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Uraemic solutes as therapeutic targets in CKD-associated cardiovascular disease

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Abstract | Chronic kidney disease (CKD) is characterized by the retention of a myriad of solutes termed uraemic (or uremic) toxins, which inflict damage to several organs, including the cardiovascular system. Uraemic toxins can induce hallmarks of cardiovascular disease (CVD), such as atherothrombosis, heart failure, dysrhythmias, vessel calcification and dysregulated angiogenesis. CVD is an important driver of mortality in patients with CKD; however, reliance on conventional approaches to managing CVD risk is insufficient in these patients, underscoring a need to target risk factors that are specific to CKD. Mounting evidence suggests that targeting uraemic toxins and/or pathways induced by uraemic toxins, including tryptophan metabolites and trimethylamine *N*-oxide (TMAO), can lower the risk of CVD in patients with CKD. Although tangible therapies resulting from our growing knowledge of uraemic toxicity are yet to materialize, a number of pharmacological and non-pharmacological approaches have the potential to abrogate the effects of uraemic toxins, for example, by decreasing the production of uraemic toxins, by modifying metabolic pathways induced by uraemic toxins such as those controlled by aryl hydrocarbon receptor signalling and by augmenting the clearance of uraemic toxins.

Chronic kidney disease (CKD) is a major public health concern, estimated to affect 13% of the global population¹. In the USA, approximately 30 million people, or one in seven individuals, have CKD, and this number is predicted to increase². Globally, CKD results in 5-10 million deaths annually, a figure that is likely to be an underestimate^{3,4}. In the USA, 340 people initiate dialysis treatment every 24 h (REF.²) and 240 patients on dialysis die daily⁵. Mortality among patients with CKD is largely attributable to an enormous cardiovascular disease (CVD) burden and an increased risk of major adverse cardiovascular events, including atherothrombotic disorders that drive myocardial infarction and stroke, heart failure, arrhythmias and sudden cardiac deaths in both adult and paediatric populations⁶⁻¹⁰. These conditions contribute to a CVD mortality in patients with CKD that is at least double that of CVD in patients without CKD11,12. CVD risk also increases with severity of CKD: 27.5% of deaths among patients with early-stage CKD (stages 1-2) can be attributed to CVD, increasing to 58% among patients with advanced-stage CKD (stages 4-5). In fact, the life expectancy of patients with advanced CKD is shortened by over 16 years owing to CVD-related mortality^{13,14}.

The previously held dogma that CVD and CKD are merely associated entities resulting from the existence

of common risk factors has been debunked by large epidemiological studies¹³. A meta-analysis of 1.4 million individuals from 30 published cohort studies suggested that after adjusting for traditional cardiovascular risk factors (such as age, sex, ethnicity, hypertension, diabetes status, high cholesterol and smoking), the risk gradient for cardiovascular mortality was evident at early stages of CKD and increased linearly with progression of CKD and albuminuria^{11,12}. Another meta-analysis that involved 1.02 million participants from 30 general population and high-risk cardiovascular cohorts and 13 CKD cohorts found that the association of CKD with cardiovascular mortality was not influenced by the presence or absence of diabetes or hypertension¹⁵. This conclusion was corroborated by findings from the Alberta Kidney Disease Network of 1.26 million participants, which demonstrated that the rate of incident myocardial infarction was substantially lower among patients with diabetes mellitus and normal kidney function than among those with concomitant CKD and proteinuria¹⁶.

Further supporting evidence that CKD is an independent risk factor for CVD stems from the observation that interventions that target conventional CVD risk factors do not adequately prevent cardiovascular events in patients with CKD¹⁷⁻¹⁹. Large clinical trials have demonstrated that statins have limited ability to reduce primary

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Key points

- Patients with chronic kidney disease (CKD) retain myriad chemical compounds, known as uraemic toxins, that mediate systemic complications including cardiovascular disease (CVD); levels of these toxins rise with CKD progression, further increasing cardiovascular risk.
- Early interventions that target conventional cardiovascular risk factors, such as obesity and hypertension, combined with approaches to directly target uraemic toxins have potential to lower the risk of CVD in patients with CKD.
- Non-pharmacological measures to target uraemic toxins include approaches to reduce their biosynthesis through dietary interventions and/or microbial manipulation; both of these approaches have limitations.
- Pharmacological strategies to suppress cellular events triggered by uraemic toxins are rapidly emerging as an attractive approach and include inhibitors of the aryl hydrocarbon receptor pathway, kinase inhibitors, Klotho or kynureninase supplementation, AST-120, meldonium and 3,3-dimethyl-1-butanol (DMB).

