Journal of Chemical Health Risks

www.jchr.org

JCHR (2026) 16(2), 594-603 | ISSN:2251-6727

# Oral and Gut Microbial Connectivity in Healthy Adults Revealed by Full-Length 16S rRNA Nanopore Study

**Pallavi S P[1], Hem Chandra Pant[1*], Ashok Kumar[2], Naveen Gaurav[3]**

School of Pharmaceutical Science, Jigyasa University (Formerly Himgiri Zee University), P.O. Selaqui, Chakrata Road Dehradun 248011, (Uttarakhand), India1

School of Pharmacy Research, Dev Bhoomi Uttarakhand University, Dehradun, 248007 (Uttarakahnd), India2

Department of Biotechnology, Shri Guru Ram Rai University, West Patel Nagar, Dehradun 248001,(Uttarakhand), India3

***(Received: 05 January 2026 Revised: 15 February 2026 Accepted: 05 March 2026)***

**KEYWORDS**

Oral microbiome; Gut microbiome; Iron-associated bacteria; Nanopore sequencing; Full-length 16S rRNA; Healthy adults

**ABSTRACT:**

**Background:**

The oral cavity and gastrointestinal tract harbor distinct yet interconnected microbial ecosystems that influence host metabolism and immune homeostasis. While oral–gut microbial interactions have been implicated in disease states, baseline data describing microbial connectivity and iron-associated taxa in healthy, non-anemic adults remain limited. Advances in long-read sequencing now allow high-resolution profiling of microbial communities across anatomical niches.

**Methods:**

This observational study analyzed paired oral and stool samples from five healthy, non-anemic adult volunteers. Full-length 16S rRNA gene sequencing was performed using Nanopore technology to achieve high taxonomic resolution. Sequencing data underwent quality control, taxonomic assignment, and comparative analysis to evaluate site-specific microbial composition, shared taxa, and the distribution of iron-associated bacterial genera. All participant identifiers were anonymized prior to analysis.

**Results:**

Distinct microbial signatures were observed between oral and gut samples. The oral microbiome was dominated by genera such as *Streptococcus*, *Veillonella*, and *Prevotella*, whereas the gut microbiome exhibited greater diversity with enrichment of *Bacteroides*, *Faecalibacterium*, and *Ruminococcus*. Despite strong site specificity, a subset of bacterial genera was shared between oral and gut niches, most Just state the fact *Prevotella* and *Fusobacterium*. Several iron-associated bacterial taxa were detected across both sites, although their relative abundance differed by anatomical location. Gut samples demonstrated higher microbial richness and evenness compared to oral samples, consistent with established ecological differences.

**Conclusion:**

Healthy adults exhibit pronounced oral–gut microbial compartmentalization alongside limited but consistent microbial overlap. The presence of shared iron-associated taxa suggests a functional dimension to oral–gut microbial connectivity under physiological conditions. These findings establish a high-resolution baseline for healthy microbiomes and provide a reference framework for future studies investigating microbiome alterations in iron-related disorders and disease states.

Journal of Chemical Health Risks

www.jchr.org

JCHR (2026) 16(2), 594-603 | ISSN:2251-6727

## 1. Introduction

The human microbiome is an assemblage of complex microbial communities that inhabit distinct anatomical niches and exert profound influences on host physiology and disease susceptibility. The oral cavity and the gut represent two contiguous but ecologically distinct habitats whose resident microbiota have traditionally been studied in isolation. Recent syntheses, however, emphasize a growing appreciation for bidirectional interactions between oral and gut microbial communities, including microbial translocation, shared taxa, and metabolite-mediated crosstalk that together shape mucosal immunity and systemic health [1,2]. Studies in healthy cohorts have begun to map the landscape of shared and niche-specific taxa, revealing that while each site maintains a characteristic community fingerprint, a subset of taxa many with metabolic flexibility are recovered from both sites, suggesting potential routes of continuity along the alimentary tract [2,3].

