

Recent Studies and Publications on Gut Microbiome, Health and Immunity

STUDIES

1. The Role Of The Gut Microbiome In Diet And Exercise Effects On Cognition: A Review Of The Intervention Literature

The purpose of this **systematic review** was to summarize findings from diet and exercise interventions that have investigated cognitive changes via effects on the microbiome.

There is evidence mainly from rodent studies supporting the notion that microbiota changes mediate the effects of diet and exercise on cognition, with potential mechanisms including end-product metabolites and regulation of local and systemic inflammation. The field lacks whole diet and exercise interventions, especially those involving human participants.

Source: Nicole D Anderson, Rotman Research Institute, Baycrest Health Sciences, Toronto, Ontario, Canada. The Role Of The Gut Microbiome In Diet And Exercise Effects On Cognition: A Review Of The Intervention Literature. The Journals of Gerontology: Series A, Volume 78, Issue 2, February (2023), Pages 195-205, <https://doi.org/10.1093/gerona/glac166>

2. Gut Microbiome Development In Early Childhood Is Affected By Day Care Attendance

In this study scientists have characterized the effect of day care on the gut microbial development throughout a single school year in 61 children from 4 different day care facilities, and in additional 24 age-matched home care children.

Study result show that *day care attendance is a significant and impactful factor in shaping the microbial composition of the growing child, the specific daycare facility and class influence the gut microbiome, and each child becomes more similar to others in their day care.*

Furthermore, in comparison to home care children, day care children have a different gut microbial composition, with enrichment of taxa more frequently observed in older populations. Hence this study provides an evidence that daycare may be an external factor that contributes to gut microbiome maturation and make-up in early childhood.

Source: Yael Haberman, Sheba Medical Center, Tel-Hashomer, Affiliated With The Tel-Aviv University, Tel-Aviv, Israel And Cincinnati Children's Hospital Medical Center And The University Of Cincinnati College Of Medicine, Cincinnati, OH, USA. Gut Microbiome Development In Early Childhood Is Affected By Day Care Attendance. Npj Biofilms Microbiomes 8, 2 (2022). <https://doi.org/10.1038/s41522-021-00265-w>

3. Transcription Shifts In Gut Bacteria Shared Between Mothers And Their Infants

This study demonstrates environment-dependent, strain-specific shifts in gut bacteria function and underscores the importance of metatranscriptomic analysis in microbiome studies.

Source: Tommi Vatanen, Liggins Institute, The University Of Auckland, Private Bag 102904, Auckland, New Zealand And The Broad Institute Of MIT And Harvard, Cambridge, MA, USA. Transcription Shifts In Gut Bacteria Shared Between Mothers And Their Infants. Sci Rep 12, 1276 (2022). <https://doi.org/10.1038/s41598-022-04848-1>

4. Caudovirales Bacteriophages Are Associated With Improved Executive Function And Memory In Flies, Mice, And Humans

This study shows that subjects with increased **Caudovirales** and **Siphoviridae** levels in the gut microbiome had better performance in executive processes and verbal memory.

Conversely, increased **Microviridae** levels were linked to a greater impairment in executive abilities. Microbiota transplantation from human donors with increased specific **Caudovirales** (>90% from the **Siphoviridae family**) levels led to increased scores in the novel object recognition test in mice and up-regulated memory-promoting immediate early genes in the prefrontal cortex. Further, supplementation of the Drosophila diet with the 936 group of **lactococcal Siphoviridae** bacteriophages resulted in increased memory scores and upregulation of memory-involved brain genes. Thus, bacteriophages warrant consideration as novel actors in the microbiome-brain axis.

Source: José-Manuel Fernández, Department Of Diabetes, Endocrinology, And Nutrition, Dr. Josep Trueta University Hospital; Nutrition, Eumetabolism, And Health Group, Girona Biomedical Research Institute (Idibgi), Girona, Spain; Centro De Investigación Biomédica En Red Fisiopatología De La Obesidad Y Nutrición (CIBEROBN), Madrid, Spain And Department Of Medical Sciences, School Of Medicine, University Of Girona, Girona, Spain. Caudovirales Bacteriophages Are Associated With Improved Executive Function And Memory In Flies, Mice, And Humans. Journal Cell Host And Microbe, Volume 30, Issue 3, 9 March (2022), Pages 340-356.e8. <https://doi.org/10.1016/j.chom.2022.01.013>

5. Combination Of Gut Microbiota And Plasma Amyloid-B As A Potential Index For Identifying Preclinical Alzheimer's Disease: A Cross-Sectional Analysis From The SILCODE Study

This study provided the evidence that the gut microbial composition was altered in preclinical Alzheimer's disease (AD). The combination of plasma A β and gut microbiota may serve as a non-invasive, cost-effective diagnostic tool for early AD screening. Further, targeting the gut microbiota may be a novel therapeutic strategy for AD.

Source: Ying Han, Department Of Neurology, Xuanwu Hospital Of Capital Medical University, Beijing; Key Laboratory Of Biomedical Engineering Of Hainan Province, School Of Biomedical Engineering, Hainan University, Haikou; Center Of Alzheimer's Disease, Beijing Institute For Brain Disorders, Beijing And National Clinical Research Center For Geriatric Diseases, Beijing, China. *Combination Of Gut Microbiota And Plasma Amyloid-B As A Potential Index For Identifying Preclinical Alzheimer's Disease: A Cross-Sectional Analysis From The SILCODE Study*. *Alz Res Therapy* 14, 35 (2022). <https://doi.org/10.1186/s13195-022-00977-x>

6. Trait Energy and Fatigue May Be Connected To Gut Bacteria Among Young Physically Active Adults: An Exploratory Study

This exploratory study investigated the correlation between mental energy (ME), mental fatigue (MF), physical energy (PE), physical fatigue (PF), and the gut microbiome. The four moods were assessed by survey, and the gut microbiome and metabolome were determined from 16 S rRNA analysis and untargeted metabolomics analysis, respectively.

Study result shows that *Bacteroidetes* (45%), the most prominent phyla, was only negatively correlated with PF. The second most predominant and *butyrate-producing phyla*, *Firmicutes* (43%), had members that correlated with each trait. However, the *bacteria Anaerostipes* was positively correlated with ME and negatively with MF and PF respectively. Diet influences the gut microbiota composition, and only one food group, processed meat, was correlated with the four moods—positively with MF and PF and negatively with ME and PE. Only the *Firmicutes genus Holdemania* was correlated with processed meat. Distinct metabolic profiles were observed, yet these profiles were not significantly correlated with the traits. The findings of this study suggest that energy and fatigue are unique traits that could be defined by distinct bacterial communities not driven by diet. Larger studies are needed to confirm these exploratory findings.

Source: Dr Ali Boolani, Department of Physical Therapy and Department of Biology, Clarkson University, Potsdam, NY, USA. *Trait Energy and Fatigue May Be Connected to Gut Bacteria among Young Physically Active Adults: An Exploratory Study*. *Nutrients* (2022), 14(3), 466. <https://doi.org/10.3390/nu14030466>

7. Metabolomic And Microbiome Profiling Reveals Personalized Risk Factors For Coronary Artery Disease

This study results highlight the utility of the serum metabolome in understanding the basis of risk-factor heterogeneity in Coronary Artery Disease(CAD).

Source: Eran Segal, Department Of Computer Science And Applied Mathematics, Weizmann Institute Of Science And Department Of Molecular Cell Biology, Weizmann Institute Of Science, Rehovot, Israel. *Metabolomic And Microbiome Profiling Reveals Personalized Risk Factors For Coronary Artery Disease*. *Nat Med* 28, 295–302 (2022). <https://doi.org/10.1038/s41591-022-01686-6>

8. Maternal Anthropometric Variables And Clinical Factors Shape Neonatal Microbiome

In this study the meconium microbiome composition and the predicted microbial metabolic pathways were analyzed in a consecutive cohort of 96 full-term newborns.

