Recent Studies and Publications on Gut Microbiome, Health and Immunity

STUDIES

1. Alterations In Gut Microbiome And Metabolomics In Chronic Hepatitis B Infection-Associated Liver Disease And Their Impact On Peripheral Immune Response

This present study aimed to characterize *gut microbiota (GM)* in patients with *chronic hepatitis B virus infection-associated liver diseases (HBV-CLD)* by combining microbiome with metabolome analyses and to evaluate their effects on peripheral immunity.

Integrated analyses of microbiome with metabolome revealed a remarkable shift of gut microbiota and metabolites in HBV-CLD patients, and disease progression and antiviral treatment were found to be two main contributing factors for the shift.

Concordant decreases in *Turicibacter* with *4-hydroxyretinoic acid* were detected to be inversely correlated with serum *aspartate aminotransferase (AST)* levels through host-microbiota-metabolite interaction analysis in cirrhotic patients. Moreover, depletion of *E.hallii group* with elevated choline was restored in patients with 5-year antiviral treatment.

Peripheral blood mononuclear cells (PBMC) exposure to bacterial extracts (BE) from non-cirrhotic patients enhanced expansion of T helper 17 cells; however, BE from cirrhotics attenuated T helper 1 cell count.

Chronic Hepatitis B (CHB) progression and antiviral treatment are two main factors contributing to the compositional shift in microbiome and metabolome of HBV-CLD patients. Peripheral immunity might be an intermediate link in gut microbe-host interplay underlying CHB pathogenesis.

2. Impact Of Tuberculosis Disease On Human Gut Microbiota: A Systematic Review

This systematic review evaluates the gut microbiota (GM) status in tuberculosis (TB) patients compared to healthy volunteers due to the disease or its treatment.

Researchers found a significant difference in GM status between the TB and healthy control (HC) groups. There was an overabundance of Phylum Proteobacteria and depletion of some short-chain fatty acid-producing bacteria genera like *Bifidobacteria, Roseburia*, and *Ruminococcus* in the TB group. Further, this review highlights that ATT exacerbates the degree of dysbiosis caused by Mycobacteria in tuberculosis disease.

3. Meat Consumption And Gut Microbiota: A Scoping Review Of Literature And Systematic Review Of Randomized Controlled Trials In Adults

This review assesses the state of available scientific literature on meat intake and gut microbiota in humans. Researchers included the 13 RCTs, comprising 18 comparisons, in the systematic review to assess the effects of higher and lower intakes of total meat and meat subtypes on the gut microbiota composition.

The bacterial composition was differentially affected by consuming diets with and without meat or with varied meat subtypes. For example, higher meat intake tended to decrease population sizes of genera *Anerostipes and Faecalibacterium (gram positive bacteria),* but it increased the population size of *Roseburia (gram positive bacteria),* across studies. However, the magnitude and directionality of most microbial responses varied, with inconsistent patterns of responses across studies. The data were insufficient for comparison within or between meat subtypes.

Further need for more well-designed prospective studies and full-feeding RCTs to address the relationships between and effects of consuming total meat and meat subtypes on gut microbiota are required.

4. Physical Activity Induced Alterations Of The Gut Microbiota Are BMI Dependent

This study examined the role of physical activity (PA) and hand-grip strength on gut microbiome composition in middle-aged adults (40–65 years, n = 350) with normal (18.5–24.9 kg/m2) and overweight (25–29.9 kg/m2) body mass index (BMI).

Overweight participants showed a higher concentration of triacylglycerols, and lower concentrations of cholesteryl esters, sphingomyelin, and lyso-phosphotidylcholine lipids compared with those with normal BMI. Additionally, overweight participants had a lower abundance of the *Oscillibacter genus*. The impact of PA duration on the gut microbiome was BMI dependent.

In normal but not overweight participants, high PA duration showed greater relative abundance of *commensal taxa such as Actinobacteria and Proteobacteria phyla, as well as Collinsella and Prevotella genera*. Furthermore, in males with normal BMI, a stronger grip strength was associated with a higher relative abundance of *Faecalibacterium and F. prausnitzii* compared with lower grip strength.

This study shows that BMI plays a significant role in modeling physical activity (PA) induced changes in gut microbiota.

5. Modulation Of The Gut Microbiome With Nisin

Nisin is a broad spectrum *bacteriocin* used extensively as a food preservative that was identified in *Lactococcus lactis* nearly a century ago.

This study shows that orally-ingested *Nisin* survives transit through the porcine gastrointestinal tract intact (as evidenced by activity and molecular weight determination) where it impacts both the composition and functioning of the microbiota.

Specifically, *Nisin* treatment causes a reversible decrease in Gram positive bacteria, resulting in a reshaping of the *Firmicutes* and a corresponding relative increase in Gram negative *Proteobacteria*. These changes were mirrored by the modification in relative abundance of pathways involved in acetate, butyrate (decreased) and propionate (increased) synthesis which correlated with overall reductions in short chain fatty acid levels in stool.

These reversible changes that occur as a result of *Nisin* ingestion demonstrate the potential of bacteriocins like *Nisin* to shape mammalian microbiomes and impact on the functionality of the community.

6. Growing Old Together: What We Know About The Influence Of Diet And Exercise On The Aging Host's Gut Microbiome

This review examines the current state of the literature regarding alterations to the gut microbiome as hosts age and drawing particular attention to the knowledge gaps in addressing how diet and exercise influence the aging microbiome.

Further, it also demonstrates the need for more controlled studies to investigate the roles that diet and exercise plays in driving the composition, diversity, and function of the microbiome in an aging population.

7. Diet Quality And The Fecal Microbiota In Adults In The American Gut Project

This study aimed to investigate the differences in fecal microbiota composition in adults from the American Gut Project based on their adherence to the Dietary Guidelines for Americans. This study was a cross-sectional analysis of the 16S sequencing and food frequency data of a subset of adults (n = 432; age = 18–60 y; 65% female, 89% white) participating in the crowdsourced American Gut Project.

Researchers found that adults with greater compliance to the Dietary Guidelines demonstrated higher diversity in their fecal microbiota and greater abundance of bacteria capable of metabolizing complex carbohydrates, providing evidence on how Dietary Guidelines support the gut microbiota.

8. Milk Protein Digestion And The Gut Microbiome Influence Gastrointestinal Discomfort After Cow Milk Consumption In Healthy Subjects

This study aimed to explore milk protein digestion and related physiological responses (primary outcome), gut microbiome and gut permeability in 19 lactose-tolerant healthy nonhabitual milk consumers [NHMCs] reporting gastrointestinal discomfort (GID) after consuming cow milk compared to 20 habitual milk consumers [HMCs] without GID.

Study result shows that, as compared to HMCs, milk consumption in NHMCs, along with GID, elicited a slower and lower increase in circulating bioactive peptides (BAPs), lower responses of ghrelin, insulin, and anandamide, a higher glucose response and serum dipeptidyl peptidase-IV (DPPIV) activity.

