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<th><strong>Title</strong></th>
<th>Preferential co-colonization of periodontopathogens in subgingival niches of periodontitis patient</th>
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<td><strong>Author(s)</strong></td>
<td>Leung, WK; Jin, LJ; Soder, PO; Corbet, EF</td>
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Chronic periodontitis is an infectious disease resulting from intricate host-pathogen interactions at the subgingival border of the tooth-supporting apparatus (Consensus Report 1996). The role of specific periodontopathogens in this disease process was being investigated dating back to the late 70’s (Socransky & Haffajee 1994). At least a dozen putative periodontopathogens were identified (Zambon 1996) while more were being put onto the list when research ability and recognition were pushed beyond the limits of traditional culture techniques (Paster et al 2001). Realizing the possible immense complexity of the microbial etiology of periodontal disease, attention was also being put towards studying the interactions between members of the subgingival microbial biofilm (Socransky et al 1988, Simonson et al 1992). Evidence accumulated in recent years pointed towards certain periodontopathic species tending to co-exist in subgingival niches of subjects with various clinical conditions (Socransky et al 1996, Jin et al 1999; 2002; 2003). Various statistical analysis protocols have been applied to the subgingival microbial data (Simonson et al 1992, Cohen 1993, Ali et al 1995, Socransky et al 1998, Jin et al 1999, 2002). Many studies employed statistical protocols focusing on two-way contingency, correlation or cluster analysis of target species. Configural frequency analysis (CFA) was recommended by Cohen (1993) as the statistical test when configurations of the target microorganisms, present or not, were studied.

The aim of the current study is therefore attempt to utilize CFA in studying the possibility of co-colonization patterns among five periodontopathogenic species. Actinobacillus actinomycetemcomitans (Aa), Porphyromonas gingivalis (Pg), Prevotella intermedia (Pi), and Treponema denticola (Td) in subgingival niches of untreated periodontitis patients.

Materials and Methods

Patients management, site selection and sampling

Microbiological samples from 85 subgingival sites of 16 untreated Chinese adults with chronic periodontitis, aged 32-55 years were studied. Related clinical information was published (Jin et al 1999, 2002).

Five to seven non-adjoining sites were sampled from each subject consisting:

- Periodontitis sites - [pocket depth (PD) > 5.0 mm, attachment loss (AL) > 3.0 mm, pocket probing depth (PPD) > 5.0 mm], 3-4 samples.
- Gingivitis sites - [gingival index (GI) > 2, positive bleeding on probing (BOP), PD < 4.0 mm, AL < 1.0 mm, BL (-)], 1 sample.

Samples were collected using paper points and analyzed for Aa, Bf, Pg, Pi and Td using species specific DNA probes (Jin et al 1999).

Following sampling, each patient received a course of non-surgical periodontal therapy within a 4-week period. Subgingival plaque samples were collected from the overall 85 sites one month after the non-surgical periodontal therapy.

Statistical analysis

The prevalence of Aa at baseline and 1-month post-therapy was low (0% and 3.5% respectively) and hence not included in the study. Stuart-Maxwell Chi square test (Fleiss & Everitt 1997) was used to analyze the change of microbial profile, i.e. presence or absence, of the four target species Bf, Pg, Pi, Td and in all possible combinations (n = 16), see Table 2 on baseline and one month post non-surgical therapy. Post hoc analysis based on McNemar's statistic with Bonferroni adjustment was carried out. A level of significance chosen was 0.05.

CFA was then applied to the data set (Cohen 1993). The protocol described by Eys (1996) was followed. In brief, a global K-factor log-linear analysis was performed in order to search for the appropriate statistical types. The first set of marginal fits described the model for mutual independence among all variables (the first-order model). The second, third, and fourth models test, respectively, models based on two-, three- and four-way interactions among the variables (Cohen 1993). The statistical types would be selected based on the component of Chi-square p-value and be put through the corresponding configuration analysis where types and/or antitypes were identified.

Results

Many of the Bf, Pg, Pi and Td co-occurrence pattern switched to none one month after treatment (p < 0.001).

References


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