GUT MICROBIOTA, DIET & NUTRITION

A selection of content from the Gut Microbiota for Health Experts Exchange 2013-2014

October 2014
Thank you for downloading the first edition of our « Best of » series! In this first issue, you have at your fingertips the best way to get up-to-date on the area of gut microbiota, diet and nutrition.

In this document, we’ve compiled website content from some of the foremost scientific experts in the field of nutrition and gut health, including Mary Ellen Sanders (our probiotics expert), Dr. Elena Verdú, Dr. Gary Wu, Prof. Jeffrey Gordon, and others.

What will you find below? A selected group of articles, summaries, and interviews from the last two years on our website, arranged around two questions: (1) How does nutrition modulate the gut microbiota? and (2) How do probiotics and prebiotics modulate the microbiota? You’ll also get a peek at some of the most popular nutrition-related tweets from our @GMFHx Twitter account.

Be sure to visit our website soon for more gut microbiota, diet and nutrition research that has been selected from the most important science journals. If you’d prefer to have the most current research delivered to your inbox twice a month, please sign up for our e-newsletter on www.gutmicrobiotaforhealth.com.

The Gut Microbiota for Health Publishing Team
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At birth, we are colonized with a complex community of microbes that reaches up to $10^{14}$ cells; ten-times the number of human cells. Normally, these microbes exist in a mutualistic relationship with the host, are critical for growth and development, and help maintain host physiology, metabolism, and immunity. Lifestyle choices, including diet and nutrition, influence the composition of the microbiota and its development following birth, which may have important implications for health and disease in both the young and the elderly. Diet in particular can rapidly induce remarkable changes in the microbiota and the Western diet (one high in fat and sugar) has been associated with increased risk for obesity, metabolic syndrome, inflammatory bowel disease and malignancies. On the other hand, interactions between the microbiota and diet/nutrition early in life are thought to contribute to malnutrition in developing countries. The possibility that diet-induced alterations to the microbiota can contribute to disease development is a global problem given that obesity is a growing cause of morbidity and mortality in Western countries. On the other hand, malnutrition is the leading cause of child mortality in developing countries.

How can we study these interactions experimentally? The use of “humanized” animal models, where a previously sterile (germ free) mouse is colonized with the microbiota from a human, has allowed us to investigate how much of a person’s biology is attributed to their microbiota. Gnotobiotic and humanized animal models allow us to determine whether the manipulation of the microbiota, by changes in diet for example, have health-related consequences and allow us to identify microbial factors and pathways that are causally associated with health and disease. Finally, they provide the ability to mimic clinical interventions and understand how the microbiota responds to successful treatment.

As discussed by Dr. Eric Brown in an interview posted on Gut Microbiota for Health on July 1st 2014 (www.gutmicrobiotaforhealth.com/interview-eric-brown-expert-malnutrition-microbiota-6171), and by Prof. Jeff Gordon during a TED talk posted on Gut Microbiota for Health on March 5th (www.gutmicrobiotaforhealth.com/jeffrey-gordon-gut-microbes-children-nutrition-2-5600), the use of animal models is critical for studying how microbe-host interactions contribute to diseases like malnutrition. The Gordon lab recently demonstrated that the microbiota may play a causal role in
a form of malnutrition called kwashiorkor (Smith et al., 2013. Science), which was highlighted by Gut Microbiota for Health on February 8th, 2013 (www.gutmicrobiotaforhealth.com/s/the-malnourished-microbiome). Using infant twin pairs they demonstrated that twin pairs that did not develop kwashiorkor had a steady maturation of their microbiota whereas the microbiota of twin pairs that developed kwashiorkor did not mature, even when treated. The transfer of healthy or kwashiorkor microbiota to germ-free mice further demonstrated that the combination of diet and the kwashiorkor microbiota contributed to weight loss in recipient mice. The Gordon lab has also been instrumental in demonstrating how the interactions between diet and our microbes can lead to obesity. Their study, which used a similar approach, demonstrated that the transfer of microbiota from obese or lean humans to mice also transferred the respective phenotype and was published in Science in 2013 (Ridaura et al., 2013. Science) and highlighted on January 13th, 2014 by Gut Microbiota for Health. Furthermore, modulating the obese microbiota in mice prevented the development of the obesity-associated phenotype (www.gutmicrobiotaforhealth.com/s/gut-microbes-diet-and-obesity-linked).

