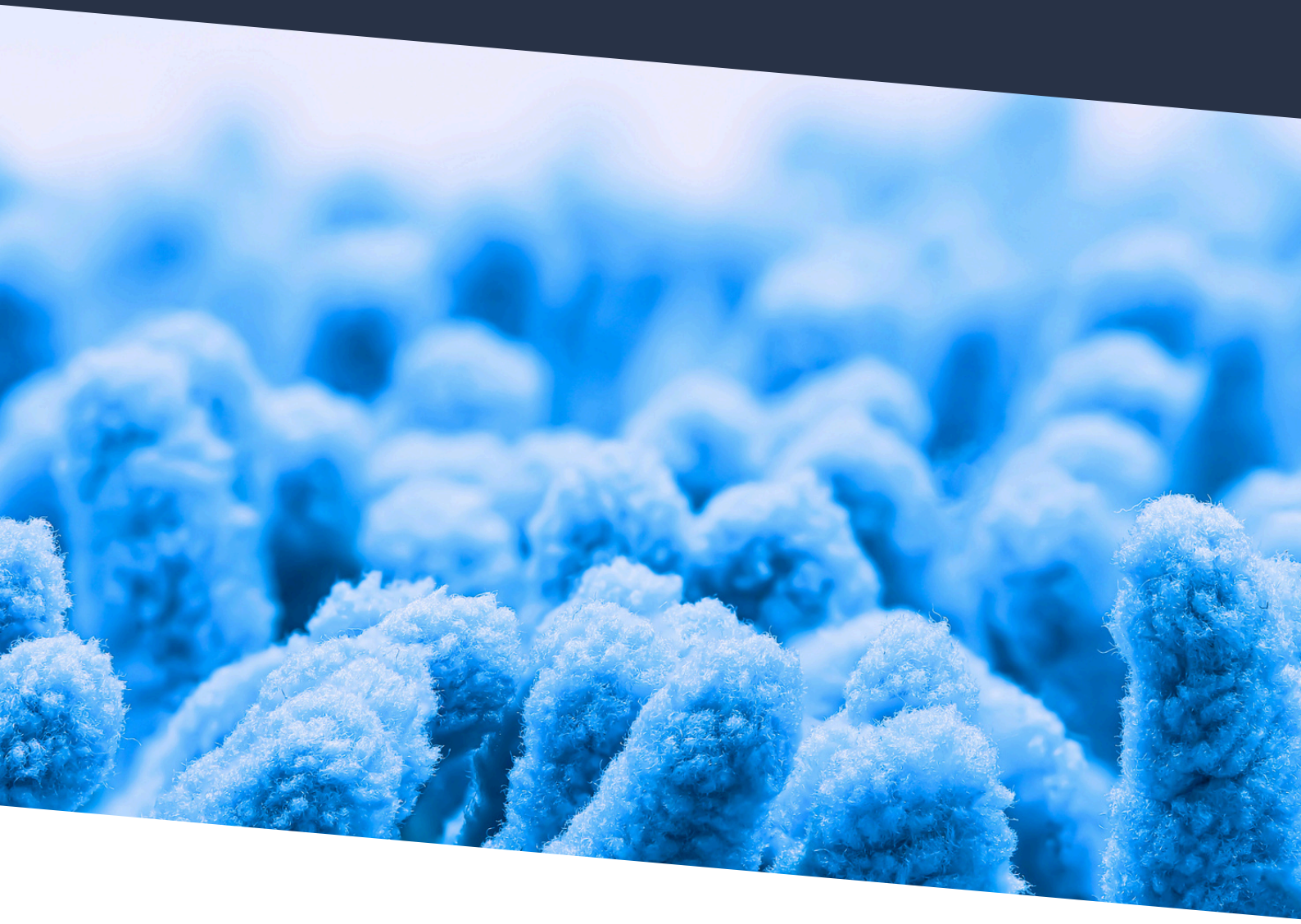
Industry Focus



Microbiology

An exclusive collection featuring top-tier articles, visionary experts, and essential industry insights

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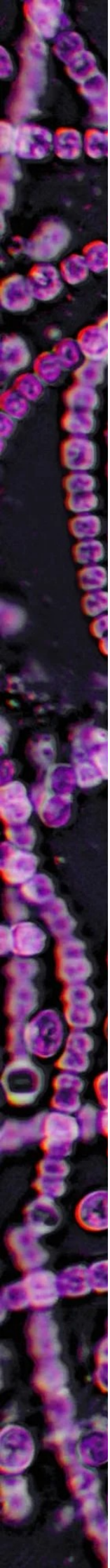
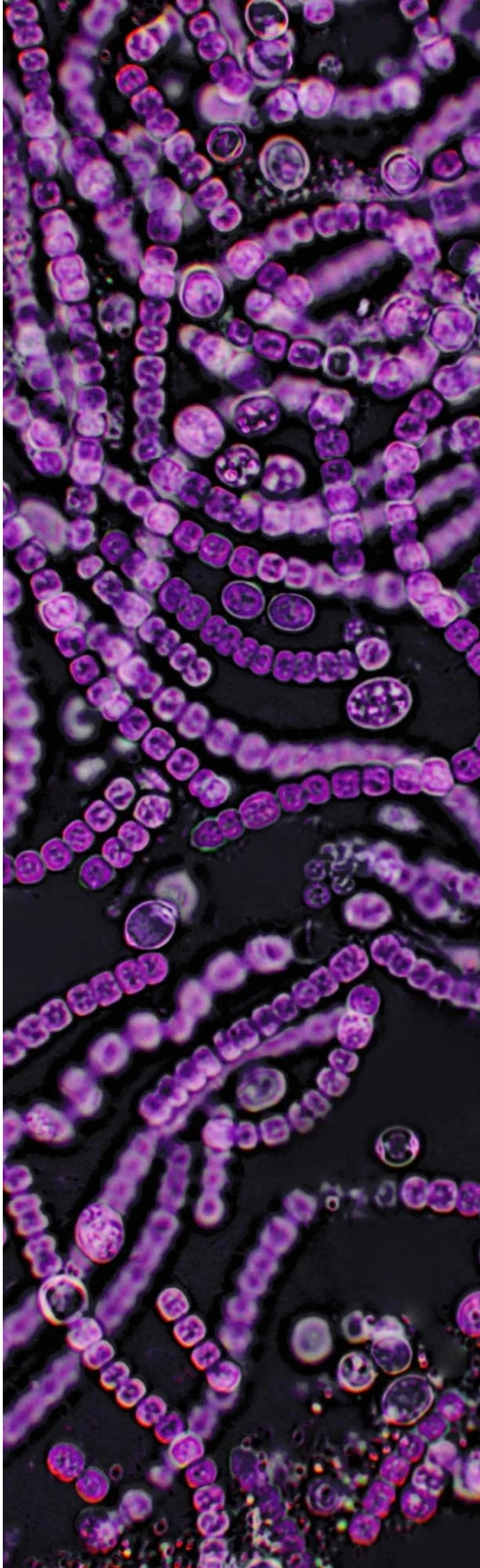




Foreword

Welcome to the latest edition of our Industry Focus eBook, where we explore the **fascinating world of microbiology**. This field continues to unveil the hidden forces shaping our health, environment, and industries, offering groundbreaking insights into the microbial communities that influence our daily lives.

In human health, microbiology plays a critical role in understanding the delicate balance of our gut microbiome. From the effects of dairy consumption—where **Milk Boosts Gut-Friendly Bacteria While Cheese Alters Microbiome Balance, Study Reveals**—to broader dietary impacts explored in **How Do Animal and Plant-Based Milks Affect Gut Health?**, these articles shed light on how what we consume shapes our internal ecosystems.

But microbiology isn't just about digestion—it also raises intriguing questions about the brain. In **Is There a Brain Microbiome?**, researchers investigate whether our minds, like our guts, are home to a microbial world of their own. Meanwhile, **Deciphering the Mysteries of the Human Microbiome** provides a deep dive into the trillions of microorganisms that influence our health in ways we are only beginning to understand.

Beyond human biology, microbiology powers industrial innovation. **Industrial Microbiology: An Overview** explores how microbes drive advancements in pharmaceuticals, food production, and environmental sustainability. And in a surprising twist, **Scientists Uncover Coffee's Surprising Effect on Gut Microbiota** reveals how one of the world's most beloved beverages interacts with our microbiome unexpectedly.

This eBook captures the latest advancements and discoveries in microbiology, offering a window into how these microscopic organisms shape our world. As you navigate these pages, we hope you find inspiration in microbiology's incredible complexity and potential—whether in health, industry or beyond.

Lily Ramsey
Editor

AZO NETWORK

Milk boosts gut-friendly bacteria while cheese alters microbiome balance, study reveals

New research reveals that milk fosters beneficial gut bacteria like Faecalibacterium and Akkermansia, while cheese reduces certain microbes—reshaping how dairy impacts digestive health.

Study: Dairy Consumption and the Colonic Mucosa-Associated Gut Microbiota in Humans—A Preliminary Investigation. Image Credit: New Africa / Shutterstock

In a recent study published in the journal ***Nutrients***, researchers in the United States explored the influence of dairy consumption on colonic mucosa-associated gut microbiota. By investigating specific bacterial composition changes linked to dairy intake, they highlighted its implications for individual and public health.

Background

Did you know that the human gut houses trillions of bacteria that influence everything from

digestion to mental health? Research increasingly points to diet as a crucial factor in shaping our gut microbiome, yet the role of dairy remains controversial. While dairy provides essential nutrients such as calcium, vitamins, and probiotics, conflicting studies raise concerns about its effects on gut health. Some research links dairy consumption to enhanced beneficial gut bacteria, while others suggest potential risks such as inflammation and metabolic disturbances. Given the global prevalence of dairy consumption, understanding its precise effects on gut microbiota is critical for shaping dietary guidelines and public health initiatives. Further research is needed to determine how specific dairy products affect different bacterial species and their long-term influence on health.

