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Regulation of Bacterial Pathogenesis by Intestinal Short-Chain Fatty Acids

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Abstract

The human gut microbiota is inextricably linked to health and disease. One important function of the commensal organisms living in the intestine is to provide colonization resistance against invading enteric pathogens. Because of the complex nature of the interaction between the microbiota and its host, multiple mechanisms likely contribute to resistance. In this review, we dissect the biological role of short-chain fatty acids (SCFA), which are fermentation end products of the intestinal microbiota, in host–pathogen interactions. SCFA exert an extensive influence on host physiology through nutritional, regulatory, and immunomodulatory functions and can also affect bacterial fitness as a form of acid stress. Moreover, SCFA act as a signal for virulence gene regulation in common enteric pathogens. Taken together, these studies highlight the importance of the chemical environment where the biology of the host, the microbiota, and the pathogen intersects, which provides a basis for designing effective infection prevention and control.

1. INTRODUCTION

1.1. Microbiota and colonization resistance

The human intestine is populated by a diverse collection of microorganisms, the composition of which is a key determinant in human health and disease. However, the complex nature of the interactions between microbial cells and their host presents challenges in elucidating the contribution of the microbiota to health or the causal relationship between the microbiota and disease. Evidence supports a role for “healthy” microbiota in protecting individuals from colonization and infection by enteric pathogens, a phenomenon commonly referred to as “colonization resistance” (Lawley & Walker, 2013). This is best illustrated with the observation that oral antibiotic usage, which disrupts the intestinal microbiota, often increases the risk of *Clostridium difficile* infection, a common hospital-acquired nosocomial infection with severe sequelae. There are likely multiple mechanisms that contribute to colonization resistance. One major resistance mechanism derives from the gut microbiota closely interacting with the host mucosal surface, the epithelium, and the immune system to modulate host responses against colonization of pathogens (Duerkop, Vaishnav, & Hooper, 2009; Hooper, Midtvedt, & Gordon, 2002; Kau, Ahern, Griffin, Goodman, & Gordon, 2011; Littman & Pamer, 2011).

The microbiota itself poses a significant barrier to foreign bacterial pathogens through niche and nutrient competition and bacteriocin production—two examples of resistance mechanisms. The colonizing microorganisms in the gut are well adapted to host physical and nutritional constraints and therefore can outcompete invading pathogens. This mechanism has been clearly demonstrated for infection by *Escherichia coli* or *C. difficile*, where colonization of nonpathogenic strains can successfully prevent subsequent challenge of pathogenic strains (Chang et al., 2004; Leatham et al., 2009; Merrigan, Sambol, Johnson, & Gerding, 2003; Sambol, Merrigan, Tang, Johnson, & Gerding, 2002). In addition, many bacteria also produce peptides with anti-microbial functions or “bacteriocins,” that can target and kill invading pathogens. Numerous reports have confirmed the antimicrobial activity of purified bacteriocins *in vitro*, and evidence for successful prevention of pathogen colonization *in vivo* is increasing (Corr et al., 2007; Cursino et al., 2006; Millette et al., 2008; Schamberger & Diez-Gonzalez, 2004). These studies support the feasibility of using live bacteriocin-producing organisms as probiotics for consumption to protect individuals against infection by enteric pathogens and to promote overall intestinal health (Corr, Hill, & Gahan, 2009; Dobson, Cotter, Ross, & Hill, 2012; Ross, Mills, Hill, Fitzgerald, & Stanton, 2010).

1.2. Intestinal SCFA production

The metabolic activity of the human gut microbiota defines the chemical environment in the intestinal lumen (Hooper et al., 2002). Nondigestible carbohydrates are broken down and oxidized incompletely in the anaerobic lumen by the intestinal microbiota releasing short-chain fatty acids (SCFA) as fermentation byproducts. SCFA can be formed through multiple pathways by the concerted effort of different members of the microbiota as depicted in the simplified schematic shown in Fig. 3.1. In general, *Bacteroidetes* represent the primary fermenters that will transform simple sugars derived from breakdown of complex carbohydrates to organic acids including SCFA and hydrogen. Secondary fermenters such as *Clostridium* species and butyrate-producing bacteria further utilize the organic acids to generate additional SCFA. Moreover, acetogens (Rey et al., 2010) can deplete the hydrogen as an energy source and contribute to the pool of acetate, the dominant component of intestinal SCFA.

The other two major constituents of intestinal SCFA are butyrate and propionate. After the formation of butyryl-CoA from condensation of acetyl-CoA, two different pathways have been proposed for the final step of butyrate production. In the first scenario exemplified by *Clostridium acetobutylicum* (Hartmanis & Gatenbeck, 1984), butyryl-CoA is converted to butyrate through the intermediate butyryl-phosphate by two separate enzymes, butyrate kinase and phosphotransbutyrylase. An alternative butyrate-producing pathway involves the butyryl-CoA:acetate-CoA transferase, which catalyzes the transfer of coenzyme A between acetate and butyrate (Duncan, Barcenilla, Stewart, Pryde, & Flint, 2002). An *in vitro* survey of 38 butyrate-producing intestinal isolates using degenerate PCR and enzymatic assays suggests the latter pathway as the major source of butyrate in the intestines (Louis et al., 2004). Finally, propionate can be formed through carbon fixation reactions from succinyl-CoA (Miller & Wolin, 1996) as demonstrated by *in vitro* analysis of a *Bacteroides fragilis* pure culture (Macy, Ljungdahl, & Gottschalk, 1978). Understanding the metabolic pathways

for butyrate and propionate productions has enabled the development of molecular markers based on genes coding for metabolic enzymes to study the functional aspects of microbial ecology in the intestines (Hosseini, Grootaert, Verstraete, & Van de Wiele, 2011).