The microbiota can be modulated. Understanding how diet-induced changes in the microbiota impact health and disease provides the opportunity to manipulate the microbiota for therapeutic or preventative purposes. Probiotics, which are live microorganisms that confer a health benefit on the host when administered in adequate amounts, and prebiotics have been widely tested as potential therapeutic options for many gastrointestinal and extra-intestinal diseases, such as irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), autism spectrum disorder, obesity, and many others. For example, in an interview with Filipe De Vadder on Gut Microbiota for Health, he recently described an important function of dietary fibre (www.gutmicrobiotaforhealth.com/deciphering-benefits-of-microbial-fermentation-via-the-gut-brain-axis-1538). Fibre is broken down in the small intestine by members of the microbiota to produce short-chain fatty acids. These SCFAs activate the intestinal gluconeogenesis pathway, which has beneficial effects on glucose
and energy homeostasis. However, as highlighted by *International Scientific Association for Probiotics and Prebiotics* and on Gut Microbiota for Health on July 23rd, 2014 the effects of probiotics seem to be strain specific as well as disease specific. This means that results from one particular study with one particular probiotic cannot be translated to other disease and other strains. Well-designed preclinical and clinical studies with well-defined primary outcomes must be performed under the appropriate conditions for different diseases (Sheridan *et al.*, 2014. *Gut Microbes*).

We are only beginning to understand the interactions between diet, microbiota and maintenance of health and disease. The diet is an easily modifiable environmental factor, but we need a more comprehensive view of normal human development that takes into account maturation of the microbiota to fully understand whether and how modulation of microbiota composition, and or metabolism, has long-lasting effects on host physiology. We have seen that diet-microbe interactions influence obesity and malnutrition, but we may only be seeing the tip of the iceberg. The continued use of gnotobiotic and humanized animal models will be critical in the future to understand how diet and probiotics can modulate the microbiota and how this influences health and disease. The challenge lies in determining the exact dietary and microbial factors that are responsible for mediating effects on the host. Finally, extrapolating these findings to the clinical setting will present an additional challenge. Many diseases are heterogeneous and whether results can be applied across different disease phenotypes remains to be tested. It has been an exciting year in microbiota-nutrition research, and can expect interesting developments in the year to come.

**Elena Verdú**  
MD, PhD, McMaster University  
Gut Microbiota for Health Board Member - Expert in Nutrition

**Heather Galipeau,**  
PhD candidate, McMaster University
Dr Elena Verdú's lab seeks to understand the complex pathophysiology of gastrointestinal diseases, with a focus on microbiota-diet interactions, to identify novel therapeutic targets for these disorders.

1 | What strikes you most in the evolution of research on gut microbiota and why?

EV: One interesting aspect relates to the way we have approached the study of the microbiota. We started off with classical culture techniques. We realized that we were only culturing a fraction of the microbiota, and moved on to heavily rely on high throughput molecular techniques. These have greatly enhanced our capacity to know “who is there”.

Moreover, metagenomic and metabolomic techniques are allowing us to understand what the microbiota “is doing”. These concepts regarding the limitations of culture techniques are undergoing some revisiting, and we are beginning to understand that what was considered unculturable before, is in fact our lack of capacity – or effort! – to culture what is there.

The groups of Dr. M Surette and Dr. P Bercik at the Farncombe Institute in McMaster University are engaged in a clinical collaborative study that investigates the recovery of microbiota by culture techniques from fecal samples from patients with irritable bowel syndrome, and compares this with state of the art molecular approaches. In a recent study presented at the Canadian Digestive Disease Week (Lau et al., 2014, Characterization of the cultivable human gut microbiota by culture-enriched molecular profiling, CDDW2014 Abstract) Surette’s group has shown that by using more than 50 different culture media and conditions, they are able to culture between 90-100% of the species detected by advanced pyrosequencing techniques.