About the study

A cross-sectional study was conducted with 34 participants who had undergone a colonoscopy at the Michael E. DeBakey Veterans Affairs Medical Center in Houston, Texas. Participants were selected based on strict eligibility criteria, excluding individuals with inflammatory bowel disease (IBD), recent antibiotic use, or major dietary changes. Self-reported dairy intake over the past year was assessed using a validated food frequency questionnaire (FFQ). Nutrient intake was adjusted for caloric consumption.

> ***Lactose may act as a prebiotic: The study found that the positive association between milk intake and Akkermansia was weakened after adjusting for lactose intake, suggesting that lactose or other dairy components might stimulate beneficial bacteria growth.***

Colonic mucosal biopsies were collected and analyzed for microbial composition using 16S ribosomal Ribonucleic acid (rRNA) gene sequencing. Bacterial Deoxyribonucleic Acid (DNA) was extracted, and the V4 region of the 16S rRNA gene was amplified and sequenced using the Illumina MiSeq platform. Operational Taxonomic Unit (OTU) classification was performed using the Unified Platform for Automated Sequence Analysis (UPARSE) and structured Identification of Lifeforms from Various Environments databases (SILVA). Alpha-diversity (species richness and evenness) and beta-diversity (community composition differences) were calculated. Statistical analyses included negative binomial regression models adjusted for demographic and lifestyle factors such as age, body mass index (BMI), smoking status, alcohol use, and dietary quality. The study included a total of 97 mucosal biopsies from these participants. False discovery rate (FDR)-adjusted p-values were used to determine statistical significance.

Study results

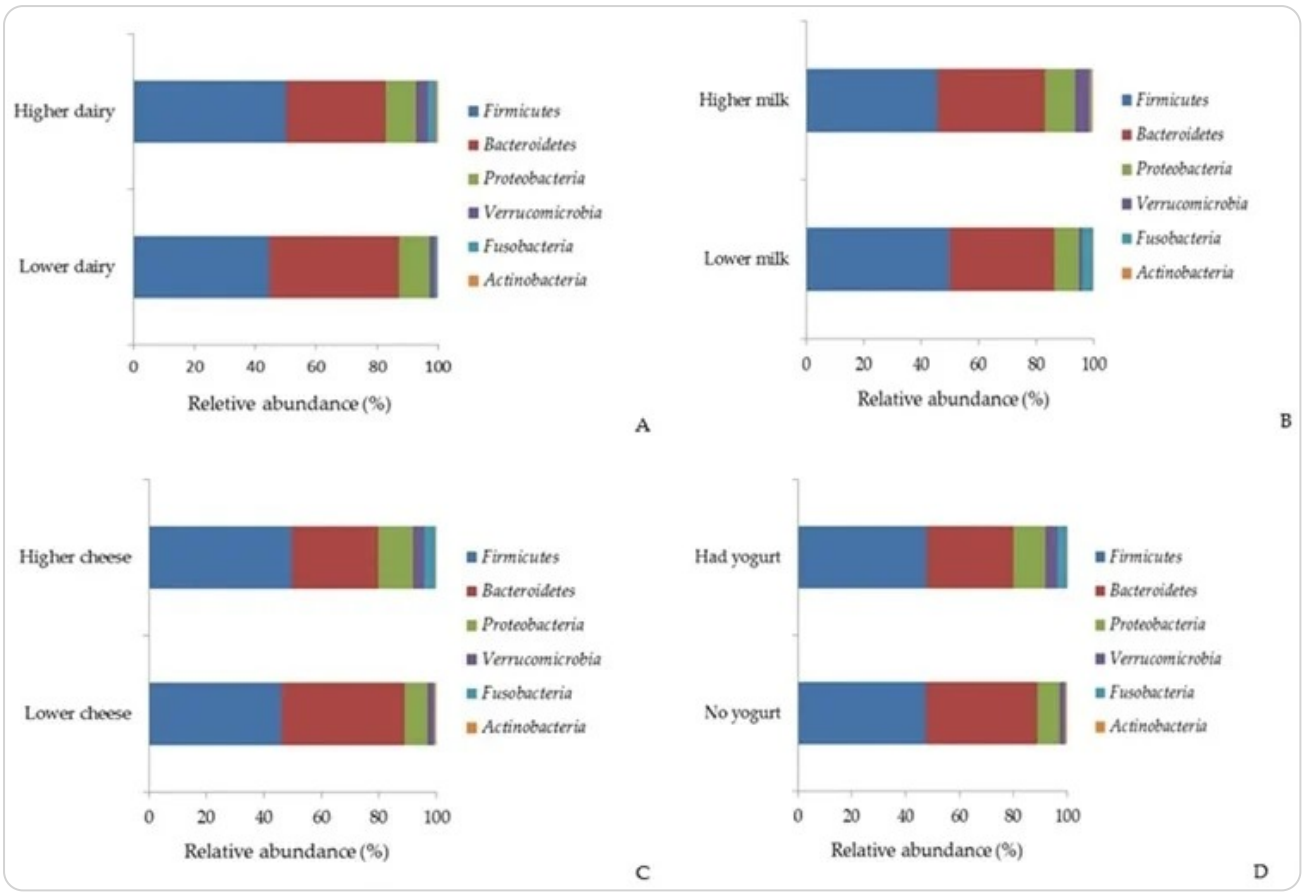
Higher consumption of total dairy and milk was associated with increased microbial alpha-diversity, indicating greater bacterial richness and evenness. In contrast, higher cheese consumption was linked to lower microbial diversity. Beta-diversity analysis revealed significant differences in gut bacterial composition based on dairy intake levels.

Bifidobacterium linked to total dairy intake: Participants who consumed more total dairy (not just milk) showed a higher abundance of Bifidobacterium, a well-known probiotic associated with digestive health and immune support.

Participants who consumed more dairy and milk exhibited a higher relative abundance of Faecalibacterium, a bacterium known for its anti-inflammatory properties. Increased milk intake was also associated with greater levels of Akkermansia, a mucin-degrading bacterium linked to improved gut barrier function and metabolic health. However, the association between Akkermansia and milk intake was attenuated after adjusting for lactose intake, suggesting that lactose or other dairy components may act as prebiotics.

Conversely, higher cheese consumption correlated with a lower relative abundance of Bacteroides and Subdoligranulum. While Bacteroides have been implicated in colorectal cancer (CRC), lower levels of Subdoligranulum have been linked to metabolic disorders. Additionally, the study found that higher total dairy intake was negatively associated with Bacteroides, suggesting a complex relationship between dairy components and microbial composition. The varying impact of milk and cheese on gut microbiota composition may be due to differences in their nutrient content and fermentation process. Milk, which contains more lactose, may promote the growth of beneficial bacteria, while cheese, which undergoes fermentation, may have distinct effects on gut microbial communities.

The study did not find significant associations between yogurt intake and microbial composition, likely due to low yogurt consumption among participants. The findings suggest that different dairy products exert varying influences on gut microbiota, which may have implications for dietary recommendations and gut health interventions.



*Relative abundance (%) of the major bacterial phyla by total dairy (**A**), milk (**B**), cheese (**C**), and yogurt (**D**).*

Conclusions

To summarize, dairy consumption significantly influences the composition and diversity of colonic mucosa-associated gut microbiota, with potential implications for individual and public health. A higher intake of total dairy and milk promotes beneficial bacteria such as Faecalibacterium and Akkermansia, whereas higher cheese consumption is linked to reductions in Bacteroides and Subdoligranulum. Notably, total dairy intake was inversely associated with Bacteroides, a genus linked to both colorectal cancer and inflammatory conditions. These findings underscore the broader impact of dairy consumption on gut health, which in turn affects metabolic, immune, and digestive functions.

Yogurt's role remains unclear: Although yogurt is often considered beneficial for gut health, this study did not find a strong association between yogurt intake and microbiota composition, likely due to low yogurt consumption among participants.

On a community level, dietary guidelines emphasizing balanced dairy consumption could

improve public health outcomes. However, the study had limitations, including a small sample size, a predominantly older male participant pool, and reliance on self-reported dietary intake, which may affect generalizability. Globally, understanding the role of dairy in gut health could inform nutrition policies, probiotic interventions, and personalized dietary recommendations. Further research using metagenomic and metabolomic approaches is needed to explore how specific dairy components influence microbial functions and their long-term effects on health.

