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Tissue metabolism and host-microbial interactions in the intestinal mucosa

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Abstract

In recent years, studies in the gastrointestinal (GI) mucosa have taught us a number of important lessons related to tissue oxygenation and metabolism in health and disease. The highly vascularized mucosa lies immediately adjacent to an anaerobic lumen containing trillions of metabolically active microbes (i.e. the microbiome) that results in one of the more austere tissue microenvironments in the body. These studies have also implicated a prominent role for oxygen metabolism and hypoxia in inflammation, so called “inflammatory hypoxia”, that results from the activation of multiple oxygen consuming enzymes. Inflammation-associated shifts in the composition of the microbiome and microbial-derived metabolites have revealed a prominent role for the transcription factor hypoxia-inducible factor (HIF) in the regulation of key target genes that promote inflammatory resolution. Analyses of these pathways have provided a multitude of opportunities for understanding basic mechanisms of both homeostasis and disease and have defined new targets for intervention. Here, we review recent advances in our understanding of metabolic influences on host-microbe interactions in the GI mucosa.

Keywords

Metabolism; Inflammation; Microbiota; Short chain fatty acid; Mucosa; Colitis; Epithelium; Murine model

1. Introduction

Recent investigations of the metabolic demands placed on the mucosa during homeostasis and disease have provided important insights into the biochemical pathways employed during host-microbe interactions. At the center of these metabolic pathways is molecular oxygen utilization. The gastrointestinal (GI) tract, for instance, is characterized by a particularly unique oxygenation profile, experiencing regular intervals of profound blood flow fluctuations [1]. Even at baseline, epithelial cells lining the mucosa exist at a relatively low oxygen tension environment, herein described as ‘physiologic hypoxia’. Countercurrent oxygen exchange mechanisms in the small intestine have revealed that oxygen from arterial

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blood supply diffuses to adjacent venules, along the crypt villus axis, resulting in graded hypoxia [2]. A steep oxygen gradient has also been documented in distal, colonic regions of the GI tract, spanning from the anaerobic lumen, across the epithelium to the richly vascularized sub-epithelial mucosa [3]. Given the high-energy requirement of the gut and the integral role of the epithelium in maintaining intestinal homeostasis, it is not surprising that these cells have evolved a number of mechanisms to cope with this austere metabolic environment [4]. Here, we will discuss how such metabolic shifts are regulated, particularly as they relate to host-microbe interactions.

2. Oxygen metabolism in healthy and inflamed tissues

The oxygenation profile of the healthy mucosa is an area of significant interest. A comparison of the lung and intestine, for example, provides a number of stark contrasts. Breathable air at sea level contains a partial O₂ pressure (pO₂) of ~145 mmHg (approximately 21% O₂). Measurements of the healthy lung alveolus have revealed a pO₂ of 100–110 mmHg [5]. Conversely, the most luminal aspect of the healthy colon exists at a pO₂ of less than 10 mmHg [3,6]. This difference is attributed primarily to the source of O₂, active local metabolism and the anatomy of blood flow [4].

Tissue oxygenation, particularly at low O₂, has been tracked using 2-nitroimidazole dyes, a class of compounds known to undergo intracellular metabolism dependent on the level of tissue oxygenation [7]. These dyes were originally developed to image the low O₂ environment of growing tumors [8] and have subsequently been used as tools to monitor levels of tissue oxygenation. Nitroimidazoles form adducts with thiol groups in proteins, peptides and amino acids where all atoms of the ring and side-chain of the 2-nitroimidazole are retained at pO₂ < 10 mmHg. Intestinal mucosal localization of these nitroimidazole dyes has revealed two striking observations. First, in the normal GI mucosa, particularly in the colon, “physiologic hypoxia” predominates [6]. Recent studies have shown that these low O₂ conditions are critical for the constitutive expression of certain innate immune factors found within the mucosa (e.g. human β defensin-1) [9]. Second, inflammatory lesions within the mucosa are profoundly hypoxic or even anoxic, similar to that seen in some tumors [4]. It is likely that there are multiple contributing factors, i.e. vasculitis, vasoconstriction, edema, increased O₂ consumption, predisposing the inflamed intestinal epithelia to decreased oxygen delivery and hypoxia [6]. These nitroimidazole compounds have shown significant clinical utility in tumor imaging and in the identification of stroke regions within the brain of patients [10]. As opposed to other imaging techniques, these molecules have the advantage that they image only viable tissue, are independent of oxygen radical accumulation and are not active in apoptotic/necrotic tissue [11].

