Gut microbiota: a potential new territory for drug targeting

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Abstract | The significant involvement of the gut microbiota in human health and disease suggests that manipulation of commensal microbial composition through combinations of antibiotics, probiotics and prebiotics could be a novel therapeutic approach. A systems perspective is needed to help understand the complex host–bacteria interactions and their association with pathophysiological phenotypes so that alterations in the composition of the gut microbiota in disease states can be reversed. In this article, we describe the therapeutic rationale and potential for targeting the gut microbiota, and discuss strategies and systems-oriented technologies for achieving this goal.

Most current searches for new drugs are focused on identifying a pharmacologically effective agent that specifically interacts with one molecular target in the eukaryotic host cell to regulate biochemical alterations in a diseased state and reestablish healthy-state biochemistry. During the past 30 years, such an approach has generated highly successful medicines. However, it does not completely exploit the complex regulatory network that has been engineered through evolutionary processes in humans, who could be viewed as ‘superorganisms’ with an indispensable internal ecosystem: the gut microbiota.

The human gastrointestinal (GI) tract is home to a complex consortia of trillions (approximately $1 \times 10^{13}$ to $1 \times 10^{14}$) of microbes, thousands of bacterial phylotypes, as well as hydrogen-consuming methanogenic archaea, colonizing the entire length of the gut with a collective genome (also termed as microbiome) that contains at least 100-times as many genes as our own genome. Although largely unexplored and under-appreciated, our gut microbiota plays an intricate and sometimes pivotal role for our health and well-being. Emerging ‘omics’ technologies, such as metagenomics and metabonomics, are now being applied to the study of the gut microbial ecology at the molecular level, generating new insights and opportunities to reveal the medical functions of the gut microbiota to human health.

Accumulating evidence indicates that the gut microbiota is instrumental in energy metabolism and immune function of the host, and has a crucial role in the development of numerous conditions including obesity, diabetes, non-alcoholic fatty liver disease, inflammatory bowel diseases, and even cancers. Unlike the human genome, which is intact and rarely manipulated by xenobiotic intervention, the composition of commensal gut microbiota is readily changeable. The plasticity of the microbiome may allow a specific or systematic manipulation of certain gut microbiota associated with host diseases. Therefore, the exploration of the gut microbiota might not only revolutionize therapeutic strategies for many diseases, but also improve the productivity of the pharmaceutical industry, which has recently made huge investments in the discovery of novel targets and drug candidates with limited success so far. With this in mind, this article provides perspectives for the therapeutic and prophylactic management of diseases and disorders that involve the gut microbiota, and suggests strategies for gut microbiota-oriented drug discovery.

A microbial organ

The human intestine is more densely populated with microorganisms than any other organ, and is a site where they exert strong influences on human biology. With this in mind, the entire system of the human gut microbiota can be pictured as a ‘microbial organ’ within the intestine, which contributes to diverse mammalian processes including protective functions against pathogens and immune-system modulation, the metabolic function of fermenting non-digestible dietary fibre, and the anaerobic metabolism of peptides and proteins that results in the recovery of metabolic energy for the host.

The intestinal mucosa is the main interface between the immune system and the external environment and therefore has an important role in the host–flora interaction. The commensal microbiota profoundly influences the development of humoral components of the gut mucosal immune system, acting as a crucial factor in the prevention of exogenous pathogen intrusion. Metabolites, including digested dietary nutrients, are absorbed by the gut, and together with various non-nutrient compounds produced by the microbiota, are co-metabolized by host enzymes such as the cytochrome P450 and conjugating enzymes in the liver. The resulting metabolites that are derived from both host and microbial processes are then returned to the gut by the bile and possibly other excretory routes for further metabolism and/or excretion. On one hand, the daily metabolism of food involving the different types of metabolic substrates and the secretion of peptic acid, bile and pancreatic fluids regulates the composition of the intestinal mucosa by hindering the colonization of the stomach and proximal small intestine by most bacteria, and changing the composition of enteric bacteria in the distal small intestine and the large intestine. On the other hand, commensal-derived metabolites and the composition of bacterial surface structures can have various effects on the host immune system. Meanwhile, commensal bacteria can modulate gene expression in the host to create a suitable environment for themselves and prevent the growth of other competitive bacteria within the ecosystem.
Being such a microbial organ, our gut flora not only plays a significant role in disease onset and progression, but also influences drug bioavailability and toxicological incidence via microbial-dependent drug metabolism. For example, the metabolism of ginsenosides, the principal bioactive components in Radix Ginseng. Ginsenoside Rb1, a saponin of protopanaxadiol, is metabolized by β-D-glucosidases in the gut microbiota into 20-O-β-D-glucopyranosyl-20(S)-protopanaxadiol, which exhibits significant antitumour and anti-allergic activities14. A toxicological research programme, the Consortium on Metabonomic Toxicology, has confirmed that the unusual metabolic profiles observed in a small proportion of the experimental rats treated with model toxic compounds are attributed to different gut microbiome contributions15, suggesting that variations in drug metabolism under identical treatment are in direct association with the inter-subject diversity of the gut microbiota.