cardiovascular events in patients with CKD^{17,18}. Similar results have been noted for other cardiovascular protective agents¹⁹. Collectively, these studies indicate that CKD is a strong and independent risk factor for CVD.

A growing body of evidence has linked the cardiovascular risk of CKD to an accumulation of uraemic toxins that occurs with progression of CKD. For patients with kidney failure, kidney transplantation represents the optimal form of kidney replacement therapy in terms of survival outcomes²⁰⁻²². Kidney transplantation is also associated with a reduced risk of cardiovascular events compared with haemodialysis^{23,24}, and in fact, has been reported to reverse end-organ toxicities, such as cardiac fibrosis²⁵, arterial stiffness²⁶ and improve remodelling and cardiovascular reserve²⁷. Importantly, and unlike haemodialysis, kidney transplantation is associated with a significant reduction in the levels of several uraemic toxins²⁸⁻³⁰, which is likely to underlie some of the benefits observed with transplantation. The identification of uraemic toxins as CKD-specific risk factors for CVD renders it imperative to consider strategies to lower their levels or abrogate their toxicity. This Review summarizes pharmacological and non-pharmacological means of abrogating the effects of uraemic toxins. Device therapies, including innovations in dialysis, have been reviewed elsewhere^{31,32} and are not covered here.

CKD: a unique milieu for CVD

CKD is characterized by the retention of several toxic metabolites and solutes that are appropriately termed uraemic toxins. These toxins are chemicals that accumulate as a result of failed elimination by the kidneys, and through interaction with biological processes produce a response that is unfavourable to the host³³. Based on physicochemical characteristics that determine their response to conventional haemodialysis, uraemic toxins are traditionally classified as either free water-soluble low-molecular-weight solutes, protein-bound (PB) uraemic toxins and middle molecules. Low-molecular-weight solutes include phosphorus, urea and creatinine; middle molecules include fibroblast growth factor 23 (FGF23) and β_2 -microglobulin; whereas PB uraemic toxins include indoxyl sulfate, indoxyl acetate, kynurenine, kynurenic acid, *p*-cresyl sulfate³³⁻³⁵ and indole-3 acetic acid. Trimethylamine N-oxide (TMAO) is another

uraemic toxin that has been linked to CVD in the general population and is also found at elevated levels in patients with CKD³⁶. The association of uraemic toxins such as phosphorus and FGF23 with CVD has been reviewed elsewhere^{37,38}; here, we focus on PB uraemic toxins.

Generation and metabolism of PB uraemic toxins

Many uraemic toxins are the products of dietary constituents. For example, *p*-cresyl sulfate is derived from tyrosine, and indoxyl sulfate, indoxyl acetate, kynurenine and kynurenic acid are products of tryptophan metabolism (FIG. 1a). Dietary tryptophan is catabolized through distinct pathways. A small fraction of tryptophan undergoes degradation in the intestine by tryptophanase-containing bacteria to generate indole. Upon absorption through the portal circulation, indole is then converted to indoxyl and then transformed into indoxyl sulfate and indoxyl acetate for excretion through the kidneys³⁹. A large proportion (>90%) of dietary tryptophan is absorbed directly through the portal circulation and is subsequently converted to N-formyl-L-kynurenine by tryptophan 2,3-dioxygenase 2 (TDO2) in the liver and indoleamine 2,3-dioxygenase 1 (IDO1) and IDO2 in the peripheral tissues to form kynurenine⁴⁰ (FIG. 1b). Kynurenine is further catabolized by kynureninase to increase subsequent downstream products such as anthranilic acid and guinolinic acid, which represents the major route of kynurenine clearance^{41,42}, or by kynurenine amino transferases to kynurenic acid⁴³. In kidney failure, an accumulation of tryptophan metabolites occurs as a consequence of its increased production in the gut owing to gut dysbiosis, alterations in enzyme activity and its ineffective excretion by the kidneys^{39,44-46}. In contrast to these PB uraemic toxins, TMAO is a low-molecular-weight metabolic product of dietary precursors L-carnitine, choline and phosphatidylcholine, which are derived from red meat, eggs, fish and poultry (FIG. 2). The intestinal microbiome degrades these precursors into trimethylamine (TMA), which is further converted into TMAO in the liver^{36,47}. Elevated TMAO levels in CKD are likely to be due to its potentially enhanced production and reduced filtration⁴⁸.

