





Analysis of Oral Microbiome using NGS



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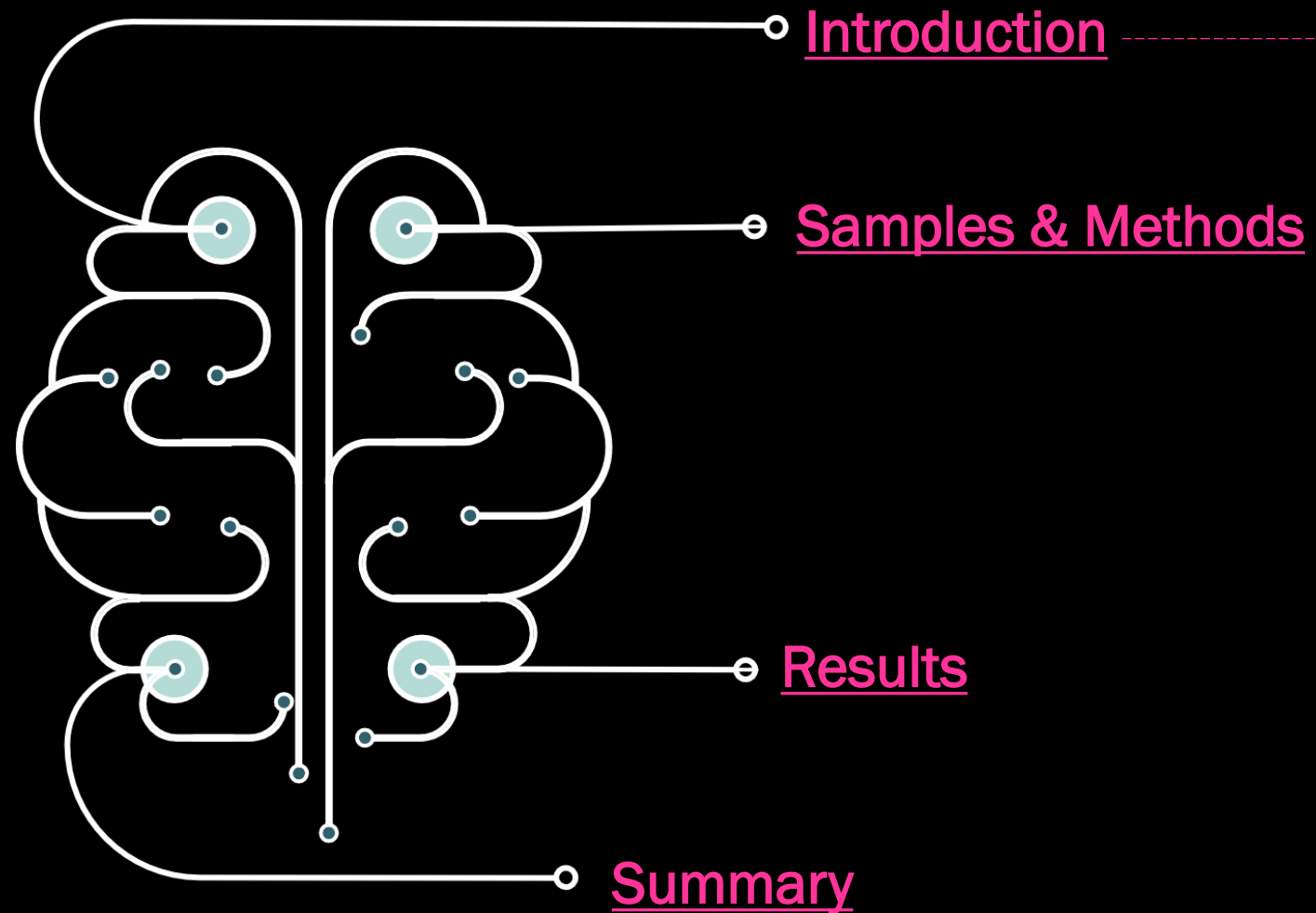
4학년 : 곽지우, 김세찬, 김은영

3학년 : 조민희, 송민준, 신태수, 이수현, 정유경

2학년 : 문소윤, 오예원, 장조은, 권주희, 김아정, 김예지, 김은아, 박가영, 임서영, 전영현, 최정훈, 류정연

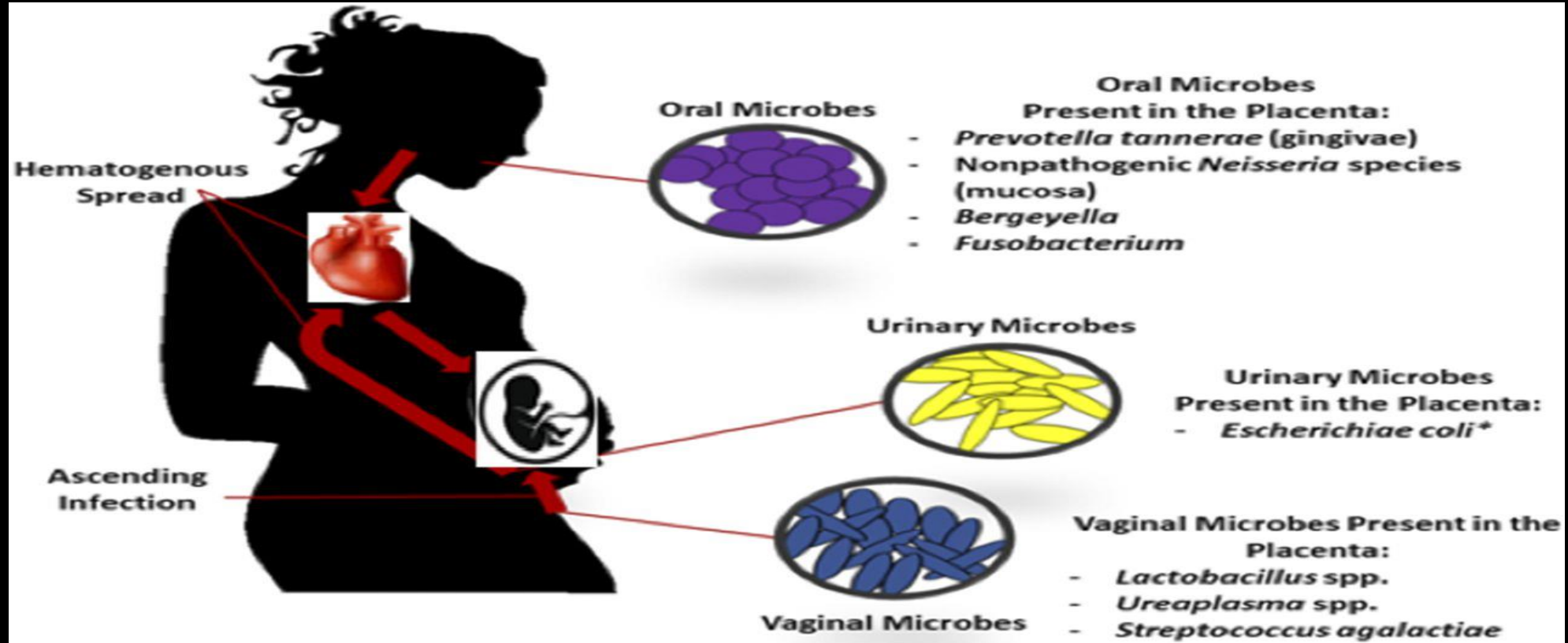
1학년 : 박민정, 조설아, 김지영, 양민주, 김혜숙, 권민주, 최한희, 김다은, 김민서, 이다영, 김성훈, 김다해, 정지연, 우수진, 김진영