Given the substantial shifts in metabolism and oxygen availability during inflammation, a number of studies have shown that stabilization of transcription factor hypoxia-inducible factor (HIF) in low oxygen environments triggers the expression of genes that are essential to epithelial barrier function [12–15]. Additionally, HIF is one of the central regulators of overall tissue metabolism [16] and has profound influences on the inflammatory response [4]. Its activity is dependent on stabilization of an O₂-dependent degradation (ODD) domain expressed on the α -subunit and subsequent nuclear translocation to form a functional

complex with HIF-1 β [17]. In normally oxygenated tissues, iron, alpha-ketoglutarate and O₂-dependent hydroxylation of two prolines (Pro564 and Pro402 of HIF-1 α) within the ODD of the alpha subunit initiates the association with the von Hippel-Lindau tumor suppressor protein (pVHL) and rapid degradation via ubiquitin-E3 ligase proteasomal targeting [18,19].

Intestinal epithelial cells express both HIF-1 α and HIF-2 α [20] and genetic studies in mice indicate that these proteins have non-redundant roles [21]. It has been suggested that distinct transcriptional responses mediated by HIF-1 α and HIF-2 α may have evolved as particular adaptations to hypoxia. For example, the transcriptional responses that coordinate metabolic adaptation through glycolytic pathways are selective for the HIF-1 α over the HIF-2 α isoform [22]. Conversely, studies addressing selectivity of the two isoforms for increased perfusion and oxygen carrying capacity (e.g. erythropoietin induction) have indicated a more prominent role for HIF-2 α [23]. Iron absorption through intestinal epithelial cells also appears to be selective for HIF-2 α [24]. While this specificity for individual gene regulation is not well understood, some evidence has shown that binding of HIF-1 α or HIF-2 α to gene promoters is dependent on interactions with STAT3 and USF2, respectively [25].

The spectrum of basal oxygenation within individual tissues is immense. Given the steep oxygen gradient due to countercurrent blood flow, colonic epithelia exist at very low pO₂ [26]. These cells have proven to be remarkably resistant to hypoxia, where even very low levels of oxygenation allow these cells to function normally [27,28]. The importance of HIF to epithelial function was originally shown by microarray analysis of intestinal epithelial cells cultured in low O₂ conditions (pO₂ ~20 mmHg) [12]. These studies were subsequently validated in murine models of colitis [6,29–33] and in diseased human tissues [34–36]. Notably, the cluster of functional proteins regulated by HIF localizes prominently to the most luminal aspect of polarized epithelia and is composed of proteins important for increased mucin production, [37] molecules that modify mucin function [38], antimicrobial defense [9], barrier function [39], xenobiotic clearance [13] and nucleotide metabolism/signaling (by ecto-5'-nucleotidase and CD73) [14,15] (see Fig. 1). Molecular studies of these hypoxia-regulated pathway(s) have shown a dependence on HIF-mediated transcriptional responses. Original studies by Karhausen, et al. generated mice expressing either mutant Hif-1 α (causing constitutive repression of *Hif-1 α*) or mutant von Hippel-Lindau (causing constitutive over-expression of HIF) targeted to the intestinal epithelial cells revealed a more severe colitic phenotype in which increased intestinal permeability was a prominent feature [6]. These findings were somewhat model-dependent, since epithelial HIF-based signaling has also been shown to promote inflammation in another study [33]. Further examination of these pathways revealed that active colonic inflammation, defined by the influx of large numbers of neutrophils, depleted local oxygen levels sufficient enough to stabilize intestinal epithelial cell HIF and imprinted a transcriptional phenotype that strongly reflected HIF stabilization [40]. This phenotype was dependent on neutrophil NADPH oxidase implicated epithelial HIF stabilization in goblet cell differentiation and the production of mucins and mucin-binding elements, which has been suggested by other studies in the colon [12,37]. Overall, these findings confirm that intestinal epithelial cells can adapt to hypoxia and that HIF may play a key role in such an adaptation.