Journal reference:

- Chen E, Ajami NJ, White DL, et al. Dairy Consumption and the Colonic Mucosa-Associated Gut Microbiota in Humans—A Preliminary Investigation. Nutrients. (2025), DOI: 10.3390/nu17030567, https://www.mdpi.com/2072-6643/17/3/567

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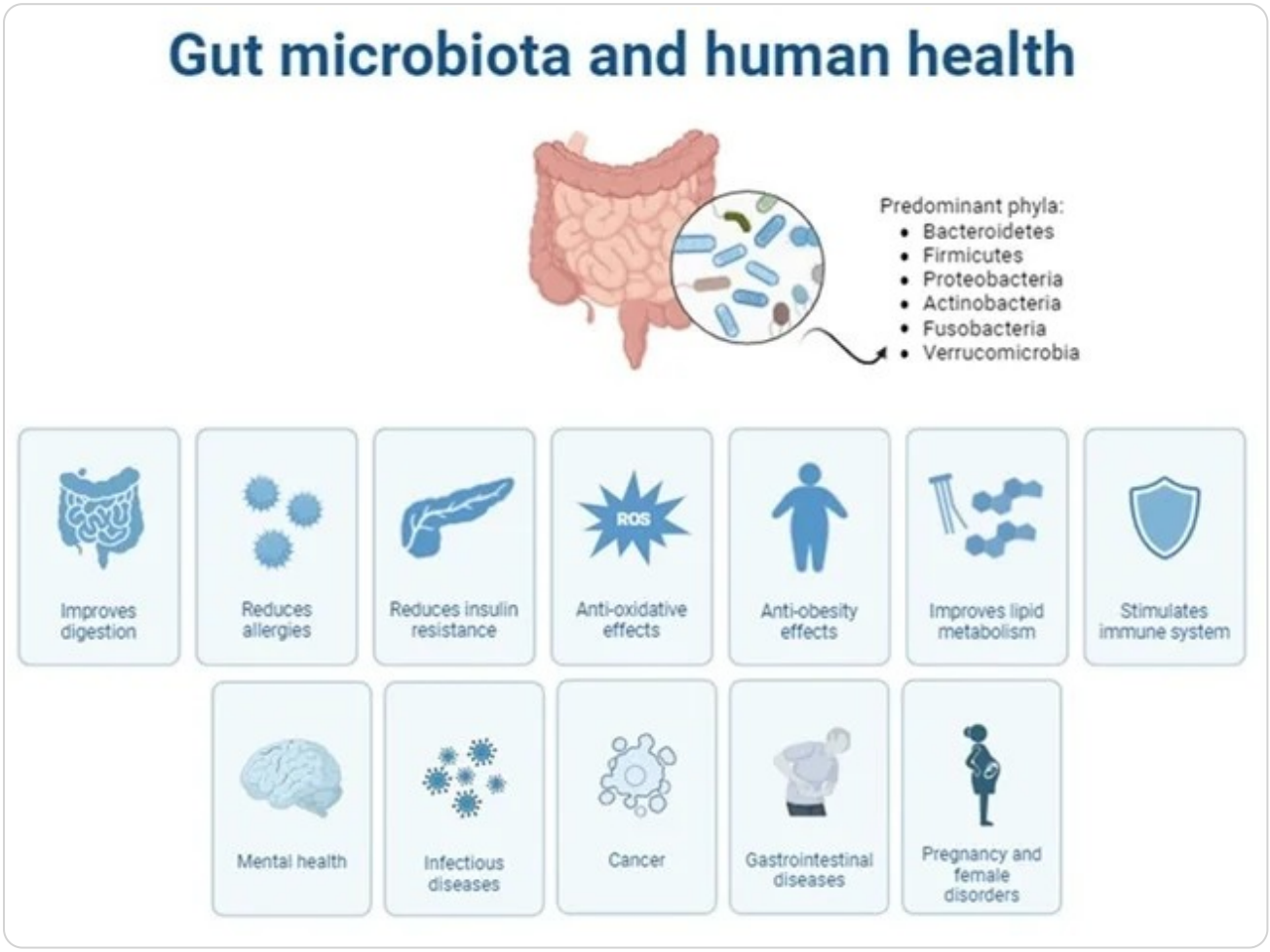
How do animal and plant-based milks affect gut health?

While both animal and plant-based milks benefit gut health, animal milk shows superior support for beneficial bacteria, raising important questions for dietary choices.



Review: Substitutive Effects of Milk vs. Vegetable Milk on the Human Gut Microbiota and Implications for Human Health

In a recent review published in the journal *Nutrients*, researchers explored how both animal milk and plant-based milk alternatives affect gut microbiota.

Their findings suggest that while both types of milk can promote gut health, animal milk generally supports a richer and more diverse microbiota, with specific components offering targeted benefits, while plant-based substitutes also contribute positively but may sometimes encourage the growth of harmful bacteria in certain contexts.

Milk and Gut Health

Milk is a vital source of nutrition for mammals, especially during infancy. It provides essential energy and nutrients needed for growth and development. Humans are unique in continuing to consume milk into adulthood.

Milk is known for being high in calcium, vitamins, and proteins, which offer anti-inflammatory benefits. These components have been linked to the prevention of diseases such as cardiovascular issues, osteoporosis, and diabetes.

Despite its many benefits, milk consumption has declined in some regions. This trend is driven by factors such as lactose intolerance, allergies, ethical concerns, and the popularity of plant-based milk alternatives.

These substitutes, made from ingredients like soy, almonds, and oats, are marketed as healthier and more sustainable. However, the research on their impact on gut microbiota remains limited, and the results vary depending on the type of milk and individual factors.

Gut microbiota plays a critical role in overall health, affecting immunity, metabolism, and even brain function. While specific components in animal milk, such as proteins and fats, have been shown to support gut health, plant-based alternatives have also been found to promote the growth of beneficial bacteria. However, some evidence suggests that certain plant-based milk alternatives might, in some cases, foster the growth of less beneficial bacteria, though this typically occurs in low proportions.

Animal-Based Milk

Animal-based milk, particularly from cows, is considered a functional food due to its bioactive molecules, including proteins, fats, and oligosaccharides. These compounds have been shown to have positive effects on gut health.

For example, studies have found that animal milk promotes the growth of beneficial bacteria like *Lactobacillus* and *Bifidobacterium*. Additionally, components such as whey proteins and lactose support gut health by acting as prebiotics, fostering the growth of beneficial bacteria while potentially offering antimicrobial effects.

> ***Mare milk, with its similarities to human milk, is particularly beneficial for individuals with allergies, supporting the growth of beneficial gut microbes while being gentle on the digestive system.***

Cow milk has been particularly noted for its ability to promote beneficial microbes and reduce harmful bacteria such as *Clostridium*. Its oligosaccharides, in combination with whey proteins, have been found to increase the production of short-chain fatty acids (SCFAs), which improve gut health by boosting satiety and immune function.

Mare milk, which shares some similarities with human milk, has also been found to support the growth of beneficial gut bacteria. This makes it particularly useful for individuals with allergies or hyperlipidemia.

Goat milk, another animal-based option, contains oligosaccharides that act as prebiotics, increasing SCFA production and improving gut barrier function. It also promotes beneficial bacteria, although in some cases, it has been linked to promoting the growth of *Helicobacter*, a bacterium associated with gastric issues.

Camel milk, known for its rich immunomodulatory proteins and antibodies, has also shown benefits for gut health. It increases beneficial bacteria while reducing harmful bacteria like *Shigella* and *Escherichia*. Its ability to boost SCFA production further enhances its positive impact on gut health and immune responses.

Plant-Based Dairy Alternatives

Plant-based milk alternatives have become increasingly popular due to their perceived health and environmental benefits. These beverages, made from ingredients like soy, almonds, and oats, have distinct nutritional profiles compared to dairy milk.

Generally lower in protein and fat, plant-based alternatives are often rich in unsaturated fats and carbohydrates. They are also free from lactose and cholesterol, making them suitable for those with lactose intolerance or milk protein allergies. In addition, these beverages contain antioxidants and phytosterols, which help reduce oxidative stress in the body.

While plant-based milk can positively impact gut health, promoting the growth of beneficial bacteria, there are some concerns. Soy milk, for instance, has been found to increase beneficial bacteria while reducing harmful ones like *Proteobacteria*.

However, some studies have shown that certain plant-based milk alternatives might encourage the growth of bacteria such as *Fusobacterium* and *Salmonella*, albeit typically in low and manageable levels.

Conclusions

The consumption of plant-based milk substitutes is on the rise globally, particularly in regions like Europe. Although these beverages can replicate some nutrients found in animal milk, significant differences remain in their protein and fat content.

Plant-based milk is also lactose- and cholesterol-free, which makes it suitable for individuals with specific dietary restrictions. While research on their impact on gut microbiota is still emerging, most findings suggest that both animal and plant-based milk can contribute positively to gut health, though with different effects and implications.

The study noted the importance of milk for gut health while highlighting certain points of concern. While animal milk appears to offer greater overall benefits for gut health, plant-based alternatives still provide some positive effects.

It is essential, however, to consider individual nutritional needs and preferences when recommending one type of milk over another, particularly given the variability in gut microbiota responses. Future studies will help clarify how both types of milk impact gut microbiota, ultimately guiding dietary choices based on personal health needs.