Cardiovascular effects of PB uraemic toxins

A wealth of clinical studies has linked the abovedescribed uraemic toxins to cardiovascular mortality in patients with CKD^{49-53} , in association with profound cardiac and vascular dysfunction. Although some phenotypic overlap exists in the profile of CVD among the general population and patients with CKD, distinct differences exist⁵⁴ imparted by the specific cardiac and vascular toxicity of TMAO^{36,53,55,56}, indoxyl sulfate^{57,58}, *p*-cresyl sulfate^{51,59}, kynurenine⁶⁰ and indole-3 acetic acid⁶¹, as reviewed elsewhere⁶⁰.

Cardiac dysfunction induced by uraemic toxins is characterized pathologically by myocardial fibrosis and remodelling abnormalities⁶² (FIG. 3). Although the pathogenesis underling these entities is likely to be multifactorial, certain uraemic toxins are implicated. For example, treatment of cultured neonatal rat cardiomyocytes with indoxyl sulfate induces protein

synthesis and increases cell volume, reminiscent of the cardiac hypertrophy observed in patients with CKD⁶³. Rats treated with indoxyl sulfate also showed increased myocardial fibrosis⁶⁴. Administration of *p*-cresyl sulfate to mice induced cardiomyocyte apoptosis — an effect that might contribute to diastolic dysfunction in patients

with CKD⁶⁵. Mechanisms such as endoplasmic reticulum and oxidative stress are also likely to contribute to myocardial damage induced by uraemic toxins^{66,67}.

Uraemic vascular disease is characterized by endothelial dysfunction, accelerated atherosclerosis, neointimal hyperplasia, a hyperthrombotic state, abnormal vascular



Fig. 1 | **Uraemic toxin production from tryptophan metabolism. a** | Tryptophan obtained through dietary sources can be degraded in the intestine by tryptophanase-containing bacteria to produce indole, which is then converted into indolic solutes such as indoxyl sulfate in the liver. Tryptophan absorbed through the portal circulation can also undergo metabolism in the liver to produce kynurenine. Indoxyl sulfate and kynurenine are considered to be uraemic toxins; they are normally excreted by the kidney but are retained in patients with chronic kidney disease (CKD). Elevated levels of these uraemic toxins in patients with CKD activate the aryl hydrocarbon receptor (AHR) to increase levels of tissue factor (TF) in the vessel wall, thereby enhancing thrombotic processes. **b** | A number of uraemic toxins, including indoxyl sulfate, indoxyl acetate, kynurenine and kynurenic acid are derived from tryptophan metabolism. Kynureninase is likely to augment the degradation of kynurenine and increase its downstream metabolites such as anthranilic acid and quinolinic acid, which are also considered to be uraemic toxins. Part **a** adapted with permission from REF.⁷⁷, American Society of Nephrology.



Fig. 2 | **TMAO synthesis.** Trimethylamine *N*-oxide (TMAO) is a multistep process and includes dietary ingredients such as choline and carnitine, which undergoes microbial processing. The intermediate γ-butyrobetaine (GBB) is rapidly converted to trimethylamine (TMA), which is then converted to TMAO, which is normally excreted via the kidneys. Allicin and 3,3-dimethyl-1-butanol (DMB) inhibit the microbiome processing and reduce the circulating levels of TMAO. A vegetarian diet supplemented with members of the Cruciferae family can reduce the activity of FMO3 — a flavin-dependent monooxygenase enzyme that is responsible for TMAO synthesis — and can therefore reduce the production of TMA from L-carnitine.