The gut permeability of the two groups was similar, while the habitual diet, which was lower in dairy products and higher in the dietary-fibre-to-protein ratio in NHMCs, possibly shaped the gut microbiome; NHMCs exhibited lower abundance of *Bifidobacteria*, higher abundance of *Prevotella* and lower abundance of *protease-coding genes*, which may have reduced protein digestion, as evidenced by lower urinary excretion of indoxyl sulfate.

9. Gut Microbiota Maturity Mediates The Protective Effect Of Siblings On Food Allergy

This study shows that the protective effect of older siblings on the risk of developing IgE-mediated food allergy during infancy which is substantially mediated by advanced maturation of the gut microbiota at age 1 year.

10. Impact Of Environmental Characteristics On Children's Gut Microbiota – A Pilot Study In Assessing The Role Of Indoor Microbiome And Metabolites

The aimed of this study was to investigate the potential influence of the indoor microbiome and metabolites on the human gut microbiota. To achieve this, researchers used culture-independent shotgun metagenomic sequencing and liquid chromatography-mass spectrometry (LC-MS) to characterize the indoor microbiome and chemical exposure in the living rooms of 56 children residing in Shanghai, China.

The study is the first to report associations between indoor microbiome/metabolites and gut microbiota, highlighting the potential role of indoor microbiome in shaping human gut microbiota.

11. Reconstruction Of The Personal Information From Human Genome Reads In Gut Metagenome Sequencing Data

Human DNA present in faecal samples can result in a small number of human reads in gut shotgun metagenomic sequencing data. A quantitative evaluation is necessary to clarify the ethical concerns related to data sharing and to enable efficient use of human genetic information in stool samples, such as for research and forensics.

In this study researchers used genomic approaches to reconstruct personal information from the faecal metagenomes of 343 Japanese individuals with associated human genotype data.

Genetic sex could be accurately predicted based on the sequencing depth of sex chromosomes for 97.3% of the samples. Individuals could be re-identified from the matched genotype data based on human reads recovered from the faecal metagenomic data with 93.3% sensitivity using a likelihood score-based method. This method also enabled to predict the ancestries of 98.3% of the samples.

This study demonstrated that the genotypes of both common and rare variants could be reconstructed from faecal samples. This included clinically relevant variants. Hence this approach can be used to quantify personal information contained within gut metagenome data.

12.   Association Of Gut Microbiota And Dietary Component Intake With Covid-19: A Mendelian Randomization Study

In this study researchers performed a two-sample bi-directional Mendelian Randomization (MR) analysis to investigate the association of gut microbiota and dietary component intake with COVID-19 outcomes. The study included 18,340 participants from 24 cohorts, most of whom were from European (N = 132,266), with 211 total taxa (131 genera, 35 families, 20 orders, 16 classes, and 9 phyla).

Scientists found that the *Ruminococcustorques* group genus was significantly associated with COVID-19. The *Ruminococcaceae* UCG013 genus and *Ruminococcus1* genus were suggestively associated with COVID-19. The *Actinobacteria class, Bifidobacteriales order, Bifidobacteriaceae genus, R. group*, and *Tyzzerella3 genus* were potentially associated with severe COVID-19.

COVID-19 was significantly associated with the *Lachnospira genus, Oscillospira,* and *RuminococcaceaeUCG009 genus* and potentially associated with the *Victivallis genus*. Severe COVID-19 was significantly associated with the *Turicibacter* and *Olsenella genus* and potentially associated with *Ruminococcus1, Candidatus Soleaferrea*, and *Parasutterella genus*.

Moreover, processed meat intake was significantly associated with COVID-19. Beef intake was suggestively associated with COVID-19. Salt added to food intake, and fresh fruit intake was suggestively associated with severe COVID-19.

13.   The Microbiota Of Pregnant Women With SARS-Cov-2 And Their Infants

Infants receive their first bacteria from their birthing parent. This newly acquired microbiome plays a pivotal role in developing a robust immune system, the cornerstone of long-term health. The objective of this study was to determine whether infection by SARS-CoV-2 during pregnancy, either at early or late stages of pregnancy or an active infection at delivery resulted in gut, vaginal, and oral microbiota changes that are passed onto the offspring. A total of 88 pregnant women, 62 with positive SARS-CoV-2 diagnosis, 26 with a negative SARS-CoV-2 diagnosis, and 68 newborns (2 sets of twins) were recruited.

This study suggested that SARS-CoV-2 infections during pregnancy, particularly early infections, are associated with lasting changes in the microbiome of pregnant women, compromising the initial microbial seed of their infant. The results of this study highlight the importance of further exploring the impact of SARS-CoV-2 on the infant's microbiome-dependent immune programming.

14.   Enterosignatures Define Common Bacterial Guilds In The Human Gut Microbiome

The human gut microbiome composition is generally in a stable dynamic equilibrium, but it can deteriorate into dysbiotic states detrimental to host health. To disentangle the inherent complexity and capture the ecological spectrum of microbiome variability, scientists used 5,230 gut metagenomes to characterize signatures of bacteria commonly co-occurring, termed *enterosignatures (ESs)*.

Researchers found five generalizable ESs dominated by either *Bacteroides, Firmicutes, Prevotella, Bifidobacterium*, or *Escherichia*. This model confirms that the key ecological characteristics known from previous enterotype concepts, while enabling the detection of gradual shifts in community structures.

Temporal analysis implies that the *Bacteroides-associated ES* is "core" in the resilience of westernized gut microbiomes, while combinations with other ESs often complement the functional spectrum. The model reliably detects atypical gut microbiomes correlated with adverse host health conditions and/or the presence of pathobionts. *ESs* provide an interpretable and generic model that enables an intuitive characterization of gut microbiome composition in health and disease.

15. Contributions Of The Early-Life Microbiome To Childhood Atopy And Asthma Development

This review captures key studies in the field that offer insights into the developmental origins of childhood atopy and asthma, providing novel insights into microbial mediators of maladaptive immunity and chronic inflammatory disease in childhood.

16. Longitudinal Gut Microbiome Analyses And Blooms Of Pathogenic Strains During Lupus Disease Flares

To investigate relationships between microbiota community resilience and disease activity, researchers performed the first longitudinal analyses of lupus gut-microbiota communities. Researchers investigated the temporal stability of longitudinal faecal samples from 16 lupus patients and 22 healthy subjects.

This study shows that unlike healthy controls, significant temporal community-wide ecological microbiota instability was common in systemic lupus erythematosus (SLE) patients, and transient intestinal growth spikes of several pathogenic species were documented. Expansions of only the anaerobic commensal, *Ruminococcus (blautia) gnavus (RG)* occurred at times of high-disease activity, and were detected in almost half of patients during *lupus nephritis (LN) disease flares*.

Whole genome sequence analysis of RG strains isolated during these flares documented 34 genes postulated to aid adaptation and expansion within a host with an inflammatory condition. Yet, the most specific feature of strains found during lupus flares was the common expression of a novel type of cell membrane-associated lipoglycan. Further, these *lipoglycans* share conserved structural features and highly immunogenic repetitive antigenic-determinants, recognized by high-level serum IgG2 antibodies that spontaneously arose, concurrent with RG blooms and lupus flares.

