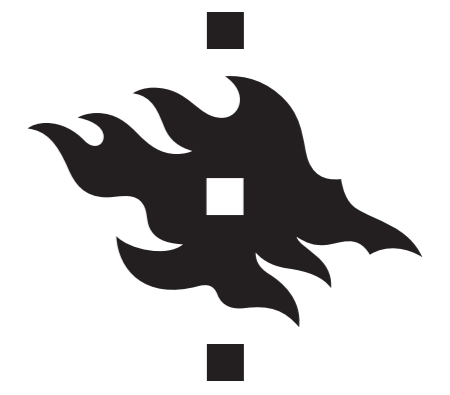


# MICROBIOME OF THE HEALTHY EXTERNAL AUDITORY CANAL



The most common bacteria in the microbiome of the healthy EAC are *Staphylococcus auricularis*, *Propionibacterium acnes*, *Alloiococcus otitis*, and *Turicella otitidis*.

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## Background

A growing number of next-generation sequencing-based microbiome studies have deepened the understanding of health and disease of many human organs. However, the microbiome of the external auditory canal (EAC) remains scarcely examined.

The aim of this study is to investigate the microbiota of the healthy EAC culture-independently and to evaluate the usefulness of the swabbing method in collecting EAC microbiota samples.

## Materials and methods

Samples were harvested with DNA-free swabs from fifty healthy working-age volunteers' asymptomatic EACs. Volunteers were staff and students from University of Helsinki, Department of otorhinolaryngology.

DNA extraction, PCR amplification, and sequencing (Illumina MiSeq platform) of the 16S rRNA gene were performed in the DNA Sequencing and Genomics Laboratory of the Institute of Biotechnology, University of Helsinki. Statistical analyses were performed in R.

## Results

The four most frequent amplicon sequence variants in the microbiota data were *Staphylococcus auricularis*, *Propionibacterium acnes*, *Alloiococcus otitis*, and *Turicella otitidis*. The swabbing method is feasible for EAC microbiota sample collection.

Typically, the dominant amplicon sequence variant in a sample was one of the most frequent bacteria, but there were also subjects where the dominant species was not among the most frequent ones (Figure 1). No significant differences were found in the bacterial compositions when compared with sex, age and sampling season (spring and autumn) (Table 1). However, ear cleaning habit with swabs altered the EAC microbiome, and more specifically, the genus *Alloiococcus* was least common in females who reported cleaning their ears (Figure 2).

Subjects with a high relative abundance of *Alloiococcus* typically had a low abundance of *Staphylococcus*, which may be a sign of the two being competing members of the microbial community.

## Conclusions

The most common bacteria in the microbiome of the healthy EAC were *Staphylococcus auricularis*, *Propionibacterium acnes*, *Alloiococcus otitis*, and *Turicella otitidis*. The EAC microbiota seems more diverse and individualized than previously thought. Also, ear cleaning habits seem to alter the EAC microbiome.