calcification, microvasculature rarefaction and suppressed angiogenesis (FIG. 3). Uraemic toxins contribute to these pathological conditions by promoting the dysfunction of several cell types including endothelial cells, endothelial progenitor cells, vascular smooth muscle cells (VSMCs), platelets and polymorphonuclear cells. For example, indolic solutes and other uraemic toxins compromise various properties of endothelial cells, including their proliferation, survival, migration, permeability, anticoagulant properties and nitric oxide-induced vasodilation⁶⁸⁻⁷¹. Of note, aryl hydrocarbon receptor (AHR) signalling⁷²⁻⁷⁵ may be particularly important for the cardiovascular effects of uraemic toxins. In endothelial cells and VSMCs, indoxyl sulfate and kynurenine bind to the ligand-binding domain of AHR, leading to AHR activation and inducing the transcription of F3, which encodes tissue factor⁷⁴ (FIG. 4). Tissue factor is the primary trigger of the extrinsic coagulation cascade and drives thrombosis after vascular injury (for example, after vascular surgery or endovascular procedures). In addition to increasing F3 transcription, ligand-activated AHR binds tissue factor in the cytosol to prevent its degradation73,76. The association of this indoxyl sulfate and the kynurenine-AHR-tissue factor axis with thrombosis has been validated in two independent patient cohorts77. Moreover, AHR activation is also implicated in the atherosclerosis of Apoe-knockout mice78. Uraemic toxins may also affect thrombotic processes via actions on endothelial cells and VSMCs. VSMC proliferation is a hallmark of intimal stenosis and VSMCs are a major contributor to thrombosis in arterial diseases. Several uraemic toxins, such as inorganic phosphate and indoxyl sulfate, induce VSMC proliferation, migration and calcification79 and augment the prothrombotic properties of VSMCs72,73,76. In addition, the CKD milieu alters platelet functions, which can contribute to atherothrombosis^{19,54,80,81}.

The profound adverse effects of uraemic toxins on cardiovascular biology⁸² indicates that therapeutic targeting of uraemic toxins or their downstream mechanisms could lead to cardiovascular benefits for patients with CKD. As described in the following sections, potential therapeutic approaches could involve non-pharmacological or pharmacological interventions. Given the complex biology of uraemic toxins, a multimodal approach may be warranted to effectively control their protean effects on the cardiovascular system.

Non-pharmacological interventions

The goal of non-pharmacological interventions is to modulate the production of and/or improve the clearance of uraemic toxins. The rationale for these interventions is built on the understanding that some uraemic toxins are derived from specific dietary constituents such as amino acids (for example, tryptophan for indoxyl sulfate, kynurenine and indoxyl acetate; tyrosine for *p*-cresyl sulfate), fatty acids or other nutrients such as choline (for TMAO) that are subsequently processed by the intestinal microbiome (FIGS 1,2). The intermediate metabolic products that arise from this processing are absorbed into the portal circulation and undergo further biotransformation in the liver through phase I metabolism and phase II metabolism. In blood, some uraemic toxins bind tightly to albumin⁸³ and are excreted in urine through tubular secretion^{84,85}. Uraemic toxins are pathologically elevated even in patients with early-stage CKD, and continue to rise with disease progression^{72,86,87}. However, the importance of uraemic toxin biogenesis and clearance to total uraemic toxin level is underscored by the fact that concentrations of uraemic toxins vary substantially between patients at the same CKD stage72,77,86-88. Indeed, uraemic toxins are influenced not only by their excretion via the kidneys but also by dietary intake, processing by

Phase I metabolism

Biochemical processing of the parent drug (by oxidation, reduction or hydrolysis) to convert it into a more polar molecule.

Phase II metabolism

A phase of drug metabolism that involves conjugation of the drug by coupling it or its metabolites to another molecule to augment its excretion.

Transamination

A biochemical process whereby an amino group from an amino acid is exchanged for a keto acid, generating an amino acid version of the keto acid and a keto acid version of the original amino acid. the intestinal microbiome and biotransformation in the liver^{39,40,89-92}, all of which can vary between individuals and may be considered as targets for intervention.