17. Deficient Butyrate-Producing Capacity In The Gut Microbiome Is Associated With Bacterial Network Disturbances And Fatigue Symptoms In ME/CFS

Myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS) is characterized by unexplained debilitating fatigue, cognitive dysfunction, gastrointestinal disturbances, and orthostatic intolerance.

This study reports a multi-omic analysis of a geographically diverse cohort of 106 cases and 91 healthy controls that revealed differences in gut microbiome diversity, abundances, functional pathways, and interactions. *Faecalibacterium prausnitzii* and *Eubacterium rectale*, which are both recognized as abundant, health-promoting butyrate producers in the human gut, were reduced in ME/CFS.

Functional metagenomics, qPCR, and metabolomics of fecal short-chain fatty acids confirmed a deficient microbial capacity for butyrate synthesis. Microbiome-based machine learning classifier models were robust to geographic variation and generalizable in a validation cohort. **The abundance of *Faecalibacterium prausnitzii* was inversely associated with fatigue severity. These findings demonstrate the functional nature of gut dysbiosis and the underlying microbial network disturbance in ME/CFS, providing possible targets for disease classification and therapeutic trials.**

18. Alterations Of The Gut Microbiome Are Associated With Epigenetic Age Acceleration And Physical Fitness

Epigenetic clocks can measure aging and predict the incidence of diseases and mortality. Higher levels of physical fitness are associated with a slower aging process and a healthier lifespan. Microbiome alterations occur in various diseases and during the aging process, yet their relation to epigenetic clocks is not explored.

In this study researchers collected metagenomic, epigenetic, and exercise-related data from eighty physically fit individuals, and applied edepigenetic clocks. They examined the relationship between gut flora, epigenetic age acceleration, and physical fitness.

Study results revealed that increased entropy in the gut microbiome is associated with accelerated epigenetic aging, lower fitness, or impaired health status. This study also revealed that, in general, accelerated epigenetic aging can be linked to the abundance of pro-inflammatory and other pathogenic bacteria and decelerated epigenetic aging or high fitness level can be linked to the abundance of anti-inflammatory bacteria. **Overall study data suggest that alterations in the microbiome can be associated with epigenetic age acceleration and physical fitness.**

19. Effects Of Unconventional Work And Shift Work On The Human Gut Microbiota And The Potential Of Probiotics To Restore Dysbiosis

The work environment is a factor that can significantly influence the composition and functionality of the gut microbiota of workers, in many cases leading to gut dysbiosis that will result in serious health problems.

The aim of this review was to provide a compilation of the different studies that have examined the influence of jobs with unconventional work schedules and environments on the gut microbiota of workers performing such work.

The study examined the potential of probiotic supplements, via modulation of the gut microbiota, in moderating the effects of sleep disturbance on the immune system, as well as restoring the dysbiosis. **Rotating shift work was found to be associated with an increase in the risk of various metabolic diseases, such as obesity, metabolic syndrome, and type 2 diabetes. Sleep disturbance or lack of sleep due to night work was also associated with metabolic diseases.**

In addition, sleep disturbance induce a stress response, both physiologically and psychologically, and disrupted the healthy functioning of the gut microbiota, thus triggering an inflammatory state. Other workers, including military, healthcare, or metallurgy workers, as well as livestock farmers or long-travel seamen, work in environments and schedules that can significantly affect their gut microbiota.

20. How Do Minerals, Vitamins, And Intestinal Microbiota Affect The Development And Progression Of Heart Disease In Adult And Pediatric Patients?

This review aimed to draw attention to the role of selected minerals and vitamins in health and the development and progression of cardiovascular diseases (CVDs) in adults and children.

In this review researchers concluded that developing a clear understanding of the gut microbiome is important for looking at its association with growth, development, and overall health. Future research is needed to elucidate the various functions of the gut microbiota and identify therapeutic targets in various metabolic disorders and diseases. Studying the various enzymes and genes that influence the impact of the gut microbiota on health and disease will be crucial.

21. Gut Microbiome And Nutrition-Related Predictors Of Response To Immunotherapy In Cancer: Making Sense Of The Puzzle

The gut microbiome is emerging as an important predictor of response to **immune checkpoint inhibitor (ICI) therapy** for patients with cancer.

This review explored the complex inter-relations between the gut microbiome, diet and patient nutritional status and the correlations with response to ICI treatment. Further, different multivariate approaches, including archetypal analysis, are discussed to help identify the combinations of features which select patients who are most likely to respond to ICI treatment.

22. Exploring The Influence Of Gut Microbiome On Energy Metabolism In Humans

In this narrative review, researchers included human studies investigating the relationship between gut microbiome and energy metabolism —i.e., energy expenditure in humans and energy harvest by the gut microbiome.

Studies found no consistent gut microbiome patterns associated with energy metabolism, and most interventions were not effective in modulating the gut microbiome to influence energy metabolism. To date, cause-and-effect relationships and mechanistic evidence on the impact of the gut microbiome on energy expenditure have not been established in humans. Further, studies are required.

23. Exploring The Relationship Between Social Jetlag With Gut Microbial Composition, Diet And Cardiometabolic Health, In The ZOE PREDICT 1 Cohort

This study explores the relationship between social jetlag (SJL), a parameter of circadian misalignment, and gut microbial composition, diet and cardiometabolic health in the ZOE PREDICT 1 cohort.

Study result shows that the SJL group (16%) had a greater proportion of males, shorter sleepers, and were younger compared to the no-SJL group. **SJL was associated with a higher relative abundance of 9 gut bacteria and lower abundance of 8 gut bacteria, in part mediated by diet. SJL was associated with unfavourable diet quality (less healthful Plant-based Diet Index), higher intakes of potatoes and sugar-sweetened beverages, and lower intakes of fruits, and nuts, and slightly higher markers of inflammation (GlycA and IL-6) compared with no-SJL and rendered non-significant after multiple testing adjustments.**

Researchers concluded that there are novel associations between SJL and more disadvantageous gut microbiomes in a cohort of predominantly adequate sleepers highlighting the potential implications of SJL for health.

24. Human Microbiome Variation Associated With Race And Ethnicity Emerges As Early As 3 Months Of Age

In this review article researchers identified that gut microbiome variation is associated with race and ethnicity that arises after 3 months of age and persists through childhood. One-third of the bacterial taxa that vary across caregiver-identified racial categories in children also vary between adults. Machine learning modeling of childhood microbiomes from 8 cohort studies (2,756 samples from 729 children) distinguishes racial and ethnic categories with 87% accuracy. Importantly, predictive genera are also among the top 30 most important taxa when childhood microbiomes are used to predict adult self-identified race and ethnicity.

The study results highlight a critical developmental window at or shortly after 3 months of age when social and environmental factors drive race and ethnicity-associated microbiome variation and may contribute to adult health and health disparities.