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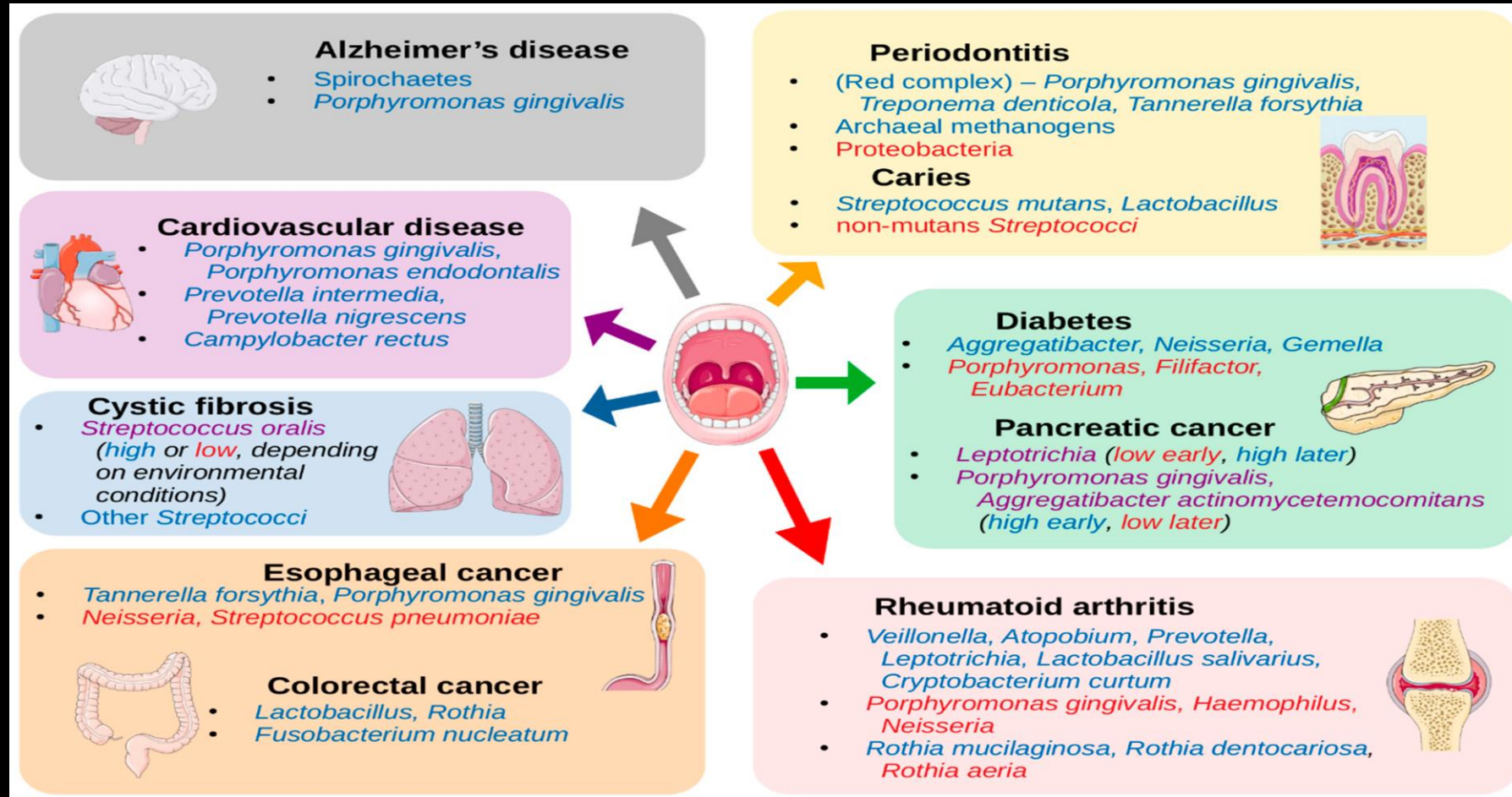
INTRODUCTION

