with the cells and matrix in the dentine-pulp complex may complement its biocompatible properties and contribute to its biological effects on dentine bridge formation and regeneration in these tissues.
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RP4

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Antibacterial effects of different root-end filling materials

Aim To evaluate the antibacterial activity of leachable components of amalgam, ProRoot MTA (Dentsply Maillefer, Switzerland), IRM (Caulk Dentsply, USA), Super Bond C&B (Sun Medical, Japan), Geristore (Den-Mat, USA), Dyract (Dentsply DeTrey, Germany) SE Bond (Kuraray, Japan) and Protect Bond (Kuraray) with Clearfil APX® (Kuraray) composite.

Methodology The direct contact test, with *E. faecalis*, *S. aureus*, and *P. aeruginosa*, was used. The walls of microtitre wells were coated with freshly mixed materials. The materials were tested immediately after application to the well (fresh samples) and after setting for 3 days (set samples). Ten μL bacterial suspensions were added to the wells for direct contact with the materials for 1 hour at 37°C. Growth of surviving bacteria was then measured in a microplate spectrophotometer hourly for 15 h at 620 nm. Automixing before each reading ensured homogenous bacterial cell suspensions. Twelve uncoated wells using identical size of inoculum for the three bacteria served as positive control. Inhibition of bacterial growth was recorded either as a delay in outgrowth in the second plate and/or a lower final number of bacteria.

Results Fresh samples of all materials showed a 3-h delay in exponential growth of both *E. faecalis* and *S. aureus*, and a 5-hr delay in growth of *P. aeruginosa*. Set samples of IRM and ProRoot cements showed generally greater antibacterial activity than the other materials: both completely inhibited *P. aeruginosa*, and both delayed and limited growth of *E. faecalis*. IRM was active also against *S. aureus*, whereas ProRoot had little if any activity towards this organism.

Conclusions The direct contact test, by being quantitative and virtually independent of solubility and diffusion, was found more suitable to assay solid root-end filling materials. IRM and ProRoot MTA were generally more potent inhibitors of bacterial growth than the other materials.

Research Posters – Microbiology

R1

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Detection of bacteraemia associated with intra-canal and extra-canal file manipulation

Aim To determine the prevalence and intensity of bacteraemia associated with intra- and extra-canal manipulation of instruments in asymptomatic teeth associated with periapical disease. The study was designed to account for confounding factors that may also potentially result in bacteraemia.

Methodology Blood and root canal samples were taken from 9 patients meeting strict selection criteria. The consented patients had a single asymptomatic tooth with apical periodontitis but were otherwise orally and generally healthy. Microbiological samples were taken from the root canals under aseptic conditions prior to root canal preparation using validated protocols. The first blood sample (baseline) was taken prior to any intra-canal filing. The root canals were then prepared to an apical size 20, maintaining the files within the terminus of the root canal system, determined by electronic and radiographic means. The second blood sample was taken 30 s following completion of this apical preparation. A size 15 instrument was then used as a patency file, 1 mm beyond the terminus of the root canal system. The third blood sample was taken 30 s after this. A period of 15 min was allowed to elapse between taking each blood sample. Blood samples were processed by lysis filtration and both blood and root canal samples were cultured under appropriate conditions. The prevalence and intensity of bacteraemia were determined.

Results Bacteria were isolated from all root canals sampled. Bacteraemias were not detected in the first (baseline) and second blood samples. Bacteraemias were detected in 5/9 (56%) of the third blood samples. The intensity of bacteraemia ranged from 1.0–5.0 CFU/6 ml.

Conclusions Only extra-canal manipulation of instruments caused bacteraemia, in just over half the cases, the intensity of which was low.

R2

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Culture-dependent and culture-independent detection of persistent bacteria retrieved by a novel apical sampling method

Aim To compare culture-dependent and culture-independent techniques to detect persistent root canal bacteria following chemo-mechanical debridement, retrieved by a novel apical sampling protocol.

Methodology Nineteen single-rooted, previously untreated teeth with radiographic evidence of a periapical lesion were subjected to root canal treatment and sampling procedures over 2 visits. Samples were obtained before and after separate preparation of the coronal (2/3) and apical (3 mm) parts of the canal using a protocol developed *in vitro*, which allowed independent sampling of the two parts of the canal. The coronal preparation was completed using ProTaper® and the apical using hand, stainless-steel instruments; NaOCl (2.5% w/w) irrigation and $Ca(OH)_2$ dressing were used in all cases. A further apical sample was taken just prior to root filling. Appropriate sterility-control measures were incorporated. Culture-dependent and culture-independent techniques were used to detect the presence of bacteria in the samples. The frequency of detection of bacteria in the apical samples using these techniques was compared using the McNemar test.

