Fluorescence \textit{in situ} hybridization (FISH) for direct visualization of bacteria in periapical lesions of asymptomatic root-filled teeth

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Whether micro-organisms can live in periapical endodontic lesions of asymptomatic teeth is under debate. The aim of the present study was to visualize and identify micro-organisms within periapical lesions directly, using fluorescence \textit{in situ} hybridization (FISH) in combination with epifluorescence and confocal laser scanning microscopy (CLSM). Thirty-nine periapical lesions were surgically removed, fixed, embedded in cold polymerizing resin and sectioned. The probe EUB 338, specific for the domain \textit{Bacteria}, was used together with a number of species-specific 16S rRNA-directed oligonucleotide probes to identify bacteria. To control non-specific binding of EUB 338, probe NON 338 was used. Alternatively, DAPI (4',6'-diamidino-2-phenylindole) staining was applied to record prokaryotic and eukaryotic DNA in the specimens. Hybridization with NON 338 gave no signals despite background fluorescence of the tissue. The eubacterial probe showed bacteria of different morphotypes in 50\% of the lesions. Rods, spirochaetes and cocci were spread out in areas of the tissue while other parts seemed bacteria-free. Bacteria were also seen to co-aggregate inside the tissue, forming microcolonies. \textit{Porphyromonas gingivalis}, \textit{Prevotella intermedia}, \textit{Tannerella forsythensis} and treponemes of phylogenetic Group I were detected with specific probes. In addition, colonies with \textit{Streptococcus} spp. were seen in some lesions. A number of morphotypes occurred that could not be identified with the specific probes used, indicating the presence of additional bacterial species. CLSM confirmed that bacteria were located in different layers of the tissue. Accordingly, the FISH technique demonstrated mixed consortia of bacteria consisting of rods, spirochaetes and cocci in asymptomatic periapical lesions of root-filled teeth.

INTRODUCTION

It has been established that bacteria play the major role in the aetiology of apical periodontitis (Kakehashi \textit{et al.}, 1965; Sundqvist 1976). In most instances endodontic infections respond well to local antimicrobial therapy of the root canal. When the root canal is properly instrumented, disinfected and obturated, follow-up studies show a treatment success rate of 80–90\% in teeth with apical periodontitis (Kerekes & Tronstad 1979; Byström \textit{et al.}, 1987). It has been generally accepted that bacteria causing endodontic infection of asymptomatic teeth are present in the root canal system, whereas the periapical lesion is free of bacteria. The defence systems mobilized by periapical inflammation are believed first to eliminate the bacteria that invade the periapex. In long-standing infections with a more or less permanently established microflora in the root canal, the host defences appear to be less effective, and findings have been made suggesting that micro-organisms can survive outside the root canal system, on the root surface and/or in the periapical lesions of asymptomatic root-filled teeth (Happonen \textit{et al.}, 1985; Tronstad \textit{et al.}, 1987, 1990; Iwy \textit{et al.}, 1990; Wayman \textit{et al.}, 1992; Gatti \textit{et al.}, 2000; Sunde \textit{et al.}, 2000a, b). Since tissue invasion is considered a major virulence factor of endodontic bacteria and complete

Abbreviations: CLSM, confocal laser scanning microscopy; DAPI, 4',6'-diamidino-2-phenylindole; FISH, fluorescence \textit{in situ} hybridization; FITC, fluorescein isothiocyanate.
healing of the periapical lesion is the ultimate goal in the
treatment of apical periodontitis, the question whether
extraradicular infection exists is of both clinical and
academic interest.

In situ hybridization has proved to be a useful method for
detection and identification of bacteria within their natural
environment (for a review see Moter & Göbel, 2000).
Recently, fluorescence in situ hybridization (FISH) has been
applied to detect bacteria in tissue embedded in cold poly-
merizing resin (Moter et al., 1998a; Hammer et al., 2001).
In these plastic sections, visualization of bacteria and excellent
histological conservation were achieved. Furthermore,
confocal laser scanning microscopy (CLSM) has been
established as a valuable tool for obtaining high-resolution
images and three-dimensional reconstructions of a variety
of biological samples (Wagner et al., 1994; Manz et al., 1995;
Moter et al., 1998a; Wecke et al., 2000).