25. Development Of The Early-Life Gut Microbiome And Associations With Eczema In A Prospective Chinese Cohort

In this study, researchers characterized the development and determinants of the gut microbiome in a prospective cohort of 112 term Chinese children by sequencing 713 stool samples collected at nine time points from birth to 3 years of age using 16S rRNA gene sequencing.

This study has revealed important associations between the gut microbiome and eczema in infancy and has established the basis for potential prevention/treatment of eczema via modulation of the gut microbiota.

26. Delayed Gut Microbiota Maturation In The First Year Of Life Is A Hallmark Of Pediatric Allergic Disease

This study shows that early-life influences and microbiome features are uniformly associated with four distinct allergic diagnoses at 5 years: atopic dermatitis, asthma, food allergy, and allergic rhinitis.

In a subset with shotgun metagenomic and metabolomic profiling researchers discovered that impaired 1-year microbiota maturation may be universal to pediatric allergies. Extending this, scientists found a core set of functional and metabolic imbalances characterized by compromised mucous integrity, elevated oxidative activity, decreased secondary fermentation, and elevated trace amines, to be a significant mediator between microbiota maturation at age 1 year and allergic diagnoses at age 5 years.

Microbiota maturation thus provides a focal point to identify deviations from normative development to predict and prevent allergic disease.

27. Gut Microbial Carbohydrate Metabolism Contributes To Insulin Resistance

This study investigated the relationship using a comprehensive multi-omics strategy in humans. Scientists combined unbiased faecal metabolomics with metagenomics, host metabolomics and transcriptomics data to profile the involvement of the microbiome in insulin resistance.

This study data reveal that faecal carbohydrates, particularly host-accessible monosaccharides, are increased in individuals with insulin resistance and are associated with microbial carbohydrate metabolisms and host inflammatory cytokines. Researchers also identified gut bacteria associated with insulin resistance and insulin sensitivity that show a distinct pattern of carbohydrate metabolism, and demonstrated that insulin-sensitivity-associated bacteria ameliorate host phenotypes of insulin resistance.

This study provides a comprehensive view of the host–microorganism relationships in insulin resistance and found the impact of carbohydrate metabolism by microbiota, suggesting a potential therapeutic target for ameliorating insulin resistance.

28. Longitudinal Dynamics Of The Gut Microbiome And Metabolome In Peanut Allergy Development

Scientists performed a longitudinal, integrative study of the gut microbiome and metabolome of infants with allergy risk factors but no Peanut Allergy (PA) from a multicenter cohort followed through mid-childhood.

Study result shows that around 28.7% of infants developed peanut allergy by mid-childhood (mean age 9 years). Lower infant gut microbiome diversity was associated with peanut allergy development. Temporal changes in the relative abundance of specific microbiota and gut metabolite levels significantly differed in children who developed peanut allergy.

Peanut allergy-bound children had different abundance trajectories of *Clostridium sensu stricto 1 sp.* decreasing over time. Metabolites associated with peanut allergy development clustered within the histidine metabolism pathway. **Positive correlations between microbiota, butyrate, and isovalerate** and **negative correlations with histamine marked the peanut allergy-free network**.

29. Unraveling The Gut Microbiome–Diet Connection: Exploring The Impact Of Digital Precision And Personalized Nutrition On Microbiota Composition And Host Physiology

The human gut microbiome, an intricate ecosystem housing trillions of microorganisms within the gastrointestinal tract, holds significant importance in human health and the development of diseases. Recent advances in technology have allowed for an in-depth exploration of the gut microbiome, shedding light on its composition and functions.

In this study, Scientists investigated the complex mechanisms that govern the diverse impacts of nutrients and specific foods on the equilibrium and functioning of the individual gut microbiome of seven volunteers (four females and three males) with an average age of 40.9 ± 10.3 years, aiming at identifying potential therapeutic targets, thus making valuable contributions to the field of personalized nutrition. **These findings have the potential to revolutionize the development of highly effective strategies that are tailored to individual requirements for the management and treatment of various diseases.**

30. Impact Of Dietary Interventions On Pre-Diabetic Oral And Gut Microbiome, Metabolites And Cytokines

Researchers conducted a six-month dietary intervention in pre-diabetic individuals, to mitigate the hyperglycemia and enhance metabolic health. The current work explored early diabetes markers in 200 individuals who completed the trial. Scientists found 166 of 2,803 measured features, including oral and gut microbial species and pathways, serum metabolites and cytokines, show significant change in response to a personalized postprandial glucose-targeting diet or the standard of care Mediterranean diet. These changes include established markers of hyperglycemia as well as novel features that can now be investigated as potential therapeutic targets.

This Study's results indicated that the microbiome mediates the effect of diet on glycemic, metabolic and immune measurements, with gut microbiome compositional change explaining 12.25% of serum metabolites variance. Although the gut microbiome displays greater compositional changes compared to the oral microbiome, the oral microbiome demonstrates more changes at the genetic level, with trends dependent on environmental richness and species prevalence in the population. **Hence this study shows that dietary interventions can affect the microbiome, cardiometabolic profile and immune response of the host, and that these factors are well associated with each other, and can be harnessed for new therapeutic modalities.**

31. The Microbiome, Epigenome, and Diet in Adults with Obesity during Behavioral Weight Loss

The objective of this study was to evaluate associations among gut microbiota (MB), DNA methylation (DNAme), and diet prior to and during a behavioral weight loss intervention. 47 Adults (age 40.9 ± 9.7 years, body mass index (BMI) 33.5 ± 4.5 kg/m2, 77% female) were included and data was collected at baseline (BL) and 3 months (3 m).

Study result shows that at BL, one MB taxon, **Ruminiclostridium**, was associated with DNAme of the genes COL20A1, COL18A1, and NT5E. At 3 m, there were 14 unique MB:DNAme associations, such as **Akkermansia** with DNAme of GUSB, CRYL1, C9, and GMDS. Among taxa associated with DNAme, no significant relationships were seen with dietary intakes of relevant nutrients, food groups, or Healthy Eating Index (HEI) scores. **The findings indicate that that microbes linked to mucin degradation, short-chain fatty acid production, and body weight are associated with DNAme of phenotypically relevant genes. These relationships offer an initial understanding of the possible routes by which alterations in gut MB may influence metabolism during weight loss.**

32. A Comparison Of The Infant Gut Microbiome Before Versus After The Start Of The Covid-19 Pandemic

In this study researchers compared gut microbiome composition among a socioeconomically and racially diverse group of 12-month old infants living in New York City who provided stool samples before the pandemic (N = 34) to a group who provided samples during the first 9-months of the pandemic (March–December 2020; N = 20).

Scientists found that infants sampled during the pandemic had lower *alpha diversity* of the microbiome, lower abundance of *Pasteurellaceae* and *Haemophilus,* and significantly different *beta diversity* based on unweighted Unifrac distance than infants sampled before the pandemic. Further, they found that gut microbiome changes to the pandemic occurred relatively quickly after the start of the pandemic and were sustained.

33. Adolescence And The Microbiome: Implications For Healthy Growth And Maturation

This review article provides an overview of adolescent development, host-microbiota interactions, and experimental models used to discern gut microbiota effects on health and disease.