Results Apical preparation using 2.5% sodium hypochlorite and subsequent dressing with calcium hydroxide both resulted in a

significant ($P < 0.05$) reduction in the number of samples with cultivable bacteria. However, the culture-independent technique revealed no significant difference in bacterial presence (no differentiation between viable or dead) between samples taken before and after chemo-mechanical preparation. There was no significant difference in the detection of bacteria in the apical samples obtained after chemo-mechanical debridement using culture-dependent or culture-independent techniques.

Conclusions The study confirmed previous findings about the effect of chemo-mechanical debridement on the bacterial flora. There was no difference in the ability of culture-dependent and culture-independent techniques to detect bacteria in the apical samples after chemo-mechanical debridement.

R3

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Microflora distribution in teeth associated with apical periodontitis determined by different microscopy techniques and protocols

Aim To compare two sample processing protocols to examine the presence and morphological distribution of bacteria in teeth associated with apical periodontitis, using three microscopy techniques [scanning electron microscopy (SEM), light microscopy (LM) and transmission electron microscopy (TEM)].

Methodology Nine root samples (7 teeth) were processed using either of two techniques (Eastman/Nair). The roots were sectioned longitudinally: the root portion designated for SEM was viewed along its entire length and descriptively divided into apical, middle and coronal thirds; semi-thin and ultra-thin sections were cut from the root portion designated for LM and TEM from each third of the root. Each third of the root was examined using all three microscopy techniques. Observations were systematically recorded.

Results Bacteria were detected in 8 of the 9 roots. A bacterial biofilm was a common finding on the root canal walls. Rods, cocci, filaments, fungal hyphae, spirochaetes and yeasts were observed. High magnification views revealed the nature of bacterial cell to cell contact via fimbriae and other cell membrane appendages. More bacteria were evident apically than coronally. Bacteria were seen in the dentinal tubules in the coronal and middle thirds but were not commonly found in the dentinal tubules apically. The roots processed using the Nair technique appeared to give more predictable results. Polymorphs (PMNs) were surprisingly found in all the root segments, mostly walling off the bacterial biofilm; although they were more commonly evident apically.

Conclusions The combination of three different microscopy techniques offered complementary views of the presence and morphological distribution of bacterial colonisation along the length of the root canal. The Nair protocol was superior to the Eastman technique in this study. The study provided further insight into the ecology of root canals and the nature and location of the host/microbial interface.

R4

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Species-richness of gram-positive coccoid morphotypes from root canals determined by phenotypic and genetic measures

Aim To compare the effect of microbial identification method on apparent species richness of gram-positive coccoid morphotypes recovered from untreated and treated root canals of teeth associated with periapical disease.

Methodology Gram-positive coccoid morphotypes ($n = 177$) recovered from untreated ($n = 105$) and treated ($n = 72$) teeth from 12 patients were identified by physiological, biochemical and commercially available enzyme detection kits (Api, bioMerieux, Lyon, France) as well as by comparative 16S rRNA gene sequence (*P*artial) (*P*reviously reported). The identities, their confidence values and biochemical test results (binary format) were analysed. The binary data were used to generate similarity matrices and dendrograms (PAUP) to compare the phenetic relatedness (TREEVIEW) of like-species from untreated and treated teeth.

Results The biochemical and molecular identities of 72% of strains matched at the genus level, 45% at the species level and 28% did not match. The method of identification influenced the species richness, regardless of the measure used (genus, species, confirmed or unconfirmed identification); 16S rRNA identification always increased the mean and range values per tooth. The greater species richness in this study compared to previous studies was probably due to a combination of sample type, method of sample retrieval, cultivation and identification procedures. A high 38% of isolates were given 'unacceptable' validity scores and were genus and sample-origin dependent. Bacteria from the treated teeth were more difficult to identify with a higher proportion of unacceptable scores (46% versus 32%), suggesting absence of such profiles in the database. Lack of direct correlation between enzyme test profile and confidence score may suggest weighting of individual tests. The dendrograms showed that same-species strains from untreated and treated teeth were often phenotypically distinct.

