The Gut Microbiome, Kidney Disease, and Targeted Interventions

Ali Ramezani and Dominic S. Raj

Division of Renal Diseases and Hypertension, The George Washington University, Washington DC

ABSTRACT

The human gut harbors >100 trillion microbial cells, which influence the nutrition, metabolism, physiology, and immune function of the host. Here, we review the quantitative and qualitative changes in gut microbiota of patients with CKD that lead to disturbance of this symbiotic relationship, how this may contribute to the progression of CKD, and targeted interventions to re-establish symbiosis. Endotoxin derived from gut bacteria incites a powerful inflammatory response in the host organism. Furthermore, protein fermentation by gut microbiota generates myriad toxic metabolites, including p-cresol and indoxyl sulfate. Disruption of gut barrier function in CKD allows translocation of endotoxin and bacterial metabolites to the systemic circulation, which contributes to uremic toxicity, inflammation, progression of CKD, and associated cardiovascular disease. Several targeted interventions that aim to re-establish intestinal symbiosis, neutralize bacterial endotoxins, or adsorb gut-derived uremic toxins have been developed. Indeed, animal and human studies suggest that prebiotics and probiotics may have therapeutic roles in maintaining a metabolically-balanced gut microbiota and reducing progression of CKD and uremia-associated complications. We propose that further research should focus on using this highly efficient metabolic machinery to alleviate uremic symptoms.

J Am Soc Nephrol 25: 657-670, 2014. doi: 10.1681/ASN.2013080905

The gut microbiota has coevolved with humans for a mutually beneficial coexistence and plays an important role in health and disease.1 Normal gut microbiota influences the well-being of the host by contributing to its nutrition, metabolism, physiology, and immune function.^{2,3} Disturbance of normal gut microbiota (dysbiosis) has been implicated in the pathogenesis of diverse illnesses, such as obesity,4 type 2 diabetes,5 inflammatory bowel disease,6 and cardiovascular disease.7,8 Quantitative and qualitative alterations in gut microbiota are noted in patients with CKD and ESRD.9-11 Preliminary evidence indicates that toxic products generated by a dysbiotic gut microbiome may contribute to progression to CKD and CKD-related complications (Figure 1).12,13

GUT MICROBIOTA: AN ENDOGENOUS ORGAN

The human gut harbors a complex community of >100 trillion microbial cells that constitute the gut microbiota. The combined microbial genome of the gut microbiota is known as the gut microbiome. In general, the adult gut is dominated by two bacterial phyla, Firmicutes and Bacteroidetes; other phyla, including Actinobacteria, Proteobacteria, Verrucomicrobia, Cyanobacteria, Fusobacteria, Spirochaetes, and TM7, are present in smaller proportions.14,15 Each species of bacteria colonizes a specific niche, leading to different bacterial composition along the intestinal tract (Table 1). Gut microbiota performs a multitude of functions and can be considered a metabolically active endogenous "organ" in itself. Under physiologic conditions, it participates in certain complementary metabolic activities that have not been fully evolved in the human host, such as breakdown of undigestible plant polysaccharides,³ synthesis of certain vitamins,¹⁶ biotransformation of conjugated bile acids,¹⁷ and degradation of dietary oxalates.¹⁸ Importantly, postnatal colonization of the intestine educates our immune system and reduces allergic responses to food and environmental antigens.¹⁹

The utility of human gut microbiota in the diagnosis, treatment, and prevention of disease requires a clear understanding of its composition, dynamics, and stability within an individual. A recent study aimed at characterizing the long-term stability of the human gut microbiota used low-error amplicon sequencing of fecal samples from 37 healthy adults collected over a period of 296 weeks.²⁰ The results revealed that on average, the microbiota was remarkably stable over time within an individual and between family members but not between unrelated individuals. These

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Published online ahead of print. Publication date available at www.jasn.org.

Correspondence: Dr. Dominic Raj, Division of Renal Diseases and Hypertension, The George Washington University School of Medicine, 2150 Pennsylvania Avenue NW, Washington, DC 20037. Email: draj@ mfa.gwu.edu

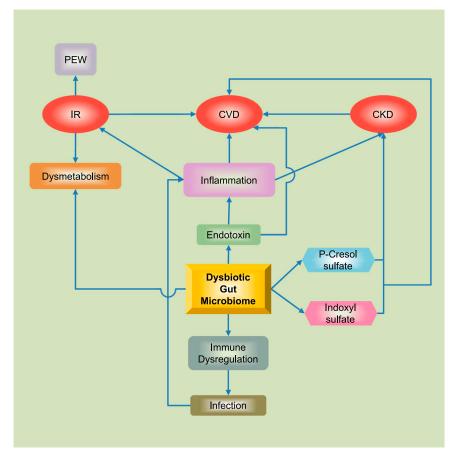


Figure 1. The human gut is host to >100 trillion bacteria with an enteric reservoir of >1 g of endotoxin. Alterations in gut microbiota and impaired intestinal barrier function in patients with CKD/ESRD have been linked to endotoxemia and accumulation of gut-derived uremic toxins leading to insulin resistance, protein energy wasting, immune dysregaulation, and atheroscleroisis. CVD, cardiovascular disease; IR, insulin resistance; PEW, protein energy wasting.

findings further emphasize the importance of the early gut colonizers, such as those acquired from parents and siblings, and their potential life-long effect on our health and disease.