Nutritional interventions

Dietary modification has long been a cornerstone in the management of patients with CKD. For example, restriction of dietary components such as proteins reduces substrates for uraemic toxin generation, and in principle reduces uraemic manifestations^{93,94}. Over time, this approach tempers the emergence of metabolic abnormalities and potentially delays the need for dialysis⁹⁵; however, the optimal amount of protein intake for patients with CKD and kidney failure remains a topic of debate⁹⁶.

Several studies have examined the effects of low protein, vegetarian or Mediterranean diets on CKD progression, but little is known about the influence of these diets on CVD events. One study of 29 healthy individuals given a high protein diet (that is, a target protein intake of >25% of total energy intake) or low protein diet (that is, a target protein intake of <25% of total energy intake) for 2 weeks reported that individuals on a low protein diet demonstrated a reduction in serum levels of indoxyl sulfate, indoxyl glucuronide, kynurenine and quinolinic acid, and reduced urinary excretion of indoxyl sulfate - demonstrating the feasibility of this approach to lowering uraemic toxin levels in patients with CKD97. A meta-analysis of 16 controlled clinical trials, each involving at least 30 patients with CKD revealed that dietary restriction of protein intake to low or very

low levels (<0.8 g/kg per day or <0.4 g/kg per day, respectively), for a time period of 6–36 months, improved levels of bicarbonate, phosphorus and blood urea nitrogen, slowed the rate of progression to kidney failure, and displayed a trend towards lower rates of all-cause mortality. Furthermore, patients on very low protein diets had slower progression of kidney failure than patients on a low protein diet⁹⁸. By contrast, the Modification of Diet in Renal Disease (MDRD) study found no beneficial effects of reducing protein intake on the progression of kidney failure, and noted a signal for malnutrition and a negative impact on survival^{99,100}. Of note, none of these studies examined the effect of protein restriction on CVD events or CVD-related mortality.

Although the optimal level of protein restriction required to ameliorate uraemic toxicity in patients with CKD is unclear, several studies have attempted to compensate for the lack of essential amino acids in a low protein diet by supplementation with ketoanalogues. The rationale for this approach is that α -ketoanalogues should convert into essential amino acids in the body via transamination and thereby compensate for the lack of dietary amino acids obtained through a low protein diet. One meta-analysis that included data from 951 patients demonstrated a benefit of this approach in terms of slowing progression of CKD without causing malnutrition. However, the effect of this intervention on patient survival or CVD mortality benefit was not evaluated¹⁰¹.

Vegetarian diets may provide different proteins and lower total protein levels than animal-based diets,



Fig. 3 | Cardiovascular consequences of uraemic toxicity. Uraemic toxins can induce a plethora of cardiac and vascular pathological conditions, including cardiac fibrosis, accelerated atherosclerosis, thrombosis, medial vascular calcification and microvascular rarefaction. These processes can, in turn, drive cardiovascular complications such as myocardial infarction, heart failure, arrhythmias, stroke, cognitive decline and peripheral artery disease.



Fig. 4 | **Consequences of AHR activation.** The aryl hydrocarbon receptor (AHR) is a ubiquitously expressed cytosolic protein that undergoes nuclear translocation upon binding with ligands such as indoxyl sulfate and kynurenine. In the nucleus, AHR induces transcription of *F3*, which encodes tissue factor (TF). In the cytosol, ligand-activated AHR protects TF from ubiquitination by STUB1 E3 ligases. Both these processes effectively increase the levels of TF in endothelial cells and vascular smooth muscle cells (VSMCs), which, upon rupture of a plaque or vascular intervention, triggers thrombosis through the extrinsic coagulation pathway.

and some evidence suggests that these differences may translate into beneficial effects on cardiovascular indices, inflammatory markers, proteinuria and glomerular filtration rate^{102,103}. Vegetarian diets also alter the microbiome in a favourable manner. For example, plant-based diets stimulate the growth of butyrate-producing bacteria and provide fibres that induce the fermentation of short chain fatty acids in the colon, both of which improve epithelial integrity, thereby preventing the release of pro-inflammatory factors from the intestine to the circulation^{104,105}. However, one study that examined the effect of the largely plant-based Mediterranean diet on gut-derived uraemic toxins found that this dietary intervention did not lower levels of the studied uraemic toxins or arterial plaque burden — a surrogate of cardiovascular health¹⁰⁶