Journal reference:

- Substitutive Effects of Milk vs. Vegetable Milk on the Human Gut Microbiota and Implications for Human Health. Portocarrero, A. C. M., Lopez-Santamarina, A., Lopez, P. R., Ortega, I. S. I., Duman, H., Karav, S., Miranda, J. M. *Nutrients* (2024). DOI: 10.3390/nu16183108, https://www.mdpi.com/2072-6643/16/18/3108

Free guide - Discover microbial single-genome sequencing

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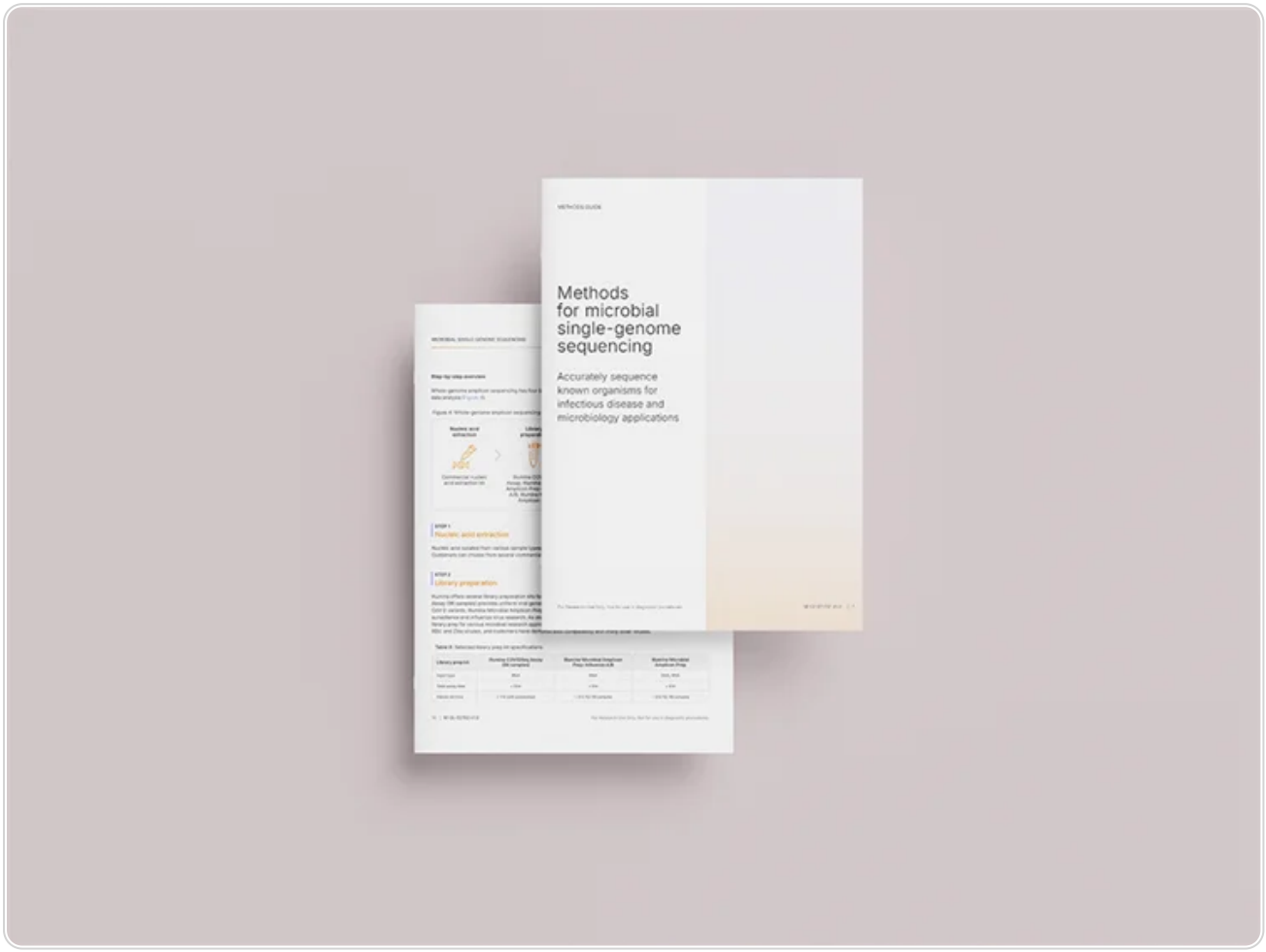

Whether you're tracking infectious disease outbreaks, analyzing bacterial evolution, or identifying antimicrobial resistance markers, this resource offers step-by-step workflows for whole-genome sequencing, targeted amplicon sequencing, and whole-genome amplicon sequencing. From nucleic acid extraction to advanced data analysis, this guide helps researchers harness next-generation sequencing (NGS) technology for high-resolution microbial profiling, ensuring accuracy and efficiency in microbiology applications.

Designed for researchers and professionals in microbiology, public health, and infectious disease surveillance, this guide equips you with trusted methods and tools to enhance your sequencing projects. Learn how to select the right sequencing workflow, optimize library preparation, and leverage powerful sequencing systems for unparalleled genomic analysis.

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Is There a Brain Microbiome?

Microbiome (a term used to describe the microorganisms present within an area) is typically associated with organs in the human body, like the gut, skin, or nasal cavities. However, an emerging body of evidence suggests the presence of a brain microbiome.

This article will describe the findings leading to this idea alongside potential pathways for its use in research and the controversy this theory has since created.

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The concept of a brain microbiome

A microbiome is a community of bacteria, fungi, and viruses living within a habitat. Thus the

hypothesis that the brain contains a microbiome postulates that bacteria, viruses, and/or fungi exist normally within the brain.

The initial suggestion of native bacterium present in the brain came from a study in 2013, initially investigating whether microbial infiltration into the brain was observed in patients with HIV/AIDS. This study by Branton et al. observed non-human RNA sequences aligning with over 170 bacteria and phages.[1]

Critically this study also transplanted the human brain tissue into immunocompromised mice, where after, the same bacterial sequences were detected. These sequences were not detected in a parallel group of mice in which the transplanted tissue was heat-treated.[1]

The appearance of microbial RNA in control brains (where the immune system should be fully functional) is not in line with the belief that the brain is a sterile organ. Further to this, the detection of microbial RNA in the non-heat-treated group suggests that the detected bacteria were living. [2]

Current techniques for detecting the presence of microorganisms in the brain rely on the recovery and reading of foreign RNA or DNA within the brain, such as in 16S RNA amplification or metagenomic high throughput sequencing.

Implications of a brain microbiome

The brain microbiome may also play a role in brain disease, alongside its presence in healthy individuals. Microorganisms have been implicated in the pathogenesis of Alzheimer's disease (AD). One study comparing samples from control brains vs brains with AD found an overabundance of bacteria and fungi species in the AD samples.[3]

Traditionally, the brain has been considered a sterile environment, meaning not containing living microorganisms. Previously, microorganism infiltration of the brain was thought of only in the context of infection, such as the Herpes Simplex Virus-1.[4]

The blood-brain barrier (BBB) is considered one of the largest contributors to the brain's immune privileged status. Under normal conditions, the BBB is near-impermeable to most large molecules, such as microorganisms.[5] Therefore, conventionally, it was thought that in individuals with a healthy BBB, microorganisms such as bacteria, should not be found in the brain.

Scientific controversy and challenges

One of the main critiques of the brain microbiome concept arises from the potential that the observed microbial sequences are a product of contamination. [6–8] This contamination may arise from the recovery of the tissue.[2] This potential for detected microorganisms to be artifacts (false positives created during the study) has led to skepticism regarding the existence of the brain microbiome.

The methodology of studies linking a potential brain microbiome with neurodegenerative disorders has been criticized for potential confounding factors that may lead to the observations of these studies.

In these studies, due to the nature of neurodegenerative disorders, participants are often older. Deterioration of the BBB leading to "leakage" is linked to increasing age in adults, with strong evidence of disruption in AD.[9,10]

Additionally, the strength of the immune system decreases with age.[11] Thus, there is the potential that microbes observed in patients with neurodegenerative disorders are secondary to infiltration after degeneration, rather than the driver of the neurodegenerative changes.[2]

Current methods used for the detection of microorganisms in the brain rely on prior knowledge of DNA/RNA sequences of microorganisms. Therefore, there is the possibility for many unknown microorganisms to be missed. Potentially meaning the brain microbiome is larger than currently hypothesized in terms of species.[2]

Potential mechanisms and pathways

Although a unified theory for microbial colonization of the brain has not been formed, multiple research groups have suggested ways this occurs. Weber et al noted that specific species of bacteria identified in studies exploring the brain microbiome in AD are normally found in the oral microbiome.[12]

Therefore, they hypothesized, that pathogenic changes in the oral cavity (often seen in AD) may damage connective tissues. This tissue destruction releases bacteria from the oral cavity, allowing for nervous system infection. Some of these bacteria can create a biofilm, through the production of amyloid proteins.[12]

These bacterial amyloids share similarities to the disease-causing versions.[13] These amyloids may then allow other native amyloid proteins to aggregate and form colonies, beginning the pathogenesis of AD.[12]

Future directions in research

The concept of the brain microbiome is still in its infancy. Whilst important steps have been made to elucidate this concept further, a true overview of the brain microbiome is still to be provided. As this field is still developing, there are still necessary steps future research should take to verify these results.

As highlighted earlier, the potential that microorganisms have been detected in brain samples may arise due to subject age and BBB deterioration, suggests studies should focus on exploring multiple age ranges. This may elucidate whether these detected microbes are due to age-related changes or are a true representation of a brain microbiome.[2]

As the human gut microbiome is potentially unique to the individual, the same thing may be true for the brain microbiome.[14] Therefore, future research may seek to analyze brain samples of individuals in parallel. This would allow researchers to observe whether detected microbes vary between individuals, which would potentially confirm the presence of a brain microbiome.[2]

As the brain microbiome may play a role in neurodegenerative disorders such as AD, a better understanding of this relationship may better inform future treatments. If microbes do drive or play a part in the associated neurodegenerative changes, there are opportunities to use targeted treatment.

In the case of the hypothesis that bacteria from the oral cavity play a role in the instigation of AD, lactoferrin may represent an important therapeutic. Lactoferrin is a protein native to the oral cavity with antimicrobial properties; typically, lactoferrin helps keep the oral microbiome in homeostasis. However, lactoferrin has also shown promise as a therapeutic in the field of neurodegenerative diseases.[12]

The brain microbiome is a fascinating concept, that is still developing. Whilst there is mounting evidence that a potential brain microbiome plays a role in human health, skepticism surrounding the methodologies used to come to these conclusions is still present. This research may prove to be incredibly important, potentially discovering new treatment routes for neurodegenerative disorders like AD.

