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Characteristics of healthy sinonasal microbiome – single-centre study in the Czech Republic

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Abstract
Introduction: The human nasal cavity and paranasal sinuses host a complex and dynamic microbiome which has a crucial role in mucosal immunity. A comprehensive profile of the healthy sinonasal microbiome remains limited. The purpose of our study was to characterize the healthy sinonasal microbiome in adults using 16S rRNA long-read sequencing to enable species-level resolution, and to assess its associations with demographical and clinical factors such as smoking, allergy history, and olfactory function.
Study design: We performed a prospective, single-centre study analysing middle meatus samples from 27 healthy individuals undergoing septoplasty in the age range from 21 to 57 years, excluding those with antibiotic and corticosteroid use and those with signs of acute or chronic rhinosinusitis.
Results: A high interindividual variability in the composition of healthy sinonasal microbiome was observed. At the phylum level, it was dominated by *Firmicutes* (48.96%), *Actinobacteria* (34.83%), and *Proteobacteria* (13.85%), while *Firmicutes* and *Actinobacteria* were consistently present in all samples. At the genus level, *Staphylococcus* spp. (32.32%), *Cutibacterium* (28.04%), and *Corynebacterium* (4.66%) were most abundant. We observed trend level correlations between phyla and some clinical factors (e.g., smoking and olfactory dysfunction) and selected phyla. However, none remained significant after false discovery rate (FDR) correction across taxa.
Conclusion: The study proposes *Staphylococcus* spp., *Corynebacterium* spp., and *Cutibacterium* spp. to be a core taxa in the healthy sinonasal microbiome. Amid the interindividual diversity in our cohort, there was evidence of a stable core microbiome potentially influenced by environmental and host factors. Our findings suggest a baseline reference for distinguishing a dysbiosis in upper respiratory disease.

Keywords: 16S rRNA sequencing; Healthy individuals; Olfactometry; Sinonasal microbiome

Highlights:
- High interindividual microbiome variability in healthy individuals.
- *Firmicutes* and *Actinobacteria* were consistently present in all samples.
- *Staphylococcus* spp., *Corynebacterium* spp., and *Cutibacterium* spp. dominate the healthy sinonasal microbiome.
- Smoking and hyposmia correlate with reduced microbial diversity.
- Trends between clinical factors (e.g., smoking, hyposmia) and phylum abundances did not remain significant after multiple comparison correction.

Introduction

A microbiome is defined as a community of microorganisms living in a specific environment under specific conditions (Marchesi and Ravel, 2015). The presence of this specific community serves a mutual symbiosis in the human organism, with essential roles in immune modulation and mucosal barrier function (Casadevall and Pirofski, 2015). A shift in this balance may lead to dysbiosis with impact on the host organism (Casadevall and Pirofski, 2015). The nasal cavity is a crucial interface between the external environment and the host immune system, which is continuously exposed to airborne microorganisms, allergens, and air pollution. The human nasal cavity and paranasal sinuses house a complex bacterial community. Recently, sinonasal microbiome has come under intensive focus (Mamiňák et al., 2024). However, most of the research focuses on the disease state, such as acute or chronic

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rhinosinusitis, while only few studies profile a healthy sinonasal microbiome. Nevertheless, differences in sampling methodology between studies are still observed, as well as a lack of understanding of the healthy core microbiome (Lu et al., 2018).

Microbiome composition is commonly characterized through sequencing of the 16S ribosomal RNA gene, which provides genus-level and, more recently, species-level resolution. This approach enables classification of bacterial communities into operational taxonomic units (OTUs), representing groups of genetically related taxa (Lladó Fernández et al., 2019). Based on genetic methods, bacteria can be assigned to 25 phyla, which are further subdivided into genera and individual species. In the sinonasal region, the most frequently represented phyla include *Firmicutes, Actinobacteria, Proteobacteria*, and *Bacteroidetes*. Dominant genera comprise *Staphylococcus, Corynebacterium, Moraxella, Heamophilus*, and *Streptococcus*. Species such as *Staphylococcus aureus* and *Corynebacterium accolens* are among the most frequently identified (Anderson et al., 2016; Bassiouni et al., 2020; Mahdavinia et al., 2018).

In a previous study, a probable core sinonasal microbiome was described to compose of *Corynebacterium, Staphylococcus, Moraxella, Streptococcus*, and *Haemophilus* genera – regardless of geography (Paramasivan et al., 2020). However, other studies presented a high burden of *Corynebacterium* and *Staphylococcus* genera, with low abundance of *Moraxella* and *Haemophilus* genera in the bacterial composition of the microbiome of healthy individuals (Aurora et al., 2013; Bassis et al., 2014; De Boeck et al., 2017; Rasmussen et al., 2000).