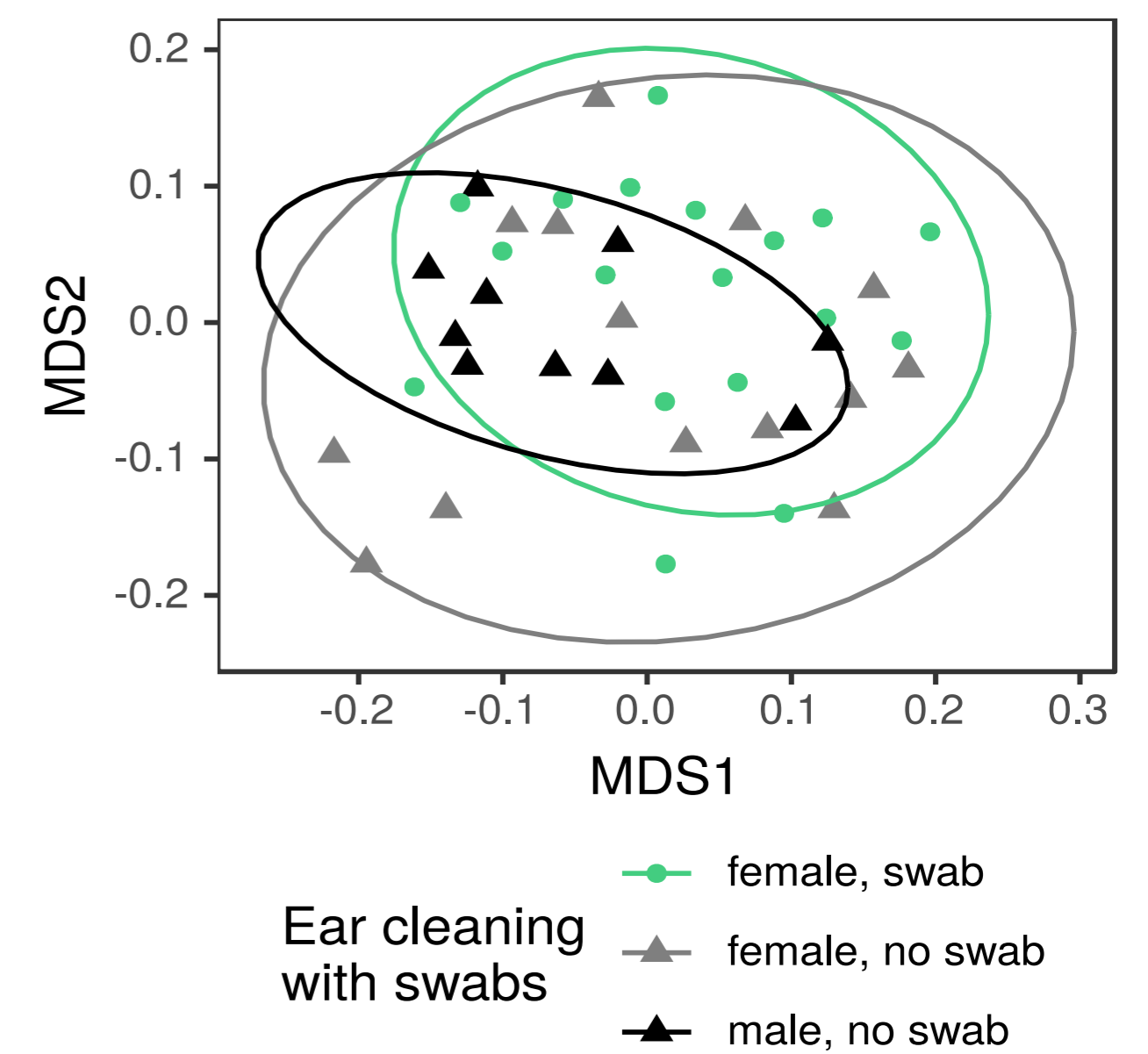


Figure 2: NMDS ordination contrasting males and females according to ear-cleaning habits. Each point is one sample, points closer to one another indicate more similar samples. Ellipses represent 90% confidence level. NMDS indicates nonmetric multidimensional scaling.

Table 1: Results of beta diversity comparisons with Adonis.

|   | P-value |
|---|---------|
| Ear cleaning with swabs                 | 0.0159  |
| Female+swab/female+no swab/male+no swab | 0.0274  |
| Sex                                     | 0.0691  |
| Dominant side                           | 0.1317  |
| Staff vs. student                       | 0.2723  |
| Age                                     | 0.3296  |
| Sampling season                         | 0.9765  |
| Allergy                                 | 0.7846  |