The aim of the present study was to visualize and identify
bacteria directly within periapical lesions by means of
FISH in combination with epifluorescence and CLSM.

METHODS

Patients. The material came from two groups of patients: Group 1
was collected in Oslo and contained 20 patients (9 men) with a
mean age of 47 years (± 11). Group 2 was collected in Bochum and
included 19 patients (11 men) with a mean age of 53 years (± 22).
The patients from both groups received surgical endodontic treat-
ment of teeth with apical periodontitis. Two surgeons performed the
surgery in Oslo and one surgeon did the surgery in Bochum. All
teeth were asymptomatic. Sinus tracts or endo-peri-to-lesions in
conjunction with the teeth to be treated were not present at the time
of surgery. Radiographs showed that the teeth referred for treatment
were root-filled and had periapical radiolucencies with diameters
between 4 and 15 mm. Each patient received treatment of one tooth
only. The patients were treated with apicoectomy. In Group 1 a sub-
marginal incision was applied during surgery, while a marginal inci-
sion was made in Group 2 (Sunde et al., 2000a).

Processing of tissue specimens. The enucleated periapical
lesions from the 39 patients were washed with sterile saline, fixed
directly with 3-7% (v/v) formaldehyde in PBS (pH 7-4) and kept at
4 °C. The embedding procedure, utilizing cold polymerizing resin
(Tecnovit 8100; Kulzer), was performed according to the manufac-
turer’s instructions. The specimens were washed overnight in PBS
containing 6-8% (v/v) sucrose, dehydrated in acetone for 1 h and
infiltrated with the plastic solution (Tecnovit 8100 base-liquid with
hardener I) for at least 6 h. After adding hardener II, the periapical
lesions were aligned properly in the wells of Histoform S (Kulzer),
sealed with cover foil and placed in the refrigerator. After polymeri-
ization, histoblocs were mounted on the specimens using Tecnovit
3040. The blocks were stored at 4 °C prior to sectioning.

The blocks were sectioned on a rotary microtome (Medim, Type DDM
0036) using steel knives with hard metal edges. Tissue sections (3 μm)
were straightened on sterile water, placed on silanized slides [Super
Frost (Medim); 3-aminopropyltrimethoxysilane (Sigma)] and stored at
4 °C. Three tissue sections from different parts of each lesion were
hybridized. The sections were examined prior to the FISH procedure
for autofluorescence.

Oligonucleotide probes. Probe EUB 338, which is complementary
to a portion of the 16S rRNA gene conserved in the domain Bacteria,
was used to visualize the entire bacterial population in the specimens
(Amann et al., 1990). The group-specific probes TRE I, TRE II and TRE IV (Choi et al., 1997; Moter et al., 1998b) were
applied to the detection of most phylogenotypes of oral treponemes of
Group I (including Treponema vincentii and Treponema medium as
cultivable members), Group II (including Treponema denticola) and
Group IV (including Treponema maltophilum and Treponema lecithi-
holyticum), respectively. For the demonstration of Streptococcus spp.,
a genus-specific probe, STREP, was used (Trebesius et al., 2000). For
visualization of Fusobacterium spp. a genus-specific probe, FUSO,
was designed, and species-specific probes were designed for
Actinobacillus actinomycetemcomitans (ACTACT), Tannerella for-
sythensis (B[T]AFO), Porphyromonas gingivalis (POGI), Prevotella
intermedia (PRIN) and Veillonella parvula (VEPA) (Table 1). All
probes have been deposited in ProbeBase (Loy et al., 2003); an online resource for rRNA-targeted oligonucleotide probes
where probe difference alignments are available (http://www.
microbial-ecology.de/probebase/index.html).

