<td>Erythromycin</td>
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<td>SOB, pyrexia</td>
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<td>S pneumoniae, B catarhalis</td>
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<tr>
<td>11</td>
<td>94</td>
<td>Renal failure, steroids COPD COPD</td>
<td>SOB, jaundice</td>
<td>NA</td>
<td>B catarhalis, MRSA</td>
<td>Amoxycillin</td>
<td>No</td>
<td>None</td>
<td>M pneumoniae, C psitaci</td>
</tr>
</tbody>
</table>

COPD, chronic obstructive airways disease; NA, chest x-ray not taken; MRSA, methicillin resistant Staphylococcus aureus; SOB, shortness of breath. *The chest x-ray of patient 1 showed pulmonary metastases. B catarhalis = Branhamella catarhalis.

Table 2: Clinical and radiological features, bacterial culture results, and treatment responses of the 11 patients who had a positive multiplex PCR result.

Normal host these infections are self limiting. The significance of the detection of C psitaci DNA in an elderly patient (No 11) with heart failure is not clear. The presence of heart failure in this case and the lack of other investigations make the assessment of response difficult.

Discussion

Previous workers have reported on the use of PCR to detect mycoplasma and chlamydia in respiratory samples. The clinical features of atypical pneumonia caused by mycoplasma and chlamydia are very similar, it is necessary to have an approach that can detect and differentiate all relevant organisms using the same sample and the same assay. Here we reported the successful development of a multiplex PCR for the simultaneous detection and differentiation of M pneumoniae, C pneumoniae, and C psitaci.

One of the problems we encountered was the fall in sensitivity when assays were combined. Although other successful multiplex assays have previously been reported, multiple mycoplasma and chlamydia PCR appears to have more sensitivity problem. In our system, the multiplex assay had a lower sensitivity of about 1 log for both M pneumoniae and C pneumoniae compared with their individual PCRs. We have not determined the sensitivity change for C psitaci. However, since the primer binding site is identical to that of C pneumoniae, we would expect its sensitivity to be similar. The detection limit of the multiplex PCR of within 10–20 organisms should be acceptable for diagnostic use. Also, the performance of the multiplex PCR with the panel suggested a sensitivity of more than 82% and a specificity of 100%. However, owing to the complexity of the variables in a multiplex PCR which includes different combinations of primer concentrations, magnesium concentrations, and annealing temperatures, the sensitivity could have been further improved by more careful optimisation. In our development, we have performed a limited optimisation using a fixed dilution of cultured materials. Ideally, a clinical sample should have been used as a standard, and a more elaborate optimisation should be performed using the format of multiple chessboard titrations, testing different combinations of the variables. Further optimisation of the annealing temperature is also desirable. It is possible that the “hot start” approach or the use of the new “temperature activated” DNA polymerases could help to improve the sensitivity. Also, the evaluation panel and the clinical samples in this study did not contain double infections. The ability of the multiplex assay to detect dual infections is therefore not known. It is important that this aspect should be addressed in future optimisation and evaluation.

The other problem encountered during the study was PCR inhibition. This was noted more often in the evaluation panel (4/53 = 7.5%) than the subsequent clinical series (9/279 = 3.2%). The evaluation panel contained much older samples that had been in storage for many years. This may have contributed to the increase in PCR inhibition. All of the samples in the clinical series with negative human DNA had detectable human DNA after dilution, suggesting that PCR inhibition rather than DNA extraction was the problem. The routine inclusion of a human DNA amplification control will help to identify both the problem of DNA extraction failure and PCR inhibition. The failure of the multiplex assay to identify two expected mycoplasma positive samples in the panel could also be related to the age of the samples, as one more sensitive individual primers PCR also failed to detect mycoplasmal DNA in these two samples.

