

REVIEW ARTICLE

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The Human Intestinal Microbiome in Health and Disease

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HUMAN-ASSOCIATED MICROBES HAVE PRIMARILY BEEN VIEWED THROUGH the lens of a single species and its environment. Advances in culture-independent technologies have shown the enormous diversity, functional capacity, and age-associated dynamics of the human microbiome (see the Glossary). A large number of diverse microbial species reside in the distal gastrointestinal tract, and gut microbiota dysbiosis — imbalances in the composition and function of these intestinal microbes — is associated with diseases ranging from localized gastroenterologic disorders to neurologic, respiratory, metabolic, hepatic, and cardiovascular illnesses. Much effort is currently concentrated on exploring potential causality and related microbiota-mediated disease mechanisms, with the hope that an improved understanding will fuel the conception and realization of novel therapeutic and preventive strategies.

Until recently, our view of human microbiology was largely shaped by culture-based studies of single microbes (bacteria, archaea, fungi, and viruses), frequently isolated from patients who had acute infection or chronic disease. However, several decades ago, environmental microbial ecologists recognized that the diversity of microbes observed by microscopy far exceeded that of organisms recovered with the use of traditional culture-based approaches.¹ A variety of culture-independent molecular assays (Table 1) for detecting and classifying microorganisms (microbiota) and assessing their encoded genes (microbiome) and gene products showed

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Glossary

Biomarker sequencing: The process of cataloguing microbes in a mixed-species community through analysis of sequence variation in a single ubiquitous gene.

Holobiont: The totality of organisms in a given ecosystem (e.g., the shared human and microbial ecosystem); also called a superorganism.

Metabolome: The complete set of small-molecule chemicals found in a biologic sample.

Metagenome: All the genetic material present in an environmental sample, consisting of the genomes of many individual organisms.

Methanogenic archaea: Methane-producing microbes of the ancient Archaea kingdom.

Microbiome: The collection of all genomes of microbes in an ecosystem.

Microbiota: The microbes that collectively inhabit a given ecosystem.

Pathobionts: Typically benign endogenous microbes with the capacity, under altered ecosystem conditions, to elicit pathogenesis.

Prebiotics: Nutritional substrates that promote the growth of microbes that confer health benefits in the host.

Probiotics: Live microbes that confer health benefits when administered in adequate amounts in the host.

Synbiotics: Formulations consisting of a combination of prebiotics and probiotics.

Table 1. Tools for Analyzing Microbiota.

Approach	Data	Platform	Pros and Cons
Biomarker sequencing (e.g., 16S rRNA gene or internal transcribed spacer region)*	Community composition	Next-generation sequencing	Is cost-effective, is semiquantitative, permits resolution of genus level and in some cases species level; shorts reads may make accurate classification difficult
Metagenomics	Generation of draft genomes, functional capacity, growth dynamics	Next-generation sequencing	Has capacity for strain-level reconstruction, is quantitative, allows for functional annotation with pathway predictions; is currently very costly, has community coverage that may be relatively shallow in more complex assemblages
Metatranscriptomics (RNA sequencing)	Gene expression	Next-generation sequencing	Highly expressed genes are more likely than others to be detected, depletion of human transcripts is possible, requires immediate preservation or processing of fresh or snap-frozen intestinal specimens
Metaproteomics	Protein expression	Liquid or gas chromatography–mass spectrometry	Primarily detects dominant proteins; makes removal of host-derived proteins impossible
Metabolomics	Metabolic productivity	Liquid or gas chromatography–mass spectrometry or magnetic resonance spectroscopy	Is semiquantitative; can be targeted or untargeted; detects metabolites that are platform- and database-dependent; detects metabolites that may originate from microbes, diet, or host

* The term rRNA denotes ribosomal RNA.

that microbes rarely exist in isolation. Instead, they subsist in complex, interactive, interkingdom, multispecies microbial communities within a habitat. As the field has developed, it has become apparent that virtually every habitat, and every organism, on earth has its own microbiota. This includes the human holobiont, a conglomerate of mammalian and multispecies microbial cells in spatially segregated ecosystems, the genomic content of which is influenced by both topography and biologic individuality.²