The chemical structures of available complex carbohydrates play a critical role in determining the kinds of fermentation products produced by the microbiota. Therefore, the level and composition of intestinal SCFA are heavily influenced by diet and the endogenous microbial community structure (Campbell, Fahey, & Wolf, 1997; Cummings, 1981; Cummings & Macfarlane, 1991; Rechkemmer, Rönnau, & Engelhardt, 1988; Roy, Kien, Bouthillier, & Levy, 2006; Topping & Clifton, 2001). There is a distinct spatial organization of the intestinal microbiota (Nava, Friedrichsen, & Stappenbeck, 2011; Pedron et al., 2012) that influences the distribution of SCFA. In general, different regions of the small and large intestines exhibit distinct levels of SCFA, which result in environments with different pH values (Cummings & Macfarlane, 1991; Macfarlane, Gibson, & Cummings, 1992; Walter & Ley, 2011). The small intestine also contains a lower microbial burden with a different composition than the large intestine (Walter & Ley, 2011). This heterogeneous distribution of microorganisms in the intestines leads to spatial variation in the relative proportions of acetate, butyrate, and propionate (Cummings, 1981). Collectively, knowledge derived from many studies suggests that an invading enteric pathogen encounters changing levels and composition of SCFA and commensal microbes as it traverses the intestines. Understanding how enteric pathogens respond to the changing intestinal environment is important in providing a framework for identifying new ways to prevent and treat enteric infections. This review will focus on how common enteric pathogens respond to intestinal SCFA by regulating virulence functions.

2. BIOLOGICAL ACTIVITIES OF SCFA

2.1. Biological activities of SCFA in the host organism

The chemical environment established through metabolic activity of the microbiota plays critical nutritional roles in the host organism. The SCFA produced by the microbiota, especially butyrate, have profound effects on energy homeostasis. Butyrate is taken up by colonocytes and used as their primary energy source (Wong, de Souza, Kendall, Emam, & Jenkins, 2006). Colonocytes from germ-free (GF) mice that are deficient in intestinal SCFA exhibit decreased intermediary metabolism that results in activation of the nutrient and energy sensor, AMPK, which eventually leads to autophagy (Donohoe et al., 2011). Butyrate, when provided exogenously, rescues the GF colonocytes from AMPK activation-directed autophagy, indicating that microbiota-derived butyrate is essential for normal host colonocyte metabolism. The authors used chemical inhibitors to further show that the requirement for butyrate to prevent autophagy was based on its contribution to energy generation, not to the known property of butyrate as a histone deacetylase (HDAC) inhibitor (Donohoe et al., 2011). In fact, the ability of normal versus transformed colonocytes to use butyrate as an energy source could be shown to alter cellular responses to butyrate. In contrast to normal cells where butyrate is the primary energy source, transformed cells rely on glycolysis as the primary source of energy generation, leading to the accumulation of

butyrate which functions in these cancerous cells predominantly as a HDAC inhibitor (Donohoe et al., 2012).

In addition to serving as metabolic substrates, SCFA also modulate host immune functions. Butyrate or propionate is taken up into immune cells through the SLC5A8 transporter, where the HDAC activity of these SCFA exerts immunomodulatory effects by blockade of dendritic cell development and by inducing Fas upregulation followed by Fas-mediated T cell apoptosis (Singh et al., 2010; Zimmerman et al., 2012). Butyrate also decreases IL-12 expression, but increases IL-23 production, by activated dendritic cells, emphasizing the importance of this microbiota-derived SCFA in gut immune homeostasis (Berndt et al., 2012).

SCFA are recognized by a family of G-protein-coupled receptors (FFAR) and can trigger signaling at both the gut epithelium and systemic sites. Several reports suggest that binding of acetate and propionate to FFAR2 (GPR43) or propionate and butyrate to FFAR3 (GPR41) regulates gut hormone production, obesity, and inflammation (Layden, Angueira, Brodsky, Durai, & Lowe, 2013; Xiong et al., 2004). Mice lacking FFAR2 or FFAR3 exhibited decreased glucagon-like peptide-1 levels *in vivo* and impaired glucose tolerance (Tolhurst et al., 2012), implicating a role for intestinal SCFA in diabetes. Furthermore, SCFA treatment appears to stimulate adipogenesis in mice by FFAR-dependent (Hong et al., 2005) and FFAR-independent mechanisms (Lin et al., 2012). FFAR2 binding of SCFA also suppressed intestinal inflammation; FFAR2-deficient mice did not resolve disease in mouse models of colitis and arthritis (Maslowski et al., 2009). Thus, accumulating evidence provides a compelling picture that implicates microbiota-produced SCFA as key regulators of energy homeostasis, gut hormone production, and inflammation. Further elucidation of the diverse mechanisms by which SCFA and their host receptors may protect against long-term development of chronic diseases, such as colitis and diabetes, will provide an evidence-based platform to examine the effects of probiotics or prebiotics on human health.

