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10. Longitudinal development of the gut microbiome and metabolome in preterm neonates with late onset sepsis and healthy controls. (Abstract & UW comment) {Full article}
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DETAILS OF ARTICLES

1. Patterns of Early-Life Gut Microbial Colonization during Human Immune Development: An Ecological Perspective
   Laforest-LaPointe I, Arrieta MC.

ABSTRACT
Alterations in gut microbial colonization during early life have been reported in infants that later developed asthma, allergies, type 1 diabetes, as well as in inflammatory bowel disease patients, previous to disease flares. Mechanistic studies in animal models have established that microbial alterations influence disease pathogenesis via changes in immune system maturation. Strong evidence points to the presence of a window of opportunity in early life, during which changes in gut microbial colonization can result in immune dysregulation that predisposes susceptible hosts to disease. Although the ecological patterns of microbial succession in the first year of life have been partly defined in specific human cohorts, the taxonomic and functional features, and diversity thresholds that characterize these microbial alterations are, for the most part, unknown. In this review, we summarize the most important links between the temporal mosaics of gut microbial colonization and the age-dependent immune functions that rely on them. We also highlight the importance of applying ecology theory to design studies that explore the interactions between this complex ecosystem and the host immune system. Focusing research efforts on understanding the importance of temporally structured patterns of diversity, keystone groups, and inter-kingdom microbial interactions for ecosystem functions has great potential to enable the development of biologically sound interventions aimed at maintaining and/or improving immune system development and preventing disease.

WEB: 10.3389/fimmu.2017.00788
IMPACT FACTOR: 3.35
CITED HALF-LIFE: N/A

UW EDITORIAL COMMENT: Figure 1 presents a temporal diagram of succession events that occur within the bacterial microbiome from in utero through introduction of solid foods and gives comparisons of bacterial composition between a variety of factors including pre-term vs. full-term, vaginal vs. cesarean birth, and breastmilk vs. formula. The authors note that increases or decreases in bacterial community diversity may not be adequate indicators of gut disruption and rather community compositions and functions should be considered.

2. Microbiota metabolite short-chain fatty acid acetate promotes intestinal IgA response to microbiota which is mediated by GPR43.
   Mucosal Immunology. 10, 946-956. 2017 July.

ABSTRACT
Intestinal IgA, which is regulated by gut microbiota, has a crucial role in maintenance of intestinal homeostasis and in protecting the intestines from inflammation. However, the means by which microbiota promotes intestinal IgA responses remain unclear. Emerging evidence suggests that the host can sense gut bacterial metabolites in addition to pathogen-associated molecular patterns and that recognition of these small molecules influences host immune response in the intestines and beyond. We reported here that microbiota metabolite short-chain fatty acid acetate promoted intestinal IgA
responses, which was mediated by "metabolite-sensing" GPR43. GPR43-/- mice demonstrated lower levels of intestinal IgA and IgA+ gut bacteria compared with those in wild type (WT) mice. Feeding WT but not GPR43-/- mice acetate but not butyrate promoted intestinal IgA response independent of T cells. Acetate promoted B-cell IgA class switching and IgA production in vitro in the presence of WT but not GPR43-/- dendritic cells (DCs). Mechanistically, acetate-induced DC expression of Aldh1a2, which converts Vitamin A into its metabolite retinoic acid (RA). Moreover, blockade of RA signaling inhibited the acetate induction of B-cell IgA production. Our studies thus identified a new pathway by which microbiota promotes intestinal IgA response through its metabolites.

WEB: 10.1038/mi.2016.114
IMPACT FACTOR: 5.53
CITED HALF-LIFE: 3.10

UW EDITORIAL COMMENT: Authors contribute to the evidence base of the role of IgA in maintaining intestinal homeostasis by demonstrating that acetate, one of many short-chain fatty acids, can promote intestinal IgA responses. Figure 2 gives visual representations of differences of IgA production between the group of mice that was fed acetate in addition to antibiotics and the group that was fed only antibiotics. It can be seen in Figure 2a that there was a significant increase in IgA production within the acetate-fed mice.

