780 Bacterial diversity of primary endodontic infections by *16SrRNA* analysis

Location: Exhibit Hall D (Miami Beach Convention Center)

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Objectives: The purpose of this study was to investigate the bacterial diversity of root canal infections by using culture-independent molecular methods based on 16S ribosomal RNA cloning. **Methods:**Samples were collected from asymptomatic root canals of twelve teeth with primary endodontic infection. Genomic DNA was isolated and *16SrRNA* amplified by PCR with universal primers. Amplicons were cloned using TOPO TA Cloning Kit and transformed into electrocompetent *E.coli* cells. The insert DNA was sequenced using ABI Prism BigDye terminator cycle sequencing. The 500 base-pair sequences were aligned and used for a BLAST sequence homology search against the GenBank database. The percentage similarity cut-off for species identification was set at 98%. **Results:** All samples were positive for Bacteria. 543 clones were sequenced (45.6±4.4 clones/sample). Three to 15 phylotypes were found per root canal sample. Sixty-one distinct bacterial taxa were identified, of which 31 (51%) are considered as-yet-uncultivated phylotypes. Most of the species belonged to the Firmicutes phyla. The most prevalent species were *Eubacterium infirmum* and *Prevotella oris*, which were identified in six and four of the twelve samples, respectively. *Dialister invisus*, *Dialister pneumosintes*, *Pseudoramibacter alactolyticus* were found each in four samples. The majority of the taxa were present in only one sample, such as *Enterococcus faecalis*, *Streptococcus mutans*, *Lachnospiraceae* oral clone BP1-14, *Eubacterium* oral clone A53MT and *Parvimonas micra*. **Conclusion:** The present study suggested a wide diversity of oral species associated with primary endodontic infections. Support FAPESP 2007/52492-3, 2006/59856-8.

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