Simplified preparation of human arterial sections for PCR analysis of *Chlamydia pneumoniae* and human DNA

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**Abstract**

**Aims** — To investigate multiple techniques for the preparation of solid tissue for polymerase chain reaction (PCR) analysis, and to identify the most simple techniques for routine use in the laboratory.

**Methods** — Techniques for the preparation of arterial tissue samples including homogenisation, ultrafiltration, and treatments involving proteinase K, GeneClean™, lectin, and Fe³⁺ specific chelators were evaluated using the PCR to amplify both *Chlamydia pneumoniae* and human DNA.

**Results** — Treatment with either GeneClean or lectin and the Fe³⁺ specific chelator deferoxamine mesylate removed PCR inhibitors from tissue homogenates. Homogenisation followed by GeneClean treatment resulted in the amplification of *C pneumoniae* DNA from within a section of atherosclerotic carotid artery, implying that *C pneumoniae* elementary bodies had been disrupted. In eight further clinical samples from patients not known to have *C pneumoniae* infection, human DNA was amplified and no cross contamination was observed between samples. These samples contained no evidence of *C pneumoniae* DNA by PCR.

**Conclusions** — A simple preparation of solid tissue for PCR analysis, involving homogenisation followed by GeneClean treatment has been developed, and is effective for the amplification of both *C pneumoniae* and human DNA.

**Keywords:** polymerase chain reaction; sample preparation; *Chlamydia pneumoniae*

Four species of *Chlamydia* have been described, of which the most prevalent is *Chlamydia pneumoniae*. Many studies have shown immunohistological and polymerase chain reaction (PCR) evidence of this infection in atherosclerotic coronary,¹ ² carotid,³ ⁴ and peripheral arteries.⁵ In contrast, however, Weiss et al found no evidence of *C pneumoniae* by PCR or culture in 57 of 58 percutaneous coronary atherectomy specimens, or by electron microscopy in all of 22 specimens.⁶ In a study from Australia, chlamydial DNA was undetectable by PCR in 49 atherosclerotic carotid and coronary artery samples from postmortems.⁷ Moreover, given the demonstration by PCR of *C pneumoniae* DNA in peripheral blood mononuclear cells of patients with coronary heart disease and healthy middle aged blood donors,⁸ there is a lingering suspicion that this organism merely contaminates preformed atheromatous material.

More studies based on PCR are needed, but there are still a number of difficulties that must be overcome before these methods can be adopted widely for routine testing.⁹ Current methods of human tissue sample preparation for amplification both of human and microbial DNA are problematic because Taq polymerase is readily inhibited by tissues. These problems are compounded by the unique life cycle of the chlamydiae,¹⁰ the first stage of which, the elementary body, is highly condensed, owing to extensive disulphide crosslinking of cysteine rich envelope proteins, and must be lysed (for example, by incubation with detergents) to release chlamydial DNA. In itself, lysis of elementary bodies runs a risk of reducing DNA template activity.

There are several preparations available for PCR based analysis of *C pneumoniae* in solid tissue, but most are time consuming, labour intensive, or both. For example, whereas some investigators simply homogenise tissue and then treat the homogenate with detergent/proteinase K and heat,¹¹ others also perform phenol/chloroform extractions and ethanol precipitation,¹² or cetyltrimethylammonium bromide (CTAB) based purification of the nucleic acids before PCR.⁷ Alternatively, samples may be homogenised directly in buffer containing detergent and RNase¹³ ¹⁴ and the resulting nucleic acids purified by conventional means¹⁵ or by using commercial ion exchange based resins.² ⁵

By examining multiple preparation techniques, each designed to eliminate known classes of PCR inhibitors, the aim of our study was to compare methods of sample preparation to simplify and improve PCR based amplification from solid tissue.

**Methods**

**TECHNIQUES FOR TISSUE PREPARATION**

All arterial sections were stored at −20°C. A tissue sample (∼ 3 mm²) containing both arterial wall and atheromatous plaque material was dissected from each section, which was returned immediately to −20°C. The sample was then homogenised. Tissue dissections were performed under sterile conditions, using sterile, disposable implements. All sample preparations were performed in a laboratory separate to that in which the PCRs were performed. Filter tips for autopipettes were used throughout.
Homogenisations were performed in sterile microcentrifuge tubes using sterile, disposable pestles (Sigma, Poole, Dorset, UK), either at room temperature in 80 µl of 1x Perkin Elmer PCR buffer (PE/Applied Biosystems, Warrington, UK) (PE buffer: 10 mM Tris/HCl, pH 8.3, 50 mM KCl, 1.5 mM MgCl₂, 0.001% gelatin) or dry, over liquid nitrogen. Homogenised samples were then treated according to one or more of the following techniques.