Conclusions Commercial enzyme tests should not be used as the sole arbiter of their identity as frequently happens in endodontic microbiology; they should be supplemented with other confirmatory tests.

R5

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Antibiotic susceptibility of gram-positive coccoid morphotypes from untreated and treated teeth with periapical disease

Aim To determine the initial Minimum Inhibitory Concentrations (MIC) of commonly prescribed antibiotics for gram-positive coccoid morphotypes from root canals of untreated and treated teeth, using agar dilution and E-test; and to compare the MIC between and within test methods, bacterial groups and sample origins.

Methodology Gram-positive coccoid morphotypes from untreated ($n = 107$) and treated ($n = 77$) teeth (isolation procedures and identification previously reported) were subjected to antibiotic (*P*enicillin, amoxicillin, metronidazole, vancomycin, erythromycin, tetracycline, clindamycin and cefaclor) susceptibility testing using agar dilution (in accordance with the recommendations of the National Committee for Clinical Laboratory Standards) and E-test (AB Biodisk protocol, 1997). The MICs from the E-tests were plotted by antibiotic/strain combination to establish frequency distributions and their relationship to interpretive categories (NCCLS 2003). The MIC and resistance status were analysed by test method, bacterial group and sample origin.

Results There was broad agreement between the agar dilution and E-test methods (80% agreement within one doubling dilution, 90% agreement within two doubling dilutions). Frequency distribution plots showed the interpretive categories to be reliable. A total of 38% of the strains exhibited resistance to at least one of the 8 antibiotics tested and the majority (86%) of the resistant strains had multiple

drug resistance. A higher proportion (53%) of strains from root-treated teeth was resistant compared to those from untreated teeth (26%); the main groups of resistant bacteria were: lactobacilli, staphylococci and enterococci. Antibiotic resistance profiles enabled strains from the same tooth to be differentiated into groups with possibly different origins. The resistant strains originated from many teeth, but a large proportion was from a select few teeth, possibly suggesting gene transfer between bacteria within root canals.
Conclusions E-test was comparable with an established method for determining MIC for root canal isolates. A high proportion of the strains exhibited resistance, especially in those from treated teeth.

R6

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Prevalence and transfer of tetracycline resistance gene [*tet*(M)] among root canal bacterial isolates

Aim To determine the prevalence of the tetracycline resistance gene [*tet*(M)] among tetracycline-resistant root canal isolates and to investigate the nature (conjugative transposon Tn*916*) and donor potential of Tn*916*-containing bacteria.
Methodology Tetracycline-resistant bacteria ($n = 15$), previously obtained from teeth with apical periodontitis, were grown in pure culture and their total DNA extracted. Previously published primers were used to amplify the following genes [16S rRNA gene, *tet*(M), Tn*916* transposon-unique sites] by PCR using the DNA as template. The 16S rRNA gene provided the bacterial identification and successful amplification of the joint of circular Tn*916* indicated its active status. Filter-mating experiments were carried out to assess the transfer of the Tn*916* elements to recipient bacteria.
Results Of the original fifteen tetracycline-resistant bacteria selected, eight were shown by PCR to contain the *tet*(M) gene; four of these contained the unique Tn*916* regions. Two of these elements were shown to be active by virtue of positive amplification of the 'joint' in a circular form. Filter-mating experiments successfully demonstrated the transfer of tetracycline resistance from one donor (*Neisseria* spp) to an enterococcal recipient.
Conclusions About half of the tested tetracycline-resistant bacteria had the *tet*(M) gene and about half of these demonstrated the presence of Tn*916*. Transfer of tetracycline resistance has been shown from one of these strains.

