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#### **REVIEW**



### Dietary polyphenol impact on gut health and microbiota

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#### **ABSTRACT**

Polyphenols are naturally occurring compounds in plants and they are the most abundant antioxidants in the human diet. Due to their considerable structural diversity, this largely influences their bioavailability. Since a large proportion of polyphenols remains unabsorbed along the gastrointestinal tract, they may accumulate in the large intestine, where most of them are extensively metabolized by the intestinal microbiota. The formation of bioactive polyphenol-derived metabolites may also benefit the health status of the subjects, although the mechanisms have not been delineated. This review aims to highlight the impact of polyphenols on gut health and the modes of action could be through modulation of intestinal barrier function, innate and adaptive immune response, signaling pathways, as well as the ability to modify gut microbiota composition. The review will conclude by presenting future perspective and challenges of polyphenols application in food products to be used for preventing or treating diseases.

#### **KEYWORDS**

Bioavailability; biotransformation; gut health; gut microbiota; metabolism; polyphenols

#### Introduction

Polyphenols are the most common plant-derived bioactive components in our diet. They are widely present in a variety of foods such as fruits, vegetables, cereals, tea, coffee and wine. More than 8000 polyphenols have been identified so far and they are categorized according to the nature of their carbon skeleton: phenolic acids, flavonoids, stilbenes and lignans (Guo, Kong, and Meydani 2009). Intake of polyphenols varies by geography, possibly due to the different diet habits, as demonstrated in a number of studies (Taguchi et al. 2017; Zamora-Ros et al. 2016). The average dietary intake of polyphenols is speculated to be about 1 g/day (Scalbert and Williamson 2000). It has been estimated that most of the total polyphenol intake remained unabsorbed in the small intestine. Unabsorbed polyphenols (90-95% of total polyphenol intake) may accumulate in the large intestine up to the millimolar range, where most of them are extensively metabolized by the intestinal microbiota (Cardona et al. 2013; Clifford 2004). The colonic microbiota therefore play an important role in the extensive breakdown of the original polyphenolic structures into a series of low-molecular-weight polyphenolic metabolites that can be readily absorbed and confer health benefits (Cardona et al. 2013). Apart from inter-individual variation in daily intake of polyphenols, inter-individual variation in gut microbiota may lead to differences in bioavailability and bioefficacy of polyphenols and their metabolites. During the last decade, there is a growing body of in vitro and in vivo evidence supporting the health-promoting effects of polyphenols, including anti-inflammatory, antioxidant,

anti-microbial, anti-carcinogenic, anti-adipogenic, anti-diabetic, cardio- and neuro-protective activities (Coates et al. 2007; Mandel and Youdim 2004; Middleton, Kandaswami, and Theoharides 2000; Pandey and Rizvi 2009; Sabu, Smitha, and Kuttan 2002; Tipoe et al. 2007; Umeno et al. 2016). The formation of bioactive polyphenol-derived metabolites and the modulation of colonic microbiota may both contribute to host health benefits, although the mechanisms have not been delineated. This review aims to highlight the impact of polyphenols on gut health, and the modes of action could be through modulation of intestinal barrier function, innate and adaptive immune response, signaling pathways, as well as the ability to modify gut microbiota composition (Figure 1).

#### Polyphenols on intestinal barrier function

Intestinal epithelial barriers are important for normal physiological functions; compromised barriers allow the entry of antigens (bacteria or toxins) and can induce inflammatory diseases. This barrier is maintained by tight junctions, adhering junction and desmosomes, which form a continuous permeability barrier surrounding the apical region of intestinal epithelial cells (IECs) (Gumbiner 1993). The trans-epithelial electrical resistance (TEER) of cell monolayers can be considered as a convenient and sensitive method to check for confluence and barrier integrity of an epithelial cell monolayer. TEER reflects the degree to which small charged particles (mainly ions) passively traverse the cell monolayer, either by transcellular or paracellular routes

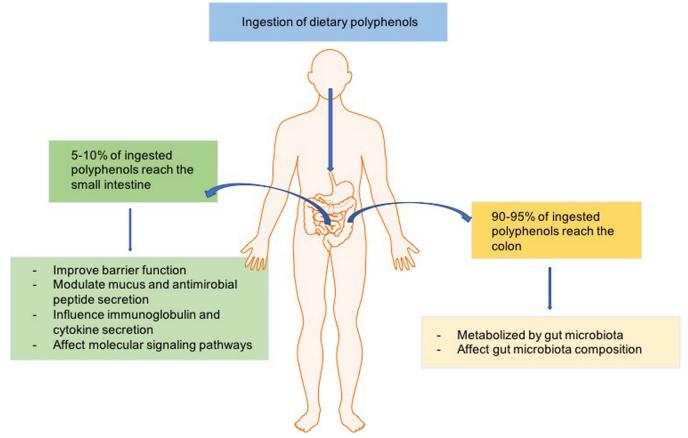


Figure 1. The impact of polyphenols on gut health and the possible modes of action.

(Madara and Trier 1994). However, the TEER measurement indeed reflects mainly the resistance across tight junctions (paracellular) instead of cell membrane (transcellular) (Madara 1983). A review article published in 2011 documented that only four flavonoids had been assessed for the protective effects on intestinal tight junctions (Suzuki and Hara 2011). On top of that, there are several other studies that have reported the effects of polyphenols on intestinal tight junctions and have been summarized previously (for review, refer to (Wan, Ling, and El-Nezami 2018)). Some of these common polyphenols, including quercetin, epigallocatechin gallate (EGCG), genistein, resveratrol, exhibit protective effects on intestinal tight junction barrier functions by increasing TEER through modulation of tight junction protein expression and/or distribution (Amasheh et al. 2012; Amasheh et al. 2008; Cao et al. 2013; Carrasco-Pozo, Morales, and Gotteland 2013; Gu et al. 2011; Ling et al. 2016; Suzuki and Hara 2009). This can prevent subsequent translocation of luminal antigens via the mucosa to the whole body, which can destroy the gut mucosal homeostasis accompanied by an increase in susceptibility to systemic infection, chronic inflammation and malabsorption (Awad, Hess, and Hess 2017).

## Polyphenols on innate and adaptive immune responses

#### Modulation of mucus layer

The luminal surface of the gastrointestinal tract is covered by a mucus gel layer that acts to protect gut epithelial cells

from the harsh luminal environment. Mucin glycoproteins (mucins) are major macromolecular components of epithelial mucus layer overlying the intestinal epithelium. Mucin forms a physiochemical barrier, which protects epithelial cells from chemical, enzymatic, mechanical and microbial damage, and limits microbial adherence and subsequent invasion (Linden et al. 2008). In the gastrointestinal tract, there are two distinctive types of mucins: secreted gel forming mucins and cell-surface mucins (Lindén, Florin, and McGuckin 2008). The gel forming mucins, mainly MUC2 secreted by the goblet cells, are the main components forming the highly viscous mucus layer; while the cell-surface mucins, such as MUC1, MUC3A/B, MUC4 and MUC12, are produced by and present on the apical membranes of all IECs. Cell-surface mucins are dominating constituents of the glycocalyx, limiting harmful molecules from accessing the cell surface (Kim and Ho 2010; Linden et al. 2008). It is expected that polyphenols can modulate the barrier properties of mucus, nutrient absorption through mucus and the viscoelastic microenvironments of intestinal bacteria (Georgiades et al. 2014). There are only two studies regarding the effects of polyphenols on intestinal mucus production. Martin et al. (2004) and Rosillo et al. (2011) reported that ellagic acid (EA) and resveratrol increased mucus production in goblet cells in colon mucosa of a rat model of Crohn's disease. Furthermore, there are also a limited number of studies related to the interaction of polyphenols with the mucus layer. Georgiades et al. (2014) have demonstrated that both naturally derived purified polyphenols, and green

Table 1. Interaction of polyphenols with the mucus gel layer, in vitro, ex vivo & in vivo.

Polyphenols (Dosages)	Cells/Models (Stimulants, if any)	Effects/Key findings	Refs.
Resveratrol (5–10 mg/kg/day)	Rat model of Crohn's disease (induced by TNBS)	<ul> <li>Resveratrol increased mucus production in goblet cells in colon mucosa.</li> </ul>	(Martin et al. 2004)
Ellagic acid (EA) (10–20 mg/kg)	Rat model of Crohn's disease (induced by TNBS)	<ul> <li>EA increased mucus production in goblet cells in colon mucosa.</li> </ul>	(Rosillo et al. 2011)
Epigallocatechin gallate (EGCG) (400, 4000 μM) Epicatechin (EC) (400, 4000 μM)	HT29 and HT29-MTX-E12	<ul> <li>The mucus layer on HT29-MTX-E12 protected the cells against EGCG toxicity.</li> <li>EC had no effect on HT29 and HT29-MTX-E12 cell viability, which may be attributed to the binding of proteins within the mucus gel layer to the galloyl ring of EGCG.</li> </ul>	(D'Agostino et al. 2012)
EC, EGCG, black and green tea extracts and EGCG-rich green tea extract	Isolated porcine gastric and duodenal mucins as model for GI mucus	<ul> <li>EGCG has the highest affinity to interact with mucins, causing precipitation and gelation, whereas EC and non- galloylated ECs do not.</li> </ul>	(Georgiades et al. 2014)

and black tea extracts can act as cross-linkers for purified gastrointestinal (GI) mucin derived from the stomach and the duodenum, which could affect the mucus layer's viscoelasticity. This could act as a selective barrier for nutrients and potentially help in defense against pathogens. D'Agostino et al. (2012) revealed that the mucus layer on HT29-MTX-E12 human colonic adenocarcinoma cells probably protected the cells against Epigallocatechin gallate (EGCG) toxicity. Epicatechin (EC) had no effect on HT29 and HT29-MTX-E12 cell viability, which may be attributed to the binding of proteins within the mucus gel layer to the galloyl ring of EGCG. Table 1 summarizes the results and details of the listed references.

