<u>Cite this as</u>: Lei XU, Zhifang WU, Yuan WANG, Sa WANG, Chang SHU, Zhuhui DUAN, Shuli DENG, 2021. High-throughput sequencing identifies salivary microbiota in Chinese caries-free preschool children with primary dentition. *Journal of Zhejiang University-Science B (Biomedicine & Biotechnology)*, **22**(4):285-294. https://doi.org/10.1631/jzus.B2000554

High-throughput sequencing identifies salivary microbiota in Chinese caries-free preschool children with primary dentition

Key words: Salivary microbiota; caries-free; preschool children; primary dentition; Illumina MiSeq; 16S rDNA V3-V4 hypervariable regions

Research Summary

The study aimed at identifying salivary microbiota in caries-free Chinese preschool children using high-throughput sequencing.

- 1.5 phyla and 13 genera were the most dominant.
- 2. The core salivary microbiome comprised 9 genera.
- 3.Microbial diversity and community structure were similar between male and female subjects.
- 4.Functional prediction revealed that the most abundant genes were related to amino acid transport and metabolism.

Research Summary



Innovation points

 Reveal the identity, composition, and structural characteristics of microorganisms in the saliva of caries-free primary dentition of preschool children.

• Lay a foundation for future research into the relationship between oral microecology and health or disease in children.