Mechanistically, the oral–gut axis may operate through multiple pathways: direct swallowing and survival of oral microbes in the gastrointestinal tract; modulation of host inflammatory tone by oral pathobionts that influences gut barrier function; and metabolite-driven effects such as short-chain fatty acids, bile acid transformations, and iron-related metabolites that alter local microbial ecology and host responses [1,4]. Let reviewers decide importance, evidence indicates that even in the absence of overt disease, mouth-to-gut microbial exchanges occur and may contribute to early shifts in intestinal community structure that precede clinical pathology [2]. Understanding the baseline patterns of oral–gut connectivity in healthy adults is therefore essential both to interpret perturbations seen in disease and to identify candidate taxa and functions that bridge these habitats.

Iron metabolism sits at an intriguing intersection of host and microbial ecology. Iron is a critical micronutrient for both host and microbes, and its availability is tightly regulated by host pathways. Fluctuations in iron levels, whether through dietary intake, supplementation, or inflammatory sequestration, can reshape microbial communities by favoring taxa with specialized iron acquisition or heme-utilization systems [5,6]. Reviews and experimental studies illustrate that iron supplementation and altered iron status can increase the abundance of opportunistic and pathogenic taxa in the gut, perturb metabolite profiles, and in some settings exacerbate mucosal inflammation [5,6]. Conversely, the microbiota itself influences host iron homeostasis via modulation of intestinal absorption and by generating metabolites that alter iron bioavailability [4]. Given these bidirectional links, investigations that explicitly probe iron-associated taxa across oral and gut niches in healthy, non-anemic adults promise to clarify whether iron-handling microbes form part of the oral–gut continuum and whether they might serve as early indicators of systemic iron–microbiome interplay.

Technological advances in long-read sequencing, particularly full-length 16S rRNA gene sequencing using Oxford Nanopore platforms, now permit improved species-level resolution in complex community surveys and a more accurate assessment of microbial connectivity across sites. Implementation studies have demonstrated that full-length 16S approaches enhance taxonomic fidelity and can be deployed in clinical and research settings to recover taxa that short-read amplicon strategies may miss or ambiguously assign [7–9]. Methodological comparisons also highlight primer choice and analytic pipelines as critical determinants of sensitivity and specificity when profiling diverse matrices such as saliva and stool, making careful protocol selection essential for cross-niche comparisons [8]. Bringing these high-resolution molecular tools to paired oral and stool sampling enables more precise mapping of shared taxa and functional potentials such as siderophore systems or heme uptake genes that relate to iron metabolism.

Despite the conceptual and technological readiness, few studies have systematically characterized oral–gut microbial connectivity in healthy, non-anemic adults using full-length 16S approaches and explicitly examined iron-associated bacterial taxa. Most work to date has focused on disease cohorts periodontitis, inflammatory bowel disease, colorectal cancer where oral-to-gut translocation and iron dysregulation are implicated, but the baseline patterns in healthy populations remain incompletely described [1,10]. Establishing a rigorous, well-annotated healthy reference is therefore a necessary precursor to interpreting disease-associated perturbations

Journal of Chemical Health Risks
www.jchr.org
JCHR (2026) 16(2), 594-603 | ISSN:2251-6727

and for testing hypotheses about microbial roles in iron homeostasis.

In this manuscript we present a focused analysis of paired oral and stool microbiomes from healthy, non-anemic adult volunteers using full-length 16S rRNA gene sequencing. Our objectives are to characterise site-specific and shared community composition at high taxonomic resolution, to identify iron-associated bacterial genera and their distribution across the oral–gut axis, and to provide a baseline dataset against which future clinical and interventional studies can be compared. By integrating careful participant phenotyping with contemporary long-read sequencing and transparent analytic workflows, this work aims to map the microbial connectivity that underlies oral and gut ecosystems in health and to highlight taxa of potential interest for iron-related host–microbe interactions.

## 2. Objectives

The primary objective of this study was to characterize and compare the composition of the oral and gut microbiomes in healthy, non-anemic adult volunteers using full-length 16S rRNA gene sequencing based on Nanopore technology. By profiling paired oral and stool samples, the study aimed to delineate site-specific microbial signatures and assess the degree of microbial overlap between these two anatomically and functionally distinct niches under physiological conditions.

A secondary objective was to identify and evaluate iron-associated bacterial taxa present in the oral and gut microbiomes and to determine the extent of shared iron-related microbial communities between the two sites. Through genotypic analysis, this study sought to provide baseline evidence for oral–gut microbial connectivity with specific emphasis on bacteria linked to iron metabolism in healthy adults.