The endogenous microbiota aid the gut epithelium in defense against attachment and invasion of enteric pathogens by stimulating production of antimicrobial peptides (AMPs) (Gallo & Hooper, 2012). One mechanism by which the microbiota may contribute to AMP production in the healthy intestine is through SCFA-dependent induction of LL-37 production demonstrated in a human colonic epithelial cell line (Termén et al., 2008). Similarly in chickens, SCFA enhanced the expression of host defense peptide gene expression, and including exogenous SCFA in feed resulted in lower *Salmonella* colonization in the cecum (Sunkara et al., 2011; Sunkara, Jiang, & Zhang, 2012). Thus, augmentation of animal feed with SCFA or with pre-biotics that promote SCFA production by the indigenous microbiota may be a viable alternative to antibiotic usage for reducing livestock colonization by potential human pathogens.

2.2. Biological activities of SCFA in bacteria

SCFA not only affect host functions but also serve as a carbon source for the endogenous microbiota (Fischbach & Sonnenburg, 2011) and at high concentration can exhibit toxic effects on bacteria. Numerous *in vitro* studies have demonstrated that the toxicity was attributable to the nonionized forms of these acids, which exist more prominently at low pH

(Baskett & Hentges, 1973; Bergeim, 1940; Hentges, 1967; Weiner & Draskoczy, 1961). These early studies also established the pleiotropic effects of weak organic acids ranging from inhibiting oxidative metabolism (Weiner & Draskoczy, 1961) to eliciting chemotactic responses (Repaske & Adler, 1981). Currently, the general mechanism for SCFA-dependent toxicity involves the entry of nonionized acids into the bacterial cytoplasm (Fig. 3.2). The non-ionized acids are small and uncharged and therefore are thought to freely diffuse across the bacterial membrane. Once inside the bacterial cytoplasm, which generally has a circumneutral pH, these nonionized acids dissociate, leading to an accumulation of protons and SCFA anions (Lambert & Stratford, 1999; Repaske & Adler, 1981; Russell, 1992; Salmond, Kroll, & Booth, 1984). On one hand, the influx of protons acidifies the intracellular compartment and dissipates proton motive force (Axe & Bailey, 1995) that can ultimately compromise metabolic reactions (Roe, O'Byrne, McLaggan, & Booth, 2002) and energy conservation. On the other hand, the accumulation of SCFA anions in the cytoplasm also significantly impacts cellular physiology, such as alterations in osmotic balance (Roe, McLaggan, Davidson, O'Byrne, & Booth, 1998).

SCFA diffusion process and the consequent toxicity are strongly influenced by external pH, which predicts the relative amount of non-ionized SCFA. Thus, SCFA toxicity is often more prevalent under acidic conditions where the pK_a value of SCFA (4.76 for acetate, 4.82 for butyrate, and 4.87 for propionate) is closer to or higher than the external pH. Furthermore, SCFA-mediated toxicity is also influenced by internal pH, which affects the transmembrane pH gradient that drives the influx of acid. Although bacterial cytoplasm is relatively resistant to pH perturbation because of the intrinsic impermeability of the membrane to protons (Raven & Beardall, 1981) and the buffering capacity established by ionizable moieties such as amino acids side chains (Booth, 1985; Slonczewski, Fujisawa, Dopson, & Krulwich, 2009), there are still various adaptive mechanisms, such as proton transporters, that are involved in active maintenance of intracellular pH (Booth, 1985). When external pH is low, organisms that are more stringent with maintaining pH at around neutral levels will face a higher transmembrane pH gradient that will enhance acid influx and thereby will be more susceptible to SCFA toxicity than those that can tolerate lower intracellular pH values (Diez-Gonzalez & Russell, 1997; Russell, 1991).

SCFA-induced toxicity often results in growth inhibition attributable to pleiotropic defects in cellular processes (Cherrington, Hinton, Mead, & Chopra, 1991) that are likely to vary by pathway, organism, and environmental condition. For example, DNA synthesis is more sensitive to propionate than synthesis of proteins, RNA, lipids, or cell walls in *E. coli* (Cherrington, Hinton, & Chopra, 1990). Similarly, amino acid uptake was inhibited in *Bacillus subtilis* after exposure to acetate and propionate (Freese, Sheu, & Galliers, 1973). However, more recent proteomic analysis showed an increased level of some amino acid transporters in *E. coli* after acetate treatment (Kirkpatrick et al., 2001), suggesting that metabolic responses to SCFA might vary by organism. The same study also demonstrated an alternative proteomic response to acetate in a defined minimal medium compared to rich medium, indicating the importance of environmental context in bacterial responses to SCFA.

