Comparison of Bacterial Community Composition of Primary and Persistent Endodontic Infections Using Pyrosequencing

**Author:** Tzanetakis et al  
**Year:** 2015  
**Journal:** JOE

**Aim**
- To investigate the composition and diversity of bacterial population in symptomatic & asymptomatic primary & persistent endodontic infections using pyrosequencing.

**Materials & Methods**
- 44 adult patients (48 teeth) were included in this study.
- Selected teeth had either a non-vital pulp or were previously treated at least 4 yrs prior with PAR.
- Clinical signs and symptoms were recorded.
- Teeth were classified into 4 groups:
  - Group 1: Primary infection & have symptoms (acute apical abscess/symptomatic AP) (13 teeth)
  - Group 2: Primary infection & have no symptoms (chronic apical abscess/asymptomatic AP) (11 teeth)
  - Group 3: Persistent infection & have symptoms (acute apical abscess/symptomatic AP) (13 teeth)
  - Group 4: Persistent infection & have no symptoms (chronic apical abscess/asymptomatic AP) (11 teeth)
- Root canal microbial samples were obtained from each tooth & DNA was extracted.
- Bacterial abundance and diversity were examined by Endodontic infection type and statistical analysis was performed.

**Results**
- Bacteroidetes was the most abundant phylum in both infection groups.
- Pyramidobacter, & Parvimonas were the most abundant in primary infections.
- Fusobacterium, Bacteroidaceae, & Prevotella were the most abundant in persistent infections.
- Persistent infections were significantly enriched for Proteobacteria and Tenericutes compared with primary ones; at the genus level including increased enrichment of persistent infections for Lactobacillus, Streptococcus, Sphingomonas, and Ralstonia.
- In primary infections, symptomatic cases were more diverse than the asymptomatic ones; in persistent infections, the opposite was found.
- Persistent infections showed higher phylogenetic diversity compared with primary infections.

**Conclusion**
- High bacterial diversity of endodontic infections and a more diverse bacterial community profile in persistent vs primary infections.

**Authors**
Giorgos Tzanetakis, Andrea Azcarate-Peril, Sophia Zachaki, Panos Panopoulos, Evangelos Kontakiotis, Phoebus Madianos & Kimon Divaris