Microbiome in oral and maxillofacial surgery

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Since Koch has reported the microorganisms are causes of infections, oral bacteria have been considered to be responsible for oral diseases such as periodontitis and dental caries. The oral cavity is the beginning of the digestive system and consists of various structures that are different from other digestive systems. Teeth are in oral cavity and there are periodontal ligaments and alveolar bone around teeth, covered by mucosa and masticatory mucosa which are keratinized epithelium. Tongue is specialized mucosa in oral cavity. Even the plaque, also known as the bacterial colony, has a very different environment depending on the supragingival and subgingival regions. Because of these various characteristics, microbiome in the oral cavity can be seen in various ways.

Microorganisms living in the human body are called microbiota. The resident microorganism is known to be more abundant than the human body. Microbiome is the genome of this microbial organism. Microbiomes have been discussed in many recent studies due to the development of genomic and gene expression analysis. Terminal restriction fragment length polymorphism (T-RFLP) method uses restriction enzymes to digest the amplicons from the 16S rRNA gene which are introduced into the oral microbiome[1].

Oral bacteria are known to have more than 700 bacterial species. Chen et al.[2] reported the results of the experiment which isolated and organized bacteria in the digestive organ including oral bacteria, using 16S rRNA gene-based methods. The goal of creating the expanded Human Oral Microbiome Database (eHOMD) is to provide the scientific community.

Currently, eHOMD includes a total of 772 microbial species and links sequence data with phenotypic, phylogenetic, clinical and bibliographic information.

All of the bacteria in the oral cavity are not related to diseases, but the site-specific bacteria are thought to be useful for identification and treatment of diseases. There are many studies for oral microbiome. A comparative study of Japanese and Korean patients could be also used for treatment and prophylactic purposes, as oral microbiomes have different compositions, which may affect periodontitis[3]. Schmidt et al.[4] studied that the microbiome may provide a framework for monitoring oral cancer development, progression and recurrence. Liu et al.[5] reported that the risk of post-operative inflammation at grafted sites might be related to the oral microbiota profile before alveolar bone grafting. Also, Pushalkar et al.[6] suggested that colonization of unique bacterial communities coupled with deficient innate immune response is likely to impact the pathogenesis of osteonecrosis of the jaw.

It would be good for oral and maxillofacial surgeons to research microbiomes associated with all diseases occurring in the oral and maxillofacial region. I hope to see more papers related to microbiome in the future.

Conflict of Interest

No potential conflict of interest relevant to this article was reported.

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