In humans, the gastrointestinal tract represents a large microbial ecosystem, housing several trillion microbial cells. An integrated catalogue of the human fecal microbial metagenome, based on data from 1200 persons in the United States, China, and Europe, identified an aggregate 9.9 million microbial genes across these fecal microbiomes.³ More than a billion years of mammalian–microbial coevolution has led to interdependency. As a result, the intestinal microbiota play a critical role in the maturation and continued education of the host immune response⁴; provide protection against pathogen overgrowth⁵; influence host-cell proliferation⁶ and vascularization⁷; regulate intestinal endocrine functions,⁸ neurologic signaling,⁹ and bone density¹⁰; provide a source of energy biogenesis¹¹ (5 to 10% of daily host energy requirements); biosynthesize vitamins,¹² neurotransmitters,⁹ and multiple other compounds with as yet unknown targets; metabolize bile salts¹³; react to or modify specific drugs; and eliminate exogenous toxins¹⁴ (Fig. 1). The relevance of these microbial activities to health probably varies across the human population. Given the diverse functional repertoire of the gut microbiota, it is not surprising that they are the focus of research into a broad range of chronic diseases, including cancer and diseases with inflammatory, metabolic, cardiovascular, autoimmune, neurologic, and psychiatric components.

GUT MICROBIOTA ACROSS THE AGES

The in utero environment has, until relatively recently, been considered sterile. However, DNA-based microbiota studies have detected bacterial species in the placentas of healthy mothers,¹⁵ in amniotic fluid of preterm infants,¹⁶ and in meconium.¹⁷ At parturition, the mode of delivery influences postnatal microbial exposure.^{18,19} A study

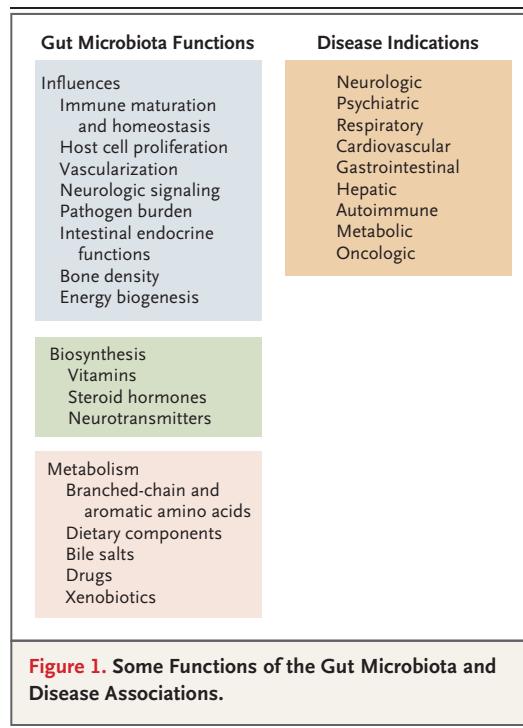
of fecal samples (collected 4 days, 4 months, and 12 months after birth) from Swedish infant-mother dyads showed that the gut microbiota of vaginally delivered neonates is taxonomically similar to the maternal gut and vaginal microbiota,¹⁹ though strain-level analyses are required to confirm the exact source of neonatal gut microbial diversity. This study also showed that the composition of the gut microbiota in infants changes to resemble adult microbiota in association with the cessation of breast-feeding (not the introduction of solid food).¹⁹ During the first postnatal years, bacterial diversity and functional capacity expand,¹² an observation that is consistent with improved cysteine metabolism and augmented fermentation pathways (encoded by lactic acid bacteria acetolactate decarboxylase [EC4.1.1.5] and 6-phosphogluconate dehydrogenase [EC1.1.1.44]), as well as more efficient bacterial foraging of intestinal mucosal mucins¹² (a capacity that confers colonization advantages²⁰).

The rapid rate of expansion in bacterial diversity that is observed in infancy slows in early childhood (between 1 and 5 years of age) (Fig. 2),²¹ and gut microbial diversity remains lower in children than in adults.²¹ In childhood, the composition of gut microbiota becomes more stable, with multiple members of Bacteroidetes, including those with butyrate-producing capacity, establishing a presence.²¹ By preadolescence (7 to 12 years of age), although the number of bacterial taxa and functional genes present in the gut microbiome is similar to that in adulthood,²² the age-differentiated microbial communities are taxonomically and functionally distinct. In preadolescents, as compared with adults, the gut microbiota are enriched in anaerovorax, bifidobacterium, faecalibacterium, and Lachnospiraceae and for pathways involved in vitamin B₁₂ and folate biosynthesis²²; folate biosynthesis is also characteristically increased in babies as compared with adults.^{12,19} Healthy adult gut microbiota are dominated by Bacteroidetes and Firmicutes but also include smaller proportions of Actinobacteria, Proteobacteria, and Verrucomicrobia,²³ as well as methanogenic archaea (primarily *Methanobrevibacter smithii*), Eucarya (predominantly yeasts), and multiple phages.²⁴ At the bacterial phyla level, the gut microbiota in adults, as compared with those in infants, are stable, but the specific microbial species and subspecies (strains) and their proportions vary enormously from one person to another.¹²