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Industrial Microbiology: An Overview

Industrial microbiology is a branch of applied microbiology that uses microbes, such as bacteria, algae, and fungi, to produce high-value products, including drugs and fuels.[1]

This field of science offers endless opportunities that include the potential to replace harmful plastics with biodegradable ones, fossil fuels with biofuels, and highly polluting chemical processes with biocompatible alternatives.

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Key concepts and technologies used in industrial microbiology

The fundamental idea of industrial microbiology is dependent on the identification of microbes from natural sources for application in large-scale fermentative processes to

produce metabolites of industrial interest.[2]

Typically, the isolated microbes are screened and characterized per specific selection criteria. The culture conditions, such as pH, temperature, nutrients, and oxygen levels, are optimized for increased production of the bioproducts.

Over the years, the advent and advancements in multiple scientific technologies have revolutionized the field of industrial microbiology. Some of the key areas are discussed below:

Synthetic biology and genetic engineering

Synthetic biology enables the creation of custom microbial strains and cell lines tailored for specific production processes.[3] Genetic engineering is employed in synthetic biology to overcome the physiological limitations of microorganisms.

This technique focuses on enhancing productivity, reducing by-product formation, improving cell growth, and stabilizing biological systems. Ultimately, these microbes undergo fermentation in a bioreactor for the production of target products.

Bioreactors

Fermentation is the core of bioprocessing. In this process, microbes are cultured in a bioreactor under controlled conditions for a high yield of the target product.[4] The bioreactor design and process are critical to optimal yield.

Real-time monitoring and regulating each step of the biomanufacturing process through process analytical technologies (PAT) and advanced control systems have ensured higher productivity and reduced variability of the final product.[5]

Advancements in bioreactor technology, such as the development of continuous fermentation systems and single-use bioreactors, have significantly improved high-scale bioprocessing efficiency.[4]

Unlike the traditional batch fermentation systems, the continuous fermentation systems operate in a steady state where nutrients are continuously added in the bioreactor and products are constantly harvested. The use of single-use bioreactors has reduced the risk of contamination and offers greater product safety.

Downstream processes

Following fermentation, the downstream process involves a series of steps to recover and purify the product from the fermentation broths or cells.

Centrifugation and filtration are common techniques used to isolate cells from the broth. Different chromatographic methods are used to test product purity. Depending on the nature of the final product, downstream processing techniques are selected.[6]

Applications of industrial microbiology

Industrial microbiology plays an important role in a wide range of sectors, including pharmaceuticals, food and beverages, agriculture, biofuel, and environment management. Some of the major applications are discussed below:

Biopharmaceuticals: Biopharmaceutical products, such as vaccines, hormones, enzymes, and monoclonal antibodies, are produced via industrial microbiology techniques. These products are used for the treatment of many diseases, including infectious diseases, cancer, and diabetics.[7]

Biofuels and bioenergy: Industrial microbiology plays a crucial role in the production of biofuels, which can be used as an alternative to fossil fuels. Microbial fermentation enables the synthesis of biogas, biofuels, and biodiesel from renewable biomass sources.[8]

The production of cellulosic ethanol from agricultural residues and woody plants has ensured the sustainability and economic viability of biofuel production. Genetically engineered yeast and bacterial strains exhibited greater efficiency in converting biomass into biofuels (e.g., bioethanol).

Food and beverage: Industrial microbiology techniques produce enzymes, such as amylases and proteases, which are used in food industries, particularly baking and brewing. These enzymes improve the texture, flavor, and shelf life of the final product.[9] Microbial fermentation techniques are widely used to develop probiotics and plant-based proteins.

Agriculture: Industrial microbiology has revolutionized the agricultural field by developing genetically engineered crops. For example, Bt corn and Bt cotton are genetically engineered crops that express a bacterial toxin that eliminates specific plant pests.[10]

Cultivation of these crops has efficiently reduced the use of chemical pesticides, prevented soil contamination, and improved crop yield.

Environmental management: Different microorganisms are used to tackle environmental challenges, including pollution and waste management.[11] Microorganisms are used for the bioremediation process that involves the detoxification of degradation of pollutants in soil, air,

and water.

Others: Industrial biotechnology is also applied in textile manufacturing processes, including bio-polishing and de-sizing, that enhance fabric quality. Bioplastics, such as polylactic acid (PLA) and polyhydroxyalkanoates (PHAs), which play a crucial role in alleviating plastic pollution, are manufactured through microbial fermentation.

Challenges and future outlook of industrial microbiology

Despite tremendous advancements in the biomanufacturing process, several challenges and limitations need to be addressed to fully harness the potential of industrial biotechnology. These challenges concern technology, regulation, the economy, and the environment.

The development of genetically modified microbial strains and cell lines requires extensive genetic engineering and metabolic pathway optimization. These methods are complex and time-consuming. Researchers also experience many challenges in maintaining the stability of these strains under industrial conditions, which is critical for large-scale applications.

Since bioreactors, raw materials, and downstream processes are often highly expensive, small-scale industries encounter significant economic challenges to establish their product.

Industrial microbiology is not without environmental challenges. The spent microbial cultures and fermentation residues must be treated to avoid adverse effects to the environment, and these steps add to the manufacturing costs.

Regulatory agencies such as the US Food and Drug Administration have strict guidelines to ensure the safety of bioproducts. The pharmaceutical industry mandates rigorous documentation and quality control measures to comply with the rules of the global regulatory agencies. A minor change in the production process requires revalidation and approval.

In the future, bioreactor design and process control could be improved to increase the scalability and efficiency of bioprocessing. Furthermore, innovations in genetic engineering and synthetic biology could focus on the development of stable and efficient microbial strains and cell lines for large-scale production in a cost-efficient manner.

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Further Reading

- All Microbiology Content
- Microbiology and Food Security
- What Can Microbiology Tell Us About Extraterrestrial Life?
- How Intelligent are Microbes?
- How Could Microbes Help to Solve Climate Change?

More...

Zurich lab imagines new possibilities in microbial research and diagnostics

In the fast-moving, ever-evolving field of medical microbiology, a team of scientists gets a boost from the new Illumina MiSeq i100

At the University of Zurich, the Institute for Medical Microbiology houses many labs including the Microbial Genomics Group. | Photo: UZH - Frank Bruderli

Tim Roloff Handschin, PhD, who coleads the Microbial Genomics Group at the Institute for Medical Microbiology (IMM), received a compact but powerful instrument at his lab on the University of Zurich campus. "The first impression we had of the instrument was that it was rather small," he says. "We were expecting a bigger machine for what it was supposed to be able to do."

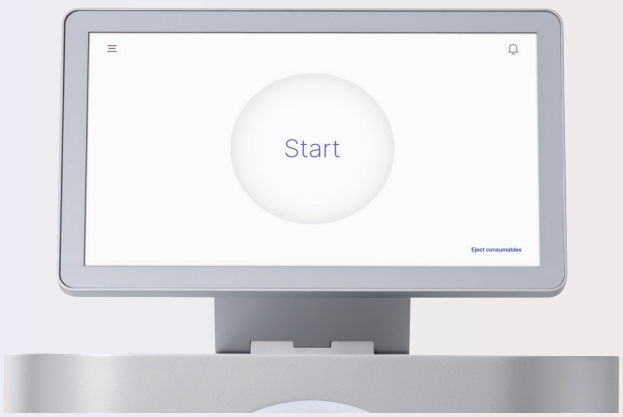
Roloff and his team were among the first to receive the new Illumina MiSeq i100 as part of alpha testing before the product was officially announced. The MiSeq i100 is Illumina's most innovative, accessible, and sustainable benchtop sequencer yet. It's easy to use and to set up: The team started their first sequencing run within half an hour of installing it.

"What has impressed us the most with this instrument is the short runtime," Roloff says. Before they received the MiSeq i100, it took his team 19 hours to complete a sequencing run on their NextSeq 1000. Now they can do the same thing in seven hours—and start two runs in a single day. "This will really be a game changer in the field of medical microbiology, because you can easily run a sequencing run in one day and then report the results within 24 hours."

Roloff's lab, one of 10 at IMM, performs whole-genome sequencing on bacteria and fungi. Their research focuses mainly on the mechanisms that lead to antimicrobial resistance, and ways to develop new diagnostic tests and antimicrobial drugs. They're also a diagnostic lab serving clinics in the Zurich metropolitan area and across Switzerland.

Roloff explains that, while bacterial genomes are small and don't require a lot of sequencing data, speed in microbiology research is still key because the ultimate goal is to provide information that prevents the spread of pathogens or leads to the correct treatment.

"The reduced run times will really speed up the process and make whole-genome sequencing much more relevant for microbial questions and diagnostics," he says. "And given the up to 100 million reads you will be able to get from the new machine, you can do a lot of experiments in parallel, a lot of bacterial genomes in parallel."



The MiSeq i100 makes index-first sequencing possible, which means users will have information early in the run about which samples have sufficient indexed representation, as well as how much data each sample will produce. In about two hours, Roloff's team can begin analyzing the sequenced indices while the rest of the fragments are still being processed. "This gives you totally new possibilities to design library prep methods that take advantage of that," Roloff says. In addition to library preparation, they can research new diagnostic tests, which "will be very interesting in our setting." He imagines developing tests that combine screening for certain bacteria with WGS. After two hours, they would be able to tell if the bacteria of interest is present. After seven hours, they could filter the full data set from the run to analyze the specific genome associated with that bacteria to determine the presence of antibiotic resistance genes, virulence factors, and more.

Tim Roloff Handschin, PhD, coleads the Microbial Genomics Group at the Institute for Medical Microbiology.

"The impact that the new instrument will have on microbial diagnostic workflows using next-generation sequencing will be massive," he says.