Human Microbiome

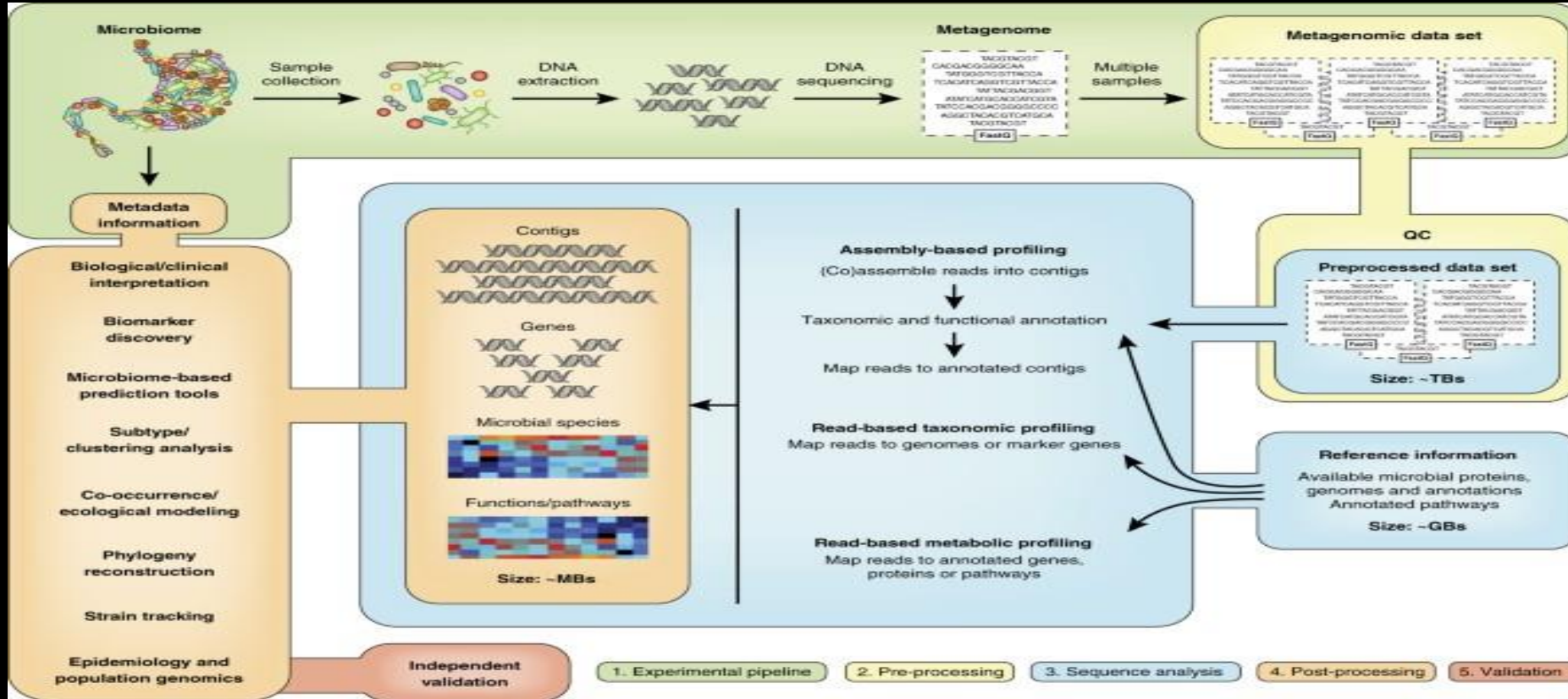


The various microbes present in the human body have symbiotic relationships with humans (hosts) while maintaining their in vivo constancy. The aggregate genetic information of microorganisms that coexist in these bodies is called microbiome. Microbiome is a compound word made by combining microbiota and genome, which can be said to be a microbial colony that contains microbes and all of their genetic information that live or coexist in all environments, including humans, animals and plants, soil, oceans, lakes, rock walls, and the atmosphere.

Correlation b/w Oral Bacteria & Human Diseases



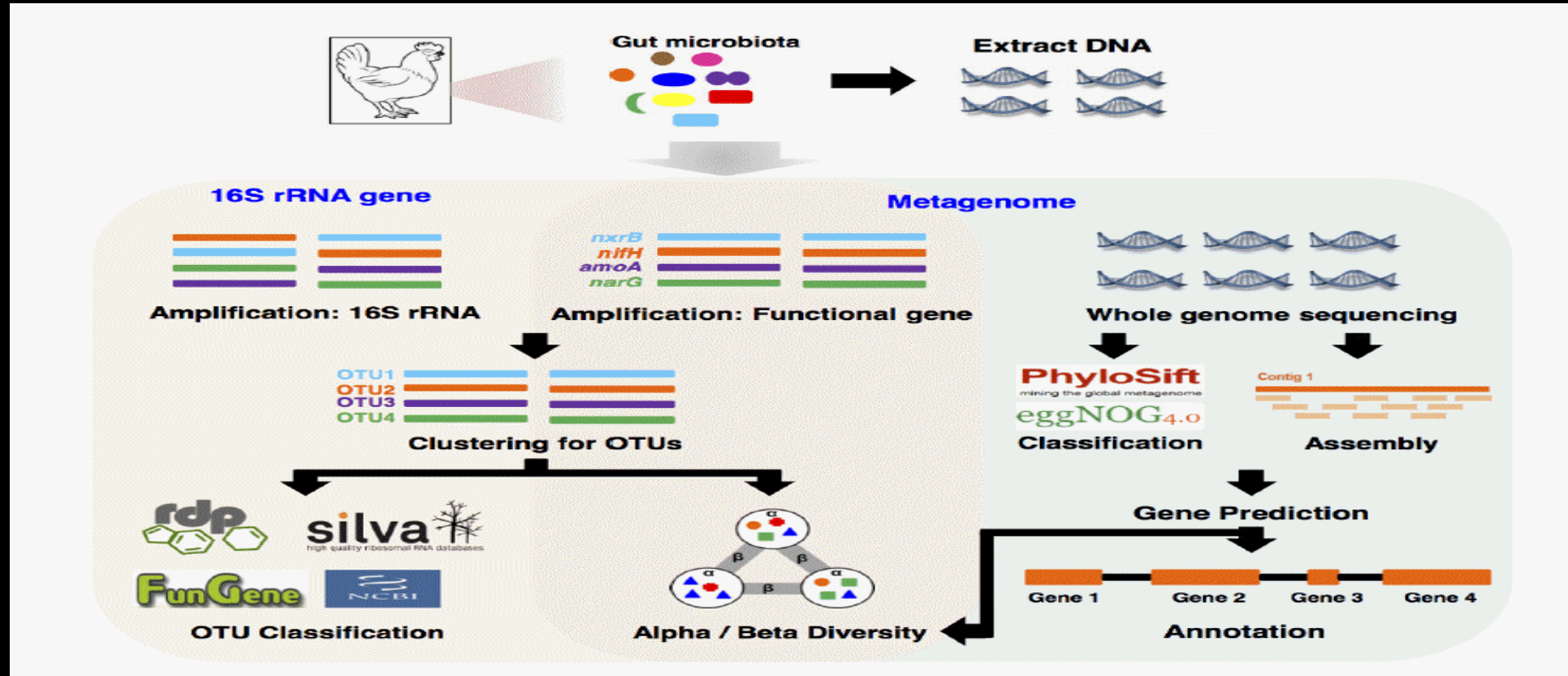
Metagenomics



While traditional microbiology and microbial genome sequencing and genomics rely upon cultivated clonal cultures, early environmental gene sequencing cloned specific genes (often the 16S rRNA gene) to produce a profile of diversity in a natural sample. Such work revealed that the vast majority of microbial diversity had been missed by cultivation-based method.

Metagenomics is the study of genetic material recovered directly from environmental samples.

16s rDNA Metagenomics



Metagenome analyzes the entire microbial genome, or 16S rRNA analysis is being usefully used. The 16S ribosomal RNA (RNA) is produced by transcription from the DNA of the prokaryotic organism and is the rRNA that forms the 30S subunit of the prokaryotic ribosomes, with the order of the 16S ribosomal RNA largely preserved, while high sequence diversity in some sections.

PURPOSE OF STUDY

Recently human microbiomes, a collection of all microbial groups that mainly exist in human epithelial cells such as human intestines, skin, mouth, respiratory and reproductive organs, have had a significant impact on the human body and studies of disease association have been reported .

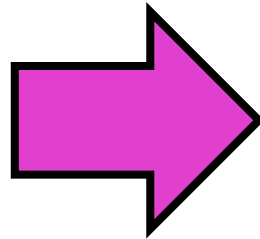
Therefore, this study tried to analyze the distribution patterns of bacteria in the mouth and the distribution and diversity of microorganisms that cause human diseases through microbiome analysis of bacteria in normal adults' mouths using NGS.