In fact, the microbial collection in each person is unique. Despite this taxonomic inter-individual variation, the functional capacity of the adult gut microbiota is relatively consistent across healthy persons,^{25,26} with pathways involved in metabolism,¹² fermentation, methanogenesis,¹² oxidative phosphorylation, and lipopolysaccharide biosynthesis.²² In the elderly, the gut microbiota become compositionally unstable and less diverse, events that are associated with coexisting conditions and age-related declines in immunocompetence²⁷ (Fig. 2).

INFLUENCES ON THE GUT MICROBIOTA

Endogenous and exogenous factors influence the gut microbiota,^{28,29} including mode of delivery of a neonate,¹⁹ host genetic features,³⁰ host immune response,³¹ diet³² (including dietary supplements, breast-feeding, and formula-feeding), xenobiotics (including antibiotics) and other drugs,^{10,33} infections,³⁴ diurnal rhythm,³⁵ and environmental microbial exposures,³⁶ several of which are established risk factors for childhood diseases such as obesity³⁷ and allergy.³⁸ The relative influence of these factors on the composition and function of the human gut microbiota, as well as the



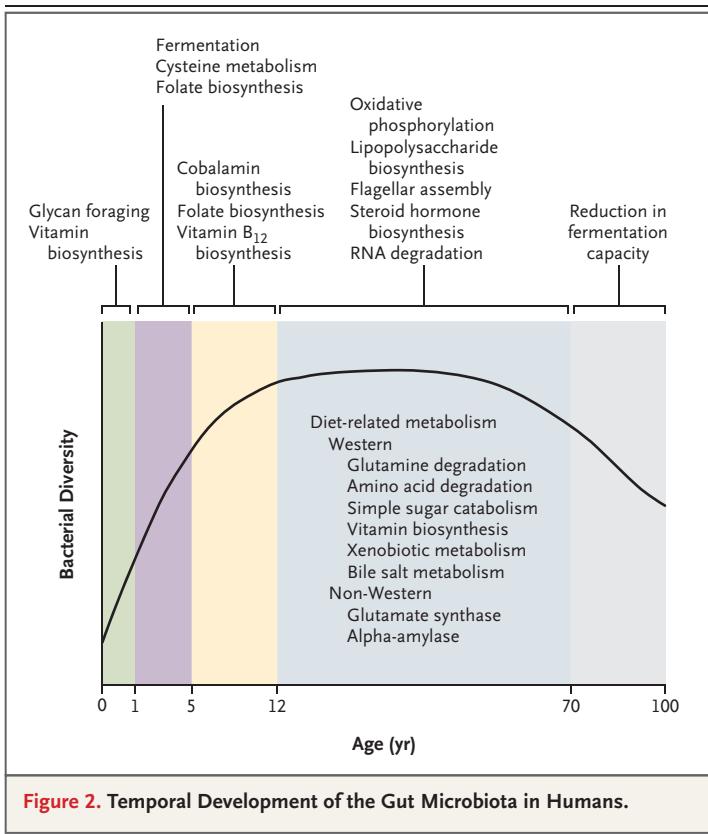


Figure 2. Temporal Development of the Gut Microbiota in Humans.

persistence of these effects, varies substantially. Sex, age, diet, exposure to antimicrobial agents, and stool consistency have been shown to exert large effects on the gut microbiota.^{12,28,29,33} The host genome has been shown to be associated with the heritability of specific bacterial families such as Christensenellaceae, which forms a co-occurrence network with other heritable bacteria and methanogenic archaea, and is associated with leanness and healthy metabolism.^{30,39} Disease-associated single-nucleotide polymorphisms of the human genome have been associated with the enrichment of specific bacterial taxa in the gut microbiota of persons with inflammatory bowel disease.⁴⁰ However, specific nongenetic factors, including the use of antimicrobial and immunosuppressant drugs and the site of intestinal biopsy sample collection, have had larger effects on the composition of the gut microbiota, indicating the need to control for such variables.⁴⁰

