# Article information:

The Human Salivary Microbiome Is Shaped by Shared Environment Rather than Genetics: Evidence from a Large Family of Closely Related Individuals | mBio  
<https://journals.asm.org/doi/full/10.1128/mBio.01237-17>

# Article summary:

1. The salivary microbiome of an extended family of Ashkenazi Jewish individuals living in several cities was studied to investigate associations with both shared household and host genetic similarities.

2. Environmental effects were found to dominate over genetic effects, with a large and significant effect of shared household on microbiome composition.

3. Host genetics played no significant role, indicating that the environment rather than host genetics is the dominant factor affecting the composition of the salivary microbiome in closely related individuals.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article provides a detailed analysis of the salivary microbiomes of an extended family of Ashkenazi Jewish individuals living in several cities and investigates associations with both shared household and host genetic similarities. The authors find that environmental effects dominate over genetic effects, with a large and significant effect of shared household on microbiome composition, while host genetics play no significant role.

The article is generally well-written and provides a thorough analysis of the data collected from this cohort. The authors have taken into account potential confounding factors such as diet, lifestyle, and Crohn’s disease status when conducting their analyses. Furthermore, they have used more accurate measures of kinship based on genome-wide single nucleotide polymorphisms (SNPs) rather than pedigree measures to assess host genetic similarity.

However, there are some potential biases in the article which should be noted. Firstly, the sample size for this study is relatively small (133 individuals from family A, 18 from family B, and 27 controls). This may limit the generalizability of the results to other populations or contexts. Secondly, it is possible that other factors such as diet or lifestyle may have influenced the results but were not accounted for due to lack of data or difficulty in controlling for them in this particular population due to cultural practices within this community (25). Finally, it should also be noted that while environmental effects appear to dominate over genetic effects in this study, further research is needed to confirm these findings across different populations or contexts before any definitive conclusions can be drawn about their relative importance in shaping microbial communities.

# Topics for further research:

* Salivary microbiome composition
* Environmental effects on microbiome
* Host genetics and microbiome
* Single nucleotide polymorphisms (SNPs)
* Diet and lifestyle influences on microbiome
* Cultural practices and microbiome

# Report location:

<https://www.fullpicture.app/item/d75335b1b468965716d51d374185d8d7>