Root canal microbiota of dogs’ teeth with periapical lesions induced by two different methods

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Objective. The microbial composition was investigated in root canals of dogs’ teeth with periapical lesions induced by 2 different methods: open versus sealed canals.

Study design. Teeth from Group I (n/H11005 16) were left open for a week, then sealed with composite resin for 120 days. The teeth from Group II (n/H11005 16) were left open for the same period. Microbiological samples from the root canals were collected and processed by the anaerobic technique for identification and counting of microorganisms after establishment of periapical reactions.

Results. Seventy-four cultivable isolates were recovered in sealed canals (Group I). Strict anaerobes accounted for 64.9% of all species isolated, and gram-negative microorganisms accounted for 55.4%. Microbial genera most frequently isolated were Prevotella, Fusobacterium, Peptostreptococcus, Streptococcus, Enterococcus, Clostridium, and Porphyromonas. Statistical analysis by Pearson chi-square or Fisher’s test revealed positive association between sealed teeth and strict anaerobes (P/H11021 < .05). In open canals (Group II), from a total of 58 cultivable isolates, 19% were strict anaerobes and 81% facultative anaerobes, with predominance of gram-positive species (75.8%). Genera most frequently isolated were Streptococcus, Propionibacterium, Staphylococcus, Neisseria, and Prevotella.

Conclusion. Strict anaerobes were most frequently found in sealed teeth rather than in the teeth with canals left exposed to the oral cavity for 4 months. Therefore, the method that induced periapical inflammatory lesions by intentional oral exposure, followed by tooth sealing, produced root canal microbiota similar to the same found in humans. (Oral Surg Oral Med Oral Pathol Oral Radiol Endod 2006;102:564-70)

Bacteria invading the root canal system may interact with host tissues and cause periradicular endodontic disease.1 A number of animal models were used to study the pathogenesis of periapical lesions,2 the dynamics of root canal infections,3 and also the response of periapical tissues after endodontic therapy.4

In the animal experimental model, certain desirable attributes must be met for the results to represent the human situation.2 The dog is a suitable animal for endodontic research,5,6 mainly because of the close similarity in the healing processes of periapical tissues found in humans and dogs.4 Moreover, as a model in endodontic research, information on the composition

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and variation of its root canal microbiota must be available.

Tissue repair in dogs’ teeth with induced periapical lesions will only occur if disinfection of the root canal system is achieved. Many investigations conducted in dogs test the antimicrobial efficacy of different medications and sealers by observing periapical repair after the root canal procedures. However, microbiological aspects of the infected root canals related to the induced periapical lesions in dogs are still unclear. There is no information on whether or not the dental root canal microbiota in dogs is comparable to the human one.

There are several techniques for experimentally infecting root canals and producing apical areas of reaction in dogs. In some investigations, after coronary opening, the teeth are submitted to pulpectomy up to the canal-dentin-cement (CDC) limit and the canals are left open and exposed to the oral environment until they show radiographic evidence of periapical radiolucent areas. In others, after pulpectomy the cavities are left open only for 5 to 7 days and then sealed. Nevertheless, it is not known, regarding the microbiological aspects, which technique is more appropriate for studying endodontic procedures in this animal model. Therefore, this work investigated the root canal microbiota of dogs’ teeth with periapical lesions induced by 2 different methods.

**MATERIAL AND METHODS**

**Procedures**

The study was conducted on 8 young adult female dogs. These were approximately 1 year old weighing from 10.0 to 15.0 kg. The operative procedures were carried out on 4 teeth from each dog, including the second and fourth lower premolars. Third premolars were excluded to keep the lesions separate.

Animals were premedicated with atropine sulphate 0.044 mg/kg (Fraga Farmáçônica S.A., Mairiporã, PR, Brazil) by subcutaneous injection 15 minutes before anaesthesia. Atropine is always included in the procedure to reduce salivation and counteract any possible arrhythmia. The anaesthetic method employed was a combination of ketamine (Francotar, Virbac do Brasil Ltda., Roseira, SP, Brazil) and xylazine (Rompum, Bayer S.A., São Paulo, SP, Brazil) by subcutaneous injection 15 minutes before anaesthesia. Atropine is always included in the procedure to reduce salivation and counteract any possible arrhythmia. The anaesthetic method employed was a combination of ketamine (Francotar, Virbac do Brasil Ltda., Roseira, SP, Brazil) and xylazine (Rompum, Bayer S.A., São Paulo, SP, Brazil). The animals were anesthetized by an intramuscular injection of ketamine 15 mg/kg and mg/kg of xylazine using the same syringe, which was supplemented when necessary. Animals were anesthetized for all procedures. Plaque and calculus were excluded to keep the lesions separate.

