Probiotics

Micronutrients, N-acetyl cysteine, probiotics and prebiotics, a review of effectiveness in reducing HIV progression.

Hummelen R¹, Hemsworth J, Reid G.

Abstract

Low serum concentrations of micronutrients, intestinal abnormalities, and an inflammatory state have been associated with HIV progression. These may be ameliorated by micronutrients, N-acetyl cysteine, probiotics, and prebiotics. This review aims to integrate the evidence from clinical trials of these interventions on the progression of HIV. Vitamin B, C, E, and folic acid have been shown to delay the progression of HIV. Supplementation with selenium, N-acetyl cysteine, probiotics, and prebiotics has considerable potential, but the evidence needs to be further substantiated. Vitamin A, iron, and zinc have been associated with adverse effects and caution is warranted for their use.

KEYWORDS:

AIDS, HIV, N-acetyl cysteine, micronutrients, prebiotics, probiotics, selenium, zinc

Supplemental Content

Altered host-microbe interaction in HIV: a target for intervention with pro- and prebiotics.

Hummelen R¹, Vos AP, van't Land B, van Norren K, Reid G.


Author information

Abstract

The intestinal immune system is severely affected by HIV and circulating microbial products from the intestinal tract that provide an ongoing source of systemic inflammation and concomitant viral replication. In addition, HIV-infected individuals can have a deregulated immune response that may hamper the anti-viral capacity of the host. Various probiotic organisms and prebiotic agents have been shown to enhance intestinal epithelial barrier functions, reduce inflammation, and support effective Th-1 responses. As these characteristics may benefit HIV patients, this review aims to provide a theoretical framework for the development of probiotic and prebiotic interventions specifically for this population.


Review

The gut microbiota shapes intestinal immune responses during health and disease

June L. Round & Sarkis K. Mazmanian

Abstract

Immunological dysregulation is the cause of many non-infectious human diseases such as autoimmunity, allergy and cancer. The gastrointestinal tract is the primary site of interaction between the host immune system and microorganisms, both symbiotic and pathogenic. In this Review we discuss findings indicating that developmental aspects of the adaptive immune system are influenced by bacterial colonization of the gut. We also highlight the molecular pathways that mediate host–symbiont interactions that regulate proper immune function. Finally, we present recent evidence to support that disturbances in the bacterial microbiota result in dysregulation of adaptive immune cells, and this may underlie disorders such as inflammatory bowel disease. This raises the possibility that the mammalian immune system, which seems to be designed to control microorganisms, is in fact controlled by microorganisms.


AIDS wasting syndrome as an enterometabolic disorder: the gut hypothesis.

Kaminski M Jr¹, Weil S, Bland J, Jan P.

Author information

Abstract

There is an interesting relationship between the HIV virus, the health of the gastrointestinal tract, and AIDS wasting syndrome, involving Tumor Necrosis Factor alpha (TNF alpha), specific and non-specific immunity in the gut, gut permeability, and oxidative stress. It is hypothesized that the progression of HIV to full-blown AIDS may be impacted by maintaining a healthy gut. A therapeutic protocol which decreases oxidative stress, inhibits TNF alpha, enhances phase I and II liver detoxification, and improves specific and non-specific immunity in the gut should be part of a therapeutic protocol for HIV-infected individuals. Through a better understanding of the pathophysiology of HIV advancing to AIDS, the practitioner can develop a treatment strategy of nutritional and lifestyle changes which could theoretically prevent an HIV infection from advancing to full-blown AIDS.

Supplemental Content


Moschen AR, Wieser V, Tilg H.

Source

Christian Doppler Research Laboratory for Gut Inflammation, Medical University of Innsbruck, Innsbruck, Austria.

Abstract
Dietary factors and the associated lifestyle play a major role in the pathophysiology of many diseases. Several diets, especially a Western lifestyle with a high consumption of meat and carbohydrates and a low consumption of vegetables, have been linked to common diseases, such as metabolic syndrome, atherosclerosis, inflammatory bowel diseases, and colon cancer. The gastrointestinal tract harbors a complex and yet mainly molecularly defined microbiota, which contains an enormous number of different species. Recent advances in sequencing technologies have allowed the characterization of the human microbiome and opened the possibility to study the effect of "environmental" factors on this microbiome. The most important environmental factor is probably "what we eat," and the initial studies have revealed fascinating results on the interaction of nutrients with our microbiota. Whereas short-term changes in dietary patterns may not have major influences, long-term diets can affect the microbiota in a substantial manner. This issue may potentially have major relevance for human gastrointestinal health and disease because our microbiota has features to regulate many immune and metabolic functions. Increasing our knowledge on the interaction between nutrients and microbiota may have tremendous consequences and result in a better understanding of diseases, even beyond the gastrointestinal tract, and finally lead to better preventive and therapeutic strategies.

