

Distinct oral bacterial communities observed between tobacco users and non-users: a longitudinal oral microbiome study

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Background and Objective

Over 700 bacterial species reside in the human oral cavity, collectively known as the oral microbiome, and these commensal bacteria are involved in different functions, many of which are important in maintaining oral health. Tobacco use is recognized to adversely affect every organ of the human body and influence changes in the oral microbiota. However, less is known about how specific tobacco products causes dysbiosis of the human oral microbiota over time. Here, we aimed to identify the temporal shifts in the bacterial communities in the oral cavity of tobacco users and compare the microbiota profiles from cigarette users and smokeless tobacco users.

Methods:

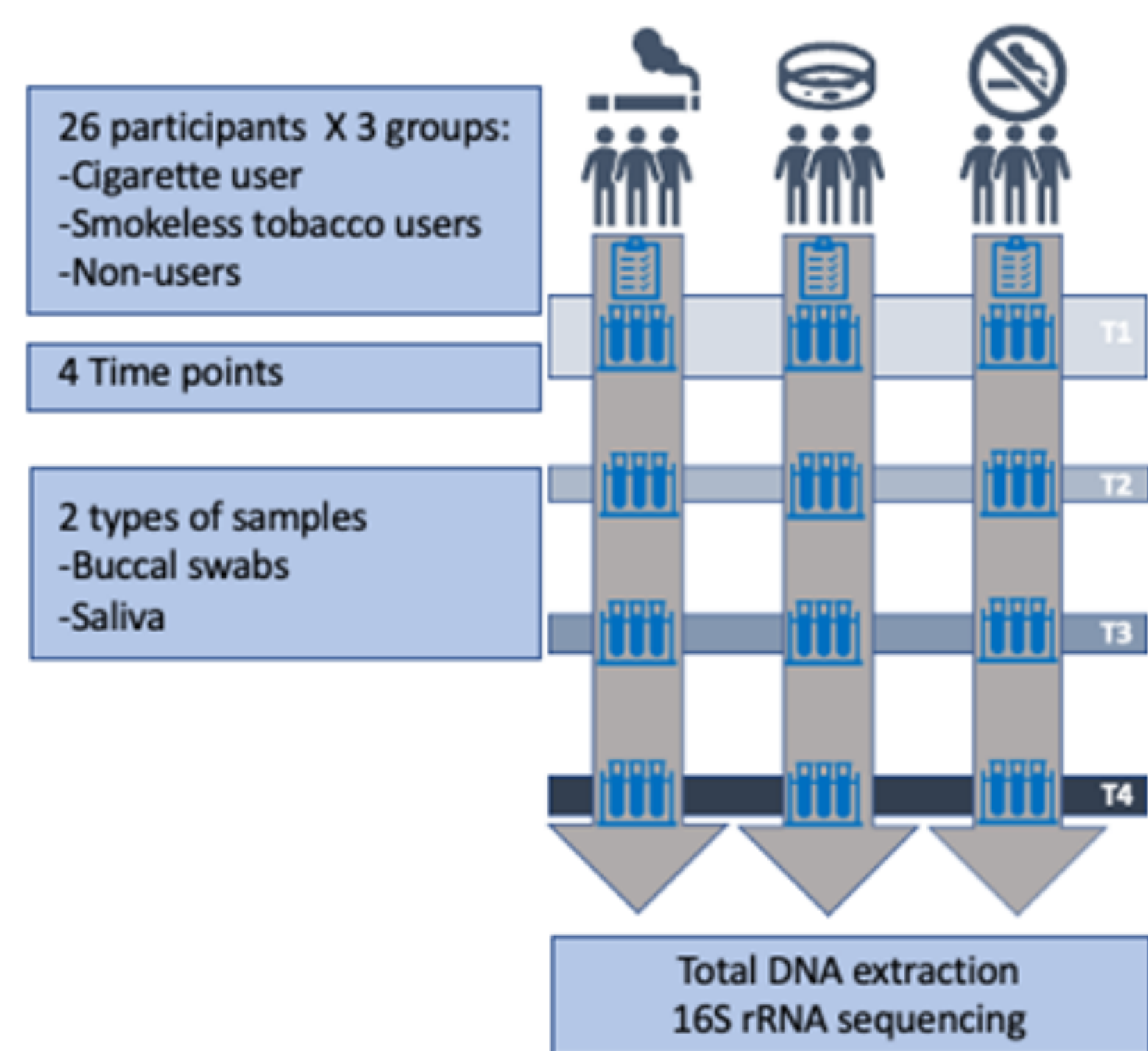


Figure 1: Longitudinal cohort study design

Results:

