The Science of the Gut: Food, Fiber, Friends and Foes

Dr. Hugo Rodier
You would not believe the stuff coming out in the journals about the gut.....

Hugo Rodier, MD
Adjunct Professor University of Utah
Department of Nutrition
College of Health
Nobel Prize in Medicine 1908

“Immunity has existed from time immemorial. It is as ancient as disease. The most simple organisms constantly struggle for their existence. They give chase to other organisms for food, and they defend themselves not to become their pray. When the aggressor in this struggle is smaller, it introduces itself into the body of the pray to destroy it by an infection, to absorb the contents of its host and multiply.”

“Immunity in Infective Diseases”, London 1905
Metabolism

“An understanding of metabolic pathways based solely on biochemistry textbooks would underestimate the pervasive role of metabolism in essentially every aspect of biology. It is evident from recent work that many human diseases involve abnormal metabolic states—often genetically programmed—that perturb normal physiology and lead to severe tissue dysfunction. Understanding these metabolic outliers is now a crucial frontier in disease-oriented research. This Review discusses the broad impact of metabolism in cellular function and how modern concepts of metabolism can inform our understanding of common diseases like cancer and also considers the prospects of developing new metabolic approaches to disease treatment.”

“Cellular Metabolism and Disease: What Do Metabolic Outliers Teach Us?”
J. Cell 2012;148:1132
Mitochondria

“Mitochondria perform diverse yet interconnected functions, producing ATP and many biosynthetic intermediates while also contributing to cellular stress responses such as autophagy and apoptosis. Mitochondria form a dynamic, interconnected network that is intimately integrated with other cellular compartments. In addition, mitochondrial functions extend beyond the boundaries of the cell and influence an organism's physiology by regulating communication between cells and tissues. It is therefore not surprising that mitochondrial dysfunction has emerged as a key factor in a myriad of diseases, including neurodegenerative and metabolic disorders.”

“Mitochondria: In Sickness and in Health,” J. Cell 2012;148:1145
The Microbiota

“The human gut harbors diverse microbes that play a fundamental role in the well-being of their host. The constituents of the microbiota—bacteria, viruses, and eukaryotes—have been shown to interact with one another and with the host immune system in ways that influence the development of disease. We review these interactions and suggest that a holistic approach to studying the microbiota that goes beyond characterization of community composition and encompasses dynamic interactions between all components of the microbiota and host tissue over time will be crucial for building predictive models for diagnosis and treatment of diseases linked to imbalances in our microbiota.”

Striking at the roots:
The Microbiome

“Our bodies, inside and out, are teeming with trillions of microbes. Most of them are our friends, helping us to digest food, strengthen our immune systems, and keep dangerous enemy pathogens from invading our tissues and organs. Evidence is building that this resident community of microbes, called the microbiome, plays a major role in health and disease. When the normal composition of the microbiome is thrown off balance, researchers say, the human host can get into serious trouble—especially because the 5 million to 8 million different microbial genes in our bodies vastly outnumber the 20,000 or so human genes. Indeed, recent research has implicated microbiome imbalances in disorders as diverse as cancer, obesity, inflammatory bowel disease, psoriasis, asthma, and possibly even autism.”

“Honor Thy Gut: Symbionts Redux,”
J. Science 8 June 2012:125
Epigenetics

“Microorganisms represent the majority of life on earth, populating a wide range of niches on its surface, underground, in the oceans, in the atmosphere, and both on and inside all multicellular organisms. This “microbiome” will clearly play a critical role as humans struggle to deal with society's major challenges—health care, agriculture, energy, and the environment. As one example, the human gut microbiome contributes 36% of the small molecules that are found in human blood, and it also plays a major role in creating susceptibility to certain human diseases. In recent years, a variety of microbial communities have been characterized through such efforts as the Human Microbiome Project and the Earth Microbiome Project. But mapping these trillions upon trillions of microbes and analyzing the vast amounts of data that are accumulating will require new integrative approaches aimed at understanding how microorganisms function and are interrelated.”

“EDITORIAL: Tackling the Microbiome,” J. Science 8 June 2012: 1209

“Exploring our gut microbial communities with new tools is allowing us to revisit old questions; to develop new concepts about our evolution, postnatal development, systems physiology, individuality, and definitions of health; and to further delineate the impact of our changing life-styles. It is also allowing us to envision exciting new ways for addressing global health problems. This area is inherently interdisciplinary, offering a wealth of opportunities to create new fields, partnerships, and educational initiatives. It is captivating to the public and carries substantial expectations. As such, participating scientists need to sponsor proactive, solution-focused discussions of its societal implications.”

