Hong-Lin Chan et al., Insights in Analytical Electrochemistry, 3:2
DOI: 10.21767/2470-9867-C1-003

MALDI biotyper system for oral microbial identification and diagnosis

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The microbiota has increasingly gained attention because of its relationship linked to the development of human diseases. Periodontal disease is one of the disorders induced by microorganisms, which cause bad breath, swollen and bleeding gums, plaque and even tooth loss. Here, we established an anaerobic MALDI Biotyper system for *in vitro* diagnosis of oral microbiota to monitor the distribution of bacteria in oral cavity of human. The Bruker database used in this study contains 5,989 species of bacteria were applied to MALDI-TOF to detect oral microbiota. We collected 45 specimens of saliva and subgingival area from healthy controls and periodontitis patients. We grouped the subjects to healthy, the age under 60 with periodontal disease, and the age above 60 with periodontal disease. In addition, P-113, an antimicrobial peptide which has been reported with the ability for reducing the periodontal disease was used to evaluate the microbiota in the saliva of healthy group. We have identified 126 species by using MALDI biotyper. Based on Socransky's classification, we found that the amount of red complex (*Porphyromonas gingivalis, Tannerella forsythia and Treponema denticola*) were higher in gingival specimens of the patients of periodontal disease than healthy controls. The isolates from periodontal disease and age above 60 patients have 16% abundance of red complex; On the other hand, only 2% of red complex were found in the patients with age under 60. Moreover, only three periodontal bacteria—*Aggregatibacter actinomycetemcomitans* (Aa), *Fusobacterium nucleatum* (Fn), *P. gingivalis* (Pg)—were present in the subgingival specimens of periodotal disease. We also found Fn and Pg in the group of age above 60 increased by 8 and 6 folds as compared to the group of age under 60. For *Streptococcus gordonii* and *S. intermedius* were higher in both saliva and subgingvial area of patients than healthy controls; *Actinomyces meyeri* and *S. constellatus*, however, are only detected in the patient group, and *Actinomyces odontolyticus*, *S. parasanguinis*, and *S. salivarius* have two-folds abundance in healthy group than the patient group. Our results further showed that S. mitis, *S. pneumonia*, Veillonella parvula are significantly decreased followed by using P-113 mouthwash. Interestingly, the number of *S. salivarius*, a dominant species in oral bacteria and has excellent potential for use as a probiotic targeting the oral cavity, was increased two-folds after P-113 treatment. Our results demonstrated that anaerobic MALDI-TOF Biotyper system could be a useful diagnostic tool for analyzing oral microbiota. We found that oral microbiota is periodontal disease- and age-dependent. We also provided a practical hygiene by using antimicrobial peptide P113. The results provide a way for clinical diagnosis and the basis for personal medicine of therapy in the future.

Biography

Hong-Lin Chan is head of the National Tsing-Hua University (Taiwan) for Quantitative Proteomics Group and has 10 years of experience in proteomic method development and application. Dr. Chan received his PhD degree from University College, University of London in 2005. After 2 year post-doctoral training in the wolfson institute for Biomedical Sciences, he took the current professorship from National Tsing-Hua University in Taiwan. Dr. Chan's group has expertise in the preparation, separation and quantification of proteins and post-translational modifications using mass spectrometry and other methods. Dr Chan was one of the first users of 2D-DIGE technology which is routinely used for protein expression profiling and the group has also established platforms which perform quantitative phosphoproteomics and redox-proteomics analysis. Dr. Chan's group is focused on: Serum biomarker discovery, characterising redox and UV stress responses in cell models, mechanisms of cellular signalling, proteomics based studies on breast cancer, prostate cancer and drug resistance formation. Methods include cell biology facilities, 2D-DIGE/MS and quantitative 2D-LC-MS/MS expression profiling.

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