Microbiota-Host Signaling

Mammalian gut microbiota forms a complex ecosystem that requires proper interaction with its host for symbiotic benefits. One of the best examples of the microbiota-host signaling is the host immunomodulation by *Bacteroides fragilis* polysaccharide A molecule, which directs the maturation of the developing immune system by mediating establishment of a proper T-helper cell (T_H1/T_H2) balance.²¹ The gut microbiota can also sense host-produced molecules. For instance, norepinephrine released in response to stress could increase the growth and production of virulenceassociated factors of Gram-negative bacteria.²² Finally, different members of the gut microbiota also communicate for establishment or maintenance of homeostasis in the intestinal ecosystem. When germ-free mice were colonized with *Bacteroides thetaiotaomicron* and *Methanobrevibacter smithii*, the latter directed *B. thetaiotaomicron* to focus on fermentation of dietary fructans to acetate, whereas *B. thetaiotaomicron*–derived formate was used by *M. smithii* for methanogenesis.²³

Intestinal Epithelial Barrier

In addition to allowing absorption of nutrients, the intestinal epithelium also functions as a barrier to prevent systemic translocation of antigens and pathogens (Figure 2A). The intestinal epithelium is a single layer of columnar epithelial cells that separates the intestinal lumen from the underlying lamina propria.24 These epithelial cells are bound together by tight junctions, making a multifunctional complex that forms a seal between adjacent epithelial cells.25 Commensal gut microbes maintain functional integrity of gut by several mechanisms, including restoration of tight junction protein structure,26 induction of epithelial heat-shock proteins,27,28 upregulation of mucin genes,29 competition with pathogenic bacteria for binding to intestinal epithelial cells,³⁰ and secretion of antimicrobial peptides.³¹ Probiotic bacteria enhance intestinal epithelial barrier function in murine models of colitis and in patients with Crohn disease.32,33 Treating human epithelial cell monolayers with metabolites secreted by Bifidobacterium infantis causes an increase in tight junction proteins ZO-1 and occludin while reducing claudin-2, thus demonstrating the ability of bacteria and bacterial products to modify ion permeability and selectivity of tight junction.26 In germ-free mice, colonization with B. thetaiotaomicron resulted in modulation in expression of genes involved in several important intestinal functions.34,35

Commensal bacteria also play an important role in maintaining the intestinal epithelial barrier by suppressing intestinal inflammation. Toll-like receptors (TLRs) comprise a family of patternrecognition receptors that detect conserved molecular products of microorganisms, such as LPS and lipoteichoic acid, recognized by TLR4 and TLR2, respectively.36 TLR2 stimulation effectively preserved tight junctionassociated barrier assembly against stress-induced damage through promotion of phosphatidylinositol 3-kinase/ protein kinase B-mediated cell survival via myeloid differentiation factor 88 (MyD88).³⁷ Microbiota signaling through mucosal TLRs was also shown to be required for maintenance of intestinal epithelial homeostasis and repair following intestinal injury.38

	Normal		CKD/ESRD	
Gastrointestinal Tract	Phyla, Families, and Genera of Dominant Bacterial Species	Microbial Number (cells/g)	Alterations from Normal Microbiota	
Stomach	Lactobacillus	10 ¹		
	Helicobacter			
Duodenum	Staphylococcus	10 ³	Human studies: increased counts ¹⁰ (10 ⁶ –10 ⁷)	
	Streptococcus			
	Lactococcus			
Jejunum	Enterococcus	10 ⁴	Human studies: increased counts ¹⁰ (10 ⁶ –10 ⁷)	
	Streptococcus			
	Lactobacillus			
lleum	Enterobacteriaceae	10 ⁷		
	Bacteroides			
	Clostridium			
	Segmented filamentous bacteria			
Colon	Firmicutes	10 ¹²	Experimental animal studies:	
	Bacteroidetes	10	increased <i>Proteobacteria</i> and Enterobacteriaceae,	
	Actinobacteria		increased Escherichia, Enterobacter, Acinetobacter,	
	Proteobacteria		Proteus, and Proteus spp, ⁸² and decreased	
	Clostridium		Lactobacillus and Bifidobacterium spp. ⁸²	
	Lactobacillaceae		Decreased Lactobacillaceae and Prevotellaceae ¹¹	
	Prevotellaceae		Human studies:	
	Fusobacteria		overgrowth of aerobic bacteria (about 100 times) ⁹	
	TM7		Decreased Bifidobacteria and higher Clostridium perfringens ⁹ Lower species richness ¹¹	

Table 1. Distribution and composition of the microbiota along the intestinal tract