The role of the gut microbiota is reviewed as it relates to adolescent: i) brain development, cognition, and behavior; ii) metabolism and adiposity, and iii) skeletal growth and bone mass accrual. Future directions are addressed including omics investigations defining mechanisms through which the gut microbiota influences adolescent development. Further, researchers discussed advancing non-invasive interventions targeting the adolescent gut microbiota that could be employed to support healthy growth and maturation.

34.   Selection Of Cross-Reactive T Cells By Commensal And Food-Derived Yeasts Drives Cytotoxic TH1 Cell Responses In Crohn's Disease

Aberrant CD4+ T cell reactivity against intestinal microorganisms is considered to drive mucosal inflammation in inflammatory bowel diseases.. In the present study, researchers identified common gut commensal and food-derived yeasts, as direct activators of altered CD4+ T cell reactions in patients with Crohn's disease (CD).

Yeast-responsive CD4+ T cells in CD display a cytotoxic T helper cell (TH1 cell) phenotype and show selective expansion of T cell clones that are highly cross-reactive to several commensal, as well as food-derived, fungal species. This indicates cross-reactive T cell selection by repeated encounter with conserved fungal antigens in the context of chronic intestinal disease.

Study results highlight a role of yeasts as drivers of aberrant CD4+ T cell reactivity in patients with CD and suggest that both gut-resident fungal commensals and daily dietary intake of yeasts might contribute to chronic activation of inflammatory CD4+ T cell responses in patients with CD.

35.   Causal Relationship Between Gut Microbiota And Gout: A Two-Sample Mendelian Randomization Study

Gout is a form of prevalent and painful inflammatory arthritis characterized by elevated serum urate (SUA) levels. The gut microbiota (GM) is believed to influence the development of gout and SUA levels. This study aimed to explore the causal relationship between gut microbiota (GM) composition and gout, as well as serum urate (SUA) levels, utilizing a two-sample Mendelian Randomization (MR) approach.

A total of 196 GM taxa from five levels were available for analysis. Researchers identified five taxa associated with SUA levels and 10 taxa associated with gout. In reverse MR analysis, researchers discovered that gout affected the composition of five GM taxa, while SUA levels influenced the composition of 30 GM taxa.

This study unveiled a potential negative feedback loop between *phylum Actinobacteria* and SUA levels, establishing connections with gout. This study also proposed two novel associations connecting GM taxa (*genus Faecalibacterium and genus Prevotella9*), SUA levels, and gout. **These findings provide compelling evidence of causal relationships between specific GM taxa with SUA levels and gout, contributing valuable insights for the treatment of gout.**

36.   Variety Of Fruit And Vegetables And Alcohol Intake Are Associated With Gut Microbial Species And Gene Abundance In Colorectal Cancer Survivor

This is a pilot cross-sectional study to explore associations between American Cancer Society (ACS) guidelines and the gut microbiome. Stool samples and questionnaires were collected from 28 CRC survivors at the University of California, San Francisco from 2019 to 2020.

Study result shows that the overall ACS score was not significantly associated with variations in the fecal microbiota. However, fruit and vegetable intake and alcohol intake accounted for 19% of variation in the microbiota, respectively.

Fruit/vegetable consumption was associated with increased microbial diversity, increased *Firmicutes*, decreased *Bacteroidota*, and changes to multiple genes and metabolic pathways, including enriched pathways for amino acid and short-chain fatty acid biosynthesis and plant-associated sugar degradation.

In contrast, **alcohol consumption was positively associated with overall microbial diversity, negatively associated with *Bacteroidota* abundance, and associated with changes to multiple genes and metabolic pathways.** The other components of the ACS score were not statistically significantly associated with the fecal microbiota.

37.   Effects Of Ramadan Intermittent Fasting On Gut Microbiome: Is The Diet Key?

This study aimed to investigate the effect of intermittent fasting during Ramadan on the gut microbiota. The study was conducted on 12 healthy adult individuals who practiced fasting 17 h per day for 29 consecutive days during the month of Ramadan.

The results show that *Firmicutes* were higher in abundance in the gut microbiota before fasting among participants, while they were significantly lower in abundance at the end of Ramadan fasting. *Proteobacteria* were significantly higher in abundance at the end of the month of Ramadan. Fasting was associated with a significant decrease in levels of seven genera: *Blautia, Coprococcus, Dorea, Faecalicatena, Fusicatenibacter, Lachnoclostridium*, and *Mediterraneibacter*.

Conversely, the abundances of two bacterial genera were enhanced at the end of the fasting month: *Escherichia and Shigella*. The results of the dietary intake analysis showed that a negative correlation was detected for three comparisons: *Ihubacter and protein, Fusicatenibacter andvegetables, and Intestinibacter and nuts.*

The results suggest that even when the fasting period during Ramadan is consistent, the types of food consumed by individuals can affect the gut microbiota.

38.   Microbiota, Diet And Acute Leukaemia: Tips And Tricks On Their Possible Connections

Acute leukaemia is probably one of the most recurrent cancers in children and younger adults, with an incidence of acute lymphoblastic leukaemia in 80% of cases and an incidence of acute myeloid leukaemia in 15% of cases.

This review shows the key role of gut microbiota in the modulation of the efficacy of leukaemia treatment as well as in the progress of many cancers, such as acute leukaemia. It also explores literature regarding the role of dietary factors and gut microbiota alterations in the development of leukaemia and suggest possible future preventive and therapeutic strategies.

39.   A Two-Cohort Study On The Association Between The Gut Microbiota And Bone Density, Microarchitecture, And Strength

Researchers investigated the association between the human gut microbiome and high resolution peripheral quantitative computed tomography scans of the radius and tibia in two large cohorts; Framingham Heart Study (FHS) and the Osteoporosis in Men Study (MrOS).

Scientists found that abundance of 37 microbial genera in FHS, and 4 genera in MrOS, were associated with various skeletal measures including the association of DTU089 with bone measures, which was independently replicated in the two cohorts. A meta-analysis of the taxa-bone associations further revealed (FDR ≤ 0.25) that greater abundances of the genera; *Akkermansia* and DTU089, were associated with lower radius total vBMD, and tibia cortical vBMD respectively. Conversely, higher abundances of the genera; *Lachnospiraceae NK4A136 group*, and *Faecalibacterium* were associated with greater tibia cortical vBMD.

Researchers also investigated functional capabilities of microbial taxa by testing for associations between predicted (based on 16S rRNA amplicon sequence data) metabolic pathways abundance and bone phenotypes in each cohort.

While there were no concordant functional associations observed in both cohorts, a meta-analysis revealed 8 pathways including the super-pathway of histidine, purine, and pyrimidine biosynthesis, associated with bone measures of the tibia cortical compartment.

This study suggests that there is a link between the gut microbiome and skeletal metabolism.