A dynamic Pachinko model of metabolism, postulated by Nicholson and Wilson, suggests that the outcome of drug metabolism in mammalian transformation systems is not pre-arranged or determined absolutely, but is probabilistic and conditional on the sequence and sites of the previous metabolic events, and strongly influenced by the distribution of key metabolizing enzymes and transporter molecules16. It is therefore reasonable for an idiosyncratic toxicity to arise in selected individuals owing to unusual metabolic fates or interactions of drugs that are due to rare, but toxic, metabolic outcomes that become favoured by unusual combinations of genetic and environmental factors. With the same perspective, disease onset at a specific time point and with a unique phenotype among individuals can be considered a result of complex and probabilistic metabolic co-regulation by the host genome and the intrinsic microbiome in response to different dietary and environmental stress factors.

The gut microbiota and diseases

Recent publications have shown that the gut microbiota has a profound influence on the onset and progression of important human diseases that are currently lacking therapeutic solutions17. For example, differences in caloric extraction efficiency from food may be determined by the composition of the microbiota, which, in turn, may contribute to differential body weights18. Gut microbial species break down non-digestible polysaccharides and promote absorption of the resulting monosaccharides from the gut lumen, facilitating the induction of de novo hepatic lipogenesis. Additionally, fasting-induced adipocyte factor (FIAF; also known as ANGPTL4), a member of the angiopoietin-like family of proteins, is selectively suppressed in the intestinal epithelium in the presence of enteric bacteria, leading to a microbiota-induced deposition of triglycerides in adipocytes19 (FIG. 1). When mice are exposed to a high-fat diet, the gut microbiota metabolism affects the conversion of choline into methyamines, reducing the bioavailability of choline to mimic the effect of a choline-deficient diet, and causing non-alcoholic fatty liver disease20. These findings raise the possibility of manipulating the microbiotic environment to treat or prevent obesity and associated diseases.

Certain environmental toxins such as dimethylnitrosamine can be metabolized by specific strains of the gut resident Escherichia coli to produce potentially toxic micrometabolites, underlying the carcinogenicity of this type of compound in the gut21. Production of toxins, particularly neurotoxins or toxic metabolic products, by such microorganisms might also mediate neurological disruptions. We anticipate that a number of neurological disorders, such as attention-deficit/hyperactivity disorder (ADHD) and Tourette syndrome, which may be associated with this type of pathogenesis22,23, will eventually find treatment solutions in the gut microbiota.

It is widely speculated, although controversial, that perturbations in the GI microbiota composition as a result of the wide use of antibiotics in modernized countries may be linked to several conditions including obesity, insulin resistance, diabetes, irritable bowel syndrome and diarrhoea24-26. The mechanism behind this speculation is that in normal conditions, the stability of the microbial structure is maintained by the equilibrium of resident bacteria. However, this may be readily disrupted by antibiotics, leading to the overgrowth of antibiotic-resistant pathogens that are associated with numerous complex disorders, such as toxigenic Clostridium difficile-associated pseudomembranous colitis27. Additionally, antibiotics can have a long-term impact on the microbial ecology in our gut; a recent study shows that a short-term antibiotic exposure can have persistent consequences for individuals for up to 2 years post-treatment28.

Taken together, it is apparent that changes in the Western lifestyle, together with the abuse of antibiotics in our body and our food chain, induce changes in the gut microbial ecology. Such changes are likely to affect the genomic and metabolic predisposition of the host towards different energy storage...
capabilities, metabolic and immune regulatory networks, and pathologies. The gut microbiota could therefore be a previously under-appreciated source of drug targets for the treatment of metabolic disorders, various conditions in the GI tract and also neurological disorders.

The gut microbiota as drug targets
The knowledge and experience obtained from the management of chronic peptic ulcers induced by *Helicobacter pylori* suggests that certain chronic diseases are derived from the growth of particular microorganisms that are not inhibited by conventional biochemical modifications in eukaryotic host cells. Such microorganisms can be causative agents of disease and are therefore therapeutic targets, which necessitate modification with antibiotics and/or nutritional intervention as a realistic means for disease management.