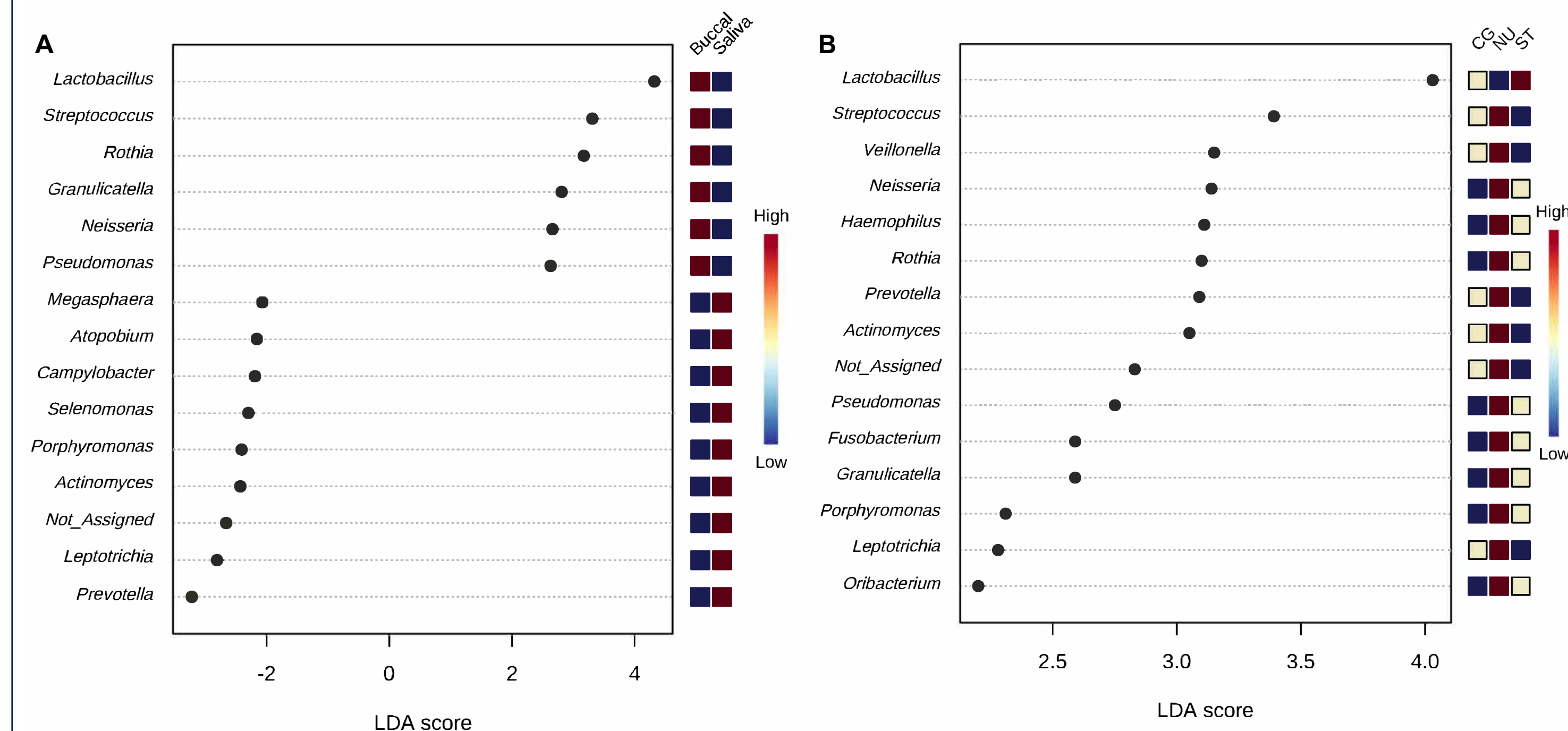


Figure 2: Linear discriminant analysis computed for top 15 differentially abundant bacterial genera between (A) sample type and (B) user groups. The log₁₀ transformed LDA scores are showed on the x-axis and the bacterial taxa are listed on the y-axis. The color coding in the squares of the right side of the plot refers to the cumulative abundance of each genus in each binned group, red means high cumulative abundance and blue means low cumulative abundance. CG: cigarette user; NU: non-user; and ST: smokeless tobacco user.