SUBJECTS & METHODS

SUBJECTS

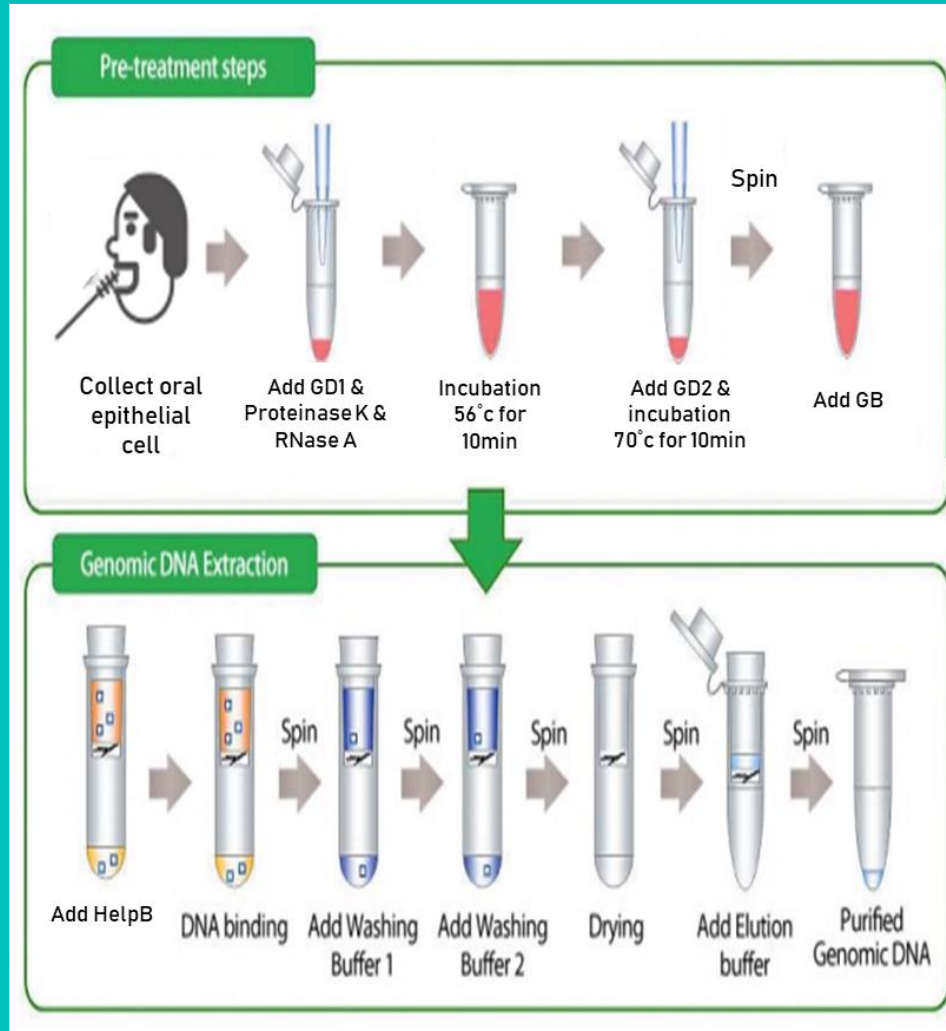
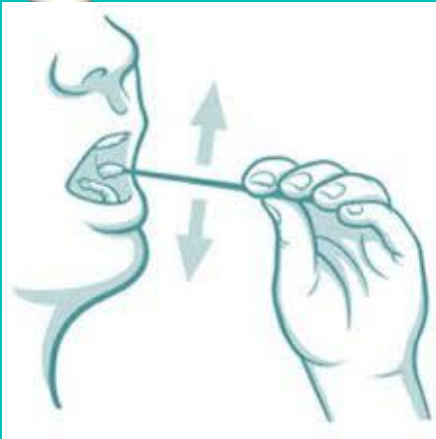