The composition and diversity of microbial community is dynamic and changes under the influence of local host-immune interactions, medications, and environmental factors. Changes in human sinonasal microbiome impacted by air pollution, tobacco smoking and vaping, and by cooking fumes have been described (Fuochi et al., 2021; Jin et al., 2023; Pfeiffer et al., 2022; Toro-Ascuy et al., 2023). Previous studies have already documented that the bacterial composition of microbiome is significantly involved in allergic inflammation of nasal cavity and paranasal sinuses (Chen et al., 2022; Lal et al., 2017; Orlandi et al., 2016). Furthermore, the use of intranasal medication and widespread use of antibiotics influence the structure of human microbiome and disrupt local immunoregulation (Fernández-Rodrígez et al., 2024; Head et al., 2016; Raita et al., 2021; Ramakrishnan et al., 2018). Previous insights into the relationship between sinonasal microbiome and olfactory function suggest a difference between the composition of sinonasal microbiome in hyposmic and normosmic healthy individuals (Han et al., 2023; Koskinen et al., 2018; Pereira et al., 2017; Thangaleela et al., 2022).

This single-centre study aimed to characterize the healthy sinonasal microbiome in healthy individuals without signs of inflammation, recent antibiotic and steroid use. For a deeper understanding of the microbiome composition in healthy nasal cavity and paranasal sinuses, and to find changes in its composition which could lead to an impact balance or support dysbiosis, we have analysed samples from healthy individuals using 16S rRNA sequencing. Samples were taken during surgery for septal deviation in standardized and endoscopy guided protocol.

The objective of this study was to define the characteristics and variability of bacterial taxa in healthy sinonasal cavity, and to explore possible associations between microbiome profiles and clinical features such as allergy, smoking, and olfactory function to determine the possibility of a shift into a disease state.

Materials and methods

Study design

We performed a prospective, original study on sinonasal microbiome in patients without chronic rhinosinusitis selected from the Department of Otorhinolaryngology and Maxillofacial surgery of Military University Hospital in Prague, from November 2022 to October 2024. We enlisted 27 patients scheduled for septoplasty, who did not meet the criteria of acute or chronic rhinosinusitis or allergic rhinitis, and presented only with septal deviation (Fokkens et al., 2020). The exclusion criterium for all enlisted patients was not having used oral or intranasal corticosteroids and antibiotics for at least 8 weeks prior to sample collection. Enlisted patients were aged over 18 and under 80. No pregnant, lactating, or patients undergoing oncologic therapy were involved. All patients signed informed consent, and the study was approved by the ethical committee of the Military University Hospital.

Clinical and demographic data collection

Clinical and demographic data were collected prior to scheduled surgery. We focused on data about age, sex, smoking, allergies, bronchial asthma and use of antibiotics, topical and systemic steroids. Allergies were assessed by patients' medical history. We also included the 22-item Sino-Nasal Outcome Test (SNOT-22) questionnaire filled prior to surgery (Hopkins et al., 2015). Examination of the sense of smell was performed by full Sniffin' Stick Identification test (Burghart Instruments, Wedel, Germany). Hyposmia is the score of the Sniffin' Stick test between the score of 8 to 11 of correct identifications (Červený et al., 2022; Wolfensberger et al., 2000). During endoscopic surgery after standard surgical skin preparation, we obtained a sample via FloQSwabs from a left middle nasal meatus regardless the presence of a septal deviation. The sample was placed in DNA/RNA Shield^{TM} Reagent R1100 and stored at –20 °C.

DNA extraction and sequencing

Acquired samples were transported to a specialized laboratory in cooled boxes. DNA from the swabs was isolated by DNeasy PowerSoil Pro Kit – QIAGEN, as per manufacturer's instructions. The DNeasy PowerSoil Pro Kit is optimized for high microbial DNA yield while minimizing host DNA contamination, it's bead-beating step and robust buffer system make it especially effective for low-biomass or complex samples (Pu et al., 2025). Quality control of extracted DNA was provided by Qubit 1× dsDNA Broad Range Assay Kit and Qubit 1× dsDNA High-Sensitivity Assay Kit. The V1–V9 regions of 16S rRNA gene of the bacterial DNA were amplified by metagenomic sequencing of bacterial 16S rDNA by Oxford Nanopore Technologies Ligation Sequencing Kit V14 (SQK-LSK114), using primer 27F (locus specific sequence AGRGTTYGATYMTGGCTCAG) and primer 1492R (locus specific sequence RGYTACCTTGTTACGACTT) (Ludwig, 2007; Weisburg et al., 1991). The acquired PCR products were paired and quality checked by Qubit 1× dsDNA High-Sensitivity Assay Kit and Quant-iTTM 1× dsDNA HS Assay. By sequencing, we obtained 3,547,119 reads in total and from 9,906–147,189 reads per sample, creating a median of 67,939 reads per sample. All reads were shortened from 5' and 3' ends by 80 nucleotides, in order to remove low sequencing quality ends. Reads below sequencing quality q15, shorter than 1,000 nucleotides, and longer than 2,000 nucleotides were eliminated.

