ORAL SYNERGISTES CLUSTER WITH THE RED COMPLEX IN CHRONIC PERIODONTITIS

Objective: The objective of this study was to explore associations among classical and new periopathogens in subgingival biofilm and to assess their relative importance to chronic periodontitis.

Method: DNA was extracted from pooled subgingival biofilm samples obtained from 40 chronic periodontitis patients and 40 healthy controls. Tagman q-PCR assays were used to determine the absolute and relative counts of Porphyromonas gingivalis, Tannerella forsythia, Treponema denticola, Prevotella micros, Filifactor alocis, oral synergistes, and oral T.s. Microbial associations were assessed using cluster analysis. Significance of differences in microbial parameters between cases and controls were sought using Mann-Whitney test and ordinal regression.

Results: The detection rate was 100% except for P. gingivalis, T. denticola, and T.s. that were detected in 71.2%, 91.2% and 95% of the samples, respectively. The median log and relative counts were lowest for T.s. (4.4 and 0.0016%, respectively) and highest for oral synergistes (7.2 and 1.4%, respectively). In cluster analysis, oral synergistes joined the red complex at a shorter distance than P. gingivalis and T. denticola, linking with T. forsythia at a 100% rescaled similarity. All species/syntypes except T.s. were significantly associated with periodontitis (P<0.005). In regression analysis, oral synergistes showed the strongest association with periodontitis, while in ROC curve analysis filter presence at log counts ≥2.2 was the best marker of periodontitis (82.5% sensitivity and specificity).

Conclusions: Oral synergistes are shown here to be members of the red complex in strong association with chronic periodontitis.

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I have a significant financial interest/arrangement or affiliation with an organization/institution whose products or services are being discussed in this session. I understand that I must disclose this information to the participants who attend my presentation. No.

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