11 subjects



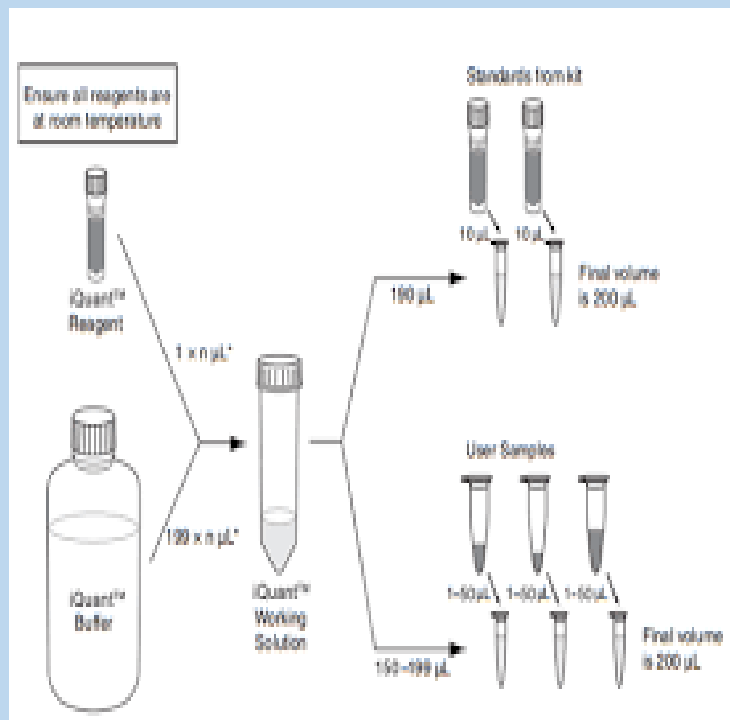


DNA extraction



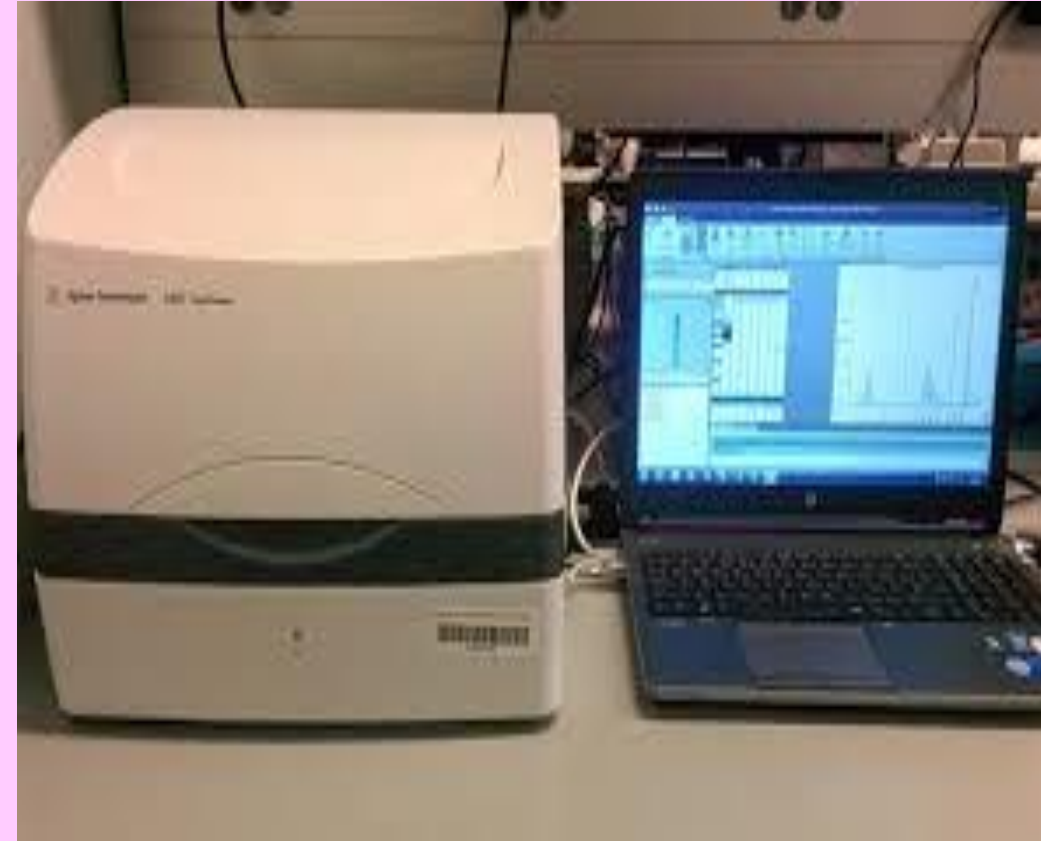
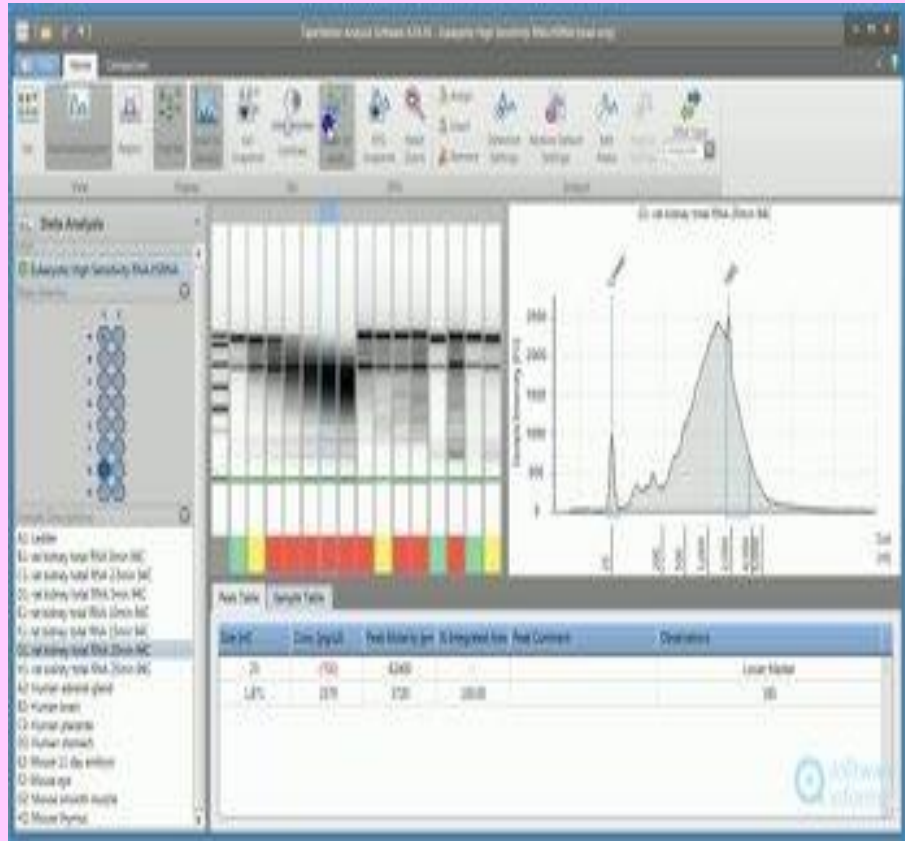