40.   Baseline Gut Microbiota And Metabolome Predict Durable Immunogenicity To SARS-Cov-2 Vaccines

In this cohort study, scientists collected blood and stool samples of 121 BNT162b2 and 40 CoronaVac vaccinees at baseline, 1 month, and 6 months post vaccination (p.v.).

Researchers found a significantly higher level of neutralising antibody (at 6 months p.v.) in BNT162b2 vaccinees that had higher relative abundances of *Bifidobacterium adolescentis, Bifidobacterium bifidum, and Roseburia faecis* as well as higher concentrations of nicotinic acid (Vitamin B) and γ-Aminobutyric acid at baseline.

CoronaVac vaccinees with high neutralising antibodies at 6 months p.v. had an increased relative abundance of *Phocaeicola dorei*, a lower relative abundance of *Faecalibacterium prausnitzii*, and a higher concentration of L-tryptophan at baseline. A higher antibody level at 6 months p.v. was also associated with a higher relative abundance of *Dorea formicigenerans* at 1 month p.v. among CoronaVac vaccinees.

The species altered following vaccination, 79.4% and 42.0% in the CoronaVac and BNT162b2 groups, respectively, recovered at 6 months. Specific to CoronaVac vaccinees, both *bacteriome and virome diversity* depleted following vaccination and did not recover to baseline at 6 months p.v. . Hence, this study identifies potential microbiota-based adjuvants that may extend the durability of immune responses to SARS-CoV-2 vaccines.

41.   Social And Psychological Adversities Are Associated With Distinct Mother And Infant Gut Microbiome Variations

In this study researchers interrogated the gut microbiome of mother-child dyads to compare high-versus-low prenatal socially disadvantaged, psychosocial stressors and maternal circulating cytokine cohorts (prospective case-control study design using gut microbiomes from 121 dyads profiled with 16S rRNA sequencing and 89 dyads with shotgun metagenomic sequencing).

Scientists found that gut microbiome characteristics is a significant predictor of social disadvantage and psychosocial stressors in the mothers and children and indicates that different discriminatory taxa and related pathways are involved, including many species of *Bifidobacterium* and related pathways across several comparisons.

The lowest inter-individual gut microbiome similarity was observed among high-social disadvantage/high-psychosocial stressors mothers, suggesting distinct environmental exposures driving a diverging gut microbiome assembly compared to low-social disadvantage/low-psychosocial stressors controls. Children's gut metagenome profiles at 4 months also significantly predicted high/low maternal prenatal IL-6, with many bacterial species overlapping those identified by social disadvantage and psychosocial stressors. These differences based on maternal social and psychological status during a critical developmental window early in life offer potentially modifiable targets to mitigate health inequities.

42.   Interplay Between The Human Microbiome And Biliary Tract Cancer: Implications For Pathogenesis And Therapy

This review article critically appraises the existing evidence pertaining to the microbiome milieu within patients afflicted by biliary tract cancer. Furthermore, it delves into potential mechanisms through which dysregulation of the human microbiome could contribute to the advancement of biliary tract cancer. Additionally, the article also expounds on its role in the context of chemotherapy and immunotherapy for biliary tract cancer.

43. Causality Investigation Between Gut Microbiota, Derived Metabolites, And Obstructive Sleep Apnea: A Bidirectional Mendelian Randomization Study

Various studies have highlighted the important associations between obstructive sleep apnea (OSA) and gut microbiota and related metabolites.

The analysis of the 196 gut microbiota revealed that *genus_Ruminococcaceae (and genus_Subdoligranulum* **were associated with an increased risk of OSA onset. Conversely,** *Family_Ruminococcaceae,* *genus_Coprococcus2, genus_Eggerthella*, **and** *genus_Eubacterium (xylanophilum_group)* **were negatively related to the risk of OSA.**

Among the 83 metabolites evaluated, 3-dehydrocarnitine, epiandrosterone sulfate, and leucine were determined to be potential independent risk factors associated with OSA. Moreover, the reverse mendelian randomization (MR) analysis demonstrated a suggestive association between OSA exposure and six microbiota taxa.

This study offers compelling evidence regarding the potential beneficial or detrimental causative impact of the gut microbiota and its associated metabolites on OSA risk, thereby providing new insights into the mechanisms of gut microbiome-mediated OSA development.

44. Gut Microbiome-Based Therapeutics in Critically Ill Adult Patients—A Narrative Review

This narrative review summarizes the curative effects and limitations of microbiome-based therapeutics in different critically ill adult patients, aiming to provide possible directions for gut microbiome-based therapeutics for critically ill patients such as ventilator-associated pneumonia, sepsis, acute respiratory distress syndrome, and COVID-19, etc.

45. Bacterial SNPs In The Human Gut Microbiome Associate With Host BMI

Genome-wide association studies (GWASs) have provided numerous associations between human single-nucleotide polymorphisms (SNPs) and health traits. Likewise, metagenome-wide association studies (MWASs) between bacterial SNPs and human traits can suggest mechanistic links, but very few such studies have been done thus far.

In this study, researchers devised an MWAS framework to detect SNPs and associate them with host phenotypes systematically. Scientists have uncovered BMI-associated SNPs in 27 bacterial species, and 12 of them shows no association by standard relative abundance analysis. They revealed a BMI association of an SNP in a potentially inflammatory pathway of *Bilophila wadsworthia* as well as of a group of SNPs in a region coding for energy metabolism functions in a *Faecalibacterium prausnitzii* genome.

The study results demonstrates the importance of considering nucleotide-level diversity in microbiome studies and pave the way toward improved understanding of interpersonal microbiome differences and their potential health implications.

46. Microbiome Diversity Is A Modifiable Virulence Factor For Cryptosporidiosis

Cryptosporidium spp. infection causes significant disease in immunosuppressed individuals and children under the age of 5 years. The severity of the pathological presentation of cryptosporidiosis is a function of the host and parasite genotypes, host immune status, and the enteric environment or microbiome of the host. Cryptosporidiosis is often presents with abdominal pain and severe diarrhoea and is associated with intestinal dysbiosis and inflammation.

This review affirms that cryptosporidiosis leads to dysbiosis of the host gut microbiome, which is characterised by an increase in bacteria in the taxa *Firmicutes (Bacillota), Proteobacteria (Psuedomoadota) and Actinomycetota*. Increases in the populations of inflammatory bacteria from numerous taxa could induce further inflammation of the gut, impact recolonisation of the GI tract, or have long-term health impacts.

In essence, diverse composition of the microbiome prior to infection does not necessarily protect against infection, but may reduce the severity of symptoms associated with disease; while probiotics are not uniformly effective at reducing oocyst output, they do show the most promise for potentially preventing severe infection in immunosuppressed individuals and subsequent infection of others should oocyst output be reduced.

47.   A Relational Framework For Microbiome Research With Indigenous Communities

In this study scientists proposed a framework centred on relation among Indigenous peoples, researchers and microbes, to guide ethical microbiome research. The framework centres accountability to flatten historical power imbalances that favour researcher perspectives and interests to provide space for Indigenous worldviews in pursuit of Indigenous research sovereignty.