We are beginning to realize that old methods will be invaluable for the isolation of species present in the microbiota, if sufficient effort is employed. When used together with molecular and metagenomic approaches and gnotobiotic technology, the renaissance of culture techniques will increase our understanding of the role of the microbiome in health and disease. We have come full circle.

2 | You are our nutrition expert on the platform. What is according to you the health potential of better understanding the gut microbiota in this area?

EV: There is little doubt that diet and nutrition affect the microbiota. Several recent studies have demonstrated that long-term diet is an important determinant of the microbiota (Wu et al., 2001. Science). On the other hand, the microbiota may be a disease-promoting factor in food intolerances because of the important role it plays in immune and functional gut homeostasis (Natividad et al., 2009. PLoSOne; Rodriguez, 2011. FEMS Microbiol Ecol; Noval Rivas, 2013. J Allergy Clin Immunol). The relationship is bi-directional. We are currently conducting studies that aim at understanding how the gut microbiota interacts with specific dietary components. Specifically we are interested in the dietary protein gluten, the trigger in celiac disease, and how the microbiota may modify disease severity and expression.

3 | How do you see the evolution of clinical applications and interventions in the field of gut microbiota?

EV: There is evidence for an association between intestinal dysbiosis and disease states, including food intolerances like coeliac disease. However, evidence demonstrating causality and mechanisms of action is lacking. The challenge will be to assign function to the microbial profiles associated with specific dietary components or interventions and how they affect expression of common diseases and their therapies. The continued use of gnotobiotic animal models in combination with clinical research will be necessary to explore this complex relationship. These studies will help develop targeted interventions directed at modulation of the microbiota to prevent or treat diseases, including food intolerance.
The definition of probiotics: twelve years later

A panel of scientific experts* assembled in London, UK, on October 23, 2013 to discuss the scope and appropriate use of the term ‘probiotic.’

The International Scientific Association for Probiotics and Prebiotics (ISAPP) organized the meeting to review the relevance of the 12-year-old FAO/WHO definition of probiotics: “Live microorganisms which when administered in adequate amounts confer a health benefit on the host” (FAO/WHO 2001).

This consensus panel was motivated by these recent developments:

• In the European Union, in the absence of approved health claims for probiotic foods, the word ‘probiotic’ is considered a health claim. Consequently, several countries have determined that the word can no longer be used on foods. The panel wanted to consider this decision in the context of amassed evidence on probiotic health effects.

• Fecal microbial transplants are being used for treatment of conditions linked to aberrant gut microbiota. The panel considered whether such preparations of live microorganisms should be considered within the scope of probiotics.

• Native human colonizing microbes are being identified as potential novel probiotics. The panel considered whether such live microorganisms should be considered within the scope of probiotics.

The conclusions of the panel were published in June 2014 as an open access paper in Nature Reviews Gastroenterology and Hepatology.

Panel conclusions:

• The panel agreed that the FAO/WHO definition for probiotics was still relevant, but advised a minor grammatical correction: “live microorganisms that, when administered in adequate amounts, confer a health benefit on the host”.

• The panel considered the general benefit of supporting a healthy digestive tract was supported by evidence gathered on a large number of different probiotic strains representing commonly studied species, such as a variety of Lactobacillus and Bifidobacterium species. “Supporting a healthy digestive tract” includes a broad array of physiological and clinical endpoints, ranging from normalizing intestinal transit to improving gut barrier function, reducing intestinal symptoms, and preventing and treating intestinal diseases. In the panel’s opinion, calling a product containing a minimum level of one of these well-studied species ‘probiotic’ is justified, even in the absence of strain-specific studies. However, any specific claim beyond “contains probiotics” must be further substantiated.

• The panel discussed whether certain microbial products fit under the framework of ‘probiotic’:
  1. ‘Live cultures’, traditionally associated with fermented foods, were determined to be outside the framework of probiotic if they were undefined and if there were no proven health benefits associated with them. Traditional fermented foods are certainly components of a healthy diet, and the microbes associated with them may impart health benefits. But there must be a convincing level of evidence to support their health effects to be considered ‘probiotics’. Note that the yogurt starter bacteria, Lactobacillus bulgaricus and Streptococcus thermophilus are considered to be probiotics due to the evidence that they help alleviate symptoms of lactose maldigestion.
2. Undefined, fecal microbiota transplants are not considered to be probiotics.