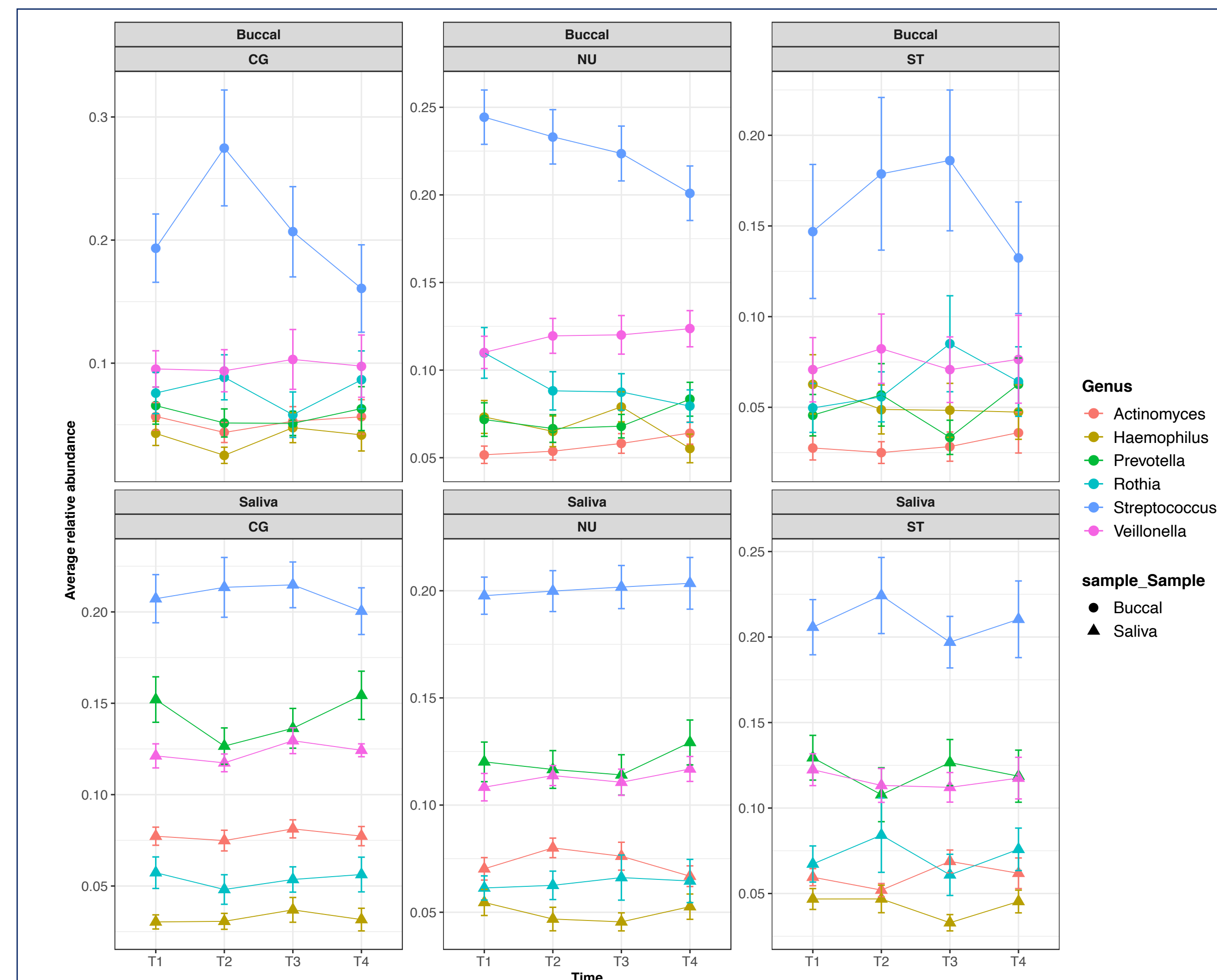


Figure 3: Average relative abundance (± SE) of top six bacterial genera present in all samples across four time points.

