Subgingival microbial profiles in refractory periodontal disease


Abstract

**Background/aim:** The purpose of the present investigation was to examine subgingival microbial profiles associated with refractory periodontitis and to seek such profiles in periodontally healthy, periodontally well-maintained elder and untreated periodontitis subjects.

**Methods:** 36 subjects were defined as refractory on the basis of further attachment loss after scaling and root planing, surgery and systemically administered antibiotics. A total of 890 subgingival plaque samples (mean/subject = 24.7) were taken from the mesial aspect of each tooth in each subject at baseline and individually processed for their content of 40 subgingival taxa using checkerboard DNA-DNA hybridization. Cluster analysis was performed on mean within subject species counts using the chord coefficient and an average unweighted linkage sort. Significant differences among clusters for individual and complexes of species were sought using the Kruskal Wallis test. The microbial profiles of the refractory subjects were compared with those of 27 periodontally healthy subjects (n plaque samples = 708), 35 periodontally well-maintained elder subjects (n plaque samples = 801) and 115 untreated adult periodontitis subjects (n plaque samples = 2871).

**Results:** 28 of 36 refractory subjects fell into 4 clusters with >29% similarity. 10 of 40 species and 4 of 7 complexes differed significantly among clusters. Profile (Cluster) I (n = 4) was characterized by high proportions of “yellow” and “green” complex species, profile II (n = 3) by low total counts and high proportions of “orange” and “purple” complex species, profile III (n = 9) by high total counts and counts of *Actinomyces* and “purple” complex species, profile IV (n = 12) by high proportions of “red” and “orange” complex species. The mean profiles of each cluster were subjected to cluster analysis with microbial data from 4380 (mean 24.7) baseline subgingival plaque samples from 27 periodontally healthy, 35 treated, well-maintained elders and 115 untreated adult periodontitis subjects. 12 clusters were formed with >41% similarity. 3 of the refractory profiles were detected in 3 cluster groups. Profile II in a cluster of 1 healthy, 1 elder and 4 untreated periodontitis subjects; profile III in a cluster of 1 healthy, 2 elder and 12 periodontitis subjects; Profile IV, with 1 healthy and 5 untreated periodontitis subjects. The profile not detected in non refractory subjects was dominated by *Streptococcus* species. 9 clusters did not harbor refractory profiles. 11.1% of healthy, 8.6% of elder and 18.3% of periodontitis subjects were in clusters exhibiting refractory microbial profiles.

**Conclusions:** 4 subgingival microbial profiles were detected among refractory subjects. “Refractory microbial profiles” could be detected in subjects who had not yet exhibited refractory disease.
occasionally concern may be expressed about the proper performance of the treatment procedures. However, in many instances the same therapist has successfully treated clinically similar cases which respond well to therapy despite exhibiting plaque levels similar to or greater than those found in refractory subjects. Thus, grudgingly the profession has recognized the likelihood that some subjects are refractory because of differences in their microbiota, their ability to respond to and cope with periodontal infections or both (Colombo et al. 1998a, b, c, Winkel et al. 1997). Among the host factors suspected of contributing to refractory disease are differences in genetic background, environmental factors such as smoking, dietary factors, systemic disease or stress. Although all of these factors may be important, and some can be modified, the major, potentially “treatable” component of refractory disease is the etiologic microbiota.

The microbiota of the refractory subject, on average, is generally similar to that of the adult periodontitis subject (Colombo et al. 1998b), although some differences have been described. For example, Magnusson et al. (1991) and Colombo et al. (1998b) have described high levels of Streptococcus constellatus/intermedius in lesions of refractory subjects, while Gordon et al. (1985) described higher levels of motile organisms and black pigmented species. Winkel et al. (1997) described a form of “refractory” periodontal disease which was characterized by high proportions of Bacteroides forsythus. Van Winkelhoff et al. (1992) found Actinobacillus actinomycetemcomitans to be frequently detected in lesions of 40 subjects with refractory periodontitis. In a 1988 paper, Haffajee et al. described 4 specific microbial complexes associated with refractory disease in 13 subjects. Three subjects had a microbial profile dominated by B. forsythus, Campylobacter rectus and Fusobacterium nucleatum; 3 subjects by Peptostreptococcus micros, Porphyromonas gingivalis and S. intermedius; 5 subjects by F. nucleatum, P. gingivalis and S. intermedius and 2 subjects by F. nucleatum and S. intermedius. All profiles contained members of the red and/or orange complexes (Socransky et al. 1998), and 3 of 4 profiles were characterized by high proportions of S. intermedius.