Scientists have found that **meconium microbiome composition** mainly included *Proteobacteria* (30.95%), *Bacteroidetes* (23.17%) and *Firmicutes* (17.13%), while for predicted metabolic pathways, the most abundant genes belonged to the class “metabolism”. They have also found a significant effect of maternal Rh factor on Shannon and Inverse Simpson indexes and a significant effect of delivery mode and maternal antibiotic exposure on Jaccard and Bray–Curtis dissimilarities, while gestational age was associated with observed richness and Shannon indexes and Jaccard and Bray–Curtis dissimilarities. The association involving maternal Rh phenotype suggests a role for host genetics in shaping meconium microbiome prior to the exposition to the most well-known environmental variables, which will influence microbiome maturation in the newborn.

Source: Cosmeri Rizzato, Department Of Translational Research And Of New Technologies In Medicine And Surgery, University Of Pisa, Via San Zeno 37, 56127, Pisa, Italy. *Maternal Anthropometric Variables And Clinical Factors Shape Neonatal Microbiome*. *Sci Rep* 12, 2875 (2022). <https://doi.org/10.1038/s41598-022-06792-6>

9. Microbiome And Metabolome Features Of The Cardiometabolic Disease Spectrum

In this study researchers have found that about 75% of microbiome and metabolome features that distinguish individuals with ischemic heart disease (IHD) from healthy individuals after adjustment for effects of medication and lifestyle are present in individuals exhibiting dysmetabolism, suggesting that major alterations of the gut microbiome and metabolome might begin long before clinical onset of IHD.

They have further categorized microbiome and metabolome signatures related to prodromal dysmetabolism, specific to IHD in general or to each of its three subtypes or related to escalation or de-escalation of IHD. Discriminant analysis based on specific IHD microbiome and metabolome features could better differentiate individuals with IHD from healthy individuals or metabolically matched individuals as compared to the conventional risk markers, pointing to a pathophysiological relevance of these features.

Source: Oluf Pedersen, Novo Nordisk Foundation Center For Basic Metabolic Research, Faculty Of Health And Medical Sciences, University Of Copenhagen, Copenhagen, Denmark. Microbiome And Metabolome Features Of The Cardiometabolic Disease Spectrum. Nat Med 28, 303-314 (2022). <https://doi.org/10.1038/s41591-022-01688-4>

10. A Posteriori Dietary Patterns Better Explain Variations Of The Gut Microbiome Than Individual Markers In The American Gut Project

This study demonstrated that in global-diet a posteriori patterns were more associated with gut microbiome variations than individual dietary features among adults in the United States. These results confirm that evaluating diet as a whole is important when studying the gut microbiome. Further, it will also facilitate the design of more personalized dietary strategies in general populations.

Source: Aurélie Cotillard, Danone Nutricia Research, Palaiseau, France A Posteriori Dietary Patterns Better Explain Variations Of The Gut Microbiome Than Individual Markers In The American Gut Project. The American Journal Of Clinical Nutrition, Volume 115, Issue 2, February (2022), Pages 432-443. <https://doi.org/10.1093/ajcn/nqab332>

11. Association Between The Mode Of Delivery And Infant Gut Microbiota Composition Up To 6 Months Of Age: A Systematic Literature Review Considering The Role Of Breastfeeding

This systematic review explores the evidence of the association between mode of delivery and infant gut microbiota up to 6 months of age and the role of breastfeeding in this association was evaluated according to PRISMA guidelines.

Researchers have found that infants born by Cesarean section (CS) had a lower abundance of *Bifidobacterium* and *Bacteroides spp.* at almost all points up to age 6 months. Populations of *Lactobacillus*, *Bifidobacterium longum*, *Bifidobacterium catenulatum*, and *Escherichia coli* were reduced in infants delivered by CS. Infants born by CS and exclusively breastfed had greater similarity with the microbiota of infants born by vaginal delivery (VD).

Source: Gilberto Kac, Department Of Social And Applied Nutrition, Federal University Of Rio De Janeiro, Josué De Castro Nutrition Institute, Rio De Janeiro, RJ Brazil. Association Between The Mode Of Delivery And Infant Gut Microbiota Composition Up To 6 Months Of Age: A Systematic Literature Review Considering The Role Of Breastfeeding. Nutrition Reviews, Volume 80, Issue 1, January (2022), Pages 113-127. <https://doi.org/10.1093/nutri/nuab008>

12. Collective Effects Of Human Genomic Variation On Microbiome Function

This study presents a new and flexible framework for examining host-microbiome genetic interactions, and provides a new dimension to the current debate around the role of human genetics on the gut microbiome.

Source: Ilana L. Brito, Meinig School Of Biomedical Engineering, Cornell University, Ithaca, NY, USA. Collective Effects Of Human Genomic Variation On Microbiome Function. Sci Rep 12, 3839 (2022). <https://doi.org/10.1038/s41598-022-07632-3>

13. Altered Gut Metabolites And Microbiota Interactions Are Implicated In Colorectal Carcinogenesis And Can Be Non-Invasive Diagnostic Biomarkers

This study underscores potential early-driver metabolites in stages of colorectal tumorigenesis. The Integrated metabolite and microbiome analysis demonstrates that gut metabolites and their association with gut microbiota are perturbed along colorectal carcinogenesis. Further, Fecal metabolites can be utilized, in addition to bacteria, for non-invasive diagnosis of colorectal neoplasia.

Source: Jun Yu, State Key Laboratory Of Digestive Disease, Li Ka Shing Institute Of Health Sciences, CUHK Shenzhen Research Institute And Department Of Medicine And Therapeutics, The Chinese University Of Hong Kong, Shatin, NT, Hong Kong, China. Altered Gut Metabolites And Microbiota Interactions Are Implicated In Colorectal Carcinogenesis And Can Be Non-Invasive Diagnostic Biomarkers. J Microbiome 10, 35 (2022). <https://doi.org/10.1186/s40168-021-01208-5>

14. Microbiome And Metabolome Profiles Of High Screen Time In A Cohort Of Healthy College Students

In this study, researchers explored the fecal microbiome and metabolome of a diverse group of college students, classified by high (≥ 75 min/day) or low (0–75 min/day) screen time.

The taxonomic profile of the microbiome, but not overall diversity, modestly differed between the two classifications of screen time. Indeed, several **health-associated microbes** such as **Bacteroides**, **Akkermansia**, **Alistipes**, **Ruminococcus**, **Sutterella**, **Oscillospira**, and **Methanobrevibacter** were found to be more associated with low screen time, even after accounting for physical activity, sex, BMI, and age.

This finding suggests that compositional differences may occur based on daily screen time. Meanwhile, the metabolome proved to be a sensitive marker of screen time; a panel of five metabolites were significant lower in the high screen time group. Predicted functional analysis of the microbiome revealed significant enrichment of numerous enzymes and taxa associated with various disease, diet, and lifestyle factors. Predicted metabolomic states indicated enrichment of several other enzymes, pathways, and disease profiles. Cumulatively, our results revealed dysfunction of amino acid metabolism which related to several key taxa.