#### Antimicrobial peptide secretion

Another mechanism of mucosal defense is the secretion of antimicrobial peptides, also known as host defense peptides, peptide antibiotics or natural antibiotics. Antimicrobial peptides play a significant role in innate immunity, having both antimicrobial and immunomodulatory activities. Currently, over 400 antimicrobial peptides have been identified in plants and animals. Antimicrobial peptides are produced by cells in the immune system and along the mucosal epithelia (Zhang, Ross, and Blecha 2000). Most antimicrobial peptides act by disrupting the integrity of the microbial cell membranes physically through peptide-lipid interactions, rather than specific receptor-mediated recognition processes, and as a result, they function as a broad-spectrum antimicrobial agent against different pathogens, including bacteria, fungi, yeasts and viruses (Smet and Contreras 2005; Zhang, Ross, and Blecha 2000). In human intestine, two types of antimicrobial peptides are present: defensins (cryptdins) and cathelicidin (Smet and Contreras 2005).

Defensins are further classified into two groups: α-defensins and  $\beta$ -defensins.  $\alpha$ -defensins have only been identified in humans, monkeys and rodents, which are expressed in different cell types, including granule-containing granulocytic leukocytes and intestinal paneth cells (Patil, Hughes, and Zhang 2004).  $\beta$ -defensins, on the other hand, are mainly expressed in epithelial cells of organs exposed to the external environment, such as the skin, gastrointestinal tract, and respiratory tract (Veldhuizen et al. 2006). In humans,

there are three enteric  $\beta$ -defensins, human  $\beta$ -defensin-1 (hBD-1), hBD-2 and hBD-3, expressed by different IECs (Smet and Contreras 2005). Studies found that hBD-1 is constitutively expressed, while hBD-2 and hBD-3 are mostly expressed in response to infection and inflammation, particularly in ulcerative colitis and Crohn's disease (Fahlgren et al. 2003; Wehkamp et al. 2002; Wehkamp et al. 2003). Antimicrobial peptides play a pivotal role in modulating the crosstalk between microbe and host cells, thereby maintaining intestinal microbiotic homeostasis (Veldhuizen et al. 2007). They also exhibit immuno-modulatory activities, through modulation of innate and adaptive immunity. These include: enhancement of phagocytosis, promotion of neutrophil recruitment, increased pro-inflammatory cytokine production, inhibition of anti-inflammatory regulation of complement activation, as well as promotion and antigen uptake of dendritic cell maturation (for review, refer to (Yang et al. 2002; Yang, Chertov, and Oppenheim 2001).

A previous study has demonstrated that the antimicrobial activity of antimicrobial peptides, such as  $\beta$ -defensins, may be associated with bacterial populations in the intestine, which naturally present a barrier limiting undesirable gut mucosal infections and preventing bacterial translocation (Veldhuizen et al. 2008). The effects of polyphenols on antimicrobial peptides have been demonstrated in few studies using non-intestinal models. For example, EGCG induced defensin secretion on gingival epithelial cells (Lombardo Bedran et al. 2014). Black tea extract, theaflavin-3,3'-digallate, as well as EGCG were able to increase the secretion of hBD-1, hBD-2 and HBD-4 on oral epithelial cells in another study (Lombardo Bedran et al. 2015). However, the effect of polyphenols on the secretion of intestinal antimicrobial peptides is poorly documented. Recently, Wan et al. (2016) reported that EGCG reduced bacterial translocation across IPEC-J2 cell monolayers by inducing secretion of antimicrobial peptides, porcine  $\beta$ -defensins 1 and 2 (pBD-1 and 2), which possessed higher antimicrobial activity against Escherichia coli. Further mechanistic studies demonstrated that EGCG up-regulated pBD-2 but not pBD-1 via the p38 mitogen-activated protein kinase (MAPK)-dependent pathway. This study suggests the potential of certain polyphenols, such as EGCG in modulating the epithelial

Table 2. Polyphenols regulation of immunoglobulin secretion in vivo

Polyphenols (Dosages)	Cells/ Models (Stimulants, if any)	Effects/ Key findings	Refs.
Curcumin, rutin, D(+)-catechin, ellagic acid and quercetin (0.5% w/w)	Male Sprague Dawley rats fed high- or low-fat diet	Only curcumin elevated fecal IgA in rats fed high-fat diet but not those fed low-fat diet	(Okazaki et al. 2010)
Cocoa, Containing a total polyphenol content of 10.62 mg/g	Female Wistar rats	<ul> <li>A continuous and high cocoaenriched diet decreased slgA concentration in intestinal wash and fecal samples.</li> <li>Gene expression data showed that cocoa intake reduced lgA and IL-6 in Peyer's patches and mesenteric lymph nodes, whereas in small intestine, cocoa decreased lgA, CCR9, CCL28, PARα and RARβ.</li> <li>Cocoa dietary intervention resulted in a differential TLR pattern and a decrease in the intestinal lgA secretion and lgA-coating bacteria.</li> </ul>	(Massot-Cladera et al. 2012; Pérez- Berezo et al. 2012)
Cocoa flavonoids (0.2% polyphenols from conventional cocoa, 0.4 and 0.8% polyphenols from non- fermented cocoa)	Male Lewis rats	<ul> <li>All cocoa polyphenol-enriched diets attenuated age-related increases of both fecal IgA and IgA-coated bacteria.</li> </ul>	(Massot-Cladera et al. 2013)
Cranberry proanthocyanins (PACs) (100 mg/kg bw)	Male ICR mice received elemental enteral nutrition (EEN)	<ul> <li>Addition to PACs to EEN increased luminal slgA levels compared with EEN alone.</li> </ul>	(Pierre et al. 2014)
Cocoa flavonoids (0.2% polyphenols from conventional defatted cocoa (PC0.2), 0.4 (PC0.4) and 0.8% (PC0.8) polyphenols from non- fermented cocoa)	Female Wistar and Brown Norway rats	<ul> <li>Significant decrease in serum IgA were found in Brown Norway rats fed with cocoa polyphenolenriched diet for 3 weeks.</li> <li>All cocoa polyphenolenriched diets partially but significantly reduced the age-dependent increase in intestinal IgA concentration in Wistar rats after 14 days of supplementation.</li> <li>Fecal IgA was reduced in Wistar rats fed with PC0.2 and PC0.8 diets at the end of the study.</li> </ul>	(Massot-Cladera et al. 2014)
Aronia polyphenol, haskap polyphenol, bilberry polyphenol (anthocyanin content 0.4%)	Sprague Dawley rats fed high- or low-fat diet	<ul> <li>Dietary polyphenols from aronia, haskap and bilberry markedly elevated the amount of fecal IgA in rats fed high-fat diet.</li> </ul>	(Taira et al. 2015)

immunological barrier function by induction of defensins expression. Further studies are necessary, to provide a better understanding of how these polyphenols exert their protective actions on intestinal epithelial barrier function against bacterial infection, and to explore if other polyphenols exhibit similar properties.

#### Immunoglobulin secretion

Secretory immunoglobulin A (sIgA) is the most abundant type of immunoglobulin in human intestinal lumen, sIgA displays an array of properties that are crucial to mucosal immunity and homeostasis (Mantis, Rol, and Corthesy 2011). The secretory component protects the sIgA from degradation, withstanding proteolytic and digestive enzymes present in the gut lumen (Phalipon et al. 2002). Unlike other antibodies, such as IgG, that are present in an almost sterile systemic environment, sIgA resides in intestinal lumen heavily infested with microbes. Therefore, sIgA functions very differently from other antibodies, via steric hindrance, receptor blockade, or immune exclusion, resulting in less inflammatory response (Mantis, Rol, and Corthesy 2011).

There is limited information on the effects of polyphenols on systemic and/or intestinal IgA secretion in vivo (Table 2). Most studies focus on the effects of cocoa polyphenols on IgA levels using different experimental designs involving rats. Cocoa polyphenols were shown to reduce the age-dependent increases in serum, intestinal and fecal IgA levels in two studies by Massot-Cladera et al. (2014; 2013). Pérez-Berezo et al. (2012) demonstrated that a continuous and high cocoa-enriched diet decreased sIgA concentration in intestinal wash and fecal samples. Long-term cocoa intake may affect IgA production by down-regulating the gene expression of cytokines, such as IL-6, which is required for the activation of B cells to become IgAsecreting cells in Peyer's patches (PPs) and mesentric lymph nodes (MLNs), chemokines and chemokine receptors such as CCR9 and CCL28, together with RARα and RAR $\beta$  which are involved in the gut homing of IgAsecreting cells. Cocoa intake was also shown to affect the gut microbiota composition in rats and this was related to an altered toll-like receptor (TLR) pattern that could be responsible for the changes observed in the intestinal immune system (Massot-Cladera et al. 2012; Pérez-Berezo et al. 2012).

Furthermore, it has been documented that certain polyphenols could increase the amount of fecal IgA in rats fed high-fat diets. Okazaki et al. (2010) reported that curcumin elevated fecal IgA in rats fed high-fat diet but not those fed low-fat diet. Whereas in another study by Taira et al. (2015), dietary polyphenols from aronia, haskap and bilberry also markedly elevated the amount of fecal IgA in rats fed high-fat diet. These studies suggest that dietary polyphenols may improve intestinal immune function in high-fat-fed animals through elevation in luminal IgA, by increasing IgA production and/or suppressing IgA degradation. This may be associated with changes in the gut microbiota composition.