Detection of seemingly unusual microbial profiles in various studies of refractory subjects leads to the question as to whether the unusual microbiotas were due to intervention of the periodontist or whether such profiles existed in individuals who had not yet received periodontal treatment. The purpose of the present investigation was to define microbial profiles associated with refractory periodontitis and to seek such profiles in periodontitis and periodontally healthy individuals.

Material and Methods
Subject population
The refractory subject population consisted of 36 subjects who had been treated by both scaling and root planing (SRP) and modified Widman flap surgery and adjunctive systemically administered tetracycline. All subjects showed either full mouth mean attachment loss or >3 sites with attachment loss >2.5 mm after each therapy. In addition, 177 other subjects were compared with the refractory group. These included 27 periodontally healthy, 35 well-maintained elders and 115 untreated adult periodontitis subjects. All subjects were >20 years of age and had at least 20 teeth. Periodontally healthy subjects had no probing pocket depths and no attachment level measurements >4 mm. However, subjects in this group could exhibit gingival inflammation. The periodontitis subjects had at least 4 sites with pocket depth >4 mm and/or 4 sites with attachment loss >4 mm. The well-maintained elders were >66 years of age. They had received regular periodontal maintenance care every 3 to 6 months for an average of 14.2 years after periodontal therapy consisting of root planing as well as both surgical and non-surgical modalities (Haffajee et al. 1998). The last group of subjects showed similar clinical characteristics to the healthy group except that they had greater mean attachment loss. Exclusion criteria for all groups included females who were pregnant or nursing, any systemic condition which might have influenced the course of periodontal disease (e.g., diabetes, AIDS), and any systemic condition which required antibiotic premedication coverage for routine periodontal procedures (e.g., heart/valve conditions, joint replacements). The mean clinical characteristics of the 4 groups are presented in Table 1.

Microbiological assessment
The microbiological sampling and the enumeration of bacterial species using checkerboard DNA-DNA hybridization have been described by Haffajee et al. (1998) and Colombo et al. (1998b). In brief, subgingival plaque samples were taken using individual, sterile Gracey curettes from the mesio-buccal aspect of each tooth, excluding 3rd molars, in each subject. The samples were individually analyzed for their content of 40 subgingival species (listed in Fig. 1) using whole genomic DNA probes, checkerboard hybridization and chemiluminescence detection. Signals were detected using Reflection NEF film (Dupont, Boston MA). 2 lanes in each run contained standards at concentrations of 10³ and 10⁶. The sensitivity of this assay was adjusted to permit detection of 10³ cells of a given species in each sample by adjusting the concentration of each DNA probe. This procedure was carried out in order to provide the same sensitivity of detection for each species. Failure to detect a sig-

| Table 1. Mean (± SD) baseline clinical characteristics of the subjects |
|---------------|----------------|----------------|----------------|---------------|
|               | Health         | Elders         | Periodontitis  | Refractory    |
| N             | 27             | 35             | 115            | 36            |
| age (years)***| 34.0±7.6       | 75.7±8.2       | 45.2±11.2      | 45.6±12.0     |
| number of missing teeth**| 1.4±1.8       | 4.9±4.0        | 2.8±2.6        | 2.9±3.1       |
| % males**     | 20             | 22             | 51             | 56            |
| mean pocket depth (mm)***| 2.4±0.2       | 2.6±0.6        | 3.2±0.6        | 3.6±0.8       |
| mean attachment level (mm)**| 1.7±0.5       | 3.1±0.8        | 2.9±1.1        | 3.4±1.1       |
| % of sites with: |
| plaque accumulation**| 48±27          | ND             | 72±29          | 63±33         |
| gingival redness*| 57±27          | ND             | 75±30          | 74±31         |
| bleeding on probing***| 14±19          | ND             | 45±33          | 63±39         |
| suppuration**| 0.0±0.0        | ND             | 1.4±3.4        | 3.4±8.9       |

