

Haffajee AD, Bogren A, Hasturk H et al. Subgingival microbiota of chronic periodontitis subjects from different geographic locations. J Clin Periodontol 2004; 31:996-1002.

Purpose: To compare the subgingival microbial profile in chronic periodontitis subjects from a specific location in Brazil, Chile, Sweden and the USA.

Materials and Methods: Fifty-eight subjects from Brazil, 26 from Chile, 101 from Sweden and 115 from USA participated in the study. For inclusion, subjects, ranging from 24-82 y.o., presented with at least 14 natural teeth, at least 4 sites with probe depths ≥ 4 mm and at least 4 sites with attachment level of ≥ 3 mm. Demographic information and smoking status was ascertained via questionnaire. Plaque accumulation, gingivitis, BOP, probe depth, attachment level were obtained at 6 sites per tooth. The data for the Chilean population was collected for a prior study utilizing a Florida probe. For the remaining 3 population pools, a North Carolina probe was used. For the Chilean, Swedish and American subjects, subgingival plaque samples were taken obtained from the MB of all teeth. Subgingival plaque from the 4 deepest sites and from 3 sites with probe depth <4 mm were sampled from the Brazilian subjects. Supragingival plaque was removed prior to collecting subgingival plaque with a sterile Gracey curette. The sample was placed in 0.15 ml Tris-EDTA + 0.15 ml of NaOH. All samples were analyzed within 3 months. Samples from Chile, Sweden and The USA were analyzed for 40 bacterial species using checkerboard DNA-DNA hybridization at The Forsyth Institute. The samples in Brazil were analyzed in Brazil by a person trained at Forsyth. The percent of the total DNA probe count was determined for each species.

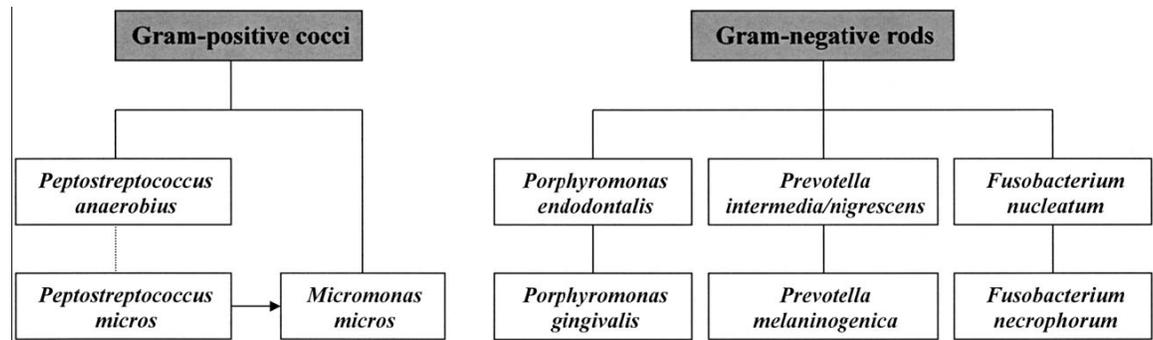
Findings and Conclusions: A total of 6036 subgingival plaque samples were analyzed. The red complex, *Tannerella forsythensis*, *Porphyromonas gingivalis* and *Treponema denticola*, were observed in different proportions in the 4 populations. *P. gingivalis* was found in significantly higher proportions in the American subjects than in the Swedish subjects. The Chileans had the highest proportion of *P. gingivalis*. The Brazilians demonstrated higher proportions of *T. denticola*, whereas the Swedes had high proportions of *T. forsythensis* and lower proportions of *T. denticola* and *P. gingivalis*. The percentage of DNA probe count for *T. forsythensis* was not significant between the Brazilian, Chilean, Swedish and American subjects. For the Chilean population, in addition to the red complex, *Prevotella melaninogenica* was noted in higher proportions than the other species. For the Brazilian subjects, the proportion of the red complex and *A. naeslundii* 1, *A. naeslundii* 2, *Prevotella intermedia* were also higher. For the Swedish and the Americans, the proportions of the bacterial species were similar except for the red complex.

Stephanopoulos PK, Kolokotronis AE, The clinical significance of anaerobic bacteria in acute orofacial odontogenic infections. Oral Surg Oral Med Oral Pathol Oral Radiol Endod 2004; 98:398-408.

Purpose: To summarize available information concerning the role of anaerobic bacteria in odontogenic infections in order to provide guidelines for effective treatment.

Materials and Methods: Literature review and Authors opinion.

Findings and Conclusions: A review of the literature on orofacial odontogenic infections indicates that the underlying microflora is typically polymicrobial, predominantly involving strictly anaerobic gram-positive cocci and gram-negative rods, along with facultative and microaerophilic streptococci. Although no single species has been consistently implicated in all of these infections, the pathogenic potential of some of these organisms has been documented by many studies. This potential can be explained by a number of virulence factors demonstrated in anaerobic bacteria, as well as by synergistic interrelationships with other members of the infectious flora.



Outline of clinically important anaerobic bacteria in orofacial odontogenic infections (arrow indicates recent reclassification of *Peptostreptococcus micros*).

<i>Factor</i>	<i>Action</i>
Superoxide dismutase	Aerotolerance
Capsular polysaccharide	Antiphagocytic, abscessogenic
Succinic acid	Antiphagocytic (leukotoxin)
Endotoxin	Cytotoxicity
Proteolytic enzymes	Tissue degradation, promotes bacterial invasion
Hydrogen sulphide	Cytotoxicity

Potential virulence factors of anaerobic bacteria isolated from orofacial odontogenic infections

Clinical and microbiologic correlations: Clinical studies in humans had underestimated the incidence of anaerobes in dentoalveolar abscesses for a long period, owing to a combination of inadequate sampling and transport together with

poor laboratory techniques, in recent years the use of novel molecular techniques has changed this perception. According to Finegold the organisms of greatest importance in mixed polymicrobial infections are those that are most virulent, those that are resistant to commonly employed antimicrobial agents, and those present in greatest numbers. Anaerobic bacteria appear to fulfill all these criteria in odontogenic infections.