IMMUNITY

Studies of mice rendered deficient for specific genes have shown that sensing of microbes by

regulatory T (Treg) cells promotes mucosal tolerance and prevents overgrowth of segmented filamentous bacteria by triggering intestinal development and synthesis of Treg cells and secretion of antimicrobial IgA.³¹ Recently, three compositionally, functionally, and metabolically distinct gut microbiota states were described in babies who were approximately 1 month of age; one of these conferred a significantly higher relative risk of allergy in 2-year-old children and of asthma in 4-year-old children. In ex vivo assays, the associated products of the high-risk microbiota state induced an increase in CD4⁺ cells that produce interleukin-4, increased interleukin-4 production, and reduced the number of CD4⁺CD25⁺FOXP3⁺ cells, indicating that perturbation of early-life gut microbiota may contribute to subclinical inflammation that precedes childhood disease development.⁴¹

DIET AND OTHER ENVIRONMENTAL INFLUENCES

Dietary habits strongly influence the selection of gut microbiota.¹² Short-term intervention studies involving healthy adults exposed to diets restricted to meat or vegetable intake have shown rapid and reproducible gut microbiota responses, with meat consumption selectively enriching for bile-metabolizing microbiota, the expansion of which is associated with inflammatory bowel disease, and vegetable consumption increasing plant polysaccharide-fermenting organisms.³² It has also been reported that persons have very different metabolic responses to identical meals. The results of a machine-learning approach applied to the integration of blood glucose levels, dietary habits, and gut microbiome data, among other factors, predicted personalized postprandial glycemic responses to real-life meals, indicating that personalized diets may be used to successfully modify blood glucose levels.⁴² Emerging data also indicate that the microbiota is distinct in house dust from residences associated with protection against, or development of childhood allergic disease.⁴³⁻⁴⁵ Moreover, either oral supplementation or nasal exposure of mice to protective house dust prevents airway sensitization,^{36,45,46} indicating that exposure to environmental microbes modulates mucosal immunity. Other influences on the gut microbiota include pathogenic infection. For example, *Vibrio cholerae* initially dominates fecal bacterial communities during a cholera infection,³⁴ and clinical recovery is associ-

ated with a restoration of the preinfection composition of the gut microbiota resembling that observed in infancy. In contrast, even if drug-induced viral suppression of human immunodeficiency virus (HIV) replication is successful, the gut microbiota of patients with HIV infection frequently remain perturbed,^{47,48} a feature related to the degree of peripheral immune activation.⁴⁷

DYSBIOSIS OF GUT MICROBIOTA

Association studies in humans and rodents⁴⁹⁻⁵³ have shown disease-related dysbioses across a wide spectrum of common chronic disorders, including atherosclerosis,⁵⁴⁻⁵⁶ metabolic disorders,⁵⁷⁻⁶⁰ asthma,^{41,61} and autism spectrum disorder.⁶² Some of these observations have been combined with experimental studies, prospective studies, or both to identify putative microbiota-derived molecular mediators of pathogenic mechanisms. Many clinical studies have used targeted sequencing of 16S ribosomal RNA (rRNA), which although economical, is limited to assessment of bacterial taxonomic composition. However, PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States),⁶³ an algorithm that uses 16S rRNA sequence data to predict conserved bacterial functional capacity, permits *in silico* bacterial metagenomic analyses. Studies have applied high-throughput methods of untargeted DNA sequencing in conjunction with the newly expanded human microbial gene catalogues,^{3,25} draft genomes,⁶⁴ and new genome assembly, permitting microbial species-level and strain-level resolution and detailed functional annotations of microbial communities.^{58-60,65-75} Such innovative approaches have facilitated the use of machine-learning algorithms to identify microbial gene- or taxon-based signatures as disease biomarkers.

