

Phenotype and genotype of enterococcus faecalis isolated from root canal and saliva of primary endodontic patients

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Deskripsi Lengkap: <https://lib.ui.ac.id/detail?id=20427801&lokasi=lokal>

Abstrak

Objective: To investigate the phenotype and genotype of *E. faecalis* isolated from the root canal and saliva of primary endodontic patients with periapical lesions.

Methods: Eight variations en adult male and female individuals suffering from primary endodontic infection, either with or without periapical lesions, were involved in this study. Root canal scraping and saliva were collected from each subject and used for bacterial quantitation using a real-time polymerase chain reaction (RT-PCR). Enterococci were isolated using ChromAgar medium and then identified using both biochemical (Gram staining and catalase tests) and molecular biology (conventional PCR) methods. Gelatinase activity, polysaccharide capsul profile and mRNA ace expression level were determined using microbiological, biochemical and molecular biology approach, respectively. Genotype of *E. faecalis* was determined based on nucleotide sequence of ace and gelE genes analyzed using web-based 3730xl DNA Analyze software.

Results: The results showed that except for its proportion, no significant difference was found in phenotypes (gelatinase activity and mRNA ace expression levels) and genotypes (polymorphism of Cps operon and variation of ace and gelE nucleotide sequences) of *E. faecalis* isolated from the root canal and saliva of primary endodontic patients had or had no periapical lesions.

Conclusion: It can be concluded that *E. faecalis* proportion had a role in the occurrence of periapical lesions in the primary endodontic patients, but not gelatinase activity, mRNA ace expression level, Cps operon polymorphism or ace and gelE nucleotide sequence variations.