Various dietary permutations have also been attempted to reduce levels of TMAO. Studies in rodents and humans have shown that a high fat diet increases postprandial levels of TMAO^{107,108}. Reducing the dietary precursors of TMAO through a reduction in dietary levels of red meat, eggs, fish and poultry may be one option for lowering TMAO levels94. A vegetarian diet supplemented with members of the Cruciferae family can reduce the activity of FMO3 - a flavin-dependent monooxygenase enzyme that is responsible for TMAO synthesis - and can thus reduce the production of TMA from L-carnitine^{109,110}. Targeted dietary manipulations to specifically inhibit other enzymes involved in TMAO synthesis have also been attempted. For example, the Mediterranean diet is thought to derive some of its known health benefits from allicin^{111,112}, a biochemical found in garlic and virgin olive oil that modulates gut microbiota through its antimicrobial properties to reduce the metabolism of carnitine to TMAO^{113,114}. Moreover, 3,3-dimethyl-1-butanol (DMB), a choline analogue found in virgin olive oil and red wine, inhibits microbial TMA lyases and also reduces TMAO production^{115,116}. However, a prospective multicentre study in Spain showing a reduction in cardiovascular events among individuals at a high cardiovascular risk following implementation of a Mediterranean diet supplemented with extra-virgin olive oil¹¹¹ did not evaluate individuals with CKD.

Cruciferae

A large family of plants with four-petalled flowers that includes cabbage, brussels sprouts, broccoli and turnips.

TMAO synthesis from dietary L-carnitine involves gut microbiota through two sequential gut microbiotadependent transformations: namely, the rapid generation of the atherogenic intermediate γ-butyrobetaine (GBB) followed by its transformation into TMA. Dietary interventions can lower the concentration of L-carnitine, but can in parallel modify microbiota to reduce TMAO production. The influence of diet on the two-step, gut-dependent process of TMAO generation has been examined in healthy individuals¹¹⁷. Ingestion of oral isotope tracers followed by extensive microbial analysis demonstrated that participants who followed a vegetarian or vegan diet had significantly lower TMAO levels than those of individuals on an omnivorous diet. Thus, reduced ingestion of L-carnitine along with alterations in gut microbiota contributes to generally lower TMAO levels among vegans and vegetarians than among meat eaters^{117,118}.

Some of the above-described studies have lacked information on uraemic toxin levels and their association with CVD events or CVD mortality. However, in the absence of such information, the potential beneficial effect of a particular diet on the cardiovascular health of patients with CKD should be carefully weighed against their putative limitations, such as increases in potassium and oxalate load94. Early and protracted dietary intervention may be required to achieve an appreciable reduction in CVD events among patients with CKD. In this case, long-term compliance may become a limiting factor. Despite these limitations, an accumulating body of evidence suggests that plant-based diets offer distinct advantages for the management of CKD, including beneficial effects on protein, carbohydrate, fat and phosphate levels, as well as improvements in acidosis⁹⁴. Pending additional longitudinal, well-powered studies, patient-tailored diets that reduce uraemic toxins and their related CVD outcomes are yet to be established.