Significant difference among groups: * p<0.05; ** p<0.01; p<0.001; Kruskall-Wallis test. ND= not determined.
Fig. 1. Stacked bar charts of the mean prevalence (% of sites colonized) and levels of the 40 subgingival species evaluated in 27 periodontally healthy, 35 well-maintained elder, 115 untreated periodontitis and 36 refractory periodontitis subjects. The species were ordered according to the microbial complexes described by Socransky et al. (1998). The % of sites colonized at different levels by each of the 40 species examined was computed for each subject and then averaged across subjects in the 4 groups. Significance of differences in mean counts and prevalence among groups was evaluated using the Kruskal-Wallis test. For counts: * $p<0.05$, ** $p<0.01$ and *** $p<0.001$; for prevalence, $p<0.05$, $p<0.01$, $p<0.001$ after adjusting for multiple comparisons (Socransky et al. 1991).

Data analysis

Microbiological data available were the counts of 40 subgingival species from the mesiobuccal aspect of each tooth in each subject. Thus, 890 samples were available from 36 refractory subjects, 708 samples from 27 periodontally healthy subjects, 801 samples from 35 well-maintained elders and 2,871 samples from 115 adult periodontitis subjects. The analyses compared microbial data expressed in 3 ways: counts $<10^5$ (levels), % DNA probe count (proportion) and % sites colonized (prevalence). In order to compare the counts of each of the bacterial species, the data were expressed as counts $\times 10^5$ at each site, averaged within a subject and then averaged across subjects in the clinical categories. The mean % DNA probe count and prevalence of each species were computed in a similar fashion in the 4 clinical categories. Significance of differences among groups for each species was sought using the Kruskal-Wallis test and adjusted for multiple comparisons (Socransky et al. 1991).

Cluster analysis was performed on the mean counts of the 40 subgingival species in the 36 refractory subjects. Similarities were computed using the chord coefficient (Ludwig & Reynolds 1988) and sorted using an average unweighted linkage sort (Sneath & Sokal 1973). The minimum cluster size accepted was 3. 4 clusters were formed with $>29\%$ similarity, while 8 subjects were considered to be outliers. Microbial profiles were constructed of the prevalence and levels of the 40 microbial taxa for subjects in the 4 refractory cluster groups. Significance of differences in bacterial species among groups was determined by averaging the counts or prevalence of each species within a subject and then across subjects in the cluster groups as described above. Pie graphs were also constructed describing the proportion that each microbial complex comprised of the total DNA probe count. The complexes described by Socransky et al. (1998) are indicated in Fig. 1.

The mean microbial profiles of counts in the 4 refractory cluster groups as well as the average microbial counts of 40 taxa for each of the 177 non-refractory subjects were run in a second cluster analysis, once more using the chord coefficient and an average unweighted linkage sort.
Refractory microbial profiles

Fig. 2. Pie charts of the mean proportion of microbial complexes in subjects in the 4 clinical groups. The % of the DNA probe count for each species was determined at each site in each subject. The proportions were then averaged within each subject and then across subjects in each clinical group. The % of the DNA probe count for each species in each complex (described by Socransky et al. (1998)) was summed and the proportion that each complex comprised was determined. The area of each pie was adjusted to reflect its size relative to the total count in the periodontally healthy group. The colors red, orange, green, yellow and purple represent the different microbial complexes; blue represents the Actinomyces species, and white represents species that do not fall into any cluster or new probes whose relationship to existing clusters has not been determined.

Fig. 4. Trellis diagram of a cluster analysis of mean microbial counts of 40 subgingival species in subgingival plaque samples from 36 refractory periodontitis subjects. The counts of 40 bacterial species were determined at each site and averaged for each species within a subject. The mean counts of the 40 taxa were employed in a cluster analysis using the chord coefficient (Ludwig & Reynolds 1988) and an average unweighted linkage sort (Sneath and Sokal, 1973). The boxes within the trellis diagram indicate the % similarity of each subject’s mean microbial profile to that of every other subject. The dark blue shading indicates similarities >46%, the light blue shading indicates similarities >29–46%, while the white shading indicates similarities <29%. 4 clusters were formed at ≥29% similarity. 8 subjects were considered to be outliers. The pie diagrams indicate the mean proportion of each microbial complex in the 4 cluster groups. The area of each pie was adjusted to reflect its size relative to the average total count for subjects in cluster I.