The teeth were accessed through the occlusal surface into the pulp chamber using sterilized spherical diamond burs at high speed and cooled with water spray. The root canal was explored with a K-file and the root pulp was removed using a file.

For contamination, the cavities were exposed, protected only by a cotton pellet in the pulp cavity. The teeth in Group I (n = 16) were left open for a week, and the teeth in Group II (n = 16) were left open for 4 months.

For the teeth in Group I, after 7 days of exposure, debris was removed from the pulp chamber, root canals were irrigated with saline and dried, and small cotton pellets were replaced at the entrance to the root canals. The occlusal cavities were then conditioned with phosphoric acid, received the adhesive (Single Bond; 3M do Brasil, Sumaré, SP, Brazil) and were sealed with composite resin Z-100 (3M).

Clinical and radiographic controls were made after 2, 3, and 4 months, until both groups showed periapical lesions in radiographs, usually after 4 months. The radiographs were taken in a standardized position using a beam guiding device. The following exposure parameters were standardized: 60 kVp and 10 mA, intraoral dental radiographic film (Kodak Ultra-speed; Eastman Kodak Company, Rochester, NY), focal distance from film 15 cm, exposure time 0.6 second, and a constant incidence of the central ray perpendicular to the film. All specimens were radiographed with the same radiographic machine (XR6010, Gnatus, Ribeirão Preto, SP, Brazil). All exposed films were machine processed. The clinical examination included registration of swellings of the mucosa over the apical region, fistula formation, and the presence of exudates in the root canals.

After 4 months, the plaque and the calculus were again removed with ultrasonic unit (Gnatus, Ribeirão Preto, SP, Brazil). A sterilized rubber dam was then applied to the affected teeth to receive the disinfection protocol. In Group II, before the placement of the rubber dam, debris was removed aseptically from the pulp chamber. Teeth and rubber dam were disinfected with 30% hydrogen peroxide and then 2.5% sodium hypochlorite. The sterility of the operation field was checked after inactivation of the antiseptic solution with 5% sodium thiosulphate. Irrigation with a sterile saline solution was performed to moisten the canal prior to sample collection.

In Group I, the composite was removed using sterilized spherical burs at high speed, and irritated with sterile saline solution after the disinfection of the field. Samples from the external surfaces of the teeth, rubber dam, and composite were previously collected to verify sterile condition.

**Microbiological sampling**

For microbial sampling, 3 sterile absorbent paper points were progressively inserted into the full length of
the canal, and kept in place for 60 seconds. The operation field was flushed with nitrogen gas during sampling by means of a sterile cannula connected to the gas cylinder. The paper point sample from the root canal was immediately transferred to individual vials with 1 mL of transport medium reduced transport fluid, and then transported to the anaerobic workstation (Don Whitley Scientific, Bradford, UK) in the microbiology laboratory. The maximum time between sample collection and laboratory processing was 4 hours.

Inside the anaerobic workstation, the transport media, containing glass beads 3 mm in diameter to facilitate mixing and homogenization of the sample, were shaken thoroughly in a mixer for 60 seconds (Vortex MA 162-Marconi, São Paulo, SP, Brazil). Serial 10-fold dilutions were made up to 1/10^4 in prereduced Fastidious Anaerobe Broth (FAB; Lab M, Bury, UK) and 50 μL of 10^-2 and 10^-4 dilution were plated onto several media, using sterile plastic spreaders, as follows: 5% defibrinated sheep blood, Fastidious Anaerobic Agar (FAA) alone, and supplemented with nalidixic acid (0.001% wt/vol), with nalidixic acid and vancomycin (0.00025% wt/vol), and neomycin (0.0075% wt/vol) for anaerobes (all of these isolation media were purchased from Lab M, Bury, UK); 5% defibrinated sheep blood Columbia agar (Oxoid, Hampshire, UK) plates for aerobes; McConkey (Oxoid) agar for enterobacteria, and Sabouraud agar (Oxoid) supplemented with 100 μg/mL of chloramphenicol for yeasts. FAA medium contains hemin and menadione for the growth of fastidious dark-pigmenting gram-negative anaerobic rods.