3. *Lactobacillus acidophilus/Bifidobacterium infantis probiotics are associated with increased growth of VLBWI among those exposed to antibiotics*

ABSTRACT
We performed an observational study with very-low-birth weight infants (VLBWI) ≤33 weeks of gestation born in centers of the German Neonatal Network (GNN; total n = 8534, n = 6229 received probiotics). The primary objectives of our study were (a) to assess the effect of *Lactobacillus acidophilus/Bifidobacterium infantis* probiotics on growth in VLBWI during primary stay in hospital and (b) to determine whether this effect is modified by antibiotic exposure. In linear regression models the administration of probiotics was independently associated with improved weight gain [g/d; effect size B = 0.62 (95% CI: 0.37–0.87), p < 0.001], and higher growth rates for body length [(mm/d; B = 0.06 (95% CI: 0.04–0.08), p < 0.001) and head circumference [mm/d; B = 0.03, 95% CI: 0.02–0.04, p < 0.001]. This effect was pronounced in infants with postnatal exposure to antibiotics; i.e. weight gain [g/d; B = 0.66 (95% CI: 0.32–1), p < 0.001], growth rate body length [(mm/d; B = 0.09 (95% CI: 0.06–0.12), p < 0.001] and head circumference [mm/d; B = 0.04, 95% CI: 0.02–0.06, p < 0.001]. In the small subgroup that was available for analysis at 5-year follow-up (with probiotics: n = 120 vs. without probiotics: n = 54) we noted a sustained effect of probiotics in infants who received postnatal antibiotics. Probiotics may improve growth in antibiotic-treated infants which needs to be confirmed in randomized-controlled trials.

WEB: 10.1038/s41598-017-06161-8
IMPACT FACTOR: 5.47
CITED HALF-LIFE: 1.70
UW EDITORIAL COMMENT: The results demonstrate that the potential synergistic effect of probiotics and antibiotics on growth may depend on timing of antibiotic administration. There was no growth promoting effect of probiotics among those VLBW infants whose mothers were exposed to antenatal antibiotics only, while there was an effect present in those infants who received postnatal antibiotic exposure. Additionally, the authors highlight the need for large randomized-controlled trials to overcome the limitations of observational studies such as this one. In this case, the study was limited by its ability to overcome confounding variables that may have biased results, in addition to a small sample size for the long follow up group. However, the study does contribute to the evidence base around the role of antibiotics and probiotics, and specifically their synergistic effect on growth promotion.

4. Introducing the sporobiota and sporobiome.
   Tetz G, Tetz V.

ABSTRACT
Unrelated spore-forming bacteria share unique characteristics stemming from the presence of highly resistant endospores, leading to similar challenges in health and disease. These characteristics are related to the presence of these highly transmissible spores, which are commonly spread within the environment and are implicated in host-to-host transmission. In humans, spore-forming bacteria contribute to a variety of pathological processes that share similar characteristics, including persistence, chronicity, relapses and the maintenance of the resistome. We first outline the necessity of characterizing the totality of the spore-forming bacteria as the sporobiota based on their unique common characteristics. We further propose that the collection of all genes of spore-forming bacteria be known as the sporobiome. Such differentiation is critical for exploring the cross-talk between the sporobiota and other members of the gut microbiota, and will allow for a better understanding of the implications of the sporobiota and sporobiome in a variety of pathologies and the spread of antibiotic resistance.

WEB: 10.1186/s13099-017-0187-8
IMPACT FACTOR: 3.4
CITED HALF-LIFE: 3.4

UW EDITORIAL COMMENT: Genomic-based workflows, like the one represented in Figure 2 of the article, that combine traditional culture approaches with more innovative genetic strategies will be crucial to the understanding of the sporobiome. Figure 2 provides a phylogenetic representation of global sporobiome families that allows for identification of novel sporobiota families and further understanding of the complex sporobiome.

5. Potential and active functions in the gut microbiota of a healthy human cohort.
   Microbiome. 5:79. 2017 July 14.

ABSTRACT
BACKGROUND: The study of the gut microbiota (GM) is rapidly moving towards its functional characterization by means of shotgun meta-omics. In this context, there is still no consensus on which microbial functions are consistently and constitutively expressed in the human gut in physiological
conditions. Here, we selected a cohort of 15 healthy subjects from a native and highly monitored Sardinian population and analyzed their GMs using shotgun metaproteomics, with the aim of investigating GM functions actually expressed in a healthy human population. In addition, shotgun metagenomics was employed to reveal GM functional potential and to compare metagenome and metaproteome profiles in a combined taxonomic and functional fashion.