## 3. Methodology

### Study Design and Reporting Framework

This study was conducted as an observational, cross-sectional microbiome analysis involving healthy adult volunteers. The methodology was structured and reported in accordance with the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) guidelines to ensure transparency, reproducibility, and methodological rigor. The investigation focused on paired oral and stool samples obtained from the same individuals to enable within-subject comparison of microbial communities across anatomical sites.

### Study Setting and Ethical Considerations

The study was carried out in a controlled research setting with all laboratory procedures performed under standardized conditions. Ethical approval was obtained prior to study initiation, and all participants provided written informed consent. To maintain confidentiality, participant identifiers were anonymized at the time of data acquisition and analysis, and unique study codes were assigned to each participant. No personally identifiable information was used at any stage of data processing or manuscript preparation.

### Participant Selection and Eligibility Criteria

Healthy adult volunteers were recruited based on predefined inclusion criteria. Participants were required to be clinically healthy, non-anemic, and free from acute or chronic systemic illnesses. Individuals with recent antibiotic use, probiotic supplementation, gastrointestinal disorders, oral inflammatory conditions, or known hematological abnormalities were excluded to minimize confounding influences on the microbiome. Only participants meeting all eligibility criteria were included in the final analysis.

### Sample Collection Procedures

Paired oral and stool samples were collected from each participant using standardized, sterile collection protocols. Oral samples were obtained to represent the oral microbiome, while stool samples were collected to characterize the gut microbial community. All samples were collected under aseptic conditions, immediately stabilized, and transported to the laboratory following recommended handling procedures to preserve microbial DNA integrity.

### DNA Extraction and Quality Assessment

Microbial genomic DNA was extracted from oral and stool samples using validated extraction protocols optimized for complex biological matrices. DNA quantity and purity were assessed prior to downstream processing to ensure suitability for sequencing. Only samples meeting predefined quality thresholds were advanced for library preparation and sequencing.

### Nanopore Sequencing and Library Preparation

Journal of Chemical Health Risks
www.jchr.org
JCHR (2026) 16(2), 594-603 | ISSN:2251-6727

Full-length 16S rRNA gene amplification was performed to enable high-resolution taxonomic profiling. Sequencing libraries were prepared according to manufacturer-recommended protocols for Nanopore sequencing platforms. Sequencing was conducted using long-read technology, allowing comprehensive coverage of the 16S rRNA gene and improved discrimination of closely related bacterial taxa across samples.

**Bioinformatic Processing and Taxonomic Assignment**

Raw sequencing reads were subjected to quality control filtering to remove low-quality and ambiguous reads. High-quality sequences were processed through a standardized bioinformatics pipeline for taxonomic classification. Taxonomic assignment was performed at multiple hierarchical levels, enabling comparative analysis of microbial composition between oral and gut samples. Genotypic data were used exclusively for all analyses, without reliance on predictive or imputed functional profiling.

**Identification of Shared and Iron-Associated Taxa**

Comparative analyses were conducted to identify microbial taxa present in both oral and gut samples within the same individuals. Particular emphasis was placed on bacterial genera known to be associated with iron acquisition, transport, or metabolism. The presence and overlap of these iron-associated taxa across anatomical sites were evaluated to explore potential oral–gut microbial connectivity under healthy physiological conditions.

**Data Management and Confidentiality**

All sequencing and analytical data were stored in secure, access-controlled systems. Data handling procedures adhered strictly to confidentiality and data protection standards. The dataset used in this study was restricted exclusively to the current manuscript and was not combined with data from other participant groups or related studies.

**Statistical Considerations**

Given the exploratory nature and limited sample size, analyses were primarily descriptive and comparative in nature. Results were interpreted cautiously, with emphasis on within-subject trends and observed microbial patterns rather than population-level inference. Methodological consistency across samples was maintained to ensure internal validity of the findings.

## 4. Results

**Study Population and Sample Overview**

A total of five healthy, non-anemic adult volunteers were included in the final analysis. Paired oral and stool samples were successfully collected and processed from all participants, yielding ten microbiome samples for sequencing. All samples passed DNA quality control and sequencing quality thresholds, allowing inclusion in downstream taxonomic and comparative analyses. Full-length 16S rRNA gene sequencing generated high-quality reads suitable for genus- and species-level classification across oral and gut microbial communities.

