

2009 PCR Detection of *Helicobacter pylori* in Saliva. K.J. KIM¹, S.H. SHIN¹, M.H. LEE², C.H. YANG, Y.H. MOON³, J.D. CHA (Wonkwang Univ., Iksan, Republic of Korea)

Many authors hypothesized that *Helicobacter pylori*, a causative agent of gastric disease, might act as a potential antigen in salivary glands. *Helicobacter pylori* has been suggested to be transmitted via oral cavity. To investigate the transmission of *Helicobacter pylori* in oral cavity, samples were taken from the saliva of patients with gastric disease. DNA was isolated from the samples, amplification was performed by the polymerase chain reaction (PCR) with a probe of standard *Helicobacter pylori* gastric isolate, and the amplified DNA fragments were sequenced by automated DNA sequencer. DNA from 7 among 24 patients (34.2%) was amplified by PCR. The sequenced nucleotides showed the homology with *Helicobacter pylori* 26895 urease (98%), and the deduced amino acid sequence were consistent with the urease alpha subunit of *Helicobacter pylori* J99. Hence, we conclude that there might be a transmission of *Helicobacter pylori* via saliva.

2010 Detection of *Lactobacilli* and *S. mutans* in patients after radioactive iodine therapy. A.K. LUEDERS¹, B. BARTSCH¹, C. DOTZENRATH², J. FELDKAMP², H. JENTSCH¹, W.H.-M. RAAB³ (Operative Dentistry, Surgery, Endocrinology, Heinrich-Heine University Duesseldorf, Operative Dentistry, University of Rostock, Germany)

Radioactive iodine treatment is common therapy in patients with thyroid cancer. In the literature, the reduction of the saliva secretion has been described as a possible side effect. The aim of our study was to determine a reduction of the saliva flow rate and to investigate the amount of *S. mutans* and *Lactobacilli* in the saliva as an indicator for necessary preventive intervention. Saliva from 14 patients who had undergone radioactive iodine treatment was sampled. Unstimulated saliva probes were taken using cotton roles (Sarstedt). The saliva was stimulated by chewing on paraffin blocs for 10 min. Microbial samples were taken after stimulation. The flow rate of the stimulated and unstimulated saliva was determined. 100 µl aliquots of the stimulated saliva samples were taken to detect the quantity of *Lactobacilli* and *S. mutans*. Each bacterium was grown on specified selective media. Data was compared to previously defined values. 35.7 % of the investigated patients showed a reduction of the unstimulated saliva flow rate (mean = 0.07 ml/min, s = 0.02). In 57.14 % of all cases, the flow rate of the stimulated saliva was reduced (mean = 0.46 ml/min, s = 0.19). The amount of bacteria in CFU/100 µl, as compared to the number of patients where those microorganisms could be detected, are demonstrated as a range:

<i>Lactobacilli</i>	12 patients	3 - 1.89 x10 ⁷ (range CFU patients +)
<i>S. mutans</i>	14 patients	9.5x10 ³ - 2.67x10 ⁷ (range CFU patients +)

These findings suggest, that patients after radioactive iodine therapy often develop a reduction of the saliva flow rate. Although *Lactobacilli* and *S. mutans* counts vary strongly in this selected group of patients, these parameters were insufficient in determining the necessity of a special preventive treatment in general.

2011 Effect of Sampling Time on Composition of Supragingival Microflora. C. WALKER, S. NANGÖ*, J. LENNON, C. YU, I. MAGNUSSON, G. ANTONSON, & E. WESTFELT (Periodontal Disease Research Clinics, Univ. of Florida, Gainesville).

It has been postulated that the time of day that supragingival plaque is harvested may influence both the quantity and the composition of the sample. Since this has an obvious impact on the scheduling and conduct of large panel studies with a microbiologic component, we were interested in determining if differences existed in plaque samples collected in the morning or in the afternoon. Plaque samples were harvested from the buccal and lingual surfaces of 4 teeth in each of 136 subjects who had abstained from all oral hygiene procedures for 12-24 h and had refrained from eating, drinking, or smoking for 4 h prior to collection. Entry required a mean MGI of at least 1.8 and plaque index of at least 2.0. Each sample was examined microscopically for 5 distinct morphological forms and enumerated on selective and non-selective media for total anaerobic and facultative counts, actinomyces and streptococci, putative periodontal pathogens, and opportunistic pathogens. A retrospective examination revealed that 85 samples were collected between 8 AM-12 noon and 51 were collected between 1 PM-4 PM. The unpaired t-test was used to determine if differences were present in the microscopic data and the Mann Whitney, a nonparametric version of the unpaired t-test, was used to examine for differences in the culture data. Essentially no differences that could be attributed to the time of collection were found either in the microscopic or in the culture data. The only statistically significant difference was that a higher number of *Bacteroides forsythus* counts (p=0.027) were recovered from the afternoon samples. This difference was contributed to the small number of samples containing *B. forsythus* rather than to collection time. Total anaerobic counts were essential the same (p=0.986) regardless of time sampled. The means for total facultative, actinomyces, and streptococci counts were all slightly higher in the afternoon; however, none of the values approached significance (p=0.519, 0.184, and 0.579, respectively). Overall, there was no tendency toward higher counts for samples collected either in the morning or in the afternoon. The time of day that plaque is harvested has no apparent effect on the microbial analyses of its composition. Supported by the Optiva Corporation