Source: Corrie Whisner, College Of Health Solutions, Arizona State University, Phoenix, AZ And Biodesign Institute Center For Health Through Microbiomes, Arizona State University, Tempe, AZ, USA. Microbiome And Metabolome Profiles Of High Screen Time In A Cohort Of Healthy College Students. Sci Rep 12, 3452 (2022). <https://doi.org/10.1038/s41598-022-07381-3>

15. Effects Of Early-Life Antibiotics On The Developing Infant Gut Microbiome And Resistome: A Randomized Trial

In this study scientists have found that there was decrease in the abundance of Bifidobacterium spp. and increased abundance of Klebsiella and Enterococcus spp. in the antibiotic treated infants compared to controls. Amoxicillin + cefotaxime show the largest effects on both microbial community composition and antimicrobial resistance gene profile, whereas penicillin + gentamicin exhibit the least effects. These data suggest that the choice of empirical antibiotics is relevant for adverse ecological side-effects.

Source: Debby Bogaert, Department Of Pediatric Immunology And Infectious Diseases, Wilhelmina Children's Hospital And University Medical Center Utrecht, Utrecht, The Netherlands And Medical Research Council And University Of Edinburgh Centre For Inflammation Research, Queen's Medical Research Institute, University Of Edinburgh, Edinburgh, UK. Effects Of Early-Life Antibiotics On The Developing Infant Gut Microbiome And Resistome: A Randomized Trial. Nat Commun 13, 893 (2022). <https://doi.org/10.1038/s41467-022-28525-z>

16. Relationship Between Gut Microbiome Characteristics And The Effect Of Nutritional Therapy On Glycemic Control In Pregnant Women With Gestational Diabetes Mellitus

The objective of this study was to explore the relationship between the characteristics of gut microbiome and the effect of medical nutrition therapy (MNT) on glycemic control in pregnant women with gestational diabetes mellitus (GDM).

Study result shows that the decrease in the abundance of characteristic gut microbiome positively correlated with blood glucose may be a factor influencing the poor hypoglycemic effect of MNT in pregnant women with GDM. Abundance of more characteristic gut microbiome negatively correlated with blood glucose could help control blood glucose in pregnant women with GDM.

Source: Mei Zhao, School Of Nursing, Anhui Medical University, Hefei, Anhui Province, The People's Republic Of China. Relationship Between Gut Microbiome Characteristics And The Effect Of Nutritional Therapy On Glycemic Control In Pregnant Women With Gestational Diabetes Mellitus. PLoS One, (2022) Apr 15;17(4):e0267045. <https://doi.org/10.1371/journal.pone.0267045>

17. Associations Of The Dietary Inflammatory Index With Total Adiposity And Ectopic Fat Through The Gut Microbiota, LPS, And C-Reactive Protein In The Multiethnic Cohort-Adiposity Phenotype Study

The aim of this study was to assess whether any associations seen between the Energy-Adjusted Dietary Inflammatory Index (E-DII score), total fat mass, visceral adipose tissue (VAT), or liver fat (percentage volume) operated through the gut microbiome (GM) or microbial related inflammatory factors, in a multiethnic cross-sectional study.

Study result shows that there were positive total effects (c) between Energy-Adjusted Dietary Inflammatory Index (E-DII) and total fat mass, visceral adipose tissue (VAT) and liver fat.

The association between E-DII score and total fat mass was mediated by LPS, *Flavonifractor*, [*Ruminococcus*] *gnavus* group, and *Tyzzere*lla. The association between E-DII score and ectopic fat occurred indirectly through *Fusobacteria*, *Christensenellaceae R-7* group, *Coprococcus 2*, *Escherichia-Shigella*, [*Eubacterium*] *xylanophilum* group, *Flavonifractor*, *Lachnospirillum*, [*Ruminococcus*] *gnavus* group, *Tyzzere*lla, [*Ruminococcus*] *gnavus* group (VAT only), and α diversity (liver fat only). Further, there was no significant association between E-DII score and adiposity phenotype through hs-CRP.

Source: Chloe P Lozano, University Of Hawaii Cancer Center, Honolulu, HI, USA. Associations Of The Dietary Inflammatory Index With Total Adiposity And Ectopic Fat Through The Gut Microbiota, LPS, And C-Reactive Protein In The Multiethnic Cohort-Adiposity Phenotype Study. *The American Journal of Clinical Nutrition*, Volume 115, Issue 5, May (2022), Pages 1344-1356. <https://doi.org/10.1093/ajcn/nqab398>

18. The Impact Of The Human Microbiome In Tumorigenesis, Cancer Progression, And Biotherapeutic Development

This systematic review concluded that research investigating the impact of the human microbiome in cancer has recently gathered pace. Vast amounts of evidence indicate the human microbiome as a potential player in tumorigenesis and progression. Promise in the development of cancer biomarkers and in targeted oncological therapies has also been demonstrated, although more studies are needed.

Despite extensive in vitro and in vivo research, clinical studies involving large cohorts of human patients are lacking. The current literature suggests that further intensive research is necessary to validate both the role of the human microbiome in cancer, and the use of microbiome modification in cancer therapy.

Source: Caitriona M. Guinane, Department Of Biological Sciences, Munster Technological University, Cork, Ireland. The Impact Of The Human Microbiome In Tumorigenesis, Cancer Progression, And Biotherapeutic Development. *BMC Microbiol* 22, 53 (2022). <https://doi.org/10.1186/s12866-022-02465-6>

19. Impact Of Intensive Lifestyle Intervention On Gut Microbiota Composition In Type 2 Diabetes: A Post-Hoc Analysis Of A Randomized Clinical Trial

Researchers have found that there were no statistical differences in the change of gut microbiota composition between treatments after 12 months, except minor and transient differences at month 3.

The shift in gut microbiota alpha diversity at all time windows did not correlate with the change in clinical characteristics, and the gut microbiota did not mediate the treatment effect on clinical characteristics. The clinical benefits of intensive lifestyle and/or pharmacological interventions in T2D are unlikely to be explained by, or causally related to, changes in the gut microbiota composition.

Source: Soren Johannes Sorensena, Section Of Microbiology, Department Of Biology, University Of Copenhagen, Copenhagen, Denmark. Impact Of Intensive Lifestyle Intervention On Gut Microbiota Composition In Type 2 Diabetes: A Post-Hoc Analysis Of A Randomized Clinical Trial. *Gut Microbes*, Volume 14, (2022) - Issue 1. <https://doi.org/10.1080/19490976.2021.2005407>

20. The Oral, Gut Microbiota And Cardiometabolic Health Of Indigenous Orang Asli Communities

The **Orang Asli** (OA) is heterogeneous indigenous population forming a national minority in Malaysia. They are the oldest inhabitants of Peninsular Malaysia. This study first assessed the cardiometabolic health in four OA communities ranging from urban, rural to semi-nomadic hunter-gatherers.

Researchers have found that the **urban Temuan** suffered from poorer cardiometabolic health while **rural OA** communities were undergoing epidemiological transition. The oral microbiota of the OA were characterized by sequencing the V4 region of the 16S rRNA gene. The OA oral microbiota were unexpectedly homogenous, with comparably low alpha diversity across all four communities. The **rural Jehai** and **Temiar PP** oral microbiota were enriched for uncharacterized bacteria, exhibiting potential for discoveries.

The **Temuan** oral microbiota were also elevated in opportunistic pathogens such as *Corynebacterium*, *Prevotella*, and *Mogibacterium*, suggesting possible oral dysbiosis in these urban settlers. The **semi-nomadic Jehai** gut microbiota had the highest alpha diversity, while **urban Temuan** exhibited the lowest. Rural OA gut microbiota were distinct from urban-like microbiota and were elevated in bacteria genera such as *Prevotella 2*, *Prevotella 9*, *Lachnospiraceae ND3007*, and *Solobacterium*. Urban Temuan microbiota were enriched in *Odoribacter*, *Blautia*, *Parabacetroides*, *Bacteroides* and *Ruminococcaceae UCG-013*.