Although many novel insights have been gained from these explorations, the study of the gut microbiome in human health and disease remains fraught with challenges. These include major intraindividual variability of the microbiome with changes in lifestyle, reproducibility issues, and statistically underpowered case-control studies, in addition to studies in which the cases and controls are phenotypically, etiologically, and microbiologically heterogeneous. These issues are compounded by a lack of stratification based on drug treatment, which potentially con-

found analytical outcomes,⁷² and a lack of statistically powered longitudinal and interventional studies involving study participants with well-defined diseases or preclinical at-risk conditions in order to explore causality. Despite evidence linking dysbiosis of the gut microbiome with disease manifestations at sites distant from the gut, most studies have not explored mechanisms outside the affected site, nor have they considered the effect of the microbiome and its varied products on the multitude of molecular pathways potentially involved. Stool samples are often used as proxies for the microbial content of the entire gastrointestinal tract, which covers more than 30 luminal intestinal square meters and contains distinct macroecosystems and microecosystems. Moreover, since bacterial genome databases are incomplete, the majority of genes in human gut microbiomes cannot be functionally assigned, a problem that is exacerbated by our lack of knowledge of both the dynamic transcriptional and translational activities of the gut microbiome and the biologic effect of the enormous numbers of polymorphisms and other structural variations of the microbiome. Finally, most studies have focused primarily on bacterial species rather than on the functional interplay among bacteria, archaea, viruses, fungi, and eukaryotes throughout the human gastrointestinal tract.

There have been few demonstrations of causality for which human studies correlating gut microbial dysbiosis with distinct clinical states have been complemented by mechanistic studies. These studies have addressed human obesity,⁷⁶ kwashiorkor,⁷⁷ childhood asthma,⁴¹ massive weight loss after bariatric surgery,⁶⁵ and the insulin-resistant state of third-trimester pregnancy.⁷⁸ In addition, a study combining analyses of human host insulin sensitivity, fasting serum metabolome, and the gut microbiome with findings from experiments in mice suggests that specific bacteria may cause insulin resistance.⁷⁹ Also, transplantation of fecal microbiota from healthy lean human donors to obese patients with insulin resistance is associated with improvement in whole-body insulin sensitivity in the recipients,⁸⁰ further supporting the notion that microbiota-associated phenotypes may be transferred and reproduced, at least to some extent, in a genetically susceptible recipient.