This study concluded that ethical inclusion of Indigenous communities in microbiome research can provide health benefits for all populations and reinforce mutually beneficial partnerships between researchers and the public.

48.   Low Short-Chain-Fatty-Acid-Producing Activity of the Gut Microbiota Is Associated with Hypercholesterolemia and Liver Fibrosis in Patients with Metabolic-Associated (Non-Alcoholic) Fatty Liver Disease

The aim of this study was to investigates the short-chain fatty acid (SCFA) activity of the gut microbiota of patients with metabolic-associated fatty liver disease (MAFLD).

Among 42 non-cirrhotic MAFLD patients, 24 had high fecal SCFA levels (group H) and 18 had low fecal SCFA levels (group L). Patients in group H had lower serum uric acid, total cholesterol, and LDL cholesterol levels but a higher BMI than those in group L. All patients in group L and only 37.9% of those in group H were found to have hypercholesterolemia. In patients with hypercholesterolemia, the level of SCFAs was lower than that in patients without hypercholesterolemia. Patients in group H had less liver fibrosis than patients in group L. A total of 50.0% of the patients in group H and 92.3% of those in group L had significant liver fibrosis (≥F2). Patients with significant liver fibrosis had lower levels of fecal SCFAs—particularly acetate and butyrate.

The fecal SCFA levels were positively correlated with gamma-glutamyl transferase, total bilirubin levels, BMI, and platelet count and were negatively correlated with FIB-4, liver stiffness, serum total, and LDL cholesterol levels.

49.   The Gut Microbiome Modulates Associations Between Adherence To A Mediterranean-Style Diet, Abdominal Adiposity, And C-Reactive Protein In Population-Level Analysis

The objective of this study was to examine the potential mediating effect of the gut microbiome on the associations between Alternate Mediterranean Diet (aMed) scores, abdominal adiposity, and inflammation in population-level analysis. It involved 670 females from Northern Germany.

This study suggests that abundance of specific taxa in the *Porphyromonadaceae* and *Peptostreptococcaceae* families contributes to the association between aMed scores, lower abdominal adipose tissue, and inflammation.

50.   Dietary- And Host-Derived Metabolites Are Used By Diverse Gut Bacteria For Anaerobic Respiration

Respiratory reductases enable microorganisms to use molecules present in anaerobic ecosystems as energy-generating respiratory electron acceptors. In this study scientists identify three taxonomically distinct families of human gut bacteria (***Burkholderiaceae, Eggerthellaceae and Erysipelotrichaceae***) that encode large arsenals of tens to hundreds of respiratory-like reductases per genome. After screening species from each family (***Sutterella wadsworthensis, Eggerthella lenta and Holdemania filiformis***), researchers discovered that 22 metabolites were used as respiratory electron acceptors in a species-specific manner.

Identified reactions transform multiple classes of dietary- and host-derived metabolites, including bioactive molecules ***resveratrol*** and ***itaconate***. Products of identified respiratory metabolisms highlights poorly characterized compounds, such as ***the itaconate-derived 2-methylsuccinate***. *Reductase* substrate profiling defines enzyme–substrate pairs and reveals a complex picture of *reductase* evolution, providing evidence that *reductases* with specificities for related cinnamate substrates independently emerged at least four times. ***These studies thus establish an exceptionally versatile form of anaerobic respiration that directly links microbial energy metabolism to the gut metabolome.***

51. Utilization Of The Microbiome In Personalized Medicine

In this Review, investigators explored the recent advances in the application of microbiome data in precision medicine across a growing number of human diseases. *Researchers also discussed the challenges, limitations and prospects of analysing microbiome data for personalized patient care.*

52. BilR Is A Gut Microbial Enzyme That Reduces Bilirubin To Urobilinogen

In this study, researchers used biochemical analyses and comparative genomics to identify BilR as a gut-microbiota-derived bilirubin reductase that reduces bilirubin to urobilinogen.

Scientists delineated the BilR sequences from similar reductases through the identification of key residues critical for bilirubin reduction and found that BilR is predominantly encoded by *Firmicutes species*. Analysis of human gut metagenomes revealed that BilR is nearly ubiquitous in healthy adults, but prevalence is decreased in neonates and individuals with inflammatory bowel disease. **This discovery sheds light on the role of the gut microbiome in bilirubin metabolism and highlights the significance of the gut–liver axis in maintaining bilirubin homeostasis.**

MISCEALLENOUS

1. Efficacy Of Faecal Microbiota Transplantation In Patients With Progressive Supranuclear Palsy Richardson's Syndrome: A Phase 2, Single Centre, Randomized Clinical Trial

This study suggest that Faecal Microbiota Transplantation (FMT) treatment significantly improved motor and nonmotor symptoms in patients with palsy-Richardson's syndrome (PSP-RS), as well as reduced intestinal inflammation and enhanced the intestinal barrier by regulating the intestinal microbiota composition.

2. Circulating Markers Of Microbial Translocation And Host Response To Bacteria With Risk Of Colorectal Cancer: A Prospective, Nested Case Control Study In Men

In this study researchers examined three complementary markers of microbial translocation and host response to bacteria, including LPS-binding protein (LBP), soluble CD14 (sCD14), and endotoxincore antibody (EndoCAb) immunoglobulin M (IgM), with subsequent risk of Colorectal Cancer (CRC).

Study result shows that microbial translocation and host response to bacteria, as reflected by sCD14, is associated with risk of incident CRC in men.

3. The Gut Microbiota Promotes Distal Tissue Regeneration Via RORγ+ Regulatory T Cell Emissaries

Specific microbial signals induce the differentiation of a distinct pool of RORγ+ regulatory T (Treg) cells crucial for intestinal homeostasis. Scientists discovered highly analogous populations of microbiota-dependent Treg cells that promoted tissue regeneration at extra-gut sites, notably acutely injured skeletal muscle and fatty liver.

Inflammatory meditators elicited by tissue damage combined with MHC-class-II-dependent T cell activation to drive the accumulation of gut-derived RORγ+ Treg cells in injured muscle, wherein they regulated the dynamics and tenor of early inflammation and helped balance the proliferation vs. differentiation of local stem cells. Reining in IL-17A-producing T cells was a major mechanism underlying the rheostatic functions of RORγ+ Treg cells in compromised tissues.

The findings highlight the importance of gut-trained Treg cell emissaries in controlling the response to sterile injury of non-mucosal tissues.

4. Etiology Of Recurrent Cystitis In Postmenopausal Women Based On Vaginal Microbiota And The Role Of Lactobacillus Vaginal Suppository

The vaginal microbiota can be altered by uropathogenic bacteria associated with **recurrent cystitis (RC)** and the vaginal administration of *Lactobacillus* has suggested certain effects to prevent RC. This study aimed to clarify the etiology of RC from vaginal microbiota and importance of vaginal *Lactobacillus*. Vaginal samples obtained from 39 postmenopausal women were classified into four groups: healthy controls; uncomplicated cystitis; RC; and prevention (prevented RC by *Lactobacillus* crispatus-containing vaginal suppositories).