Efforts to investigate community acquired pneumonia are generally poor. As illustrated in...
this study, of the retrospective sputum samples collected over one winter in a large teaching hospital, only 36 of 244 (14.8%) had an acute blood sample sent for investigation and none had a convalescent sample. Many cases of atypical infection would have gone unrecognised without proper investigation. The use of PCR on sputum, which is usually collected when pneumonia is suspected, will help to improve the diagnosis. Prolonged and asymptomatic shedding of mycoplasma and chlamydia has been reported in both healthy individuals and immunodeficient patients.15–34 Prolonged shedding of M pneumoniae from the respiratory tract has been demonstrated for up to seven months after acute infection.35 During an epidemic, 13.5% of healthy volunteers was found to carry M pneumoniae in the throat, but this fell to 4.6% during the interepidemic period.35 C pneumoniae has also been found to persist in atherosclerotic lesions and in peripheral blood mononuclear cells.36–38 However, one should be aware that using a sensitive PCR technique it is possible to detect persistent non-viable bacterial genome for a prolonged period. The diagnostic relevance should therefore be examined carefully in each case. For patients who had clinical respiratory infection, detection of these organisms in respiratory samples in the absence of other respiratory pathogens should be considered as potentially important. Owing to the lack of other supportive investigations and the retrospective nature of the study, the analysis of the case notes of the 11 patients in this series did not provide a clear cut answer as to whether the episode of illness was caused by the identified organism. Several of the patients (Nos 1, 3, 4, 5, and 8) were initially treated with antibiotics not appropriate for mycoplasma or chlamydia and appeared to have a prolonged illness (table 2). In contrast, two younger patients (Nos 6 and 7) with no underlying illness who had detectable C pneumoniae DNA in their sputum appeared to get better when treated with an inappropriate antibiotic. If C pneumoniae were the causative agents in these two patients, this may reflect the self limiting nature of this infection in otherwise healthy young individuals. The detection of C psittaci DNA in an elderly patient with heart failure is puzzling. The lack of investigations and detailed clinical history in this case make assessment difficult. Amoxyclillin is not recommended as a treatment for C psittaci but it may have some effect on chlamydia. Also, the strategy for diagnosis of C psittaci in this multiplex PCR assay was that of exclusion and it is possible that there may be other forms of unrecognised but related respiratory chlamydial infection. Overall, we believe that in at least eight patients in this series, the finding of mycoplasma or chlamydia could be clinically relevant.

The prevalence of atypical organisms in this clinical series was much lower than in other similar studies,35 and no dual infections were detected. However, our clinical series was comparatively small and was only collected over one winter, which was not in an epidemic year for M pneumoniae. Also, although some samples in this series were sent to the hospital by general practitioners, most were from within the hospital which also restricted the spectrum of disease studied.44 The collection also explained the predominance of older patients with underlying predisposing factors. Mycoplasma and chlamydia were thought to be the cause of pneumonia mainly in young adults.1 However, the importance of these organisms to the elderly population has recently been emphasised.39 In this study, the exclusive use of sputum as a sample has restricted the spectrum of disease that we investigated as most patients with atypical pneumonia had non-productive cough. A study of throat swabs or nasopharyngeal swabs in such circumstances may provide a greater yield.

To conclude, we have successfully developed a multiplex PCR that can simultaneously detect and differentiate three causative agents of atypical pneumonia. Further optimisation may improve its sensitivity further. To study the usefulness of this assay in a clinical context, it is necessary to carry out prospective studies covering both epidemic and non-epidemic years, using different types of respiratory samples in both hospital and primary care settings.

This study was funded by the NHS North West biomedical research funding scheme (RD02/3). The late Dr T Trehan of the Institute of Ophthalmology, London, kindly supplied us with the C pneumoniae IOL207 strain. We thank A Kearns of the Newcastle Public Health Laboratory for supplying the M pneumoniae strain.


Multiplex polymerase chain reaction for the simultaneous detection of Mycoplasma pneumoniae, Chlamydia pneumoniae, and Chlamydia psittaci in respiratory samples.

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*J Clin Pathol* 1999 52: 257-263
doi: 10.1136/jcp.52.4.257

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