Basic data analysis and raw data processing

Raw data were automatically processed by MinKnow 24.11.8 software interface (ONT) in default settings. The basecalling was carried out using DORADO basecalling software version 0.8.3. Demultiplexed reads filtering was based on reads length using NanoFilt version 2.8.0. Relative abundance analysis was done by EMU software version 2.28, using Silva database with keep read counts. Reads from mt 16SrDNA were expelled during the alignment step to Silva database (Bars-Cortina et al., 2023).

Positive and negative controls and microbial standards were used as a standard internal quality check of sequencing outcomes in the laboratory.

Statistical analysis

Clinical and demographic characteristics of patients were analyzed in R software (v4.3.3) using *t*-test, Wilcoxon test, Chi-square test, and Fisher's Exact test. All subsequent microbiome analyses were conducted in Python (v3.12.7). Filtered sequencing data was used to evaluate bacterial diversity, relative abundance, and composition of the microbiome. Relative proportions of bacterial phyla, genera, and species displays were performed using Mann–Whitney *U*-tests. The most abundant taxa were visualized using stacked bar plots and horizontal bar charts. To evaluate correlations between clinical and demographic variables and microbial abundances, Spearman rank correlation coefficients or Mann–Whitney *U*-tests were computed (Feng et al., 2022). Correlation heatmaps were generated using Seaborn, with significance thresholds set at $p < 0.05$ (*), $p < 0.01$ (**), and $p < 0.001$ (***). Reported *p*-values were adjusted for multiple testing using the Benjamini–Hochberg false discovery rate (FDR) procedure, applied within each clinical variable across all taxa. We report FDR adjusted q values with significance set at $q < 0.05$. The study power was calculated as 70.6 % for medium effect size.

Ethical approval and consent to participate

All patients signed an informed consent form. The study was approved by the ethical committee of the Military University Hospital, Number 108/16-49/2021 (Project of Ministry of Health NU 22-09-00493).

Table 1. Demographic characteristics

Characteristic	HC (mean ± SD or count %)
Age	39.22 ± 9.85
SNOT-22	24.93 ± 14.23
Male	22 (81.5%)
Allergy	14 (51.9%)
Asthma	5 (18.5%)
Smoking	6 (22.2%)
Anosmia	0 (0.0%)
Hyposmia	10 (37.0%)
OERP	22 (81.5%)

Note: Demographic and clinical data of studied cohort ($n = 27$) demonstrated in mean with SD (standard deviation) or in percentage. Age was calculated in years at the time of sampling ($n = 27$). HC stands for healthy individuals. Male, Female, and Other gender was obtained by questionnaire. SNOT-22 stands for 22-item Sino-Nasal Outcome Test. Allergy stands for any kind of allergy without signs of allergic rhinitis. Asthma means Bronchial Asthma in medical history. Anosmia and Hyposmia were tested by Sniffin' Stick test.

Results

The age range of patients was from 21 to 57 years, with a mean age of 39. In the studied group, male gender was highly predominant (81.5%). From anamnestic data collection, we observed that 14 (52%) of patients had some kind of allergy and 5 (18.5%) individuals suffered from bronchial asthma. 6 (22.2%) patients were tobacco smokers, 10 (37%) presented with hyposmia, and no patients presented with anosmia. The mean SNOT-22 outcome was 24.93, which can be influenced by the septal deviation. All described demographic and clinical data are presented in Table 1.

Statistical analysis of present bacterial phyla in the studied cohort was performed by Mann–Whitney *U*-tests on mean relative abundance of the phyla. The most abundant phylum in the healthy sinonasal group was *Firmicutes*, comprising 48.96% of the total bacterial sequences on average. This result suggests that they may play a central role in maintaining mucosal health and immune regulation in the sinonasal cavity. Known genera like *Staphylococcus* spp. and *Streptococcus* spp. belong to the *Firmicutes* phylum. The second most abundant phylum was *Actinobacteria* in a mean relative abundance of 34.83%. This is associated with a beneficial commensal like *Corynebacterium* spp. Phylum *Proteobacteria*, including genera like *Haemophilus* spp. and *Pseudomonas* spp. was the third most abundant in 13.85% of sequences. *Bacteroides* and *Cyanobacteria* are present in low mean relative abundance (1.57% and 0.36%, respectively), proposing a minor however possibly functional presence in the ecosystem. These top five phyla are shown in Fig. 1. The dominance of *Firmicutes* and *Actinobacteria* with low abundance of inflammatory-associated phyla suggests homeostatic microbial profiles (Chen et al., 2022). Fig. 2. Shows the relative proportions of bacterial phyla in all studied individuals. The most dominant phyla across samples in varying proportions are *Firmicutes, Actionobacteria*, and *Proteobacteria*, though *Bacteroides, Fusobacteria*, and *Cyanobacteria* phyla appear sporadically and in low proportions. Fig. 2. shows a notable variability in microbial composition across samples, which may indicate a personalized sinonasal microbiome even among healthy individuals. Despite the diversity, *Firmicutes* and *Actinobacteria* are present in nearly all samples, indicating these as core components of a healthy sinonasal microbiome.