As we only possess limited knowledge of our gut microbiota and lack most of the molecular details of host–flora interactions, it may be too early to propose a clear microbiota-based drug discovery strategy or therapeutic modality. However, initial considerations of target candidates are expected to centre on those indigenous bacterial species with known genome sequences and biochemical functions. For example, *Bacteroides thetaiotaomicron* is a Gram-negative anaerobe and a dominant member of the normal distal intestinal microbiota, which devotes a large proportion of its genome to metabolic processes that benefit the host and other communal species. It has an elaborate apparatus for acquiring and hydrolysing otherwise indigestible dietary polysaccharides and influences the transport and regulation of mammalian peroxisome proliferator-activated receptor-γ (PPARγ), an intranuclear receptor that is highly expressed in host adipose tissue and involved in the mechanism of human insulin resistance. Certain pathogenic microbial species, which differ distinctly from healthy populations as a result of xenobiotic intervention and pathological development, could be identified as targets of interest for relevant treatment strategies.

Compositional structures or patterns of the gut microbiota that are associated with certain diseases constitute a new type of drug target. Such a concept evolves from recent work comparing the distal gut microbiota of genetically obese mice and their lean littermates, as well as those of obese and lean human volunteers, in which obesity was found to be associated with changes in the relative abundance of the two dominant bacterial divisions, the *Bacteroidetes* and the *Firmicutes*, and a dominant archaeon, *Methanobrevibacter smithii*. Recent comparative genomic profiling analysis has revealed a wide distribution of the type III secretion system in commensal bacteria and pathogens, which is not only a specific outcome of host cell infection, but also an indication of interactive communication between commensal bacteria and the host. Therefore, we speculate that different compositional structures of the gut microbiota in association with certain diseases may use different secretion patterns or modes to communicate with host cells and participate in the host metabolic network. These different secretion patterns may produce a characteristic secretome or small-molecule metabolome that could be measured by biochemical analysis of urinary and faecal samples. Further studies are expected to determine whether commensal bacteria with certain compositional structures will mediate the host immune surveillance in the gut by means of specific secretion patterns. Moreover, the ‘omics’ sciences such as metagenomics and proteomics can be utilized to monitor the subtle variation resulting from different compositional structures of commensal bacteria under certain pathological conditions.

Gut microbiota-targeted therapies
We envisage that two strategies may be taken for the development of future gut microbiota-targeted therapies. The first is the direct elimination or modification of a well-defined, specific gut microorganism, or certain species of bacteria, as disease target(s), in a similar way to the treatment of chronic peptic ulcer induced by *H. pylori* using antibiotics. An alternative method for such a strategy is vaccination using an antigenic epitope of a bacterium or toxin of interest to elicit an immune response capable of interacting with the gut flora upon microbe proliferation in the gut. However, limitations of these methods may include the lack of specificity of the broad-spectrum antibiotics and the vaccination systems available, which will result in unexpected destruction of the beneficial microbial community and a long-term disturbance of gut ecology. Additionally, the frequent exposure of the gut microbiota to antibiotics or vaccines
may induce rapid genetic modification of the gut microbiota, which would accelerate the development of resistance to such therapeutic means. A thorough molecular understanding of host–flora interactions and pathologies is a prerequisite for these therapeutic approaches to be effectively conducted with minimal long-term adverse consequences.

The second strategy is to take a holistic approach, similar to that practiced in traditional Chinese medicine, in which various diseases and conditions are categorized into different syndromes based on a patient’s clinical manifestations such as pulse, tongue images and information of urine and excrements, before a treatment is applied. In this strategy, different structural patterns of the gut microbiota that are associated with different clinical manifestations are identified and categorized using profiling methods such as metabonomics and metagenomics. The metabolomic or genomic profiling of the gut microbiota from plasma, urinary or faecal samples could allow a stratification of certain gut microbiota structures in association with disease phenotypes. Combinations of antibiotics, probiotics, prebiotics and perhaps laxatives could be used to manipulate the gut microbiota to achieve a therapeutically effective regimen and, eventually, restore the homeostasis of gut ecology in the host (Fig. 2).

Probiotics are live microorganisms that are traditionally believed to be *Bifidobacterium* spp. and *Lactobacillus* spp., prebiotic ingredients may work through the selective stimulation of various indigenous beneficial strains to exert antimicrobial effects, or to modulate immune responses of the host and compete with pathogens for receptors.