Supplemental Content


Gut microbial flora, prebiotics, and probiotics in IBD: their current usage and utility.


Source

Department of Internal Medicine, Gastroenterology Division, Catholic University of Sacred Hearth, Policlinico "A. Gemelli" Hospital, lgo Gemelli 8, 00168 Roma, Italy.
francoscaldaferri@libero.it

Abstract

Inflammatory bowel diseases are chronic diseases affecting the gastrointestinal tract, whose major forms are represented by Crohn's disease (CD) and ulcerative colitis (UC). Their etiology is still unclear, although several factors have been identified as major determinants for induction or relapses. Among these, the role of the "forgotten organ", gut microbiota, has become more appreciated in recent years. The delicate symbiotic relationship between the gut microbiota and the host appears to be lost in IBD. In this perspective, several studies have been conducted to assess the role of prebiotics and probiotics in gut microbiota modulation. This is a minireview aimed to address in an easy format (simple questions-simple answers)
some common issues about the theme. An update on the role of selected constituents of gut microbiota in the pathogenesis of IBD is presented together with the analysis of the efficacy of gut microbiota modulation by prebiotics and probiotics administration in the management of IBD.

Supplemental Content

**Anti-inflammatory effects of resveratrol, curcumin and simvastatin in acute small intestinal inflammation.**


Source

Institut für Mikrobiologie und Hygiene, Charité-Universitätsmedizin Berlin, Berlin, Germany.

Abstract

**BACKGROUND:**

The health beneficial effects of Resveratrol, Curcumin and Simvastatin have been demonstrated in various experimental models of inflammation. We investigated the potential anti-inflammatory and immunomodulatory mechanisms of the above mentioned compounds in a murine model of hyper-acute Th1-type ileitis following peroral infection with Toxoplasma gondii.

**METHODOLOGY/PRINCIPAL FINDINGS:**

Here we show that after peroral administration of Resveratrol, Curcumin or Simvastatin, mice were protected from ileitis development and survived the acute phase of inflammation whereas all Placebo treated controls died. In particular, Resveratrol treatment resulted in longer-term survival. Resveratrol, Curcumin or Simvastatin treated animals displayed significantly increased numbers of regulatory T cells and augmented intestinal epithelial cell proliferation/regeneration in the ileum mucosa compared to placebo control animals. In contrast, mucosal T lymphocyte and neutrophilic granulocyte numbers in treated mice were reduced. In addition, levels of the anti-inflammatory cytokine IL-10 in ileum, mesenteric lymph nodes and spleen were increased whereas pro-inflammatory cytokine expression (IL-23p19, IFN-γ, TNF-α, IL-6, MCP-1) was found to be significantly lower in the ileum of treated animals as compared to Placebo controls. Furthermore, treated animals displayed not only fewer pro-inflammatory enterobacteria and enterococci but also higher anti-
inflammatory lactobacilli and bifidobacteria loads. Most importantly, treatment with all three compounds preserved intestinal barrier functions as indicated by reduced bacterial translocation rates into spleen, liver, kidney and blood.

CONCLUSION/SIGNIFICANCE:

Oral treatment with Resveratrol, Curcumin or Simvastatin ameliorates acute small intestinal inflammation by down-regulating Th1-type immune responses and prevents bacterial translocation by maintaining gut barrier function. These findings provide novel and potential prophylaxis and treatment options of patients with inflammatory bowel diseases.


Role of endogenous microbiota, probiotics and their biological products in human health.

Howarth GS, Wang H.