A "common ground" hypothesis (Fig. 3), which

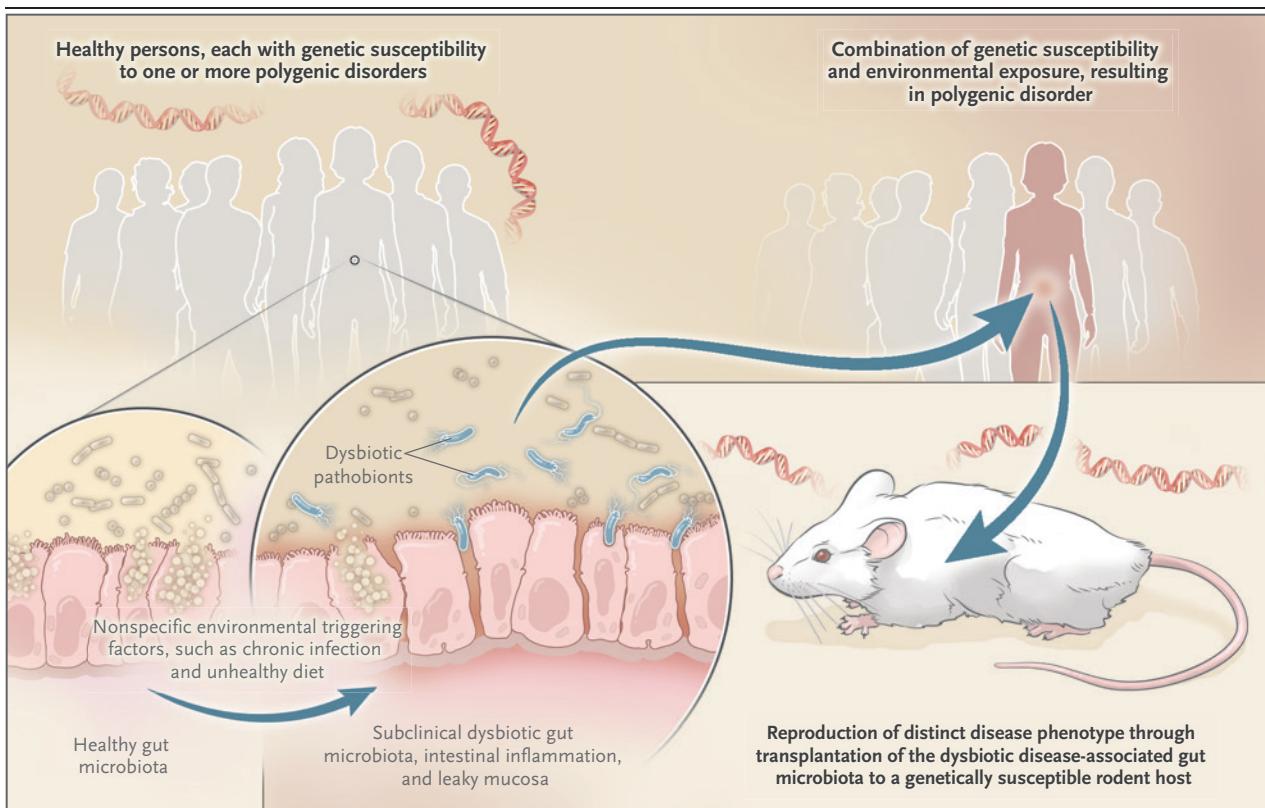


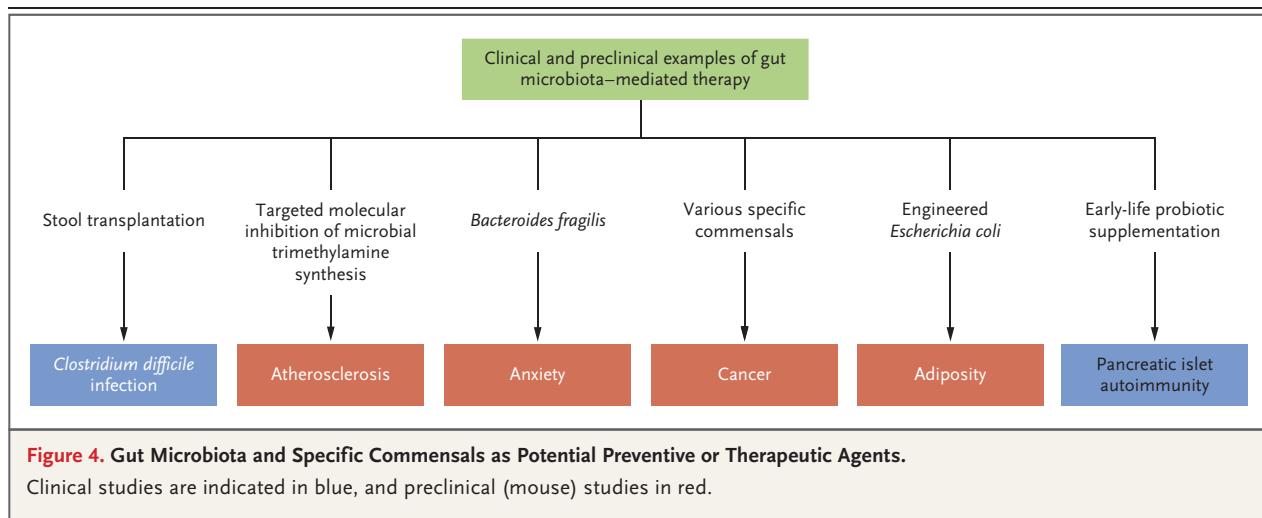
Figure 3. “Common Ground” Hypothesis of Pathogenesis Caused by Dysbiotic Gut Microbiota.

has yet to be rigorously examined, has been proposed⁸¹ to explore the question of whether imbalances of gut microbial communities are a consequence or a cause of chronic polygenic diseases. This hypothesis posits, first, that various endogenous or exogenous factors, or combinations of such factors, trigger an increase in gut permeability (“leaky mucosa”) or mucosal inflammation either directly or through selective pressure on the gut microbiota; second, that in persons who are genetically susceptible to one or more chronic disorders, the subclinical intestinal abnormalities favor the expansion of opportunistic microbes and the transition to pathobionts; third, that microbial gene products from the dysbiotic pathobiont gut communities promote local or systemic morphologic and functional changes that are pathogenic; and finally, that once disease-associated gut microbiota have been expressed in a genetically susceptible person, they can be transferred from that person to a genetically sensitive recipient, acting as a continual and contributing pathogenic mechanism.