“Honor Thy Gut: Symbionts Redux,”
J. Science 8 June 2012: 125
“Bacterial cells in the body outnumber human cells by a factor of 10 to 1. Yet only recently have researchers begun to elucidate the beneficial roles these microbes play in fostering health. Some of these bacteria possess genes that encode for beneficial compounds that the body cannot make on its own. Other bacteria seem to train the body not to overreact to outside threats. Advances in computing and gene sequencing are allowing investigators to create a detailed catalogue of all the bacterial genes that make up this so-called microbiome. Unfortunately, the inadvertent destruction of beneficial microbes by the use of antibiotics, among other things, may be leading to an increase in autoimmune disorders and obesity. Biologists once thought that human beings were physiological islands, entirely capable of regulating their own internal workings. Our bodies made all the enzymes needed for breaking down food and using its nutrients to power and repair our tissues and organs. Signals from our own tissues dictated body states such as hunger or satiety. The specialized cells of our immune system taught themselves how to recognize and attack dangerous microbes—pathogens—while at the same time sparing our own tissues. Over the past 10 years or so, however, researchers have demonstrated that the human body is not such a neatly self-sufficient island after all. It is more like a complex ecosystem—a social network—containing trillions of bacteria and other microorganisms that inhabit our skin, genital areas, mouth and especially intestines. In fact, most of the cells in the human body are not human at all. Bacterial cells in the human body outnumber human cells 10 to one. Moreover, this mixed community of microbial cells and the genes they contain, collectively known as the microbiome, does not threaten us but offers vital help with basic physiological processes—from digestion to growth to self-defense.”

“How Bacteria in Our Bodies Protect Our Health: Researchers who study the friendly bacteria that live inside all of us are starting to sort out who is in charge—microbes or people?” J. Scientific American June 2012, p7
More Evidence
www.hugorodier.com

“The hybrid science of diet, microbes, and metabolic health,”
Am J Clin Nutr 2011 94: 1


“Peripheral education of the immune system by colonic commensal microbiota,” J. Nature 2011;478; 250


“The Gut's Clostridium Cocktail,” J. Science 2011;331:289

“Gut Microbes May Drive Evolution: The bacteria that live quietly in our bodies may have a hand in shaping evolution,”
J. Scientific American, February 23, 2012
The best evidence
“Probiotics can have inflammatory activities in both healthy and IBD tissue. Valid preclinical data on proper model systems should therefore be obtained before specific probiotic strains enter the clinics, especially if administered during acute inflammatory responses. Postbiotics may be a safe alternative for the treatment of patients with IBD in the acute inflammatory phase.”

Pharmaceuticals: Protection, Modulation and “Buggutexx”

1. **NSAIDS, Antibiotics, Acid blockers,**
   “Microflora, Helminths and the Immune system. Who Controls Whom?” NEJM 010;363:15
   “Probiotics for Antibiotic-Associated Diarrhea,” JAMA 2012;307;1959

2. “A mechanistic understanding of how the gut **microbiota directly and indirectly affects drug metabolism** is beginning to emerge.”
   “Is It Time for a Metagenomic Basis of Therapeutics?” J. Science 8 June 2012: 1253

3. “**Gut Microbes: From Bugs to Drugs**”
   American J. Gastroenterology 2010;105:275
By fixing the gut “everything” gets better: examples

Host-microbe cross talk

Commensal-pathogen cross talk

Commensal-commensal cross talk

Generation and maintenance of balanced gut microbiota and mucosal homeostasis
"Bacteria in intestinal tract are not regulating allergic immune response as effectively as they did in the past, so children are reacting to more potential allergens."

"Treatment Rather Than Avoidance May Be Within Reach for Children With Food Allergies," JAMA 2012;307:345

Obesity

“The composition and activity of the gut microbiota codevelop with the host from birth and is subject to a complex interplay that depends on the host genome, nutrition, and life-style. The gut microbiota is involved in the regulation of multiple host metabolic pathways, giving rise to interactive host-microbiota metabolic, signaling, and immune-inflammatory axes that physiologically connect the gut, liver, muscle, and brain.”