Source: Maude Elvira Phipps, Jeffrey Cheah School Of Medicine & Health Sciences, Monash University Malaysia And Tropical Medicine And Biology Multidisciplinary Platform, School Of Science, Monash University Malaysia, Bandar Sunway, Malaysia. The Oral, Gut Microbiota And Cardiometabolic Health Of Indigenous Orang Asli Communities. *Front. Cell. Infect. Microbiol.*, 22 April 2022, Sec. Microbiome in Health and Disease, Volume 12 - (2022). <https://doi.org/10.3389/fcimb.2022.812345>

21. A Guide To Dietary Pattern-Microbiome Data Integration

This systematic review identified a substantial and growing body of literature that explores links between the microbiome and dietary patterns. 54 studies were identified in this review which used ≥ 7 different methods to assess diet.

This review summarizes the current state of the art for diet-microbiome data integration and highlights ways dietary data could be paired with microbiome data in future studies to improve the detection of diet-microbiome signals.

Source: Abigail J Johnson, Division Of Epidemiology And Community Health, University Of Minnesota, School Of Public Health, Minneapolis, MN. A Guide To Dietary Pattern-Microbiome Data Integration. *The Journal Of Nutrition*, Volume 152, Issue 5, (2022), Pages 1187-1199, ISSN 0022-3166. DOI: 10.1093/jn/nxac033

22. Mycobiota Composition And Changes Across Pregnancy In Patients With Gestational Diabetes Mellitus (GDM)

The human mycobiota is a neglected component of the microbiome, including all the different fungal species living in the human host. This study aimed to analyze the fecal mycobiota of GDM patients during the second (T₂) and third (T₃) trimester of pregnancy and to compare it with the mycobiota of pregnant normoglycemic women (controls).

Researchers have found that GDM mycobiota was composed almost exclusively of *Ascomycota* phylum; *Basidiomycota* accounted for 43% relative to the controls. *Kluyveromyces*, *Metschnikowia*, and *Pichia* showed a significantly higher frequency in GDM patients, while *Saccharomyces* were more prevalent in controls. From T₂ to T₃, a reduction in fungal alpha diversity was found in GDM patients, with an increase of the relative frequency of *Candida*, and the reduction of some pro-inflammatory taxa. Many associations between fungi and foods and nutrients were detected. Finally, several fungi and bacteria showed competition or co-occurrence.

Patients with GDM showed a predominance of fungal taxa with potential inflammatory effects when compared to normoglycemic pregnant women, with a marked shift in their mycobiota during pregnancy, and complex bacteria-fungi interactions.

Source: Simona Bo, Department Of Medical Sciences, University Of Torino, Torino, Italy. Mycobiota Composition And Changes Across Pregnancy In Patients With Gestational Diabetes Mellitus (GDM). *ci Rep* 12, 9192 (2022). <https://doi.org/10.1038/s41598-022-13438-0>

23. The Vaginal Microbiome And The Risk Of Preterm Birth: A Systematic Review And Network Meta-Analysis

The aim of this systematic review and meta-analysis was to investigate the association between the vaginal microbiome, defined as community state types (CSTs, i.e. dominance of specific *lactobacilli* spp, or not (low-lactobacilli)), and the risk of preterm birth.

Researchers have found that women with "low-lactobacilli" vaginal microbiome were at increased risk for delivering preterm compared to *Lactobacillus crispatus* dominant women. Further, network meta-analysis supports the microbiome being predictive of preterm birth, where low abundance of *lactobacilli* is associated with the highest risk, and *L. crispatus* dominance the lowest.

Source: Unnur Gudnadottir, Department Of Microbiology, Tumor And Cell Biology (MTC), Centre For Translational Microbiome Research, Karolinska Institutet, Solna/Stockholm, Sweden. The Vaginal Microbiome And The Risk Of Preterm Birth: A Systematic Review And Network Meta-Analysis. *Sci Rep* 12, 7926 (2022). <https://doi.org/10.1038/s41598-022-12007-9>

24. The Promise Of The Gut Microbiome As Part Of Individualized Treatment Strategies

This systematic review discussed six broad disease groups: infectious disease, cancer, metabolic disease, cardiovascular disease, autoimmune or inflammatory disease, and allergic and atopic diseases. It highlights current knowledge on the gut microbiome in disease pathogenesis and prognosis, efficacy, and treatment-related adverse events and its promise for stratifying existing treatments and as a source of novel therapies. It also highlights the potential implications of the microbiome as a tool to individualize treatment strategies in clinical practice.

Source: Purna C. Kashyap, Division Of Gastroenterology And Hepatology, Mayo Clinic, Rochester And Department Of Physiology And Biomedical Engineering, Mayo Clinic, Rochester, MN, USA. The Promise Of The Gut Microbiome As Part Of Individualized Treatment Strategies. *Nat Rev Gastroenterol Hepatol* 19, 7-25 (2022). <https://doi.org/10.1038/s41575-021-00499-1>

25. Gut Virome Profiling Identifies A Widespread Bacteriophage Family Associated With Metabolic Syndrome

This study shows **gut virome changes** associated with metabolic syndrome (MetS), a highly prevalent clinical condition preceding cardiometabolic disease, in 196 participants by combined sequencing of bulk whole genome and virus like particle communities.

Researchers found that MetS gut viromes exhibit decreased richness and diversity. They are enriched in phages infecting *Streptococcaceae* and *Bacteroidaceae* and depleted in those infecting *Bifidobacteriaceae*. Differential abundance analysis identifies eighteen viral clusters (VCs) as significantly associated with either MetS or healthy viromes. Among these are a MetS-associated *Roseburia* VC that is related to healthy control-associated *Faecalibacterium* and *Oscillibacter* VCs.

Further analysis of these VCs revealed the *Candidatus Heliusviridae*, a highly widespread gut phage lineage found in 90+% of participants. The identification of the temperate *Ca. Heliusviridae* provides a starting point to studies of phage effects on gut bacteria and the role that this plays in MetS.

Source: Hilde Herrema, Departments Of Internal And Experimental Vascular Medicine, Amsterdam University Medical Centers; Amsterdam Gastroenterology Endocrinology Metabolism, Endocrinology, Metabolism And Nutrition And Amsterdam Cardiovascular Sciences, Diabetes & Metabolism, Amsterdam, The Netherlands. Gut Virome Profiling Identifies A Widespread Bacteriophage Family Associated With Metabolic Syndrome. Nat Commun 13, 3594 (2022). <https://doi.org/10.1038/s41467-022-31390-5>

26. The Gut Microbiome And Mental Health: Advances In Research And Emerging Priorities

This **review article** explores the recent advances in gut microbiome–brain interactions, the mechanistic underpinnings of these relationships, and the ongoing challenge of distinguishing association and causation.

Source: Geraint B. Rogers, Microbiome And Host Health, South Australian Health And Medical Research Institute, Adelaide And Infection And Immunity, Flinders Health And Medical Research Institute, College Of Medicine And Public Health, Flinders University, Bedford Park, Australia. The Gut Microbiome And Mental Health: Advances In Research And Emerging Priorities. Mol Psychiatry 27, 1908–1919 (2022). <https://doi.org/10.1038/s41380-022-01479-w>

27. Personal Diet–Microbiota Interactions And Weight Loss

This **systematic review** provides an overview of how person-specific interactions between diet and the gut microbiota could play a role in affecting diet-induced weight loss responses.

Source: Henrik M. Roager, Department Of Nutrition, Exercise And Sports, University Of Copenhagen, Frederiksberg, Denmark. Personal Diet–Microbiota Interactions And Weight Loss. Proceedings Of The Nutrition Society , Volume 81 , Issue 3 , September (2022) , Pp. 243 – 254. <https://doi.org/10.1017/S0029665122000805>

28. The Common And Unique Pattern Of Microbiome Profiles Among Saliva, Tissue, And Stool Samples In Patients With Crohn’s Disease

This study aimed to elucidate common and unique microbiome patterns in saliva, intestinal tissue biopsy, and stool samples from patients with Crohn’s disease (CD).