3. Host-microbial metabolism and tissue hypoxia

The gastrointestinal tract of mammals is host to trillions of bacteria. This finely tuned host-microbe relationship exists on the surface of the intestinal mucosa, where microbes are essential for host health, but can also initiate and perpetuate disease [41]. These microbes, in addition to aiding in digestion, produce a number of vitamins and benefit the host through the local synthesis of short-chain fatty acids (SCFAs), including butyrate, propionate, and acetate.

SCFAs are end products of bacterial fermentation, primarily derived from resistant starches, dietary fibers and undigested proteins [42]. Anaerobic bacteria in the colon, particularly members of the Phyla *Firmicutes* [43], produce butyrate through the conversion of microbial acetyl-CoA to the butyryl-CoA via β -oxidation of fatty acids. The final conversion from butyryl-CoA to butyrate is either catalyzed by butyryl-CoA: acetate CoA transferase or butyrate kinase. Due the presence of highly conserved regions these enzymes can be used for the identification of butyrate-producing bacterial communities in molecular analyses [44–46]. Amino acids can also serve as a substrate for SCFA production. Acetate can be produced through microbial metabolism of several amino acids, including glycine, alanine, threonine, glutamate, lysine and aspartate [42]. Propionate can be synthesized from alanine and threonine and butyrate from lysine and glutamate. Acetate and propionate are utilized primarily by muscle and liver cells, respectively [42], whereas butyrate is the primary metabolic substrate for colonocytes (see below).

The majority of both human and mouse microbiota is composed of members of the *Firmicutes* and *Bacteroidetes* phyla [47]. In IBD, there is an overall decrease in microbial diversity, including decreased abundance of these major phyla. The majority of butyrate in the colon is derived from Clostridial clusters IV, XIVa, and XVIII, members of the *Firmicutes* phylum. Laser capture microdissection experiments demonstrated an enrichment of *Firmicutes* in the inter-fold regions of the colon when compared to the luminal microbiome population [48].

Potentially related to its biogeographic position in the colon, butyrate is efficiently absorbed and metabolized by the epithelium and very little butyrate is released into portal circulation [49]. Butyrate generates energy by stimulating expression of pyruvate dehydrogenase kinase, which in turn inhibits the pyruvate dehydrogenase complex [50] (see Fig. 1). This inhibition prevents conversion of glucose-derived pyruvate to acetyl-CoA effectively shifting colonocyte metabolism to butyrate from glucose. In addition, it has been suggested that the function of butyrate is dependent on its concentration and location. Butyrate is selectively taken up by the colonocytes (through several transporters including SMCT1 and MCT1) and provides the epithelium with up to 70% of their energy. Other SCFA such as acetate and propionate are primarily transported to muscle and liver, respectively [51]. High concentrations of butyrate are found in the lumen of the colon and may exist at levels exceeding 30 mM [49]. Butyrate concentrations that exceed the metabolic capacity of the cell (~0.5 mM) enter the nucleus to act as an HDAC inhibitor, effectively inhibiting proliferation and inducing apoptosis in colonocytes. In this role, butyrate may promote colonocyte turnover through homeostatic mechanisms [51]. Most cancer cells use glucose as

their primary energy source, termed the Warburg effect. Studies comparing the effects of butyrate on normal colonocytes and cancerous colonocytes suggest that butyrate has the capability of exhibiting a differential influence on cells depending on concentration and the metabolic state of the cell. In this report, butyrate stimulated the proliferation of normal colonic epithelia but inhibited cell growth of colorectal cancer cells [52]. This variable function of butyrate is referred to as the “butyrate paradox” and is thought to be, at least in part, related to epigenetic changes exerted by butyrate. A study from 2011 found that butyrate oxidation in UC was significantly lower than controls but, interestingly, saturation of butyrate kinetics was achieved from 1 mM in both UC and control subjects and replacement of butyrate to higher levels does not restore metabolism ([53]). Interestingly, as in cancer cells, actively inflamed colonic epithelia were found to have impaired butyrate oxidation.