GeneClean™ is a commercial preparation that purifies nucleic acid of proteins and other contaminants. In essence, a crude mixture containing DNA is added to fine glass beads under high salt conditions. Under these conditions, nucleic acids adhere to the glass beads, whereas contaminants such as proteins, carbohydrates, and ions do not. The beads are washed in a proprietary mixture of salts and ethanol to remove unbound, contaminating material. DNA is then eluted from the beads by a water wash because, under low salt conditions, nucleic acids do not adhere to the glass beads. GeneClean treatments were performed according to the manufacturer's instructions (Anachem, Luton, UK).

Proteinase K was dissolved in 1x PE buffer and added to homogenised samples to a final concentration of 10 µg/µl. Triton X-100 was added to a concentration of 0.5% and the mixture was incubated at 55°C for one hour. The enzyme was inactivated by heating to 95°C for five minutes. Samples were microfuged at 14 000 × g for 30 seconds and the supernatant removed for use in PCR assays.

The Fe³⁺ specific chelators ethylenediamine-N,N'-diacetic acid (EDDA) and deferoxamine mesylate (Sigma) were dissolved in 0.1 M NaOH to final concentrations of 10 mg/ml. Stock solutions were then added to the PCR mixtures, to final concentrations of 0.2 mg/ml, before cycling.

The lectin concanavalin A (Sigma) was dissolved in 1x PE buffer and added to the tissue homogenate to a concentration of 30 µg/µl. The mixture was incubated on ice for 30 minutes, with vortexing at five minute intervals. Samples were microfuged at 14000 × g for 30 seconds and the supernatant removed for use in PCR assays.

For ultrafiltration, 15 µl of treated homogenate was processed through a Microcon® -30 microconcentrator (Millipore, Watford, UK) and the DNA was recovered from the upper reservoir according to manufacturer’s instructions, in 10 µl sterile distilled H₂O.

PCR AMPLIFICATIONS
PCR amplifications were optimised according to the following strategy:
Buffer selection → Mg²⁺ concentration → Quantity of Taq DNA polymerase → dNTP concentration → Primer concentration

MATERIALS
Genomic DNA was purified from C pneumoniae elementary bodies by Dr Cunningham (University of Southampton, UK) and from C. pseuodotuberculosis by Dr D Storey (University of Manchester, UK). Taq DNA polymerase was obtained from Perkin Elmer (PE/Applied Biosystems).

Oligonucleotide primers: CP1, 5'-GTGATTCGTAGCGGATC-3'; CP2, 5'-AGTAGCATATAAGCTGGCC-3'; H1, 5'-ACTCTCCTCGTTGTATTCACCC-3'; and H2, 5'-TTC TGCGATCCACATG-3' were synthesised on a Beckman Oligo1000 DNA synthesiser or purchased from Applied Biosystems. Primers CP1 and CP2 anneal to the major outer membrane protein (MOMP) gene of C pneumoniae strain IOL207, as sequenced by Carter and colleagues.3 Primers CP1 and CP2 correspond to bases 670–687 and the reverse complement of bases 970–987 of sequence M64064, respectively. Primers H1 and H2 anneal to exon 2 of the human ß-globin gene, which is contained within the human ß-globin region of chromosome 11 (Genbank accession number U01317). Primer H1 corresponds to the first 18 bases (19755–19772, U01317) and primer H2 corresponds to the reverse complement of bases 198–215 (19953–19970, U01317) of this exon.

Atheromatous plaque material was collected between September 1995 and September 1996. Patients were recruited after selection for carotid, coronary, or peripheral endarterectomy (for established atheromatous disease) by consultant vascular or cardiothoracic surgeons at the City Hospital, Birmingham and Walsgrave Hospital, Coventry. Exclusion criteria were known or suspected immunodeficiency or hepatitis B viral infection, or apparent risk of acquiring serum hepatitis or human immunodeficiency virus infection. All patients gave informed consent and the study was approved by the district ethics committee.

Results
DEVELOPMENT OF PCR ASSAYS
Two PCR assays were developed to test the methods of sample preparation. One amplified hypervariable region IV of the C. pneumoniae MOMP gene and the second was a simple amplification of human DNA, encompassing exon 2 of the human ß-globin gene. The first PCR is technically more demanding because of the need to lyse C pneumoniae elementary bodies. Conditions were therefore optimised for this amplification using the strategy outlined above, with purified C pneumoniae genomic DNA as a template.
Preparation of arterial sections for PCR was observed (data not shown).

Under the optimised conditions, PCRs with annealing temperatures of 45 °C, 50 °C, and 55 °C were examined. Increasing temperature gave no diminution of product yield. The highest temperature (55 °C) was therefore used in subsequent analyses. Figure 1 shows that a significant increase in amplicon yield was achieved.

