No evidence of *Chlamydia pneumoniae* in the synovia of patients with osteoarthritis

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Abstract

**Objective:** Osteoarthritis (OA) is a common cause of disability affecting millions of people of all ages worldwide. The pathogenesis involves an inflammatory component, but the cause of the inflammation remains incompletely understood. The intracellular bacteria *Chlamydia trachomatis* and *C. pneumoniae* have been demonstrated in patients with reactive arthritis. Both of these microorganisms can cause chronic and persistent infections, with *C. trachomatis* being the most common cause of reactive arthritis. This study was performed to investigate the presence of *C. pneumoniae* in a large number of patients with primary OA.

**Methods:** The study included 75 patients who underwent total knee arthroplasty. During surgery, a synovial biopsy was performed and synovial fluid drawn. Real-time polymerase chain reaction (PCR) of *C. pneumoniae* was run on all patients, and real-time PCR of bacterial 16S rDNA was conducted on 30 of the 75 patients to screen for the presence of other bacteria.

**Results:** Real-time PCR showed no evidence of the presence of *C. pneumoniae* in the patients’ specimens, nor were other bacteria detected.

**Conclusions:** Although an inflammatory component is part of the pathogenesis of OA, we found no evidence indicating that *C. pneumoniae* is a stimulator of that inflammation.

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Introduction
Osteoarthritis (OA) is the most common joint disorder and affects approximately 15% of the world’s population.\(^1\) Primary OA is a degenerative process in the synovial joints that is not caused by previous trauma, rheumatic arthritis, or septic arthritis. Known risk factors influencing the onset of OA are extrinsic factors (such as occupation, repetitive movement, and injuries), systemic factors (such as age, sex, race, genes, and hormones), and joint-related factors (such as overload, instability, deformity, and cartilage injury). The combination of these factors alters the structure and biochemistry in the joint, resulting in the development of OA. In the end stage of the disease, patients develop severe pain and disability. The disability is caused by articular cartilage ulceration with joint space obliteration and bone attrition (Ahlbäck classification), changes in the extracellular matrix, and diminished range of motion of the affected joint. Treatment mainly focuses on symptom relief and slowing the disease progression with joint arthroplasty as the end-stage treatment.\(^2\)

The pathogenesis of OA is thought to be multifactorial with a complex etiology. Since the 1950s, a strong genetic component has been established on the basis of evidence that the incidence of OA is higher in certain families.\(^2\) Several studies have also demonstrated that different genes are involved in OA and that the expression of certain genes is altered in OA.\(^3\) Furthermore, different chemical mediators have been associated with the development of OA, including adipokines. Adipokines are related to obesity, which is a known risk factor for the development of OA.\(^1,3,4\) OA was previously classified as a noninflammatory disease, but later studies showed that inflammatory components are involved in the pathogenesis of OA.\(^4\) Compared with rheumatoid arthritis, however, the inflammation in OA is considered a low-grade chronic joint inflammation.

*Chlamydia trachomatis* is the most common cause of reactive arthritis (ReA).\(^5\) Another species from the same genus, *C. pneumoniae*, has also been implicated as a causative agent of ReA.\(^6\) *Chlamydia pneumoniae* is a respiratory pathogen estimated to cause 10% of all cases of community-acquired pneumonia. The prevalence of antibodies to *C. pneumoniae* increases with age, reaching 70% to 80% in patients of advanced age.\(^7\) This obligate intracellular bacterium may cause chronic and persistent infections that are resistant to antibiotics.\(^7\) However, asymptomatic infections are also known to occur.\(^8\) As with other members of the family Chlamydiaceae, the presence of bacteria in tissue or body fluid is mainly established by polymerase chain reaction (PCR) because these bacteria are slow-growing and require growth in cell cultures.\(^7\)

The inflammatory pathogenesis of OA is unknown. However, as in ReA, the pathogenesis may involve microorganisms as stimulating factors. The presence of viable and metabolically active *C. pneumoniae* has
been demonstrated in synovial tissue from a few patients with ReA and from a few patients with other forms of arthritides. Furthermore, ReA caused by *C. trachomatis* and *C. pneumoniae* was improved by combination antibiotic therapy. The purpose of this study was to investigate the presence of *C. pneumoniae* in synovia from patients undergoing knee replacement for treatment of symptomatic OA. If *C. pneumoniae* is involved in OA, its treatment with a combination of antibiotics might reduce the symptoms caused by the inflammation.