3. VIRULENCE REGULATION OF ENTERIC PATHOGENS BY SCFA

3.1. *Salmonella* spp

According to Centers for Disease Control and Prevention, *Salmonella* infection is one of the most common foodborne illnesses with more than 1 million cases estimated per year in the United States. Among thousands of known serotypes that can cause human disease, *Salmonella enterica* serotypes Enteritidis, Typhimurium, and Newport are responsible for more than 60% of all laboratory confirmed incidences in 2011. A critical component of *Salmonella* pathogenesis after adherence to the host cells involves the delivery of bacterial effector proteins into host cytosol through two Type III Secretion Systems (T3SS) (Galan, 2001). During the gastrointestinal phase of the infection, *Salmonella* must navigate within the luminal environment rich in SCFA before gaining access to the host epithelium. Therefore, understanding how *Salmonella* responds to SCFA will reveal key aspects of pathogenesis that can ultimately provide useful insight into designing prevention and treatment strategies.

Molecular responses to SCFA have been extensively studied in *Salmonella* species. In general, *Salmonella* can assimilate SCFA, such as propionate (Horswill & Escalante-Semerena, 1999), as a carbon source when provided at low concentrations. At higher levels and low pH, SCFA strongly inhibit the growth of *Salmonella* (Goepfert & Hicks, 1969; McHan & Shotts, 1993; Van Immerseel et al., 2003), an activity that has been the basis for using SCFA in food preservatives or poultry feed to minimize *Salmonella* contamination (Wales, Allen, & Davies, 2010). As a foodborne pathogen that encounters several host environments with low pH and high SCFA levels in the gastrointestinal tract, *Salmonella* adopts a variety of active mechanisms to survive the acid stress by eliminating proton accumulation in the cytosol (Álvarez-Ordóñez et al., 2011).

In addition to serving as metabolic precursors and agents of acid stress, SCFA also regulate *Salmonella* virulence gene expression *in vitro* in a pH- and species-specific manner (Boyen et al., 2008; Cardenal-Muñoz & Ramos-Morales, 2011; Durant, Corrier, & Ricke, 2000; Gantois et al., 2006; Gong et al., 2009; Huang, Suyemoto, Garner, Cicconi, & Altier, 2008; Zabala Díaz & Ricke, 2004). In *Salmonella dublin*, all SCFA with two to six carbons induce genes *spvABCD*, which are important for virulence (El-Gedaily, Paesold, & Krause, 1997). In contrast, single supplementation of butyrate (four carbons) or propionate (three carbons), but not acetate (two carbons), reduces expression of invasion genes in WT *S. enterica* Typhimurium. Mixtures representing colonic SCFA concentrations, which contain higher total SCFA as well as relative proportions of butyrate and propionate, exhibit a greater inhibitory effect than ileal SCFA concentrations, suggesting spatial orientation for *S. enterica* Typhimurium colonization in the host intestines (Lawhon, Maurer, Suyemoto, & Altier, 2002). Detailed analyses to study the molecular mechanisms of inhibition have highlighted the importance of SCFA metabolism, for example, formation of acetyl-phosphate and propionyl-CoA from acetate and propionate, respectively, in regulation of virulence gene expression (Hung et al., 2013; Lawhon et al., 2002).

The effect of SCFA on virulence gene expression *in vitro* has been tested during *Salmonella* interactions with the host using both tissue culture and animal infection models. As observed

in gene expression analyses *in vitro* (Durant et al., 2000), the effect of SCFA on *S. enterica* Typhimurium association and invasion into HEp-2 cells depends heavily on the medium pH. All three SCFA tested, acetate, butyrate, and propionate reduced cell association more efficiently at pH 6 than at pH 7 (Durant et al., 1999). Pre-treatment of *S. enterica* Enteritidis with butyrate reduces invasion of the avian intestinal cell line DIV-1 (Van Immerseel et al., 2003) and primary chicken cecal epithelial cells (Van Immerseel et al., 2004). While these studies collectively suggest a protective role of SCFA during *Salmonella* infections, they overlook the host response to SCFA that may affect the infection outcome. In animal models of infection where SCFA exposure is shared by host epithelium and invading *Salmonella*, supplementing SCFA in feed reduced the *Salmonella* number in ceca of chicks (McHan & Shotts, 1992) and pigs (Boyen et al., 2008), agreeing with the protective effects of SCFA against *Salmonella* colonization demonstrated in tissue culture models of infection. Furthermore, antibiotic-treated mice that have an altered microbiota composition and decreased levels of SCFA are more susceptible to *Salmonella* infection (Garner et al., 2009). Taken together, these studies suggest that individuals with sufficient levels of intestinal SCFA, specifically butyrate and propionate, are less likely to be susceptible to *Salmonella* infections.

3.2. Escherichia coli

Enterohemorrhagic *E. coli* (EHEC) is one of the leading foodborne pathogens that causes attaching and effacing lesions of the intestinal epithelium through delivery of effector proteins into host cells by the T3SS (Wong et al., 2011). Key virulence determinants including the T3SS for EHEC are encoded on a chromosomal locus for enterocyte effacement (LEE). Based on protein and transcriptomic analyses, expression of LEE genes in EHEC strain Sakai is strongly induced by sodium butyrate but not by sodium acetate or sodium propionate (Nakanishi et al., 2009). This particular response to butyrate relies on the transcriptional regulator Lrp or leucine-responsive regulatory protein (Nakanishi et al., 2009), which belongs to a group of related proteins that are widely distributed among bacteria and Archaea and are often involved in metabolic responses to nutrient availability (Brinkman, 2003; Calvo & Matthews, 1994; Newman & Lin, 1995; Yokoyama et al., 2006). Based on analyses of site-directed Lrp mutants, butyrate may interact with the Lrp ligand-binding domain and thereby affect Lrp activity (Nakanishi et al., 2009).

