National Institute for Public Health and the Environment
Ministry of Health, Welfare and Sport

Factsheet Microbiome
PIENTER 3 study results

Background

The human body hosts a vast and interconnected ecosystem of microorganisms (i.e. bacteria, viruses, fungi, and more) collectively known as the human microbiome. These microbial communities colonize various body sites such as the skin, gut, and respiratory tract, profoundly influencing digestion, metabolism, and immune regulation. The microbiome acts as both a guardian and a modulator of health, shaping immune development and protecting against pathogens.
Recent studies show that the microbiome also influences the outcomes of infectious diseases and the variability in vaccine responses. Understanding the complex interplay between the immune response and the microbiome provides a foundation for novel microbiome-based approaches to improve disease prevention and treatment strategies.
The PIENTER-3 study offered an opportunity to investigate microbiome composition and function within a large, representative sample of the Dutch population. By integrating microbiome profiling with extensive demographic, environmental, and health data, this project characterized baseline microbial diversity across the lifespan and identified determinants of microbiome variation, ultimately relevant to public health.

Results

Gut microbiome
Using samples from approximately 4,000 participants, the gut microbiome study provided critical insights into age-related microbial dynamics and their association with health indicators.

- Age-related diversity and composition:

Microbial diversity was lowest and most variable in infants (<1 year old), increasing sharply during childhood and adolescence (10–12 years) and stabilizing in adulthood. This developmental trajectory underscores the strong influence of diet, environment, and genetics on microbiome maturation.

- Determinants of microbiome variation:

In younger participants, dietary patterns were key drivers of microbial composition, while in adults, factors such as ethnic background and body mass index (BMI) were more strongly associated with diversity and function. These results emphasize the importance of life stage–specific microbiome characteristics.

- Defining the healthy core microbiome:

Building upon this work, we explored how overall health status, derived from validated health indices, correlated with gut microbial signatures. This approach aimed to identify microbial features associated with general well-being and healthy aging in the population.

- Antimicrobial resistance:

In a case-control sub-study, we studied how asymptomatic carriage of extended-spectrum beta-lactamase (ESBL)-producing Escherichia coli was not associated with major alterations in gut microbiome composition or resistome structure, suggesting resilience of the gut ecosystem to certain resistant strains.
These findings and others in preparation contribute to a growing reference framework for understanding how gut microbial communities evolve across the human lifespan and influence health outcomes.

Respiratory Microbiome
Complementing the gut data, the respiratory microbiome component examined over 3,100 saliva/oropharyngeal (OP) and 2,500 nasopharyngeal (NP) samples from 3,160

participants (0–87 years old). This represents the largest population-level investigation of the upper respiratory tract (URT) microbiota to date.

- Age and niche-specific microbiota:

Age was identified as the dominant factor shaping microbial diversity and composition in the URT. The nasopharyngeal microbiota matured gradually until approximately 15–24 years of age, with children showing lower diversity but higher bacterial density compared to adults. Each niche (NP and OP) exhibited distinct microbial communities, reflecting unique ecological environments.

- Environmental and lifestyle factors:

The nasopharyngeal microbiota was primarily influenced by environmental exposures, such as living or working with children, suggesting microbial transmission between age groups, as well as by season and sex. In contrast, the oral/oropharyngeal microbiota was more strongly shaped by lifestyle factors including alcohol and tobacco use.

- Health associations:

Viral infections were linked to increased abundance of Streptococcus pneumoniae in the nasopharynx, particularly among individuals with fever or recent pneumonia. These findings highlight the interplay between the microbiota and host susceptibility to respiratory pathogens.

Collectively, these analyses and others in preparation, establish critical reference data for the Dutch population, contributing to a better understanding of how microbiome composition influences respiratory health and disease risk across the lifespan.

Conclusion / discussion

The PIENTER-3 microbiome research, including both gut and respiratory niches, offered a comprehensive view of the human microbiome from infancy to old age in a general population context. The integration of these data enhances our understanding of microbial ecology, antimicrobial resistance, and the interplay between microbes, immunity, infection, and ultimately of health. As we continue to unlock the microbiome's role in shaping health, these findings lay the groundwork for several approaches towards public health, including microbiome-informed strategies or targeted prevention of infectious diseases.

Publications

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