R7

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Induction of resistance by serial exposure of root canal isolates to sub-inhibitory doses of antiseptics

Aim To investigate induction of resistance and cross-resistance by serial exposure of root canal isolates to sub-inhibitory doses of antimicrobial agents.
Methodology Initial Minimum Inhibitory Concentrations (MIC) were calculated for 20 strains of bacteria isolated from untreated and treated teeth with apical periodontitis, using several antimicrobial agents (chlorhexidine gluconate, povidone-iodine, calcium hydroxide and sodium hypochlorite). Doubling dilutions of these agents were prepared in 96-well microtitre plates and the strains inoculated into the wells. After 72 hours, MIC values were recorded and strains from the ½ MIC well were sub-cultured on blood agar plates. The ½ MIC sub-cultures were re-inoculated into another 96-well plate and the exposure repeated; this was carried out 12 times. Following this serial exposure, the MICs were re-calculated and the strains maintained either by sub-culturing without antimicrobial challenge or by freezing for one month. After 1 month the stability of the MICs was determined.
Results An increase in MIC was observed for 70% (14/20) of the strains for at least one antimicrobial agent following serial exposure. Considering the combination of strain and antimicrobial, 23% (18/80) showed an increase in MIC. The MIC changes were strain/antimicrobial-dependent but no obvious genus- or species-dependent patterns were evident. The MIC for other antimicrobial agents also increased concurrently with that of the test agent, without exposure to them for 10 strains. The induced change occurred for one specific or all of the non-test antimicrobials. The increase was stable after frozen storage but returned to pre-exposure levels on sub-culture without antimicrobial challenge.
Conclusions Serial exposure to sub-inhibitory doses of antimicrobials may cause reversible increases in MIC; withdrawal of exposure reduced the MIC to pre-exposure levels but not if the strains were frozen. Induced resistance may be accompanied by cross-resistance to other agents. The phenomenon was strain/antimicrobial-dependent but no genus/species patterns were evident.

R8

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Antimicrobial effect of calcium hydroxide, chlorhexidine digluconate and their combination in a human dentine block model

Aim To evaluate *in vitro* the antibacterial effect of calcium hydroxide (CH), chlorhexidine digluconate (CHX) and their combination (CH+CHX) against *Enterococcus faecalis* in a dentine block model with and without the use of EDTA.
Methodology Root canals of 48 human dentine blocks were prepared and smear layer removed by rinsing with EDTA (17%) and NaOCl (0.5%). The blocks were placed in Tryptic Soy Broth (Oxoid), autoclaved, inoculated with *E. faecalis* (A197A) and incubated at 37°C for 3 weeks. The blocks were rinsed with EDTA ($n = 24$) or sterile water ($n = 24$). In each group, 6 root canals were dressed either with CH (1 : 1 w/v in water), CH + CHX (1 : 1 w/v CH in 2% CHX), calcium carbonate (CC) + CHX (1 : 1.5 w/v) or CC (1 : 1.5 w/v in water) (negative control) for one week. Dentine samples obtained with a reamer were sampled in phosphate buffered saline. The samples were cultured on Tryptic Soy Agar (Oxoid) and the number of colony-forming units (CFU) was determined.
Results CH + CHX was the most effective dressing (mean log10CFU ± SD = 2.11 ± 2.06), followed by CH (2.80 ± 3.19), CC + CHX (3.37 ± 3.60) and CC (4.66 ± 4.36). Rinsing with EDTA did not demonstrate antibacterial efficacy.
Conclusions CHX improves the efficacy of CH, whereas EDTA rinsing does not seem to have a direct killing potential in dentine disinfection. Quantification of bacteria residing in dentine is difficult as indicated by the high SD.

R9

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Prevalence of oral enterococci among endodontic retreatment patients and dental students

Aim To investigate the prevalence of enterococci in four different sites of the oral cavity among patients undergoing root canal retreatment (P-group) and a group of dental students (S-group).
Methodology The P-group ($n = 101$, mean age 56 years) consisted of patients referred to the department of Endodontology for retreatment of apical periodontitis in a root filled tooth and showing >10 dental restorations. The S-group ($n = 100$, mean age 31 years), was recruited among dental students at Göteborg University with a high level of oral health (<4 dental restorations and no root filled tooth). Oral hygiene was classified as poor, fair or good and smoking habits were recorded. Microbiological samples were obtained from four different sites: subgingival and supragingival plaque, the tongue and cheeks. Samples were transported to the laboratory of oral microbiology using VMGA III and plated on Enterococcosel Agar. The specimens were incubated aerobically and bacterial growth was classified as present or absent.
Results Enterococci were more prevalent among individuals in the P-group (62%) than in the S-group (20%) ($P < 0.001$). Enterococci were recovered from 144 sites and were most frequently identified in supragingival samples (54 sites) and in samples from the tongue (48 sites). In four individuals enterocci were present in samples from all sites and in 44 persons from only one site. In the S-group poor oral hygiene and smoking were factors associated with presence of enterococci ($P = 0.002$ and $P = 0.002$, respectively). No such correlations were found in the P-group.
Conclusions Oral enterococci were common among patients undergoing root canal retreatment but were also found among a group of dental students with good oral health.