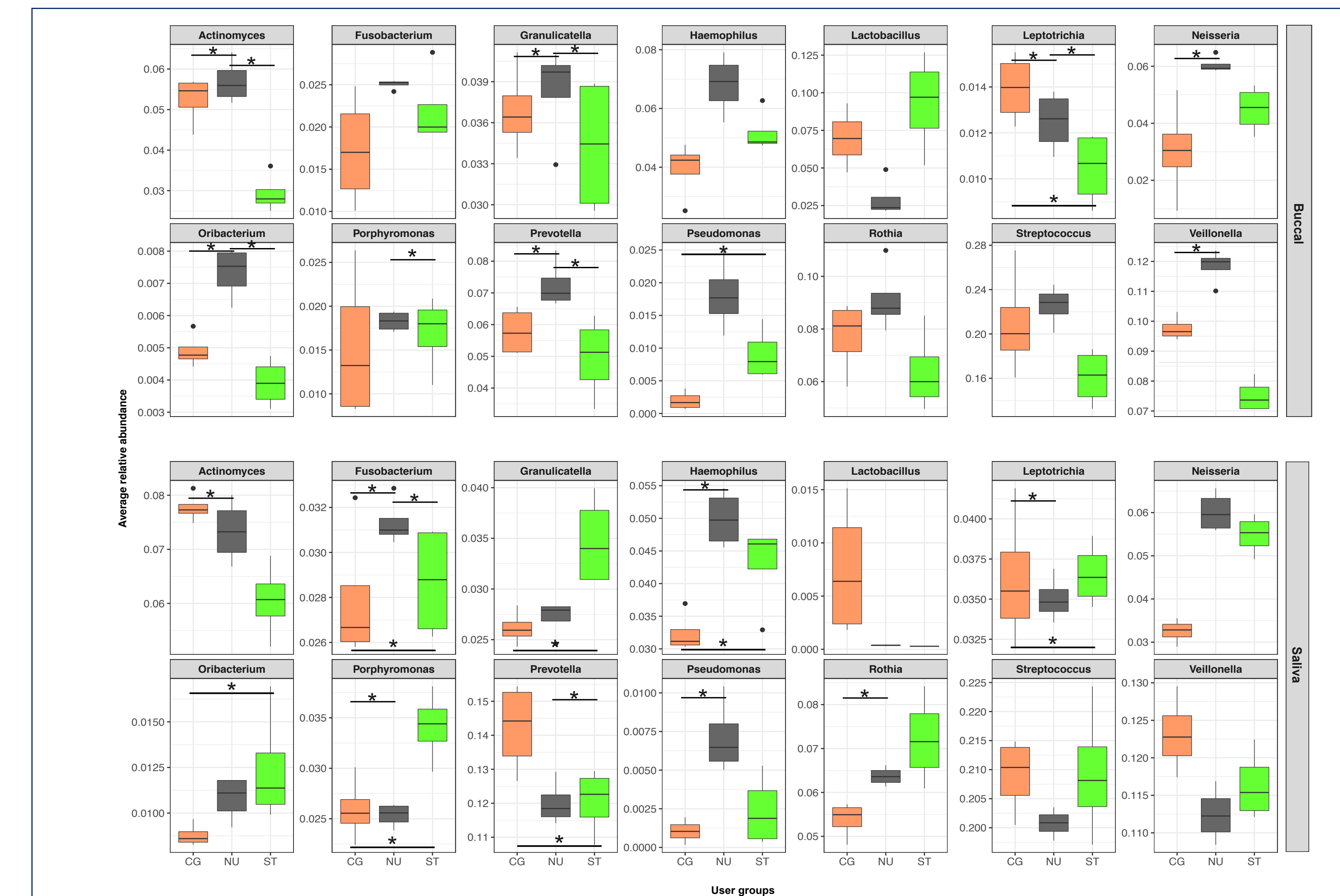


Figure 5: Box plots of relative abundance of top 14 bacterial genera by user groups (CG (orange), grey (NU), green (ST)).