### Modulation of cytokines and chemokines expression

Cytokines, and also chemokines, are small proteins, which are important mediators that are involved in regulation of a wide range of biological functions, including innate and adaptive immunity, and inflammatory responses. Cytokines can be produced by a broad range of cells, including immune cells such as dendritic cells, macrophages, lymphocytes, but also cells other than immune cells such as intestinal epithelial cells (IECs). Several cytokines, including transforming growth factor alpha (TGF)-α, interleukin (IL)-1, IL-6, IL-10, IL-15, IL-18 and granulocyte-macrophage colony-stimulating factor (GM-CSF) are constitutively expressed by the intestinal epithelium for maintenance of epithelial cell growth and homeostasis (Stadnyk 2002), but some cytokines, such as IL-8, monocyte chemotactic protein-1 (MCP-1), GM-CSF, tumor necrosis factor (TNF)-α are markedly up-regulated in response to bacterial infection (Jung et al. 1995). In the case of intestinal inflammation, several cytokines and chemokines were also produced, which include IL-6, IL-8, IL-1 $\beta$ , and TNF- $\alpha$ . The secretion of these inflammatory cytokines may be an integral part of the immune response, dysregulation of these cytokines balance plays a key role in the pathogenesis of inflammatory bowel diseases (IBDs), encompassing Crohn's disease and ulcerative colitis. Therefore, it is vital to control the secretion of these cytokines for maintenance of intestinal homeostasis (Son, Satsu, and Shimizu 2005).

It is well known that polyphenols have significant antiinflammatory activity and therefore it is proposed that polyphenols could be used as an alternative natural approach to prevent or treat chronic inflammatory diseases, particularly gastrointestinal diseases. Indeed, numerous studies have shown the effects of polyphenols on intestinal inflammation (Table 3). To mimic intestinal inflammation in vivo, IECs were treated with a cocktail of pro-inflammatory substances, including IL-1 $\beta$ , TNF- $\alpha$ , IFN- $\gamma$  and lipopolysaccharides (LPS), which were reported as prominent and synergistic contributors in the development of IBDs (Puleston et al. 2005). The inflammatory state was characterized by an overexpression of mRNA and/or protein levels for pro-inflammatory markers such as IL-6, IL-8, MCP-1, etc. Treatment with polyphenols, for example genistein, ellagic acid, green

tea polyphenols, EGCG, quercetin, cyanidin-3-O-glucoside (C3G), pinoresinol can provoke a decrease in the expression of these cytokines (During et al. 2012; Ferrari et al. 2016; Oz and Ebersole 2010; Romier et al. 2008; Ruiz and Haller 2006; Sergent et al. 2010).

Dextran sulfate sodium (DSS) and 2, 4, 6-trinitrobenzene sulfonic acid (TNBS) have commonly been used to chemically induce colitis in animal models, which displays symptoms similar to those observed in human ulcerative colitis (Okayasu et al. 1990) and Crohn's disease (Antoniou et al. 2016). There are numerous studies reported on the effects of polyphenols against DSS- or TNBS-induced colitis (Table 3). For example, piceatannol (Kim et al. 2008), resveratrol (Martin et al., 2004; Sánchez-Fidalgo et al. 2010; Singh et al. 2010), curcumin (Isabel, Susana, and Alarcón 2011), naringenin (Azuma et al. 2013), ellagic acid (Marín et al. 2013), gallic acid (Pandurangan et al. 2015), thearubigin (Maity et al. 2003) have been shown to alleviate or prevent DSS- or TNBS-induced colitis by suppressing pro-inflammatory cytokines such as IL-1 $\beta$ , IL-6, IL-8, TNF- $\alpha$ , IFN- $\gamma$  and sometimes IL-12 p40. These results showed that polyphenols might present an alterative way to improve intestinal inflammation, such as IBD. However, so far, there is no definite mechanism that could explain all polyphenols effects and it is reported that the anti-inflammatory response of polyphenols is dependent on the cell type and is signal specific (Romier et al. 2009; Tunon et al. 2009). Therefore, further investigations are necessary to validate the potential beneficial role of polyphenols and also to understand the underlying mechanisms responsible for modulation of intestinal inflammation.

#### Polyphenols on molecular signaling

Studies from the last decade have demonstrated that polyphenols are able to confer their anti-oxidative, anti-inflammatory, anti-cancer through modulation of cellular molecular signaling pathways. A notable property of polyphenols is their ability to regulate the redox status in cells (Ramos 2008). Reactive oxidative species (ROS) are by-products of normal cellular metabolism or environmental triggers that are useful for signaling. However, at high levels, ROS can cause oxidative stress and damage DNA, lipids and proteins. Oxidative stress occurs when there is an imbalance between reactive ROS and antioxidants, and it is found in chronic gastrointestinal disorders such as IBD (Liu et al. 2017). Oxidative stress markers are also elevated in various kinds of cancers, including colorectal cancer (CRC) (Liou and Storz 2010). For example, nitric oxide, lipid peroxides, catalase (CAT), glutathione peroxidase (GPx) levels are increased in CRC cells (Haklar et al. 2001; Perše 2013; Rainis et al. 2007). It is suggested that the anti-oxidative properties of polyphenols, which are attributed to their free radical scavenging ability and antioxidant enzyme modulation, could counter oxidative stress to achieve chemoprevention (Link, Balaguer, and Goel 2010; Ross and Kasum 2002). Several dietary polyphenols, including resveratrol, EGCG and curcumin, are found to upregulate NF-E2-related

Table 3. Polyphenols regulation of intestinal cytokine expression and secretion in vitro, in vivo and ex vivo.

Polyphenols (Dosages)	Cells/ Models (Stimulants, if any)	Effects/ Key findings	Refs.
Red wine polyphenol	Zinc-deficient male Sprague-Dawley rats	<ul> <li>Treatment with red wine polyphenol decreased the expression of zinc deficiency induced pro-inflammatory cytokines such as tumor necrosis factor (TNF)-α, cytokine-induced neutrophil chemoattractant (CINC), whereas that of the anti-inflammatory interleukin (IL)—10 in jejunum.</li> </ul>	(Canali et al. 2000)
Green tea polyphenol (5 g/L in water)	IL-2 <sup>-/-</sup> C57BL/6J mice	<ul> <li>Green tea polyphenol-treated mice demonstrated a significant reduction in the spontaneous release of IFN-γ and TNF-α from colon explants and lamina propria lymphocytes.</li> </ul>	(Varilek et al. 2001)
Thearubigin (10–100 mg/kg/day)	Female Balb/c mice with trinitrobenzene sulfonic acid (TNBS)-induced colitis	<ul> <li>Thearubigin reduced T-helper 1 cytokines (e.g. IFN-γ and IL-12 p40) and induced T-helper 2 cytokine (IL-4) mRNA in colon tissue samples of TNBS- treated mice.</li> </ul>	(Maity et al. 2003)
Resveratrol (5–10 mg/kg/day)	TNBS-induced male Wistar rats	<ul> <li>Resveratrol reduced mucosal level of IL- 1β in colitic rats.</li> </ul>	(Martın et al. 2004)
Green tea extract	Rats with dinitrobenzene sulfonic acid (DNBS) induced colitis	<ul> <li>Green tea extract attenuated colitis induced by DNBS by a remarkable amelioration of the disruption of the colonic architecture, significant reduction of colonic myeloperoxidase and TNF-α.</li> </ul>	(Mazzon et al. 2005)
Genistein (100 μmol/L)	TNF and IL-1 $eta$ treated Mode-K cells	<ul> <li>Genistein inhibited TNF and IL-1β induced IL-6 production in cell supernatants.</li> </ul>	(Ruiz and Haller 2006)
Ellagic acid, genistein, EGCG, resveratrol (50 μmol/L)	IL-1 $\beta$ -treated Caco-2 cells	<ul> <li>Ellagic acid, genistein and EGCG decreased IL-1β induced IL-8 secretion</li> <li>Resveratrol increased significantly IL-8 secretion.</li> </ul>	(Romier et al. 2008)
Piceatannol (1, 2.5, 5 or 10 mg/ kg bw)	Dextran sulfate sodium (DSS)-induced female Balb/c mice	• Piceatannol prevented significant increases in IL-1 $\beta$ , IL-6 and TNF- $\alpha$ in colon of DSS-induced mice.	(Kim et al. 2008)
Apple procyanidins (ACT) (0.0013, 0.0025, 0.005%)	Phorbol 12-myristate 13-acetate (PMA)- induced Caco-2 cells	<ul> <li>ACT inhibited PMA-induced secretion of IL-8 in cell supernatants.</li> </ul>	(Yoshioka et al. 2008)
Grape seed, cocoa, sugar cane, oak, mangosteen and pomegranate polyphenolic extract (50 µM of gallic acid equivalent/l)	IL-1 $\beta$ induced Caco-2 cells	<ul> <li>Grape seed, sugar cane, oak and pomegranate polyphenolic extract reduced IL-1β induced IL-8 secretion.</li> </ul>	(Romier-Crouzet et al. 2009)
Green tea polyphenols (0.1, 0.25, 0.5 and 1%)	DSS-induced male ICR mice	<ul> <li>DSS-induced increase in IL-1β and MIF production in colonic mucosa were attenuated by 0.1% green tea polyphenols.</li> <li>The levels of IL-1β were increased by 0.5% and 1% green tea polyphenols treatment groups with DSS-induced colitis.</li> </ul>	(Mihye et al. 2010)
Grifola frondosa water extract (1 g/kg)	Sprague-Dawley rats with TNBS- induced colitis	<ul> <li>The polyphenol-enriched extract inhibited the TNBS-induced TNF-α expression in the colon tissue.</li> </ul>	(Lee et al. 2010)
Grifola frondosa water extract (10, 50 and 100 μg/ml)	TNF- $\alpha$ induced HT29 cells	<ul> <li>The polyphenol-enriched extract inhibited TNF-α induced MCP-1 and IL-8 mRNA and protein levels.</li> </ul>	(Lee et al. 2010)
EGCG and genistein (50 μM)	Caco-2 cells exposed to a cocktail of IL-1 $\beta$ , IFN- $\gamma$ , TNF- $\alpha$ and LPS	EGCG reduced significantly the secretion of IL-6 and IL-8, whereas genistein lowered significantly the levels of IL-6 and MCP-1.	(Sergent et al. 2010)
Resveratrol (10, 50, 100 mg/kg bw)	DSS-induced C57BL/6 mice	<ul> <li>Resveratrol decreased IFN-γ, TNF-α, IL-6 and IL-1β in serum of mice with acute colitis.</li> </ul>	(Singh et al. 2010)
Resveratrol (3 mg/kg bw)	DSS-induced female C57BL/6 mice	• Resveratrol reduced DSS-induced increase in TNF- $\alpha$ and IL-1 $\beta$ , and caused	(Sánchez-Fidalgo et al. 2010)
Ellagic acid (60 mg/kg bw)	1,2-Dimethylhydrazine-induced male Wistar albino rats	<ul> <li>a reduction in IL-10 in colon tissues.</li> <li>Ellagic acid reduced the expression of TNF-α and IL-6 in rat colon tissues as confirmed by immunohistochemical, immunoblot and immunofluorescence analysis.</li> </ul>	(Syed and Ganapasam 2010)
Green tea polyphenols (50, 200 and 400 μg/ml)	TNF- $\alpha$ stimulated IEC-6 cells	<ul> <li>Green tea polyphenols prevented TNF-α induced IL-8 release in a dosedependent manner.</li> </ul>	(Oz and Ebersole 2010)