GUT MICROBIOTA IN OBESITY AND INSULIN RESISTANCE

Data from the US Renal Data System shows an epidemic of obesity among the ESRD population.³⁹ Insulin resistance is common in patients with CKD⁴⁰ and is in part due to a high prevalence of shared risk factors, such as obesity and sedentary lifestyle. Recent findings suggest that our gut microbiota might be involved in the development of obesity and related disorders, such as insulin resistance.41-44 Weight gain is associated with an increase in the capacity of the microbiota to extract nutrients from the diet and in inducing metabolic changes in the host, such as increased fatty acid oxidation in muscle and increased triglyceride storage in the liver.43,45 Germ-free mice ingesting a high-fat diet do not gain weight or develop adiposity; however, reconstitution of germ-free mice gut with microbiota from lean mice or from genetically or diet-induced obese mice causes weight gain.⁴⁶ Gut microbiota composition is significantly different in genetically obese mice and obese patients compared with lean controls.^{4,41} A high-fat (Western) diet modifies the gut microbiota by reducing the relative abundance of Bacteroidetes and increasing the relative abundance of Firmicutes.⁴¹ An increase of genes involved in the import and processing of sugars in the gut metagenome was also found in mice fed with Western diet.⁴⁴

The role of the gut microbiota in type 1 and 2 diabetes has been researched in mouse models. The development of type 1 diabetes in MyD88-deficient nonobese diabetic (NOD) mice depended on the presence or absence of the gut microbiota, and nearly all germ-free MyD88-deficient NOD mice developed diabetes, whereas colonization of these germ-free MyD88-deficient NOD mice with a defined gut microbiota (representing bacterial phyla normally present in human

gut) attenuated type 1 diabetes.⁴⁷ Another study compared the fecal microbiota profile in lean control, obese diabetic, and obese nondiabetic participants and noted that diabetes was associated with a reduction of *Faecalibacterium prausnitzii* species.⁴⁸ A case-control study of type 2 patients with diabetes found decreased *Bacteroides vulgatus* and *Bifidobacterium* genus in the diabetic group compared with a healthy control group.⁴⁹ Thus, altered gut microbiota could play an important role in the development of obesity, insulin resistance, and diabetes.

INTESTINAL DYSBIOSIS IN CKD/ ESRD

Gut Microbiome in CKD/ESRD

Uremic patients show greatly increased counts of both aerobic (approximately 10⁶ bacteria/ml) and anaerobic (approximately 10⁷ bacteria/ml) organisms in the