3. New commensals and consortia comprising defined strains from human samples, with adequate evidence of safety and efficacy, are probiotics.

This Consensus Statement provides updates to the probiotic concept that reflect important developments in human microbiota research, such as fecal microbial transplants, as well as the evidence on probiotic efficacy that has amassed since 2001.

Mary Ellen Sanders, PhD
Gut Microbiota for Health Board Member - Expert in Probiotics


Panel of scientific experts: Glenn Gibson, Chair, University of Reading, UK; Colin Hill, Alimentary Pharmabiotic Centre, Ireland; Roberto Berni Canani, University of Naples Federico II, Italy; Harry Flint, University of Aberdeen, Scotland; Francisco Guarner, University Hospital vall d’Hebron, CEBERehd, Barcelona, Spain; Dan Merenstein, Georgetown University, USA; Lorenzo Morelli, Università Cattolica del Sacro Cuore, Piacenza, Italy; Bruno Pot, Institut Pasteur – Lille, France; Gregor Reid, University of Western Ontario, Canada; Seppo Salminen, University of Turku, Finland; and Mary Ellen Sanders, ISAPP Executive Science Officer, USA. Philip Calder (UK), was unable to be present at the meeting in person, but participated fully in developing the conclusions from the discussion and in preparation of the manuscript.
Interview with Eric Brown, expert on gut microbiota and malnutrition
Published in: GUT MICROBIOTA - NUTRITION I Written on July 1, 2014 by Kristina Campbell

Eric Brown, Ph.D., of the University of British Columbia (Canada) recently gave a seminar as part of the Collège de France symposium: The Impact of Malnutrition on Host-Microbial Interactions in the Small Intestine. Afterward, he took the time to answer some questions about the event.

1 | Can you give us a brief overview of your Collège de France symposium talk?

For my talk, I presented the research I have carried out over the past 3 years in researching the interactions between malnutrition, the gut microbiome and immunity. Specifically, I am interested in a disorder called environmental enteropathy. This is characterized by chronic inflammation, malabsorption, growth stunting and villous blunting in the small intestine independent of any known infectious etiology. This is primarily seen in developing countries with poor nutrition and sanitation. This disorder is now recognized as a major cause of childhood malnutrition. My hypothesis is [that] the microbiome plays a factor in the disorder. There is not much known about enteropathy, since it presents in the small intestine which is difficult to study in humans. Thus I sought to create an animal model to mimic this disease in order to understand the basic biology better. The research I presented was my work so far developing the animal model, which is at a point right now close to publication. I exposed mice to a malnourished diet, alongside a cocktail of microbes which triggered symptoms of enteropathy in mice. I see dysbiosis in the small intestinal microbiota, increased intestinal permeability, alongside changes in villous height and growth rate. With this model, we may be able to understand the disease mechanisms better.

There are not a lot of people studying enteropathy; however, interest is beginning to mount especially with the Gates Foundation funding so much of the research. There is always lots of talk on whether mice are the best models. You just need to be aware of the limitations and strengths of rodent models. If you ask the right questions they will give you relevant answers for human biology. People were also interested in my data from the small intestine microbiota since most studies were done on feces.

2 | What struck you most during the Collège de France event?

As a North American, what struck me the most was meeting and hearing about the vibrant microbiome research community in Europe. Most if the speakers were European and it was an interesting look at the topics and research done in Europe. Many of the conferences I had been to in the past were much more USA-centric. Expanding [my] network by meeting more international researchers gave me some great perspectives on the state of microbiome research. Also, there was a lot of research nutrition-wise on obesity and the microbiome but I was the only speaker talking about malnutrition and microbiome. I think in the future this area is going to expand in relevance, based on feedback from my talk, and research from Jeff Gordon’s lab.

Eric Brown’s 2012 TEDx talk, “How a Toilet Can Save Your Life”, can be viewed here.