Polyphenols (Dosages)	Cells/ Models (Stimulants, if any)	Effects/ Key findings Refs.
Kiwifruit extracts	Intestinal epithelial cells isolated from the large intestine of C57BL/6J and	<ul> <li>Kiwifruit extracts inhibited LPS-induced (Edmunds et al. 2011)</li> <li>IL-6, TNF-α and IFN-γ secretion in</li> </ul>
Curcumin (0.6% diet)	IL10-/- mice, stimulated by LPS DSS-induced C57BL/6 mice	culture supernatants.  • Curcumin resulted in down-regulation (Isabel et al., 2011)
Apple polyphenols	DSS-induced female C57BL/6 mice	of colonic IFN-γ and TNF-α levels.  • Apple polyphenols dampened the mRNA expression of IFN-γ, TNF-α, IL-1β, IL-6, IL-17, IL-22, and macrophage inflammatory protein (MIP)-1α in
Apple polyphenol extract	Rats with TNBS-induced colitis	colon tissues.  • Apple extract reduced the TNBS- (D'Argenio et al. 2012) induced increase in TNF-α mRNA and
Quercetin and pinoresinol (50 μmol/L)	IL-1 $eta$ stimulated Caco-2 cells	<ul> <li>protein in colon mucosa.</li> <li>Quercetin decreased IL-1β induced IL-6 (During et al. 2012) and IL-8 levels.</li> <li>Pinoresinol had a significant inhibitory</li> </ul>
Aqueous cinnamon extract	Freshly isolated intestinal enterocytes	effect on IL-6 secretion.  • Cinnamon extract inhibited the mRNA (Qin et al. 2012)
Cocoa polyphenolic extract (10 μg/ml)	TNF- $\alpha$ stimulated Caco-2 cells	<ul> <li>expression of IL-1β, IL-6 and TNF-α.</li> <li>Cocoa polyphenolic extract treatment protected TNF-α induced IL-8 secretion.</li> </ul>
Apple peel polyphenols (phenolic acids, flavonol glycosides, flavan-3-ols, procyanidins)	Caco-2/15 cells induced by iron- ascorbate and lipopolysaccharide (LPS)	• Apple peel polyphenols abolished the increase in TNF- $\alpha$ and IL-6 protein expression induced by iron-ascorbate (Denis et al. 2013)
Naringenin (0.3% diet)	DSS-induced male Balb/c mice	<ul> <li>and LPS.</li> <li>Gene expression of IFN-γ, IL-6, MIP-2 and IL-17A in colons of DSS-induced mice were attenuated by feeding naringenin.</li> </ul>
Sardinian wine extracts (30 and 60 μM)	Oxysterol induced Caco-2 cells	Sardinian wine extracts reduced (Biasi et al. 2013) oxysterol induced IL-6 and IL-8 protein levels.
Ellagic acid (2%)	DSS-induced female Balb/c and C57BL/ 6 mice	• Ellagic acid inhibited DSS-induced TNF- (Marín et al. 2013) $\alpha$ , IL6 and IFN- $\gamma$ protein levels in the colon.
Red wine extract (100, 200, 400 and 600 µg/ml)	HT29 cells stimulated with TNF- $\alpha$ , IL-1 and IFN- $\gamma$	<ul> <li>Red wine extract partially suppressed (Nunes et al. 2013) cytokines-induced IL-8 production.</li> </ul>
Cyanidin-3-glucoside (25 μM)	HT29 cells	<ul> <li>Cyanidin-3-glucoside inhibited IL-8 production by cells induced by cytokines (IL-1α, TNF-α and IFN-γ).</li> </ul>
Grape marc meal extract (GSGME) or spent hops (SH) (Total polyphenol content 8.5% and ~5% for GSGME and SH, respectively)	Weaned pigs	<ul> <li>GSGME reduced mRNA of intercellular adhesion molecule (ICAM-1) and IL-8 in duodenum, ICAM-1, IL-1β, IL-8 and TNF-α in both ileum and colon.</li> <li>SH lowered mRNA of IL-1β and IL-8 in</li> </ul>
Chlorogenic acid (20 and 50 mg/kg)	LPS challenged Sprague-Dawley rats	<ul> <li>duodenum and ileum, and of IL-1β and TNF-α in colon.</li> <li>Chlorogenic acid significantly reduced concentrations of TNF-α and IFN-γ in jejunum and colon of weaned rats.</li> <li>Only chlorogenic acid at 50 mg/kg affected the concentration of IL-10 in</li> </ul>
Green tea, cocoa and red wine polyphenols (50 μM total polyphenols, calculated as GA equivalents)	LPS induced Caco-2 cells	the jejunum.  • Wine and green tea polyphenols (Nicod et al. 2014) reduced basolateral IL-6 secretion from Caco-2 monolayers grown on Transwells and challenged with LPS.
Cranberry phenolic compounds (250 µg/ml)	Caco-2/15 cells induced by iron- ascorbate and LPS	<ul> <li>Cranberry phenolic compounds were able to significantly decrease TNF-α and</li> </ul>
Chlorogenic acid (CHA), caffeic acid (CA) and quinic acid (QA) (0.5- 2 mmol/L)	TNF- $\alpha$ and H <sub>2</sub> O <sub>2</sub> -induced Caco-2 cells	IL-6 production.  • CHA and CA significantly inhibited TNF- (Shin et al. 2015) $\alpha$ and H <sub>2</sub> O <sub>2</sub> -induced IL-8 secretion, but not for QA.
Chlorogenic acid (CHA) and caffeic acid (CA) (354 mg/kg for CHA, 180 mg/kg for CA))	DSS-induced female C57BL/6 mice	<ul> <li>CHA significantly reduced colonic mRNA (Shin et al. 2015) levels of macrophage inflammatory protein (MIP)—2 and IL-1β.</li> <li>CA inhibited only IL-1β mRNA</li> </ul>
Gallic acid (10 mg/kg bw)	DSS-induced male Balb/c mice	expression induced by DSS.  Gallic acid attenuated mRNA expression (Pandurangan et al. 2015) levels of TNF-α, IL-1β, IFN-γ, IL-6, and
Tea polyphenols (0.03, 0.06 and 0.09 g/kg bw)	Broiler chickens	IL-17 in colon. • Tea polyphenols reduced intestinal IL- (Li et al. 2015) $1\beta$ , IL-4, IL-6, IL-10 and IFN- $\gamma$ mRNA expression.

Table 3. Continued

Polyphenols (Dosages)	Cells/ Models (Stimulants, if any)	Effects/ Key findings	Refs.
Red grape pomace extracts (Total phenolic content 1.16 mg/g diet)	DSS-induced male Wistar rats	<ul> <li>Red grape pomace extracts abolished the colonic increase of IL-1α, IL-6 and IFN-γ and significantly reduced TNF- α levels.</li> </ul>	(Boussenna et al. 2016)
Dried apple peel powder (DAPP) (200 and 400 mg/kg/day)	DSS-induced male C57BL6 mice	<ul> <li>DAPP significantly suppressed intrinsic TNF-α and IL-6 elevations in DSS- induced mice.</li> </ul>	(Denis et al. 2016)
Cyanidin-3-O-glucoside (C3G) (20 and 40 μM)	TNF- $\alpha$ induced Caco-2 cells	<ul> <li>C3G reduced TNF-α induced IL-6 mRNA expression.</li> </ul>	(Ferrari et al. 2016)
Resveratrol (50 μM)	IPEC-J2 cells stimulated with dexoxynivalenol (DON)	<ul> <li>Resveratrol reduced DON-induced secretion of IL-6 and IL-8.</li> </ul>	(Ling et al. 2016)
Resveratrol (5 and 20 μM)	TNF-α stimulated Caco-2 endothelial EA.hy926 coculture	<ul> <li>Resveratrol significantly reduced the secretion of IL-8 and ICAM-1 in culture media.</li> </ul>	(Toaldo et al. 2016)
Mango polyphenols (include gallic acid and gallotanins)	DSS-induced male Sprague-Dawley rats	• Mango polyphenols reduced IL-1 $\beta$ and TNF- $\alpha$ mRNA, as well as IL-1 $\beta$ , TNF- $\alpha$ and IL-6 protein levels in the intestinal mucosa.	(Hyemee et al. 2017)
Pomegranate polyphenols (Ellagic acid as major polyphenol)	DSS-treated Sprague-Dawley rats	• Pomegranate polyphenols reduced TNF- $\alpha$ and IL-1 $\beta$ mRNA, and TNF- $\alpha$ , IL-1 $\beta$ and IL-6 protein levels in intestinal mucosal samples.	(Kim et al. 2017)
Black carrot polyphenols	TNF-α stimulated Caco-2 endothelial EA.hy926 coculture	<ul> <li>Black carrot polyphenols reduced the secretion of IL-8, monocyte chemoattractant protein (MCP)—1 and ICAM-1 under both non-inflammatory and inflammatory conditions.</li> </ul>	(Kamiloglu et al. 2017)

factor-2 (Nrf-2), a transcription factor related to oxidant resistance, and several antioxidant enzymes, to ameliorate oxidative stress (Cheng et al. 2012; Ghanim et al. 2011; González-Reyes et al. 2013; Sahin et al. 2010). Interestingly, the effect of polyphenols on redox modulation can be different depending on cell lines. While they act as anti-oxidants to normal, healthy cells, it can be pro-oxidant to cancerous cells (Amawi et al. 2017). This is also known as "oxidative therapy", where cancer cells are killed from damage caused by oxidative stress. Khan et al. (2014) suggested the signal/ cell-specific aspect of polyphenols may be due to the different amount of copper ions present in normal cells and cancer cells. In their study, EGCG, resveratrol, apigenin and luteolin did not inhibit growth of normal cells, unless they were cultured in copper-supplemented media. Since the anti-cancer effects of polyphenols in colorectal cancer are not the main focus of this review, readers may refer to León-González, Auger, and Schini-Kerth (2015) and Lee, Huang, and Shyur (2013) for more comprehensive view of the relationship between polyphenols and cancer pathways.

