

Microbial community in persistent apical periodontitis : a 16S rRNA gene clone library analysis

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論文題名 Microbial community in persistent apical periodontitis:a 16S rRNA

gene clone library analysis

(16S rRNA 遺伝子クローンライブラリー法を用いた根尖性歯周炎に関する細菌群集構成の同定)

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論 文 内 容 の 要 旨

Aim To characterize the microbial composition of persistent periapical lesions of root filled teeth using a molecular genetics approach.

Methodology Apical lesion samples were collected from 12 patients (23-80 years old) who visited the Kyushu University Hospital for apicectomy with persistent periapical lesions associated with root filled teeth.. DNA was directly extracted from each sample and the microbial composition was comprehensively analyzed using clone library analysis of the 16S rRNA gene. *Enterococcus faecalis*, *Candida albicans* and specific fimA genotypes of *Porphyromonas gingivalis* were confirmed using Polymerase Chain Reaction (PCR) analysis with specific primers.

Results Bacteria were detected in all samples, and the dominant findings were *Porphyromonas gingivalis* (19.9%), *Fusobacterium nucleatum* (11.2%), and *Propionibacterium acnes* (9%). Bacterial diversity was greater in symptomatic lesions than in asymptomatic ones. In addition, the following bacteria or bacterial combinations were characteristic to symptomatic lesions: *Prevotella* spp., *Treponema* spp., *Peptostreptococcaceae* sp. HOT-113, *Olsenella uli*, *Slackia exigua*, *Seimonas infelix*, *P. gingivalis* with type IV fimA, and a combination of *P. gingivalis*, *F. nucleatum*, and *Peptostreptococcaceae* sp. HOT-113 and predominance of *Streptococcus* spp.. On the other hand, neither *Enterococcus faecalis* nor *Candida albicans* were detected in any of the samples.

Conclusion While a diverse bacterial species were observed in the persistent apical lesions, some characteristic patterns of bacterial community were found in the symptomatic lesions. The diverse variation of community indicates that bacterial combinations as a community may cause persistent inflammation in periapical tissues rather than specific bacterial species.