“Host-Gut Microbiota Metabolic Interactions,”
J. Science 8 June 2012: 1262

“Mitochondrial lipid oxidation is impaired in cultured myotubes from obese humans,”
International J. of Obesity 2012;36:1025

“Infant antibiotic exposures and early-life body mass, “
International J. of Obesity, Epub August 22nd 2012

“The Microbiome and Obesity: is obesity linked to our gut flora?”
J. Current Gastroenterology Reports 2009;11:307

“Gut Microbiota and Its Possible Relationship with Obesity,”
J. Mayo Clinic Proceedings 2008;83:460
Insulin Resistance, Diabetes

“Bacterial Endotoxin Activity in Human Serum Is Associated With Dyslipidemia, Insulin Resistance, Obesity, and Chronic Inflammation,”
*J. Diabetes Care* 2011; 34:1809

“*Helicobacter pylori* Infection Is Associated With an Increased Rate of Diabetes,”
*J. Diabetes Care* 2012;35:520

“Association of Diabetes and HbA$_{1c}$ Levels With Gastrointestinal Manifestations,”
*J. Diabetes Care* May 2012;35:1053
Detoxification

“Do Interactions Between Gut Ecology and Environmental Chemicals Contribute to Obesity and Diabetes?”
J. Environmental Health Perspectives 2012;120:a123

“An Environmental Link to Obesity; A Growing List of Potential Obesogens,”
J. Environmental Health Perspectives 2012;120:a62

“Inflammasome-mediated dysbiosis regulates progression of NAFLD and obesity,”
J. Nature 2012;482:179
Immune-detox system

“The large numbers of microorganisms that inhabit mammalian body surfaces have a highly coevolved relationship with the immune system. Although many of these microbes carry out functions that are critical for host physiology, they nevertheless pose the threat of breach with ensuing pathologies. The mammalian immune system plays an essential role in maintaining homeostasis with resident microbial communities, thus ensuring that the mutualistic nature of the host-microbial relationship is maintained. At the same time, resident bacteria profoundly shape mammalian immunity. Here, we review advances in our understanding of the interactions between resident microbes and the immune system and the implications of these findings for human health.”

“Interactions Between the Microbiota and the Immune System,”
J. Science 2012;336: 1268

“99th Dahlem Conference on Infection, Inflammation and Chronic Inflammatory Disorders: The normal gut microbiota in health and disease,”
J. Clinical & Experimental Immunology 2010;160:80

“Peripheral education of the immune system by colonic commensal microbiota,”
J. Nature 2011;478:250
hormones

Healthy gut bacteria more efficiently breaks down estrogen; lower risk of breast cancer,
J. Clinical Endocrinology & Metabolism Epub September 11 2014.
Colitis, IBS

“Commentary on Prebiotic Utility in Colitis: Will Inflammasomics Hold the Key?”
J. Nutrition 2012;142: 1189

“Probiotic and postbiotic activity in health and disease: comparison on a novel polarized ex-vivo organ culture model,”
J. Gut 2012;61:1007

“Microbiome: That healthy gut feeling;
J. Nature 2011;480:S88

“Novel pathophysiological concepts of inflammatory Bowel Disease,”
J. Gastroenterology 2006;41:10

“Postinfectious Irritable Bowel Syndron A Genetic Link Identified?”
J. Gastroenterology 2010;138:1246
Rheumatoid problems


“The gut in Ankylosing Spondylitis and other spondyloarthropaties: inflammation beneath the surface,” J. Rheumatology 2003;30:11

“Subclinical intestinal inflammation and sacroiliac changes in relatives of patients with Ankylosing Spondylitis,” J. Gastroenterology 2003;125:1598

“The Gut's Clostridium Cocktail,” J. Science 2011;331:289
Endotoxemia

“A High Fat Meal Induces Low-Grade Endotoxemia: evidence of a novel mechanism of postprandial inflammation,” AJCN 2007;86:1286

“Does the Western Diet Promote Endotoxemia and Inflammation?”
J. Gastroenterology 2012 May 21st, Epub
Small Intestinal Bacterial Overgrowth: A Framework for Understanding Irritable Bowel Syndrome

Henry C. Liu, MD

**CONCEPT** Irritable bowel syndrome (IBS) is a common diagnosis that affects 11% to 14% of the population. Currently, IBS is diagnosed primarily on the basis of nonspecific clinical criteria. This symptom-based approach has been used because no consistent biological marker or unifying framework has been available to explain the different symptoms and findings of IBS. The varying symptoms in IBS have led to efforts looking at differences rather than similarities between patients.