This study shows that the vaginal microbiota of postmenopausal women with RC is differed from healthy controls and uncomplicated cystitis in terms of lack of *Lactobacillus* and relatively dominant of *Enterobacteriaceae*. Vaginal administration of *Lactobacillus*-containing suppositories can prevent RC by stabilizing vaginal dysbiosis and causing a loss of pathogenic bacteria virulence.

5. Integrating Respiratory Microbiome And Host Immune Response Using Machine Learning For Diagnosis Of The Lower Respiratory Tract Infections

At present, the diagnosis of lower respiratory tract infections (LRTIs) is difficult and there is an urgent need for better diagnostic methods. This study enrolled 136 patients from 2020 to 2021 and collected bronchoalveolar lavage fluid (BALF) specimens.

Study result showed that the diversity of the lower respiratory tract microbiota in LRTIs significantly decreased, manifested by a decrease in the abundance of normal microbiota in the oropharynx and an increase in the abundance of opportunistic pathogenic bacteria. The upregulated differentially expressed genes (DEGs) in the LRTIs group were mainly enriched in infection immune response-related pathways. *Klebsiella pneumoniae* had the most significant increase in abundance in LRTIs, which was associated with upregulation of the host gene CMTM1, which belongs to the chemokine-like factor family. Researchers combined clinical information, lower respiratory tract microbiome, and host transcriptome data to construct a machine learning model with 70 screened features to predict LRTIs. The results showed that the model trained by random forest in the validation set had the best performance (ROC AUC: 0.957). The independent external dataset showed an accuracy of 88.2% for this model.

This study suggests that the prediction model integrating clinical information, lower respiratory tract microbiome, and host transcriptome data can be an effective tool for lower respiratory tract infections (LRTIs) diagnosis.

6. Fecal Microbiota Transplantation Plus Anti-PD-1 Immunotherapy InAdvanced Melanoma: A Phase I Trial

Fecal microbiota transplantation (FMT) represents a potential strategy to overcome resistance to immune checkpoint inhibitors in patients with refractory melanoma. Researchers conducted a multicenter phase I trial combining healthy donor FMT with the PD-1 inhibitors nivolumab or pembrolizumab in patients with advanced melanoma.

This clinical research study shows that FMT from healthy donors is safe in the first-line setting and warrants further investigation in combination with immune checkpoint inhibitors.

7. Cracking Cancer With Engineered Skin Commensals

The use of engineered bacteria to boost antitumor immunity is a fast-developing field in cancer research. **In this study scientists engineered a commensal bacterium of the human skin microbiota to cross-present tumor antigens to T cells and counteract tumor progression.**

8. Greengenes2 Unifies Microbial Data In A Single Reference Tree

Shotgun metagenomics and 16S rRNA gene amplicon (16S) studies are widely used in microbiome research, but investigators using these different methods typically worked hard to reconcile the results. This lack of standardization across methods limits the utility of the microbiome for reproducible biomarker discovery.

This study introduced Greengenes2, a reference tree that unifies genomic and 16S rRNA databases in a consistent, integrated resource.

Researchers found that by inserting sequences into a whole-genome phylogeny the 16S rRNA and shotgun metagenomic data generated from the same samples agree in principal to coordinates space, taxonomy and phenotype effect size when analyzed with the same tree.

9. Behaviour And Sun Exposure In Holidaymakers Alters Skin Microbiota Composition And Diversity

This study aimed to investigate the effects of sun exposure on the skin microbiota and its relationship with individual skin phototypes.

Study result shows that the major bacterial phyla were *Actinobacteria, Proteobacteria* and *Firmicutes*. There was a significant change in microbial beta diversity at day 28 post-holiday, compared to baseline, for all participants. However, when participants were segregated into three cohorts dependent on the degree of skin tanning response between baseline (pre-holiday) and immediately one-day post-holiday, there was a reduction in Proteobacteria in the sun-seeking participants 1 day after the holiday, which recovered over time. Hence, **these findings suggest that sun exposure can affect the diversity and composition of the skin microbiota, which may have downstream effects on skin health.**

10.   Microbiome And Metabolome In Home-Made Fermented Soybean Foods Of India Revealed By Metagenome-Assembled Genomes And Metabolomics

This study explores the microbiome, their functional annotations, metabolites and recovery of metagenome-assembled genomes (MAGs) in Grep-chhurpi, peha, peron namsing and peruñyaan fermented soybean foods prepared by the native people of Arunachal Pradesh in India.

Metagenomes revealed that the dominance of bacteria was 97.80 % with minor traces of viruses, eukaryotes and archaea. *Bacillota* is the most abundant phylum with *Bacillus subtilis* as the abundant species. Metagenome also revealed the abundance of lactic acid bacteria such as *Enterococcus casseliflavus, Enterococcus faecium, Mammaliicoccus sciuri* and *Staphylococcus saprophyticus* in all samples. *B. subtilis* was the major species found in all products. Predictive metabolic pathways showed the abundance of genes associated with metabolisms.

Metabolomics analysis revealed that both targeted and untargeted metabolites, contribute in flavour development and therapeutic properties. Researchers identified high-quality MAGs (B. *subtilis, Enterococcus faecalis, Pediococcus acidilactici* **and B.** *velezensis*) **which showed the presence of several biomarkers corresponding to various bio-functional properties. Gene clusters of secondary metabolites (antimicrobial peptides) and CRISPR-Cas systems were also detected in all MAGs. Further, this study also showed the key elements related to the cultivability of identified species of MAGs for future use as starter cultures in fermented soybean food product development. Additionally, comparison of microbiome and metabolites of grep-chhurpi, peron namsing and peruñyaan with that of other fermented soybean foods of Asia revealed a distinct difference.**

11. Fecal Microbiota Transplantation Plus Tislelizumab And Fruquintinib In Refractory Microsatellite Stable Metastatic Colorectal Cancer: An Open-Label, Single-Arm, Phase II Trial (RENMIN-215)

The aim of this study was to explore the efficacy and safety of the combination of fecal microbiota transplantation (FMT) and *tislelizumab* and *fruquintinib* in refractory microsatellite stable (MSS) metastatic colorectal cancer (mCRC).

Study result show that nineteen patients (95%) experienced at least one treatment-related adverse event (TRAE). Six patients (30%) had grade 3–4 TRAEs, with the most common being albuminuria (10%), urine occult blood (10%), fecal occult blood (10%), hypertension (5%), hyperglycemia (5%), liver dysfunction (5%), hand-foot skin reaction (5%), and hypothyroidism (5%). No treatment-related deaths occurred. Responders had a high-abundance of *Proteobacteria* and *Lachnospiraceae family and a low-abundance of Actinobacteriota and Bifidobacterium*. The treatment did not change the structure of peripheral blood TCR repertoire. However, the expanded TCRs exhibited the characteristics of antigen-driven responses in responders.

Researchers concluded that FMT plus tislelizumab and fruquintinib as third-line treatment improves survival and helps in manageable safety in refractory MSS mCRC, suggesting a valuable new treatment option among patient.