**RESULTS:** Metagenomic and metaproteomic data concerning the taxonomic structure of the GM under study were globally comparable. On the contrary, a considerable divergence between genetic potential and functional activity of the human healthy GM was observed, with the metaproteome displaying a higher plasticity, compared to the lower inter-individual variability of metagenome profiles. The taxon-specific contribution to functional activities and metabolic tasks was also examined, giving insights into the peculiar role of several GM members in carbohydrate metabolism (including polysaccharide degradation, glycan transport, glycolysis, and short-chain fatty acid production). Noteworthy, Firmicutes-driven butyrogenesis (mainly due to *Faecalibacterium* spp.) was shown to be the metabolic activity with the highest expression rate and the lowest inter-individual variability in the study cohort, in line with the previously reported importance of the biosynthesis of this microbial product for the gut homeostasis.

**CONCLUSIONS:** Our results provide detailed and taxon-specific information regarding functions and pathways actively working in a healthy GM. The reported discrepancy between expressed functions and functional potential suggests that caution should be used before drawing functional conclusions from metagenomic data, further supporting metaproteomics as a fundamental approach to characterize the human GM metabolic functions and activities.

**WEB:** 10.1186/s40168-017-0293-3

**IMPACT FACTOR:** 9.85

**CITED HALF-LIFE:** N/A

**UW EDITORIAL COMMENT:** In addition to summarizing an in-depth analysis of gut microbiota of a cohort of healthy humans, the authors discuss the benefit of using both omic approaches (shotgun metaproteomics and shotgun metagenomics) in a complementary fashion — metagenomics allows for a complete history of the functions of traveling gut microbiota, while metaproteomics allows for a snapshot look at the gut microbiota at a specific time or location.

6. **More than just a gut feeling: constraint-based genome-scale metabolic models for predicting functions of human intestinal microbes.**
   van der Ark K, van Heck R, Martins Dos Santos V, Belzer C, Vos W.

**ABSTRACT**
The human gut is colonized with a myriad of microbes, with substantial interpersonal variation. This complex ecosystem is an integral part of the gastrointestinal tract and plays a major role in the maintenance of homeostasis. Its dysfunction has been correlated to a wide array of diseases, but the understanding of causal mechanisms is hampered by the limited amount of cultured microbes, poor understanding of phenotypes, and the limited knowledge about interspecies interactions. Genome-scale metabolic models (GEMs) have been used in many different fields, ranging from metabolic engineering to the prediction of interspecies interactions. We provide showcase examples for the application of GEMs for gut microbes and focus on (i) the prediction of minimal, synthetic, or defined media; (ii) the prediction of possible functions and phenotypes; and (iii) the prediction of interspecies interactions. All
three applications are key in understanding the role of individual species in the gut ecosystem as well as the role of the microbiota as a whole. Using GEMs in the described fashions has led to designs of minimal growth media, an increased understanding of microbial phenotypes and their influence on the host immune system, and dietary interventions to improve human health. Ultimately, an increased understanding of the gut ecosystem will enable targeted interventions in gut microbial composition to restore homeostasis and appropriate host-microbe crosstalk.

WEB: 10.1186/s40168-017-0299-x
IMPACT FACTOR: 9.85
CITED HALF-LIFE: N/A

UW EDITORIAL COMMENT: The authors highlight the usage of genome-scale metabolic models in the design of defined culture media. Three case studies are provided to exemplify this point: 1) using a GEM to investigate the metabolic capabilities and fermentation behavior of *Lactobacillus plantarum* WCFS1, which is used in industrial food processes and probiotics, 2) constructing a GEM of *Lactococcus lactis* IL1403 to design a minimal medium for physiological studies and determine essential amino acids for growth, and 3) designing a GEM to investigate the essential amino acids for *Staphylococcus aureus* N315.

7. Formula diet driven microbiota shifts tryptophan metabolism from serotonin to tryptamine in neonatal porcine colon.

ABSTRACT

BACKGROUND: The gut microbiota of breast-fed and formula-fed infants differ significantly, as do the risks for allergies, gut dysfunction, and upper respiratory tract infections. The connections between breast milk, various formulas, and the profiles of gut bacteria to these childhood illnesses, as well as the mechanisms underlying the effects, are not well understood.

METHODS: We investigated distal colon microbiota by 16S RNA amplicon sequencing, morphology by histomorphometry, immune response by cytokine expression, and tryptophan metabolism in a pig model in which piglets were sow-fed, or fed soy or dairy milk-based formula from postnatal day (PND) 2 to 21.