**Sequencing Output and Read Characteristics**

**Table 1. Sequencing yield and quality metrics of oral and stool samples**

| Sample ID | Sample Type | Total Reads | Mean Read Length (bp) | Q-score (Mean) | Assigned Reads (%) |
|---|---|---|---|---|---|
| P1 | Oral | 68,420 | 1,465 | 12.4 | 94.2 |
| P1 | Stool | 72,315 | 1,482 | 12.7 | 95.1 |
| P2 | Oral | 64,890 | 1,458 | 12.1 | 93.5 |
| P2 | Stool | 75,104 | 1,490 | 12.9 | 95.6 |
| P3 | Oral | 70,332 | 1,470 | 12.6 | 94.8 |
| P3 | Stool | 73,889 | 1,486 | 12.8 | 95.0 |
| P4 | Oral | 66,578 | 1,452 | 12.0 | 93.1 |

Journal of Chemical Health Risks
www.jchr.org
JCHR (2026) 16(2), 594-603 | ISSN:2251-6727

| | | | | | |
|---|---|---|---|---|---|
| P4 | Stool | 71,450 | 1,488 | 12.7 | 94.9 |
| P5 | Oral | 69,201 | 1,468 | 12.5 | 94.5 |
| P5 | Stool | 74,220 | 1,491 | 12.9 | 95.8 |

Sequencing generated consistently high read counts across all oral and stool samples, with a slightly higher yield observed in stool specimens. Mean read lengths approximated the expected full-length 16S rRNA gene size, confirming successful long-read amplification. Average Q-scores exceeded acceptable quality thresholds for Nanopore-based taxonomic analysis. A high proportion of reads were successfully assigned to bacterial taxa, indicating robust sequencing depth and minimal data loss during quality filtering. These metrics collectively demonstrate the reliability and comparability of sequencing data between oral and gut samples, providing a strong foundation for subsequent microbial composition analyses.

**Overall Microbial Composition of Oral and Gut Samples**

**Table 2. Dominant bacterial genera identified in oral and gut microbiomes**

| Genus | Oral Microbiome (Mean %) | Gut Microbiome (Mean %) |
|---|---|---|
| Streptococcus | 32.4 | 1.8 |
| Veillonella | 14.7 | 2.3 |
| Prevotella | 12.9 | 8.6 |
| Neisseria | 9.5 | 0.4 |
| Fusobacterium | 7.1 | 1.2 |
| Bacteroides | 1.6 | 34.8 |
| Faecalibacterium | 0.8 | 16.5 |
| Roseburia | 0.4 | 9.2 |
| Ruminococcus | 0.6 | 11.7 |
| Akkermansia | 0.2 | 6.4 |

Distinct microbial signatures were observed between oral and gut microbiomes. Oral samples were predominantly enriched with Streptococcus, Veillonella, Prevotella, and Neisseria, reflecting taxa commonly associated with the oral cavity. In contrast, gut samples showed marked dominance of Bacteroides, Faecalibacterium, Ruminococcus, and Roseburia, which are characteristic anaerobic gut commensals. Although some genera such as Prevotella were present in both niches, their relative abundance differed substantially. These findings highlight strong site-specific microbial specialization while also indicating partial compositional overlap between oral and intestinal ecosystems.

Journal of Chemical Health Risks
www.jchr.org
JCHR (2026) 16(2), 594-603 | ISSN:2251-6727

**Alpha Diversity Comparison Between Oral and Gut Microbiomes**

**Table 3. Alpha diversity indices of oral and gut samples**

| Diversity Index | Oral Microbiome (Mean ± SD) | Gut Microbiome (Mean ± SD) |
|---|---|---|
| Observed OTUs | 112 ± 18 | 245 ± 32 |
| Shannon Index | 2.84 ± 0.41 | 4.12 ± 0.36 |
| Simpson Index | 0.79 ± 0.06 | 0.91 ± 0.04 |

Alpha diversity analysis demonstrated significantly greater microbial richness and evenness in gut samples compared to oral samples. The gut microbiome exhibited higher observed operational taxonomic units and elevated Shannon and Simpson indices, reflecting a more complex and evenly distributed microbial community. Oral samples showed lower diversity, consistent with ecological constraints and selective pressures within the oral cavity. These findings suggest that while the oral microbiome is taxonomically distinct and less diverse, the gut microbiome maintains a broader and more stable microbial ecosystem in healthy individuals.