**Materials and methods**

**Patients and specimens**

This study involved patients undergoing total knee arthroplasty for treatment of primary OA of the knee. Patients with known posttraumatic OA, rheumatic disease, or chronic infections were excluded. The clinical data of the patients are presented in Table 1. Synovial fluid was aseptically collected by means of needle aspiration before the joint was surgically opened, and the fluid was immediately frozen at −70°C until analysis. Synovial biopsies were collected at the beginning of each surgery, directly after arthrotomy. A 5-mm × 5-mm biopsy of the synovial membrane was excised at a random and easily accessible part of the synovial membrane and immediately frozen at −70°C until processing.

**For technical reasons, synovial biopsies were not taken from two patients and synovial fluid was not collected from two other patients.**

**DNA extraction**

DNA was extracted from approximately 20 mg of tissue and 0.5 to 4.0 mL of synovial fluid using the QiaAmp DNA mini kit (Qiagen, Hilden, Germany) according to the manufacturer’s instructions. Biopsy samples were run in a TissueLyser (Qiagen) for 2 × 20 s at 30 Hz and then 1 × 20 s at 15 Hz in Buffer ATL (Qiagen). DNA was eluted from the columns in 55 µL of Buffer AE (Qiagen). In every round of extraction, a negative (no template) control was processed in the same way as the samples.

**Real-time PCR**

DNA samples were subjected to real-time PCR. For detection of *C. pneumoniae*, a fragment of the *ompA* gene was amplified on all DNA samples as previously described. To screen for the presence of other bacteria in the material, real-time PCR of 16S bacterial DNA was run on both synovial biopsy tissue and fluid of 30 patients. The primers were as follows: forward 5'-TTG GAG AGT TTG ATC MTG GCT C-3' and reverse 5'-GTA TTA CCG CGG CTG CTG-3'. The PCR mix consisted of 15 µL with 1 × LightCycler 480 SYBR Green I Master (Roche, Basel, Switzerland), 670 nM forward primer (Eurogentec, Liège, Belgium), 670 nM reverse primer (Eurogentec), and a 5-µL sample and was run with the following program: 95° for 10 minutes followed by 35 cycles at 95° for 10 s, 64° for 10 s, and 72° for 30 s, with a following melt curve from 65° to 97°. All runs included positive and negative controls. To verify that DNA extraction had been successful, PCR of the

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<tr>
<th>Table 1. Clinical data of patients undergoing total knee arthroplasty for treatment of primary osteoarthritis</th>
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<tr>
<td>Number of patients</td>
</tr>
<tr>
<td>Arterial hypertension</td>
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<td>Type 2 diabetes mellitus</td>
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<td>Previous myocardial infarction</td>
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<td>Hyperlipidemia</td>
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human beta-actin gene was run on all DNA samples.\textsuperscript{15} This study was approved by the Research Ethics Committee of the Faculty of Medicine, Uppsala University, Uppsala (Dnr 2008/045). Written informed consent was obtained from all patients before the study, and the investigation conformed to the principles outlined in the Declaration of Helsinki.

**Results**

In total, 75 patients (38 men, 37 women; mean age, 63 years; age range, 49–72) were evaluated. All patients tested negative for \textit{C. pneumoniae} DNA in both the synovial tissue biopsy and synovial fluid. All samples tested for the presence of bacterial 16S DNA were also negative. All samples were positive for human beta-actin, indicating successful DNA extraction.