Butyrate may exert additional influences on cell growth through the promotion of physiologic hypoxia. Kelly et al., recently demonstrated that butyrate increases epithelial O₂ consumption depleting local O₂ to levels of hypoxia that stabilize HIF [54,55]. In vivo, these same studies revealed that depletion of the microbiota using antibiotics reduced colonic butyrate and HIF expression, both of which were restored by butyrate supplementation. Moreover, the barrier protection afforded by butyrate was not appreciated in cells lacking HIF, suggesting that butyrate provides barrier protection in a HIF-dependent manner. These results reveal that the butyrate-HIF axis is a novel pathway in butyrate driven host-microbe interactions (Fig. 1).

Analysis of germ-free (GF) mice has revealed nearly no retention of O₂-sensitive dyes and significantly decreased HIF stabilization at baseline [57]. Work by Donohoe et al. [58], demonstrated that colonocytes from GF mice are significantly energy deprived, with markedly diminished levels of ATP and NADH/NAD⁺ in addition to decreased capacity for oxidative phosphorylation. Such metabolic deficits were shown to activate AMP kinase and profoundly increase epithelial autophagy, in which cytoplasmic targets are engulfed by a double-membrane vacuole termed the autophagosome which fuses with lysosomes and undergoes hydrolase-mediated digestion. There is much interest in understanding autophagy in the intestine, as variants in several genes involved in the autophagy pathway have emerged as risk alleles for inflammatory bowel disease (IBD), including autophagy-related 16 like 1 (*ATG16L1*) [59,60] and immunity-related GTPase family M (*IRGM*) [61,62].

The metabolic abnormalities associated with GF mice were shown to be proportional to decreased levels of butyrate. The addition of butyrate or butyrate-producing microbes rescued these defects in autophagy and tissue energetics, including the deficits in oxidative phosphorylation [58]. These same studies showed that the protection afforded by butyrate occurred through the provision of energy and not through its function as an HDAC inhibitor.

The hypoxic microenvironment can be shaped as well as perturbed by the microbiome. A recent study by Rivera-Chavez et al. [63] revealed that aerobic respiration enzymes encoded within the bacterial genome might prove beneficial for the expansion of *Salmonella*, particularly in conditions where anaerobes become depleted (e.g. following antibiotic use). These studies employed *Salmonella enterica* subsp. *Typhimurium* (*S. Typhimurium*) mutants

lacking functional cytochrome *bd* subunits and examined competitive fitness advantages in vitro and in vivo. Results from these studies revealed that mice depleted of major anaerobic microorganisms (especially *Clostridia*) generate a more aerobic luminal environment that allows for the expansion of aerobic *S. Typhimurium*. These experiments revealed that the lack of cytochrome *bd* oxidase resulted in a growth disadvantage for *S. Typhimurium* that manifested only in antibiotic-treated animals. Further analysis revealed that cytochrome *bd* oxidase synergizes with nitrate reductases to drive post-antibiotic *S. Typhimurium* expansion and recovery of targeted *S. Typhimurium* nitrate respiration mutants were nearly 10-fold less than wild-type *S. Typhimurium* following antibiotic-mediated depletion of anaerobes. This same group recently demonstrated that the elevation of inducible nitric oxide synthase (iNOS) associated with post-antibiotic treatment results in the selective oxidation of certain monosaccharides by the host, namely galactose and glucose, and provides a fitness advantage for expansion of *S. Typhimurium* [64]. Finally, it is notable that inflammation-associated luminal expansion of select members of the microbiota can also include facultative anaerobes. It has been shown, for example, that some Enterobacteriaceae selectively expand through the local generation of electron acceptors that can be used for anaerobic respiration (esp. nitrate) [65,66]. Conditions associated with ongoing inflammation (i.e. inflammatory hypoxia) provide the ideal environment to promote the localized generation of reactive oxygen and nitrogen-containing electron acceptors.

4. Microbial metabolism in mucosal inflammation

Surprisingly little is known about the influence of tissue metabolism on the expansion and retraction of specific components of the gut microbiome. There is increasing evidence that the pathogenesis of IBD is largely influenced by an intestinal dysbiosis and perturbation of the microbial population, though it remains unclear whether such dysbiosis is a cause or consequence of the inflammation associated with IBD [67]. It is clear, however, that the host immune system exists in close proximity to the microbiome and is capable of detecting and responding to components of its constituents from microbial-associated molecular patterns (MAMPs) to bacterial metabolites, such as SCFAs.