For anaerobic culture, the plates were incubated at 37°C in an atmosphere of 10% H₂, 10% CO₂, and 80% N₂ for 2, 5, and 14 days. Columbia and McConkey agar plates were incubated aerobically at 37°C for 2 days, and Sabouraud agar plates were kept at room temperature for up to 5 days.

Following incubation, each plate was examined and different colony types were subcultured nonselectively onto blood-FAA plates to obtain a pure culture. Colony appearance was used to select the colonies for further study. All microbiological analysis was carried out quantitatively. Pure cultures were initially identified according to their Gram morphology, ability to produce catalase, and gaseous requirements established by incubation for 2 days aerobically and anaerobically.

These procedures permit the primary identification of the strain as gram-positive or -negative, coccus or bacillus, catalase-positive or -negative, and aerobic or anaerobic. Based on these primary results, the appropriate kit for identification was selected, as follows: Rapid ID 32 A (BioMérieux S.A., Marcy-l’Etoile, France) for obligately anaerobic gram-negative and -positive rods; RapID ANA II System (Innovative Diagnostic Systems Inc., Atlanta, GA) for obligately anaerobic gram-positive cocci; API Staph (BioMérieux) for staphylococci and micrococci; Rapid ID 32 Strep (BioMérieux) for streptococci; Rapid NH System (Innovative Diagnostic Systems Inc) for Eikenella, Hae-mophilus, Neisseria, and Actinobacillus; API 20 E (BioMérieux) for enterobacteria; and ID 32 C Kit (BioMérieux) for yeast identification. Miniapi software (BioMérieux SA) was used to automatically read ID 32 tests.

The identification of enterobacteria via an oxidase test was done before biochemical identification through the kit API 20 E. The identification of black-pigmenting gram-negative anaerobes was performed by the following additional tests:

- fluorescence under long-wave (366 nM) UV light;
- haemagglutination of 3% sheep erythrocytes;
- lactose fermentation by application of the fluorogenic-substrate 4-methylumbelliferonyl-β-galactoside (Sigma Chemical Co., St. Louis, MO, M-1633), according to Alcoforado et al. ;
- trypsinlike activity by application of the synthetic fluorogenic peptide 7-(N-carbobenzoxy-glycylglycyl-larginin-7-amido)-4methyl coumarin.HCl (C-9396).

Statistical analysis

The data collected for each case were typed onto a spreadsheet and statistically analyzed using SPSS for Windows (SPSS Inc., Chicago, IL). The Pearson chi-square test or the 1-sided Fisher’s Exact test, as appropriate, was chosen to test the null hypothesis that there was no relationship between the method of lesion induction and the presence of a specific group of bacteria in the root canals sampled.

RESULTS

None of the sterility controls of the surgical fields showed growth.

In sealed canals (Group I), the average number of cultivable microorganisms was 2.3 × 10⁵ (range, 1.2 × 10⁵ to 3.4 × 10⁵). Seventy-four cultivable isolates were recovered from 16 teeth examined, with an average of 5 species per canal. Strict anaerobes accounted for 64.9% of all species isolated, and gram-negative microorganisms accounted for 55.4%. The microbial genera most frequently isolated were Prevotella, Fusobacterium, Peptostreptococcus, Streptococcus, Enterococcus, Clostridium, and Porphyromonas (Fig. 1). Statistical analysis by Pearson chi-square or Fisher’s test revealed positive asso-
ciation between sealed teeth and strict anaerobes ($P < .05$).

In open canals (Group II), the average number of bacterial cells and species was $1.1 \times 10^5$ cells (range, $1.9 \times 10^5$ to $3.5 \times 10^5$) and 4 species per canal. However, there was no significant difference between the mean number of species in open and closed teeth. From a total of 58 cultivable isolates, 19% were strict anaerobes and 81% facultative anaerobes, with predominance of gram-positive species (75.8%). The most frequently genera isolated were *Streptococcus*, *Propionibacterium*, *Staphylococcus*, *Neisseria*, and *Prevotella* (Fig. 1).