In contrast to butyrate promoting bacterial adherence, all three major SCFA induce production of flagella in EHEC through both Lrp-dependent and -independent mechanisms (Tobe, Nakanishi, & Sugimoto, 2011). As adherence and flagellar motility exert opposing effects on bacterial cells, the authors postulate an *in vivo* scenario in which EHEC expresses flagella inside the intestinal lumen and only initiates adherence as butyrate levels increase in the large intestine leading to colonization and delivery of T3SS effector proteins (Tobe et al., 2011). This hypothesis is consistent with the observation that EHEC has the ability to inhibit butyrate uptake in the human colonic Caco-2 cell line (Borthakur et al., 2006), thereby increasing local butyrate level near the epithelium for optimal induction of the T3SS. Moreover, a recent study (Herold, Paton, Srimanote, & Paton, 2009) demonstrated in three different EHEC strains that colonic but not ileal levels of SCFA induce expression of *iha*, which encodes an outer membrane protein involved in adherence, supporting the ability

of EHEC to navigate within different intestinal environments by responding to SCFA levels. However, these studies do not agree with the observation that bovine colonic tissues incubated with SCFA support a reduced load of EHEC (Cobbold & Desmarchelier, 2004). Therefore, additional *in vivo* studies will be necessary to better elucidate the complex functions of SCFA in EHEC pathogenesis.

3.3. *Listeria monocytogenes*

Listeria monocytogenes is a prevalent contaminant in food products that are slightly acidic in nature such as dairy products or food with organic acid preservatives because of its ability to survive and grow under acid conditions. After ingestion, the bacterium must survive acid stress in the stomach and the SCFA challenge in the lower intestines for colonization and pathogenesis to occur. Therefore, understanding *L. monocytogenes* acid response is of particular importance from the perspective of food safety as well as bacterial pathogenesis.

Prior acid exposure enhances *L. monocytogenes* survival of subsequent acid stress (Davis, Coote, & O’Byrne, 1996; Kroll & Patchett, 1992; O’Driscoll, Gahan, & Hill, 1996). This adaptive behavior, termed acid tolerance response (ATR) (Cotter & Hill, 2003; Ryan, Hill, & Gahan, 2008), encompasses three major cellular adaptations in response to the decreased intracellular pH (Shabala et al., 2002) as shown in Fig. 3.2. The glutamate decarboxylase system (Cotter, Gahan, & Hill, 2001; Cotter, O’Reilly, & Hill, 2001; Cotter, Ryan, Gahan, & Hill, 2005; Wiedmann, Arvik, Hurley, & Boor, 1998), the F₁F₀ ATPase (Bowman, Hages, Nilsson, Kocharunchitt, & Ross, 2012; Bowman, Lee Chang, Pinfold, & Ross, 2010; Cotter, Gahan, & Hill, 2000; Datta & Benjamin, 1997; Phan-Thanh & Mahouin, 1999), and the arginine and agmatine deiminase system (Ryan, Begley, Gahan, & Hill, 2009) all function to reduce the intracellular level of protons. In addition to survival in acid stress, ATR plays a critical role in promoting *L. monocytogenes* virulence (Conte et al., 2000; Conte et al., 2002; Marron, Emerson, Gahan, & Hill, 1997).

ATR studies using *in vitro* survival assays (Ferreira, 2003) or proteomics approaches (O’Driscoll et al., 1997) all reported that organic acids eliciting a distinct response from inorganic acids. This can be explained by the intracellular accumulation of organic acid anions, which are carbon metabolites, interfering with metabolic reactions. For example, exposure to butyrate significantly alters membrane fatty acid composition (Julotok, Singh, Gatto, & Wilkinson, 2010; Sun, Wilkinson, Standiford, Akinbi, & O’Riordan, 2012) because of butyrate assimilation into straight chain fatty acids, which normally represent a minor component of membrane fatty acids. This response is notably different from changes in membrane fatty acid composition caused by exposure to HCl, acetic acid, or lactic acid (Mastronicolis et al., 2010). Moreover, high levels of butyrate strongly inhibit virulence factor production in *L. monocytogenes* at the transcriptional level (Sun et al., 2012), suggesting a protective effect of intestinal SCFA against *L. monocytogenes* infection.

Work published as early as 1979 revealed that GF animals show increased susceptibility to *Lm* colonization and that the intestinal microbiota, introduced either individually or as a community, is capable of decreasing *Lm* colonization of GF mice (Archambaud et al., 2012; Bambirra et al., 2007; dos Santos et al., 2011; Nakamura et al., 2012; Vieira et al., 2008; Zachar & Savage, 1979) and rats (Czuprynski & Balish, 1981). Although these studies do

not provide clear mechanisms for colonization resistance, they nevertheless demonstrate a functional requirement for the gut microbiota in protection against *L. monocytogenes* infection. Thus, mechanistic understanding of how intestinal SCFA affect *L. monocytogenes* virulence gene regulation and pathogenesis *in vivo* remains to be determined.

