R-16. Distribution of Periodontal Pathogens in Korean Aggressive Periodontitis

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연구 배경

Microbial associations in aggressive periodontitis versus different ethnic origins are substantially unknown. We undertook this study to determine the prevalence of 7 putative periodontopathogens in Korean patients and to evaluate microbial differences in localized and generalized aggressive periodontitis patients.

연구방법 및 재료

Thirty-nine aggressive periodontitis patients between 20 and 35 years old were selected according to clinical criteria. The patients were subclassified into 17 localized and 22generalized aggressive periodontitis patients. In each of 39 individuals, subgingival plaque samples were collected from 4 diseased teeth ($\geq$6mm pocket depth, 156 sites) and 1 healthy site ($\leq$3mm pocket depth, 39 sites). Polymerase chain reaction (PCR) of the 16S ribosomal RNA gene fragments (about 530 bp) of plaque bacteria and their subsequent detection by dot blot hybridization using specific oligonucleotide probes was performed to determine the presence of 7 periodotopathogens.

연구결과

The prevalences were 75% for *Actinobacillus actinomycetemcomitans*, 94.2% for *Bacteroides forsythus*, 99.4% for *Fusobacterium* sp., 85.9% for *Peptostreptococcus micros*, 96.8% for *Porphyromonas gingivalis*, 78.8% for *Prevotella intermedia*, and 96.8% for *Treponema* sp. The prevalences of these bacteria were significantly higher in diseased sites than in healthy sites. The logistic regression analysis showed that *P. intermedia*was more significantly associated with generalized aggressive periodontitis than the localized form, the odds ratio being 3.28 (95% C.I. 1.26-8.56, p=0.015).

결론

Our results demonstrate that the 7 periodontal pathogens analyzed are strongly associated with Korean aggressive periodontitis. In particular, *P. intermedia* are more associated with generalized aggressive periodontitis, a more severe and progressive form, than with localized aggressive periodontitis.