Targeting microbiota

Intestinal microbiota have an integral role in the maintenance of intestinal barrier integrity and regulation of host immunity and metabolic processes, and have been linked to hallmarks of CVD, including hypertension¹¹⁹ and atherosclerosis¹²⁰. The accumulation of uraemic toxins in patients with CKD and consumption of antibiotics, such as macrolides, β -lactams and fluroquinolones, can profoundly affect the composition of intestinal microbiota, resulting in 'uraemic gut dysbiosis'¹²¹. One mouse model of CKD demonstrated intestinal dysbiosis of various proteobacteria, increased translocation of bacteria across the intestinal barrier and increased serum levels of bacterial endotoxin¹²². The dysbiosis of patients with CKD is characterized by a decrease in the abundance of Clostridia and Bacillus spp.¹²². and an increase in several bacterial families that contain urease (for example, Alteromonadaceae and Cellulomonadaceae), uricase (for example, Cellulomonadaceae and Dermabacteraceae) and tryptophanase (for example, Enterobacteriaceae and Verrucomicrobiaceae)123. An analysis of 19 intestinal microbial families that were overexpressed in patients with kidney failure compared with levels in healthy individuals demonstrated that 12 possessed urease, 5 possessed uricase and 4 possessed indole and p-Cresolforming enzymes¹²³. These changes would be expected to augment the production of urea, uric acid and indole, and compromise intestinal barrier function, resulting in the translocation of bacteria and toxins into the circulation^{124,125}. A notable depletion of short-chain fatty acids such as butyrate and propionate in patients with CKD indicates a shift away from saccharolytic fermentation (indicative of gut microbiome homeostasis) towards proteolytic fermentation (resulting in the production of harmful uraemic toxins from amino acids and proteins). These perturbations negatively affect the cardiovascular health of patients with CKD, as reviewed elsewhere¹²⁶. Collectively, these findings underlie the rationale to restore the microbiome balance in patients with CKD.

The microbiome can be manipulated using a number of strategies, including ingestion of unprocessed fibre-rich food items, avoidance of certain drugs such as proton pump inhibitors and/or administration of prebiotics (such as arabinoxylan oligosaccharides or non-digestible oligo and polysaccharides), probiotics, or synbiotics, as summarized in detail elsewhere¹²⁷. Human studies of prebiotics in patients with CKD have yielded mixed results¹²⁸. A 12-week study in which patients with CKD were given muffins loaded with pea hull and the prebiotic inulin¹²⁸, based largely on the hypothesis that the increased fibre load would aid delivery of the prebiotic to the colon and thereby increase saccharolytic fermentation, found that this intervention reduced levels of *p*-cresyl sulfate in blood. Following the same rationale, administration of an α-glucosidase inhibitor (acarbose)¹²⁹ and the sodium-glucose co-transporter 2 inhibitor canagliflozin130 to block carbohydrate absorption in the small intestine and increase levels of carbohydrates for saccharolytic fermentation in the large colon of mice also reduced serum concentrations of p-Cresol sulfate. That study used mice with normal kidney function and this approach should be applied to a CKD mouse model to examine the effect of this intervention on uraemic toxins.

In animal models of hypertension without CKD, dietary supplementation with the probiotic *Lactobacillus murinus* or use of a high-fibre diet combined with acetate (again, to improve saccharolytic fermentation) reduced blood pressure, cardiac fibrosis and left ventricular hypertrophy^{131,132}. Probiotics have also been investigated in patients with CKD. In one 6-week randomized, placebo-controlled, crossover trial, administration of *Streptococcus thermophilus*, *Lactobacillus*

with CKD reduced plasma levels of p-Cresol sulfate but not indoxyl sulfate¹⁰⁵. Studies of synbiotics have shown similarly variable effects on uraemic toxins^{133,134}. In one study, administration of a combination of prebiotics (high-molecular-weight inulin, fructo-oligosaccharides and galacto-oligosaccharides) and probiotics (nine different strains across the Lactobacillus, Bifidobacterium, and Streptococcus genera) to patients with non-dialysis CKD for 6 weeks led to a significant reduction in levels of p-Cresol sulfate but not indoxyl sulfate¹⁰⁶. Except for changes in the stool microbiome (characterized by an increase in Bifidobacterium spp. and depletion of Ruminococcaceae spp.), no alterations in parameters such as inflammatory cytokines and oxidative stress biomarkers were noted. Prospective clinical trials are underway to examine the effects of dietary interventions and approaches to manipulating the intestinal microbiota on CKD outcomes135; however, these studies are typically short-term and not powered to examine CVD events.

acidophilus and Bifidobacterium longum to patients

Investigations of the effects of probiotic supplements on TMAO levels have vielded inconsistent results^{127,136,137}. One small randomized study found that administration of the multi-strain probiotic VSL#3 did not significantly attenuate the increase in plasma levels of TMAO induced by a 4-week, high-fat diet in non-obese men¹³⁷. Other approaches have involved fecal transplantation or ingestion of genetically engineered bacteria to modulate uraemic toxin-producing enzymes or approaches to scavenge and/or neutralize endotoxins in the circulation as a result of barrier dysfunction caused by gut dysbiosis¹³⁸. Targeting of gut bacteria that harbour the indoxyl sulfate substrate, tryptophanase, or the TMAO substrate, TMA, can lower circulating levels of indoxyl sulfate and TMAO in mice^{139,140}. Targeting of the small molecules produced by microbiota (the secretome) has also been suggested as an approach to modulating host-microbiome interactions as a strategy for lowering uraemic toxins141.