Another way we have emphasized the difference rather than the similarity is in the grouping of one set of symptoms of these patients as IBS and another set of symptoms as belonging to some other diagnosis. The clinical criteria for IBS do not include the extraintestinal symptoms that are common to these patients such as fatigue or myalgia. Instead, these complaints are viewed as symptoms of other diagnoses that coexist with IBS such as “chronic fatigue syndrome” and fibromyalgia. This separation may be an artifact of medical specialization. A unifying framework for understanding IBS that could account for both the gastrointestinal and extraintestinal symptoms of these patients would better warrant serious consideration.

**EVIDENCE ACQUISITION**

Ovid MEDLINE was searched through May 2004 for articles using combinations of the terms “malingering,” gas, IBS, postinfectious IBS, small intestinal bacterial overgrowth (SIBO), intestinal inflammation, and IBS. Relevant articles were cited where indicated. A unifying framework for understanding IBS that could account for both the gastrointestinal and extraintestinal symptoms of these patients would better warrant serious consideration.

**EVIDENCE SYNTHESIS**

Postinfectious IBS as a Unifying Symptom of IBS

Regardless of whether an IBS patient is troubled predominately by constipation, diarrhea, or IBS symptoms, the patient will often have extraintestinal symptoms, such as fatigue or myalgia, as well. Extraintestinal symptoms may be the major complaint in some patients, with gastrointestinal symptoms being more subtle.

**Author Affiliation** Division of Gastroenterology and Nutrition, Department of Medicine, and Institute for Clinical and Translational Science, University of Southern California, Los Angeles.

Corresponding Author: Henry C. Liu, MD. Division of Gastroenterology and Nutrition, Department of Medicine, University of Southern California, 1220 N. State St., Los Angeles, CA 90033. E-mail: hliu@med.usc.edu

Cancer

“The Human Microbiome Project: Getting to the Guts of the Matter in Cancer Epidemiology,” J. Cancer Epidemiology Biomarkers & Prevention 2008 17; 2523
Brain-gut connection


“Many of the immune and metabolic changes occurring during normal pregnancy also describe metabolic syndrome. Gut microbiota can cause symptoms of metabolic syndrome in nonpregnant hosts. … Microbial interactions that impact host metabolism can occur and may be beneficial in pregnancy.”

“The human microbiome and its potential importance to pediatrics”
J. Pediatrics 2012;129:950

“Potential Association Between the Oral Tetracycline Class of Antimicrobials Used to Treat Acne and Inflammatory Bowel Disease,”
Am J Gastroenterol 2010;105: 2610

Well documented:
   “Hygiene hypothesis:”
   Asthma, atopy, allergies
   Diarrhea
   NICU. Dr. Chan, UUMC
Cholesterol, heart disease

“Microbiologist Zhao Liping combined prebiotics with a diet based on whole grains, he lost 20 kilograms in 2 years. His blood pressure, heart rate, and cholesterol level came down.”
“My Microbiome and Me,” J. Science 8 June 2012:1248


Gut increases risk of MI in young patients with low risk, J. Family Practice News, June 15th 2011, p16
Why? Dysbiosis

“The human gastrointestinal tract harbors trillions of bacterial cells belonging to more than 1000 species, and **there are 10 times as many bacterial cells within the gastrointestinal tract as there are human cells within our bodies.** The gastrointestinal microbiota plays essential roles in human nutrition, physiology, development, immunity, and behavior, such that disrupting the structure and balance of this community leads to dysbiosis and disease. This important balance between host and microbiota can be severely disrupted by environmental stimuli. One of the most common insults to the microbiota that induces **dysbiosis** is infectious diseases.”

“Virulence or Competition?”
*J. Science 8 June 2012: 1238*
4 Fs

• Food & supplements
• Fiber
• Friends
• Foes
1. Food

Week(s) 1-2
Lean meats, veggies, nuts

Week(s) 3-4
Fruits

Week(s) 5-6
Legumes

After that
Introduce a whole grain

Q3 days

BEST DIETS:
DASH, Mediterranean, Glycemic I.