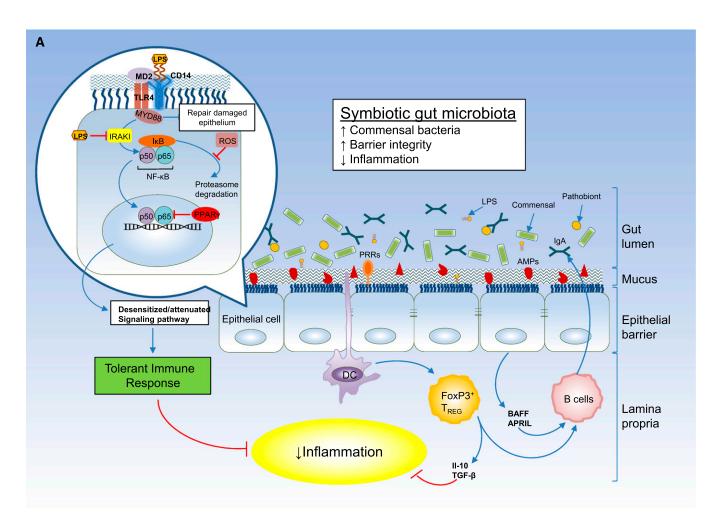


Figure 2. (A) Intestinal epithelial barrier and inflammatory responses in symbiotic and dysbiotic gut microbiota. A symbiotic gut microbiota leads to development of a functional barrier, with normal amounts of mucus, pattern recognition receptors (PRRs), antimicrobial peptides (AMPs), and secreted IgA, which in turn contain the microbiota in the intestinal lumen and away from the intestinal epithelial cells. As a result, the intestinal immune system becomes largely tolerant to the resident commensals. Similar to immune cells, the signaling cascades that occur downstream of TLRs (enlarged on the left) are used by epithelial cells to detect microbes through PRRs, such as the TLR4. Briefly, upon LPS ligation, the MYD88 is recruited, which activates the NF-κB pathway and leads to production of antimicrobial proteins and proinflammatory cytokines. In a symbiotic gut, epithelial cells are desensitized by continuous exposure to LPS¹⁶⁸ or are attenuated by (1) LPSmediated downregulation of the IL-1 receptor-associated kinase 1 (IRAK1), which is the proximal activator of the NF-κB cascade;¹⁶⁸ (2) LPS-mediated induction of peroxisome proliferator-activated receptor- γ (PPAr γ), which can divert NF- κ B from the nucleus;¹⁶⁹ or (3) commensal bacteria-derived reactive oxygen species (ROS)-mediated inhibition of polyubiquitylation and degradation of the aortic inhibitor of KB.¹⁷⁰ (T bars indicate the checkpoints that are controlled by the microbiota.) Exposure to LPS induces epithelial cells to secrete TGF-β, B-cell-activating factor of the TNF family (BAFF), and a proliferation-inducing ligand (APRIL), all promoting the development of tolerogenic immune cell responses to the microbiota. CD103⁺ dendritic cells (DCs) support the development of regulatory T (Treg) cells secreting IL-10 and TGF- β , and together they stimulate the production of commensal-specific IgA.¹⁷¹ (B) Increased intestinal concentration of uremic toxins associated with the progression of CKD leads to microbial dysbiosis and overgrowth of pathobionts. Pathobiont overgrowth leads to the loss of barrier integrity and the breach in the epithelia barrier. Translocation of bacteria and bacterial components triggers the intestinal immune system to direct a potentially harmful proinflammatory response to clear invading bacteria by secreting IL-1 and -6 from intestinal epithelial cells, promoting a $T_{\rm H}$ 1 and $T_{\rm H}$ 17 response by DCs and macrophages and producing higher levels of commensal-specific IgG by B cells. In this context, LPS binding to its receptor complex on macrophages (enlarged on the left) results in enhanced production of inflammatory cytokines including IFN- β , IFN- γ , IL-1 β , IL-6, TNF α , and IL-12, the production of which has been shown to require activation of p38MAPK.¹⁷² Subclinical endotoxemia is a potential cause of inflammation in CKD.^{90–92} Dysregulated immune response and chronic production of proinflammatory cytokines lead to systemic inflammation, which could further accelerate the progression of CKD and development of cardiovascular disease. ΙκΒ, inhibitor of NF-κΒ.

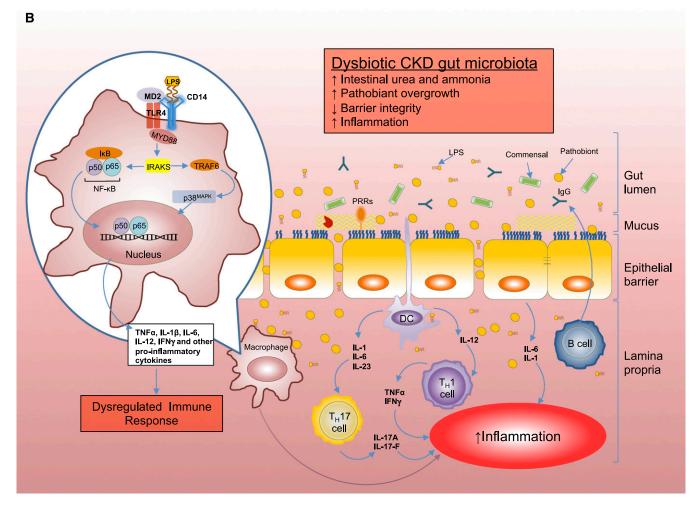


Figure 2. Continued.

duodenum and jejunum, normally not colonized heavily by bacteria in healthy persons (Table 1).10 Lower intestinal microbial flora has also been shown to be altered in patients with CKD, most notably with decreases in both Lactobacillaceae and Prevotellaceae families.11 Hida et al.9 studied the colonic composition of microbiota in healthy controls and hemodialysis patients. Analysis of the fecal microbiota revealed a disturbed composition of the microbiota characterized by an overgrowth of aerobic bacteria. Although this study did not show a significant difference in the total number of bacteria, the number of aerobic bacteria, such as Enterobacteria and Enterococci species, was approximately 100 times higher in hemodialysis patients. Of the anaerobic bacteria, hemodialysis patients had significantly lower numbers of Bifidobacteria and higher Clostridium perfringens.9 Patients with ESRD were also at a high risk of Clostridium difficile-associated diarrheas.50 Vaziri et al.11 showed significant differences in the abundance of 190 microbial operational taxonomic units (OTUs) between the patients with ESRD and the normal control individuals. To isolate the effect of renal failure, the investigators also examined the gut microbiota in nephrectomized rats.11 The study revealed substantially lower species richness as measured by the number of operational taxonomic units in the nephrectomized rats compared with the controls.