**Shared Microbial Taxa Between Oral and Gut Niches**

**Table 4. Bacterial genera shared between oral and gut microbiomes**

| Genus | Oral Presence (%) | Gut Presence (%) |
|---|---|---|
| Prevotella | 100 | 100 |
| Streptococcus | 100 | 80 |
| Veillonella | 80 | 60 |
| Fusobacterium | 80 | 60 |
| Actinomyces | 60 | 40 |
| Rothia | 60 | 20 |

Several bacterial genera were identified as shared between oral and gut microbiomes across participants. Prevotella was consistently detected in both niches in all individuals, suggesting strong oral–gut continuity. Streptococcus and Veillonella were frequently observed in gut samples despite being predominantly oral taxa. The presence of these shared genera indicates potential microbial transmission or ecological compatibility between oral and intestinal environments. However, differences in prevalence and abundance suggest that while certain taxa can inhabit both sites, their ecological roles may vary depending on anatomical location.

**Iron-Associated Bacterial Taxa in Oral and Gut Microbiomes**

**Table 5. Iron-associated bacterial genera detected in oral and gut samples**

| Genus | Oral Microbiome | Gut Microbiome | Functional Association |
|---|---|---|---|
| Prevotella | Present | Present | Iron utilization |

Journal of Chemical Health Risks
www.jchr.org
JCHR (2026) 16(2), 594-603 | ISSN:2251-6727

| | | | |
|---|---|---|---|
| Bacteroides | Low | High | Heme/iron transport |
| Streptococcus | High | Moderate | Iron acquisition systems |
| Veillonella | Moderate | Low | Iron-dependent metabolism |
| Fusobacterium | Moderate | Moderate | Iron uptake mechanisms |

Multiple iron-associated bacterial genera were identified in both oral and gut microbiomes of healthy participants. Prevotella emerged as a consistently shared genus across both niches, highlighting its potential role in iron-related microbial ecology. Bacteroides demonstrated strong enrichment in the gut, aligning with its known involvement in iron and heme utilization. Oral-associated genera such as Streptococcus and Veillonella were also detected in gut samples, albeit at lower abundance. These findings suggest that iron-associated bacteria form a shared functional subset linking oral and gut microbiomes even in non-anemic individuals.

## 5. Discussion

This study used full-length 16S rRNA Nanopore sequencing to compare paired oral and gut microbiomes in a small cohort of healthy, non-anemic adults and to examine the presence and overlap of iron-associated bacterial taxa across the two niches. The principal findings were consistent with well-established ecological differences between oral and intestinal habitats: oral communities were dominated by canonical oral taxa, whereas gut communities were richer, more even, and dominated by obligate anaerobes typical of the colon. Nevertheless, a modest set of genera, notably *Prevotella* and *Fusobacterium*, were detectable in both sample types and included taxa commonly described as iron-responsive or possessing iron-acquisition systems. These observations align with prior reports showing that site specificity and ecological filtering largely determine microbial distributions in healthy adults, with only limited cross-niche persistence..

The strong compartmentalization of oral and gut communities observed here echoes findings from large population surveys which show that, under homeostatic conditions, the distal gut maintains a distinct taxonomic composition relative to the oral cavity [11]. That work and others have emphasized that apparent detection of oral taxa in stool should be interpreted cautiously in healthy individuals, because routine exposure to oral microbes through swallowing does not necessarily translate to successful colonization of the distal gut [11]. Nevertheless, pathophysiological states and specific anatomical contexts can permit ectopic persistence of oral taxa; for example, studies of small-intestinal and enteropathy syndromes in children have documented oral taxa colonizing proximal intestinal sites and contributing to functional disruption [12,13]. These context-dependent examples suggest a useful heuristic: in health, oral-gut overlap is limited and low-abundance, while meaningful colonization or dominance of oral taxa in gut samples often signals altered barrier function, ecological decompartmentalization, or disease processes [11–13].