### Table 1: Examples of gut microbiota-related diseases and therapeutic strategies

<table>
<thead>
<tr>
<th>Disease or disorder</th>
<th>Association of gut microbiota with disease</th>
<th>Evidence of gut microbiota-targeted therapy</th>
<th>Refs</th>
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<tbody>
<tr>
<td>Chronic peptic ulcer</td>
<td><em>Helicobacter pylori</em> infection is the pathogenic key to the development of most chronic peptic ulcers</td>
<td>Regimen of <em>H. pylori</em> eradication with antibiotics and proton-pump inhibitory agents</td>
<td>26,57</td>
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<td>Antibiotic-associated diarrhoea</td>
<td>The suppression of antibiotic-sensitive bacteria and overgrowth of antibiotic-resistant species lead to intestinal dysfunction</td>
<td>Treatment with probiotics, such as the yeast <em>Saccharomyces boulardii</em>, together with antibiotics is effective in the prevention of antibiotic-associated diarrhoea</td>
<td>58,59</td>
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<td>Ulcerative colitis</td>
<td>Abnormal immune response to commensal bacteria, and increased numbers of intestinal microorganisms, but reduced numbers of protective bacteria such as <em>Lactobacilli</em> and <em>Bifidobacteria</em></td>
<td>Short-term benefits were observed with antibiotic or probiotic/synbiotic therapy</td>
<td>42,60</td>
</tr>
<tr>
<td>Crohn’s disease</td>
<td>Inadequate clearance of ingested microorganisms by dysfunctional intestinal macrophages (hypothesized mechanism)</td>
<td>Reinstating the balance of intestinal microflora with probiotics, prebiotics and/or antibiotics, such as the non- absorbable antibiotic rifaximin</td>
<td>61,62</td>
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<td>Obesity</td>
<td>The relative abundance of the two predominant bacterial divisions, the <em>Bacteroidetes</em> and the <em>Firmicutes</em>, affect the efficiency of energy harvest from diet</td>
<td>It is suggested that manipulation of the commensal microbial composition could be a novel therapeutic approach for obesity</td>
<td>5,6</td>
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<tr>
<td>Diabetes</td>
<td>No gut microbiota-related mechanism is established, but it appears that diabetes is associated with the gut microbiota</td>
<td>Oral administration of probiotics shows a significant antidiabetic effect in diabetic models</td>
<td>34–38</td>
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<tr>
<td>Colorectal cancer</td>
<td>Conversion of dietary procarcinogens into DNA-damaging agents or generation of carcinogens by particular commensal bacteria are thought to be certain causes of colorectal cancer</td>
<td>Reduced prevalence of colon cancer was observed in interleukin 10 knockout mice by probiotic <em>Lactobacillus</em> administration, and strong antitumour activity was achieved by <em>Bifidobacterium longum</em> therapy in vivo</td>
<td>63,64</td>
</tr>
<tr>
<td>Idiopathic parkinsonism</td>
<td>Partial involvement of microorganisms such as <em>H. pylori</em> is thought to be important in the aetiology/pathogenesis of idiopathic parkinsonism and useful for disease categorization and subsequent treatment</td>
<td><em>H. pylori</em> is important in the aetiology/pathogenesis of idiopathic parkinsonism and useful for disease categorization and subsequent treatment</td>
<td>65–67</td>
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Probiotics are a group of non-digestible food ingredients including inulin, oligosaccharides, lactulose and resistant starch that are fermented by colonic commensal microbiota to potentially improve host health by selectively stimulating the growth of certain gut bacteria. Efficient probiotic strains have been found in different bacterial genera including *Bifidobacteria*, *Lactobacilli*, *Streptococci* and non-pathogenic *E. coli*, and even nematode parasites. Many probiotic effects, including resistance to infection, improvement of allergic diseases and anti-inflammatory properties, are achieved by modifying the host immune response. For example, the enhancement of phagocytic activity of peripheral blood leukocytes and natural killer cells, and the stimulation of both nonspecific secretory immunoglobulin A (IgA) and a specific antibody response.