Similarly, we analyzed the mean relative abundance of sequenced bacteria on the genus and species level. On the genus level, the most dominant bacteria found was *Staphylococcus* genus, with a mean relative abundance of 32.32% — including both commensal and opportunistic species. The second most abundant genus was *Cutibacterium* (28.04%), formerly known as *Propionibacterium*. The remaining of the five most abundant genera were *Pseudomonas, Corynebacterium*, and *Peptoniphilus* (in low mean abundance of 5.11%, 4.66%, and 4.11%, respectively). *Pseudomonas* genera contain both commensal and opportunistic members. *Corynebacteium* is known to inhibit the growth of *S. aureus* (Huang et al., 2022; Paramasivan et al., 2020). The role of *Peptoniphilus* genera is unclear. Relative proportions of bacterial genera in all studied individuals are proportionally displayed in Fig. 3. On the other hand, Fig. 4. contains the ten most relative abundant species found in the obtained samples. The most abundant bacterium was *Cutibacterium acnes* (21.13%), the second most present was *Staphylococcus aureus* (14.07%), suggesting possible carriage in healthy

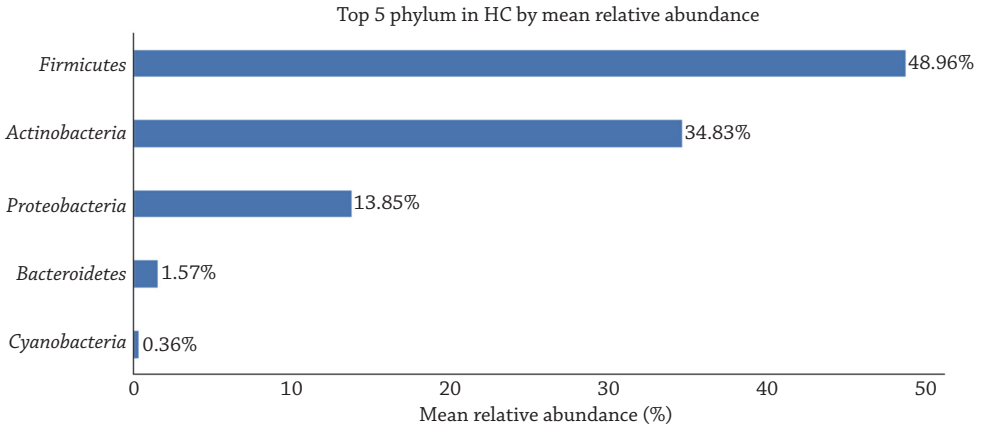

Fig. 1. Top five most abundant bacterial phyla processed on relative proportions of by using Mann–Whitney *U*-tests are shown and displayed in horizontal bar charts with percentage. HC stands for healthy individuals (n = 27).