There is increasing evidence supporting a homeostatic role for SCFA in colonic inflammation in both strengthening the intestinal barrier and promoting healing of colitis [49,68]. The protection afforded by high fiber diets in experimental colitis are thought to be dependent on SCFA production, particularly butyrate [69–71]. In support of these data, administration of exogenous butyrate in the form of the triacylglyceride tributyrin has been shown to promote resistance to antibiotic-mediated damage in experimental colitis models [71,72]. Furthermore, pharmacologic inhibition of β -oxidation of fatty acids, thus butyrate production, by sodium 2-bromo-octanoate induces colitis similar to ulcerative colitis (UC) [74].

Ulcerative colitis, a form of IBD, has been described as an energy deficient disease. Two genes associated with the development of UC, SLC22A5 (OCTN2) and uncoupling protein 2 (UCP2) are critical components of mitochondrial energy metabolism and are required for intestinal barrier function [75]. Interestingly, conplastic mice with mitochondrial polymorphisms resulting in increased intracellular ATP production were found to be

resistant to chemically-induced colitis likely secondary to a corresponding increased rate of enterocyte proliferation allowing for epithelial repair [75]. Kaiko et al. recently demonstrated that butyrate was a potent inhibitor of intestinal stem cell proliferation through a Foxo3-dependent mechanism and due to intestinal crypt architecture these cells are not exposed to this microbial metabolite except in the setting of damage or colitis, potentially impeding the necessary regeneration required for epithelial repair [76]. Alternatively, these latter studies could implicate the intestinal crypt as a metabolic sensor of energy availability through SCFA.

SCFAs also regulate blood flow in the colon by stimulating perfusion. Mortensen et al. utilized resected colonic segments and determined that SCFA produced dose-dependent vasodilation at concentrations as low as 3 mM [77]. Furthermore, SCFA have been shown to promote post-surgical healing in the human rectum by increasing mucosal blood flow following 10–14 days of SCFA instillation [78]. The concentration of SCFA that colonic vessels are exposed to in vivo is not clear, but SCFA are present in high levels within the healthy intestinal lumen. In the setting of chronic, long-standing inflammation, there is diminished mucosal perfusion and impaired wound healing. In contrast, acute inflammation is characterized by tissue hyperemia resulting from dilation of small vessels [79]. While SCFA stimulates colonic blood flow, the role of low SCFA in diminished blood flow and oxygenation in chronic gut inflammation has not been studied in detail but could represent a possible mechanism to explain this phenomenon.

As in rodent models, there is mounting evidence connecting intestinal dysbiosis to the development of IBD in humans. While monozygotic twin concordance studies suggest a greater environmental component to the development of ulcerative colitis compared to Crohn's disease, germ-free studies in experimental colitis models strongly suggest that the development of IBD is not purely genetic but requires bacterial colonization. For example, diversion colitis develops after surgery resulting in exclusion of fecal material, the microbiome and its metabolites, from a portion of the colon. This condition is treated most effectively with SCFA enemas. To this point, multiple studies have revealed lower concentrations of luminal butyrate and reduced abundance of butyrate-producing organisms (e.g., certain *Roseburia* and *Faecalibacterium* genera) in patients with inflammatory bowel disease [80–82]. This is further supported by data demonstrating that increasing fecal butyrate levels decreases intestinal inflammation and symptoms in ulcerative colitis patients [83]. A recent meta-analysis of 25 studies of patients with UC was notable for a 65% clinical response rate to fecal microbiota transplant (FMT) with a corresponding increase in microbial diversity including an increase in key butyrate producers, *Firmicutes* and *Clostridium clusters IV, XIVa, XVIII* [84].

The intestinal microbiota shifts have a profound impact on colonic inflammation, however it remains unclear if inflammation or dysbiosis is the primary driver of colitis [85]. Several lines of evidence support an important role for host-microbe interactions in the regulation of intestinal barrier function. Perturbations in microbial metabolism and epithelial autophagy disrupt multiple aspects of barrier function. Recent studies, for example, defined a central role for autophagy in colonic goblet cell mucus secretion. Conditional epithelial knockout studies of *Atg5*, *Atg7* and *Lc3b* in mice revealed that autophagy is required for efficient