R10

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Microbiological evaluation using T-RFLP analysis of the flora in necrotic teeth of patients irradiated in the head and neck region

Aim To evaluate the root canal flora in necrotic teeth in patients irradiated in the head and neck region by use of terminal restriction fragment-length polymorphism (T-RFLP) analysis and to compare the results with the flora from necrotic teeth in a control group.
Methodology Bacterial samples from necrotic root canals in patients treated for radiation caries following irradiation in the head and neck region (group a) and in healthy controls (group b) were analysed. Each sample in group a was taken from a different tooth (all were single rooted teeth, in total 13 root canals in 9 patients). Group b consisted of 11 patients of which 11 teeth were sampled (each time, 1 necrotic canal was sampled (in multi-rooted teeth, the root with easiest access was sampled). T-RFLP was used as identification technique. The 16S rRNA genes (rDNAs) of oral bacteria in root canals were amplified by PCR with universal primers. The 16S rDNAs were digested with the BstUI restriction enzyme and analysed by capillary electrophoresis (ABI310). T-RFLP patterns were numerically analysed using Basehopper, an in-house developed computer program. Bacterial species were assigned to terminal restriction fragments (T-RFs) by comparison with culture and cloning of 16S rRNA genes.
Results In group a, 3 samples were tested PCR negative, none in group b. A total of 50 different T-RFs were detected in the T-RFLP profiles (44 in group a and 28 in group b). Each T-RF represents one bacterial species or a cluster of bacterial species. Fifteen T-RF's could not be identified using the web-library. A mean of 13.20 T-RFs in group a and 6.55 T-RF's in group b were found per sample. This difference was statistically significant ($P < 0.05$). A total of 22 different T-RF's were found in group a that were not found in group b. These mainly comprised of subspecies of Lactobacillus spp., Capnocytophagae spp. and Actinomyces spp.
Conclusions The flora in root canals of patients irradiated in the head and neck region (xerostomia) were significantly more diverse than the flora in a control group.
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R11

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Assessment of the bacterial load in root canals using real-time PCR

Aim To evaluate the bacterial load of root canals with the diagnosis of chronic apical periodontitis by means of quantitative real-time PCR depending on the method for root canal disinfection.
Methodology Twenty teeth with radiographically documented periapical lesions were included. Ten of these teeth had a deficient root filling; the other 10 had not been treated. After removal of either pulp tissue or root canal filling, bacterial samples were obtained with sterile paper points, using measures to prevent contamination. Root canals were prepared using rotary instruments. During preparation, in each group 5 teeth were rinsed with either NaOCl 2% or chlorhexidine 0.1%. A second set of samples were taken immediately after treatment and the third samples after a period of 14 days during which the canals were filled with a calcium hydroxide dressing.
Results In the NaOCl group the mean total number of bacteria was 1.96 E7 (SD: 5.64 E7) before root canal preparation. The bacterial load was statistically significant reduced to 4.56 E4 (SD: 9.33 E4) immediately after treatment ($P < 0.05$). After the 14 days period during which the root canals were filled with calcium hydroxide, the number of bacteria was 3.9 E5 (SD: 8.29 E5). In the chlorhexidine group the corresponding values were 4.86 E7 (SD: 6.33 E7) before root canal preparation, 2.66 E4 (SD: 2.42 E4) immediately after treatment and 8.77 E3 (SD: 6.85 E3) after 14 days ($P < 0.05$). In teeth with insufficient root canal fillings, the total number of bacteria was lower and the reduction of the bacterial load was not statistically significant.
Conclusions The novel method of quantitative real-time PCR appears to be well suited to evaluate various disinfection protocols during root canal treatment.