2012 Comparison of cariogenic microflora in plaque of minority subjects. S.H. KHAN*, H.A.B. LINKE, E.O. KUYINU, O.O. OLAWOYE, M.M. IMAM, A.O. IHIONKHAN R.Z. LEGEROS (New York University College of Dentistry, NY, NY)

Microbiological factors in dental plaque, previously implicated in dental caries formation, were studied using samples from four caries positive (DMFS > 10) adult ethnic groups: Hispanic (n=55), Asian (n=53), Black (n=69) and Caucasian (n=42). Pooled plaque (approx. 50 mg) was collected in 1ml RTF transport medium from each subject for the enumeration of total cultivable microorganisms (T; Blood agar), streptococci (S; Mitis Salivarius agar), mutans streptococci (MS; MSB and MSFA agar) and lactobacilli (L; Rogosa SL agar). All data are expressed in cfu/plaque sample. The mean values obtained for each group were as follows, (1) T: Black, 10.4 x10⁶; Hispanic, 9.8 x10⁶; Asian, 7.3 x10⁶; and Caucasian, 5.3 x10⁶. (2) S: Black, 1.9 x10⁶; Hispanic, 1.4 x10⁶; Asian, 2.3 x10⁶; and Caucasian, 1.5 x10⁶. (3) MS: Black, 11.6 x10⁶; Hispanic, 1.6 x10⁶; Asian, 4.1 x10⁶; and Caucasian, 4.2 x10⁶. (4) L: Black, 5.7 x10⁴; Hispanic, 28.4 x10⁴; Asian, 1.7 x10⁴; and Caucasian, 3.6 x10⁴. No statistical significant differences were found in regards to the type of bacteria and the four ethnic groups. Moreover, in 58/219 subjects, yeast were detected in their plaque samples (22/53 Asians, 13/55 Hispanic, 12/42 Caucasian, 11/69 Black). Conclusion: microbial composition in dental plaque was not associated with ethnicity. Sponsored by grant no. DE-10593 (Research Center for Minority Oral Health, NYUCD/Forsyth) from NIDCR/NIH.

2013 Study of Oral Microbial Flora on Diabetes Mellitus Patients. T. MUTOH*, E. HONDA, K. MATSUMOTO, M. MORITO, M. KANAZAWA, N. MAEDA (Tsurumi University School of Dental Medicine, Tokyo Medical University)

It has well been known that diabetes mellitus (DM) patients are compromised hosts. In fact the incidence of oral infections increases when comparing DM patients to healthy subjects. The purpose of this study is to investigate the oral microbial flora of DM patients. The DM patients were divided into following 2 groups, DM I group (n=31, mean age 46.3 ± 10.3 years old) whose fasting blood sugar (FBS) level > 200 mg/dl, and DM II group (n=22 mean age 42.6 ± 10.0 years) whose FBS ≤ 200 mg/dl. We investigated salivary flow rate and buffering capacity, the levels of lysozyme and secretory IgA (sIgA) in saliva, and counted the numbers of staphylococci and *Candida* on the tongue, and the number of lactobacilli and mutans streptococci in saliva. The level of lysozyme and the numbers of lactobacilli in saliva and *Candida* on tongue were significantly higher in DM II group than in DM I group (respectively p < 0.01, p < 0.01 and p < 0.05). Comparing with DM I group, DM II group showed higher levels of sIgA and mutans streptococci in saliva, and lower levels of salivary flow rate and buffering capacity. These result suggested hyperglycemia upper than 200 mg/dl increased the number of oral microorganisms such as lactobacilli, mutans streptococci and *Candida*, and decreased the salivary flow rate and buffering capacity.