The intestinal dysbiosis may be due to iatrogenic causes or uremia *per se*.^{51,52} Loss of kidney function leads to secretion of urea into the gastrointestinal

tract. Subsequent hydrolysis of urea by urease expressed by some gut microbes, results in the formation of large quantities of ammonia, which could affect the growth of commensal bacteria.^{51,52} Other contributing factors include decreased consumption of dietary fiber,^{53–55} frequent use of antibiotics,^{56,57} slow colonic transit,^{58,59} metabolic acidosis,^{60,61} intestinal wall edema,^{62–64} and possibly oral iron intake.^{65,66}

There is high prevalence of insufficiency or deficiency in vitamin K among patients with CKD and ESRD.^{67,68} Pioneering work of Almquist and Stokstad has recognized the biosynthesis of vitamin K by intestinal bacteria as an important source in animals and humans.⁶⁹ Investigators have shown that certain strains, such as *B. fragilis, Bifidobacteria* species, *Clostridia* species, and *Strepto-coccus faecalis*, are involved in the biosynthesis of vitamin K.⁷⁰ The lower part of the intestinal tract, where the bacterial density is highest, is most likely site for the absorption of the vitamin. Consistent with these findings, the intestinal flora has been associated with symptomatic vitamin K deficiency and severe hemorrhage.^{71–73}

Gut Barrier Function in CKD

The gastrointestinal system is at the interphase between the blood and the potentially toxic contents of the gut.74 Histologic changes, including reduction of villous height, elongation of the crypts, and infiltration of lamina propria with inflammatory cells are noted in CKD (Figure 2B).⁵² Uremia increases intestinal permeability, both in uremic rats and in patients with CKD.75,76 The disruption of colonic epithelial tight junction could subsequently lead to translocation of bacteria and endotoxin across the intestinal wall.77-79 Studies in uremic rats have shown marked azotemia, systemic oxidative stress, and marked depletion of the key protein constituents of the epithelial tight junction (claudin-1, occludin, and ZO1) in the stomach, jejunum, and ileum,80 as well as penetration of bacteria across the intestinal wall and localization in the mesenteric lymph nodes.52 Hemodialysisinduced systemic circulatory stress and recurrent regional ischemia may also damage the mechanical barrier of the gut.81 In addition, factors that promote intestinal dysbiosis may also contribute to the leaky gut in CKD. Gut microbiome dysbiosis is associated with bacterial translocation, thereby contributing to microinflammation in experimental uremia⁸² as well as in patients with ESRD.⁸³

Endotoxin as a Cause of Inflammation in CKD

Endotoxin, the hydrophobic anchor of LPS, is a phospholipid that constitutes the outer membranes of most Gramnegative bacteria. It is continuously produced in the gut and is transported into intestinal capillaries through a TLR4-dependent mechanism.⁸⁴ Endotoxin

circulates in the plasma of healthy humans at low concentrations (between 1 and 200 pg/ml).85,86 It is taken up by liver and mononuclear phagocyte cells and eventually cleared.87 Endotoxin provokes an array of host responses by binding to the 55-kD glycosyl-phosphatidyl-inositolanchored myeloid differentiation antigen, CD14.88 LPS-binding protein is a key modulator of cellular response to endotoxin.89 Endotoxin stimulates cells of the immune system, particularly macrophages and the endothelial cells, to become activated and to synthesize and secrete a variety of effector molecules that cause an inflammatory response. Recent evidence indicates that subclinical endotoxemia is a potential cause for inflammation in patients with CKD.90-92

Endotoxin and Atherosclerosis

The association between bacteria and atherosclerosis has been known for more than two decades.93 Recently, focus has shifted from bacteria to its product, endotoxin, for its role in the development of atherosclerosis.85,94 Endotoxin is a key factor in initiation and progression of atherosclerosis through mediation of endothelial cell injury, promotion of recruitment of monocytes, transformation of macrophages to foam cells, and procoagulant activity.95,96 Furthermore, vascular smooth muscle cells exhibit profound responsiveness to even very low levels of endotoxin.97,98 The Bruneck study showed that elevated endotoxin level is a strong risk factor for the development of atherosclerosis in the general population.85 Elevated plasma level of sCD14 is noted in patients with unstable angina and is related to increased aortic stiffness and carotid plaque formation.99,100 Szeto et al.79 showed that circulating endotoxemia in patients undergoing peritoneal dialysis is related to systemic inflammation and features of atherosclerosis. Using two separate cohorts, we demonstrated that sCD14 is associated with mortality in patients with ESRD.92,101

Gut-Derived Uremic Toxins

Certain intestinal bacteria can generate uremic toxins that are absorbed into the

blood and are normally cleared by the kidney. Protein fermentation by gut microbiota results in the generation of different metabolites, including phenols¹⁰² and indoles.¹⁰³ Aronov et al.¹⁰⁴ compared plasma from hemodialysis patients with and without colon and confirmed the colonic origin of indoxyl sulfate and p-cresol. These are prototype members of a large group of proteinbound uremic toxins that are resistant to clearance by dialysis.¹⁰⁵ P-cresol, a 108-Da protein-bound solute, is a colonic fermentation product of the amino acid tyrosine and phenylalanine.106 Most of the p-cresol generated by the intestinal flora is conjugated to p-cresyl sulfate in the intestinal wall and to p-cresyl glucuronide in the liver.107 Intestinal bacteria also have tryptophanase that converts tryptophan to indole, which is subsequently absorbed and metabolized to indoxyl sulfate in the liver.106