R12

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The effect of canal filling with Gutta-percha or Resilon on *Enterococcus faecalis* in bovine dentinal tubules

Aim To observe the effect of canal filling on survival of *E faecalis* remaining in dentinal tubules and to compare the sealing ability of Gutta-percha and Resilon (SybronEndo, USA).
Methodology Bovine teeth were sectioned to produce specimens 4 mm thick with 6 mm external diameter and 2.3 mm of internal diameter. *E. faecalis* was inoculated into the specimens and incubated. The outer surface was coated with nail varnish and the internal diameter was increased to 2.5 mm by using an ISO 025 round bur. The dentine specimens were divided into 5 groups by canal filling method. Group 1 was the negative control. Group 2 was the positive control. In Group 1 and 2, the internal surface of the dentine blocks was coated with nail varnish. Group 3 was filled with ZOE based sealer and Gutta-percha, Group 4 with resin based sealer and Gutta-percha, and Group 5 with resin based sealer and Resilon. After 24 h at room temperature, the blocks were incubated at 37°C for 1, 2, 3 and 4 weeks on BHI agar plates. The internal layer of the dentine blocks was removed using ISO 027, 029, 031, 035 round burs and the resultant dentine chips were incubated on culture medium at 37°C; for 24 h. Following incubation, the optical density of the medium was measured using spectrophotometer.
Results There was a statistically significant reduction in the number of *E. faecalis* in the group where dentinal tubules were completely sealed with nail varnish in comparison with the groups obturated with gutta-percha or Resilon. In group 5, the number of *E. faecalis* in the dentinal tubules decreased significantly with time, whereas in group 3 and 4, there was no reduction.
Conclusions Canal sealing ability of both Gutta-percha and Resilon was not complete since *E. faecalis* in dentinal tubules survived after canal filling. Evidence emerged that the resin based sealer and Resilon would exhibit a better root canal sealing ability in the long-term.

Research Posters – Canal Preparation

R13

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Procedural errors during shaping root canals to increased apical preparation sizes using Lightspeed rotary instruments

Aim To evaluate the incidence of procedural errors following root canal treatment with Lightspeed (LS) rotary instruments with increased apical enlargement.
Methodology A total of 80 patients (117 teeth with 287 roots) underwent root canal treatment which was carried out under standardized conditions by a trained operator using Lightspeed rotary instruments (85 molars, 25 premolars, 7 incisors). The apical portion was enlarged to sizes varying on average between sizes 40 to 60. The mean apical preparation size was 52.5. Sixty-three teeth were recalled after a mean interval of 25 months. Initial and recall radiographs were assessed using the periapical index (PAI). Procedural errors such as instrument fractures, perforations and root canal transportation were noted.
Results Only three LS instrument fractures occurred (sizes 37.5, 40, 52.5), all in the apical portion of the canal. The presence of the fractured LS instruments had no impact on apical healing. One perforation was noted in the middle third of the canal. No root canal transportation was observed.
Conclusions In the hands of a trained operator, root canal treatment with Lightspeed rotary instruments was a safe technique, allowing apical enlargement to sizes larger than commonly recommended.

R14

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Shaping ability of ProTaper in comparison to a ProTaper–Profile combined technique in simulated root canals

Aim To compare the shaping ability of ProTaper (Dentsply Maillefer, Switzerland) instruments and the combined use of ProTaper and ProFile (Dentsply Maillefer) instruments in severely curved simulated root canals.
Methodology Thirty simulated canals with curvature of 40° and different shapes in terms of position of curvature (straight section before curve: 8 and 12 mm) were prepared using two different preparation methods: group A with the ProTaper instrument set (apical preparation to F3) according to the recommendations of the manufacturer; group B with ProTaper preparation of the coronal two thirds (S1 to F1) and apical enlargement with ProFile .04 taper (sizes 20–35). Pre-operative, sequential and post-operative pictures, recorded using a digital camera, were superimposed. Measurements were carried out at 5 different points: canal orifice (O); half-way to the orifice in the straight section (HO); beginning of the curve (BC); apex of the curve (AC); endpoint (EP).
Results In both canal types the total canal width was significantly higher in group A compared to group B at points HO, BC and AC ($P < 0.05$); a similar result was found for the transportation of the central axis at the apex of the curve (AC, $P < 0.05$). Mean transportation was towards the inner aspect of the curve in all canal types at BC, towards the outer aspect in canals with 12 mm straight section at AC. In both canal types, the mean transportation was significantly higher in group A at point AC ($P < 0.05$).
Conclusions Under the conditions of this study, apical enlargement of curved canals with ProFile .04 taper instead of ProTaper instruments resulted in less apical transportation and a more centred preparation shape in and beyond the apex of the curve.