Longitudinal and population scale studies provide an important perspective on baseline variability and the limits of cross-niche inference. Large longitudinal cohorts demonstrate that gut microbial composition shows both intra- and inter-individual temporal dynamics, yet core features remain stable in healthy adults, reinforcing the idea of a resilient gut community that resists invasion by transient taxa [14,15]. Similarly, the oral microbiome is structured by biofilm architecture and localized microenvironments, which select for taxa adapted to salivary flow, oxygen gradients, and frequent perturbations (e.g., chewing, hygiene) [16]. Therefore, the pattern we observed site specificity with a small shared subset fits within a broader framework in which ecological filters (pH, redox potential, host secretions, bile acids, resident competitors) largely prevent wholesale oral colonization of the distal gut in the absence of pathology [11,14–16].

A central motivation for this study was to examine iron-associated bacterial taxa as a potential functional link between oral and gut communities. Iron availability is a

Journal of Chemical Health Risks
www.jchr.org
JCHR (2026) 16(2), 594-603 | ISSN:2251-6727

potent ecological variable and bacteria have evolved diverse acquisition strategies that modulate their fitness across environments. Recent mechanistic studies demonstrate that microbiota-derived metabolites can influence host iron uptake and immune cell function and, reciprocally, that host iron handling shapes microbial community structure [17,18]. For example, microbiota-assisted iron uptake has been shown to promote regulatory T cell differentiation in the gut, linking microbial metabolism to mucosal immune tolerance [17]. At the same time, alterations in dietary iron or supplementation have repeatedly been shown to shift gut communities sometimes toward taxa associated with inflammation highlighting the sensitivity of microbial networks to iron perturbation [18,19].

In this context, shared iron-associated genera such as Prevotella and Fusobacterium were detectable across oral and gut samples in healthy volunteers. *Prevotella* species are recognized for their ecological versatility and presence across multiple mucosal sites; they frequently appear in studies of oral–gut overlap and have been suggested to survive transit into the proximal gut via swallowed saliva [20]. *Fusobacterium* spp., particularly *F. nucleatum*, have attracted interest for their capacity to adhere, invade, and influence host responses in extra-oral sites, and their consistent detection across compartments in disease cohorts has bolstered hypotheses of oral-to-gut translocation in pathological states [21]. In the healthy phenotype we sampled, these genera were present but not dominant in the stool, a pattern compatible with limited persistence or transient passage rather than established colonization.

The enrichment of gut-adapted taxa with established iron-handling capabilities, particularly Bacteroides in stool samples, reflects distinct functional niches and metabolic networks across sites. *Bacteroides* species possess sophisticated heme and iron transport systems and are well adapted to the nutrient milieu of the colon; their dominance in stool aligns with prior biochemical and genomic studies demonstrating Bacteroidetes reliance on iron-sensitive regulons for competitive fitness [22]. These divergent functional specializations reinforce the interpretation that iron-associated microbes do not distribute uniformly along the alimentary tract but rather occupy site-appropriate niches governed by substrate availability, host physiology, and microbial interactions.

Methodological considerations also shape the interpretation of oral–gut comparisons. Full-length 16S rRNA gene sequencing using long-read Nanopore platforms provides enhanced species-level resolution compared with short-read amplicon sequencing, thereby reducing taxonomic ambiguity and improving detection of low-abundance and shared taxa across complex microbial communities [23,24]. This improved resolution is particularly relevant when investigating oral–gut microbial overlap, where closely related taxa may otherwise be misclassified. Nevertheless, primer selection, DNA extraction efficiency, and reference database completeness remain important sources of analytical bias that can influence cross-site comparisons and should be carefully considered when interpreting findings from small exploratory cohorts [25].

The findings indicate that, in healthy adults, oral and gut microbiomes remain largely distinct while sharing a limited number of taxa with ecological flexibility that have ecological flexibility and potential iron-related functions. These shared taxa may represent a reservoir of organisms poised at mucosal interfaces able to transiently occupy multiple niches; their relative abundances and functional expression likely shift under perturbation (e.g., iron supplementation, mucosal inflammation, altered gastric acidity), which could tip the balance from transient passage to ectopic persistence with downstream pathophysiological consequences [12,17–19]. These patterns suggest that a small subset of taxa with shared metabolic traits may link anatomically distinct microbiomes, a hypothesis that warrants further investigation.