A total of 42 different microbial species were identified from the root canals of dogs’ teeth. Individual root canals yielded a maximum of 7 microbial species each. **Tables I** and **II** indicate the microbial species found in the root canals of sealed and opened teeth, respectively. Some microorganisms were identified only according to their Gram morphology, ability to produce catalase, and gaseous requirements.

![Figure 1](image-url)
DISCUSSION

In this study, dogs were used to test 2 different methods of lesion induction by comparing the microbiological aspects of the root canals associated with the induced lesions. In both groups, the number of bacterial cells (> $10^5$) present in the dogs’ root canals was comparable to that found in the human canals (between $10^2$ to $10^4$). Likewise, the average number of bacterial species found in the dogs’ root canals was also similar to the that found in humans when cultural methods were used: 4 to 5 and 5 to 7 different species per canal, respectively. This further confirms that the mean number of species in infected root canals as revealed by culture studies is low and includes only a limited assortment as compared to the breadth of bacterial diversity in the oral cavity. However, molecular studies have revealed a far higher number of species in infected root canals. Species that are difficult to be cultured have been identified by the latter techniques (e.g., Tannerella forsythia, Treponema denticola, Filifactor alocis, Pseudorambacter alactolyticus, Dialester pneumosintes, Olsenella spp., Centipedes periodontii). Therefore, this study may have failed to detect microorganisms that do not grow reliably on culture media.

In general, the human and dog oral cavity florae have some similarities. Both of them comprise gram-positive cocci (mainly genus *Streptococcus*, and also the genera *Micrococcus*, *Staphylococcus*, and *Peptostreptococcus*); gram-positive rods and filaments (*Actinomyces* and *Propionibacterium*); gram-negative cocci (*Neisseria* and *Veillonella*); and gram-negative rods (including the facultative anaerobic and capnophilic genera *Haemophilus*, *Actinobacillus*, *Eikenella*, and *Capnocytophaga*; and the obligate anaerobic genera *Porphyromonas*, *Prevotella*, and *Fusobacterium*). However, the most striking difference in the oral microbial flora of

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**Table I.** Microbial species found in the root canals of 16 sealed teeth (Group I)

<table>
<thead>
<tr>
<th>Teeth</th>
<th>Microorganisms</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td><em>Porphyromonas gingivalis</em>, <em>Streptococcus constellatus</em>, <em>Enterococcus avium</em>, <em>Peptostreptococcus anaerobius</em>, <em>Staphylococcus xylosus</em></td>
</tr>
<tr>
<td>2</td>
<td><em>Prevotella loescheii</em>, <em>Prevotella bivia</em>, <em>Prevotella oris</em>, <em>Bacteroides fragilis</em>, <em>Enterococcus faecalis</em>, <em>Fusobacterium nucleatum</em>, <em>Fungi</em></td>
</tr>
<tr>
<td>3</td>
<td><em>Prevotella oralis</em>, <em>Prevotella bivia</em>, <em>Prevotella denticola</em>, <em>Streptococcus bovis</em>, <em>Capnocytophaga sp.</em></td>
</tr>
<tr>
<td>4</td>
<td><em>Streptococcus bovis</em>, <em>Bacteroides thetaiotaomicron</em>, <em>Rod-shaped G– anaerobe</em></td>
</tr>
<tr>
<td>5</td>
<td><em>Prevotella oralis</em>, <em>Propionibacterium acnes/granulosum</em></td>
</tr>
<tr>
<td>6</td>
<td><em>Porphyromonas endodontalis</em>, <em>Prevotella bivia</em>, <em>Fusobacterium necrophorum</em>, <em>Clostridium difficile</em>, <em>Neisseria sicca/subflava</em>, <em>Enterococcus faecalis</em></td>
</tr>
<tr>
<td>7</td>
<td><em>Porphyromonas gingivalis</em>, <em>Peptostreptococcus anaerobius</em>, <em>Neisseria sicca/subflava</em>, <em>Enterococcus faecalis</em>, <em>Staphylococcus xylosus</em>, <em>Cocci Rod-shaped G– anaerobe</em></td>
</tr>
<tr>
<td>8</td>
<td><em>Porphyromonas endodontalis</em>, <em>Peptostreptococcus spp.</em>, <em>Cocci Rod-shaped G– anaerobe</em></td>
</tr>
<tr>
<td>9</td>
<td><em>Prevotella oralis</em>, <em>Fusobacterium nucleatum</em>, <em>Peptostreptococcus anaerobius</em>, <em>Eubacterium limosum</em>, <em>Capnocytophaga sp.</em>, <em>Enterococcus faecalis</em></td>
</tr>
<tr>
<td>10</td>
<td><em>Prevotella loescheii</em>, <em>Porphyromonas gingivalis</em>, <em>Prevotella oralis</em>, <em>Fusobacterium nucleatum</em>, <em>Peptostreptococcus anaerobius</em>, <em>Gemella morbillorum</em>, <em>Streptococcus spp.</em></td>
</tr>
<tr>
<td>11</td>
<td><em>Enterococcus faecalis</em></td>
</tr>
<tr>
<td>12</td>
<td><em>Peptostreptococcus anaerobius</em>, <em>Clostridium difficile</em>, <em>Neisseria sicca/subflava</em>, <em>Streptococcus spp.</em></td>
</tr>
<tr>
<td>13</td>
<td><em>Prevotella oralis</em>, <em>Fusobacterium nucleatum</em>, <em>Clostridium bifermentans</em>, <em>Streptococcus spp.</em></td>
</tr>
<tr>
<td>14</td>
<td><em>Prevotella oralis</em>, <em>Fusobacterium nucleatum</em>, <em>Clostridium bifermentans</em>, <em>Peptostreptococcus spp.</em>, <em>Cocci Rod-shaped G– anaerobe</em></td>
</tr>
<tr>
<td>15</td>
<td><em>Clostridium bifermentans</em>, <em>Clostridium sordelli</em>, <em>Rod-shaped G+ facultative</em>, <em>Rod-shaped G– anaerobe</em>, <em>Rod-shaped G+ anaerobe</em></td>
</tr>
<tr>
<td>16</td>
<td><em>Fusobacterium necrophorum</em>, <em>Haemophilus parainfluenzae</em>, <em>Propionibacterium granulosum</em>, <em>Escherichia coli</em>, <em>Rod-shaped G– facultative</em></td>
</tr>
</tbody>
</table>