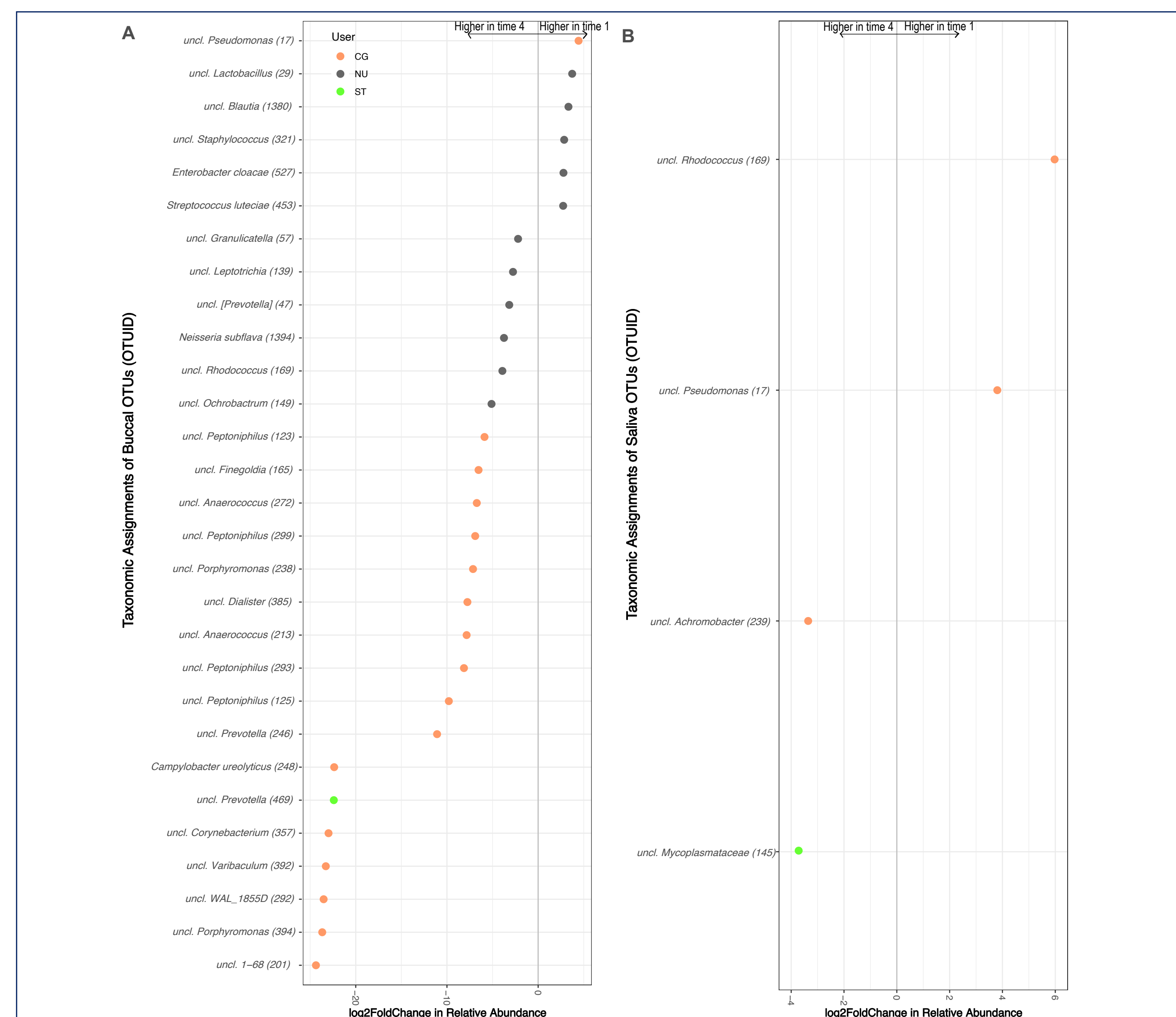


Figure 4: Differential relative abundance of bacterial OTUs in (A) buccal mucosa and (B) saliva samples that were statistically significantly different (p<0.05) between time-point 1 and 4. A positive log₂-fold change value denotes an OTU that is significantly higher in time-point1 samples, while a negative log₂-fold change indicates an OTU that is significantly higher in time-point4 samples. The grey line highlight the conversion in log₂-fold change from negative to positive values.

Discussion and conclusion:

- Oral bacterial communities are dominated by *Streptococcus*, *Prevotella*, *Haemophilus*, *Neisseria*, and *Veillonella*, regardless of tobacco use status (non-user, cigarette user, and smokeless user).
- Tobacco users had a larger and more diverse set of core bacterial species, with either significant co-occurrence or co-exclusion relationships, than non-users.
- Tobacco users had a lower relative abundance of *Proteobacteria* compared to non-users. *Haemophilus* was significantly higher (p<0.05) in the non-users, when compared to the smokers and *Streptococcus*, was least impacted by smoking status.
- Cigarette users showed a significantly higher (p<0.05) relative abundance of *Rothia mucilaginosa*, *Haemophilus parainfluenzae*, *Neisseria subflava*, and *Veillonella dispar*; while smokeless tobacco users showed significantly (p<0.05) higher relative abundance of *Actinomyces* and *V. dispar* when compared to the non-users.
- Significant difference (p<0.05) in the diversity of bacterial communities was also observed between buccal mucosa and saliva samples. *Haemophilus*, *Lactobacillus*, *Pseudomonas*, and *Rothia* showed higher while *Leptotrichia*, *Oribacterium*, *Porphyromonas*, and *Prevotella* showed lower relative abundance in buccal mucosa samples when compared to saliva samples.
- Our results indicate using tobacco products significantly changes the oral microbiome, even though it remains consistent over time. Alterations in the prevalence of some of the opportunistic pathogens in the smokers' samples indicate poor oral health, which could lead to the initiation of smoking-related diseases.
- Overall, these results provide a more holistic understanding of the structure of microbial communities in the oral cavity, and some clues about how smoking exposures may govern their assembly and lead to disease states.

Funding: This work was supported by the University of Maryland Tobacco Center of Regulatory Science (UMD TCORS) "Rapid Response Characterization of New and Manipulated Tobacco Products" awarded by the National Institute of Health (NIH) and the Food and Drug Administration (FDA)—Award # P50-CA-180523-01.