**Limitations**

This study has several limitations. The sample size was small and drawn from a narrowly defined population of healthy, non-anemic adults; consequently, generalisability is limited and population heterogeneity (age, diet, geography) could alter both composition and the extent of oral–gut overlap. The cross-sectional design precludes temporal assessment of stability or transient dynamics; longitudinal sampling would clarify whether shared taxa

Journal of Chemical Health Risks
www.jchr.org
JCHR (2026) 16(2), 594-603 | ISSN:2251-6727

represent persistent colonizers or episodic transients. Use of full-length 16S rRNA sequencing enhances taxonomic resolution but does not provide direct functional gene information; inference about iron-handling capacity therefore remains indirect and should be validated by shotgun metagenomics, metatranscriptomics, or targeted functional assays. Finally, the study focused on relative abundance measures and lacked paired host iron metrics (e.g., ferritin, hepcidin) that would enable integrated host–microbe correlation analyses.

**Future implementation**

Future work should prioritize larger, longitudinal cohorts with diverse demographics and concurrent host iron phenotyping to map how oral–gut microbial connectivity varies with iron status. Integration of shotgun metagenomics and targeted assays for siderophore biosynthesis genes, heme transporters, and iron-responsive regulons will be essential to move from taxonomic association to functional causation. Interventional studies that manipulate iron availability (dietary modulation or controlled supplementation) in controlled settings would test whether iron is a causal driver of oral–gut microbial shifts. Finally, mechanistic models from in vitro co-culture systems to gnotobiotic animal experiments can validate whether candidate oral taxa can survive transit, acquire iron in the intestinal environment, and alter host absorptive or immune processes.

In conclusion, the present analysis provides a high-resolution taxonomic baseline demonstrating strong oral–gut compartmentalization in healthy adults with a modest shared subset of iron-associated taxa. The results refine our understanding of oral–gut microbial connectivity under physiological conditions and identify candidate genera for mechanistic follow-up that could illuminate how iron availability shapes mucosal microbial ecology across the alimentary tract.

## 6. Conclusion

This study provides a high-resolution comparison of oral and gut microbiomes in healthy, non-anemic adults using full-length 16S rRNA Nanopore sequencing. Clear site-specific microbial signatures were observed, with the oral cavity and gut maintaining distinct yet biologically connected microbial ecosystems. A limited subset of shared taxa, including iron-associated genera, was consistently identified across both niches, supporting the concept of oral–gut microbial connectivity under physiological conditions. The predominance of gut-adapted anaerobes alongside transient or low-abundance oral taxa in stool highlights strong ecological filtering in health. Iron-associated bacteria emerged as a potential functional link between oral and intestinal communities. Together, these findings establish a baseline reference for healthy adults and provide a framework for future studies exploring microbiome alterations in iron-related disorders and disease states.

## 7. References

[1] Tan, X.; Wang, Y.; Gong, T. The Interplay between Oral Microbiota, Gut Microbiota and Systematic Diseases. J. Oral Microbiol. 2023, 15, 2213112.

[2] Costa, C. F. F. A.; Correia-de-Sá, T.; Araujo, R.; Barbosa, F.; Burnet, P. W. J.; Ferreira-Gomes, J.; Sampaio-Maia, B. The Oral–Gut Microbiota Relationship in Healthy Humans: Identifying Shared Bacteria between Environments and Age Groups. Front. Microbiol. 2024, 15, 1475159.

[3] Rajasekaran, J. J.; Krishnamurthy, H. K.; Bosco, J.; Jayaraman, V.; Krishna, K.; Wang, T.
Oral Microbiome: A Review of Its Impact on Oral and Systemic Health. Microorganisms 2024, 12, 1797.

[4] Yan, Y.; Zhang, W.; Wang, Y.; Yi, C.; Yu, B.; Pang, X. Crosstalk between Intestinal Flora and Human Iron Metabolism. Microbiol. Res. 2024, 282, 127667.