Recent research in enteric bacteria indicates that the use of probiotics is rapidly advancing from the field of nutrition or dietary supplementation towards therapeutic applications for various conditions. Oral administration of *Lactobacillus casei* in diabetic KK-Ay mice has been shown to significantly decrease plasma glucose levels and inhibit the production of B-cell specific CD4+ T cells and cytokines — interferon-γ (IFNγ) and interleukin 2 (IL2) — which are leading factors involved in the induction of autoimmune diabetes. In addition, studies have found that *L. casei* could inhibit the alloxan-induced disappearance of pancreatic B cells in mice, which can also inhibit the autoimmune destruction of pancreatic B cells in non-obese diabetic mice. Similarly, *Lactobacillus* GG feeding delays the development of glucose intolerance and hyperglycaemia in streptozotocin-induced diabetic rats, and a significant anti-diabetic effect of a probiotic containing *Lactobacillus acidophilus* and *L. casei* has been observed in high-fructose fed rats. Additionally, some probiotics may also induce defensins in epithelial cells, which are natural antimicrobial peptides secreted in the intestine.

Prebiotics are a group of non-digestible food ingredients containing inulin, oligosaccharides, lactulose and resistant starch that are fermented by colonic commensal microbiota to potentially improve host health by selectively stimulating the growth of certain gut bacteria. Although their targets are traditionally believed to be *Bifidobacterium* spp. and *Lactobacillus* spp., prebiotic ingredients may work through the selective stimulation of various indigenous beneficial strains to exert antimicrobial effects, or to modulate immune responses of the host and compete with pathogens for receptors.
Both prebiotics and probiotics have been shown to decrease the incidence and severity of infantile diarrhoea, and prevent antibiotic-induced diarrhoea or food allergies\(^{41}\). Additionally, dietary intervention using a combination of probiotics and prebiotics, known as symbiotics, is a feasible treatment strategy and has proven to be efficacious in volunteer trials in patients with active ulcerative colitis\(^{42}\). Examples of gut microbiota-related diseases and therapeutic strategies are provided in Table 1.

The fact that a significant portion of bioactive metabolites produced in animals and medicinal plants are found to be synthesized or co-synthesized by their commensal microbiota suggests that the gut microbiota itself may be a largely untapped source of novel drugs or drug leads\(^{41}\). Several anticancer metabolites from marine sponges, including discodermolide, halichondrin B and bryostatin 1, have progressed to preclinical or clinical-trial phases, and are thought to be products derived from their microbiotic consortia\(^{42}\). Therefore, the commensal microbiota can potentially be engineered as a bioreactor using new cloning and biosynthetic expression strategies for the controlled secretion of biologically active molecules and vaccines. A new class of pharmaceutical compounds derived from the uncultured commensal microorganisms in appropriate in vitro or animal models may be produced to develop a long-term host immunotherapy for diseases such as inflammatory bowel disease. Currently, the application of culture-independent metagenomic technology sheds light on the opportunities of drug discovery from the gut microbiota. The integration of high-throughput DNA sequencing and bioinformatics tools enables the identification of genes encoding bioactive compounds from the commensal microbiota. The genes of interest, isolated directly from commensal bacteria or screened from a clone library using genome-sequence tags, could be cloned into optimal vectors and transformed into surrogate hosts to encode biosynthesis of novel therapeutic products.

**Platform technologies for the microbiota**

The development and utilization of appropriate technologies that allow comprehensive and robust analyses for various microorganisms, most of which are non-culturable, are crucial for understanding the impact of the gut microbiota on the host. The established metabolic profiling approach has a powerful capacity for detecting various metabolites originating from microorganisms that are commonly found in mammals. Several analytical techniques, including high resolution nuclear magnetic resonance (NMR) spectroscopy\(^{46} \) and various gas/liquid chromatography–mass spectrometry (GC–MS, LC–MS) techniques\(^{48,49}\) are currently used to generate spectral profiles from which information pertaining to pathophysiology can be extracted. For example, the aromatic region of a typical 1H NMR spectrum of urine provides a clear window for visualization of metabolic signature of microbial products, dietary metabolites or parasite-related metabolites\(^{46,47}\). On the basis of a metabolic profiling approach, the concept of pharmacometabonomics, proposed by Clayton et al.\(^{48}\) in 2006, highlights the application of such technology to personalized treatment, in which drug-induced responses in individuals can be predicted from a pre-dose metabolic signature. This concept was demonstrated in two classic rat models of dietary-induced obesity and streptozotocin-induced diabetes, in which only certain animals acquired obese or hyperglycaemic phenotypes\(^{48}\).

The different outcomes of streptozotocin or dietary intervention were closely associated with variations in pre-dose urinary metabolites that had been reported to originate from gut microbiota metabolism\(^{52}\), therefore linking the phenotypic variations to the different pre-dose compositional structures of the gut microbiota (Fig. 5).