Change in Microbiome 24 hrs after diet change
“The Impact of the Gut Microbiota on Human Health: An Integrative View,”
J. Cell 2012;148:1258
1a Food: addiction


“Neural Cortex Food Addiction,”
“Blood pressure, heart rate, fructose, and a variety of other metabolic biomarkers were measured. Fructose area under the curve and maximum concentration, dose-normalized glucose area under the curve and maximum concentration, relative bioavailability of glucose, changes in postprandial concentrations of serum uric acid, and systolic blood pressure maximum levels were higher when HFCS-sweetened beverages were consumed as compared with sucrose-sweetened beverages. Compared with sucrose, HFCS leads to greater fructose systemic exposure and significantly different acute metabolic effects.”

“Effects of high-fructose corn syrup and sucrose on the pharmacokinetics of fructose and acute metabolic and hemodynamic responses in healthy subjects,” J. Metabolism Clinical and Experimental 2012;61:641
1c Food: energy & Information

“Why obese patients don’t lose weight with low calorie diets?”  
AJCN 2007;85:346

“Personal metabolomics ”  
J. Nutrition 2003;133:4260

“Changes in Diet and Lifestyle and  
Long-Term Weight Gain in Women and Men,”  
NEJM 2011;364:2392

“Weight Loss and Weight Loss Maintenance,”  
JAMA 2012;307:2617
1d Food: misinformation

“The quality of carbohydrates, as characterized by their glycemic index, is dismissed as unimportant, whereas we believe the evidence strongly suggests the opposite. The original Food Guide Pyramid, which encouraged substituting grain products for dietary fat (irrespective of their nutritional quality), may have inadvertently contributed to epidemics of metabolic syndrome and related chronic diseases by increasing refined-starch consumption. 

1e Food: supplements

• Omega oils
• Vitamin D3
• B complex
• Digestive enzymes
• 2nd team: one thing in common
  Curcumin
  Alpha Lipoic acid
  SAMe
  N-Acetyl-Cysteine

Up to 1990, 80% of drugs came from herbs and nutrients. Now it’s 50%
“Drug Discovery and Natural Products: end of an era or an endless frontier?”
J. Science 2009;325:161
2. Fiber = prebiotics

“Dietary fiber is important in digestion, and its relationship with chronic disease has been a topic of great interest for many years. A fiber-rich diet similar to that of early man is probably healthier than current Western-type diets,"

“Do the Health Benefits of Dietary Fiber Extend Beyond Cardiovascular Disease?: Comment on "Dietary Fiber Intake and Mortality in the NIH-AARP Diet and Health Study" J. Arch Intern Med. 2011;171:1069


Commercial brands for intestinal cleansing:
Glutamine, Turmeric, Slipepry Elm, NAC, Boswellia, Ginger, Quercetin, Grape seed extract, Pectin, assorted antioxidants
3. Friends: “buggutexx?”

“Probiotics can have inflammatory activities in both healthy and IBD tissue. Valid preclinical data on proper model systems should therefore be obtained before specific probiotic strains enter the clinics, especially if administered during acute inflammatory responses. Postbiotics may be a safe alternative for the treatment of patients with IBD in the acute inflammatory phase.”


“Gut microbiota fermentation of prebiotics [fiber] increases satietogenic and incretin gut peptide production with consequences for appetite sensation and glucose response after a meal,” Am J Clin Nutr 2009;90: 1236

“Prescribing an Antibiotic? Do Not Forget the Probiotic,” J. Gastroenterology 2009;137:1846
4. Foes

“The Gut's *Clostridium* Cocktail,”
J. Science 2011;331:289

“Antibiotic Therapy in Inflammatory Bowel Disease: A Systematic Review and Meta-Analysis,”
Am J Gastroenterol 2011;106:661

“Targeting the Human Microbiome with Antibiotics, Probiotics and Prebiotics: gastroenterology enters the metagenomics era,”
J. Gastroenterology 2009;136:2015

Antibiotics, probiotics helpful in IBS,
Annual Mtg Am Coll of physicians, New Orleans 2012,
J. Family Practice News, June 15\textsuperscript{th} 2012, page 16

**My experience:**
Gentamycin, Vancomycin
Terbinafine, Nystatin
Ivermectin, Mebendazole/Tinidazole
Effects of selective decontamination of digestive tract on mortality and acquisition of resistant bacteria in intensive care: a randomised controlled trial

Evert de Jonge, Marcus J Schultz, Lodewijk Spanjaard, Patrick M M Bossuyt, Margaretha B Vroom, Jacob Dankert, Jozef Kesecioglu

Summary

Background Selective decontamination of the digestive tract (SDD) is an infection-prevention regimen used in critically ill patients. We assessed the effects of SDD on intensive-care unit (ICU) and hospital mortality, and on the acquisition of resistant bacteria in adult patients admitted to intensive care.