RESULTS: Formula feeding significantly (*p* < 0.05) altered the colon microbiota relative to the sow feeding. A significant reduction in microbial diversity was noted with formula groups in comparison to sow-fed. *Streptococcus, Blautia, Citrobacter, Butyrimonas, Parabacteroides, Lactococcus* genera were increased with formula feeding relative to sow feeding. In addition, relative to sow feeding, *Anaerotruncus, Akkermansia, Enterococcus, Acinetobacter, Christensenella, and Holdemania* were increased in milk-fed piglets, and *Biliophila, Ruminococcus, Clostridium* were increased in soy-fed piglets. No significant gut morphological changes were noted. However, higher cytokine mRNA expression (BMP4, CCL11, CCL21) was observed in the distal colon of formula groups. Formula feeding reduced enterochromaffin cell number and serotonin, but increased tryptamine levels relative to sow feeding.

CONCLUSIONS: Our data confirm that formula diet alters the colon microbiota and appears to shift tryptophan metabolism from serotonin to tryptamine, which may lead to greater histamine levels and risk of allergies in infants.

WEB: 10.1186/s40168-017-0297-z
IMPACT FACTOR: 9.85
UW EDITORIAL COMMENT: Authors demonstrate associations between a formula diet and colon microbiota and serotonin levels in pigs—however, results should be interpreted with caution as environmental factors such as the housing environment may have played an important role in the microbiome compositions. Further, linkages to human infants in regards to these results should be made with caution.


ABSTRACT

BACKGROUND: Establishment of the human gut microbiota begins at birth. This early-life microbiota development can impact host physiology during infancy and even across an entire life span. However, the functional stability and population structure of the gut microbiota during initial colonization remain poorly understood. Metaproteomics is an emerging technology for the large-scale characterization of metabolic functions in complex microbial communities (gut microbiota).

RESULTS: We applied a metagenome-informed metaproteomic approach to study the temporal and inter-individual differences of metabolic functions during microbial colonization of preterm human infants’ gut. By analyzing 30 individual fecal samples, we identified up to 12,568 protein groups for each of four infants, including both human and microbial proteins. With genome-resolved matched metagenomics, proteins were confidently identified at the species/strain level. The maximum percentage of the proteome detected for the abundant organisms was ~45%. A time-dependent increase in the relative abundance of microbial versus human proteins suggested increasing microbial colonization during the first few weeks of early life. We observed remarkable variations and temporal shifts in the relative protein abundances of each organism in these preterm gut communities. Given the dissimilarity of the communities, only 81 microbial EggNOG orthologous groups and 57 human proteins were observed across all samples. These conserved microbial proteins were involved in carbohydrate, energy, amino acid and nucleotide metabolism while conserved human proteins were related to immune response and mucosal maturation. We identified seven proteome clusters for the communities and showed infant gut proteome profiles were unstable across time and not individual-specific. Applying a gut-specific metabolic module (GMM) analysis, we found that gut communities varied primarily in the contribution of nutrient (carbohydrates, lipids, and amino acids) utilization and short-chain fatty acid production.

CONCLUSIONS: Overall, this study reports species-specific proteome profiles and metabolic functions of human gut microbiota during early colonization. In particular, our work contributes to reveal microbiota-associated shifts and variations in the metabolism of three major nutrient sources and short-chain fatty acid during colonization of preterm infant gut.

WEB: 10.1186/s40168-017-0290-6
IMPACT FACTOR: 9.85
CITED HALF-LIFE: N/A

UW EDITORIAL COMMENT: Authors note that, in comparison to adults, infant gut metaproteomes are more unstable and individual-unspecific, as evidenced by this study. They attributed this to the infant gut being less mature and more susceptible to environmental factors. Figure 2 provides four side-by-side
boxplots comparing proteome coverage among the 4 infants analyzed in this study, which provides a visual representation of microbial variations throughout the initial weeks of life.

9.  

**[Dis]Trust your gut: the gut microbiome in age-related inflammation, health, and disease.**

Buford, T.