Results

The mean prevalence and levels of a number of taxa differed significantly among periodontally healthy, “well-maintained” elder, untreated adult periodontitis and refractory periodontitis subjects (Fig. 1). Most notable were the elevated prevalence and levels of red complex species and orange complex species in periodontitis and refractory subjects when compared with periodontally healthy or well-maintained elder subjects. The red complex species, B. forsythus, P. gingivalis and T. denticola, were significantly higher in counts ($p<0.001$) and proportions ($p<0.001$) even after adjusting for 40 comparisons. Fig. 2 summarizes the proportions of the microbial complexes in the 4 clinical groups. Periodontitis and refractory subjects exhibited significantly higher proportions of red and orange complex species and significantly lower proportions of purple complex and Actinomyces species compared with the healthy and well-maintained elder subjects. The areas of the pies were sized to reflect the average total count in each clinical group relative to the healthy subjects. The total counts were highest in the periodontitis subjects and lowest in the refractory subjects. Fig. 3 highlights the major difference in the subgingival microbiota among the clinical groups. The counts and proportions of red complex species were elevated in the periodontitis and refractory subjects while Actinomyces species were higher in levels and proportions in periodontally healthy and well-maintained elder individuals. The ratio of counts of Actinomyces to counts of red complex species ranged from 7.2 in healthy subjects to 1.3 in periodontitis, while proportions of these taxa ranged from 42.4 in healthy subjects to 0.89 in refractory periodontitis subjects. These data suggest that, on average, refractory and periodontitis subjects have similar microbiotas while the microbiotas in periodontal health and well maintained elders are on average quite similar.

However, there was a great deal of heterogeneity in the patterns of colonization in subjects with refractory disease. Cluster analysis of the microbial profiles revealed 4 distinct clusters and 8 outlier subjects (Fig. 4). The mean proportions of each of the microbial complexes differed significantly among the 4 cluster groups and the outliers. The mean proportions of red complex species were significantly elevated in cluster group IV and at very low levels.
in cluster group II. The proportions of orange complex species were highest in cluster groups II and IV. The proportions of yellow complex species were strikingly elevated in cluster group I, while green complex species were high in cluster group I and low in cluster group II. Purple complex species were elevated in proportion in cluster groups II and III, while Actinomyces species were markedly elevated in cluster group III. Thus, the microbial pattern of cluster group I featured very high proportions of “yellow” and “green” complex species. The microbial pattern associated with cluster group II consisted of very high proportions of “orange” and “purple” complex species in subjects who exhibited very low total bacterial counts. Cluster group III consisted of 9 subjects who had an overall microbial profile similar to that observed in many subjects with moderate periodontitis; i.e., moderate levels of “red” and “orange” complex species and higher levels of Actinomyces and “purple” complex species. Cluster group IV consisted of 12 subjects who exhibited very high proportions of “red” and “orange” complex species (a mean of 79.5% of the microbiota) and low proportions of Actinomyces species.

The differences among the 4 Clusters for the 40 species individually are shown in Fig. 5. Subjects in cluster group I had a high prevalence and levels of the Streptococcus species of the yellow complex. Cluster group II showed remarkably low prevalence and counts of the taxa tested. However, the orange complex species were relatively more commonly detected in this group compared to the other taxa evaluated. Cluster group III showed a much wider distribution and higher counts of most taxa examined than the other 3 clusters. Most noticeable in this cluster was the high prevalence and counts of A. naeslundii genospecies 2 and V. parvula compared with the other clusters. Cluster group IV was characterized by a wide distribution and higher counts of red and orange complex species. Of note, was the high prevalence and levels of B. forsythus. It is worth noting the high prevalence of S. constellatus and to a lesser extent S. intermedius in all cluster groups. The mean baseline clinical characteristics of the subjects in the 4 cluster groups and the outliers did not differ significantly. However, cluster group II subjects, who exhibited the lowest mean counts, also showed the lowest mean pocket depth and mean attachment level. The deepest mean pocket depths were found in subjects of cluster group IV and the outliers.