Source

School of Animal and Veterinary Sciences, The University of Adelaide, Roseworthy Campus, South Australia 5371, Australia. gordon.howarth@adelaide.edu.au

Abstract

Although gut diseases such as inflammatory bowel disease, mucositis and the alimentary cancers share similar pathogenetic features, further investigation is required into new treatment modalities. An imbalance in the gut microbiota, breached gut integrity, bacterial invasion, increased cell apoptosis to proliferation ratio, inflammation and impaired immunity may all contribute to their pathogenesis. Probiotics are defined as live bacteria, which when administered in sufficient amounts, exert beneficial effects to the gastrointestinal tract. More recently, probiotic-derived factors including proteins and other molecules released from living probiotics, have also been shown to exert beneficial properties. In this review we address the potential for probiotics, with an emphasis on probiotic-derived factors, to reduce the severity of digestive diseases and further discuss the known mechanisms by which probiotics and probiotic-derived factors exert their physiological effects.

Supplemental Content

Lactic acid bacteria contribution to gut microbiota complexity: lights and shadows.

Pessione E.

Source

Dipartimento di Scienze della Vita e Biologia dei sistemi - Life Sciences and Systems Biology, University of Torino Torino, Italy. enrica.pessione@unito.it

Abstract

Lactic Acid Bacteria (LAB) are ancient organisms that cannot biosynthesize functional cytochromes, and cannot get ATP from respiration. Besides sugar fermentation, they evolved electrogenic decarboxylations and ATP-forming deiminations. The right balance between sugar fermentation and decarboxylation/deimination ensures buffered environments thus enabling LAB to survive in human gastric trait and colonize gut. A complex molecular cross-talk between LAB and host exists. LAB moonlight proteins are made in response to gut stimuli and promote bacterial adhesion to mucosa and stimulate immune cells. Similarly, when LAB are present, human enterocytes activate specific gene expression of specific genes only. Furthermore, LAB antagonistic relationships with other microorganisms constitute the basis for their anti-infective role. Histamine and tyramine are LAB bioactive catabolites that act on the CNS, causing hypertension and allergies. Nevertheless, some LAB biosynthesize both gamma-amino-butyrate (GABA), that has relaxing effect on gut smooth muscles, and beta-phenylethylamine, that controls satiety and mood. Since LAB have reduced amino acid biosynthetic abilities, they developed a sophisticated proteolytic system, that is also involved in antihypertensive and opioid peptide generation from milk proteins. Short-chain fatty acids are glycolytic and phosphoketolase end-products, regulating epithelial cell proliferation and differentiation. Nevertheless, they constitute a supplementary energy source for the host, causing weight gain. Human metabolism can also be affected by anabolic LAB products such as conjugated linoleic acids (CLA). Some CLA isomers reduce cancer cell viability and ameliorate insulin resistance, while others lower the HDL/LDL ratio and modify eicosanoid production, with detrimental health effects. A further appreciated LAB feature is the ability to fix selenium into seleno-cysteine. Thus, opening interesting perspectives for their utilization as antioxidant nutraceutical vectors.

Supplemental Content

**Lactobacillus acidophilus, Bifidobacterium lactis and Lactobacillus F19 prevent antibiotic-associated ecological disturbances of Bacteroides fragilis in the intestine.**

Sullivan A, Barkholt L, Nord CE.

Source

Department of Laboratory Medicine, Huddinge University Hospital, Karolinska Institutet, SE-141 86 Stockholm, Sweden.

Abstract

**OBJECTIVE:**

The objective of this study was to compare the effect of clindamycin on the intestinal microflora in subjects ingesting yogurt with added probiotic microorganisms with the microflora in subjects ingesting placebo yogurt.

**MATERIALS AND METHODS:**

Twenty-four healthy subjects were included in the study. All subjects received 150 mg clindamycin four times daily for 7 days and 250 ml yogurt twice daily for 14 days. Faecal samples were collected before, during and after administration of clindamycin.

**RESULTS:**

In the aerobic intestinal microflora, the numbers of enterococci increased after treatment in both groups, whereas other Gram-positive microorganisms decreased. In both groups, the numbers of Escherichia coli also decreased, whereas there was a concomitant increase in numbers of other Gram-negative bacilli. In the anaerobic microflora in subjects receiving yogurt with added microorganisms, the numbers of lactobacilli and bacteroides remained at the same levels throughout the study, whereas the numbers decreased in the placebo group. Other anaerobic bacteria decreased in both groups. The minimum inhibitory concentration of clindamycin against strains of bacteroides increased in both groups during the study.