Methods We did a prospective, controlled, randomised, unblinded clinical trial. 934 patients admitted to a surgical and medical ICU were randomly assigned oral and enteral polymyxin E, tobramycin, and amphotericin B combined with an initial 4-day course of intravenous cefotaxime (SDD group n=466), or standard treatment (controls n=468). Primary endpoints were ICU and hospital mortality and the acquisition of resistant bacteria.

Findings In the SDD group 69 (15%) patients died in the ICU compared with 107 (23%) in the control group (p=0.002). Hospital mortality was lower in the SDD groups than in the control groups (113 [24%] vs 146 [31%]; p=0.02). During their stay in intensive care, colonisation with gram-negative bacteria resistant to certazidime, ciprofloxacin, imipenem, polymyxin E, or tobramycin occurred in 61 (13%) of 466 SDD patients and in 104 (26%) of 395 patients in the control group (p=0.001). Colonisation with vancomycin-resistant enterococci occurred in five (1%) SDD patients and in four (1%) controls (p=1.0). No patient in either group was colonised with meticillin-resistant Staphylococcus aureus.

Interpretation In a setting with low prevalence of vancomycin-resistant enterococci and meticillin-resistant S aureus, SDD can decrease ICU and hospital mortality and colonisation with resistant gram-negative aerobic bacteria.

Lancet 2003; 362: 1011–16

See Commentary page 1006

Introduction

Selective decontamination of the digestive tract (SDD) is an infection-prophylaxis regimen that was introduced into intensive-care medicine in 1984. Nosocomial infections contribute substantially to morbidity and mortality of patients treated in intensive-care units (ICUs). Most of these infections are thought to be preceded by oropharyngeal and intestinal colonisation with pathogenic microorganisms. SDD is based on the concept of colonisation resistance, according to which the indigenous intestinal flora has a protective effect against secondary colonisation with gram-negative aerobic bacteria. The approach aims to eradicate colonisation of aerobic potentially pathogenic microorganisms from the oropharynx, stomach, and gut, while leaving the indigenous anaerobic flora largely undisturbed. The classic SDD regimen consists of two components. Topical non-absorbed antibiotics, generally polymyxin E, tobramycin, and amphotericin B, were applied orally and through a nasogastric tube, and treatment with parenteral antibiotics, most frequently cefotaxime, was added for the first 4 days to prevent early infections. The belief that SDD reduces mortality in ICU patients was fostered by three meta-analyses, each reporting decreased mortality among patients who were treated with combined topical and systemic antibiotics. Yet, the meta-analyses on SDD were based partly on unpublished studies and the quality of methods in the published studies has been challenged. Controversy exists about the effect of SDD on mortality and on antibiotic resistance. Studies with antibiotic resistance as an endpoint would ideally focus on the effect of SDD on the ICU environment as well as on individual patients. We, therefore, did a controlled randomised study with mortality and the acquisition of resistant bacteria as primary endpoints.

Patients and methods
Goals of 4F program: Fix leaky gut, remodel microbiota

“Altered intestinal permeability is a key pathogenic factor if idiopathic bowel inflammation. A large variety of bacterial populations with different pathogenic potentials and a high concentration of chemicals and bacterial toxins are constantly challenging the structure and function of the colonic mucosal barrier... leading to changes in the intestinal permeability... facilitating the penetration of proinflammatory antigens that challenge the immune system,” J. Gut 2001;48:503

“Regulation of Tight Junction Permeability by Intestinal Bacteria and Dietary Components,” J. Nutrition 2011;141:769
Fecal Flora Transplant?

“Long-Term Follow-Up of Colonoscopic Fecal Microbiota Transplant for Recurrent Clostridium difficile Infection,”
Am J Gastroenterol 2012:107:1079
Summary

Intestinal flora is influenced by multiple factors including diet, stress, medical drugs, microorganisms, climate, nutrient absorption, medical drugs, gastrointestinal function, and infections. These factors can lead to changes in the immune system, ageing, and allergies.
Now, I have to go back to my office...