**Table II.** Microbial species found in the root canals of 16 teeth with open pulp space (Group II)

<table>
<thead>
<tr>
<th>Teeth</th>
<th>Microorganisms</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td><em>Prevotella oralis</em></td>
</tr>
<tr>
<td>2</td>
<td><em>Porphyromonas gingivalis</em>, <em>Prevotella oralis</em>, <em>Peptostreptococcus anaerobius</em>, <em>Clostridium spp.</em></td>
</tr>
<tr>
<td>3</td>
<td><em>Streptococcus intermedius</em>, <em>Rod-shaped G– facultative</em></td>
</tr>
<tr>
<td>4</td>
<td><em>Neisseria sicca/subflava</em></td>
</tr>
<tr>
<td>5</td>
<td><em>Propionibacterium acnes</em>, <em>Staphylococcus intermedius</em>, <em>Neisseria sicca/subflava</em>, <em>Streptococcus bovis I</em>, <em>Rod-shaped G+ facultative</em></td>
</tr>
<tr>
<td>6</td>
<td><em>Prevotella oralis</em>, <em>Streptococcus bovis I</em>, <em>Streptococcus bovis II</em>, <em>Propionibacterium propionicum</em>, <em>Neisseria sicca/subflava</em></td>
</tr>
<tr>
<td>7</td>
<td><em>Actinomyces odontolyticus</em>, <em>Propionibacterium acnes</em></td>
</tr>
<tr>
<td>8</td>
<td><em>Peptostreptococcus spp.</em>, <em>Neisseria sicca/subflava</em>, <em>Streptococcus suis II</em>, <em>Streptococcus capitis</em>, <em>Propionibacterium propionicum</em>, <em>Propionobacterium acnes</em>, <em>Rod-shaped G– anaerobe</em></td>
</tr>
<tr>
<td>9</td>
<td><em>Prevotella oralis</em>, <em>Bifidobacterium spp.</em>, <em>Streptococcus bovis I</em>, <em>Streptococcus bovis II</em>, <em>Propionibacterium propionicum</em>, <em>Propionibacterium acnes</em></td>
</tr>
<tr>
<td>10</td>
<td><em>Enterococcus faecium</em>, <em>Aerococcus viridans</em>, <em>Streptococcus suis II</em>, <em>Streptococcus bovis I</em>, <em>Propionibacterium propionicum</em></td>
</tr>
<tr>
<td>11</td>
<td><em>Neisseria sicca/subflava</em>, <em>Enterococcus avium</em>, <em>Aerococcus viridans</em>, <em>Staphylococcus epidermidis</em> (aureus), <em>Rod-shaped G+ facultative</em></td>
</tr>
<tr>
<td>12</td>
<td><em>Staphylococcus intermedius</em></td>
</tr>
<tr>
<td>13</td>
<td><em>Bifidobacterium spp.</em>, <em>Streptococcus bovis I</em>, <em>Staphylococcus xylosus</em>, <em>Abiotrophia adiacens</em></td>
</tr>
<tr>
<td>14</td>
<td><em>Streptococcus salivarius</em>, <em>Staphylococcus aureus</em></td>
</tr>
<tr>
<td>15</td>
<td><em>Lactis lactis cremoris</em>, <em>Streptococcus suis</em>, <em>Staphylococcus aureus</em>, <em>Streptococcus lentus</em>, <em>Neisseria sicca/subflava</em></td>
</tr>
<tr>
<td>16</td>
<td><em>Lactis lactis cremoris</em>, <em>Streptococcus salivarius</em>, <em>Neisseria sicca/subflava</em>, <em>Rod-shaped G+ facultative</em></td>
</tr>
</tbody>
</table>
humans and dogs is the higher number of species detected in humans. This difference is due mainly to the higher isolation rate of anaerobic bacteria in humans compared with animals. Another remarkable distinction is the much higher prevalence of enterobacteria in dogs. Species from the genera Enterococcus, Klebsiella, Escherichia, Citrobacter, and Enterobacter have been isolated from the oral cavity of dogs. Bacillus and Clostridium species have been also isolated. Furthermore, some species, such as Pasteurella spp., have only been recovered from dogs and not from humans, especially P. multocida and P. fluorescens.