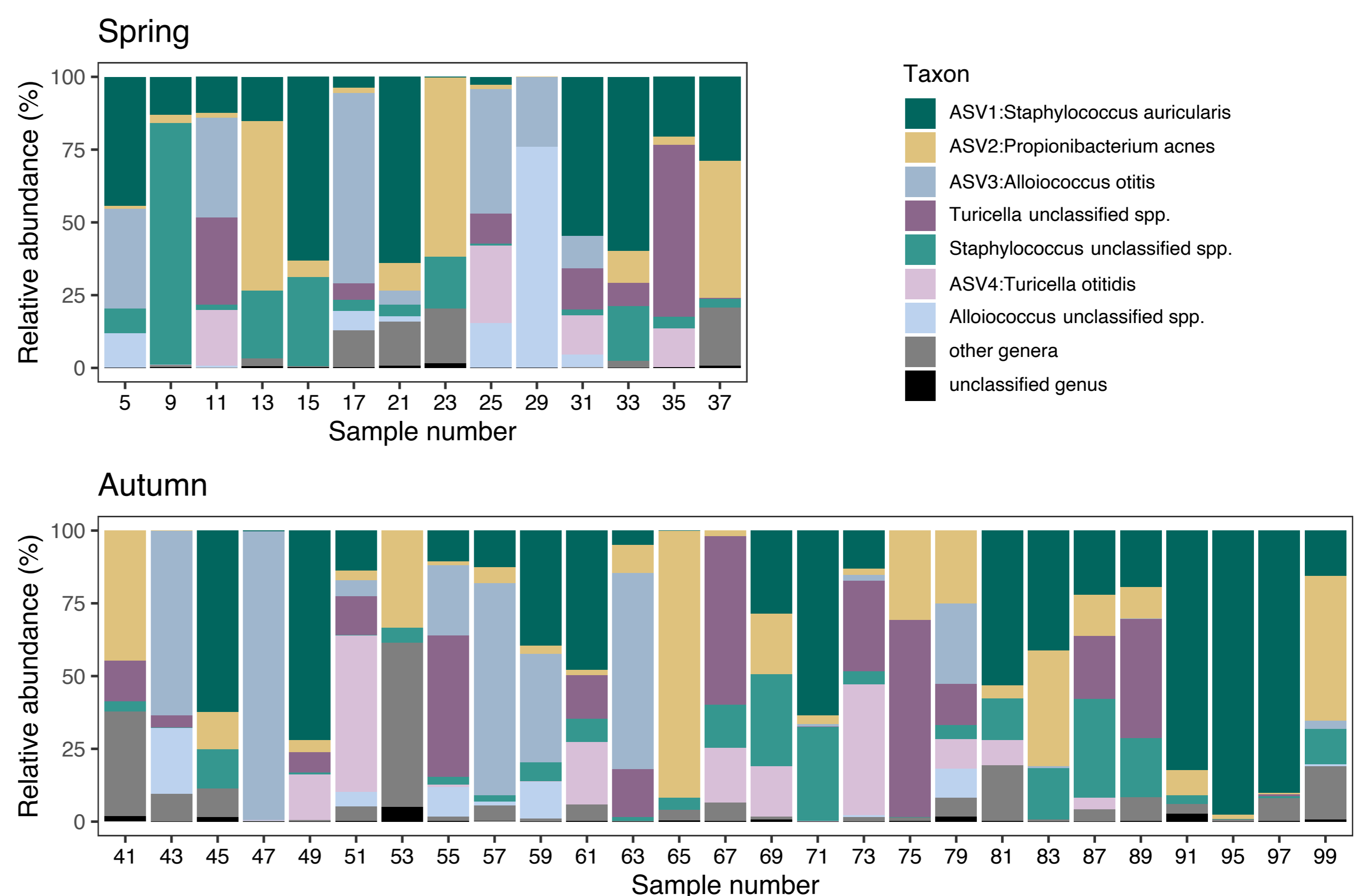


Figure 1: The relative abundances of the most common taxa in the data for each right ear sample, grouped by sampling season/batch