The University of Hong Kong The HKU Scholars Hub



Title	16S rDNA sequence analysis of periodontitis microbiota: a pilot study
Author(s)	Leung, WK; Ng, CHC; Wong, APK
Citation	The 82nd General Session and Exhibition of the International Association for Dental Research, Honolulu, HI., 10-13 March 2004. In Journal of Dental Research, 2004, v. 83 Sp Iss A, abstract no. 3657
Issued Date	2004
URL	http://hdl.handle.net/10722/53636
Rights	Creative Commons: Attribution 3.0 Hong Kong License

3657 16S rDNA sequence analysis of periodontitis microbiota: A Pilot Study

<u>W.K. LEUNG</u>, C.H.C. NG, and A.P.K. WONG, University of Hong Kong, Faculty of Dentistry, Hong Kong

Aim: To study the microbial diversity of periodontal subgingival microbiota by cloning and partial sequencing of 16S rDNA gene. Method: Bacterial DNA from a subgingival plague sample of an untreated periodontitis patient was extracted and amplified using universal 16S rDNA primers: forward - D88, reverse - E94. Correct size amplicons were isolated and cloned using pCR 2.1 vector into an E. coli host (TA cloning kit). 50 transformants were picked randomly and the plasmids carrying the amplified 16S rDNA were extracted and were sequenced using an ABI 310 sequencer. Identity of cloned 16S rDNA sequences were matched against a public access data base (NCBI). 16S rDNA clone identification was established when i) ≥ 400bp (range: 403 -1470bp) were sequenced, and ii) ≥ 98% sequence match could be identified. Results: A total of 22 species were detected including: Filifactor alocis (26%), unidentified oral bacterium AP60-5 (26%), Streptococcus sanguinis (6%), Fusobacterium nucleatum subsp. nucleatum (4%), Fusobacterium sp. oral clone CZ006 (4%), Abiotrophia para-adiacens (2%), Bacteriodes sp. oral clone FX069 (2%), Bacteriodes-like sp. oral clone X083 (2%), Capnocytophaga sp. oral clone CZ006 (2%), uncultured Eubacterium sp. (2%), unidentified Fusobacterium sp. (2%), Haemophilus paraphrophilus (2%), Lautropia sp. oral clone APO09 (2%), Selenomonas sp. oral clone EW09 (2%), unidentified Streptococcus sp. (2%), Streptococcus constellatus (2%), Streptococcus oligofermentans (2%), two independent unidentified Veillonella sp. (2% each), and three independent uncultured bacteria (2% each). Conclusion: When studied using culture independent method, a fair proportion of periodontitis subgingival microbiota remain poorly characterized indicating more research efforts should be directed to the study of periodontitis associated subgingival biofilm. Supported by RGC Hong Kong.

Seg #372 - Clinical Microbiology Poster

10:15 AM-11:30 AM, Saturday, 13 March 2004 Hawaii Convention Center Exhibit Hall 1-2

Back to the Microbiology / Immunology and Infection Control Program
Back to the IADR/AADR/CADR 82nd General Session (March 10-13, 2004)