Concentrations of indoxyl sulfate and p-cresyl sulfate in the serum are negatively correlated with the level of kidney function.12 A prospective, observational study performed in 268 patients with CKD indicated that baseline levels of indoxyl sulfate and p-cresyl sulfate were predictors of CKD progression.13 Animal studies suggest that these uremic toxins may damage renal tubular cells.¹⁰⁸ In uremic rats, administration of indoxyl sulfate mediates the renal expression of genes related to tubulointerstitial fibrosis, such as TGF- β 1, tissue inhibitor of metalloproteinases, and pro- α 1, accompanied by a significant decline in renal function and worsening of glomerular sclerosis.109 Indoxyl sulfate also induces nephrotoxicity via organic anion transporter-mediated uptake in the basolateral membrane of renal proximal tubular cells,^{110,111} where it activates NF-*k*B and plasminogen activator inhibitor type 1 expression.^{110,112}

Barreto *et al.*¹¹³ showed that an elevated level of indoxyl sulfate is associated with vascular stiffness, aortic calcification, and higher cardiovascular mortality. Indoxyl sulfate is a potential vascular toxin that induces oxidative stress in endothelial cells,¹¹⁴ increases shedding of endothelial microparticles,¹¹⁵ impairs endothelial cell repair mechanism,¹¹⁶ and increases vascular smooth muscle cell proliferation.¹¹⁷ Bammens *et al.*¹¹⁸ reported that free serum levels of p-cresol is associated with mortality in hemodialysis patients. *In vitro* evidence indicates that p-cresol inhibits cytokine-stimulated expression of endothelial adhesion molecules intercellular adhesion molecule 1 and vascular cell adhesion molecule ¹¹⁹ and induces increase in endothelial permeability.¹²⁰ Thus, gut-derived uremic toxins contribute to progression of CKD as well as cardiovascular disease.

TARGETED INTERVENTIONS TO TREAT INTESTINAL DYSBIOSIS

Recent advances in our understanding of the gut microbiome's physiologic functions and pathologic consequences of dysbiosis have led to exploration of various ways of reestablishing symbiosis. Most therapies targeting the colonic microenvironment in CKD aim to modulate gut microbiota, block LPS or attenuate inflammation, or target adsorption of uremic toxin end products of microbial fermentation. Some of these approaches are briefly discussed below (reviewed in Table 2).

Modulation of Gut Microbiota Prebiotics

A prebiotic is a nondigestible (by the host) food ingredient that has a beneficial effect through its selective stimulation of the growth or activity of one or a limited number of bacteria in the colon.121,122 The candidate prebiotics include inulin, fructo-oligosaccharides, galacto-oligosaccharides, soya-oligosaccharides, xylo-oligosaccharides, and pyrodextrins. Prebiotics promote the growth of Bifidobacteria and Lactobacilli species at the expense of other groups of bacteria in the gut, such as Bacteroides species, Clostridia species, and enterobacteria.123 Preliminary evidence indicates that prebiotic oligofructose-enriched inulin (p-inulin) promotes growth of Bifidobacteria species, mediates weight loss, reduces inflammation, and improves metabolic function.124-126 High dietary fiber intake

is associated with lower risk of inflammation and reduced mortality in patients with CKD.¹²⁷ Meijers *et al.*¹²⁸ reported that serum concentrations of p-cresol and indoxyl sulfate are reduced by the oral intake of p-inulin in hemodialysis patients.

One of the mechanisms by which p-inulin mediates weight loss may be by enhancing satiety due to bacterial fermentation and increased production of short-chain fatty acids in the gut lumen.¹²⁶ Short-chain fatty acids stimulate secretion of glucagon-like peptide 1 (GLP-1)¹²⁹ and peptide YY (PYY).¹³⁰ GLP-1 has antiobesity and antidiabetic actions by such mechanisms as inhibiting food intake, stimulating insulin secretion, and inducing β -cell proliferation.¹³¹ PYY colocalizes with GLP-1 in the intestinal L cells and is also considered an anorexigenic peptide.133 Plasma concentrations of GLP-1¹³³ and PYY¹³⁴ are reduced in obese individuals, and oligofructose supplementation in rats resulted in reductions in energy intake and increased plasma GLP-1 and PYY concentrations.135

Probiotics

Probiotics are defined by the United Nations' Food and Agriculture Organization and the World Health Organization as "live microorganisms" that when administered in adequate amounts confer a health benefit on the host.¹³⁶ Probiotics consist of living bacteria, such as Bifidobacteria species, lactobacilli, and streptococci,137 that can alter gut microbiota and affect the inflammatory state.138,139 Treatment with Bacillus pasteurii and Sporlac slowed the progression of kidney disease and prolonged the life span of fifth/sixth nephrectomized Sprague-Dawley rats.140 Hemodialysis patients treated with oral Lactobacillus acidophilus showed decreased serum dimethylamine, a potential uremic toxin.¹⁰ In another study, treatment with L. acidophilus ATCC-4356 reduced the atherosclerotic burden in ApoE^{-/-} mice.141 This was accompanied by an inhibition of translocation of NF- κ B p65 from cytoplasm to nucleus, suppression of degradation of a ortic inhibitor of $\kappa B \alpha$, and improvements in gut microbiota distribution. Prakash *et al.*¹⁴² reduced BUN in uremic rats by orally administering microencapsulated, genetically engineered live cells that contained living urease-producing *Escherichia coli*–DH5.