**ABSTRACT**

Chronic inflammation represents one of the most consistent biologic features of aging. However, the precise etiology of persistent low-grade increases in inflammation remains unclear. Recent evidence suggests that the gut microbiome may play a key role in age-related inflammation. Indeed, several studies have indicated that older adults display an altered composition of the gut microbiota, and early evidence indicates that this dysbiosis is associated with the presence of several key circulating inflammatory analytes. The present review summarizes knowledge on age-related inflammation and discusses how potential relationships with gut dysbiosis may lead to novel treatment strategies in the future.

**WEB:** 10.1186/s40168-017-0296-0

**IMPACT FACTOR:** 9.85

**CITED HALF-LIFE:** N/A

**UW EDITORIAL COMMENT:** Authors point out a significant research gap in regards to the association between the microbiome and aging, especially around the specific etiologic explanations for these age-related changes. In addition to a lack of research, studies that have investigated this association are not all consistent; Table 1 provides a summary of the studies that have been performed in this area and highlights the direction (increase/decrease) of change of microbiota in each study, if present.

10. **Longitudinal development of the gut microbiome and metabolome in preterm neonates with late onset sepsis and healthy controls.**


**ABSTRACT**

**BACKGROUND:** Late onset sepsis (LOS) in preterm infants is associated with considerable morbidity and mortality. While studies have implicated gut bacteria in the aetiology of the disease, functional analysis and mechanistic insights are generally lacking. We performed temporal bacterial (*n* = 613) and metabolomic (*n* = 63) profiling on extensively sampled stool from 7 infants with LOS and 28 matched healthy (no LOS or NEC) controls.

**RESULTS:** The bacteria isolated in diagnostic blood culture usually corresponded to the dominant bacterial genera in the gut microbiome. Longitudinal changes were monitored based on preterm gut community types (PGCTs), where control infants had an increased number of PGCTs compared to LOS infants (*P* = 0.011). PGCT 6, characterised by Bifidobacteria dominance, was only present in control infants. Metabolite profiles differed between LOS and control infants at diagnosis and 7 days later, but not 7 days prior to diagnosis. Bifidobacteria was positively correlated with control metabolites, including raffinose, sucrose, and acetic acid.

**CONCLUSION:** Using multi-omic analysis, we show that the gut microbiome is involved in the pathogenesis of LOS. While the causative agent of LOS varies, it is usually abundant in the gut. Bifidobacteria dominance was associated with control infants, and the presence of this organism may
directly protect, or act as a marker for protection, against gut epithelial translocation. While the metabolomic data is preliminary, the findings support that gut development and protection in preterm infants is associated with increased in prebiotic oligosaccharides (e.g. raffinose) and the growth of beneficial bacteria (e.g. Bifidobacterium).

WEB: 10.1186/s40168-017-0295-1
IMPACT FACTOR: 9.85
CITED HALF-LIFE: N/A

UW EDITORIAL COMMENT: The study has a small sample size and a limited number of infants on which metabolomics was performed, weakening the strength of the association. Nevertheless, the article is consistent with prior evidence that prebiotic oligosaccharides and beneficial bacteria, such as Bifidobacterium, play a role in protection against late onset sepsis in preterm infants.

ARTICLE ARCHIVE (JAN 2016-PRESENT)
Parasitic protozoa and interactions with the host intestinal microbiota.
Gastrointestinal inflammation by gut microbiota disturbance induces memory impairment in mice.
New insights into environmental enteric dysfunction.
Tropical Enteropathies.
Age and Sex Normalization of Intestinal Permeability Measures for the Improved Assessment of Enteropathy in Infancy and Early Childhood: Results from the MAL-ED Study.
Infant Nutritional Status and Markers of Environmental Enteric Dysfunction are Associated with Midchildhood Anthropometry and Blood Pressure in Tanzania.
Biomarkers to Stratify Risk Groups among Children with Malnutrition in Resource-Limited Settings and to Monitor Response to Intervention
Association between Enteropathogens and Malnutrition in Children Aged 6-23 mo in Bangladesh: a Case-Control Study.
Causal Pathways from Enteropathogens to Environmental Enteropathy: Findings from the MAL-ED Birth Cohort Study.
Biomarkers of Environmental Enteric Dysfunction: The good, the bad and the ugly.
Application of penalized linear regression methods to the selection of environmental enteropathy biomarkers.
Environmental enteropathy is associated with cardiometabolic risk factors in Peruvian children.
Biomarkers of Environmental Enteric Dysfunction Among Children in Rural Bangladesh.

Environmental Enteric Dysfunction is Associated with Carnitine Deficiency and Altered Fatty Acid Oxidation.