3.4. *Campylobacter jejuni*

Campylobacter jejuni is the most common bacterial foodborne pathogen causing diarrheal disease in humans with more than 2 million cases per year according to reports available at the Centers for Disease Control and Prevention. As contaminated chickens are considered the main source of exposure, numerous studies are conducted to establish proper housing regimens to minimize the spread of *C. jejuni* (Hermans et al., 2011), including those specifically testing the effect of SCFA in animal feed on *C. jejuni* colonization (Heres, Engel, Urlings, Wagenaar, & van Knapen, 2004; Heres, Engel, Van Knapen, Wagenaar, & Urlings, 2003; Van Deun, Haesebrouck, Van Immerseel, Ducatelle, & Pasmans, 2008). These studies have not reported a consistent protective effect by SCFA. Studies that evaluated *C. jejuni* virulence responses to SCFA using a tissue culture infection model showed that pretreating *C. jejuni* with SCFA did not compromise its invasion into human colonic epithelium-derived Caco-2 cell, but pretreating Caco-2 cells significantly reduced subsequent *C. jejuni* invasion (Van Deun, Pasmans, Van Immerseel, Ducatelle, & Haesebrouck, 2008). Therefore, it is possible that SCFA are not involved in bacterial virulence gene regulation in *C. jejuni* but provide a protective value to the host against *C. jejuni* infection.

3.5. *Shigella* spp

Shigella represents another model enteric pathogen that is widely studied to probe host-pathogen interactions. Islam et al. (2001) has demonstrated that *Shigella* infection causes a downregulation in the production of cathelicidin, an AMP that is part of the innate defense repertoire, in both human rectal mucosal biopsies and in a tissue culture model of infection (Van Deun, Pasmans, Van Immerseel, Ducatelle, & Haesebrouck, 2008). This bacterial modulation of host immune defense is thought to be important for colonization and pathogenesis but can be overcome by oral administration of butyrate or bolus infusion of SCFA into the colon, both of which significantly improve clinical manifestations in an adult rabbit infection model (Rabbani et al., 1999; Raqib et al., 2006). The potential health benefit of SCFA proposed by these studies is mainly based on upregulation of rabbit cathelicidin, which efficiently eliminates *Shigella*. This was subsequently tested in a human clinical trial where patients with *Shigella* infections receiving butyrate-containing enemas showed improved pathology and higher expression of cathelicidin compared to patients receiving the placebo control (Raqib et al., 2012). Although there may be multiple effects of SCFA on *Shigella* virulence regulation that remain to be defined, they likely include indirect effects on *Shigella* pathogenesis by protective stimulation of host defense mechanisms.

4. APPLICATIONS OF SCFA

4.1. Food safety

The food industry has been taking advantage of the toxic effect of SCFA on microbes to enhance food safety. SCFA can be added to food products as preservatives that will inhibit bacterial growth (Carpenter & Broadbent, 2009; Ricke, 2003). Moreover, as contaminated poultry is believed to be the main source of human *Salmonella* infections (Callaway, Edrington, Anderson, Byrd, & Nisbet, 2008), many research efforts have investigated the effects of adding SCFA into poultry feed to control *Salmonella* colonization in poultry (Cox & Pavic, 2010; Defoirdt, Boon, Sorgeloos, Verstraete, & Bossier, 2009; Dibner & Buttin, 2002; Jones, 2011; Ricke, 2003; Van Immerseel et al., 2006; Wales et al., 2010). In this regard, addition of SCFA in animal feed in theory has the potential to prevent colonization and shedding of pathogenic organisms, thereby lowering the initial risk of contamination in the food production line. However, other hygienic controls are also important considering that SCFA additives in feed at best only reduce but do not eliminate *Salmonella* colonization (Van Immerseel et al., 2005).

4.2. Prebiotics

The concept of prebiotics was introduced by Gibson et al. and defined as a food ingredient that can modulate the gut microbiota to confer health benefits (Gibson, Probert, Loo, Rastall, & Roberfroid, 2004; Gibson & Roberfroid, 1995). Inulin, fructo-oligosaccharides, and galato-oligosaccharides, which are complex carbohydrates nondigestible by humans, represent the best-studied types of prebiotics. As recommended by the World Gastroenterology Organisation, dietary supplementation with these prebiotics can confer significant health benefits and often leads to enrichment in selective members of the gut microbiota, mainly bifidobacteria and *Lactobacillus* species and increases in the level of SCFA (Macfarlane, Steed, & Macfarlane, 2008). The health benefits of prebiotics shown in these studies do not dismiss the concern that individual variation in gut microbiota composition (Schloissnig et al., 2013) may make it difficult to predict the efficacy of prebiotics that target specific community members of the microbiota. This is particularly relevant in diseased individuals that may lack the target microbiota members and therefore will not benefit from prebiotic supplementation. One solution to this challenge is the concept of "synbiotics" where prebiotics are provided simultaneously with live commensal bacteria or "probiotics," to ensure the presence of the desired species. Further research in this field may reveal novel and beneficial strategies to prevent disease and promote human health.