The average profile for each of the 4 clusters was computed and the 4 mean profiles were run in a second cluster analysis with the microbial profiles of 27 healthy, 35 well-maintained elder and 115 untreated periodontitis subjects (Fig. 6). 3 of the 4 mean refractory profiles clustered with clusters formed by subjects in the 3 other clinical categories (Fig. 6). Refractory profile II consisting of high proportions of orange complex species was observed in a cluster consisting of 1 healthy, 1 well maintained elder and 4 periodontitis subjects. Cluster analysis profile III was observed in a cluster consisting of 1 healthy, 2 well maintained elder and 12 adult periodontitis subjects, while refractory profile IV was observed in a cluster of 1 healthy and 5 periodontitis subjects. This last pattern exhibited very high levels of red and orange complex species. Table 2 summarizes the number of subjects and the % distribution of the refractory profiles in the 3 “non refractory” clinical groups. Refractory profile III was detected in 15 total subjects representing 8.5% of the non-refractory subjects examined. Profiles II and IV

Fig. 3. Bar charts of the mean total DNA probe counts ($\times 10^5$, ±SEM; left panel) and % of the DNA probe counts (right panel) of Actinomyces and red complex species in 27 periodontally healthy, 35 well-maintained elder, 115 periodontitis and 36 refractory periodontitis subjects. The bars indicate the means and the whiskers the SEM. The counts of Actinomyces species and red complex species were computed at each site, averaged within a subject and then across subjects for each clinical group separately. In a similar fashion, the % DNA probe counts for the Actinomyces and red complex species were determined at each site in each subject, averaged within each subject and then across subjects in each clinical group. The number over the bars represent the ratio of Actinomyces species to red complex species for each clinical group for both the counts and proportions.
Fig. 5. Stacked bar charts of the mean prevalence (% of sites colonized) and levels of the 40 subgingival species evaluated in the 4 cluster analysis groups. The format is as described in Fig. 1. The shaded area represents microbial complexes that were found in higher proportions in the individual cluster groups. Significance of differences in mean counts and prevalence among groups was evaluated using the Kruskal-Wallis test. For counts: *p < 0.05, **p < 0.01 and ***p < 0.001; for prevalence, * p < 0.05, ** p < 0.01, *** p < 0.001. Because of the small number of subjects in each group, the analyses were not adjusted for multiple comparisons.

were found in 6 subjects each (each comprised 3.4% of the non-refractory subjects). Refractory profile I, harboring high levels of Streptococcus species, was not detected in the non-refractory clusters.

Discussion

The subject with “refractory” periodontal disease has evoked considerable interest and controversy for some time. Some investigators feel that refractory periodontitis subjects have inadequate plaque control and/or have received inappropriate periodontal therapy. Others suggest that the refractory subject may differ from successfully treated periodontitis subjects in terms of the nature of their subgingival microbiota and/or the ability of the host to cope with periodontal infection. The present investigation demonstrated that, on average, the composition of the subgingival microbiota in refractory subjects was similar to that found in untreated periodontitis subjects prior to therapy, but different from that found in subjects who were periodontally healthy or periodontally well-maintained elders. Differences in the composition of the subgingival microbiota among periodontally healthy, well-maintained elder and periodontitis subjects have been described previously (Haffajee et al. 1998). These consisted primarily of a higher prevalence and levels of red complex species in subjects with periodontitis than in healthy or well-maintained elder subjects. The present investigation extends these findings by demonstrating that the microbiota of refractory subjects, on average, is similar to that found in subjects with periodontitis who had not yet received therapy. In addition, refractory subjects exhibited a lower prevalence of Actinomyces species.

The mean values for the 4 clinical groups failed to show the heterogeneity that exists in the subgingival microbiota in subjects within each clinical group. This heterogeneity was examined in more detail in the subjects with refractory periodontitis. Cluster analysis demonstrated 4 cluster groups with distinct microbial profiles in the refractory subjects. In addition, 8 outlier subjects were detected with distinctly different profiles from the cluster groups and from one another (Fig. 4). The most common pattern detected was that observed in 12 subjects (cluster IV) who exhibited very high counts and proportions of red and orange complex species and very low proportions of Actinomyces species and Veillonella parvula. Particularly noteworthy in this group was the high prevalence and counts of B. forsythus (Fig. 5).
which was in accord with the microbial data from 27 “refractory” patients described by Winkel et al. (1997). This profile is likely to be particularly threatening to the subjects in that species thought to be pathogens or likely to be pathogens comprise about 80% of the microbiota examined. Also of concern in this group was the low proportions of species thought to be host compatible such as Actinomyces species and V. parvula. A 2nd refractory cluster (cluster II) was comprised of high proportions of orange complex species and low proportions of most other taxa examined. Individuals with this pattern also demonstrated very low total counts of bacteria in their subgingival plaque samples. A 3rd refractory cluster (cluster III) demonstrated microbial complexes that were similar in levels and proportions to that of a relatively common profile (cluster) observed in untreated periodontitis patients as well as periodontally healthy and well-maintained elders (Figs 5, 6). This profile was marked by quite high proportions of Actinomyces sp. and V. parvula and moderate levels of red and orange complex species. Subjects in this group may have had more virulent strains of the periodontal pathogens, pathogenic species not examined in the test battery, or may have been compromised in terms of host response. The 4th refractory cluster analysis profile (cluster I) was dominated by members of the yellow complex comprised of Streptococcus species. This profile was not detected in any subject when cluster analysis was performed examining microbial profiles in periodontally healthy, well-maintained elder and periodontitis subjects (Fig. 6).