Experimental evidence indicates that bacterial synergism between bacterial strains isolated from odontogenic infections may enhance the pathogenic potential of the infectious flora.

Emergence of antimicrobial resistance: Antibiotic resistance is an important consideration in the management of orofacial odontogenic infections. Although it is not considered a virulence factor per se, B-lactamase activity among gram-negative anaerobic rods may be responsible for clinical failures with penicillin treatment.

Antibiotic selection for orofacial odontogenic infections: Focus on anaerobes: Penicillin remains the recommended agent for the nonallergic patient with mild to moderate infection. However, in more severe cases where there is a narrow margin of acceptance of possible therapy failure it is recommended to resort to agents with adequate anaerobic spectrum such as clindamycin or combinations of an aminopenicillin with b-lactamase inhibitor; broader antimicrobial coverage is indicated for patients with impaired host defenses. Even with active antimicrobial therapy, the majority of orofacial odontogenic infections tend to be suppurative, requiring surgical drainage together with definitive treatment of the offending tooth.

Susceptibility of oral anaerobic pathogens to selected antimicrobial agents (compiled data)

<i>Agent</i>	<i>GPAC species</i>	<i>Prevotella species</i>	<i>Porphyromonas species</i>	<i>Fusobacterium nucleatum</i>	<i>Eubacterium species</i>
Penicillin G	+++	+/-	++	++	+++
Amoxicillin/ clavulanate	+++	+++	+++	+++	+++
Cefoxitin	+++	+++	+++	+++	++
Imipenem	+++	+++	+++	+++	+++
Clindamycin	+++	+++	+++	+++	++
Metronidazole	+++	+++	+++	+++	+/-
Azithromycin	++	++	+++	++	++
Moxifloxacin	+++	+++	+++	+++	+++

+++ = excellent activity; ++ = good activity, clinically useful; + = moderate activity, clinically unpredictable; - = poor activity.

Haffajee AD, Japlit M, Bogren A, Kent Jr RL, Goodson JM, Socransky SS. Differences in the subgingival microbiota of Swedish and USA subjects who were periodontally healthy or exhibited minimal periodontal disease. J Clin Periodontol 2005; 32: 33–39.

Purpose: To determine whether there were differences in the subgingival microbiotas of Swedish and American subjects who exhibited periodontal health or minimal periodontal disease.

Materials and Methods: For this study 158 periodontally healthy or minimally diseased subjects (79 from Sweden and 79 from USA) who were already enrolled in preventive studies were recruited. Included subjects were >20 years of age and had at least 24 natural teeth. Periodontally healthy subjects exhibited no pockets >4mm or attachment level measurements >3 mm. Minimally diseased subjects had no more than 2 sites with pocket depth >4mm or 2 sites with attachment level measurements >4 mm. Subjects were measured at baseline for plaque, gingivitis, BOP, suppuration, pocket depth and attachment level at 6 sites per tooth. Subgingival plaque samples were taken from the mesial aspect of each tooth at baseline (excluding third molars). Samples were individually analyzed, in one laboratory, for their content of 40 bacterial species using checkboard DNA–DNA hybridization. % DNA probe counts comprised by each species was determined for each site and averaged across sites in each subject. Significance of differences in proportions of each species between countries was determined using ancova adjusting for age, mean pocket depth, gender and smoking status.

Findings and Conclusions: On average, all species were detected in samples from subjects in both countries. The majority of the species did not differ significantly in adjusted mean proportions from country to country. After adjusting for multiple comparisons: 5 species were in significantly higher adjusted mean percentages in Swedish than American subjects *Actinomyces naeslundii* genospecies 1; *Streptococcus sanguis*; *Eikenella corrodens*; *Tannerella forsythensis* and *Prevotella melaninogenica*. *Leptotrichia buccalis* was in significantly higher adjusted mean percentages in American than Swedish subjects. Two species that differed significantly in mean counts between countries were examined further. The mean counts of *A. naeslundii* genospecies 1 and *L. buccalis* in Swedish and American subjects who were subset according to smoking status and mean full mouth pocket depth of >2.4mm. The data confirmed the notion that differences in mean pocket depth or smoking status for subjects in the 2 countries had less effect on the mean bacterial counts than the geographic location of the sampled subject. Cluster analysis grouped 121 subjects into 8 microbial profiles, while 37 subjects were not assigned to any cluster group. 24 of the 40 test species examined differed significantly among cluster groups. Five clusters were dominated by American subjects and 2 clusters by Swedish subjects. 73% of the Swedish subjects fell into 1 cluster group dominated by high proportions of *A. naeslundii* genospecies 1, *Prevotella nigrescens*, *T. forsythensis* and *P. melaninogenica*. Different clusters were characterized by high proportions of the following: *Actinomyces gerencseriae*, *Veillonella parvula*, *Prevotella intermedia*,

Eubacterium saburreum (Cluster 3), *Capnocytophaga gingivalis* & *L. buccalis* (Cluster 6) and *Neisseria mucosa* (Cluster 4). All cluster groups and the “not in cluster” group had mean proportions of red complex species that were <4% of the microbiota. Swedish and American subjects who exhibited periodontal health or minimal disease had different microbial profiles of subgingival plaque samples.