[5] Puga, A. M.; de L. Samaniego-Vaesken, M.; Montero-Bravo, A.; Ruperto, M.; Partearroyo, T.; Varela-Moreiras, G. Iron Supplementation at the Crossroads of Nutrition and Gut Microbiota.Nutrients 2022, 14, 1926.

[6] Malesza, I. J.; Bartkowiak-Wieczorek, J.; Winkler-Galicki, J.; Nowicka, A.; Dzięciołowska, D.; Błaszczyk, M. The Relationship between Iron, Inflammation and Gut Microbiota. Nutrients 2022, 14, 3478.

[7] Vanhee, M.; Floré, K.; Vanthourenhout, S.; Hellemans, J.; Muyldermans, A.; Reynders,

Journal of Chemical Health Risks

www.jchr.org

JCHR (2026) 16(2), 594-603 | ISSN:2251-6727

M.Implementation of Full-Length 16S Nanopore Sequencing. Diagn. Microbiol. Infect. Dis. 2023, 116156.

[8] Waechter, C.; Chaberny, I. F.; Kumpitsch, C. Comparative Analysis of Full-Length 16S rRNA Sequencing. Front. Genet. 2023, 14, 1213829.

[9] Aja-Macaya, P.; Conde-Pérez, K.; Trigo-Tasende, N.; Buetas, E.; Nasser-Ali, M.; Nión, P. Nanopore Full Length 16S rRNA Gene Sequencing. Sci. Rep. 2025, 15, 26486.

[10] Elzayat, H.; Mesto, G.; Al-Marzooq, F. Impact of Gut and Oral Microbiome on Gut Health. Nutrients 2023, 15, 3377.

[11] Rashidi, A.; Ebadi, M.; Weisdorf, D. J.; Costalonga, M.; Staley, C. No Evidence for Colonization of Oral Bacteria in the Distal Gut. Proc. Natl. Acad. Sci. U.S.A. 2021, 118, e2114152118.

[12] Vonaesch, P. Ectopic Small Intestinal Colonization by Oral Bacteria.Proc. Natl. Acad. Sci. U.S.A. 2022, 119, e2209589119.

[13] Chen, R. Y.; Kung, V. L.; Das, S. Duodenal Microbiota in Stunted Children. N. Engl. J. Med. 2020, 383, 321–333.

[14] Suzuki, T. A.; Fitzstevens, J. L.; Schmidt, V. T. Codiversification of Gut Microbiota with Humans.Science 2022, 377, 1328–1332.

[15] Olsson, L. M.; Boulund, F.; Nilsson, S. Dynamics of the Normal Gut Microbiota. Cell Host Microbe 2022, 30, 726–739.

[16] Hajishengallis, G.; Lamont, R. J.; Koo, H. Oral Polymicrobial Communities. Cell Host Microbe 2023, 31, 528–538.

[17] Zhu, L.; Li, G.; Liang, Z. Microbiota-Assisted Iron Uptake. Nat. Commun. 2023, 14, 2790.

[18] Baldi, A. Effects of Iron Supplements on the Gut Microbiome. Nat. Commun. 2024, 15.

[19] Seyoum, Y.; Baye, K.; Humblot, C. Iron Homeostasis in Host and Gut Bacteria. Gut Microbes 2021, 13, 1–19.

[20] Könönen, E. Oral Prevotella Species. Front. Cell. Infect. Microbiol. 2022.

[21] Abed, J. Fusobacterium nucleatum and Colorectal Cancer. Front. Cell. Infect. Microbiol. 2022, 12, 400.

[22] Ndeh, D. Metabolism of Glycosaminoglycans by Bacteroides. Nat. Commun. 2020, 11.

[23] Hoffbeck, C.; Middleton, D. M. R. L.; Nelson, N. J.; Taylor, M. W. Benchmarking 16S rRNA Gene-Based Approaches. Int. J. Microbiol. 2025, 2025, 7563096.

[24] Aja-Macaya, P.; Conde-Pérez, K.; Trigo-Tasende, N. Nanopore Full-Length 16S rRNA Gene Sequencing. Sci. Rep. 2025, 15, 26486.

[25] Monteagudo-Mera, A. Impact of Inorganic Iron on the Human Gut Microbiota. Front. Microbiol. 2023, 14, 1074637.