The microbial profiles observed in this investigation had many features in common with earlier descriptions of diverse refractory microbial profiles (Haffajee et al. 1988). Both investigations emphasized the importance of red and orange complex species including B. forsythus, P. gingivalis, Fusobacterium, Campylobacter, Prevotella and Peptostreptococcus species. S. intermedius was found to be elevated in proportion in 3 of 4 refractory microbial profiles described by Haffajee et al. (1988). This species and other Streptococcus species were elevated in cluster I in the present investigation and S. constellatus/intermedius was of major importance in distinguishing refractory from periodontitis subjects in the study of Colomb et al. (1998b).

The unusual profiles observed in the refractory subjects led to the question of whether some or all of these profiles might have resulted from prior, perhaps very aggressive, periodontal therapy. For this reason, 4 mythical persons, with the average microbial profiles observed in the 4 refractory cluster groups, were constructed and run in a cluster analysis with the microbial profiles detected in healthy, well-maintained elder and periodontitis subjects. Three of 4 refractory profiles were found to cluster with subjects who were not considered to have refractory disease. This suggests that these 3 profiles were probably not caused by dental intervention, but may represent profiles that might be difficult to control by periodontal treatment. One suspects, without any supportive evidence at this time, that subjects in these 3 groups are more at risk for poor treatment re-
response than subjects who exhibited other microbial profiles. It is worth noting that the largest cluster observed in Fig. 6 consisted of 40 periodontally healthy, well-maintained elderly and untreated periodontitis subjects. The subjects in this group did not exhibit microbial profiles in common with subjects in the refractory group. This suggests that a relatively common subgingival microbial profile may respond well to conventional forms of periodontal therapy.

The fourth microbial profile (cluster I) which had a disproportionately high level of Streptococcus species may have resulted from repeated periodontal therapy since this profile was not observed in the non refractory subject groups. The possibility that periodontal therapy may have contributed to this unusual profile is supported by the work of Feres et al. (2001) who demonstrated that systemically administered amoxicillin increased the proportion of yellow complex species and decreased the proportion of Actinomyces species in subjects receiving this agent for the treatment of adult periodontitis. In that study, the proportions of streptococci decreased once the course of amoxicillin had been completed, although the Actinomyces species were still found at lower proportions at one year post therapy. Conceivably, repeated use of amoxicillin or other chemotherapeutic agents might distort the subgingival microbiota to one dominated by Streptococcus species including those that could be pathogenic for that species in subjects receiving this species in subjects receiving this agent for the treatment of adult periodontitis.