Scientists found that the composition of major microbial taxa was similar between tissue and stool samples. The microbial community in saliva was significantly distinct from that in tissue and stool. The major species of microbiota and their composition also differed significantly from those of tissue and stool samples. However, *Streptococcus* and *Prevotella* are common genera in saliva, tissue, and stool microbiome. The abundance of *Streptococcus*, *Pantoea*, and *Actinomyces* from the saliva sample group was significantly different, varying with the location of the inflammation. Saliva has a distinct microbial community compared with tissues and stools in patients with CD. *Prevotella* and *Streptococcus*, which are commonly observed in saliva, stool, and tissue, can be considered a potential biomarker related to the diagnosis or prognosis of CD.

Source: Dong Il Park, Division Of Gastroenterology, Department Of Internal Medicine And Inflammatory Bowel Disease Center, Kangbuk Samsung Hospital And Medical Research Institute, Kangbuk Samsung Hospital, Sungkyunkwan University School Of Medicine, Seoul, Korea. The Common And Unique Pattern Of Microbiome Profiles Among Saliva, Tissue, And Stool Samples In Patients With Crohn’s Disease. Microorganisms (2022), 10(7), 1467. <https://doi.org/10.3390/microorganisms10071467>

29. Gut Microbiota–Derived Metabolite Trimethylamine-N-Oxide And Multiple Health Outcomes: An Umbrella Review And Updated Meta-Analysis

This **review and meta-analysis** summarizes health outcomes related to circulating Trimethylamine-N-Oxide (TMAO) concentrations. Scientists have concluded that TMAO might be a novel biomarker related to human health conditions including all-cause mortality, hypertension, cardiovascular diseases (CVD), Diabetes Mellitus (DM), cancer, and kidney function. Further studies are needed to investigate whether circulating TMAO concentrations could be an intervention target for chronic disease.

Source: Xue Li, Department Of Big Data In Health Science, School Of Public Health, Center Of Clinical Big Data And Analytics Of The Second Affiliated Hospital, Zhejiang University School Of Medicine, Hangzhou, China. Gut Microbiota–Derived Metabolite Trimethylamine-N-Oxide And Multiple Health Outcomes: An Umbrella Review And Updated Meta-Analysis. The American Journal Of Clinical Nutrition, Volume 116, Issue 1, July (2022), Pages 230–243. <https://doi.org/10.1093/ajcn/nqac074>

30. Impact of Environmental Pollutants on Gut Microbiome and Mental Health via the Gut–Brain Axis

This systematic review discussed how various environmental pollutants such as phthalates, heavy metals, Bisphenol A and particulate matter may alter the intricate microbiota–gut–brain axis thereby impacting neurological and overall mental health.

Source: Ravinder Nagpal, Department Of Nutrition And Integrative Physiology, Florida State University, Tallahassee, USA. *Impact of Environmental Pollutants on Gut Microbiome and Mental Health via the Gut–Brain Axis. Microorganisms* (2022), 10(7), 1457; <https://doi.org/10.3390/microorganisms10071457>

31. Mode Of Delivery Modulates The Intestinal Microbiota And Impacts The Response To Vaccination

The gut microbiota in early life, when critical immune maturation takes place, may influence the immunogenicity of childhood vaccinations. This study assessed the association between mode of delivery, gut microbiota development in the first year of life, and mucosal antigen-specific antibody responses against pneumococcal vaccination in 101 infants at age 12 months and against meningococcal vaccination in 66 infants at age 18 months.

Researchers have found that birth by vaginal delivery is associated with higher antibody responses against both vaccines. Relative abundances of vaginal birth-associated *Bifidobacterium* and *Escherichia coli* in the first weeks of life are positively associated with anti-pneumococcal antibody responses, and relative abundance of *E. coli* in the same period is also positively associated with anti-meningococcal antibody responses.

Source: Debby Bogaert, Department Of Paediatric Immunology And Infectious Diseases, Wilhelmina Children's Hospital And University Medical Centre Utrecht, Utrecht; Centre For Infectious Disease Control, National Institute For Public Health And The Environment, Bilthoven, Netherlands And Medical Research Council And University Of Edinburgh Centre For Inflammation Research, Queen's Medical Research Institute, University Of Edinburgh, Edinburgh, UK. *Mode Of Delivery Modulates The Intestinal Microbiota And Impacts The Response To Vaccination. Nat Commun* 13, 6638 (2022). <https://doi.org/10.1038/s41467-022-34155-2>

32. Impacts Of Breast Cancer And Chemotherapy On Gut Microbiome, Cognitive Functioning, And Mood Relative To Healthy Controls

This cross-sectional study explored the associations of self-reported cognitive functioning, depression, and anxiety symptoms, and gut microbiome diversity and community composition in women who were diagnosed with and undergoing chemotherapy treatment for breast cancer (BC) compared to cancer-free healthy controls (HC).

Study result shows that the BC group displayed higher rates of cognitive dysfunction and depressive symptoms relative to HC. There was a significant difference in microbiome community composition between BC and HC, particularly characterized by a decreased relative abundance of the mucin-degrading genus Akkermansia in BC compared to HC. Association models identified significant associations among group, cognitive, depression, and microbiome variables. Overall, the study identified that BC participants experienced significant differences in self-reported cognitive functioning, self-reported depression symptoms, microbiome community composition, and mucin-degrading bacteria of the gut-mucosal barrier, relative to HC. Further, this study is consistent with the hypothesis that gut microbiome community composition impacts a woman's experience with breast cancer and treatment suggesting that microbiome-based interventions have potential for improving quality of life outcomes in individuals with breast cancer.

Source: Emily Bilenduke, Department Of Psychology, University Of Colorado Denver, Denver, CO, USA. *Impacts Of Breast Cancer And Chemotherapy On Gut Microbiome, Cognitive Functioning, And Mood Relative To Healthy Controls. S Sci Rep* 12, 19547 (2022). <https://doi.org/10.1038/s41598-022-23793-7>

33. Evaluation Of The Effects Of The Tritordeum-Based Diet Compared To The Low-FODMAPS Diet On The Fecal Metabolome Of IBS-D Patients: A Preliminary Investigation

In this study researchers have investigated the impact of *Tritordeum-Based Diet (TBD)* and *Low-FODMAPS Diet (LFD)* on the fecal metabolome composition in 38 IBS-D patients randomly allocated to the two diets for 12 weeks.

Scientists have found that at baseline, the profile of fecal volatile organic compounds (VOCs) of IBS-D patients was not significantly different in the two groups. After treatment, significant changes were observed in the two groups regarding the VOCs content since some of them increased in the TBD group (namely, decanoic acid), whereas others (i.e., nonanal and ethanol) increased in the LFD one. Further, at baseline, short-chain fatty acids were positively related to inflammation and showed a significant decreasing trend after both diets compared to baseline values (namely, acetic and propanoic acid). TB Diet are the combination of durum wheat (*Triticum durum*) and wild barley (*Hordeum chilense*) whereas FODMAPs Diet includes low-fermentable oligosaccharides, disaccharides, monosaccharides and polyols.

This study suggests a potential positive intervention of TBD and LFD affecting the fecal metabolome composition in IBS-D patients.