To evaluate their specificity in FISH, all specific oligonucleotide probes
were tested against Treponema vincentii (ATCC 35580), Treponema
denticola (ATCC 35405), Treponema maltophilum (ATCC 51395),
Treponema socranski subsp. socranski (ATCC 35536), Treponema
socranski subsp. buccale (ATCC 35534), Fusobacterium nucleatum
subsp. nucleatum (ATCC 25586), Porphyromonas gingivalis (ATCC
33277), Prevotella intermedia (ATCC 25611), Veillonella parvula
(ATCC 10790), Veillonella dispar (ATCC 17748), Actinobacillus
actinomycetemcomitans (ATCC 43718), Campylobacter rectus (ATCC
33287), Capnocytophaga gingivalis (MCC 00858), Streptococcus
viridans (clinical isolate), Haemophilus influenzae (clinical isolate) and
Tannerella forsythus (formerly Bacteroides forsythus) (ATCC 43037).

Table 1. Oligonucleotide probes

<table>
<thead>
<tr>
<th>Probe</th>
<th>Sequence (5’–3’)</th>
<th>Target species</th>
<th>Formamide (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACAC</td>
<td>TCCATAAGACAGATTCC</td>
<td>Actinobacillus actinomyctemcomitans</td>
<td>30</td>
</tr>
<tr>
<td>B(T)AF0</td>
<td>CGTATCCATTTTATTCGCCCGTTATTC</td>
<td>Tannerella forsythus</td>
<td>20</td>
</tr>
<tr>
<td>POGI</td>
<td>CAATACCGTGTTGCGCTTTAC</td>
<td>Porphyromonas gingivalis</td>
<td>20</td>
</tr>
<tr>
<td>PRIN</td>
<td>CTTTACGTCCCAACAAAAAAGCAGTTTACAA</td>
<td>Prevotella intermedia</td>
<td>20</td>
</tr>
<tr>
<td>FUSO</td>
<td>CTACGGGAGACCGAAGCTC</td>
<td>Fusobacterium spp.</td>
<td>30</td>
</tr>
<tr>
<td>VEPA</td>
<td>TCTAATCTGTTGCGAAGGAGTGCTT</td>
<td>Veillonella parvula</td>
<td>30</td>
</tr>
</tbody>
</table>

*Percentage formamide in the hybridization buffer for optimal hybridization conditions in FISH experiments.
Fig. 1. (a) Simultaneous hybridization with the Bacteria-specific probe EUB338-FITC (green) and the complementary control probe NON EUB-Cy3 (red) on a tissue section from a periapical endodontic lesion localized several EUB338 FITC (green)-positive bacteria of different morphotypes spread among lesion cells and fibres. (b) Only background fluorescence of the tissue could be seen with the Cy3 filter on the same tissue section as shown in (a). (c) DAPI staining of a tissue section from a periapical endodontic lesion. Blue signals show staining of host cells and bacterial DNA. (d) FISH on a tissue section from a periapical granuloma using the Bacteria-specific probe EUB 338-FITC. A small area of tissue necrosis and EUB 338-detected bacteria of different morphologies can be seen. No bacteria could be detected with specific probes. (e) FISH on a tissue section from a periapical endodontic lesion. Hybridization with the Bacteria-specific probe EUB 338-FITC shows a microcolony of co-aggregated bacteria of different morphotypes. No bacteria could be detected with specific probes. Bars, 10 μm.
using fixed cells (Moter et al., 1998a). Control slides with a selection of these fixed bacterial cells were included in every hybridization experiment together with tissue sections.

Besides *A. actinomycetemcomitans*, probe ACTACT also matches *Pasteurella* sp. MCCM02539, a sequence submitted while this work was in progress. Therefore, we could not exclude hybridization with this species. The closest negative control for ACTACT was *Haemophilus influenzae* with a single mismatch as determined by sequencing, that was not detected by the probe. Similarly, probe POGI has none or one single mismatch to the recently published species *Porphyromonas gulae*, isolated from the gingival sulcus of various animal hosts (Fournier et al., 2001). Therefore, we cannot exclude cross-hybridization with this species that so far has not been detected in humans. *V. dispar* was the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized. Probe B(T)AFO detects 13 sequences in the closest negative control for probe VEPA and yielded only weak signals when hybridized.