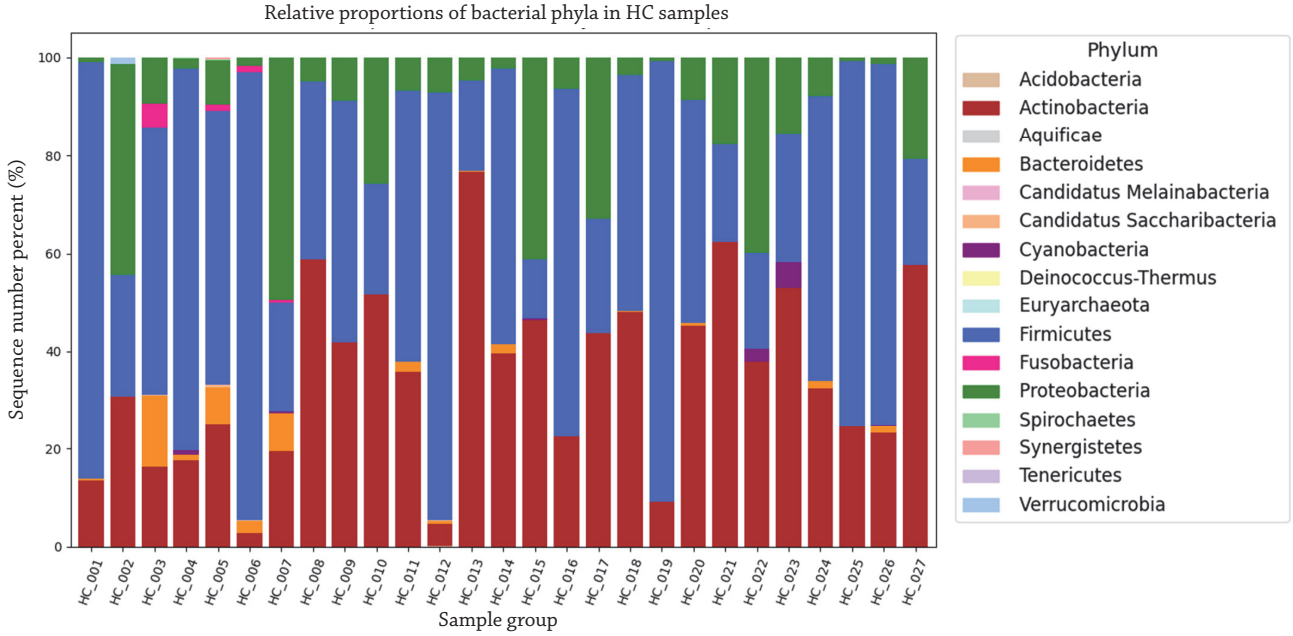

Fig. 2. Relative proportions of bacterial phyla were performed using Mann–Whitney *U*-tests. Relative proportions are visualized using stacked bar plots for every studied individual. Bacterial phyla are shown by colours assigned in the legend in the right upper corner (n = 27).

individuals without overt inflammation. In an almost similar abundance of 13.56% was *Staphylococcus epidermidis*. An opportunistic bacterium, *Pseudomonas putida*, was present in low abundance (4.27%), as well as anaerobic commensal *Peptophilus lacrimalis* (3.91%). *Corynebacterium accolens*, a commensal associated with the inhibition of *S. aureus*, was present in a very low abundance of 2.46%.

We have correlated clinical and anamnestic features of the studied cohort in a relationship to bacterial phyla burden by Spearman rank correlation coefficients and created a heatmap (Fig. 5). The heatmap reveals generally weak to moderate correlations between certain bacterial phyla and clinical or demographic variables. Positive correlations are shown in blue and negative in red. No statistically significant correlations were found. Correlations of bacterial phyla with age are generally weak across all samples, showing no associations between age and bacterial composition in healthy individuals. Slight negative correlations with smoking and bacterial phyla *Fusobacteria* (r = –0.33), *Bacteriodetes* (r = –0.33), and *Spirochetes* (r = –0.37) were observed at the uncorrected level. SNOT-22 outcome was positively correlated at the uncorrected level with phyla in low abundance (*Spirochetes* and *Verrucomicrobia*, r = 0.30 and r = 0.28). Association of bacterial phyla and allergy has shown light positive correlation with *Firmicutes* (r = 0.22) and negative correlation with *Proteobacteria* (r = –0.33) at the uncorrected level. Negative correlation between hyposmia and *Cyanobacteria* is the strongest observed correlation of medium effect r = –0.5 (p < 0.01) at the uncorrected level. Negative correlation between hyposmia and *Spirochetes* was present at r = –0.38 (p < 0.05). Negative correlation with *Proteobacteria* (r = –0.37) was observed at the uncorrected level. None of the stated correlations remained significant after FDR correction ($q \geq 0.05$).