THERAPEUTIC AND PREVENTIVE OPPORTUNITIES

INFECTION WITH *CLOSTRIDIUM DIFFICILE*

Fecal microbial transplantation for severe cases of recurrent diarrhea caused by antibiotic-resistant *C. difficile* infection is efficacious in approximately 90% of affected patients. This finding remains the prime proof of principle that healthy gut microbiota can reproducibly correct a severe and specific microbial dysbiosis and that transplantation of healthy microbiota is therefore medically actionable.⁸² For chronic inflammatory bowel diseases, clinical remission is less predictable, and success rates are more modest.⁸³ Because many persons dislike aspects of fecal microbial transplantation and, more important, because transplantation carries the potential risk of transferring to recipients infections and other phenotypes that are clinically silent in donors, several preclinical and clinical initiatives^{84,85} are under way. These investigations test and develop single commensals, mixtures of defined species or



strains, or cocktails of microbiota-derived molecules targeting specific microbial species or pathways that are enriched in the disease state, in an effort to treat or prevent various common disorders (Fig. 4). The outcomes of selected preclinical studies are discussed below. The findings suggest that microbial-based therapeutics or preventives may have an advantage over interventions with synthetic drugs. They may be less likely to have severe side effects, given the coevolution of human-derived microbial strains and humans.

ATHEROSCLEROSIS AND PRODUCTS OF THE MICROBIOTA

Studies have shown that gut microbiota metabolism of dietary phosphatidylcholine and L-carnitine produces trimethylamine, which subsequently undergoes flavin monooxygenase 3-dependent oxidation to trimethylamine-N-oxide (TMAO); elevated circulating levels of TMAO appear to be a strong risk factor for atherosclerosis in humans and animals.^{55,56} A study of a mouse model showed how oral application of a structural analogue of choline, 3,3-dimethyl-1-butanol, inhibited commensal microbial trimethylamine production, lowered plasma TMAO levels, and prevented atherosclerosis without apparent side effects, despite a pro-atherosclerosis diet.⁸⁶

Bacteriocins represent another class of products of the mammalian gut microbiota. These high-potency peptide toxins may offer leads for the development of species-specific or strain-specific alternatives to current antibiotics.⁸⁷ For example, screening in human stool has identified 13 bacteriocin-producing bacterial strains.⁸⁸

Identifying target microbial species that exclude pathogens is equally important. With the use of mathematical modeling of gut microbiota, *C. scindens*, a secondary bile acid-producing bacterium, was identified as promoting resistance against *C. difficile* colonization.⁸⁹ Given the interactive nature of microbiomes, therapies targeting a network of interacting organisms that provide protection against or precipitate disease are likely to be more efficacious than therapies targeting a single species.

BEHAVIOR

Exploration of the therapeutic potential of microbial species at the preclinical level has been undertaken in several mouse models, including the maternal immune activation (MIA) model. The offspring of MIA mice exhibit autistic-like behavior, gut microbiota dysbiosis, increased gut mucosa permeability, and an altered serum metabolome, with an increase in 4-ethylphenylsulfate (4EPS) by a factor of 46.⁶² Injection of this neurotoxin into the blood of healthy mice resulted in an anxiety phenotype. Feeding MIA mice a strain of *Bacteroides fragilis* ameliorated the intestinal dysbiosis, restored the integrity of the mucosal barrier, and diminished behavioral abnormalities in conjunction with significant decreases in circulating 4EPS levels.⁶² Similar studies have been performed in mouse models of allergic airway disease in which oral supplementation with *Lactobacillus johnsonii*, a human vaginal commensal species, provides airway protection against both allergen challenge and respiratory viral infection.³⁶

CANCER

Gut microbial species are being explored in the field of oncology. Of specific interest is the capacity of some commensal bacteria to modulate the tumor microenvironment and anticancer therapies.^{90,91} It is well known that T-cell infiltration of solid tumors is associated with a positive therapeutic response. A recent study comparing melanoma growth in mice with distinct gut commensals support the hypothesis that certain microbes enhance the efficacy of cancer immunotherapy.⁹² Oral administration of a mixture of bifidobacterium species modulates the activation of dendritic cells, which in turn helps improve the effector function of tumor-specific CD8+ T cells. Bifidobacterium supplementation improved tumor control to the same degree as anti-PD-L1 (programmed cell death ligand 1) therapy (checkpoint blockade) in an animal model, and combination treatment (bifidobacterium supplementation and anti-PD-L1 therapy) almost completely eliminated tumor expansion.⁹² Similarly, studies in both humans and mice have shown that the antitumor effect of treatment with antibodies against cytotoxic T-lymphocyte-associated antigen 4 (CTLA-4) is potentiated by specific members of the gut microbiota. T-cell responses specific for *B. thetaio-taomicron* or *B. fragilis* were associated with the efficacy of CTLA-4 blockade, and the introduction of *B. fragilis* to tumorigenic, germ-free mice, which do not have a response to CTLA-4 treatment, brought about a response.⁹³ The discovery of a tumor-inhibiting molecule produced by a probiotic strain was recently made. *L. casei* strain ATCC 334 produces ferrichrome, which has been shown to inhibit progression of colon cancer by means of apoptosis mediated through the c-Jun N-terminal kinase pathway.⁹⁴