As mentioned in Section "Modulation of cytokines and chemokines expression and secretion", polyphenols can regulate the expression and production of various cytokines and chemokines, to attenuate inflammation. This is because polyphenols are inhibitors of NF- $\kappa$ B, a key transcription factor for inflammatory response. Shakibaei et al. (2007) reported that curcumin reduced inflammatory response by downregulation of cyclo-oxygenase-2 (COX-2) and matrix metalloproteinase-9 (MM-9) via the NF- $\kappa$ B pathway. Mice fed with grape seed proanthocyanidins experienced less inflammation, because the phenolic compounds inhibited NF- $\kappa$ B that was activated by the high-fat diet (Liu et al. 2017). There are many more studies displaying the anti-inflammatory

properties of polyphenols, including resveratrol (Ma et al. 2015), tea polyphenols (Tang et al. 2009), and quercetin (Ruiz et al. 2007). Hence, they are proposed to be used for treatments and preventives for several diseases, including inflammatory bowel disease (IBD), colitis and cancer (Amawi et al. 2017; Shapiro et al. 2007).

# Reciprocal interaction between polyphenols and gut microbiota

The human intestines house a diverse community of microbial species, which comprises mainly of bacteria (Eckburg et al. 2005). Some consider the gut microbiota to be a "metabolic organ" that can modulate nutrient absorption and interact with the immune system (Guinane and Cotter 2013; Kau et al. 2011; Krajmalnik-Brown et al. 2012). A "healthy composition" of gut microflora can form a physical barrier against infections, whereas disturbance in the balance of gut ecology (dysbiosis) causes higher susceptibility to pathogens. Multiple literature has discussed the linkage between dysbiosis and disease development, including obesity, IBD and cancer (Everard and Cani 2013; Ni et al. 2017; Ridaura et al. 2013; Zitvogel et al. 2015). Therefore, understanding the interactions between polyphenols and gut microbiota is crucial to giving insight on their implications on gut health.

#### Biotransformation and bioavailability of polyphenols

Due to their complex structures and high molecular weights, up to 95% of the consumed dietary polyphenols cannot be absorbed in the small intestines, but are passed on to the colon and metabolized by the residing bacteria (Cardona

et al. 2013; Marín et al. 2015). Biotransformation of polyphenols in the gut has been demonstrated in a number of in vitro studies by inoculating phenolic compounds with intestinal bacteria. Aura et al. (2005) discovered that gut bacteria deconjugate anthocyanins by cleaving their glycosidic bonds, to form lower molecular weights metabolites. Parkar, Trower, and Stevenson (2013) reported the catabolism of four common polyphenols, including rutin, quercetin, chlorogenic acid and caffeic acid, by a mixture of bacteria representing the gut microbiota, to smaller phenolic acids. Lee et al. (2006) revealed that the content of flavonoids and phenolic acids initially present in tea extracts decreased after 24-hour incubation with fecal bacteria, coupled by an emergence of aromatic metabolites (Lee et al. 2006). Interestingly, the catabolism of polyphenols is associated to the gut microbiota composition, as illustrated by an investigation conducted by Sánchez-Patán et al. (2015, 2012) and Tzounis et al. (2008). In both studies, polyphenols were incubated with fecal samples collected from different volunteers. Flavonoids and anthocyanins in wine were gradually catabolized to simpler phenols and phenolic acids over the course of 48 hours, while (-)-epicatechin (EC) and (+)-catechin (C) were degraded to more polar metabolites (Torres and Rosazza 2001; Tzounis et al. 2008). However, the rates and extent of polyphenol biotransformation in each inoculum were different, implying that dietary intake is not the only factor in the bioavailability of polyphenols and their metabolites. The finding is in line with previous studies that showed varying capacities of different bacteria to metabolize different polyphenols and produce different derivatives (Ozdal et al. 2016; Schoefer et al. 2003). Multiple studies and reviews have demonstrated how phenolic compounds are metabolized in the gut (refer to (Marín et al. 2015; Ozdal et al. 2016; Selma, Espín, and Tomás-Barberán 2009)).

#### Modulation of gut microbiota by polyphenols

While the bioavailability and bioactivity of polyphenols are largely dependent on bacterial metabolism, it should be noted that polyphenols can shape the composition of the gut bacteria. The most studied aspect in this regard is polyphenols' ability to inhibit growths of specific bacteria. Foods rich in dietary polyphenols have been studied for their antimicrobial activities against common foodborne pathogens and profiled for their phenolic contents. These studies range from simple in vitro studies, where food extracts were incubated with selected microbes, to comprehensive in vivo studies, where fecal bacteria were analyzed before and after exposure to polyphenols. Table 4 summarizes the results and details of the listed references.

In in vitro settings, incubation of phenolic acids and bacteria revealed that pathogenic E. coli, S. aureus and C. albicans were susceptible to most phenolic acids tested (Burdulis et al. 2009). Lee et al. (2006) reported inhibition of most tested bacteria, in particular pathogenic E. coli, S. typhimurium and C. perfringens, by tea polyphenols, and their derivatives. They then examined the antimicrobial capacities of each phenolics and metabolites individually. It

was found that the metabolites, especially the ones with an aromatic ring in their structure, were more adept at bacterial inhibition than their parent polyphenols. This is of no surprise as it is known that the metabolites resulting from gut bacterial transformation of polyphenols often exhibit different, if not enhanced, bioefficacy than their original forms, due to the altered chemical structure and bioavailability (Blaut and Clavel 2007). In another similar study, green tea extracts were also shown to inhibit growths of several strains of bacterial pathogens, including L. monocytogenes, P. aeruginosa, S. aureus and B. cereus (Sourabh et al. 2013). Chan et al. (2011) compared the antimicrobial properties and polyphenol concentrations in different types of teas. They found that the teas were only effective against gram-positive bacteria, with green tea being the best antibacterial. However, in other studies, tea extracts were able to inhibit also gram-negative bacteria, albeit to a lesser extent (Chan et al. 2011; Lee et al. 2006; Sourabh et al. 2013). This could be due to the different solvents used during extraction in these studies, which in turn affects the amount of tea polyphenols extracted. Among the tea polyphenols extracted, EGCG showed the highest antibacterial potential, followed by (-)-epicatechin-3-gallate (ECG) and (-)-epigallocatechin (EGC) (Lee et al. 2006). Several studies found that phenolic compounds in blueberries, such as quercetin and chlorogenic acid, can inhibit growth of several pathogens, including Listeria monocytogenes, Salmonella enteritidis, H. pylori, Bacillus cereus, etc. (Burdulis et al. 2009; Nohynek et al. 2006; Shen et al. 2014). More recently, Singh et al. (2019) showed that the interesting role of urolithin A, a major microbial metabolite derived from polyphenolics of berries and pomegranate fruits in barrier integrity in addition to anti-inflammatory effects. Since gut microbiota play an important physiological role in catabolizing dietary components into absorbable metabolites, it is speculated that it is the interaction of polyphenol together with the antimicrobial peptides (e.g. bacteriocins) produced by certain gut microbiota, for example lactic acid bacteria, provides greater health benefits. However, there are only a few studies on the synergistic effects of polyphenols and probiotics on antimicrobial effects or gut microbiota modulation (de Souza et al. 2019; Westfall, Lomis, and Prakash 2018). Also, there are only few studies discussing polyphenols' synergy with probiotics to manage inflammation and prevent diseases (Banerjee and Dhar 2019; Rupasinghe, Parmar, and Neir 2019) but these studies do not explain what causes the synergy (i.e. whether it's the bacterial products that interact with polyphenols or the bacteria itself).

Apart from acting as antimicrobial agents against pathogens, polyphenols are also suggested to confer their protective effects as prebiotics. Prebiotic is defined to be a "nonviable food component that confers a health benefit on the host associated with modulation of the microbiota" (Pineiro et al. 2008). Polyphenols may be able to fit into this description because of their specificity against pathogens, while beneficial bacteria remain unaffected, if not stimulated, by polyphenols. Tzounis et al. (2008) demonstrated that epicatechin and catechin not only inhibited foodborne



Table 4. Effect of polyphenols and polyphenol-rich foods on microbial growth, in vitro, ex vivo & in vivo.