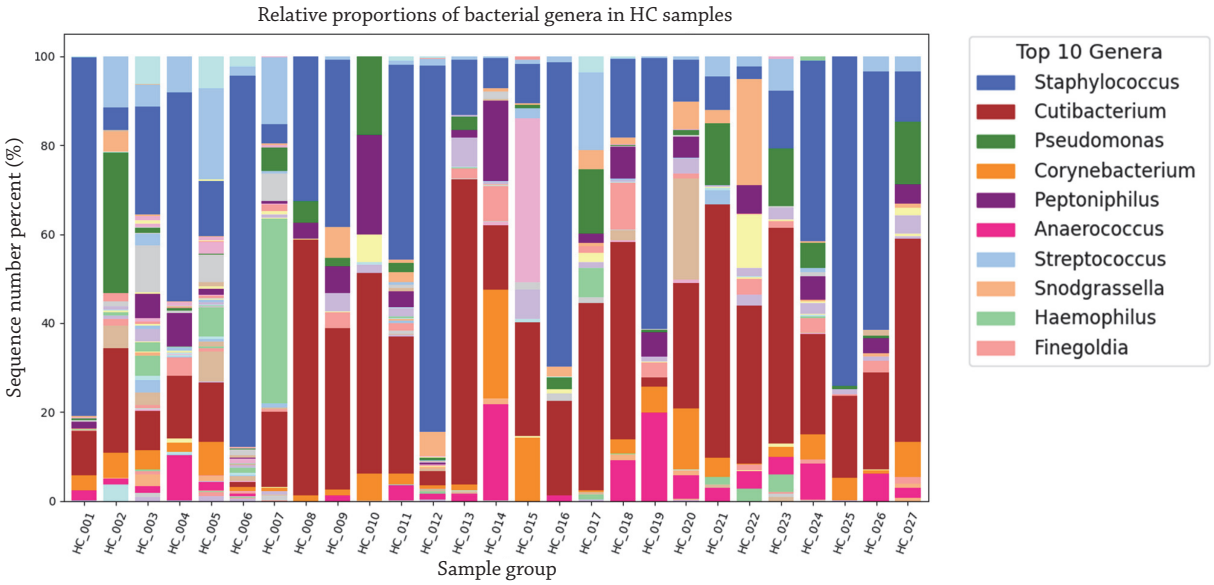

Fig. 3. Relative proportions of bacterial genera were performed using Mann–Whitney *U*-tests. Relative proportions are visualized using stacked bar plots for every studied individual. Bacterial genera are shown by colours assigned in the legend in the right upper corner (n = 27).

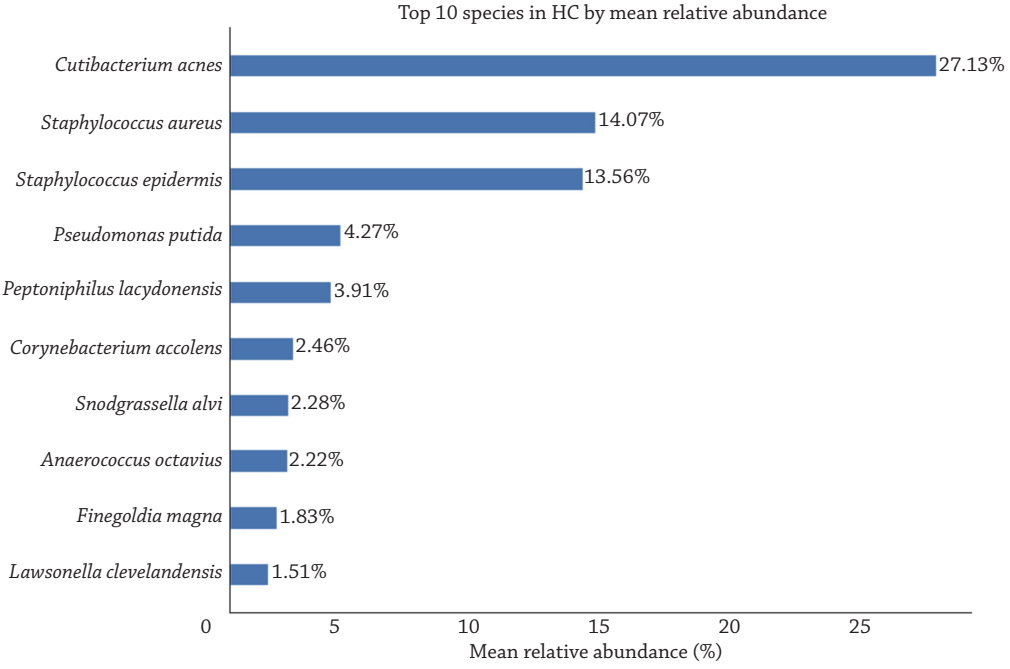

Fig. 4. Top ten most abundant bacterial species processed on relative proportions of by using Mann–Whitney *U*-tests are shown and displayed in horizontal bar charts with percentage. HC stands for healthy individuals (n = 27).