Read the original post online at: www.gutmicrobiotaforhealth.com/interview-eric-brown-expert-malnutrition-microbiota-6171
Interview with Paul O’Toole, expert on gut microbiota in elderly populations
Published in: GUT MICROBIOTA - NUTRITION | Written on June 28, 2014 | by Kristina Campbell

Professor Paul O’Toole of University College Cork (Ireland) recently gave a seminar as part of the Collège de France symposium: Diet-Microbiota-Health Interactions in Elderly People. Afterward, he took the time to speak with Gut Microbiota for Health about the event.

Paul O’Toole, University College Cork.

1 I Can you give us a brief overview of your Collège de France symposium talk?

I began by reviewing what’s been published about our studies on the elderly gut microbiota. The first major observation being that where you live determines your microbiota type. It transpired that that was driven by diet... people living in long-term residential care tend to eat a narrower range, a less diverse diet. Then they get a low-diversity microbiota as a consequence. The main outcome of [our] study was the fact that the low-diversity gut microbiota correlated with poor health indices across a range of different parameters. And the main ones were sarcopenia, inflammation, and loss of cognitive function. That work was published in Nature two years ago.

We believe that loss of diversity in different ways is impactful in different conditions at different stages in the life span. But the key question is: What actually is changing in the microbiota? [That is to say,] what metabolic activities are being lost? I went on to describe briefly a European community project called NU-AGE [pronounced «new age»], which is a dietary intervention in 1250 European citizens across five recruitment centres, and that’s still ongoing. And then I described our analyses of the stability of the microbiota, because there’s an interest in how stable your gut microbiota is, and it seems that in healthy adults it’s relatively stable. It turned out that the lower the diversity of the microbiota, the less stable it was. Which fits with general ecological theory, whereby a diverse ecosystem is more robust and more resilient to external perturbations, whereas if the rainforest only has three tree species left it’s going to be pretty shaky.

I talked a little bit about methanogens – these are a species of Archaea – so they’re a different domain of life, they’re not bacteria and they’re not eukaryotes, they’re ancient microbes. And they make methane. We described the fact that the elderly people in our study have a very peculiar community of methanogens in their guts, which we’re still working on. And the last thing I mentioned in my talk is that, in the past, I always get the question, ‘Ok, it’s fine if you’re living in the community and buying your own food and cooking it yourself, you’ve got a good diet. If you’re in long term care you’ll probably have a Sunday dinner every day and you’ll have a bad microbiota. What about people who live in the community who’ve got a low-quality diet?’ We went and found those internal positive controls, I call them, to show that, regardless of your initial health status, if you live in the community and you’ve got a low-diversity, poor-quality diet, you’ll have a correspondingly low-quality microbiota. So it sort of confirms what we showed in the cross-sectional analysis, and this also correlated with inferior health stats. So even if you’re living at home, the moral of the story is you have to have a high-diversity diet to have a high-diversity microbiota.

And then I gave some of my general hypotheses on the diagnostic value of the microbiota. So I believe in profiling the microbiota of people in a
clinical situation to know what their current health status is, but more importantly what their health trajectory is. In other words, if you have a person who’s been retired for five years, they’ve probably changed their diet but you don’t actually know what their current diet is. We can actually infer the diet with quite a bit of accuracy just from profiling the microbiota. Because we’ve got good correlative databases. And we can also tell from the microbiota profile where they stand in terms of these health indices I’ve talked to you about, like inflammation, muscle loss, and cognitive function. We believe the microbiota has diagnostic and prognostic value in elderly healthcare management.

What struck you most during the Collège de France event?

It’s probably the fact that awareness of the microbiota is permeating so many different fields of human biology. So for example there was a talk about microbiota and regulation of bone mass. Osteopenia: we all know that post-menopausal women are particularly at risk for fractures. And some of that is driven by inflammation. And inflammation is controlled to a degree by the gut microbiota... So I think that after a period of around five years where people have been describing correlations of the microbiota with this and that, things are calming down a bit. We’re a little better positioned to develop hypotheses based on research. And all of these exciting physiological connections. It’s not going to be easy because there’s only so much you can do in animal models and ultimately you want to be applicable to humans. I mean, the physiology of mice is different from humans, never mind the microbiota. So we’re going to have to do a lot of work in humans.