Roloff and his team were excited to hear that the MiSeq i100 reagents can be shipped at room temperature and can be stored that way, because that meant there would be less waste and they would not need any freezers or refrigerators. This would save money on storage. "It actually makes each sequencing run cheaper."

Roloff says they hadn't realized the additional flexibility that room-temperature storage would give them. Being able to bypass thawing time meant they could begin a run at a moment's notice.

"Turnaround time is really what has been the problem in the past," he says. "We've seen in the COVID crisis that NGS results were always lagging behind and you could only retrospectively analyze, for instance, which lineage was there." The workflow in Roloff's lab took approximately a week to report whole-genome sequencing data. "PCR was just much faster."

A significantly reduced turnaround time essentially removes the reliance on PCR or other methods, which look at only a single factor and don't provide as much information.

One final advantage the team found in the MiSeq i100, which comes with DRAGEN software on board: The data quality was as good as or better than they expected, and they could immediately get the output on the screen. "You don't need any bioinformatician waiting for the data and analyzing what you have produced," Roloff says. "Even the technician can directly report the results of a sequencing run.

"With this new instrument, Illumina makes benchtop sequencing much more valuable for medical microbiology, because it's much faster to analyze bacteria, it's cheaper and easier to store your reagents, and the ease of use actually reduces the amount of personnel you need around sequencing—the service technicians, bioinformaticians, and so on. We were very excited to join this test of the new instrument, but we were actually positively surprised by all the possibilities we suddenly had."

illumina® | Learn more at **illumina.com/MiSeqi100**

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Deciphering the Mysteries of the Human Microbiome

The human microbiome is made up of trillions of microorganisms, including bacteria, viruses, fungi, and other microbes, that live in and on the human body. In recent years, we've gained significant insights into these microbial communities, from their role in the gut-brain axis to promising research on how they could influence cancer immunotherapy responses. However, much remains to be discovered, and we are still at the frontier of microbiome research.

In this interview, we speak with Se Jin Song, Ph.D., Managing Director at The Microsetta Initiative, about the progress in understanding the human microbiome and how both cutting-edge research and public participation are shaping this journey.

Can you start by giving us an overview of The Microsetta Initiative and its primary goals?

The Microsetta Initiative (TMI) is a highly collaborative microbiome research study based out of the Knight Lab and the Center for Microbiome Innovation (CMI) at the University of California San Diego (UC San Diego).

The study's primary goal is to better understand our microbiomes, like those on our gut or skin, and their connections to diet, lifestyle, age, health, medical history, demographics, and other relevant conditions. Participants submit samples, such as stool, which we then sequence to discover what bacteria and other microbes are present. We pair these data with information participants provide about their personal characteristics and habits.

By analyzing the combination of microbial composition and survey responses, we're able to tease out novel associations that not only expand our knowledge of human microbiomes but also create new avenues of research to determine how and why these associations exist. Beyond our in-house research and analysis, we also put fully anonymized data into the public domain for anyone to reuse. This way, scientists worldwide can use these data to further our understanding.

The origins of this initiative started with the American Gut (2012) and the British Gut (2014) Projects, which were localized citizen science efforts aimed at collecting microbiome data provided by participants in the US and the UK, respectively.

TMI became the next natural step that provided a framework for generalizing the project's reach.

> *The "Microsetta" name is intended to reflect a conceptual relationship to the Rosetta Stone (which helped scholars decipher the code of hieroglyphics).*

Along the same lines, we hope that TMI's output will expand microbiome data from many populations so researchers can ask how results from one population translate to another.

What motivated you to pursue research in the field of microbiomes?

In 2010, I was a graduate student in need of summer funding, and I answered a call put out by Rob Knight, then a professor at the University of Colorado Boulder, for help collecting samples for a study.

The study was about whether a person's microbiome is shaped by the other people and animals that live with them. At the time, I had a background in genetics and ecology but wasn't familiar at all with the concept of microbiomes. As I got more involved in the study and learned more about the field, I got hooked. I was fascinated by the idea that we and all other animals on earth are entire ecosystems, home to multitudes of microbial beings and that we still understood so little about them and our relationship with them. I went on to lead that 'family study' into my first publication, and this study is why you see questions about who and what animals you live with in TMI's questionnaire.

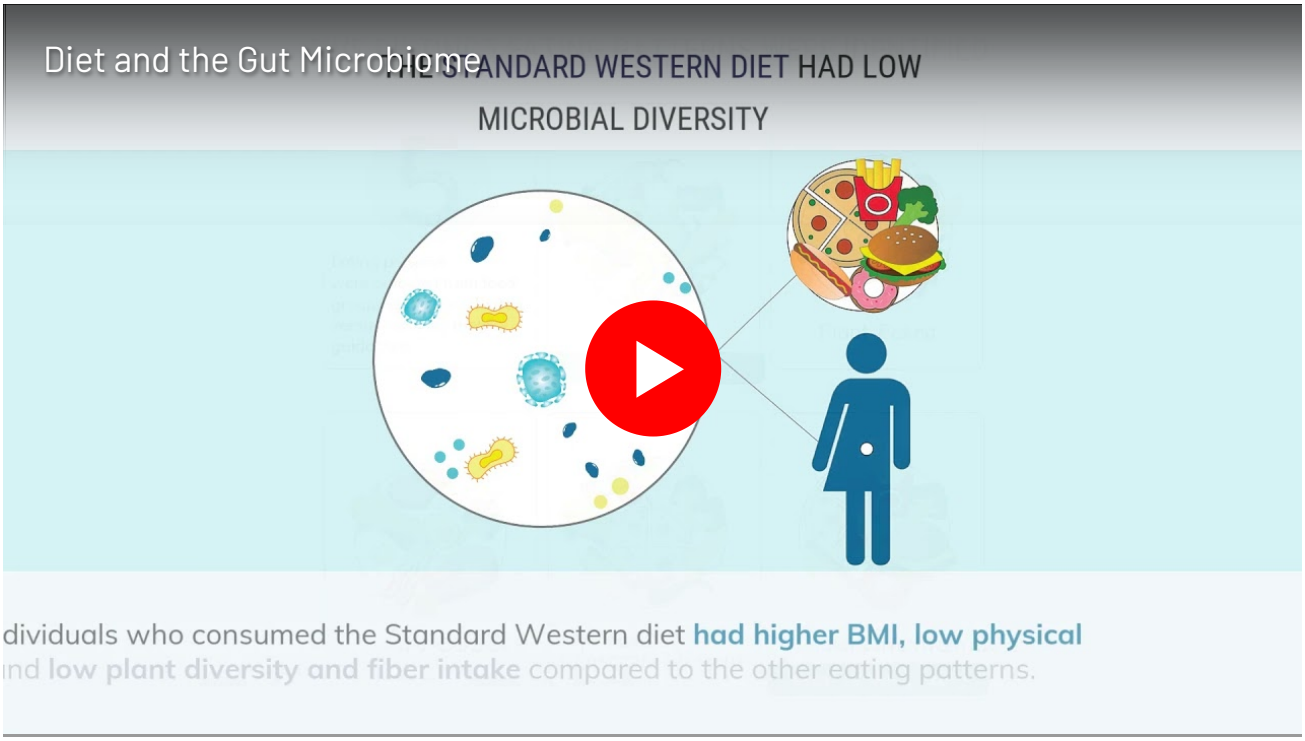
What are some of the most significant discoveries or findings that have emerged from The Microsetta Initiative so far?

One of the most impactful discoveries we've found is the connection between the variety of plants you eat and the diversity of your gut microbiome. If you've seen the recent Netflix documentary, "Hack Your Health: The Secrets of Your Gut," you're probably familiar with the 60-plant smoothie, or you may have seen references to the 30-plant challenge. While throwing

everything but the kitchen sink into your blender isn't strictly necessary, the concept is built on findings from our study.

In our 2018 publication, "American Gut: An Open Platform for Citizen Science Microbiome Research," we found that participants who reported eating 30 or more types of plants per week had more diverse gut microbiomes than participants who reported eating fewer than ten types of plants. This finding was particularly exciting because it wasn't something we were expecting a priori.

When we dug further, we found that those people also tended to have more of certain compounds and microbes that are thought to play beneficial roles, such as a compound called conjugated linoleic acid (CLA) and microbes putatively identified as *Faecalibacterium prausnitzii* and *Oscillospira*. Bacteria like these are important because they can produce short-chain fatty acids (SCFAs), compounds that are beneficial for human health.



Another significant finding is that age can be estimated from the microbiome. The skin microbiome is particularly good for this. For this analysis, we combined the TMI data with data from other studies to ensure that this finding was robust to different studies and populations. We are now working on improving these estimations using more advanced methods.

Could you elaborate on the methodologies and technologies employed in The Microsetta Initiative to analyze and understand microbiomes?

Our lab uses metagenomic DNA sequencing, also known as shotgun metagenomic sequencing, to determine the microbes in a sample. This method involves taking random snippets from all of the DNA found in a sample and sequencing them. We then match those DNA sequences to sequences from known microbial genomes to estimate the types and relative amounts of microorganisms present.

For the 2018 publication, we used a then widely used approach called 16S amplicon sequencing, which sequenced just one part of one gene present in all microbes. While that method was already very effective, metagenomic sequencing provides a more detailed picture of microbiome samples by allowing us to cover more parts of the genomes, which gives us insight into not just which microbes are there but also what they can do.

How does microbiome research fundamentally change our understanding of human biology, and what potential does it hold for revolutionizing medical treatments and public health strategies?

