

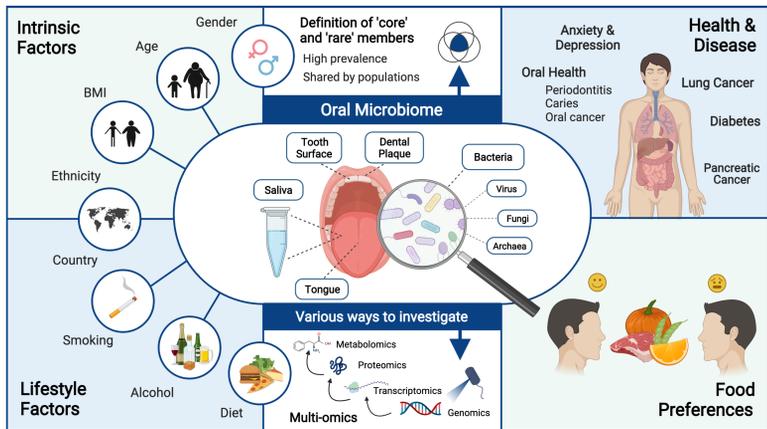
The salivary microbiome shows a high prevalence of core bacterial members yet variability across human populations

Xinwei Ruan¹, Jiaqiang Luo¹, Pangzhen Zhang¹ and Kate Howell¹

¹ School of Agriculture and Food, Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Parkville 3010, Australia



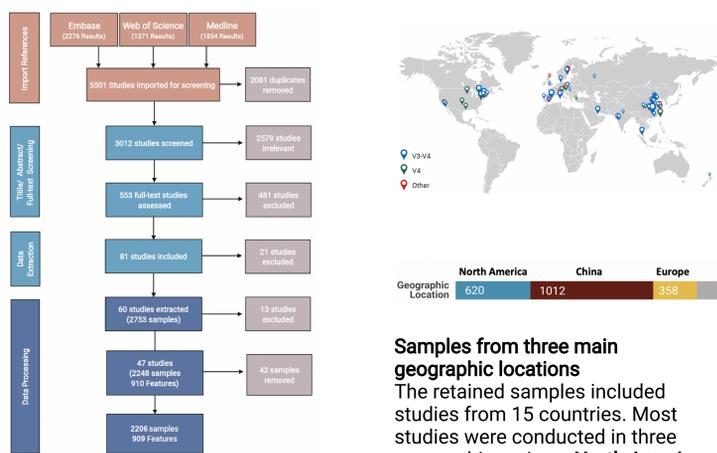
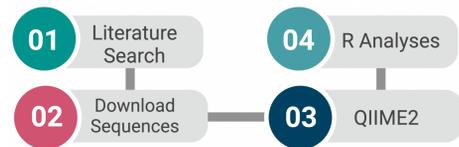
INTRODUCTION



Sensory perception is an essential driver of personal preference during food consumption. **Human saliva**, especially the diverse **microbial profile**, can change the induced perception during the mixing with food products. Many **host characteristics** have been shown to have an impact on the composition of the salivary microorganisms, including age, ethnicity, gender, smoking, alcohol use, body mass index, and the type of stimulation.

METHODS

This study use a **meta-analysis** approach to define and explore the core membership of the human salivary microbial community by collecting and re-analysing raw **16S rRNA amplicon sequencing data** from **47 studies** with **2206 saliva samples**¹.



Systematically review available public studies
A literature search was performed in EMBASE, MEDLINE and Web of Science.

Samples from three main geographic locations
The retained samples included studies from 15 countries. Most studies were conducted in three geographic regions: **North America**, **Europe**, and **China**. We further combined samples from North America and Europe into a single group, "**Western**."

CONCLUSION

In summary, we have defined a **core bacterial community** in saliva from healthy humans, and this core demonstrated both stability and variability among populations. We have revealed the influence of various host factors, such as **geographic locations**, on the salivary microbiome. We also identified microbial and functional biomarkers to differentiate the **Chinese and Western** people, underlying the potential relationship between salivary microbiota and **sensory perception**.

Data availability

The sequencing data supporting the conclusion of the meta-analysis are available in publicly accessible databases. The sequencing data generated and/or analysed during the current study are available in the NCBI Bioproject repository, PRJNA786805. Original scripts generated during the current study are available in Github (https://github.com/XINWEIR/SalivaryMicrobiome_MetaAnalysis).

Acknowledgements

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References

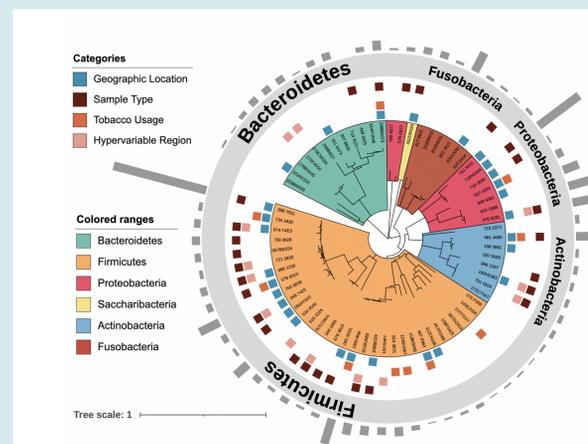
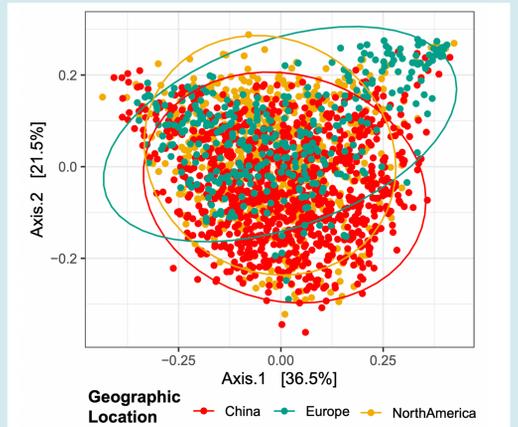
1 Ruan, X., Luo, J., Zhang, P. & Howell, K. (2022). "The salivary microbiome shows a high prevalence of core bacterial members yet variability across human populations" bioRxiv: 2021.2012.2013.471511 10.1101/2021.12.13.471511
2 Luo, J. et al. (2021). "Can variation in wine preference amongst consumers be explained by salivary protein composition?" Poster presented at the Institute of Food Technologists annual meeting 2020, Chicago, IL

