## 東北大学大学院歯学研究科 インターフェイスロ腔健康科学 第66回学術フォーラム

Forum for Interface Oral Health Science

## The Oral Microbiome in Health and Disease

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## 平成25年4月3日 (水) 17:00~18:00 歯学部B1講義室

The human oral cavity harbours a complex commensal microbiota including fungi, protozoa, viruses, Archaea and Bacteria. The Bacteria are numerically dominant and around 1200 bacterial species belonging to 15 phyla are listed in the Human Oral Microbiome database (www.homd.org). The oral microbiome is generally stable in adults and little geographical variation has been found. Culture-independent methods targeting 16S rRNA have revealed numerous novel lineages of oral bacteria, many of which are predicted to be obligate anaerobes. Around half of oral bacteria cannot be cultured and this has been a major obstacle to understanding their role in health and disease. It has been hypothesised that one reason for unculturability is that members of certain taxa are adapted to growing in mixed-species biofilms and have thus become dependent on the presence of other taxa for growth. Members of the previously uncultivated Synergistetes Cluster A have been successfully grown in co-culture in vitro and following extended incubation and passaging, have been domesticated so that they can grown on agar media with a single co-culture partner. The recently described Fretibacterium fastidiosum strain SGP1 was grown in this way which has enabled its genome sequence to be obtained. A systematic approach to the culture of the remaining as yet uncultivated oral anaerobic lineages is required. The introduction of next generation high throughput sequencing methods such as pyrosequencing has facilitated the characterisation and comparison of the oral microbiota in health and disease. These methods have been used in studies to determine the changes in microbiota in experimental gingivitis and periodontitis and have identified new potential pathogens associated with these conditions.

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