Jeffrey Gordon: gut microbes and children under nutrition

Published in: GUT MICROBIOTA - NUTRITION | Written on March 5, 2014 by Yohanan Winogradsky

Prof. Jeffrey Gordon was invited to give a TED talk at the TEDxGatewayArch. His talk introduces the ideas of microbiota and microbiome, a new view to our connection to the microbial world as humans. He goes on detailing how our microbiome is for us a new way of considering our human evolution: it’s a part of evolution that goes much faster than that portrayed in our Homo sapiens genome, occurring at the level of our microbiome.

It’s an opportunity to look at some of the most pressing health issues worldwide. In this perspective, Gordon offers to address the question of malnutrition and its possible connection with the gut microbiota. He describes how malnutrition is a complex dynamic, where gut microbiota represents one more factor. Is the microbiota causally related to risk for childhood undernutrition?
Diet and the intestinal microbiome: associations, functions, and implications for health and disease
Published in: NUTRITION I Written on February 10, 2014 by Julien Tap

A review about how diet affects the structure and metabolome of the human intestinal microbiome, and may contribute to health or pathogenesis of disorders such as coronary vascular disease and inflammatory bowel diseases.

Source: *Gastroenterology*

Read the original post online at: www.gutmicrobiotaforhealth.com/s/diet-and-the-intestinal-microbiome-associations-functions-and-implications-for-health-and-disease

Gut microbes, diet and obesity linked
Published in: NUTRITION I Written on January 13, 2014 by Yohanan Winogradsky

“A new study by researchers in the [Washington University in St. Louis] School of Medicine is helping to illuminate how diet and gut microbes interact to affect weight gain. Microbes of the gut number in the trillions, vary substantially from person to person, and help break down food and synthesize nutrients and vitamins from our diets.”

Source: *Science*

Read the original post online at: www.gutmicrobiotaforhealth.com/s/gut-microbes-diet-and-obesity-linked

Diet rapidly and reproducibly alters the human gut microbiome
Published in: NUTRITION I Written on January 2, 2014 by Julien Tap

This study based on 10 subjects showed that diet could impact rapidly the microbiota. Microbial activity mirrored differences between herbivorous and carnivorous mammals, reflecting trade-offs between carbohydrate and protein fermentation.

Source: *Nature*

Read the original post online at: www.gutmicrobiotaforhealth.com/s/diet-rapidly-and-reproducibly-alters-the-human-gut-microbiome
The malnourished microbiome
Published in: NUTRITION | Written on February 8, 2013  by Joël Doré

The gut microbiome may be a causal factor of kwashiorkor, a form of severe malnutrition, researchers from Washington University in St. Louis report in Science. WashU’s Jeffrey Gordon and his colleagues studied the gut microbiomes of 317 Malawian twin pairs until they turned three. They then focused on nine, well-nourished, same-gender twin pairs and 13 same-gender twin pairs in which one twin developed kwashiorkor. The microbiomes of the healthy twins became more diverse, but as Ed Yong at Not Exactly Rocket Science puts it, “the bacteria of kwashiorkor children stagnated.”

Source: Science
Smith, M et al., 2013. Gut microbiomes of Malawian twin pairs discordant for kwashiorkor. Science DOI: 10.1126/science.1229000

Read the original post online at: www.gutmicrobiotaforhealth.com/s/the-malnourished-microbiome
Deciphering benefits of microbial fermentation via the gut brain axis
Published in: GUT BRAIN AXIS - METABOLIC CONDITIONS - NUTRITION | Written on January 18, 2014 by Julien Tap

Filipe De Vadder is a molecular biologist in Gilles Mithieux group and published recently an important article in Cell journal which illustrate how gut microbiota fermentation product could impact neural communication. He accepted for GMFH to give us some highlights.

What is the context of this study?
Dietary fiber has long been known for its beneficial effects on health, including insulin sensitivity. However, no study had provided a clear mechanism explaining the beneficial metabolic effects of dietary fiber. Given the fact that the effects of dietary fiber are quite similar to those of intestinal gluconeogenesis (which we first described in our lab in the beginning of the 2000s decade), we hypothesized that this unique metabolic feature could be the key linking dietary fiber and beneficial metabolic effects. Furthermore, when dietary fiber is metabolized by the gut microbiota, it produces short-chain fatty acids such as propionate, which is classically described as a liver gluconeogenic precursor. This is in contradiction with the benefits of propionate on glucose homeostasis, so we thought that, before reaching the liver, propionate could act as a glucose precursor in the gut.