Acarbose

Acarbose is an inhibitor of α -glucosidase enzymes in the intestinal brush-border that blocks the hydrolysis of poly- and oligosaccharides to glucose and other monosaccharides. The undigested oligosaccharides that enter the colon act as fermentable carbohydrates. Evenepoel *et al.*¹⁴³ showed that treatment with acarbose reduces the colonic generation of p-cresol in healthy persons.

Gut Microbiome Transplantation

Manichanh *et al.*¹⁴⁴ examined the longterm effects of exogenous microbiota transplantation alone and combined with antibiotic pretreatment in a rat model. A short intake of antibiotics produced profound long-term effects on the rat intestinal microbiome, with reduced gut microbial diversity. Transplantation of a rich pool of exogenous bacteria led to an increase in bacterial diversity and changing the microbiome of the recipients to resemble that of the donor. Human fecal transplantation has demonstrated efficacy against *Clostridium difficile* colitis.¹⁴⁵

Essential Oils

The potential of essential oils as agents to treat dysbiosis was examined in an *in vitro* study.¹⁴⁶ Results indicated that *Carum carvi, Lavandula angustifolia, Trachyspermum copticum,* and *Citrus aurantium var. amara* essential oils displayed the greatest degree of selectivity, inhibiting the growth of potential pathogens at concentrations that had no effect on the beneficial bacteria examined.¹⁴⁶ More research is needed, however, to evaluate tolerability and safety concerns and to verify the selective action of these agents.

Blocking of LPS/Attenuation of Inflammation

Sevelamer

Sevelamer is a large cationic polymer phosphate binder that binds endotoxin in

Reference	Reference Patient Type/Model Intervention (number)		Comments
Uremic toxins			
Simenhoff et al. ¹⁰	hoff et al. ¹⁰ HD patients (8) <i>L. acidophilus</i>		↓ Serum dimethylamine
			↓ Nitrosodimethylamine
Prakash et al. ¹⁴²	Uremic rats	Genetically engineered E. coli	↓ Plasma urea
Ranganathan et al. ¹⁷³	Nephrectomized rats	Various combinations of probiotics	↑ Lifespan
			↓ BUN
Ranganathan et al. ¹⁷⁴	Patients with CKD (13)	S. thermophilus, L. acidophilus,	↓ BUN
		and B. longum	↓ Uric acid concentration
Ranganathan <i>et al.</i> ¹⁷⁵	Patients with CKD (246)	S. thermophilus, L. acidophilus, and B. longum	↓ BUN
Meijers et al. ¹²⁸	HD patients (22)	Oligofructose-enriched inulin	\downarrow Serum p-cresyl sulfate and generation rate
de Preter <i>et al.</i> ¹⁷⁶	Healthy persons (50)	Oligofructose-enriched inulin	↓ Urinary excretion of p-cresol
Nakabayashi <i>et al.</i> ¹⁷⁷	HD patients (7)	Galacto-oligosaccharides, L. casei, and B. breve	↓ Serum p-cresyl sulfate
Swanson et al. ¹⁷⁸	Healthy persons (68)	Fructooligosaccharides and/or	↓ Fecal protein catabolites (beneficial)
		L. acidophilus	with fructooligosaccharides
			↑ Fecal protein catabolites (harmful)
			with L. acidophilus
Atherosclerosis			
Chen et al. ¹⁴¹	ApoE ^{-/-} mice	L. acidophilus	↓ Atherosclerotic burden
Uchida et al. ¹⁷⁹	Rabbits on a high cholesterol diet	Exopolysaccharide	↓ Atherosclerotic lesions
Oxman et al. ¹⁸⁰	Sprague-Dawley rats	L. bulgaricus-51	↓ Reperfusion tachyarrhythmia
			↑ Functional recovery of the ischemic rat hearts
			↓ Norepinephrine release
Naruszewicz et al. ¹⁸¹	Healthy persons (36)	L. plantarum 299v	↓ Systolic BP and fibrinogen
			\downarrow F ₂ -Isoprostanes and IL-6
			↓ Monocyte adhesion to endothelial cells
Inflammation			
Neyrinck et al. ¹⁸²	Mice	High-molecular-weight arabinoxylane	↑ Bifidobacteria
			↓ Inflammation
Cani et al. ¹²⁴	Mice	Oligofructose	↓ Endotoxemia and proinflammatory cytokines
Dewulf et al. ¹⁸³	Obese women (30)	Inulin/oligofructose	↓ Endotoxemia
Andreasen <i>et al</i> . ¹⁸⁴	Patients with T2DM (45)	L. acidophilus NCFM75	Preserved insulin sensitivity
0 1 105			↓ Inflammation
Schiffrin et al. ¹⁸⁵	Elderly persons (74)	Oligosaccharides	\downarrow TNF- α and IL-6 mRNAs
			↓Serum sCD14
Andreasen <i>et al.</i> ¹⁸⁴	Patients with T2DM (45)	L. acidophilus	Preserved insulin sensitivity
A l			Did not affect systemic inflammation
Anderson <i>et al.</i> ¹⁸⁶	Elective surgical	Combination of probiotics	No measurable effect on bacterial translocation
K	patients (137)	Deditoria da se tel la la se	or systemic inflammation
Kotzampassi <i>et al.</i> ¹⁸⁷	Trauma patients	Probiotics along with and inulin, oat	↓ Rate of systemic inflammatory response,
		bran, pectin, and resistant starch	syndrome, infections, severe sepsis, and mortalit