**CONCLUSIONS:**

The probiotic microorganisms evaluated in this study prevented ecological disturbances in the numbers of intestinal Bacteroides fragilis group species during clindamycin administration.

Supplemental Content
Microbiota restoration: natural and supplemented recovery of human microbial communities.

Reid G¹, Younes JA, Van der Mei HC, Gloor GB, Knight R, Busscher HJ.

Author information

Abstract

In a healthy host, a balance exists between members of the microbiota, such that potential pathogenic and non-pathogenic organisms can be found in apparent harmony. During infection, this balance can become disturbed, leading to often dramatic changes in the composition of the microbiota. For most bacterial infections, nonspecific antibiotics are used, killing the non-pathogenic members of the microbiota as well as the pathogens and leading to a substantial delay in the restoration of a healthy microbiota. However, in some cases, infections can self-resolve without the intervention of antibiotics. In this Review, we explore the mechanisms underlying microbiota restoration following insult (antibiotic or otherwise) to the skin, oral cavity, and gastrointestinal and urogenital tracts, highlighting recovery by natural processes and after probiotic administration.

Supplemental Content

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The effects of commensal bacteria on innate immune responses in the female genital tract.


Source
Department of Immunology/Microbiology, Rush University Medical Center, Chicago, IL 60612, USA.

Abstract

The innate and adaptive immune systems are important mechanisms for resistance to pathogens in the female lower genital tract. Lactobacilli at this site help maintain a healthy vagina by producing several factors including lactic acid. Indeed, bacterial vaginosis, a condition in which the genital microbiota is altered, is strongly associated with increased rates of a number of infections including HIV. However, the precise factors that contribute to increased rates of microbial and viral infections in bacterial vaginosis remain to be elucidated. We have studied the effects of bacterial microbiota in the lower genital tract on innate immunity and have found that Toll-like receptor ligands and short chain fatty acids, produced by bacterial microbiota, have dramatic effects on immune function. In this review, we will discuss these results, in addition to some recent articles that we believe will enhance our understanding of how microbes might interact with the immune system.

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Supplemental Content


The restoration of the vaginal microbiota after treatment for bacterial vaginosis with metronidazole or probiotics.


Source

State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, the First Affiliated Hospital, College of Medicine, Zhejiang University, Hangzhou, Zhejiang, China. lingzongxin_lzx@163.com

Abstract

Whether or not treatment with antibiotics or probiotics for bacterial vaginosis (BV) is associated with a change in the diversity of vaginal microbiota in women was investigated. One hundred fifteen women, consisting of 30 healthy subjects, 30 BV-positive control
subjects, 30 subjects with BV treated with a 7-day metronidazole regimen, and 25 subjects with BV treated with a 10-day probiotics regimen, were analyzed to determine the efficacy and disparity of diversity and richness of vaginal microbiota using 454 pyrosequencing. Follow-up visits at days 5 and 30 showed a greater BV cure rate in the probiotics-treated subjects (88.0 and 96 %, respectively) compared to the metronidazole-treated subjects (83.3 and 70 %, respectively \( p = 0.625 \text{ at day 5 and } p = 0.013 \text{ at day 30} \)). Treatment with metronidazole reduced the taxa diversity and eradicated most of the BV-associated phylotypes, while probiotics only suppressed the overgrowth and re-established vaginal homeostasis gradually and steadily. Despite significant interindividual variation, the microbiota of the actively treated groups or participants constituted a unique profile. Along with the decrease in pathogenic bacteria, such as Gardnerella, Atopobium, Prevotella, Megasphaera, Coriobacteriaceae, Lachnospiraceae, Mycoplasma, and Sneathia, a Lactobacillus-dominated vaginal microbiota was recovered. Acting as vaginal sentinels and biomarkers, the relative abundance of Lactobacillus and pathogenic bacteria determined the consistency of the BV clinical and microbiologic cure rates, as well as recurrent BV. Both 7-day intravaginal metronidazole and 10-day intravaginal probiotics have good efficacy against BV, while probiotics maintained normal vaginal microbiota longer due to effective and steady vaginal microbiota restoration, which provide new insights into BV treatment.

**Supplemental Content**

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