Because there is appreciable homology between the MOMP genes of *C. pneumoniae* and *C. psittaci*, a PCR under the optimised conditions was performed using purified *C. psittaci* DNA as a template. No amplification was observed (data not shown).

**Figure 1** Optimisation of *Chlamydia pneumoniae* PCR. PCR amplifications of *H. O* (negative controls) and *C. pneumoniae* genomic DNA were performed with primers CP1 and CP2 as described under standard (1x PE buffer, 100 µM dNTPs, 0.4 µM primers, 2 U Taq DNA polymerase) or optimised (1x AB buffer IV; 100 µM dNTPs, 0.6 µM primers, 4 U Taq DNA polymerase) conditions, as indicated. Lane 1, negative control; lane 2, *C. pneumoniae* amplification; lane 3, negative control; lane 4, *C. pneumoniae* amplification. MW, molecular weight marker (1 µg of a pBR322/HaeIII digest (Sigma)).

Amplification in a standard potassium containing buffer (Perkin Elmer) was compared with that in an ammonium sulphate containing buffer (Advanced Biotechnologies). Each buffer system was used with MgCl₂ at concentrations of 1.5 mM, 2.0 mM, 2.5 mM, and 3.0 mM. No appreciable difference was noted between the different magnesium concentrations, but amplification in the ammonium sulphate containing buffer gave a consistently greater yield of PCR product. The ammonium sulphate containing buffer with 1.5 mM MgCl₂ was therefore used in subsequent analyses. Using this buffer system, the quantity of Taq DNA polymerase was optimised. PCR reactions with 1, 2, 3, 4, and 5 U of enzyme/reaction were performed. A great increase in product yield between 1 and 2 U and a minimal further increase between 2 and 4 U was observed. Therefore, 4 U of Taq DNA polymerase were used during the remaining optimisation reactions.

The nucleotide concentration was then optimised: dNTP concentrations of 20, 50, 100, 150, and 200 µM were tested. A large increase in PCR product yield was observed between 20 and 100 µM dNTPs, but no further increase in yield was observed above this point. A concentration of 100 µM dNTPs was therefore used for future assays.

Primer concentrations between 0.2 µM and 2 µM in 0.2 µM stages were then examined. Amplicon yield plateaued at a concentration of 0.6 µM of primers. Consequently, this concentration was used. Finally, the optimum annealing temperature was investigated.

Under the optimised conditions, PCRs with annealing temperatures of 45 °C, 50 °C, and 55 °C were examined. Increasing temperature gave no diminution of product yield. The highest temperature (55 °C) was therefore used in subsequent analyses. Figure 1 shows that a significant increase in amplicon yield was achieved.

Because there is appreciable homology between the MOMP genes of *C. pneumoniae* and *C. psittaci*, a PCR under the optimised conditions was performed using purified *C. psittaci* DNA as a template. No amplification was observed (data not shown).
successful amplifications from samples 5, 7, and 8 were obtained (fig 2B). Although no native chlamydial DNA was detected in any of these samples, chlamydial DNA was successfully amplified in the spiked reactions, with a yield of: sample 5 > sample 8 > sample 7.

Collectively, these results demonstrate that either GeneClean or combined lectin/chelator treatment of the crude homogenate is sufficient to remove PCR inhibitors. Because the GeneClean treatment gave the highest yield of product in the spiked reaction and was shown to disrupt C pneumoniae elementary bodies (fig 2A), this method was used for future analyses. The lack of amplification of native chlamydial DNA in the second analysis (fig 2B) suggests either that this original tissue sample contained no C pneumoniae, or that the PCR reaction was insufficiently sensitive on this occasion.

PCR ANALYSIS OF CLINICAL SAMPLES

The sample preparation technique of tissue homogenisation followed by GeneClean treatment was applied to clinical samples from patients A–H, who were not known to be infected with C pneumoniae. Tissue samples were homogenised dry over liquid nitrogen and were then suspended in 80 µl 1× PE buffer and purified using a GeneClean Spin Kit™ (Anachem). Dry homogenisation and the GeneClean Spin Kit were introduced to minimise the potential for cross contamination between samples, whereas treatment of the entire homogenate was performed to improve the yield of template DNA. To monitor potential cross contamination, a blank homogenisation/purification containing only 1× PE buffer was performed between that of each tissue sample. Each sample was then used as a template both for the C pneumoniae PCR and for PCR of the human ß-globin gene. No C pneumoniae amplicon resulted from any of the samples (data not shown). However, successful amplification of human DNA was seen for all tissue samples (fig 3), confirming that tissue homogenisation followed by GeneClean treatment is an effective preparation of solid tissue for PCR.