Polyphenols (Dosages)	Models	Effects/ Key findings	Refs.
Apple peel polyphenol-rich extract (APPE) (150 or 300 mg/kg/day)	C57BL6/J mice	<ul> <li>APPE inhibited growth of H. pylori after the mice were infected with the pathogen.</li> </ul>	(Pastene et al. 2010)
Blueberry extract containing chlorogenic acid, quercetin, ellagic acid, quercetin-3-galactoside (112.5–900 mg/mL)	L. monocytogenes and S. enteritidis	<ul> <li>Blueberry extract inhibited the growth of L. monocytogenes and S. enteritidis.</li> </ul>	(Shen et al. 2014)
Blueberry extract (1% v/v for Fecal Batch Culture Fermentation; or 10–25% v/v for Plate count) Blueberry extract (4 mL/kg/d)	Lactobacillus rhamnosus NZRM 299 and Bifidobacterium breve NZRM 3932 Female Sprague Dawley rats	<ul> <li>Blueberry extract significantly increased number of Lactobacillus rhamnosus and Bifidobacterium breve.</li> <li>Rats gavaged with blueberry extract for 6 days had increased amount of Lactobacillus rhamnosus and</li> </ul>	(Molan et al. 2009)
Blueberry drink (25 g blueberry powder/d)	Healthy human individuals	<ul> <li>Bifidobacterium breve in the cecum.</li> <li>6 weeks consumption of the wild blueberry drink increased the amount of Bifidobacterium spp. in</li> </ul>	(Vendrame et al. 2011)
Bilberry extract and blueberry extract (anthocyanidins are the major polyphenols) (50 μL/well)	Bacteria: Listeria monocytogenes ATCC 19117, Staphylococcus aureus ATCC 25923, Bacillus subtilis ATCC 6633, Enterococcus faecalis ATCC 29212, Escherichia coli ATCC 25922, Pseudomonas aeruginosa ATCC 27853, Citrobacter freundii ATCC 8090, and Salmonella typhimurium ATCC 14028	the human intestines.  Blueberry and bilberry extracts showed similar inhibitory effects against all tested bacteria, but the yeast strains were not affected.	(Burdulis et al. 2009)
	Yeast: Debaryomyces hansenii, Trichosporon cutaneum, Kluyveromyces marxianus var. lactis, Sacharomyces cerevisiae, Candida parapsilosis, Torulaspora delbrueckii, Pichia kluyveri, and Rhodotorula rubra		
Benzoic acids, including butyl gallate, ethyl 3,5-dihydroxybenzoate, 3,4-dihydroxy-benzoic acid methyl ester, 2,4-dihydroxy-3,6-dimethylbenzoic acid, isopropyl 3,4,5-trihydroxybenzoate, methyl 3,5 dihydroxybenzoate	S. aureus CNRZ3, B. subtilis ATCC6633, L. monocytogenes ATCC 19115, E. coli ATCC 25922, P. aeruginosa ATCC 27853, S. Enteritidis E0220	<ul> <li>Ethyl 3,5-dihydroxybenzoate inhibited growth of <i>E. coli ATCC 25922</i>, <i>S. Enteritidis E0220 and B. subtilis ATCC6633</i></li> <li>3,4-dihydroxy-benzoic acid methyl ester inhibited growth of <i>E. coli ATCC 25922</i>, <i>S. Enteritidis E0220</i>, <i>L. monocytogenes ATCC 19115 and B. subtilis ATCC6633</i></li> <li>Methyl 3,5 dihydroxybenzoate inhibited <i>B. subtilis ATCC6633</i>, <i>S. Enteritidis E0220 and E. coli ATCC 25922</i></li> <li>Isopropyl 3,4,5-trihydroxybenzoate inhibited <i>E. coli ATCC 25922</i>, <i>S. Enteritidis E0220 and B. subtilis ATCC6633</i></li> <li>2,4-dihydroxy-3,6-dimethylbenzoic acid promoted growth of <i>E. coli ATCC 25922 but inhibited S. Enteritidis E0220</i></li> <li>Butyl gallate inhibited all tested bacteria except <i>P. aeruginosa</i></li> </ul>	(Bouarab-Chibane et al. 201
Berry extracts (1 mg/mL, contains >400 mg polyphenols/g dry wt of berries)	B. cereus ATCC 9139, C. jejuni LMG 8841, C. albicans NCPF 3179, C. perfringens ATCC 13124, E. coli ATCC 11775, H. pylori NCTC 11637, L. rhamnosus VTT E-97800, L. rhamnosus GG VTTE-96666, S. enterica sv. Infantis VTT E-97738, S. enterica sv. Typhimurium SH-5014,	<ul> <li>ATCC 27853</li> <li>H. pylori and B. cereus were inhibited by all berry extracts.</li> <li>Cloudberry, raspberry and strawberry extracts were most effective against all bacteria strains.</li> </ul>	(Nohynek et al. 2006)

Table 4. Continued.

Polyphenols (Dosages)	Models	Effects/ Key findings	Refs.
71	S. enterica sv. Typhimurium VTT E- 981151, S. aureus ATCC 6538, S. aureus ATCC 25923, S. aureus ATCC 12600 and S. epidermis DSM 20044		
Berry extracts (containing 230–470 mg/g extract depending on the berries) (1 mg/mL)	Bifidobacterium lactis VTT-E-94508 (Bb- 12), Enterococcus faecalis VTT E-93203T (DSM 20478), E. coli 50 VTT E-94564T (ATCC 11775), E. coli CM 871, Lactobacillus crispatus VTT E-96725 (M247), Lactobacillus johnsonii VTT E-97797 (LJ1), Lactobacillus paracasei F19 VTT E- 94510 (LMG P-17806), Lactobacillus plantarum VTT E-78076, Lactobacillus reuteri VTT E-97849 (ATCC 55730), Lactobacillus rhamnosus VTT E-97800, Lactobacillus rhamnosus GG VTT E- 96666 (ATCC 53103) and Salmonella enterica ser. Typhimurium SH5014	<ul> <li>In liquid culture, E. coli CM 871 and E. coli 50 were inhibited by all the berry extracts, except for black currant extract.</li> <li>Salmonella enterica ser. Typhimurium SH5014 was inhibited by all berry extracts except for blueberry extract.</li> <li>Lactobacillus group remained unaffected by berries in liquid culture.</li> </ul>	(Puupponen-Pimiä et al. 2001
Berry extracts (50 μL/disc)	Clostridium perfringens ATCC 19404, Bacillus subtilis ATCC 6633, Listeria innocua ATCC 33090, Staphylococcus aureus ATCC 6538, Sarcina lutea ATCC 934, Micrococcus flavus ATCC 40240, Escherichia coli ATCC 25922, Pseudomonas aeruginosa ATCC 9027, Salmonella enteritidis ATCC 13076, Shigella sonnei ATCC 25931, Klebsiella pneumoniae ATCC 10031	<ul> <li>Blackthorn, European cornel and wild blackberry extracts inhibited all the tested gram-positive bacteria, including <i>C. perfringens</i>, <i>B. subtilis</i>, <i>L. innocua</i>, <i>S. aureus</i>, <i>S. lutea</i>, and <i>M. flavus</i>.</li> <li>For gram-negative, <i>E. coli</i>, <i>P. aeruginosa</i>, <i>S. enteritidis</i> and <i>S. sonnei</i> were susceptible to all berry extracts, but P. vulgaris was only inhibited by blackthorn and</li> </ul>	(Radovanović et al. 2013)
Cinnamic acid, including, caffeic acid, caffeic acid 1,1-dimethylallyl ester, chicoric acid, cinnamyl-3,4-dihydroxy-α-cyanocinnamate, 2,4-dihydroxycinnamic acid, ethyl 3,4-dihydroxycinnamate, chlorogenic acid, CU-CPT22 acid	and Proteus vulgaris ATCC 8427 S. aureus CNRZ3, B. subtilis ATCC6633, L. monocytogenes ATCC 19115, E. coli ATCC 25922, P. aeruginosa ATCC 27853, S. Enteritidis E0220	<ul> <li>European cornel extracts.</li> <li>Chlorogenic acid promoted growth of <i>B. subtilis ATCC6633 but inhibited L. monocytogenes ATCC 19115</i></li> <li>Caffeic acid inhibited <i>S. aureus CNRZ3, L. monocytogenes ATCC 19115, S. Enteritidis E0220 and E. coli ATCC 25922</i></li> <li>Caffeic acid 1,1-dimethylallyl ester inhibited <i>S. aureus CNRZ3, B. subtilis ATCC6633, L. monocytogenes ATCC 19115 and S. Enteritidis E0220</i></li> <li>CU-CPT22 acid inhibited <i>S. aureus CNRZ3, B. subtilis ATCC6633 and E. coli ATCC 25922</i></li> <li>Chicoric acid inhibited <i>, L. monocytogenes ATCC 19115 and S. Enteritidis E0220</i></li> <li>Ethyl 3,4-dihydroxycinnamate inhibited <i>B. subtilis ATCC6633, L. monocytogenes ATCC 19115 and S. Enteritidis E0220</i></li> <li>Cinnamyl-3,4-dihydroxy-α-cyanocinnamate inhibited all tested bacteria</li> </ul>	(Bouarab-Chibane et al. 2019)
Cocoa powder (10 or 20 g/d)	Male pigs	<ul> <li>tested bacteria</li> <li>Pigs fed with flavanol-enriched cocoa powder had more Lactobacillus and Bifidobacterium</li> </ul>	(Jang et al. 2016)
Cocoa flavanols (23 or 494 mg/d)	Healthy human volunteers	<ul> <li>species in the colon.</li> <li>Consumption of cocoa flavanols for 4 weeks changed the abundance of Bifidobacterium spp., C. histolyticum group, E. rectale-C. coccoides group and Lactobacillus and Enterococcus spp. compared to control.</li> </ul>	(Tzounis et al. 2011)