mucin granule accumulation and secretion from goblet cells [86]. Interestingly, this work implicates NADPH oxidase-derived ROS at the autophagosome-endosome interface as critical mediators of mucus secretion. Likewise, butyrate has been shown to enhance epithelial barrier function and selectively induce the tight junction protein claudin-1 through a mechanism involving the transcription factor Sp1 [87]. A so-called “tight claudin,” claudin-1 plays an integral role in determining barrier function in IECs [56]. Given the association between butyrate levels and HIF stabilization [57], our own studies have revealed that HIF is an important regulator of claudin-1 [39]. These studies showed that cells lacking HIF harbored a number of barrier defects. Global HIF-1 α chromatin immunoprecipitation (ChIP) analysis identified claudin-1 as a prominent HIF target gene and overexpression of CLDN1 in HIF-deficient cells resulted in resolution of morphological abnormalities and restoration of barrier function. It is noteworthy that claudin-1 was not hypoxia-inducible *per se*, rather, this gene appears to be regulated basally by mechanisms involving constitutive HIF stabilization (i.e. physiologic hypoxia) [9]. While not completely clear at present, it is intriguing to speculate that such physiologic hypoxia could be proportional to luminal butyrate levels, thereby providing an important host-microbial crosstalk critical for fundamental tissue functions such as barrier.

It has been shown that microbial signals, such as those delivered by a mix of *Clostridial* species, specifically members of cluster IV, XIVa and XVIII, induce mucosal tolerance and healing by enhancing regulatory T cells expansion and differentiation (Fig. 2). The IL-23/Th17/IL17 pathway is important in the regulation of IBD; pro-inflammatory Th17 is increased in mucosa and serum of IBD patients. Butyrate is a major product of tolerogenic *Clostridial* species [88]. Butyrate administration has been shown to increase blood Treg and levels of anti-Th17 cytokines (IL-10 and IL-12) while also suppressing IL-17 levels ([89,90] (see Fig. 2). Furthermore, butyrate is shown to enhance histone H3 acetylation in the promoter and conserved non-coding regions of the Foxp3 locus, which provides a mechanism for butyrate’s regulation of Treg differentiation [89]. Under such conditions, butyrate differentiated T cells attenuated colitis induced by adoptive transfer of CD4+ CD45RBhi T cells in Rag1 $^{-/-}$ mice [89]. In addition to functioning as a direct energy source, SCFAs can signal through a series of G-protein coupled receptors (GPR) to mediate their biological functions [91,92]. In mice, deletion of *Gpr41* and *Gpr43* mediate protective immunity in inflammatory models [91,92]. Also notable is the observation that treatment of mice with propionate promotes colonic protection during inflammation [92] and that the butyrate receptor (GPR109a) functions to suppress colonic inflammation [93].

5. Conclusions

In the past decade, much work has been accomplished unraveling the host-microbe interactions on the intestinal mucosa however further work is required to deepen this understanding. Of particular interest are the unique locales in which these interactions occur within the length of GI tract: juxtaposed between a microbial-rich anaerobic lumen and the highly vascularized submucosa. The epithelium has evolved and adapted to this “physiologic hypoxia” through the stabilization of HIF. Recently, microbial-derived SCFA butyrate has been discovered to stabilize epithelial HIF and enhance intestinal barrier function through a HIF mechanism. Further, butyrate has also been implicated as a key player in the expansion

and differentiation of Tregs by acting as a HDAC inhibitor and suppressing colonic inflammation by binding to surface GPCR's (e.g. GPR109a). Ongoing studies to better understand the host-microbial crosstalk are becoming increasingly recognized as important to health and disease. Knowledge from these pathways may provide new avenues for the treatment of intestinal disease, such as IBD.