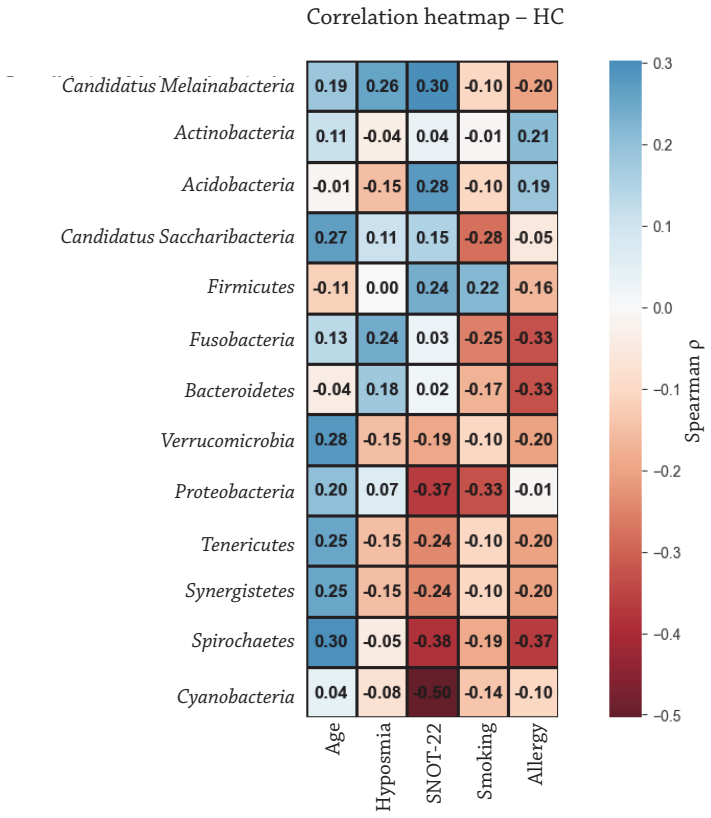

Fig. 5. Associations between demographical and clinical data using Spearman rank correlation coefficients were computed. Correlation heatmap was generated using Seaborn, with significance thresholds set at $p < 0.05$ (*), $p < 0.01$ (**), and $p < 0.001$ (***). *P*-values were adjusted for multiple testing using FDR (Benjamini–Hochberg) within each clinical variable; no associations met $q < 0.05$. The heatmap shows thirteen bacterial phyla in correlation with anamnestic and evaluated data from all healthy individuals ($n = 27$). SNOT-22 stands for 22-item Sino-Nasal Outcome Test ($n = 27$). Age was calculated in years at the time of sampling ($n = 27$). Hyposmia was tested by Sniffin' Stick test ($n = 10$). Allergy stands for any kind of allergy without signs of allergic rhinitis ($n = 14$). Smoking stands for tobacco smoking in medical history ($n = 6$).

Discussion

This study was a single centre performed research focused on investigating characteristics of a healthy sinonasal microbiome. We performed standardized sample acquisition and 16S rRNA sequencing on bacterial species level. We preferred using Oxford Nanopore Technologies Ligation Sequencing analysis with long-reads to obtain results to the species level. It is more fitting to small cohort analysis, giving it a distinct advantage over the commonly used short-read Illumina sequencing method that has higher error rate in small cohorts and only delivers analysis to genus level (Quail et al., 2008; Sheka et al., 2021). Bacterial taxa 16S results were not analyzed by qPCR, which we acknowledge as a study limitation.

Although several authors distinguish the term 'bacteriome', we use 'microbiome' in line with prevailing usage in sinonasal literature. The microbiome composition was not affected by use of antibiotics and corticosteroids, acute or chronic inflammation of nasal cavity and paranasal sinuses. However, quite a small cohort of healthy individuals was investigated. There is a notable variability in the microbial composition across study samples, indicating a personalized sinonasal microbiome – even in healthy individuals.

Most studies focusing on sinonasal microbiome describe changes in microbiome in a disease state, but few focus on exploring the composition of this microbiome in a healthy state. We found *Firmicutes* (48.96%) and *Actinobacteria* (34.83%) phyla in dominant abundance – and their presence in nearly all samples. This reflects their probable role in mucosal immune regulation and colonization resistance. *Staphylococcus* spp. (*Firmicutes* phylum) together with *Corynebacterium* spp. (*Actinobacteria* phylum) formed a significant part of total bacterial abundance (36%).

Paramasivan et al. (2020) described a core sinonasal microbiome in multicentric study to be similar in healthy individuals as in patients with chronic rhinosinusitis (CRS). This healthy core microbiome was composed of *Corynebacterium, Staphylococcus, Moraxella, Streptococcus*, and *Haemophilus* genera. Kumpitsch et al. (2019) and Toro-Acuy et al. (2023) also delineated *Corynebacterium, Staphylococcus, Moraxella, Streptococcus*, and *Haemophilus* spp. as the most common genera in healthy nasal cavities.

In contrast, *Moraxella* and *Haemophilus* genera were found in very low abundance in our studied cohorts, suggesting that the healthy core microbiome could be composed only from *Staphylococcus* spp., *Streptococcus* spp., and *Corynebacterium* spp. Supporting our findings, Bassis et al. (2014) also presented a high abundance of *Corynebacterium* spp., *Propionibacterium* (now *Cutibacterium*), and *Staphylococcus* spp. in all samples from healthy individuals together with low abundance of *Moraxellacae* spp.

Ramakrishnan et al. (2018) also investigated a healthy sinonasal microbiome from middle nasal meatus sampling

founding a high prevalence and abundance of *Corynebacterium* spp., *Staphylococcus* spp. and *Propionibacterium* (now *Cutibacterium*). Recent findings indicate the core sinonasal microbiome of healthy individuals is composed of *Corynebacterium* spp. and *Staphylococcus* spp., with wide interindividual differences in the rest of the microbial composition (Aurora et al., 2013; Bassis et al., 2014; Ramakrishnan et al. 2018; Rasmussen et al., 2000).