What was the most challenging part of this study?
The precise quantification of intestinal glucose fluxes is always quite challenging because it involves surgery, radioactive measurements and you have to be very careful to sample blood. I also think that sequencing and analyzing the gut microbiota was quite a long and difficult step.

What were the main findings?
In this study, we find that propionate initiates a portal-brain neural communication. Furthermore, butyrate and propionate both induce intestinal glucose production, but through different complementary mechanisms. Using mice that are unable to produce glucose specifically in the intestine, we showed that intestinal gluconeogenesis provides a causal link for benefits of dietary fiber.

What are limitations?
This is a study on rodents, so of course they are a model that has some limits.

How your study could help clinicians in the future?
Intestinal gluconeogenesis has actually been described in humans so the mechanisms that take place in rodents are very likely to take place in humans too. I think this study could help clinicians to treat obese and diabetic patients with a dietary supplement in fiber. But probably the most important message would be to say that we can prevent this diseases by increasing our intake of dietary fiber.

Read the original post online at:
A modified *E. coli* strain reduces food intake and obesity in mice

In an article published online on June 24, 2014 in the Journal of Clinical Investigation, Zhongyi Chen and Lilu Guo, from the Vanderbilt University, Nashville, Tennessee, USA, showed that the administration of a modified bacteria expressing therapeutic factors in the gut microbiota could reduce food intake and obesity.

By adding an engineered NAPE-expressing *E. coli* Nissle 1917 strain in the drinking water of mice for 8 weeks, despite a high-fat diet, Zhongyi Chen and Lilu Guo demonstrated a reduction of the levels of obesity in mice.

Mice receiving the modified *E. coli* strain had lower food intake, adiposity, insulin resistance, and hepatosteatosis compared with mice receiving standard water or control bacteria. The protective effects persisted for at least 4 weeks after removal of the modified strain in drinking water.

Moreover, administration of NAPE-expressing bacteria to TallyHo mice, a polygenic mouse model of obesity, inhibited weight gain.

This study is a first step for the development of potential new treatments for obesity and other related diseases, based on the incorporation of appropriately modified bacteria into the gut microbiota.

* NAPE: N-acylphosphatidylethanolamine.

Source: *Incorporation of therapeutically modified bacteria into gut microbiota inhibits obesity* J Clin Invest. doi:10.1172/JCI72517.

Read the original selection online at: www.gutmicrobiotaforhealth.com/s/modified-e-coli-strain-reduce-food-intake-obesity-mice

Several probiotic strains reduce fatty liver disease in obese rats

This study, published in PLoS ONE, set out to document the effects of three probiotic strains on hepatic steatosis (fatty liver disease) in obese rats: *Lactobacillus paracasei* CNCM I-4034, *Bifidobacterium breve* CNCM I-4035 and *Lactobacillus rhamnosus* CNCM I-4036.

After 30 days, measures of triacylglycerols had decreased in rats that were fed *L. rhamnosus*, *B. breve*, or the mixture of *B. breve* and *L. paracasei*. The research showed that certain probiotic strains reduced fatty liver disease and had anti-inflammatory effects in obese rats.

Source: *PLoS ONE*


Read the original selection online at: www.gutmicrobiotaforhealth.com/s/several-probiotic-strains-reduced-fatty-liver-disease-obese-rats
Recommendations on probiotic and prebiotic treatments to improve nutritional status

Published in: PROBIOTICS  I  Written on July 23, 2014  by Kristina Campbell

This article is a collaboration of representatives from academia, medicine, and industry who came together at a workshop during the International Scientific Association for Probiotics and Prebiotics (ISAPP) held in Cork, Ireland in October, 2012. The goal of the workshop was to assess evidence on the link between the microbiome and under-nutrition, focusing specifically on probiotic and prebiotic treatments. Participants hoped to answer the question of whether probiotics and prebiotics can improve nutritional status in at-risk groups like children, pregnant women, the elderly, and individuals with disease-associated malnutrition.