Source: Francesco Russo, National Institute Of Gastroenterology "S. De Bellis" Research Hospital, Castellana Grotte, Italy. *Evaluation Of The Effects Of The Tritordeum-Based Diet Compared To The Low-FODMAPS Diet On The Fecal Metabolome Of IBS-D Patients: A Preliminary Investigation. Nutrients* (2022), 14(21), 4628. <https://doi.org/10.3390/nu14214628>

34. Impact Of Total Parenteral Nutrition On Gut Microbiota In Pediatric Population Suffering Intestinal Disorders

This systematic review synthesizes the current evidence on the effects of Parenteral Nutrition (PN) on gut microbiome in infants and children suffering from diverse gastrointestinal diseases, including necrotizing enterocolitis (NEC), short bowel syndrome (SBS) and subsequent intestinal failure, liver disease and inflammatory bowel disease (IBD). They have also discussed the potential use of pre-, pro- and/or synbiotics as promising therapeutic strategies to reduce the risk of severe gastrointestinal disorders and mortality.

Source: Cristina Campoy, EURISTIKOS Excellence Centre For Paediatric Research, Biomedical Research Centre; Department Of Paediatrics, School Of Medicine, University Of Granada, Granada; And Spanish Network Of Biomedical Research In Epidemiology And Public Health (CIBERESP), Granada's Node, Carlos III Health Institute, Avda. Monforte De Lemos, Spain. Impact Of Total Parenteral Nutrition On Gut Microbiota In Pediatric Population Suffering Intestinal Disorders. Nutrients (2022), 14(21), 4691. <https://doi.org/10.3390/nu14214691>

35. The Role Of Gut Microbiota—Gut—Brain Axis In Perioperative Neurocognitive Dysfunction

This systematic review highlights the mechanism of the role of gut microbiota-gut-brain axis in Perioperative Neurocognitive Dysfunction (PND) which helps to explore reasonable early treatment strategies.

Source: Youming Zong, Department Of Anesthesiology, The Second Hospital Of Jiaxing, The Second Affiliated Hospital Of Jiaxing University, Jiaxing And Department Of Anesthesiology, Bengbu Medical College, Bengbu, China. The Role Of Gut Microbiota—Gut—Brain Axis In Perioperative Neurocognitive Dysfunction. Front. Pharmacol., 14 June (2022), Sec. Neuropharmacology, Volume 13 - 2022. <https://doi.org/10.3389/fphar.2022.879745>

36. The Heart And Gut Relationship: A Systematic Review Of The Evaluation Of The Microbiome And Trimethylamine-N-Oxide (TMAO) In Heart Failure

This systematic review explores the current state of the science on the evaluation and testing of the gut biome in persons with HF. Researchers have identified 51 HF (heart failure) biome investigations between 2014 and 2021. 30 studies were included in the review, six were 16S rRNA and nineteen trimethylamine-N-oxide (TMAO), and three both TMAO and 16S rRNA, and two bacterial cultures. A limited range of study designs were represented, the majority involving single cohorts (n=10) and comparing individuals with HF to controls (n=15).

Study results show that patients with HF had less biodiversity in fecal samples compared to controls. TMAO is associated with age, BNP, eGFR, HF severity, and poor outcomes including hospitalizations and mortality. Inconsistent across studies was the ability of TMAO to predict HF development, the independent prognostic value of TMAO when controlling for renal indices, and the relationship of TMAO to LVEF and CRP. Gut microbiome dysbiosis is associated with HF diagnosis, disease severity, and prognostication related to hospitalizations and mortality. Gut microbiome research in patients with HF is developing.

Further longitudinal and multi-centered studies are required to inform interventions to promote clinical decision-making and improved patient outcomes.

Source: Kelley M. Anderson, School Of Nursing & Health Studies, Georgetown University, 3700 Reservoir Rd NW, Washington, DC, USA. Lack Of Biodiversity In The Gut Or Elevated Metabolites Associated With Heart Failure Severity. The Heart And Gut Relationship: A Systematic Review Of The Evaluation Of The Microbiome And Trimethylamine-N-Oxide (TMAO) In Heart Failure. Heart Fail Rev 27, 2223-2249 (2022). <https://doi.org/10.1007/s10741-022-10254-6>

37. Western-Style Diet, Pks Island-Carrying Escherichia Coli, And Colorectal Cancer: Analyses From Two Large Prospective Cohort Studies

Evidence supports a carcinogenic role of Escherichia coli carrying the pks island that encodes enzymes for colibactin biosynthesis. In this study researchers have explored the association of the Western-style diet (rich in red and processed meat) with colorectal cancer incidence might be stronger for tumors containing higher amounts of pks+ E coli.

This study concluded that the Western-style diet is associated with a higher incidence of colorectal cancer containing abundant pks+ E coli, supporting a potential link between diet, the intestinal microbiota, and colorectal carcinogenesis.

Source: Shuji Ogino, MD, Ph.D., MS, Program In MPE Molecular Pathological Epidemiology, Department Of Pathology, Brigham And Women's Hospital, Boston, MA. Western-Style Diet, Pks Island-Carrying Escherichia Coli, And Colorectal Cancer: Analyses From Two Large Prospective Cohort Studies. Gastroenterology, Volume 163, Issue 4, P862-874, October (2022). <https://doi.org/10.1053/j.gastro.2022.06.054>

38. Rethinking Healthy Eating In Light Of The Gut Microbiome

In this **systematic review**, scientists have discussed contemporary nutritional recommendations from a microbiome science perspective, focusing on mechanistic evidence that established host-microbe interactions as mediators of the physiological effects of diet. Researchers have applied this knowledge to inform discussions of nutrition controversies, advance innovative dietary strategies, and propose an experimental framework that integrates the microbiome into nutrition research.

Further, the congruence of key paradigms in the nutrition and microbiome disciplines validates current recommendations in dietary guidelines, and the systematic incorporation of microbiome science into nutrition research has the potential to improve and innovate healthy eating.

Source: Jens Walter, APC Microbiome Ireland, School Of Microbiology, And Department Of Medicine, University College Cork, Cork, Ireland. Rethinking Healthy Eating In Light Of The Gut Microbiome. Cell Host & Microbe, Volume 30, Issue 6, P764-785, June 08, (2022). <https://doi.org/10.1016/j.chom.2022.04.016>

39. The Role Of The Microbiome In The Metabolic Health Of People With Schizophrenia And Related Psychoses: Cross-Sectional And Pre-Post Lifestyle Intervention Analyses

Researchers have found that there was no difference in α -diversity between groups at baseline, but microbial composition differed by 21 taxa between the established schizophrenia group and controls. In people with established illness pre-post comparison of α -diversity showed significant increases after the 12-week lifestyle intervention.

This study adds to the current literature about detailed compositional differences in the gut microbiota of people with schizophrenia compared to those without mental illness and suggests that lifestyle interventions may increase gut microbial diversity in patients with established illness. These results show that microbiome studies are feasible in patients with established schizophrenia. Further, studies are required.

Source: Maryanne O'Donnell, Discipline Of Psychiatry And Mental Health, School Of Medicine And Health, University Of New South Wales, Kensington And Eastern Suburbs Mental Health Service, South Eastern Sydney Local Health District, Randwick, Australia. The Role Of The Microbiome In The Metabolic Health Of People With Schizophrenia And Related Psychoses: Cross-Sectional And Pre-Post Lifestyle Intervention Analyses. Pathogens (2022), 11(11), 1279; <https://doi.org/10.3390/pathogens11111279>

40. Influence Of Food And Nutrition On The Gut Microbiome And Implications For Intestinal Health

This **systematic review** summarizes the current knowledge regarding the impacts of major food components and their metabolites on the gut and health consequences, specifically within the GI tract. The influence of the diet on the gut microbiome-host immune system interaction in IBD is also discussed. Further, understanding the influence of the diet on the interaction of the gut microbiome and the host immune system will be useful in developing nutritional strategies to maintain gut health and restore a healthy microbiome in IBD.