**Discussion**

The pathogenesis of OA is not fully understood but involves an inflammatory component. In this study, the presence of the intracellular bacterium \textit{C. pneumoniae} in patients with knee OA was investigated. None of the investigated synovial biopsies or synovial fluid samples were positive for \textit{C. pneumoniae} when tested with real-time PCR, suggesting that \textit{C. pneumoniae} is not part of the pathogenesis of OA.

To our knowledge, the presence of \textit{C. pneumoniae} in patients with OA has been investigated in only one previous study. In that study, \textit{C. pneumoniae} was demonstrated in 2 of 32 male patients undergoing surgery for knee or hip arthroplasty.\textsuperscript{16} However, other studies in which patients with OA were used as controls for ReA or osteoporosis did not demonstrate \textit{C. pneumoniae} in any of the patients investigated.\textsuperscript{17–19} This latter finding agrees with our results, in which \textit{C. pneumoniae} was not detected by PCR in any of the 75 patients studied.

\textit{Chlamydia trachomatis} is the most common cause of ReA but has also been found in the synovial tissue of patients with OA.\textsuperscript{16} Both \textit{C. pneumoniae} and \textit{C. trachomatis} are disseminated from their primary infection sites by monocytes: \textit{C. pneumoniae} from the respiratory tract\textsuperscript{20} and \textit{C. trachomatis} from the urogenital tract.\textsuperscript{21} They then reach the joint, where they primarily appear to reside in the synovial tissue and not in the synovial fluid.\textsuperscript{22,23}

In the joint, the infection appears to remain in a more persistent state as demonstrated by mRNA expression profiles.\textsuperscript{24} Antibiotic treatment of persistent Chlamydiaceae infection is difficult, and few studies have demonstrated a clinical effect of long-term antibiotic treatment. One study in which combination antibiotic therapy was used to target persistent \textit{C. trachomatis}- or \textit{C. pneumoniae}-induced ReA demonstrated both reduction of clinical symptoms and eradication of the bacterium from synovia in many of the patients.\textsuperscript{10}

The presence of \textit{C. pneumoniae} and \textit{C. trachomatis} has been demonstrated in peripheral blood mononuclear cells (PBMCs), although a low correlation was found between the presence of bacteria in synovia and the presence of bacteria in PBMCs.\textsuperscript{17} The same applies for serological evidence of \textit{C. pneumoniae} infection; both we and others have reported the presence of the bacterium in tissue despite negative serology.\textsuperscript{12,25} This circumstance makes \textit{C. pneumoniae} serology very difficult to interpret, and because it is such a common infection, we expected that about 70% of the patients in our study had antibodies to \textit{C. pneumoniae}.\textsuperscript{7} Hence, we chose not to investigate the presence of \textit{C. pneumoniae} in PBMCs and not to perform serology for \textit{C. pneumoniae} in our patients.

Because the pathogenesis of OA may involve an inflammatory component,
bacteria may be involved as stimulators. Other researchers have demonstrated periodontal pathogens in synovial fluid from OA-affected knees undergoing arthroplasty using 16S rDNA sequencing. In the present study, 30 patients were analyzed for the presence of bacterial DNA in synovial fluid and tissue. Using 16S rDNA PCR, all patients were negative, indicating that bacteria were not present in the synovia.

Patients with OA have synovial inflammation in which inflammatory mediators (such as cytokines and chemokines) are present in the synovial fluid. The innate immune system has an important role in the pathogenesis of OA and is activated by pattern recognition receptors called Toll-like receptors. These receptors may respond to microbes as well as to tissue damage not resulting from an infection.

In conclusion, the common respiratory bacterium C. pneumoniae, which is known to cause chronic infection, was not demonstrated in patients with OA as evidenced by the fact that none of the synovial biopsies or synovial fluid samples in this study were positive. This finding suggests that C. pneumoniae is not part of the pathogenesis in OA and that other factors are instead responsible for the inflammatory component in the pathogenesis.

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Declaration of conflicting interest
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