

Scientific release
from the European
Federation of
Periodontology

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Study:



Oral Microbiome in Chinese Patients with Aggressive Periodontitis and their family members

Li Y, Feng X, Xu L, Zhang L, Lu R, Shi D, Wang X, Chen F, Li J, Meng H.
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**Relevant
background
to study:**

Aggressive periodontitis (AgP) is a rare form of inflammatory periodontal disease characterised by rapid attachment loss and alveolar bone destruction observed at an early age. AgP presents with a familial aggregation, which may be explained by both genetic and environmental factors together with intra-familial transmission of infectious periodontal microorganisms. According to the

consensus report of the 1999 international classification of periodontal diseases, AgP patients presented with higher proportions of either *Aggregatibacter Actinomycetemcomitans* (Aa.) or *Porphyromonas gingivalis* (Pg.) in different populations. However, it has been reported that in some Asian AgP patients Aa. could not be identified as being present.

Study aims:

The purpose of this study was to demonstrate the microbial composition of Chinese patients with AgP and to compare bacterial profiles between AgP patients and their first-degree blood relatives using the 16S rRNA gene pyrosequencing technique.

Methods:

Saliva and subgingival plaque samples from 10 AgP patients and 10 first-degree blood relatives with chronic periodontitis were collected. Genomic DNA was isolated from saliva and subgingival

plaque samples. Bacterial 16S rRNA gene amplification and sequencing of PCR products were performed.

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Results:

- The unweighted unifracs distance between AgP patients and their family members was significantly lower than those in unrelated participants.
- The relative abundance of Pg. and red complex pathogens in subgingival plaque samples of AgP patients was higher than their first-degree blood relatives.
- The relative abundance of Pg. and red complex pathogens in saliva samples of AgP patients were similar to their first-degree blood relatives.
- The relative abundance of Pg. and red complex pathogens in subgingival plaque samples were higher than in saliva samples for both AgP patients and their first-degree blood relatives.
- The relative abundance of Pg. and red complex pathogens in saliva correlated strongly with levels in subgingival plaque samples for each AgP patient

**Limitations,
conclusions
and impact:****Limitations:**

- Small sample size.
- Age difference between AgP patients and relatives.

Conclusions:

Similar phylogenetic architecture of microbial composition in AgP patients and first-degree blood relatives were observed, thus evidence for microbial transmission within family members was proposed. Additionally, Pg. may be the predominant periodontal pathogen in Chinese AgP patients.

Impact:

Findings of the study are crucial for the treatment and prophylaxis of Chinese AgP patients.