The high abundance of *Staphylococcus aureus* (14.07%) in our samples in individuals with no signs of acute or chronic inflammation supports the theory of a commensal carrier state, in which the healthy host-microbiome balance suppresses its pathogenic behaviour (Chen et al., 2022; Huang et al., 2022; Krismer et al., 2017; Lal et al., 2017; Lu et al., 2018; Toro-Ascuy et al., 2023). This theory also supports the presence of *Corynebacterium accolens* (2.46%), the bacteria known to inhibit *Staphylococcus aureus* shifting into a pathogenic state (Huang et al., 2022; Konovalovas et al., 2024).

Similar findings were stated in the study by Paramasivan et al. (2020). They observed a depletion in abundance of *Corynebacterium* spp. and over-presentation of *Staphylococcus* spp. in samples from healthy individuals collected from Amsterdam in comparison with samples from Asia, Australia and America, addressing it as a possible unique European profile.

Aurora et al. (2013) presented the importance of *Cyanobacteria, Bacteroides*, and *Propionibacterium* (*Cutibacterium* spp.) in healthy nasal cavity, high abundance of *Cutibacterium acnes* (21.13%) in our studied cohort supports these findings. *Bacteroides* and *Cyanobacteria* phyla were present at lower levels of abundance in our samples, indicating their niche role in the sinonasal environment. These uncommon phyla are also assumed to be environmentally impacted (Gisler et al., 2021; Kaspar et al., 2016; Raita et al., 2021; Yan et al., 2013). They were similarly depleted in our patients who were smokers and had an olfactory dysfunction.

It has already been described that tobacco smoking and vaping supress microbial diversity (Fuochi et al., 2021; Gisler et al., 2021; Pfeiffer et al., 2022). Our correlation analysis revealed depletion in abundance of majority of bacterial phyla in smoking healthy individuals, however any of these correlations were statistically significant. The mild positive correlation between *Firmicutes* and allergic status found in our cohort is supported by similar results in the study by Chen et al. (2022). The SNOT-22 slightly elevated mean result may be altered by the septal deviation and not necessarily reflect dysbiosis or ongoing inflammation, since we have not found any correlation with increase or decrease of the bacterial phyla (Buckland et al., 2003).

Olfactory function may be impacted by nasal obstruction, local inflammation, head trauma, or nasal surgery. Changes in composition of the sinonasal microbiome can also play a role in decreasing olfactory function. Koskinen et al. (2018) found that *Proteobacteria, Actinobacteria, Firmicutes*, and *Bacteroidetes* were associated with poor odor identification.

In our study, only *Firmicutes* phylum was positively correlated with olfactory dysfunction, while *Actinobacteria* and *Bacteroidetes* had no correlation. We also observed trend-level negative correlations of olfactory dysfunction with *Cyanobacteria, Spirochetes*, and *Proteobacteria*, suggesting that low abundance of these phyla may play a role in olfactory pathways. However, these did not remain significant after FDR correction (Song et al., 2025). *Cyanobacteria* are considered to be non-resident transient organisms in the human microbiome. Biswas et al. (2023) did not observe any significant differences in bacterial diversity between bacterial samples from individuals with olfactory dysfunction and those with normal olfactory function.

It should be stated that a partial nasal obstruction in septal deviation could influence our results in terms of hyposmia. More olfaction-focus studies analyzing microbial composition and microbial diversity should be performed to further explore these interactions based on the difference between recent findings. Standard statistical analysis of binary demographic data was not performed due to the small size of the studied cohort, which is acknowledged as a serious study limitation.

Conclusion

We presented data supporting possible characteristics of a healthy core sinonasal microbiome, with individual diversity resulting from environmental, geographical, and host-immune factors. *Staphylococcus* spp., *Cutibacterium* spp. and *Corynebacterium* spp. emerged as the most abundant genera, supporting their central role in microbiome balance maintenance and mucosal immune regulation. The definition of a stable core microbiome in a healthy individual can create a baseline to recognize disease severity, according to its composition changes. The observed association in olfactory dysfunction and microbiome changes highlights a potential microbial component in a sense of olfaction loss. Further investigation of healthy sinonasal microbiome on a larger scale and multi-centre composition is necessary to bring new perspectives on healthy core sinonasal microbiome.

Authors' contributions

MK was the first author of this publication. *JA* and *MK* were involved in the design of this study. *MK, JK*, and *HR* were involved in the recruitment of patients and data collection. *MK, HR, FT*, and *KD* were responsible for the microbiome sampling of patients. *PA* performed data analyses and manuscript review. *JA* was the supervisor of the project and contributed to the manuscript. All authors discussed the results and read and approved the final manuscript.

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Ethical aspects and conflict of interest

The authors have no conflict of interest to declare.

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