Table 2. Effect of probiotics and prebiotics on uremic toxins, inflammation, and atherosclerosis

HD, hemodialysis; T2DM, type 2 diabetes mellitus.

both *in vitro* and *in vivo* studies.^{147,148} A cross-sectional study in hemodialysis patients showed that endotoxin level was lower in patients using sevelamer.¹⁴⁸ Subsequently, a prospective, randomized, open-label study further confirmed that treatment with sevelamer reduced endotoxin and sCD14 levels in hemodialysis patients.¹⁴⁹ Potential interaction

between sevelamer and fat-soluble vitamins, including vitamin A, D, E, and K, has been proposed but remains to be determined.¹⁵⁰

Synthetic TLR4 Antagonists

he biologic activity of LPS resides almost entirely in its lipid A component.¹⁵¹ The synthetic lipid A analogue eritoran (E5564) and the lipid A mimetic CRX-526¹⁵² inhibit LPS signaling.^{153,154} In healthy persons, E5564 blocked all of the effects of LPS, with significant reductions in white blood cell count, C-reactive protein levels, and cytokine levels (TNF- α and IL-6).¹⁵⁵ More recently, C34, a 2-acetamidopyranoside, was developed. It inhibited TLR4 in enterocytes and macrophages *in vitro* and reduced systemic inflammation in mouse models of endotoxemia and necrotizing entero-colitis.¹⁵⁶

Adsorption of Uremic Toxins

Oral Adsorbents

AST-120 is an oral adsorbent consisting of microspheres made from porous carbon material. Administration of AST-120 partially restored the epithelial tight-junction proteins and reduced plasma endotoxin and markers of oxidative stress and inflammation in CKD rats.157 In another study, AST-120 decreased serum levels of indoxyl sulfate and slowed the progression of CKD by reducing the profibrotic gene expression in the rat remnant kidney.¹⁵⁸ In patients with CKD, administration of AST-120 significantly decreased the serum and urine levels of indoxyl sulfate and improved the slope of the 1/serum creatinine-time plot.159,160 AST-120 treatment of patients with CKD has also delayed the time to dialysis initiation.¹⁶¹

Miscellaneous

The 3-hydroxy-3-methylglutaryl coenzyme A reductase inhibitors (statins) are lipid-lowering drugs with anti-inflammatory properties.¹⁶² Abe et al.¹⁶³ demonstrated that statins partially attenuated the development of adipose tissue inflammation in obese mice, which might be associated with an inhibitory effect of statins on TLR4-triggered expression of IFN- β via MyD88-independent signaling pathway in macrophages. Atorvastatin is known to affect LPS indirectly by causing impaired TLR4 recruitment into the lipid raft, thereby affecting anti-inflammatory responses.164 In a small study, optimized BP control with antihypertensive agents decreases endotoxin levels.165 The mechanism of this beneficial effect is unknown.

CONCLUSIONS AND FUTURE DIRECTIONS

Resident microbiota outnumber the human host cells by 10-fold, with metabolic activity in excess of that of the liver and a combined microbiome that is estimated

to be 100 times greater than that of the human.166 In 2007, the Human Microbiome Project was established to characterize the human microbiome and analyze its role in health and disease.¹⁶⁷ The project serves as a "roadmap" for discovering the roles these microorganisms play in human health and disease, with the goal of metagenomic characterization of microbial communities from 300 healthy individuals over time. Not long ago, the products of intestinal putrefaction were considered the primary uremic toxins. The recent explosion of knowledge on the metabolic potential of gut microbiome and its critical role in the pathogenesis of several chronic inflammatory diseases has led the nephrologist to refocus on the gut as a potential cause of CKD-related complication and a target organ for attenuating uremiarelated complications. Therefore, it is time for more clinical and basic research studies to further our understanding of the role of the gut microbiome in progression of CKD and its associated complications. Finally, interventions aimed at establishing gut symbiosis and blocking microbiome-related pathogenic biochemical pathways should be explored in order to develop interventions to ameliorate uremic syndrome.

ACKNOWLEDGMENTS

D.S.R. is supported by National Institutes of Health grants 1R01DK073665-01A1, 1U01DK099924-01, and 1U01DK099914-01.

DISCLOSURES

None.

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