DNA Quantitation



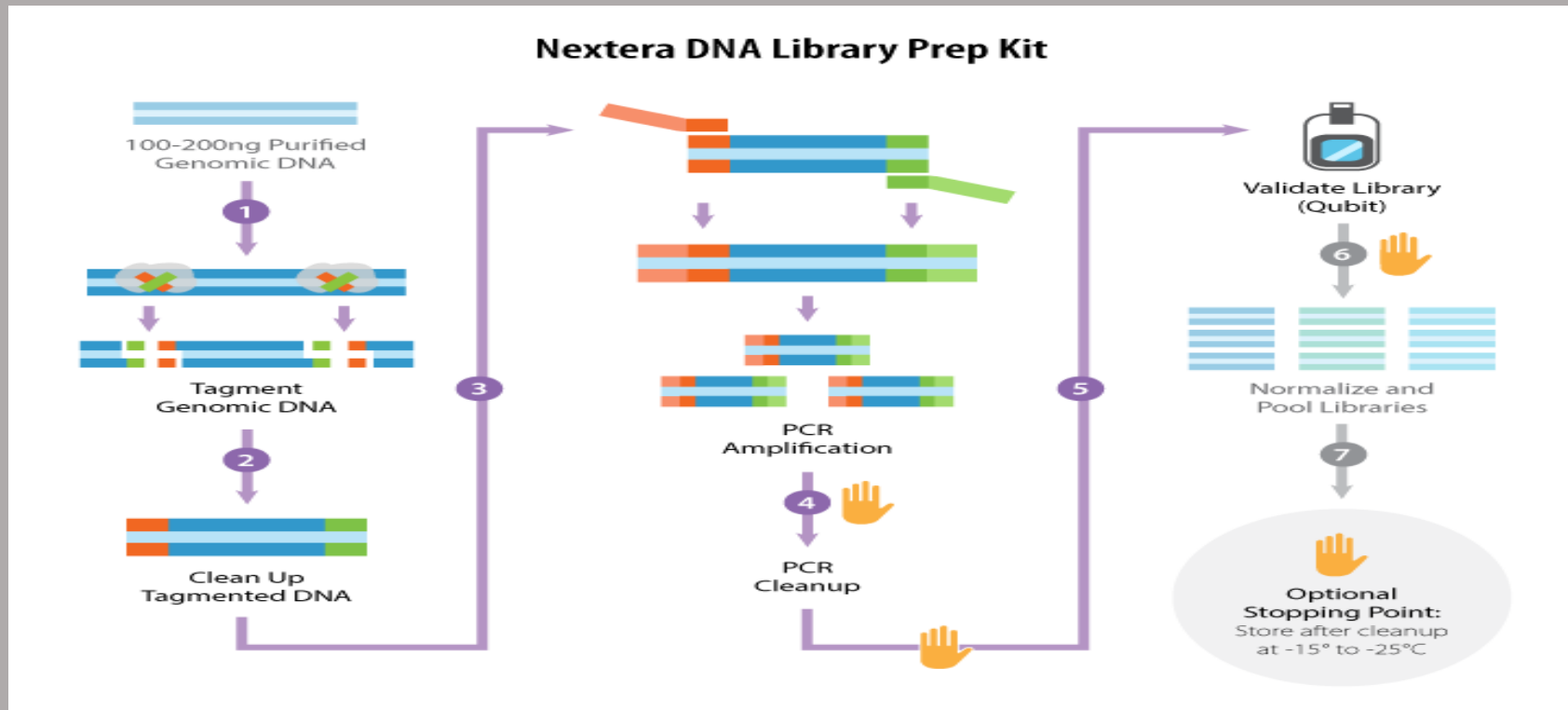


DNA Qualification



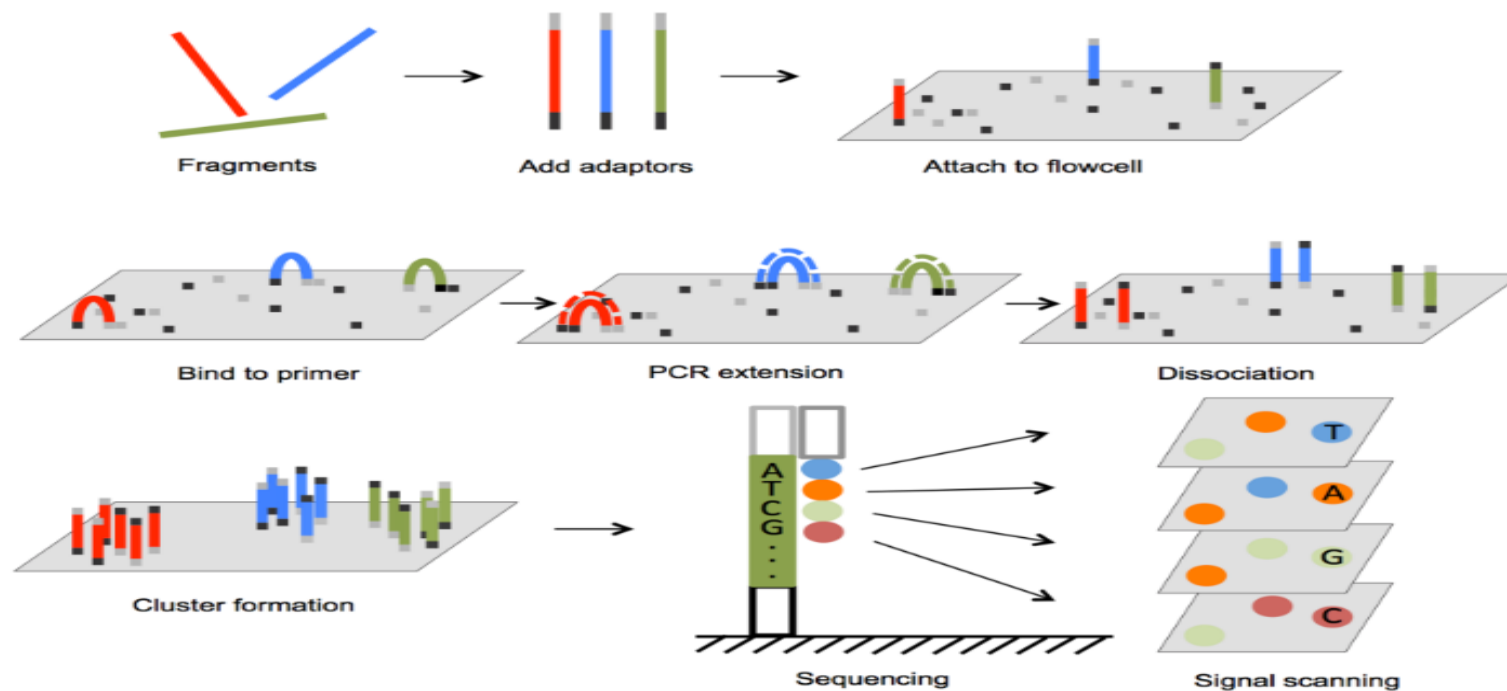


DNA Library Construction





16 rDNA Sequencing by NGS using MiSeq



RESULTS



Distribution of Major Bacterial Species In The Oral Cavity

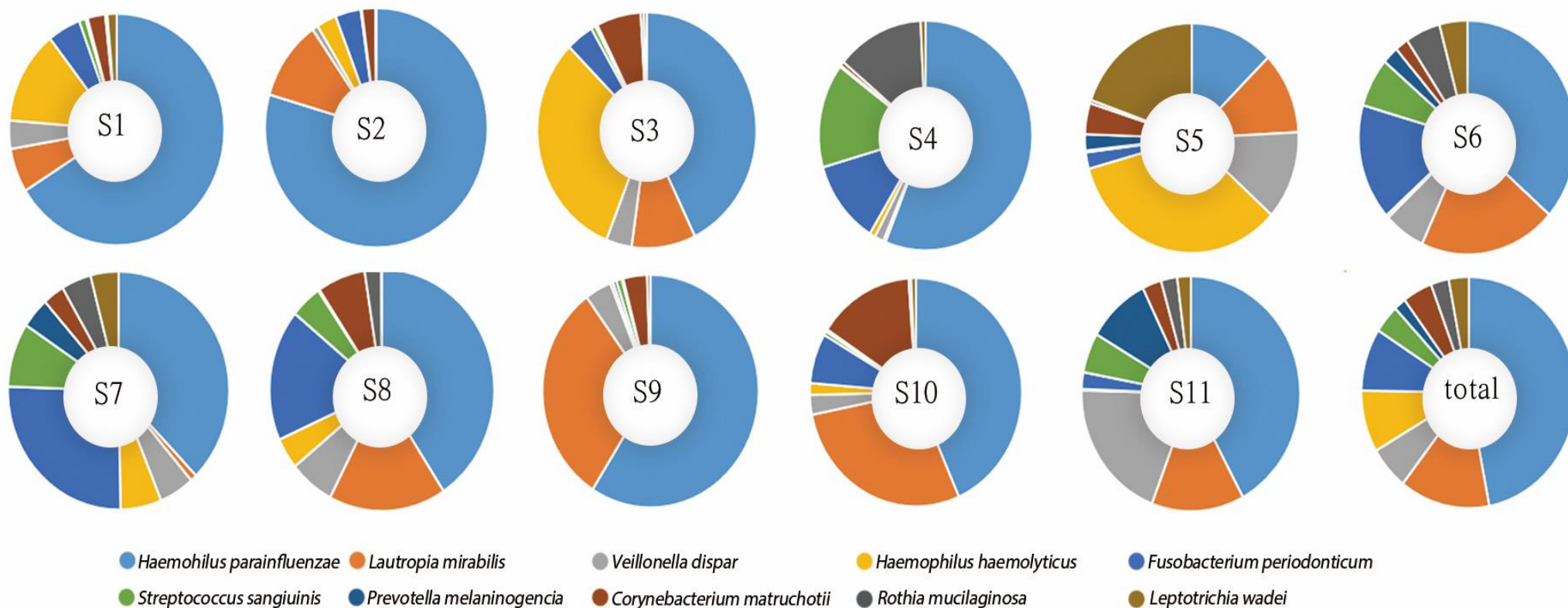