Figure 2 Summary of tissue preparation methods and their effectiveness for PCR amplifications. Tissue samples were prepared by homogenisation and supplementary treatments as indicated. Aliquots (1 µl) of the prepared tissue samples were subjected to PCRs of the human ß-globin gene (H); the Chlamydia pneumoniae major outer membrane protein (MOMP) gene (CP); and the C pneumoniae MOMP gene, in the presence of C pneumoniae genomic DNA (CP+) as indicated. MW, molecular weight marker; -ve, control in which 1 µl H2O replaced the prepared tissue sample; +ve, control in which 1 µl C pneumoniae genomic DNA replaced the prepared tissue sample. (A) Preparation methods and PCR analyses of samples 1–4; (B) preparation methods of samples 5–13 and PCR analyses of samples 5, 7, and 8.

Figure 3 PCR amplification of human genomic DNA from tissue samples and blank preparations. Tissue samples A–H and interspersed blank aliquots of buffer were prepared by homogenisation and GeneClean™ treatment. PCRs of the human ß-globin gene were performed on 1 µl aliquots of each sample as indicated. -ve, interspersed blank preparations; MW, molecular weight marker.
Discussion
Chlamydia pneumoniae is even more difficult to culture than the other chlamydiae, so epidemiological evidence relating to it derives mainly from serological studies. In general, such studies have supported the view that C pneumoniae infection occurs throughout the world, in both affluent and deprived communities, in some of which it has been endemic at least since the late 1950s. Chlamydia pneumoniae is a common respiratory pathogen in children as well as adults, and persistent asymptomatic infection also appears to be common.

Chronic coronary artery disease and acute myocardial infarction are associated with atherogenic serum cholesterol profile. C pneumoniae infection is also associated with atherosclerosis, implying that they may be virulence factors. Serological evidence of previous C pneumoniae infection is also associated with a proatherogenic serum cholesterol profile. Chlamydia pneumoniae has also been cultured from atherosclerotic material, and has been demonstrated by immunohistochemistry in three cell types known to be important in atherogenesis, namely: endothelial cells, macrophages, and smooth muscle cells, all of which support C pneumoniae growth in vitro. In animal models, chlamydiae disseminate at an early stage to peripheral blood mononuclear cells, spleen, and peritoneal macrophages, where they multiply. Using PCR and immunocytochemistry, C pneumoniae has been shown to spread preferentially to cardiovascular tissue, where infection is followed by arterial lesions that resemble atherosclerosis. Enzyme immunoassays have been developed for IgG and IgA antibodies to C pneumoniae, but there is no indication that their sensitivity and specificity are superior to those of micro-immunofluorescence. Moreover, concentrations of antichlamydial IgG, IgA, and IgM antibodies measured in atherosclerotic lesions by micro-immunofluorescence may show no correlation with direct detection by PCR. PCR of C pneumoniae can detect 10<sup>10</sup> g of DNA, approximately equivalent to one chlamydial elementary body. It has been combined with enzyme immunoassay, and this combined test (PCR-EIA) used to screen throat swab and bronchoalveolar lavage specimens for C pneumoniae. A two stage PCR has also been described, which detects C psittaci as well as C pneumoniae in the first stage, but amplifies only C pneumoniae DNA in the second stage.

In our study, we have described two simple techniques for the preparation of solid tissue for PCR analysis. One, homogenisation followed by GeneClean treatment, has been performed on several tissue samples. The lack of contamination in blank samples suggests that this method is not prone to cross contamination. As an alternative, we have also described the preparation of tissue samples by homogenisation, followed by treatment with the Fe chelator deferoxamine mesylate.

In addition, we have developed an optimised PCR for the MOMP gene of C pneumoniae and demonstrated amplification of C pneumoniae DNA from a clinical sample. This result implies that our combined procedure of homogenisation and GeneClean treatment lysed C pneumoniae elementary bodies effectively. Interestingly, however, no C pneumoniae DNA was detected in a second sample of the same tissue. Although this result may be an artefact caused by insufficient sensitivity of the PCR reaction, it might also arise from patchy localisation of C pneumoniae within the arterial wall (analogous to localised bacterial colonies on the surface of an agar plate). Such a distribution of this organism would necessarily result in sporadic PCR results, because only some samples of the tissue would contain C pneumoniae DNA. Previous sporadic amplifications of C pneumoniae DNA from different sections of the same atherosclerotic lesion have been rationalised similarly. No C pneumoniae DNA was amplified from clinical tissue samples A–H. This might have resulted either from the absence of C pneumoniae DNA in those samples or from insufficient sensitivity of the PCR reaction. However, in the context of previous PCR based studies, failure to detect C pneumoniae in only eight atheromatous plaques is unsurprising. The successful amplification of human DNA from all clinical samples demonstrates that tissue homogenisation followed by GeneClean treatment is an effective preparation of solid tissue for PCR.
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