**RESULTS**

**Bacteria detected with probe EUB 338**

With the universal eubacterial probe EUB 338-FITC, bacteria could be detected by FISH in 10 of the 20 samples investigated in Group 1 and in 10 of the 19 samples examined in Group 2. In all specimens where bacteria were observed, they were seen in localized areas of the lesions, while large areas of the lesions seemed to be bacteria-free. The observed bacteria were located within the tissue and could not be seen at the tissue borders.

Most often rods, cocci and especially spirochaetes of different sizes hybridized with the EUB 338 probe only. These bacteria were often seen spread among cells and fibres in the tissue (Fig. 1a). Simultaneously, hybridization with the probe EUB 338-FITC and the control probe NON 338-Cy3 showed several bacteria with the FITC filter while no signals could be seen with the Cy3 filter (Fig. 1b).

Bacteria of different morphologies could also be detected with DAPI staining (Fig. 1c).

In three lesions, areas of tissue necrosis were apparent and micro-organisms of different morphologies were observed (Fig. 1d). In some lesions the EUB 338 probe detected co-aggregated bacteria of different morphologies within microcolonies (Fig. 1e). In addition, single colonies of EUB 338-detected cocci were also seen.

A distinct morphotype of large, curved bacterial rods was detected with the EUB 338 probe in several lesions (Fig. 2a).

**Bacteria detected with specific probes**

*Tannerella forsythensis* (Fig. 2b), *Prevotella intermedia* and *Porphyromonas gingivalis* (Fig. 2c) were observed in three different lesions. The TRE I probe reacted specifically in one lesion (Fig. 2d). The treponemes were seen spread between eukaryotic cells and fibres in the tissue and some treponemes seemed to migrate around the periapical cells. The probe for the genus *Streptococcus* reacted specifically in three different lesions. In one of these a homogeneous colony with *Streptococcus* spp. was detected, while in two lesions mixed colonies of *Streptococcus* and other cocci detected with the EUB 338 probe, were observed (Fig. 3a–c).

CLSM allowed three-dimensional reconstruction of the tissue and confirmed that the cells observed were bacteria located in different tissue layers (Fig. 4). With this technique we could also see the spatial distribution of the bacteria. The organisms were located between fibres and cells, whereas no bacteria were visible within tissue cells.

**DISCUSSION**

This is the first investigation of the periapical microflora of asymptomatic apical periodontitis where the FISH and...
CLSM techniques have been used. FISH, which turned out to be a powerful method for visualizing micro-organisms in their natural environment, demonstrated bacteria in 50% of the periapical lesions. The method was additionally improved by using CLSM, which allowed optical sectioning, three-dimensional reconstruction and therefore exact localization and observation of the spatial distribution of bacteria in different layers of the periapical lesion and around periapical cells.

By using the control probe NON 338 and DAPI staining, non-specific binding could be excluded, which gave confidence to the results achieved, especially when unusual and large morphotypes of bacteria were observed. In addition, autofluorescence was excluded by viewing the sections prior to the FISH procedure. No bacteria were observed at the borders of the lesions, indicating that contamination had been prevented. This was consistent with the results of a previous methodological study of
extraradicular infection where our surgical technique proved to be adequate for microbial sampling of periapical lesions (Sunde et al., 2000a).

In most cases, bacteria were detected with the eubacterial probe EUB 338 only. The organisms were spread between tissue cells and fibres in the lesion or were co-aggregated, forming microcolonies. The bright signal intensities of the bacteria indicated a high amount of rRNA, which is evidence for physiological activity of the cells at the time of sampling (Kemp et al., 1993; Wallner et al., 1993).

In all lesions where bacteria were observed, they seemed to colonize localized parts of the lesions while other parts seemed to be bacteria-free. Co-aggregation and accumulation of bacteria may suggest that a synergistic interaction is taking place between the organisms involving use of food chains and consorted degradation of complex host and bacterial exopolymers. Positive interactions between

Fig. 3. (a) FISH on a tissue section from a periapical granuloma. Simultaneous hybridization with the Bacteria-specific probe EUB 338-FITC and the genus-specific probe for Streptococcus-Cy3 shows a mixed colony of streptococci (orange) and other cocci detected with the EUB 338 probe (green). Calcified tissue can be seen in the bottom right corner. (b) The same tissue section as in (a) seen with the Cy3 filter showing only streptococcal cells. (c) The same tissue section showing all cocci detected with the EUB 338 probe as seen with the FITC filter. Bar, 10 μm.