Refractory microbial profiles

Proportionen des “organen” und “purpur- nen” Komplexes, Profil III (n=9) durch hohe Gesamtkomplexenzahl und Anzahl von Acti- nomycies sowie “purpurinen” Spezies und Profil IV (n=12) durch hohe Anteile von Spe- zies des “roten” und “grünen” Komplexes charakterisiert. Die Mittelwertprofile eines jeden Clusters wurden einer Clusteranalyse mit mikrobiologischen Daten von 4380 (Mittelwert 24.7) subgingivalen Plaqueproben von 27 parodontal gesunden, 35 parodontal erfolgreich betreuten älteren und unbehandelten parodontal erkrankten Personen unterzogen. Es wurden 12 Cluster mit einer Übereinstimmung von >41% generiert. 3 der refraktären Profile wurden in 3 der Clustergruppen gefunden: Profil II in einem Cluster aus 1 gesunden, 1 älteren und 4 unbekan- delteten parodontal erkrankten Personen; Profil III in einem Cluster aus 1 gesunden, 2 älteren und 12 unbehandelten Personen; Profil IV in einem Cluster aus 1 gesunden und 5 unbehandelten Personen. Das Profil, das nicht in nichtrefraktären Clu- stern gefunden wurde, war von Streptoco- coccus-Spezies dominiert. 9 Cluster wiesen keine refraktären Profile auf. 11.1% der gesunden, 8.6% der älteren und 18.3% der unbehandel- ten Personen wurden Clustern zugeordnet, die refraktäre Profile aufwiesen. Schlussfolgerungen: 4 subgingivale mikrobiolo- gische Profile konnten bei Patienten mit therapierefraktären Parodontitis identifiziert werden. Solche refraktären Profile konnten auch bei Patienten gefunden werden, die bisher keine refraktäre Erkrankung entwickelt hatten.

Résumé

Profils microbiens sous-gingivaux lors de la maladie parodontale réfractaire

Origin, but: Le propos de cette recherche était d’examiner les profils microbiens sous- gingivaux associés avec la parodontite réfra- tactaire et de rechercher de tels profils chez des sujets au parodonte sain, des sujets âgés bien maintenus et des sujets atteints de parodontite non traité.

Méthodes: 36 sujets furent diagnostiqués comme étant réfractaires sur la base de pertes d’attache persistantes après détartrage et sur- façage radiculaire, chirurgie et antibiothérapie par voie générale. Un total de 890 échantillons de plaque sous-gingivale (moyenne par sujet=24.7) furent prélèvés sur la face mésiale de chaque dent chez chaque sujet initialement et examinés individuellement pour la présence de 40 taxons sous-gingivaux par hybridation ADN-ADN en damier. Une analyse d’échan- tillon fut réalisée pour la moyenne des comp- tages d’espèces des sujets par le coefficient de chord et par tri de lien moyen non pondéré. Des différences significatives parmi les grou- pes pour les individus et les complexes d’espè- ces furent recherchées par le test de Kruskal Wallis. Les profils microbiens des sujets réfrac- taires furent comparés avec ceux de 27 sujets au parodonte sain (n échantillons de plaque= 708), à 35 sujets âgés bien maintenus (n’échan- tillons de plaque=801) et 115 adultes ayant
une parodontite non traitée (n échantillons de plaque=2871)

Résultats: 28 des 36 sujets réfractaires se trouvaient dans 4 groupes avec plus de 29% de similarité. 10 des 40 espèces et 4 des 7 complexes différaient significativement entre les groupes. Le profil (groupe) 1 (n=4) était caractérisé par une forte proportion d’espèces des complexes jaune et vert, le profil (groupe) 2 (n=3) par un comptage total bas et de fortes proportions d’espèces des complexes orange et violet, le profil 3 (n=9) par de forts comptages totaux, d’actinomyces et d’espèces du complexe violet, le profil 4 (n=12) par de fortes proportions des espèces des complexes rouge et orange. Les profils moyens de chaque groupe furent soumis à une analyse de groupe avec les données microbiennes de plaque sous ginvale de 27 sujets sains, 35 sujets traités, des sujets âgés bien maintenus et 115 sujets adultes présentant une parodontite non traitée. 12 groupes furent formés avec 41% de similarité. 3 des profils réfractaires furent détectés dans 3 groupes. Le profil 2 dans un groupe de 1 patient sain, 1 sujet âgé et 4 sujets non traités. Le profil 3 dans un groupe de 1 sujet sain, 2 âgés et 12 patients présentant une parodontite. Le profil 4 avec 1 sujet sain et 5 patients non traités. Le profil non détecté chez les sujets non réfractaires était dominé par les espèces streptococcus. 9 groupes ne présentaient pas le profil réfractaire. 11% des sujets sains, 8.6% des sujets âgés et 18.3% des sujets atteints de parodontite étaient dans des groupes présentant des profils microbiens réfractaires.

Conclusions: Les profils microbiens sous-gingivaux ont été détectés entre les sujets réfractaires. “Les profils microbiens réfractaires” pouvaient être détectés dans les sujets qui n’avaient pas encore montré réfractaire la maladie.

References

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