5. PERSPECTIVES

SCFA exert protective effects against enteric pathogen colonization and infection by multiple mechanisms and can act to regulate virulence in different pathogens as diagrammed in Fig. 3.3. The chemical nature of SCFA allows easy penetration into bacterial cells and subsequent incorporation into common metabolic pathways. Therefore, the effects of SCFA on bacterial virulence may vary depending on the metabolic processes involved in different pathogens. For example, it is possible that *C. jejuni* will respond to SCFA differently than other enteric pathogens because of its inability to utilize carbohydrates (Dasti, Tareen,

Lugert, Zautner, & Groß, 2010) and may be better adapted to utilize SCFA as a source of carbon and energy in the intestines. While metabolism of intracellular bacteria has received increasing attention and has an established role in intracellular pathogenesis (Eisenreich, Dandekar, Heesemann, & Goebel, 2010; Muñoz-Elías & McKinney, 2006), defining metabolism of extracellular pathogens while inside the host (Alteri & Mobley, 2012) is equally crucial. Defining the relationship between SCFA metabolism and SCFA-dependent virulence responses will enhance our understanding in bacterial virulence processes in the context of the host environment and its resident microbiota.

The recognition of SCFA as a signal for virulence regulation in enteric pathogens and as a potential health determinant conferring protection against enteric infections argues for a closer look at the importance of chemical homeostasis in the intestinal environment. As most intestinal levels of SCFA are reported based on bulk analysis, their values likely do not reflect the microenvironment experienced by enteric pathogens. Moreover, there is likely a cross-sectional SCFA gradient that cannot be revealed by bulk analysis. The gradient can be established because SCFA are produced in the lumen and absorbed by the epithelium. The aerobic environment near the epithelium also provides a thermodynamically more favorable condition than the anaerobic lumen to promote complete oxidation of the same carbon source, thereby potentially reducing the production of fermentation products. The chemical environment near the epithelium is further complicated by the fact that absorption rates for individual SCFA are different and might lead to distinct local pools of SCFA. Consequently, it will be important to develop better *in vivo* tools to measure local levels of SCFA and to determine if the SCFA concentration near the host epithelium still maintains modulatory activity on the virulence regulation of enteric pathogens.

6. CONCLUSION

The multifaceted interaction between the gut microbiota and its host exerts profound influence in many aspects of host development and physiology. The close association of the gut microbiota with human health and disease is now widely accepted, but the mechanistic details involved in how the microbiota contributes to human health require much more in-depth analysis. Nevertheless, these early studies of the chemical messages that mediate interactions between intestinal bacteria and their host have led to a more comprehensive picture of human biology. In this review, we have focused on the role of a particular class of chemical messages, microbiota-derived SCFA, during interactions between the host and enteric pathogens. Based on the literature summarized in this review, SCFA provide an important resistance mechanism against pathogen by exerting toxic acid stress. However, some enteric pathogens have adapted to the intestinal gradient of SCFA and have evolved mechanisms to regulate virulence gene expression that allow successful colonization of the host. In summary, SCFA provide a key link between the microbiota, the host, and invading enteric pathogens. It is likely that the studies reviewed here are just a small representation of the many chemical interactions of the microbiota that drive health and disease. Future studies that further characterize the role of SCFA in the complex interactions taking place in the intestine will enhance our ability to control and prevent food contamination and to improve human digestive health.

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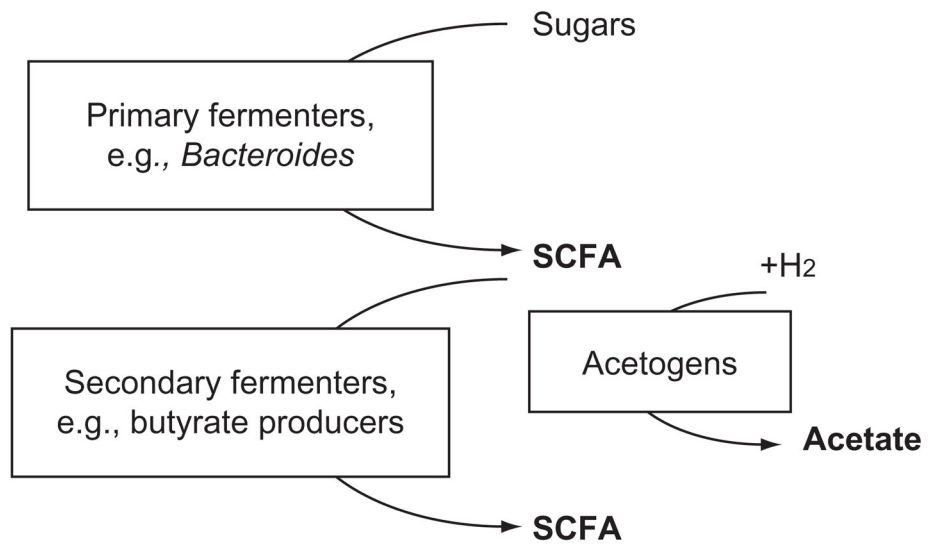
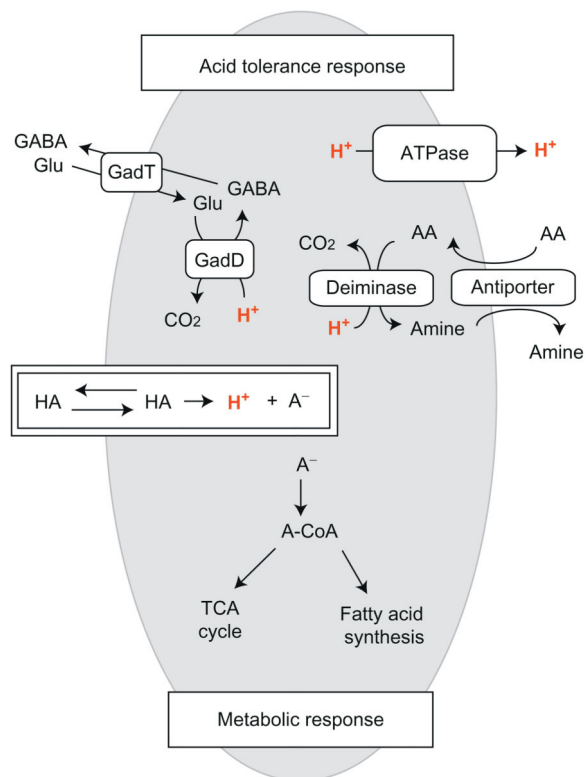