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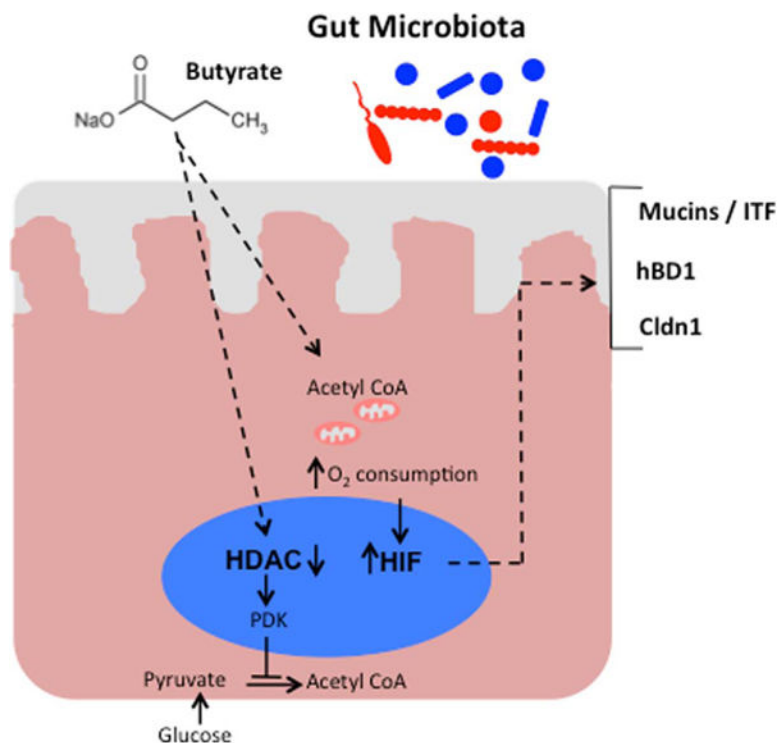


Fig. 1. Preferential oxidation of butyrate by intestinal epithelium stabilizes HIF and contributes to barrier function

Microbiota-derived butyrate is absorbed apically and acts to inhibit histone deacetylation. One consequence is increased expression of pyruvate dehydrogenase kinase (PDK), which inactivates pyruvate dehydrogenase. This precludes oxidative metabolism of pyruvate, allowing for the majority of acetyl CoA that is used for oxidative metabolism to be derived from β -oxidation of butyrate. Oxidative respiration leads to increased oxygen consumption, stabilization of HIF, and expression of HIF target genes important in barrier regulation (Muc3/ITF, hBD1, Cldn1).

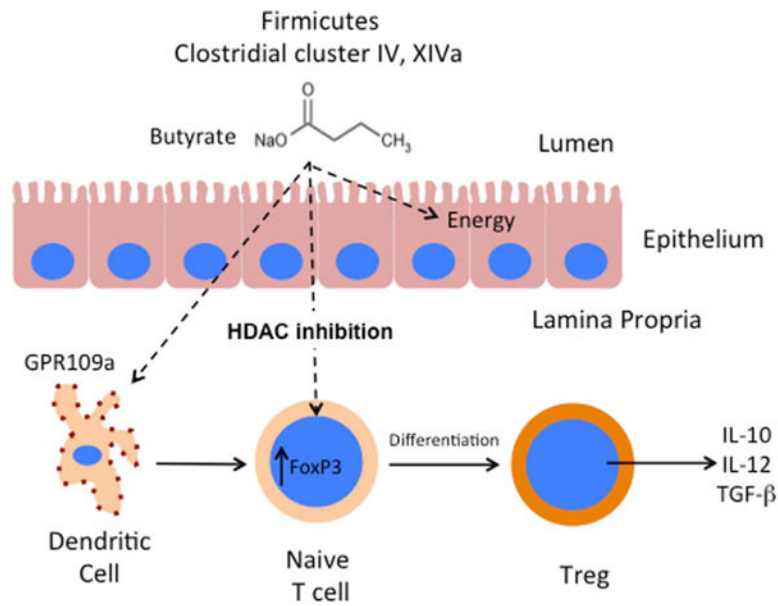


Fig. 2. Microbial-derived butyrate enhances regulatory T cell (Treg) expansion and differentiation to promote mucosal tolerance and healing. Butyrate produced from the metabolism of undigested carbohydrates by Firmicutes and Clostridial cluster IV and XIVa are selectively taken up by the colonic epithelium and serves as the primary energy source (~70% of total energy) for healthy epithelial cells. Further, small quantities of butyrate cross the epithelium to bind GPR109a on dendritic cells (DC) and induce Treg generation via HDAC inhibition. Butyrate treatment enhances acetylation at histone H3 lysine 27 (H3K27) at the Foxp3 promoter leading to Foxp3 induction and promotes the conversion of naïve CD4⁺T cells to Tregs. This action of butyrate in the mucosa results in increased expression of immunosuppressive cytokines within the lamina propria.