Dolumbanals (Dasses)	Models	Effected Von Goding	D-f-
Polyphenols (Dosages)		Effects/ Key findings	Refs.
Coumarins, including baicalein, 3',5'- dihydroxyflavone, 5,7-dihydroxy-4- phenylcoumarin, 5,7-dihydroxy-4- propylcoumarin, 5,7-dihydroxy-4- methylcoumarin	S. aureus CNRZ3, B. subtilis ATCC6633, L. monocytogenes ATCC 19115, E. coli ATCC 25922, P. aeruginosa ATCC 27853, S. Enteritidis E0220	<ul> <li>The group that consumed 494 mg cocoa flavanols per day had a more significant increase in <i>Lactobacillus, Enterococcus</i> and <i>Bifidobacterium spp.</i>, and decreased the amount of <i>C. histolyticum</i> group, compared to the group who consumed less cocoa flavanols.</li> <li>Baicalein inhibited <i>L. monocytogenes ATCC 19115</i></li> <li>5,7-dihydroxy-4-propylcoumarin inhibited <i>S. aureus CNRZ3 and L. monocytogenes ATCC 19115</i></li> <li>5,7-dihydroxy-4-phenylcoumarin inbhited <i>S. aureus CNRZ3, B. subtilis ATCC6633 and L. monocytogenes ATCC 19115</i></li> <li>3',5'-dihydroxyflavone inhibited all bacteria except <i>B. subtilis ATCC6633</i></li> <li>5,7-dihydroxy-4-methylcoumarin inhibited <i>L. monocytogenes</i></li> </ul>	(Bouarab-Chibane et al. 2019)
Cranberry extract	Staphylococcus aureus ACTT 25923	<ul><li>ATCC 19115</li><li>Cranberry extract inhibited the</li></ul>	(Lian et al. 2012)
(-)-epicatechin (EC) and (+)-catechin (C) (150 or 1000 mg/L)	Human fecal samples	<ul> <li>growth of <i>S. aureus</i>.</li> <li>24-hour incubation with EC increased the growth of <i>C. coccoides-E. rectale</i> group in fecal samples significantly.</li> <li>C increased the amount of <i>C. coccoides-E. rectale</i> group, <i>Bifidobacterium spp.</i>, and <i>E. coli</i>, but</li> </ul>	(Tzounis et al. 2008)
Flavonoids, including cardamonin, dihydromyricetin, diosmin, epigallocatechin gallate, myricetin, myricitrin, quercetin 3-β-D-glucoside, rutin, silibinin, taxifolin, wedelolactone	S. aureus CNRZ3, B. subtilis ATCC6633, L. monocytogenes ATCC 19115, E. coli ATCC 25922, P. aeruginosa ATCC 27853, S. Enteritidis E0220	<ul> <li>inhibited <i>C. histolyticum</i>.</li> <li>Taxifolin inhibited <i>S. aureus CNRZ3</i> and <i>L. monocytogenes ATCC 19115</i></li> <li>Myricitrin dihydrate promoted growth of <i>B. subtilis ATCC6633 but inhibited L. monocytogenes ATCC 19115</i></li> <li>Diosmin inhibited <i>S. Enteritidis E0220, S. aureus CNRZ3 and L. monocytogenes ATCC 19115</i></li> <li>Rutin hydrate inhibited <i>B. subtilis ATCC6633, E. coli ATCC 27853</i></li> <li>Myrecitin inhibited <i>E. coli ATCC 27892 and P. aeruginosa ATCC 27853</i></li> <li>Myrecitin inhibited <i>E. coli ATCC 27922, S. Enteritidis E0220 and S. aureus CNRZ3</i></li> <li>Dihydromyricetin inhibited <i>S. aureus CNRZ3 and L. monocytogenes ATCC 19115</i></li> <li>Cardamonin inhibited <i>S. aureus CNRZ3, B. subtilis ATCC6633, L. monocytogenes ATCC 19115, E. coli ATCC 25922</i></li> <li>Quercetin 3-β-D-glucoside inhibited <i>S. aureus CNRZ3 and L. monocytogenes ATCC 19115</i></li> <li>Silibinin promoted growth of <i>S. Enteritidis E0220</i></li> <li>Epigallocatechin gallate inhibited all tested bacteria except <i>E. coli ATCC 25922</i></li> <li>Wedelolactone promoted growth of <i>S. Enteritidis E0220</i></li> <li>Epigallocatechin gallate inhibited all tested bacteria except <i>E. coli ATCC 25922</i></li> </ul>	(Bouarab-Chibane et al. 2019)
Flavonoids, including naringenin, hesperidin, quercetin and rutin (2, 20 or 100µg/mL)	B. bifidum, B. adolescentis	<ul> <li>S. Enteritidis E0220</li> <li>For B. bifidum, naringenin only inhibited its growth at 2μg/mL at 2 hours incubation, while other concentrations and incubation time did not affect bacterial growth. Hesperidin, quercetin and rutin all inhibited bacterial growth first at 0.5 incubation hour, then promoted bacterial growth at 2 hour</li> </ul>	(Gwiazdowska et al. 2015)

Table 4. Continued.

Polyphenols (Dosages)	Models	Effects/ Key findings	Refs.
Grape pomace concentrate (GPC) and grape seed extract (GSE) (60 g GPC/kg; 7.2 g GSE/kg)	Broiler chicks	incubation which then returned to comparable rates as control at longer incubation time points.  • At 100μg/mL, B. adolescentis growth was inhibited by naringenin, hesperidin, and quercetin after 2 hours incubation. But as incubation time increased, the growth inhibition effect became diminished. Rutin only inhibited its growth in the first 0.5 hour.  • GPC and GSE increased the number of <i>Enterococcus</i> , but decreased the amount of <i>Clostridium</i> in the ileum	(Viveros et al. 2011)
		<ul> <li>after 21 days.</li> <li>In the cecum, GPC and GSE increased the number of Escherichia coli, Lactobacillus, Enterococcus, and Clostridium.</li> <li>GPC and GSE increased the population of phenol-degrading bacteria in the chicks.</li> <li>GPC and GSE increased the biodiversity of the gut microbiota of the birds.</li> </ul>	
Grape seed extract (GSE) (1% w/w in 2 kg diet)	Crossbred female pigs	<ul> <li>6-day GSE diet increased the amount of Lachnospiraceae, Clostridales, Lactobacillus and Ruminococcacceae in feces.</li> </ul>	(Choy et al. 2014)
Grape seed extract (GSE) (flavan-3-ol fraction) (600 mg/L)	Human fecal samples	<ul> <li>GSE increased the population of Lactobacillus and Enterococcus but reduced the number of C. histolyticum group.</li> </ul>	(Cueva et al. 2013)
Grape seed proanthocyanidin extract (GSPE) and gallic acid (500 mg/kg)	Female Wistar rats	<ul> <li>8-day treatment with GSPE increased the abundance of <i>Bacteroides</i>, <i>Parabacteroides</i>, <i>Sutterella Phascolarctobacterium</i>, and <i>Bilophila</i> in the cecum.</li> <li>Amount of <i>Ruminococcus</i>, <i>Oscillospira</i>, <i>Coprococcus</i> and <i>Dehalobacterium</i> were reduced by GSPE.</li> </ul>	(Casanova-Martín et al. 2018
Grape seed proanthocyanidins (GSPs) (250 mg/kg)	Crossbred weaned piglets	<ul> <li>GSPs increased the diversity and abundance of gut microbiota in the piglets significantly.</li> <li>GSPs decreased the amount of <i>Lactobacillaceae</i>, but increased the abundance of <i>Clostridiaceae</i> in the piglets.</li> </ul>	(Han et al. 2016)
Hydroxycinnamic phenolic acids, including <i>p</i> -cumaric acid, ferulic acid, sinapic acid, caffeic acid, and chlorogenic acid (2, 20 or 100μg/mL)	B. bifidum, B. adolescentis	<ul> <li>p-cumaric acid and caffeic acid promoted growth of B. bifidum at 2-hour incubation, but not at longer incubation periods</li> <li>Ferulic acid, at 100μg/mL, inhibited B. bidfidum growth for 2 hours.</li> <li>The phenolic acids used did not affect B. adolescentis growth significantly.</li> </ul>	(Gwiazdowska et al. 2015. )
Naphtoquinones, including 5,8- dihydroxy-1,4-naphthoquinone, 2,3-dichloro-5,8-dihydroxy-1,4- naphthoquinone	S. aureus CNRZ3, B. subtilis ATCC6633, L. monocytogenes ATCC 19115, E. coli ATCC 25922, P. aeruginosa ATCC 27853, S. Enteritidis E0220	<ul> <li>5,8-dihydroxy-1,4-naphthoquinone inhibited all tested bacteria except <i>P. aeruginosa ATCC 27853</i></li> <li>2,3-dichloro-5,8-dihydroxy-1,4-naphthoquinone inhibited <i>S. Enteritidis E0220, S. aureus CNRZ3, B. subtilis ATCC6633, and L. monocytogenes ATCC 19115</i></li> </ul>	
Phenolic acids, including benzoic acids, phenylacetic acids and phenylpropionic acids (62.5, 125, 250, 500 and 1000 μg/mL)	E. coli ATCC 25922, E. coli O157:H7, E. coli lpxC/tolC, Lactobacillus paraplantarum LCH7, Lactobacillus plantarum LCH17, Lactobacillus fermentum LPH1, L. fermentum CECT 5716,	The nonpathogenic strain of <i>E. coli</i> ATCC 25922 was only inhibited by 4 out of 13 phenolic acids tested, whereas the pathogenic <i>E. coli</i> O157:H7 was inhibited by most phenolic acids	(Cueva et al. 2010)

Table 4. Continued.