Figure 3.1.

An overview of short-chain fatty acid (SCFA) production in the intestines. Primary fermenters such as *Bacteroides* species oxidize mono- and oligosaccharides and release SCFA that can be subsequently utilized by secondary fermenters to generate additional SCFA. Acetogens also utilize hydrogen released from fermentation reactions along with carbon dioxide to form acetate, thereby contributing to intestinal SCFA content.

**Figure 3.2.**

A representative schematic of bacterial responses to weak organic acids. Nonionized organic acids, symbolized as “HA,” can diffuse across bacterial membrane and dissociate into protons (H⁺) and anions (A⁻) in the circumneutral cytoplasm. This influx of proton will induce the acid tolerance response (ATR) that functions to maintain intracellular pH homeostasis by removing cytoplasmic protons. ATR, in general, includes a glutamate decarboxylase system (GadD, glutamate decarboxylase; GadT, glutamate-GABA antiporter), an F₀F₁-ATPase, and a deamination system (e.g., AA, arginine; amine, ornithine). The organic anions accumulated in the cytoplasm can feed into metabolic pathways such as TCA cycle or membrane fatty acid synthesis after addition of coenzyme A.

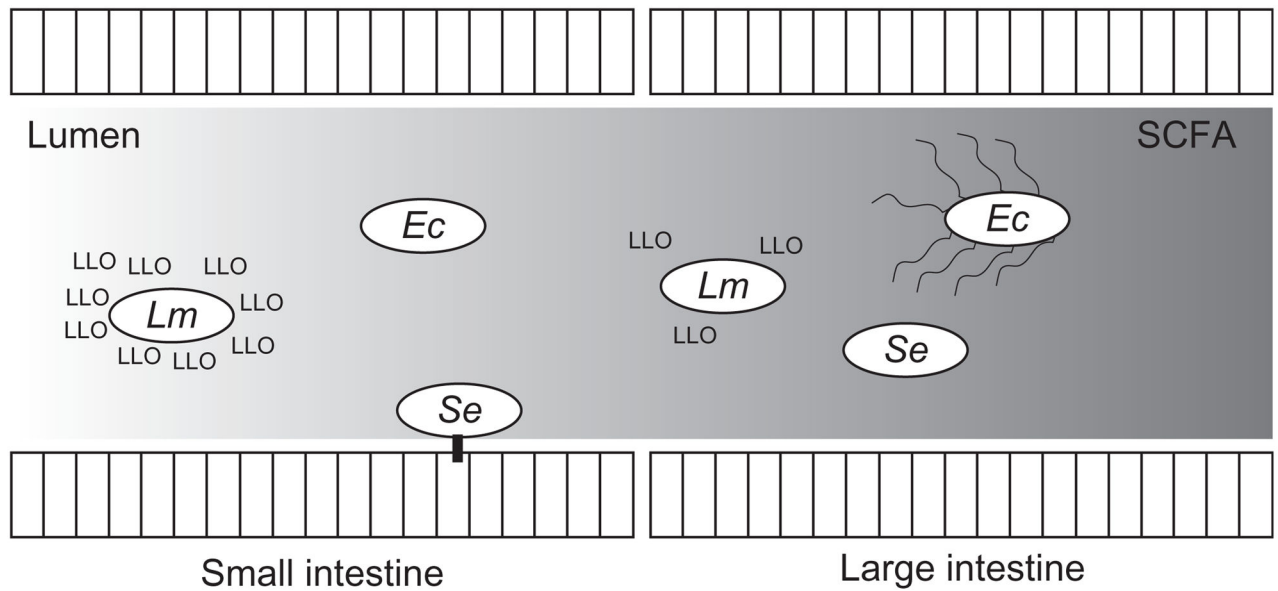


Figure 3.3.

A model depicting virulence functions of representative enteric pathogen in response to an intestinal gradient of short-chain fatty acids (SCFA). *Ec*, Enterohaemorrhagic *Escherichia coli*, upregulates flagella synthesis in response to butyrate. *Lm*, *Listeria mono-cytogenes*, reduces production of the pore-forming toxin, listeriolysin O, in response to butyrate. *Se*, *Salmonella enterica*, decreases production of Type III Secretion System in response to colonic mixtures of SCFA.