> *Microbiome research has opened our eyes to the immense complexity and variability of the microorganisms that live around, on, and within us and how much we rely on them. Each of us has a unique assemblage of microbes shaped by everything from our genetics and the way we were born to the foods we eat and where we live.*

While we have more questions than answers at this stage, research has found that microbes are heavily associated with human health and biology in ways that we didn't fully appreciate just a couple of decades ago. Not only do they train our immune systems, but we're finding that they also play a part in metabolic health, how we respond to drugs and immunotherapies, and even mental health.

A key public health issue we face is the ongoing loss of microbial diversity due to activities associated with westernization, urbanization, and environmental change. Many human studies have shown that Westernized and urban populations have much lower microbial diversity than populations that have maintained more traditional lifestyles. Environmental change is also likely to deplete plant, animal, and soil microbial communities in irreversible ways.

Researchers are still grappling with the precise effects of these losses. Still, we've observed on a larger scale that when species of animals or plants are lost to extinction, it generally has a negative impact on the ecosystems and communities of which they were a part. Human

microbiomes are likely subject to similar risks, as researchers believe that decreases in microbial diversity are linked to the increased prevalence of chronic diseases and reduce our collective resilience against pathogens.

With diversity loss, we're additionally losing opportunities to discover microbiota as sources of novel drugs, therapeutics, or supplements. The Microbiota Vault is an international consortium working to preserve existing diversity in much the same way as the Svalbard Seed Vault safegaurds plant diversity. TMI is honored to be a member of the coalition.

From the perspective of medical treatments informed by or derived from microbiome research, the ultimate goal is highly personalized, precision medicine. However, the fact that the microbiome can be so variable from one individual to the next means that getting to this kind of application will likely rely on enormous amounts of data and new technologies like AI to help decipher that information. Large population studies that are both rich and diverse, like the one we are building with The Microsetta Initiative, will be important to these types of approaches.

The Microsetta Initiative involves collaboration with various institutions and researchers. How do these collaborations enhance the scope and impact of your research?

Every collaboration is unique and rewarding in its own way, but one of the overarching themes is that it connects us with specific subsets of the population who might be under-represented in our existing dataset. And in many cases, the study is clinically focused or designed to understand or address a real-world issue. Other collaborations help us reach foreign populations by bridging the logistical and cultural gaps involved.

For example, through a study funded by Danone and collaboration with local institutions, we were recently able to study cohorts in the United Kingdom, Mexico, Spain, and Japan and compare those data to what we collected from American participants. In all cases, the data are collected and generated under a common protocol, which means that with each added study, the overall dataset becomes that much more powerful for detecting complex associations. It also becomes a richer resource for the research community to be able to pick and choose from a variety of criteria to meet their research needs.

Image Credit: Edge Creative/Shutterstock.com

Public participation is a key element of The Microsetta Initiative. How do you engage with the public, and what role do citizen scientists play in your research?

Given the crowdsourced beginnings and nature of The Microsetta Initiative, public participation isn't just a key element—it's foundational to our work. While we do recruit targeted cohorts from time to time and run focused studies with collaborators, it would be nearly impossible for us to reach wide-scale participation without people discovering our project and proactively contributing.

We're especially grateful for our most ardent supporters, who not only participate in the project themselves but also evangelize the project to their friends and families. As much as the day-to-day mechanics of microbiome research can sometimes feel like a slog, it's refreshing and rewarding to see that there are people who are genuinely excited about the work we do.

For us, public engagement is built on principles of education, scientific rigor, and continuous improvement:

- **Education** - We're committed to sharing our findings both with other researchers and the general public. But critically, we strive to make information approachable and accessible for as many audiences as possible.
- **Scientific rigor** - Emerging fields of research are often fertile ground for exciting claims. And while we hope that our work leads to impactful discoveries for human health, we ensure that everything we share with participants is well-supported by scientific evidence.
- **Continuous improvement** - Microbiome research is a rapidly evolving field, and our communication with participants reflects that.

Whenever we develop new analyses or improve our microbiome sample report, we share those changes with past participants and apply the new features to their data, even if they contributed their sample several years ago.

What are some of the main challenges you face in conducting research within The Microsetta Initiative, and how do you address them?

Managing participants' expectations is a frequent challenge. Over the past several years, microbiomes and their relationships with health have gone from a research niche to a commonly discussed concept. However, like many emerging scientific fields that enter the public consciousness, microbiomes' popularity has given rise to both misunderstandings and misinformation.

One of the most prevalent issues is that people think that measuring the microbial composition of a given sample can infer actionable advice. In many cases, this comes from a place of hope for which we have great empathy. People contact us because they have long-standing gut health issues or conditions their doctors have been unable to resolve, and they hope to discover a microbial silver bullet, whether it's eliminating some bacteria from their gut or encouraging another to grow.

Unfortunately, for most conditions, that sort of approach isn't currently backed by scientific research. Human microbiomes are incredibly complex ecosystems whose constituents are rarely outright "good" or "bad." A given microbe can be beneficial in some contexts but harmful in others.

While we hope to one day reach a point where microbiome-based precision medicine is a realistic avenue, we're not there yet. We try to temper expectations by being transparent about what they will learn about their microbiomes and not over-promising the results or

overreaching what they may mean.

While this sometimes leads to an initial sense of disappointment, most participants are still excited to learn more about their microbiomes and to know that they are helping to push the field forward. The opportunity to provide education and outreach while carrying out our study provides a sort of symbiotic enrichment for both participants and researchers.

What future directions or expansions do you foresee for The Microsetta Initiative in the coming years?

We're excited about continuing to expand our platform to broaden support for microbiome research. The latest research program powered by our platform is the Skin Biome Initiative, which aims to build a large public repository of skin microbiome data. The pilot study, funded by L'Oréal Research & Innovation, will recruit over 2350 participants over the next three years, but the Initiative also plans to open for general participation.

Looking further into the future, we'd like to open our study to residents of other countries. Microbiome datasets are known to be heavily biased towards European and North American populations, yet large portions of microbiome diversity are contained within other populations.

Collecting microbiome data from diverse populations is one of the foundational goals of the Microsetta Initiative, and expanding internationally is a key component of that. While there are logistical challenges to consider, the study and its supporting technologies have all been built with internationalization in mind.

We're continuously seeking new collaborators to help diversify the project and expand its reach. We encourage organizations to reach out and explore mutually beneficial ways we can work together. Companies bring resources that help us overcome logistical challenges while they benefit from leveraging our expertise and infrastructure to accelerate research.

At the same time, we frequently work with academic investigators on highly targeted studies. Our platform allows any group to conduct efficient and impactful cohort studies, and these collaborations are integral to the project's growth.

What aspects of leading The Microsetta Initiative do you find most rewarding, and how has it influenced your perspective on microbiome research?

The most rewarding part of leading this project is working with people who are clearly passionate about the science and the work being done. This includes everyone from the outreach and communications team to the sample processing team and the data analysts, and this has allowed this project to advance and improve while continuing to be grounded in good science—and mind you, this has been without the kind of resources that private companies have.

On the other hand, I love hearing from supporters who are excited about the research and often have insightful questions. This project is a constant reminder to me of how important it is to not only do quality research but also translate the research findings responsibly and in accessible ways.

Where can readers find more information?

- Our website: https://microsetta.ucsd.edu/
- Our crowdfunding site: https://fundrazr.com/microsetta
- Facebook: https://www.facebook.com/Microsetta/
- Twitter: https://x.com/microsetta
- A link to our main paper: https://journals.asm.org/doi/10.1128/msystems.00031-18

About Se Jin Song

As the Director of Research Programs at CMI, which manages The Microsetta Initiative, Se Jin's role is to help bridge the gap between academia and industry, overseeing joint projects that leverage the expansive knowledge and expertise at UC San Diego towards real world applications. Her expertise comes from nearly 15 years in the field of microbiome science, leading studies ranging from the microbes we share with co-habitants, to large-scale patterns of microbiome composition across vertebrates, to technical solutions for microbiome studies, to microbial signatures associated with skin aging. She has been on Clarivate's list of Highly Cited Researchers list in 2021, 2022, and 2023.

Scientists uncover coffee's surprising effect on gut microbiota

Discover how your daily coffee habit fuels gut health by fostering unique bacterial growth, unlocking new pathways to wellness!

Study: Coffee consumption is associated with intestinal Lawsonibacter asaccharolyticus abundance and prevalence across multiple cohorts. Image Credit: Shutterstock AI

Scientists identify a metabolic link between coffee consumption and the abundance of specific gut microorganisms across different human populations.

The study is published in the journal *Nature Microbiology*.

Background

Coffee is a popular beverage worldwide, with a range of health benefits. Studies have shown that coffee intake can reduce the risks of diabetes, non-alcoholic fatty liver disease, cancer, and all-cause and cardiovascular mortality.

The health benefits of coffee can be attributed to its polyphenol content. Chlorogenic acid, a key polyphenol in coffee, is metabolized by gut microorganisms into caffeic acid, quinic acid, and other metabolites. The gut microbiota that helps metabolize coffee has also been found to

mediate its health effects. Several studies have reported that coffee intake can lead to changes in the gut microbiota composition and diversity in healthy individuals.

The scientists of the current study have previously reported that among more than 150 food items, coffee exhibits the highest correlation with the gut microbiota composition in over 1,000 individuals.

In the current study, scientists have conducted a multi-omic analysis of metagenomic samples obtained from more than 22,000 individuals who provided detailed reports on long-term coffee consumption. Additionally, they integrated these findings with public data from over 54,000 samples, encompassing diverse populations, including non-Westernized groups, newborns, and individuals with specific diseases.

Study Design

The study analyzed more than 35,000 metagenomic samples from three study cohorts, including the ZOE Personalized Responses to Dietary Composition Trial (PREDICT) metagenomics study, the Mind–Body Study (MBS), and the Men's Lifestyle Validation Study (MLVS).