Fig. 1. NGS를 이용한 검사자 11명의 검출된 구강내 세균의 종 분포 분석 결과



Analysis of Major Bacterial Species Present in The Patient's Oral Cavity

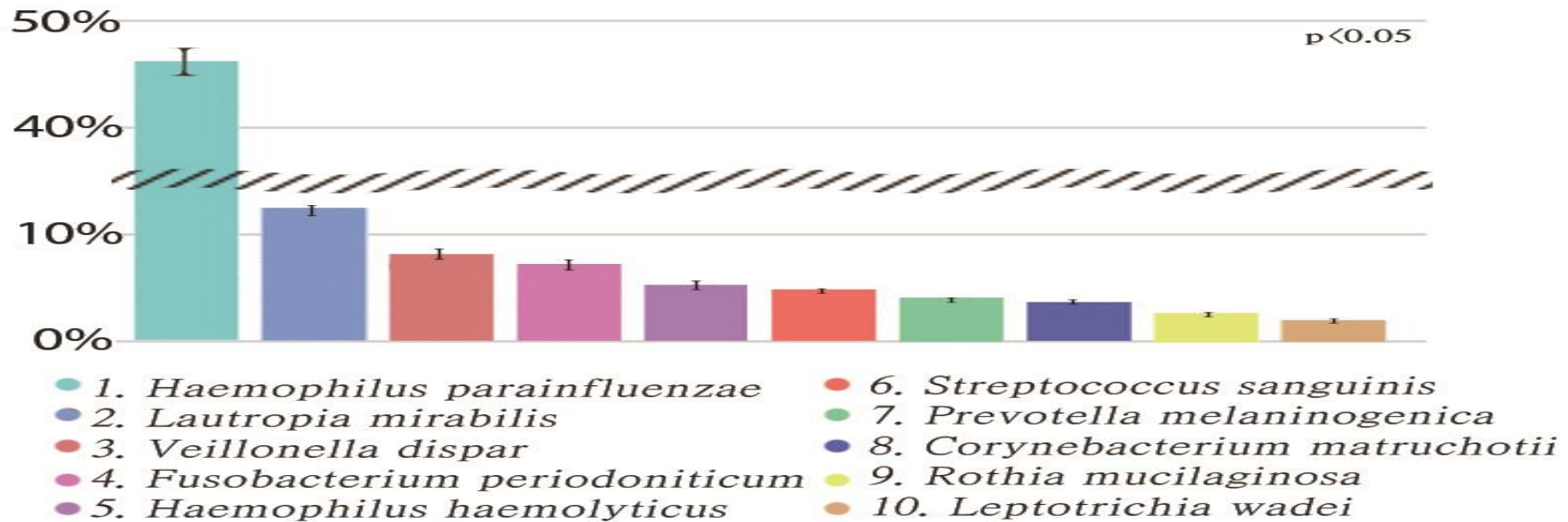
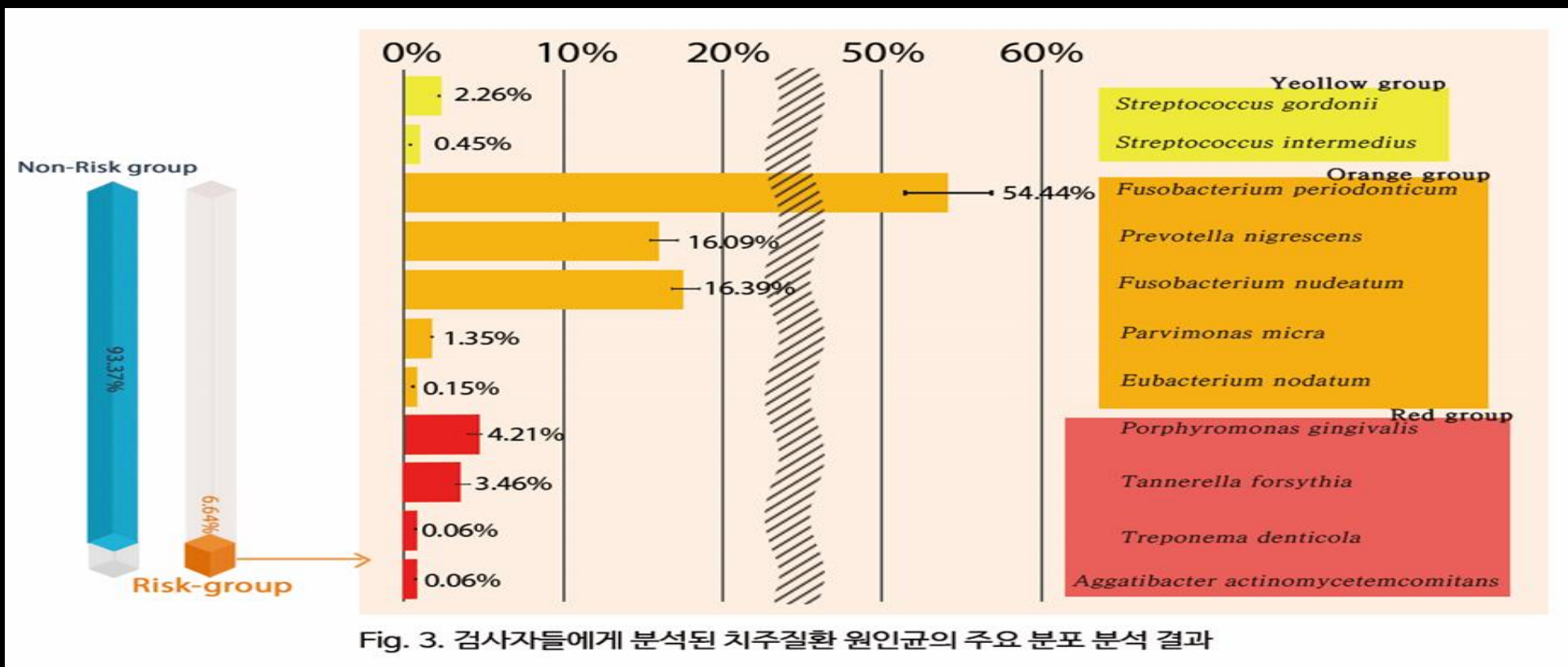


Fig. 2. 검사자들에게서 분석된 주요 균종 분석 결과



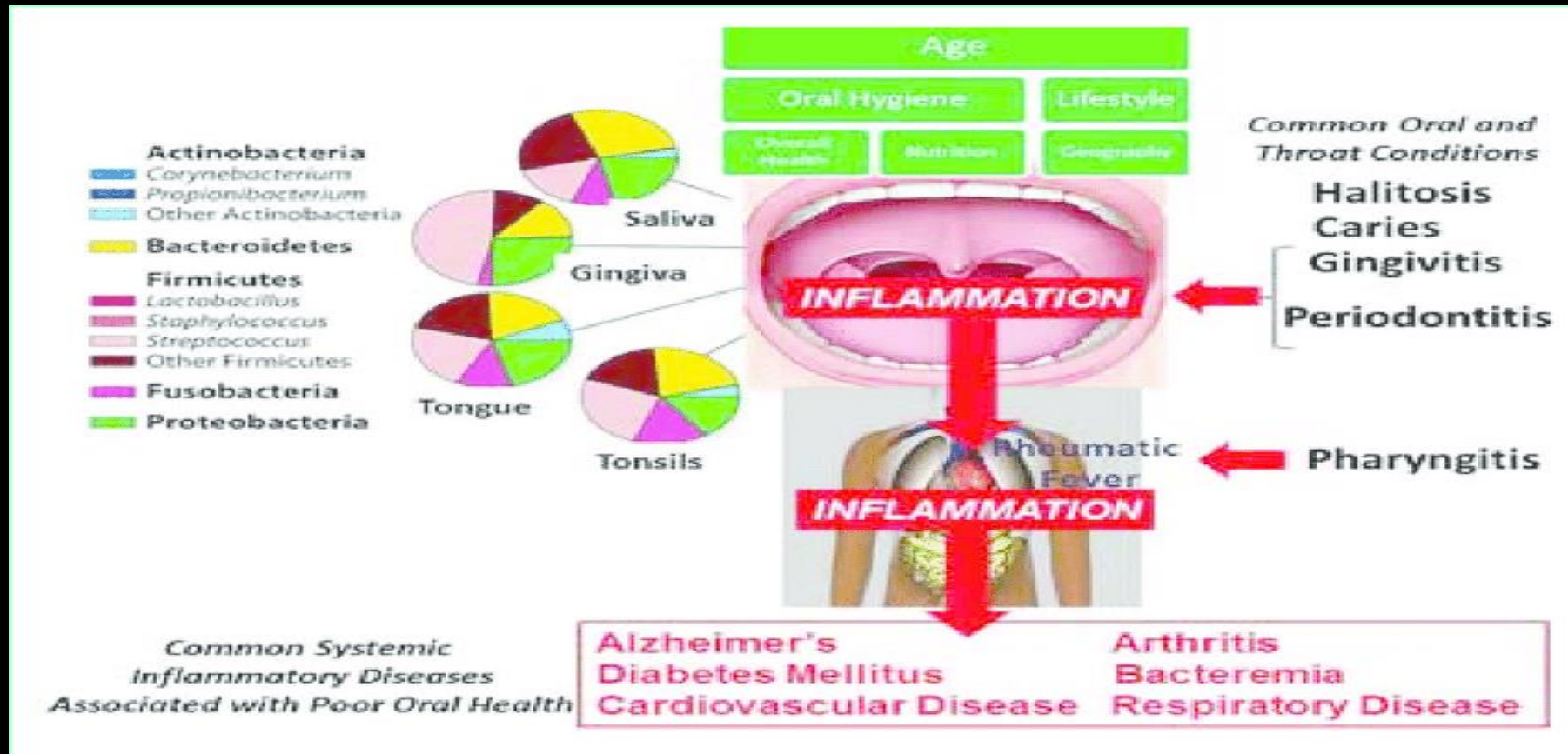
Distribution of Causative Bacteria Causing Periodontal Disease