The group came up with four recommendations for clinicians and researchers (presented verbatim below):

(1) The categories of malnourished individuals need to be differentiated.

To improve treatment outcomes, subjects should first be categorized based on the cause of malnutrition, additional health-concerns, differences in the gut microbiota, and sociological considerations.

(2) Define a baseline “healthy” gut microbiota for each category.

Altered nutrient requirement (for example, in pregnancy and old age) and individual variation may change what constitutes a healthy gut microbiota for the individual.

(3) Perform studies using model systems to test the effectiveness of potential probiotics and prebiotics against these specific categories.

These should illustrate how certain microbiota profiles can be altered, as members of different categories may respond differently to the same treatment.

(4) Perform robust well-designed human studies with probiotics and/or prebiotics, with appropriate, defined primary outcomes and sample size.

These are critical to show efficacy and understand responder and non-responder outcomes.

Source: Gut Microbes

Read the original selection online at: www.gutmicrobiotaforhealth.com/s/recommendations-probiotic-prebiotic-treatments-improve-nutritional-status

Microbiota modulate behavioral and physiological abnormalities associated with neurodevelopmental disorders

Published in: GUT BRAIN AXIS  I  Written on January 24, 2014  by Yohanan Winogradsky

[Abstract]

Neurodevelopmental disorders, including autism spectrum disorder (ASD), are defined by core behavioral impairments; however, subsets of individuals display a spectrum of gastrointestinal (GI) abnormalities. We demonstrate GI barrier defects and microbiota alterations in the maternal immune activation (MIA) mouse model that is known to display features of ASD. Oral treatment of MIA offspring with the human commensal Bacteroides fragilis corrects gut permeability, alters microbial composition, and ameliorates defects in communicative, stereotypic, anxiety-like and...
sensorimotor behaviors. MIA offspring display an altered serum metabolomic profile, and *B. fragilis* modulates levels of several metabolites. Treating naive mice with a metabolite that is increased by MIA and restored by *B. fragilis* causes certain behavioral abnormalities, suggesting that gut bacterial effects on the host metabolome impact behavior. Taken together, these findings support a gut-microbiome-brain connection in a mouse model of ASD and identify a potential probiotic therapy for GI and particular behavioral symptoms in human neurodevelopmental disorders.

Source: *Cell*


Read the original selection online at: www.gutmicrobiotaforhealth.com/s/microbiota-modulate-behavioral-and-physiological-abnormalities-associated-with-neurodevelopmental-disorders
In this section, we propose a listing of the 5 most popular tweets related to gut microbiota, diet and nutrition on our account Twitter.com/GMFHx.

1. **GutMicrobiota Health**
   - Now therapies in #colicadisease: Dr Elena Verdu reports the latest trends, including the possible role of #probiotics gutmicrobiotaforhealth.com/?p=5920
   - Retweets: 10, Favorites: 1
   - [Link](http://twitter.com/GMFHx/status/459255266761277440)

2. **GutMicrobiota Health**
   - "Gut Microbiota, Probiotics and Their Impact Throughout the Lifespan", a symposium to be held @harvardmed in Sept.
gutmicrobiotaforhealth.com/event/gut-micro...  
   - Retweets: 7, Favorites: 2
   - [Link](http://twitter.com/GMFHx/status/49377348190703370)

3. **GutMicrobiota Health**
   - Food intolerance and food digestion are two important factors in IBS #GMFH2014
   - Retweets: 7, Favorites: 1
   - [Link](http://twitter.com/GMFHx/status/4233281845907040)

4. **GutMicrobiota Health**
   - Gluten-free diet for pregnant mice changed their gut microbiota and reduced incidence of diabetes in their offspring: diabetes.journals.org/content/early/…
   - Retweets: 7
   - [Link](http://twitter.com/GMFH/status/470441043704293129)

5. **GutMicrobiota Health**
   - Danish study finds that babies establish their gut 'enterotype' between 9 and 36 months, depending on breastfeeding:
   - Retweets: 7
   - [Link](https://twitter.com/GMFH/status/46477755593045472)