The study analysis also included more than 54,000 metagenomic samples from public sources, including healthy individuals, non-Westernized individuals, newborns and infants, ancient microbiome samples, non-human primates, and individuals with a specific disease.

Important Observations

The study investigated the association between coffee intake and gut microbiota composition by categorizing the participants into three coffee-drinking levels: never-drinking, moderate-drinking, and high-drinking.

> ***Beyond Caffeine: The research showed that even decaffeinated coffee stimulates the growth of Lawsonibacter asaccharolyticus, highlighting the role of coffee's polyphenols rather than caffeine.***

The findings revealed a strong correlation between coffee intake and gut microbiota composition across different study populations. The gut microbiota exhibited distinct compositions in coffee drinkers compared to non-drinkers, with a modest effect on differentiating the level of coffee drinking.

In general, coffee showed stimulatory rather than inhibitory effects on the abundance of gut

microbial species. The strongest association of coffee intake was observed with the abundance of the Gram-positive bacterium *Lawsonibacter asaccharolyticus.* This association remained the same for both decaffeinated and caffeinated coffee.

The abundance of *Lawsonibacter asaccharolyticus* was 4- to 8-fold higher among high coffee drinkers compared to that among non-drinkers. Among moderate drinkers, the abundance was 3- to 4-fold higher than non-drinkers.

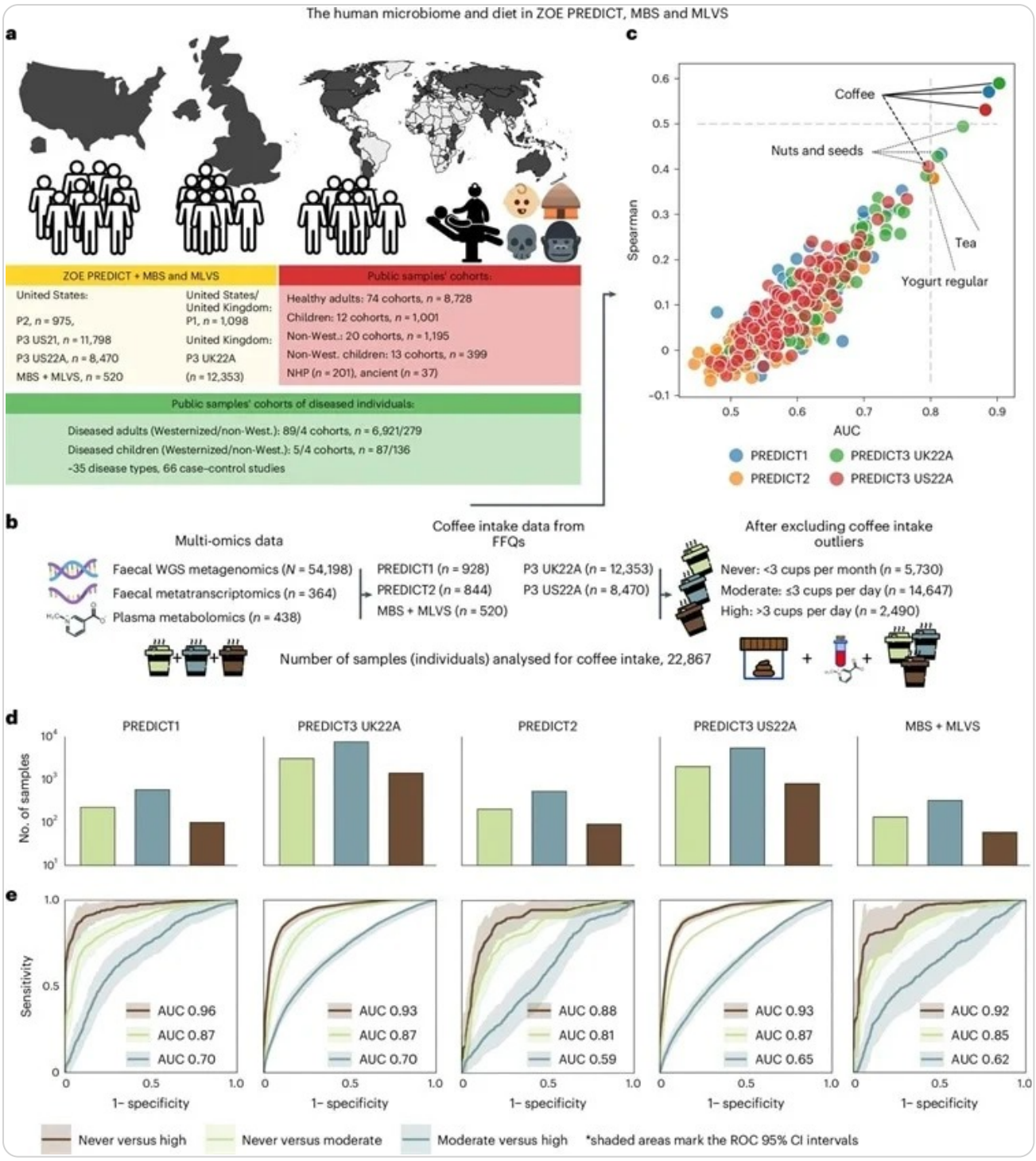
The study conducted a set of in vitro experiments to confirm the observed association further. In these experiments, coffee was added to the culture media of *Lawsonibacter asaccharolyticus.*

The findings revealed that coffee significantly increased the growth of *Lawsonibacter asaccharolyticus* by 3.5-fold, irrespective of the types (moka brewed and instant coffee) and the presence of caffeine.

The study also identified a panel of 115 gut microbial species positively associated with coffee consumption, highlighting coffee's broader influence on the microbiota.

Besides the coffee-mediated increased abundance of *Lawsonibacter asaccharolyticus* at the individual level, the study found that the overall prevalence of the bacterium in a population can be driven by the population-level consumption of coffee.

The analysis of 438 plasma metabolomes identified several metabolites enriched among coffee drinkers, with quinic acid and its potential derivatives associated with coffee and *Lawsonibacter asaccharolyticus.* Unannotated metabolites potentially derived from quinic acid were also highlighted, emphasizing the need for future biochemical investigations.



a, Five UK and/or US PREDICT cohorts (*n* = 975, 11,798, 8,470, 1,098, and 12,353), the MBS and the MLVS (*n* = 213 and *n* = 307, respectively) were used to assess diet–microbiome relationships (total *n* = 35,214). For later comparisons of microbiome distributions across different populations, we retrieved *n* = 18,984 metagenomic samples from public sources, including healthy adult individuals, newborns, non-Westernized (non-West.) individuals, ancient samples, and non-human primates (NHP). P1, PREDICT1; P2, PREDICT2; P3, PREDICT3. **b**, We combined fecal metagenomics (*n* = 54,198), fecal metatranscriptomics (*n* = 364), and plasma metabolomics (*n* = 438) with the latter two from the MBS and MLVS cohorts. FFQs surveyed the nutritional habits of the participants from four PREDICT cohorts, MBS, and MLVS (*n* = 22,867 after removing individuals above the 99th percentile of coffee intake in the PREDICT cohorts

as outliers). Participants were categorized as 'high', 'moderate' and 'never' coffee drinkers as previously established[25]. **c**, Median Spearman's correlation and median AUCs from a random forest regressor and a random forest classifier trained on the microbiome composition estimated by MetaPhlAn 4 . **d**, The number of never (light green), moderate (dark cyan) and high-coffee drinkers (brown). **e**, ROC and AUC of random forest classifiers discriminating participants between pairs of the three coffee drinker classes, assessed in a tenfold, ten times repeated cross-validations (CV) that benefited from the other cohorts during the training phase as in the leave-one-dataset-out approach (LODO). The shaded areas represent the 95% confidence intervals (CIs) of a linear interpolation over all the folds of the test.

Study Significance

The study finds a strong correlation between coffee intake and gut microbiota composition across five US and UK populations.

A positive association has been observed between coffee intake and a set of 115 gut microbial species. Among these microorganisms, the strongest association has been observed for *Lawsonibacter asaccharolyticus*.

The observed stimulatory effect of coffee on the growth of *Lawsonibacter asaccharolyticus* provides a background for future studies aiming to decipher the extent of this stimulatory effect. Such studies should investigate the effect of different concentrations of coffee on the growth rates of a panel of coffee-associated gut microorganisms.

The study also identified variations in the prevalence of *Lawsonibacter asaccharolyticus* between Western and non-Western populations, potentially linked to differences in coffee availability and consumption habits.

The metabolomic analysis carried out in this study reveals that quinic acid, trigonelline, and other potential metabolites are significantly enriched in coffee drinkers carrying *Lawsonibacter asaccharolyticus*.

Chlorogenic acid is one of the main polyphenols in coffee. Gut microorganisms metabolize it to caffeic acid, quinic acid, and several other metabolites. Gut microorganisms responsible for this biotransformation include *Bifidobacterium animalis*, *Bifidobacterium lactis*, *Escherichia coli*, and *Lactobacillus gasseri*.

The caffeine-independent strong association between *Lawsonibacter asaccharolyticus* abundance and coffee intake indicates that it may also respond to activities within these

polyphenol metabolism pathways.

Caffeine and its derivatives were prioritized in the study because of their association with *Lawsonibacter asaccharolyticus*. However, the enrichment of microorganisms in decaffeinated coffee drinkers indicates that caffeine does not occupy the central position in this complex crosstalk. Instead, quinic acid and its derivatives may play a pivotal role.

Overall, the study provides a framework for understanding microbial dietary responses at the biochemical level.

Journal reference:

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