INFLAMMATORY AND METABOLIC DISEASES

Given the tight interplay between gut microbes and host immunity,^{95,96} efforts have focused on the isolation of human gut microbial species with therapeutic potential in inflammatory disorders. A mixture of 17 human clostridium strains has been shown to diminish the severity of experimentally induced allergic colitis in rodents through mechanisms that promote the expansion and activity of Treg cells, although it remains to be determined which bacterial molecules mediate these effects.⁹⁷ More recently, a substantially broader range of human gut bacterial strains were shown

to promote the expansion of Treg cells.⁹⁸ In addition, *Lactococcus lactis* expressing interleukin-10, an antiinflammatory cytokine, has been shown to be safe in a phase 1 clinical trial⁹⁹ and was effective in reducing inflammation in mouse models of colitis¹⁰⁰ and allergic airway inflammation.¹⁰¹

Within the area of metabolism, studies suggest that proteins secreted by *Escherichia coli*, including ClpB, a chaperone protein and a mimic of alpha-melanocyte-stimulating hormone, affect food intake and meal patterns in rodents, with the magnitude of the effect depending on the bacterial growth phase. *E. coli* proteins stimulated intestinal hormones, glucagon-like peptide 1 (a potent antihyperglycemic hormone), and peptide YY (produced in the ileum in response to feeding) and activated anorexigenic pathways in the brain, inducing those that mediate satiety.¹⁰² Bioengineered commensals may also have a role in future microbiota-mediated therapy.^{99,103} In a preclinical setting, an *E. coli* strain was genetically manipulated to biosynthesize precursors of the anorexigenic *N*-acylethanolamides, which are produced in the ileum in response to feeding and serve to reduce food intake and, thus, obesity. Introduction of this engineered strain in obese mice fed a high-fat diet resulted in lower food intake, an increased basal metabolic rate, and a pronounced loss of adiposity, which endured for 4 weeks after cessation of bacterial supplementation.¹⁰⁴ Similarly, in studies of rats with diabetes, commensals engineered to synthesize and release glucagon-like peptide 1 have been shown to stimulate epithelial secretion of insulin, thereby improving carbohydrate metabolism.^{105,106}

CAUTION IN EXTRAPOLATING BASIC FINDINGS

The examples discussed above involve introduction of human commensals or their products in isogenic rodents under highly controlled conditions during defined stages of pathogenesis. Predictions of similar effects in humans with preclinical or overt disease should be viewed with caution. Controlled clinical trials have shown relatively modest therapeutic effects of traditional probiotics in adults with various established disorders.¹⁰⁷ In contrast to these findings in adults, a recent prospective study showed the effect of probiotics on predisease autoimmune signatures in newborns in a large birth cohort that was followed to the start of school age.¹⁰⁸ In this study, neonatal probiotic supple-

mentation (administered between 0 and 27 days after birth) was associated with a 60% reduction in the risk of pancreatic islet autoimmunity before school age, as compared with either no supplementation or intervention after 27 days, with the association accounted for by high-risk children with the HLA-DR3/4 genotype. This finding raises the question of whether the introduction of more targeted formulations in neonates who are at increased risk for autoimmunity would prevent the subsequent development of autoimmune disorders.

DIETARY INTERVENTIONS TARGETING GUT MICROBIOTA

On the basis of studies in both animals and humans, dietary intake appears to be a major short-term and long-term regulator of the struc-

ture and function of gut microbiota.^{32,42,109} Still, only a relatively small number of randomized, clinically controlled dietary interventions targeting the gut microbiota have been reported in humans, and these show that energy restriction and diets rich in fiber and vegetables are associated with gut microbial changes that, in turn, are associated with a health benefit.^{70,110-112} Although investigation of the relevance of the gut microbiome to health and disease is in an early phase, the findings, in aggregate, support the view that specific dietary regimens, used alone or combined with the administration of mixtures of microbial species that have been validated and approved by regulatory authorities (next-generation synbiotics),¹¹¹ may hold potential for enhancing public health.

Disclosure forms provided by the authors are available with the full text of this article at NEJM.org.

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