Polyphonols (Dosagos)	Models	Effects / Koy findings	Refs.
Polyphenols (Dosages)		Effects/ Key findings	Reis.
	Lactobacillus brevis LCH23, Lactobacillus coryniformis CECT 5711, C. albicans MY1055, S. aureus EP167 and P. aeruginosa PAO1	<ul> <li>Lactobacillus paraplantarum LCH7 and Lactobacillus coryniformis CECT 5711 were inhibited by most phenolic acids but the rest of the Lactobacillus group was not affected.</li> <li>Pathogen S. aureus EP167 was inhibited by the phenolic acids.</li> </ul>	
Purple sweet potato (PSP) polyphenols (0.16% (w/v))	Fresh pig feces	<ul> <li>PSP polyphenols increased the relative abundance of <i>Bifidobacterium</i> in the presence of cellulose, but lowered relative abundance of <i>Bifidobacterium</i> in the presence of inulin</li> <li>PSP polyphenols lowered the relative abundance of <i>Proteobacterium</i>, with or without dietary fiber</li> <li>PSP polyphenols, mixed with cellulose, increased the relative</li> </ul>	(Kilua et al. 2019)
Red wine polyphenols	Human fecal samples	<ul> <li>abundance of Actinobacteria</li> <li>Red wine extract inhibited the growth of C. histolyticum group in human fecal inoculum.</li> </ul>	(Sánchez-Patán et al. 2012)
Red wine polyphenols (272 mL/d)	Healthy human males	<ul> <li>4-week consumption of red wine polyphenols increased the number of Enterococcus, Prevotella, Bacteroides, Bifidobacterium, Bacteroides uniformis, Eggerthella lenta, and Blautia coccoides-Eubacterium rectale groups</li> </ul>	(Queipo-Ortuño et al. 2012)
Stilbenes, including hapontin, resveratrol and pinosylvin	S. aureus CNRZ3, B. subtilis ATCC6633, L. monocytogenes ATCC 19115, E. coli ATCC 25922, P. aeruginosa ATCC 27853, S. enteritidis E0220	<ul> <li>Resveratrol inhibited all tested bacteria</li> <li>Pinosylvin inhibited all tested bacteria except for <i>P. aeruginosa ATCC 27853</i></li> </ul>	(Bouarab-Chibane et al. 2019)
Tea extracts	M. luteus, S. aureus and B. cereus	<ul> <li>Green tea extract inhibited all 3 bacteria while black tea and white tea only inhibited M. luteus and B. cereus.</li> </ul>	(Chan et al. 2011)
Tea polyphenols (0.1% w/v)	Human fecal bacteria, and 28 strains of bacteria (refer to (Lee et al. 2006))	<ul> <li>Tea polyphenols strongly inhibited growth of pathogenic <i>C. perfringens, C. difficile,</i> and <i>Bacteroides spp.</i></li> <li>Commensal bacteria and probiotics were less affected by the tea polyphenols.</li> </ul>	(Lee et al. 2006)
Tea polyphenols (1.2 g/d)	Healthy human individuals	<ul> <li>4-week consumption of tea polyphenols lowered the number of C. perfringens and other Clostridium spp. in the volunteers' feces, while number of Bifidobacterium spp. increased.</li> </ul>	(Okubo et al. 1992)

pathogens, but also increased the count of probiotics like Lactobacillus, and Bifidobacterium spp. and Eubacterium rectale-C. coccoides. A follow-up study by Tzounis et al. (2011) supplied volunteers with high or low amounts of cocoa flavanols. After 4 weeks, even the total count of fecal bacteria remained unchanged, the number of Lactobacillus and Bifidobacterium spp. was increased. The increase was also dose-dependent to concentrations of consumed flavanols. Similar findings were produced in pigs that were fed cocoa flavanols, which saw an increase in Lactobacillus and Bifidobacterium spp. in the feces (Jang et al. 2016). Another in vivo experiment showed that 4-week consumption of red wine polyphenols resulted in a significant increase in Enterococcus, Prevotella, Bacteroides, Bifidobacterium spp., and Blautia coccoides-Eubacterium rectale groups (Queipo-

Ortuño et al. 2012). Broiler chicks fed with grape extracts had more Lactobacillus spp. in their intestines, and a more diverse gut microbiota, which is associated with gut health (Guinane and Cotter 2013; Viveros et al. 2011). Meanwhile, the count of Clostridium spp., which are linked to Irritable Bowel Syndrome (IBS) and IBD, was lowered (Ghoshal et al. 2012; Morgan et al. 2012; Wehkamp et al. 2003). This finding is in line with a recent in vitro study where Clostridium spp. was decreased after inoculation with red wine extracts (Sánchez-Patán et al. 2012). Grape seed and wine polyphenols were found to lower amount of Firmicutes in the intestines, which are associated with metabolic disorders (Queipo-Ortuño et al. 2012). An interesting human study performed by Mayta-Apaza et al. (2018) demonstrated that polyphenol-induced change in gut microbiota

composition is also dependent on the preexisting gut microbes. Ten healthy individuals consumed tart cherry juice for 5 days, and their stool was examined before and after the intervention. Mayta-Apaza et al. (2018) discovered that, before the intervention, there was already significant difference in gut microbiota among the individuals, marked by the abundance of Bacteroides. The group with fewer Bacteroides had a different response to the cherry polyphenols than the group with more Bacteroides. The former had an increase in Bacteroides and Bifidobacterium after the intervention, while the latter experienced a decrease in those bacterial groups. However, the authors acknowledged that the differential response may be due to different dietary habits in each individual. Similar to this study, a major drawback in most human studies for the effects of polyphenols is the lack of a control diet. In the human studies mentioned above, polyphenols were often consumed by volunteers in the form of juice or powder supplements. The studies did not take into account of the amount of polyphenols in study participants' normal diet. The effects observed may not be entirely due to the polyphenols that were tested in the studies, but a combined effect of various polyphenols found in the supplements and diet. Therefore, more welldevised clinical trials may be required for us to fully understand the effects of polyphenols in humans.

A recurring theme in these studies is that the bioactivity of polyphenols against bacteria is structure-dependent, and the bacterial susceptibility to polyphenols is strain-dependent. For example, tea polyphenols are more effective against gram-positive bacteria, whereas berry polyphenols are more effective against gram-negative bacteria. The authors attributed the selective actions of phenolic compounds to the different structures of gram-positive and gram-negative bacteria. In the case of tea polyphenols, the presence of negatively-charged lipopolysaccharides (LPS) on the cell membrane in gram-negative bacteria may repulse and reduce cell uptake of tea phenolics, making them more resistant. Taguri, Tanaka, and Kouno (2004) observed that the most effective antibacterial polyphenols, such as ECG and EGC, all contained a galloyl group in their chemical structure(Taguri, Tanaka, and Kouno 2004). Bouarab-Chibane et al. (2019) studied the effects of 35 polyphenols on 6 bacterial strains, where they also noted the strain-specific nature of polyphenols' antibacterial properties. Rarely was any of the tested polyphenols effective against all grampositive or gram-negative bacteria. They concluded that the antibacterial effects of polyphenols cannot be categorized according the polyphenol class. Even within the same phylum, bacteria may respond differently to the same polyphenolic compound. Gwiazdowska et al. (2015) observed the effects of flavonoids and phenolic acids on the in vitro growth of different strains of bifidobacterium over the span of 48 h. Bacterial growths were either inhibited or promoted, depending on strain, polyphenolic compound, concentration of polyphenol and incubation time. Also, different flavonoids or phenolic acids exerted different effects on the same bacterial strain, compared with other polyphenolic compounds of the same class.

Current studies provide us some insight on how a single polyphenolic compound affects the growth of selected few bacteria in vitro, or composition of the gut microbiota in vivo. And most in vivo studies only demonstrate the general effects of polyphenols on certain bacterial phylum, for example cocoa flavanols and grape anthocyanidins increase the abundance of Bifidobacterium. However, much still remains unknown, when polyphenols of the same category, such as flavonoids, favanols, anthocyanins, etcetera, can have varying effects on the same bacterial strain in in vitro settings. And in vivo, there are large variations in gut microbiota among individuals, which may result in a different response to the same polyphenol, due to the different polyphenolic metabolites and bacterial metabolites. Also, there are many things to consider when assessing the in vivo effects of polyphenols, including the interaction of polyphenols and other components in diets, which could interfere with polyphenol-bacterial interactions. For example, a recent study (Kilua et al. 2019), demonstrated that the same purple sweet potatoes polyphenols modulates swine gut microbiota, but the extent to which the polyphenols promote or inhibit bacterial growth depended on the type of dietary fiber in the mix. And Mansoorian et al. (2019) showed that fermentable fibers changed the way rutin was metabolized by fecal bacteria. Therefore, it is difficult to conclude how polyphenols in a whole changes bacterial growth or affects the gut microbiota or vice versa with studies at hand.

#### Future perspective and challenges for the use of polyphenol

Because of the anti-oxidative, anti-inflammatory, and anticarcinogenic properties of polyphenols, they have been proposed to be promising candidates in preventing and combating various gastrointestinal diseases. However, much is still unknown about polyphenols. A crucial challenge in the use of polyphenols is determining the dosage. Given how polyphenol concentrations vary in different food source, and can be altered by food preparation methods (Manach et al. 2004), or the fact that polyphenols can interact with other food substances and the gut microbiota, we should consider how much is needed to achieve the desired effect while avoiding side-effects from overconsumption. Although there is a general consensus that polyphenols are anti-oxidants, some evidence showed that they can be prooxidant in excess (Halliwell 2008). In a study done by Jones and Hughes (1982), there was a far more detrimental effect than oxidative stress induced by high amounts of polyphenols. Mice fed with too much quercetin in a long term experienced premature death. Moreover, there is a lack of clinical trials to tackle the optimal dose of polyphenols, or to observe potential side-effects of long term exposure in humans (Balentine et al. 2015). Without them, it would be difficult to develop polyphenol-based treatments, even though animal models demonstrate promising results. The same challenge goes with using polyphenols as prebiotics, as the concentration of polyphenols to allow them to act as



prebiotics vary from different probiotic strains (de Souza et al. 2019).

#### Conclusion

There is increasing evidence in literature to show and emphasize the positive effects of polyphenol-rich plants, their extracts, and also individual compounds, on gut health, which may be used as alternative approach for prevention or treatment of different diseases related to oxidative stress and inflammation, such as IBD. The impact of polyphenols on gut health and the modes of action could be through modulation of intestinal barrier function, innate and adaptive immune response, signaling pathways, as well as the ability to modify gut microbiota composition. A clear understanding of these mechanisms is necessitated, which will allow for appropriate polyphenol(s) to be selected for certain applications, and may lead to discovery of new therapeutic targets that could be modulated through more conventional pharmacological approaches. Extensive human clinical trials are also indispensable to confirm that polyphenols could in fact constitute a preventive or therapeutic approach for specific types of diseases. Although polyphenols exist abundantly in most dietary sources such as fruits, vegetables, tea and wine, more detailed studies are still needed to determine their absorption and bioavailability. Provided that polyphenols may undergo considerable degree of modifications during digestion and absorption and that the modified forms may have different biological properties and potencies, future work should also consider the activity of their metabolites, which may affect the health outcomes.

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