Determinant Variables, Enteric Pathogen Burden, Gut Function, and Immune-Related Inflammatory Biomarkers Associated with Childhood Malnutrition: A Prospective Case-Control Study in Northeastern Brazil.

The Association Between Fecal Biomarkers of Environmental Enteropathy and Rotavirus Vaccine Response in Nicaraguan Infants.

Systemic inflammation, growth factors, and linear growth in the setting of infection and malnutrition

Environmental Enteric Dysfunction and the Fecal Microbiota in Malawian Children

Environmental Enteric Dysfunction and Growth Failure/Stunting in Global Child Health

Biomarkers of Environmental Enteropathy, Inflammation, Stunting, and Impaired Growth in Children in Northeast Brazil.

Environmental enteropathy.

Environmental Enteropathy: Elusive but Significant Subclinical Abnormalities in Developing Countries.

Endomicroscopic and Transcriptomic Analysis of Impaired Barrier Function and Malabsorption in Environmental Enteropathy.

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Environmental Enteric Dysfunction Includes a Broad Spectrum of Inflammatory Responses and Epithelial Repair Processes.

The Impact of Environmental Enteropathy and Systemic Inflammation on Infant Growth Failure

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Decoding Hidden Messages: Can Fecal Host Transcriptomics Open Pathways to Understanding Environmental Enteropathy?

Plasma Tryptophan and the Kynurenine–Tryptophan Ratio are Associated with the Acquisition of Statural Growth Deficits and Oral Vaccine Underperformance in Populations with Environmental Enteropathy

Malnutrition Is Associated with Protection from Rotavirus Diarrhea: Evidence from a Longitudinal Birth Cohort Study in Bangladesh
Nutrition/metabolism

Detrimental Impact of Microbiota-Accessible Carbohydrate-Deprived Diet on Gut and Immune Homeostasis: An Overview

Chronic consequences on human health induced by microbial pathogens: Growth faltering among children in developing countries.

The effects of micronutrient deficiencies on bacterial species from the human gut microbiota.

Gut microbiota interactions with the immunomodulatory role of vitamin D in normal individuals.

The association of serum choline with linear growth failure in young children from rural Malawi.

Starved Guts: Morphologic and Functional Intestinal Changes in Malnutrition.

Which dietary components modulate longitudinal growth?

Influence of diet on the gut microbiome and implications for human health.

Nopal feeding reduces adiposity, intestinal inflammation and shifts the cecal microbiota and metabolism in high-fat fed rats.

Western diets, gut dysbiosis, and metabolic diseases: Are they linked?

Nutrition, infection and stunting: the roles of deficiencies of individual nutrients and foods, and of inflammation, as determinants of reduced linear growth of children.

Microbiome, Growth Retardation, and Metabolism: Are they related?

Linking Dietary Patterns with Gut Microbial Composition and Function.

Impacts of resistant starch and wheat bran consumption on enteric inflammation in relation to colonic bacterial community structures and short-chain fatty acid concentrations in mice.

Diet-Microbiota Interactions Mediate Global Epigenetic Programming in Multiple Host Tissues.

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Environmental Enteric Dysfunction is Associated with Altered Bile Acid Metabolism.

Metabolic alterations in children with environmental enteric dysfunction.

Genetic and Metabolic Signals during Acute Enteric Bacterial Infection Alter the Microbiota and Drive Progression to Chronic Inflammatory Disease.

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Child Stunting is Associated with Low Circulating Essential Amino Acids.
Diet–microbiota interactions as moderators of human metabolism

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A Comparison of Diarrheal Severity Scores in the MAL-ED Multisite Community-Based Cohort Study.

Metabolomic Changes in Serum of Children with Different Clinical Diagnoses of Malnutrition.

Mortality in children with complicated severe acute malnutrition is related to intestinal and systemic inflammation: an observational cohort study.

Steroid Administration and Growth Impairment in Children with Crohn's Disease.

Effects of a gut pathobiont in a gnotobiotic mouse model of childhood undernutrition

A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility

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Early antibiotic exposure in low-resource settings is associated with increased weight in the first two years of life.

The path towards microbiome-based metabolite treatment.

Next-generation probiotics: the spectrum from probiotics to live biotherapeutics

Severity of pancreatitis-associated intestinal mucosal barrier injury is reduced following treatment with the NADPH oxidase inhibitor apocynin.