2014 Oral Flora in Renal Transplant Recipients Taking Immunosuppressive Drugs. K. TAKANO*, K. TSUKADA, U. YASUNARI, M. OKAMOTO and N. MAEDA (Tsurumi University, School of Dental Medicine, Yokohama, Japan)

The renal transplant recipients have to take the immunosuppressive agents, such as cyclosporin or tacrolimus (FK 506), in order to reduce the graft versus host reaction for a long time. The aim of this study is to investigate the effects of the immunosuppressive agents on the oral flora in the renal transplant recipients. A total 31 patients (RTR group) who had transplanted the kidney were examined the floras in the saliva, the tongue and gingival sulcus. An age matched 32 healthy subjects (control group) were compared as a control. We tested the salivary buffering capacity, the levels of lysozyme and sIgA, the number of *Streptococcus mutans* group and lactobacilli in saliva, and the number of *Candida* and staphylococci on the tongue, and the prevalence and number of the black-pigmented anaerobic rods (BPRs) in gingival sulcus. The results were as follows. The level of sIgA of the RTR group was significantly higher than that of the control group (P < 0.05). The salivary buffering capacity of the RTR group was weaker than the control group (P < 0.01). However, no significant differences of the levels of lysozyme; the number of *Streptococcus mutans* group and lactobacilli in saliva, and the number of *Candida* and staphylococci on the tongue, and the prevalence and number of the BPRs in gingival sulcus between the RTR and control groups were observed. It is suggested that the immunosuppressive drugs less influenced on the change of oral flora in renal transplant recipients.

2015 The Microflora of Root Surface Caries in Southern Chinese. S. SHEN*, L.P. SAMARANAYAKE, H.K. YIP, J.E. DYSON (Faculty of Dentistry, The University of Hong Kong, Hong Kong SAR, China)

Root surface caries is emerging as a significant problem in the middle aged and elderly. As little data is available on the microbiology of root surface caries in Chinese cohorts, we evaluated, both qualitatively and quantitatively, 28 such lesions in elderly, institutionalized, ethnic Chinese residing in Hong Kong. Samples of carious dentine were aseptically taken (J Dent Res 1993;73:623-629) from root caries lesions of 18 subjects (mean age 79.67 ± 8.57, 5 males and 13 females). The cultivable flora, both aerobic and anaerobic, were isolated and identified using standard methods and API 20 Strip (bioMérieux s.a. Marcy-l'Etoile, France) and RapID ANA II (Innovative Diagnostic Systems, L.P., Norcross, GA, USA) identification kits (Oral Microbiol Immunol 1998;13:1-10). The main findings were: i) of the total isolates, 91.30% were Gram positive and 8.70% were Gram negative bacteria; ii) the proportions of cocci and rods were 36.03% and 63.96%, respectively; iii) the predominant groups of organisms isolated were *Streptococcus* spp., *Lactobacillus* spp., *Staphylococcus* spp. and *Actinomyces* spp. with isolation frequencies of 100%, 89.29%, 71.43% and 67.86%, respectively; iv) the isolation frequency of yeasts belonging to *Candida* spp. (60.71%) was notably high although the proportion of yeasts within each sample was low (0.01%). This study provides baseline information on the microbiological features of root surface caries in the Southern Chinese living in Hong Kong. The data on the most predominant bacteria isolated concur with those reported from other regions of the world. This study was supported by CRCG grant (a/c 10201963), the University of Hong Kong.

2016 Taxonomic Characterization of Novel Asaccharolytic Gram-positive Rods from Human Oral Cavities.

F. NAKAZAWA*, S. E. POOCO, JR., M. SATO, T. IKEDA, and E. HOSHINO. (Oral Microbiol., Niigata Univ., Japan). Several strains of culture-difficult Gram-positive, obligately anaerobic rods were isolated from human necrotic pulp and tongue plaque. When phenotypic characteristics of the novel five strains were examined according to the VPI manual, they most resembled *Eubacterium timidum* among the established species, i.e. they were non-motile, non-spore-forming, short rods, and inert in most biochemical tests and produced phenylacetate as a sole metabolic end-product in peptone-yeast-extract broth. However, SDS-PAGE protein profile and GC content (41-42 mol%) revealed that they were distinct from other oral *Eubacterium* species. Comparative 16S rDNA sequence analysis demonstrated that the unknown isolates were closely related to the *Mogibacterium* species but these novel strains were phylogenetically distinct from the previously described species of asaccharolytic Gram-positive rod. Based on both phenotypic and phylogenetic evidences, it is proposed that the unknown bacterial strains represent new species in genus *Mogibacterium*. (Grants: 09470390, 10922050 and JSPS P99174)