In this study, the dogs’ root canals constantly contaminated by saliva for 4 months showed a higher isolation frequency of facultative anaerobes and gram-positive species, such as Streptococcus, Propionibacterium, and Staphylococcus. Strict anaerobes, for example Prevotella and Peptostreptococcus, were less frequently isolated. This may have been a result of ecologic determinants in the open canals, such as the availability of nutrients and oxygen. Moreover, the anatomy of the dogs’ premolar teeth may have contributed to sustaining aerobic conditions in the root canals.

On the other hand, in the closed teeth group studied, the microbiota was predominantly anaerobic, with approximately equal proportions of gram-negative and gram-positive bacteria. These results are in accordance with previous investigations in humans and monkeys. The latter authors have showed that, in a closed root canal, the relative proportion of strict aerobic bacterial strains increases with time. In this study, after 120 days, the strict anaerobes accounted for 64.9% of all species isolated. The anaerobic microbial genera most frequently isolated were Prevotella, Fusobacterium, Peptostreptococcus, and Porphyromonas. The importance of anaerobic bacteria, gram-negative as well as gram-positive, is related to their power of producing a number of virulence factors that play a key role in mixed endodontic infections. Gram-negative bacteria such as Prevotella, Fusobacterium, and Porphyromonas contain various bioactive cell surface components, such as fimbriae, capsules, peptidoglycans, outer membrane proteins, and lipopolysaccharides (LPSs). LPS-endotoxin may therefore be one of the bacterial products that acts as an inflammatory agent in the etiology of apical periodontitis. The cell walls of gram-positive bacteria such as Peptostreptococcus include peptidoglycans and lipoteichoic acids that can influence inflammatory reactions and enhance the pathogenicity of gram-negative species.

In this study, despite the similarities found between the microbiota of closed root canals in the dogs’ teeth and that found in human necrotic pulps, some differences are apparent. For example, Enterococcus and Clostridium species, frequently isolated in the dogs’ root canals studied, are rarely found in human necrotic pulps when cultural procedures are used. Such differences may have occurred because of the peculiarities found in the microflora of a dog’s oral cavity as discussed above.

Overall, when 2 methods of lesion induction in dogs are compared, the results indicate the method that induced periapical lesions by intentional oral exposure, followed by tooth sealing, produced a root canal microbiota similar to humans. These findings may help validate studies that use the latter method for testing, in dogs, the antimicrobial efficacy of endodontic medicaments.

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REFERENCES


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