Fig. 4. FISH on a tissue section from a periapical granuloma. Bacteria were detected with the EUB 338 probe as shown by CLSM. Analysis of different optical sections using CLSM allows localization of spirochaete- and rod-like bacteria within the tissue (white frames). Bar, 10 μm.
different species occur in the periodontal pocket (van Winkelhoff et al., 1987; Socransky et al., 1998) and in the root canal (Fabricius et al., 1982; Sundqvist 1992), and it is likely that positive interactions also exist between bacteria living in periapical lesions.

In one lesion, Group I treponemes were observed. Treponema vincentii and/or Treponema vincentii-related organisms, which are Group I treponemes, have been associated with human periodontal diseases (Choi et al., 1994; Moter et al., 1998b; Willis et al., 1999; Dewhirst et al., 2000), but have to our knowledge not previously been reported in the root canal or in periapical lesions. In a previous epidemiologic study on oral treponemes, the parallel use of oligonucleotide probes specific for cultivable and as-yet-uncultivable treponemes of Group I, II and IV (Moter et al., 1998b), suggesting the presence of novel yet unknown organisms at a high frequency. In the present study several spirochaete-like organisms of different sizes were detected with the universal probe EUB 338, but no specific signals could be obtained with the treponeme-specific probes. The explanation may be that the probes did not enable detection of all treponemes present, emphasizing the considerable genetic diversity of this group of organisms (Choi et al., 1994; Dewhirst et al., 2000). Previously, our group has described a large uncultivable spirochaete-like organism of 180–2000 μm in diameter, which are Group I treponemes, have been observed in the root canal (Dahle et al., 1993), and in a previous study with transmission and scanning electron microscopy spiral-form bacteria were commonly seen in ‘sulfur granules’ from periapical lesions (Sunde et al., 2002). The detection of these strict anaerobic bacteria suggested that both the root canal and periapical lesion contain highly reduced microenvironments. Because spirochaetes are difficult or even sometimes seemingly impossible to cultivate, their prevalence in endodontic infections is probably underestimated.

Other noteworthy observations in the present study were the positive signals obtained from Porphyromonas gingivalis, Prevotella intermedia and Tannerella forsythensis appearing in three different lesions. These organisms have been associated with periodontal disease (Ashimoto et al., 1996; Socransky et al., 1998), similar to oral treponemes. Their presence in periapical lesions is consistent with recent observations from the root canal and periapical lesions based on molecular methods (Conrads et al., 1997; Gatti et al., 2000; Sunde et al., 2000b; Jung et al., 2001; Roças et al., 2001).

Streptococci were observed in microcolonies in several lesions. They are considered important pathogens in dental caries and have often been isolated from the root canal and periapical lesions.

Most of the probes used did not show specific reaction with any of the observed bacteria. One possibility of non-detection is interference from elastin, collagen and blood cells causing bright autofluorescence. This could have decreased the signal-to-noise ratio and it cannot be excluded that some specific fluorescent signals were masked, particularly from small spirochaetes.

It is also possible that some strict anaerobic bacteria may not be detected by the FISH technique due to their low metabolic activity and the small number of rRNA copies, resulting in low signal intensity and false negative results. However, many of the detected micro-organisms seem to be not yet cultured isolates or are not so-called oral pathogens.

In conclusion, direct visualization of bacteria with the FISH technique provided additional support to the notion that bacteria are present in periradicular tissue of asymptomatic teeth with apical periodontitis, that the bacteria here constitute a consortium of different species and that some of them are probably as yet uncultivable. This technique may also have a potential value in elucidating the aetiology/pathogenesis of extraradicular infection. However, more FISH studies combined with epifluorescence and CLSM should be done with a battery of specific probes for visualization and identification of additional bacteria, including uncultivable ones. No doubt, the endodontic microflora needs to be revisited.

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REFERENCES


FISH-detected bacteria in periapical lesions