Source: Ping Zhang, Center for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Menglun, China. Influence Of Food And Nutrition On The Gut Microbiome And Implications For Intestinal Health. I Int. J. Mol. Sci. (2022), 23(17), 9588. <https://doi.org/10.3390/ijms23179588>

41. A Review Of The Preclinical And Clinical Studies On The Role Of The Gut Microbiome In Aging And Neurodegenerative Diseases And Its Modulation

In this **review** researchers have reviewed the role of the gut microbiome in aging and neurodegenerative diseases, as well as provided a comprehensive review of recent findings from preclinical and clinical studies to present an up-to-date overview of recent advances in developing strategies to modulate the intestinal microbiome by probiotic administration, dietary intervention, fecal microbiota transplantation (FMT), and physical activity to address the aging process and prevent neurodegenerative diseases.

Source: Suzana Makpol, Department Of Biochemistry, Faculty Of Medicine, Universiti Kebangsaan Malaysia Medical Centre, Kuala Lumpur, Malaysia. A Review Of The Preclinical And Clinical Studies On The Role Of The Gut Microbiome In Aging And Neurodegenerative Diseases And Its Modulation. Front. Cell. Neurosci., 03 November 2022, Sec. Cellular Neuropathology, Volume 16, (2022). <https://doi.org/10.3389/fncel.2022.1007166>

42. Metagenomic Profile Of The Fecal Microbiome Of Preterm Infants Consuming Mother's Own Milk With Bovine Milk–Based Fortifier Or Infant Formula: A Cross-Sectional Study

The goal of this study was to evaluate the metagenomic potential of the fecal microbiome of Preterm (PT) infants consuming mother's own milk (MOM) with bovine milk–based fortifier compared with PT formula alone.

Study result shows that the primary function of the fecal microbiome of PT infants was characterized by a high abundance of biosynthesis pathways. A set of core features was identified; these belonged to pathways for amino acid metabolism and vitamin K-2 biosynthesis. Five pathways significantly differed between the MOM and formula group. Pathways for fatty acid and carbohydrate degradation were significantly higher in the MOM group. Taxonomically, members of *the phylum Actinobacteria* and the *genus Bifidobacterium* were higher in PT infants exposed to MOM.

Source: Sharon M Donovan, Division Of Nutritional Sciences, University Of Illinois Urbana-Champaign, Urbana, IL, USA. Metagenomic Profile Of The Fecal Microbiome Of Preterm Infants Consuming Mother's Own Milk With Bovine Milk–Based Fortifier Or Infant Formula: A Cross-Sectional Study. The American Journal Of Clinical Nutrition, Volume 116, Issue 2, August (2022), Pages 435-445. <https://doi.org/10.1093/ajcn/nqac081>

43. Effects Of A Mediterranean Diet On The Gut Microbiota And Microbial Metabolites: A Systematic Review Of Randomized Controlled Trials And Observational Studies

This systematic review explores the effects of the Mediterranean diet on the composition and metabolism of the gut microbiota in both randomized controlled trials and observational studies.

Although some evidence from a small number of studies indicated a positive impact of a Mediterranean diet on select microbiota, the findings of this systematic review suggest that dietary pattern does not consistently alter microbiota composition or metabolism. The lack of a consistent effect could be related to methodological differences between studies, especially differences in the composition of the Mediterranean diet administered.

Source: John. C. Mathers, Human Nutrition Research Centre, Centre For Healthier Lives, Population Health Sciences Institute, Newcastle University, UK. Effects Of A Mediterranean Diet On The Gut Microbiota And Microbial Metabolites: A Systematic Review Of Randomized Controlled Trials And Observational Studies. Crit Rev Food Sci Nutr. (2022) Apr 1;1-22. <https://doi.org/10.1080/10408398.2022.2057416>

44. Associations Of The Dietary Inflammatory Index With Total Adiposity And Ectopic Fat Through The Gut Microbiota, LPS, And C-Reactive Protein In The Multiethnic Cohort–Adiposity Phenotype Study

The objective of this study was to assess whether there are any associations between the Energy-Adjusted Dietary Inflammatory Index (E-DII score), total fat mass, visceral adipose tissue (VAT), or liver fat (percentage volume) operated through the GM or microbial related inflammatory factors, in a multiethnic cross-sectional study.

Study result shows that there were positive total effects (c) between E-DII and total fat mass, VAT and liver fat. The association between E-DII score and total fat mass was mediated by *LPS*, *Flavonifactor*, [*Ruminococcus*] *gnavus* group, and *Tyzzarella*. The association between E-DII score and ectopic fat occurred indirectly through *Fusobacteria*, *Christensenellaceae R-7 group*, *Coprococcus 2*, *Escherichia-Shigella*, [*Eubacterium*] *xylanophilum* group, *Flavonifactor*, *Lachnoclostridium*, [*Ruminococcus*] *gnavus* group, *Tyzzarella*, [*Ruminococcus*] *gnavus* group (VAT only), and α diversity (liver fat only). There was no significant association between E-DII score and adiposity phenotype through hs-CRP.

Source: Chloe P Lozano, University Of Hawaii Cancer Center, Honolulu, HI, USA. Associations Of The Dietary Inflammatory Index With Total Adiposity And Ectopic Fat Through The Gut Microbiota, LPS, And C-Reactive Protein In The Multiethnic Cohort–Adiposity Phenotype Study. The American Journal Of Clinical Nutrition, Volume 115, Issue 5, May (2022), Pages 1344-1356. <https://doi.org/10.1093/ajcn/nqab398>

45. Mapping The Human Gut Mycobiome In Middle-Aged And Elderly Adults: Multiomics Insights And Implications For Host Metabolic Health

This study depict the socio-demographic and dietary determinants of human gut mycobiome in middle-aged and elderly individuals, and further reveal that the gut mycobiome may be closely associated with the host metabolic health through regulating gut bacterial functions and metabolites.

Source: Ju-Sheng Zheng, Key Laboratory Of Growth Regulation And Translational Research Of Zhejiang Province, School Of Life Sciences, Westlake University; Westlake Intelligent Biomarker Discovery Lab, Westlake Laboratory Of Life Sciences And Biomedicine And Institute Of Basic Medical Sciences, Westlake Institute For Advanced Study, Hangzhou, Zhejiang, China. Mapping The Human Gut Mycobiome In Middle-Aged And Elderly Adults: Multiomics Insights And Implications For Host Metabolic Health. Gut2022;71:1812-1820. DOI: 10.1136/gutjnl-2021-326298

46. A Posteriori Dietary Patterns Better Explain Variations Of The Gut Microbiome Than Individual Markers In The American Gut Project

This study demonstrated that global-diet a posteriori patterns were more associated with gut microbiome variations than individual dietary features among adults in the United States. These results confirm that evaluating diet as a whole is important when studying the gut microbiome. It will also facilitate the design of more personalized dietary strategies in general populations.

Source: Aurélie Cotillard, Danone Nutricia Research, Palaiseau, France. A Posteriori Dietary Patterns Better Explain Variations Of The Gut Microbiome Than Individual Markers In The American Gut Project. *The American Journal Of Clinical Nutrition*, Volume 115, Issue 2, February (2022), Pages 432-443. <https://doi.org/10.1093/ajcn/nqab332>

47. Bidirectional Brain–Gut Axis Effects Influence Mood And Prognosis In IBD: A Systematic Review And Meta-Analysis

This systematic review and meta-analysis concluded that bidirectional effects of the brain–gut axis are present in IBD and may influence both the natural history of the disease and psychological health.