Metagenomics, also known as community genomics, provide an insight into the genetic potential of complex microbial communities, including uncultured species, using culture-independent approaches\(^{53}\). It has been used in digestive ecosystems to discover novel hydrolase genes in uncultured rumen bacteria and β-glucanase genes affiliated with uncultured microbiota that colonized the large bowel of mice. Currently, screening approaches for intestinal metagenomic
libraries have not been fully established. With the progress in molecular technologies, the most comprehensive 16S ribosomal DNA (rDNA) sequence-based metagenomic approach has been successfully applied in the analysis of the distal gut and faecal microbiota. This analysis revealed significant differences in community membership between healthy adults5–7, which may contribute to variations in physiology between individuals or in factors that predispose to disease.

Transplantation of human gut microbiota into surrogate hosts, such as mice or rats, may allow the generation of animal models that mimic human flora and facilitate the in-depth research on human gut microbiota-associated metabolism, pharmacology and immunity5–7. However, the intrinsic differences between rodents and humans in anatomy and physiology make it difficult to directly extrapolate the results. A new human flora-associated piglet model was recently established by the transplantation of human GI microbiota to germ-free piglets with minimal individual variation and ageing patterns that are similar to those observed in humans5–7. Such a human flora-mimicking piglet model provides a new platform for pharmacological and biochemical research for gut pathology, nutraceutical and pharmaceutical compound screening, and drug metabolism.

Concluding thoughts: a systems approach

Gut microbiota-oriented pharmaceutical research requires a progressive, experimental pipeline approach that is dedicated to such a process. Understanding the global relationships between the gut microbiota and humans — for example, a common aetiology for both GI and neurological/metabolic disorders — is the first step towards establishing novel diagnostic, therapeutic and preventive modalities for such diseases. Strategies that are guided by systems thinking need to be adopted in order to understand the essential elements that are involved in the onset and development of many complex human diseases that are associated with variations in the gut microbiota. Focusing on the totality of the microbiota and, therefore, capturing the global change of the gut microbiota with pathological and pharmacological significance is the key to generating comprehensive molecular descriptions of the disease and multifaceted, system-wide drug responses, so that the breadth of biochemical changes contributing to a disease or drug response can be taken into account. Research programmes focusing on certain clinical manifestations or phenotypic variations of a disease associated with altered gut microbiota need to be conducted to classify the disease so that different therapeutic strategies can be implemented for different subtypes or states of gut ecology associated with different structures of the microbiota. Bioanalytical profiling technologies, such as metabonomics and metagenomics, of patient urinary and faecal samples can be utilized to provide holistic and dynamic biochemical information to assist the medical staff on disease diagnosis, stratification and personalized gut microbiota-targeted treatment. Meanwhile, elucidating the molecular details of host–flora interactions during a pathological process should be pursued to obtain a mechanistic understanding to aid drug development. Such a top-down strategy is crucial to achieving a complete coverage of the biochemical mechanisms contributing to the disease to generate feasible treatment measures.

So far, engineering ecologies (the living environments outside and inside of our bodies) has not been that successful because of an incomplete understanding of the systems involved. Currently, we still have limited mechanistic knowledge regarding how indigenous microorganisms have shaped our genome and biology in postnatal development. Emerging technologies, such as metabonomics and metagenomics, have provided information indicating that symbiotic microbes affect metabolic phenotypes and enzyme induction states, which ultimately affect the outcome of interventions4. Growing evidence continues to reveal important functions of the gut microbiota in human health and provides new therapeutic targets for the drug industry that, so far, has been focusing exclusively on the human genome. We assert that the value of gut microbiota-targeted drug discovery and therapies can only be fully realized by a major shift from studying the parts of living systems in isolation, or the reductionist approach, to studying the intricate interrelationship within our superorganism by integrating results from different scientific disciplines — the systems approach. The host–flora interaction must be composed of complex, networked communications involving convergent, divergent and redundant signalling pathways. Considering the infrastructures for platform technologies to be established and the need to attract cross-disciplinary research personnel, a long-term agenda and research strategy, perhaps 15–20 years in duration, is required for the full development of this field. With the progress of metagenomics in conjunction with other ‘omics’ technologies, the composition and specific biological functions of the human gut microbiota will be gradually uncovered, opening up an entirely new approach to drug discovery and therapy.


Acknowledgements

This work was financially supported by the National Basic Program of China (2007CB811700) and the International Collaborative Project. Chinese Ministry of Science and Technology (2006DFA02700).