RESULTS

Intrinsic and lifestyle factors have a significant effect on the host salivary microbiome

Large variability between studies was observed in the taxonomic profile, and alpha diversity. The beta-diversity analyses showed that all metadata categories measured have a **significant** ($p < 0.001$) effect on the bacterial profile of human saliva. However, only **limited** variation among samples has been explained by these factors ($R^2 < 10\%$).

Figure 1. Principal coordinate analysis (PCoA) showing the differences between samples from North America, Europe, and China.



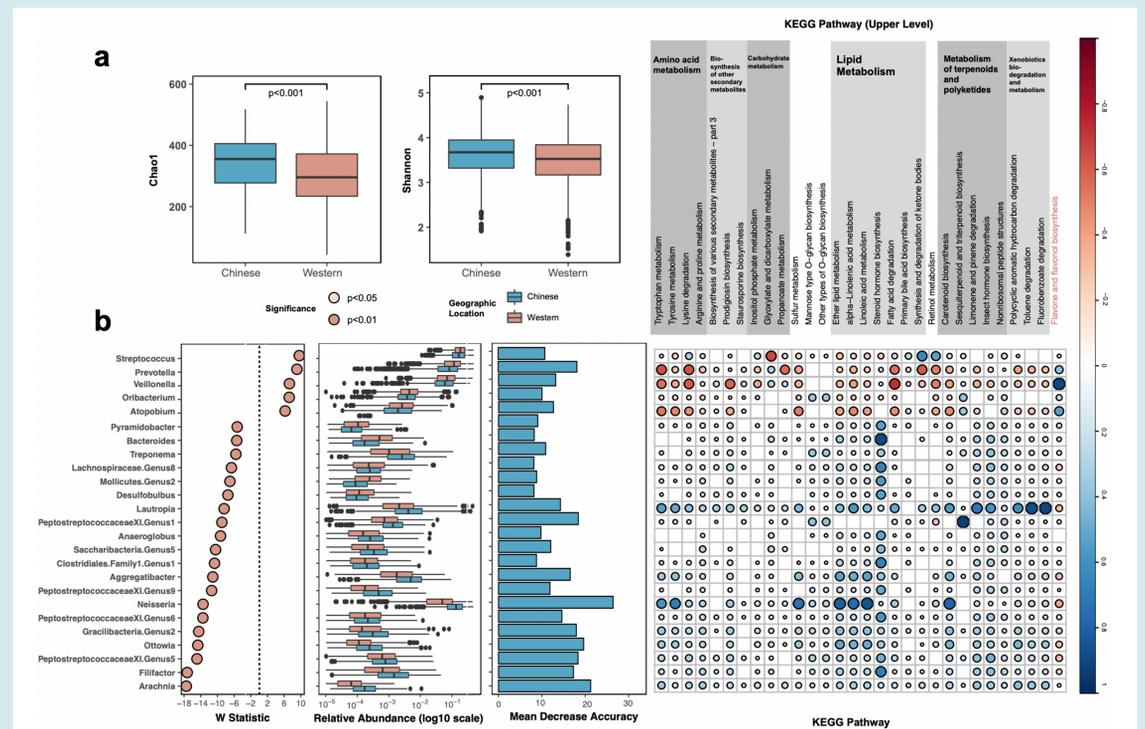
Identifying the core OTUs

We found **68** core OTUs that were consistently detected across studies.

Differential OTUs

We determined the **core** microbiome that can be used as **biomarkers** to differentiate people categorised by **intrinsic and lifestyle factors**.

Figure 2. Phylogenetic tree indicates the taxonomic information of 68 core OTUs. The coloured squares indicate the OTUs that were defined by the Random Forest model as "important". The bars on the outmost ring showing the mean relative abundance of OTUs.



Functional Prediction (PICRUSt 2)

Here, we showed that *Veillonella* was generally higher in **Western** samples. Such differences may influence the **flavone and flavonol biosynthesis pathways** in the oral cavity. We speculate it may lead to the different **sensory responses** of Western-born and Chinese-born experts to **wine** we observed in a previous study².

Figure 3.
a Differences in alpha-diversity at genus level.
b Spearman's correlation coefficients were calculated between each pairwise comparison of differential genus and KEGG pathway.

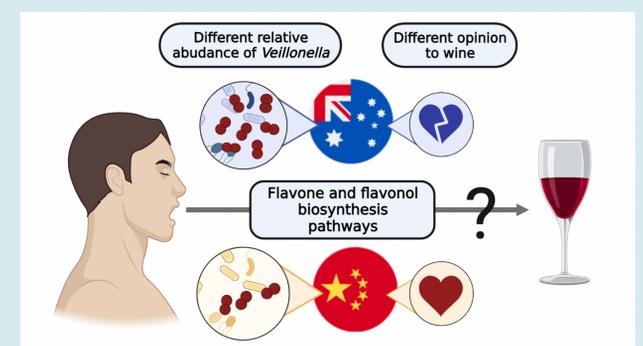


Figure 4. Inferred relationship between oral bacteria and sensory responses