Source: Alexander C Ford, Leeds Gastroenterology Institute And Leeds Institute Of Medical Research At St. James's, University Of Leeds, Leeds, UK. Bidirectional Brain–Gut Axis Effects Influence Mood And Prognosis In IBD: A Systematic Review And Meta-Analysis. *Gut*. (2022) Sep; 71(9):1773-1780. DOI: 10.1136/gutjnl-2021-325985.

48. Multi-Omics Analyses Of Airway Host–Microbe Interactions In Chronic Obstructive Pulmonary Disease Identify Potential Therapeutic Interventions

Multi-omics data were integrated using sequential mediation analysis, to assess in silico associations of the microbiome with two primary chronic obstructive pulmonary disease (COPD) inflammatory endotypes, neutrophilic or eosinophilic inflammation, mediated through microbial metabolic interaction with host gene expression.

Hypotheses of microbiome–metabolite–host interaction were identified by leveraging microbial genetic information and established metabolite–human gene pairs. A prominent hypothesis for neutrophil-predominant COPD was altered tryptophan metabolism in airway lactobacilli associated with reduced indole-3-acetic acid (IAA), which was in turn linked to perturbed host interleukin-22 signalling and epithelial cell apoptosis pathways.

In vivo and in vitro studies showed that airway microbiome-derived IAA mitigates neutrophilic inflammation, apoptosis, emphysema and lung function decline, via macrophage–epithelial cell cross-talk mediated by interleukin-22. Intranasal inoculation of two airway lactobacilli restored IAA and recapitulated its protective effects in mice. These findings provide the rationale for therapeutically targeting microbe–host interaction in COPD.

Source: Zhang Wang, Institute Of Ecological Sciences, South China Normal University, Guangzhou, China. Multi-Omics Analyses Of Airway Host–Microbe Interactions In Chronic Obstructive Pulmonary Disease Identify Potential Therapeutic Interventions. *Nat Microbiol* 7, 1361–1375 (2022). <https://doi.org/10.1038/s41564-022-01196-8>

49. Gut Microbiota And Acylcarnitine Metabolites Connect The Beneficial Association Between Equol And Adiposity In Adults: A Prospective Cohort Study

This study examined the association of equol production with obesity and explored the mediating roles of equol-related gut microbiota and microbial carnitine metabolites.

The study shows that *urinary equol*, but not daidzein and genistein, is independently and inversely associated with the obesity-related indicators of BMI, %FM, and a biomarker (TGs). Equol producers (EPs) have lower odds of adiposity conditions and a reduced risk of 6.6-y obesity progression than non-EPs among total participants.

Gut microbial analyses indicated that EPs had higher microbiome species richness and significantly different β -diversity of gut microbiota compared with the non-EP group with 20 of 162 species differing significantly. EPs had higher abundances of *Alistipes senegalensis* and *Coprococcus catus* but lower abundances of *Ruminococcus gnavus*.

Among the 7 determined fecal *acylcarnitine* metabolites, *palmitoylcarnitine*, *oleylcarnitine* 18:1, and *stearylacarnitine* were inversely associated with EPs but positively correlated with obesity conditions and progression. Path analyses indicated that the beneficial association between equol and obesity might be mediated by gut microbiota and decreased production of 3 acylcarnitines in feces.

Source: Yu-Ming Chen, Department Of Epidemiology, Guangdong Provincial Key Laboratory Of Food, Nutrition And Health, School Of Public Health, Sun Yat-Sen University, Guangzhou, China. Gut Microbiota And Acylcarnitine Metabolites Connect The Beneficial Association Between Equol And Adiposity In Adults: A Prospective Cohort Study. *The American Journal Of Clinical Nutrition*, Volume 116, Issue 6, December (2022), Pages 1831-1841. <https://doi.org/10.1093/ajcn/nqac252>

50. Strong Pathogen Competition In Neonatal Gut Colonization

This study highlights the importance of systematic surveillance of bacterial gut pathogens, not only from disease but also from carriage state, to better inform therapies and preventive medicine in the future.

Source: Tommi Mäklän, Helsinki Institute For Information Technology HIIT, Department Of Computer Science, University Of Helsinki, Helsinki, Finland. Strong Pathogen Competition In Neonatal Gut Colonization. *Nat Commun* 13, 7417 (2022). <https://doi.org/10.1038/s41467-022-35178-5>

51. Stool Energy Density Is Positively Correlated To Intestinal Transit Time And Related To Microbial Enterotypes

The findings of this study suggest that gut microbial energy harvest is diversified among individuals by intestinal transit time and associated gut microbiome ecosystem variations. A better understanding of these associations could support the development of personalized nutrition and improved weight-loss strategies.

Source: Henrik M. Roager, Department Of Nutrition, Exercise And Sports, University Of Copenhagen, Frederiksberg, Denmark. Stool Energy Density Is Positively Correlated To Intestinal Transit Time And Related To Microbial. Microbiome 10, 223 (2022). <https://doi.org/10.1186/s40168-022-01418-5>

52. The Microbiome In Health And Disease From The Perspective Of Modern Medicine And Ayurveda

The role of the microbiome in health and disease helps to provide a scientific understanding of key concepts in Ayurveda. It is now recognized that virtually every aspect of human physiology and health is influenced by the collection of microorganisms that live in various parts of the body, especially the gut microbiome. There are many external factors which influence the composition of the gut microbiome but one of the most important is diet and digestion.

This systematic review points out that Ayurveda and other systems of traditional health have for thousands of years focused on diet and digestion. Recent research has helped us understand the connection between the microbiome and the many different prevention and therapeutic treatment approaches of Ayurveda.

Source: Robert Keith Wallace, Department Of Physiology And Health, Maharishi International University, Fairfield, USA. The Microbiome In Health And Disease From The Perspective Of Modern Medicine And Ayurveda. Medicina (2020), 56, 462. <https://doi.org/10.3390/medicina56090462>

53. Investigating Efficacy Of “Microbiota Modulation Of The Gut-Lung Axis” Combined With Chemotherapy In Patients With Advanced NSCLC: Study Protocol For A Multicenter, Prospective, Double Blind, Placebo Controlled, Randomized Trial

This study explores the combination of intestinal microecological regulation and chemotherapy to provide new treatment strategies and basis for lung cancer patients.

Source: Lihong Fan, Institute Of Energy Metabolism And Health, Tongji University School Of Medicine, No. 301, Middle Yangchang Rd, Shanghai, 200072, China. Investigating Efficacy Of “Microbiota Modulation Of The Gut-Lung Axis” Combined With Chemotherapy In Patients With Advanced NSCLC: Study Protocol For A Multicenter, Prospective, Double Blind, Placebo Controlled, Randomized Trial. BMC Cancer 21, 721 (2021). <https://doi.org/10.1186/s12885-021-08448-6>

54. Consumption Of Fermented Foods Is Associated With Systematic Differences In The Gut Microbiome And Metabolome

Public interest in the effects of fermented food on the human gut microbiome is high, but limited studies have explored the association between fermented food consumption and the gut microbiome in large cohorts. In this study researchers used a combination of omics-based analyses to study the relationship between the microbiome and fermented food consumption in thousands of people using both cross-sectional and longitudinal data.

This review revealed that fermented food consumers have subtle differences in their gut microbiota structure, which is enriched in conjugated linoleic acid, thought to be beneficial. Further studies of specific kinds of fermented food and their impacts on the microbiome and health are required.

Source: Muriel Derrien, Danone Nutricia Research, Palaiseau, France. Consumption Of Fermented Foods Is Associated With Systematic Differences In The Gut Microbiome And Metabolome. mSystems. (2020) Mar 17;5(2):e00901-19. <https://doi.org/10.1128/mSystems.00901-19>

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