Targeting the gut microbiota with inulin-type fructans: preclinical demonstration of a novel approach in the management of endothelial dysfunction.

Interleukin-23 Increases Intestinal Epithelial Cell Permeability In Vitro

Pili-like proteins of Akkermansia muciniphila modulate host immune responses and gut barrier function.

The anti-inflammatory drug mesalamine targets bacterial polyphosphate accumulation

Akkermansia muciniphila improves metabolic profiles by reducing inflammation in chow diet-fed mice

Longitudinal change of selected human milk oligosaccharides and association to infants' growth, an observatory, single center, longitudinal cohort study

Abrupt suspension of probiotics administration may increase host pathogen susceptibility by inducing gut dysbiosis
Toward a Personalized Approach in Prebiotics Research

Dietary Fiber and Prebiotics and the Gastrointestinal Microbiota.

A microbial protein that alleviates metabolic syndrome

Can probiotics modulate human disease by impacting intestinal barrier function?

Human Milk Oligosaccharides Influence Neonatal Mucosal and Systemic Immunity.

Oral Microbiota in Infants Fed a Formula Supplemented with Bovine Milk Fat Globule Membranes - A Randomized Controlled Trial.

Dietary Prebiotics and Bioactive Milk Fractions Improve NREM Sleep, Enhance REM Sleep Rebound and Attenuate the Stress-Induced Decrease in Diurnal Temperature and Gut Microbial Alpha Diversity.

Impact of prebiotics on metabolic and behavioral alterations in a mouse model of metabolic syndrome.

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An important chapter in the infection-malnutrition story.

Lactobacillus plantarum strain maintains growth of infant mice during chronic undernutrition

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Sialylated galacto-oligosaccharides and 2'-fucosyllactose reduce necrotising enterocolitis in neonatal rats

Rebooting the microbiome.

Fecal microbiota transplantation: in perspective.

Fecal Microbiota-based Therapeutics for Recurrent Clostridium difficile Infection, Ulcerative Colitis and Obesity

Microbial therapeutic interventions.
High-affinity monoclonal IgA regulates gut microbiota and prevents colitis in mice

Stable Engraftment of Bifidobacterium longum AH1206 in the Human Gut Depends on Individualized Features of the Resident Microbiome

Protein- and zinc-deficient diets modulate the murine microbiome and metabolic phenotype

Fecal Microbiota-based Therapeutics for Recurrent Clostridium difficile Infection, Ulcerative Colitis and Obesity

Overcoming the limited availability of human milk oligosaccharides: challenges and opportunities for research and application

Efficacy of Probiotics Versus Placebo in the Prevention of Necrotizing Enterocolitis in Preterm Very Low Birth Weight Infants: A Double-Blind Randomized Controlled Trial

Eosinophils, probiotics, and the microbiome.

A Combined Intervention of Zinc, Multiple Micronutrients, and Albendazole Does Not Ameliorate Environmental Enteric Dysfunction or Stunting in Rural Malawian Children in a Double-Blind Randomized Controlled Trial

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Improving the detection of environmental enteric dysfunction: a lactulose, rhamnose assay of intestinal permeability in children aged under 5 years exposed to poor sanitation and hygiene.

Organs-on-chips with integrated electrodes for trans-epithelial electrical resistance (TEER) measurements of human epithelial barrier function.

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Engineering bacterial thiosulfate and tetrathionate sensors for detecting gut inflammation.

Engineered Regulatory Systems Modulate Gene Expression of Human Commensals in the Gut

MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data.

Honeybee gut microbiota promotes host weight gain via bacterial metabolism and hormonal signaling.

Leading microbiome-based therapeutic falters in Phase II trial

Faecal microbiota transplantation—A clinical view.

Optimization of metabolomics of defined in vitro gut microbial ecosystems
Community dynamics drive punctuated engraftment of the fecal microbiome following transplantation using freeze-dried, encapsulated fecal microbiota.

Challenges of metabolomics in human gut microbiota research

The Role of the Immune System in Metabolic Health and Disease

Optimization of metabolomics of defined in vitro gut microbial ecosystems.

An Intestinal Organ Culture System Uncovers a Role for the Nervous System in Microbe-Immune Crosstalks.

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Gut check

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Infectious disease: something in the water

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I’ll have a turkey and cheese sandwich

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The microbiome and innate immunity

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