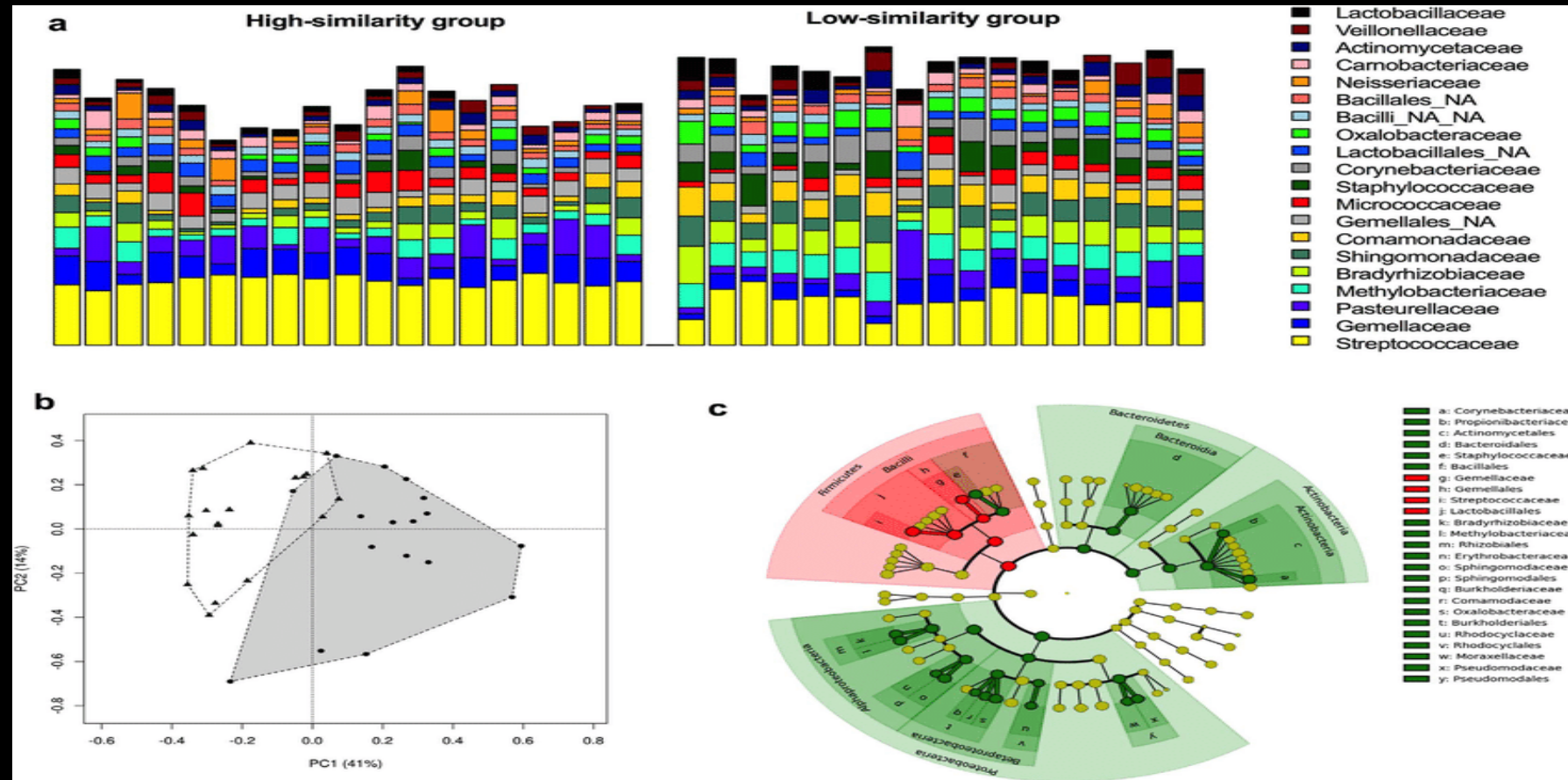
SUMMARY

- In the oral cavity, most of the bacteria irrelevant to periodontal disease accounted for more than 93.36%. In particular, *Haemophilus parainfluenzae* was distributed at an average of 47.16% in all oral bacteria in most testers, and *Lautropia mirabilis* was distributed at 13.15% and *Veillonella dispar* at 7.76%.
- Periodontal disease causative bacteria that cause bacterial oral disease account for 6.64% of the total bacterial distribution. Of these, the orange group, the moderate group for periodontal disease, 5.88%, the red group 0.59%, the high-risk group, and 0.18% the yellow group, the low-risk group.
- It was analyzed that *Porphyromonas gingivalis* occupied the highest distribution in the high risk group with 0.28%, *Fusobacterium periodonticum* 3.62% in the moderate group, and *Streptococcus gordonii* 0.15% in the low risk group.

CONCLUSION



In order to know the bacteria that cause oral disease, there have been attempts to find the causative bacteria by culturing plaques formed of biofilm on the tooth surface. However, since many bacteria in the oral cavity are mostly anaerobic bacteria, it has not been well cultured by general culture methods, so it has not been adopted as a clinical test technique to diagnose the risk of oral disease.



Recently, as microbiome analysis using NGS has become possible, the overall picture of oral-resident bacteria and pathogens has been known, and a new perspective on the association of oral microbiome in oral diseases is starting.



As such, oral microbiome analysis has the potential to bring a new direction to the etiology of oral inflammatory diseases including periodontal disease.

Thank
you