Despite the potential of these approaches to reduce uraemic toxins, the effect of such interventions on CVD risk in patients with CKD remains unclear. Studies involving manipulation of the microbiome have produced conflicting results, potentially because the influence of host factors, such as age, sex, ethnicity, dietary patterns, comorbidities and medication intake, on the microbial landscape remains incompletely defined. Successful translation of microbiome-targeted therapies would also require major obstacles to be addressed, such as the need to maintain a stable microbial ecosystem in the gut of patients despite frequent changes in their environment resulting from exposure to hospital or dialysis units and/or antibiotics, which may threaten the stability of microbiota communities142. Most importantly, the ability of these interventions to effectively reduce levels of a range of uraemic toxins over a protracted period of time with resultant clinically meaningful CVD outcomes in patients with CKD is yet to be demonstrated. Marginal reductions in circulating uraemic toxin levels may not be sufficient to derive biological benefits, as demonstrated by a study in which even

Prebiotics

Components of food that induce the growth or activity of beneficial microorganisms to maintain microbial homeostasis.

Probiotics

Live microorganisms that can improve or restore the gut flora to maintain microbial homeostasis.

Synbiotics

A combination of probiotics and prebiotics that are intended to improve the survival and activity of beneficial microorganisms in the gut.

low levels of uraemic toxins were still able to drive prothrombotic processes⁷². Adding to the complexity of this topic, emerging work casts doubt on the contribution of the microbiome to levels of uraemic toxins. A study of 141 patients showed an increase in levels of PB uraemic toxins with CKD progression; however, the levels of these toxins and their precursors remained unchanged in feces¹⁴³. Anaerobic culture of fecal samples from the patients showed no difference in the rate of p-Cresol sulfate, indole and indole-3 acetic acid production, strongly suggesting that increased plasma levels primarily result from the retention of uraemic toxins as a consequence of impaired kidney function rather than an increase in uraemic toxin generation. These results encourage careful reconsideration of alterations in the microbiome as a therapeutic strategy to reduce the burden of uraemic toxins and as such, microbial intervention remains an experimental pre-clinical modality.

Albumin displacers

Human serum albumin (HSA) is the most abundant protein in plasma and the main carrier of PB uraemic toxins¹⁴⁴. The fatty acid binding sites of HSA serve as ligand binding domains for PB uraemic toxins¹⁴⁵⁻¹⁴⁷, allowing the hydroxyl group of indoxyl sulfate to interact with Tyr410 of HSA while its amide group interacts with Leu430 (REF.¹⁴⁸) of HSA (FIG. 5a). Indoxyl sulfate also forms salt bridges, hydrogen bounds and van der Wall interactions with other residues in that binding domain¹⁴⁸. Once bound to HSA, the ability of haemodialysis and haemodiafiltration to clear PB uraemic toxins is limited^{149,150}. For example, concentrations of indoxyl sulfate and p-Cresol sulfate are reduced by only 10-35% with haemodialysis, whereas the concentration of more tightly bound uraemic toxins, including 3-carboxy-4-methyl-5-propyl-2-furanproprionic acid, remained unchanged or increased after haemodialysis¹⁵¹. Techniques such as fractionated plasma separation and adsorption (so-called albumin dialysis) have been proposed as an approach to clear PB uraemic toxins, but this approach is labour intensive, not easily scalable and fraught with complications such as bleeding and thrombosis¹⁵².

Certain ligands can affect the structure of HSA or alter its affinity to ligands such as indoxyl sulfate¹⁴⁴. This approach could potentially be used to displace indoxyl sulfate from HSA and increase the amount of HSA-free indoxyl sulfate for clearance by haemodialysis (FIG. 5b). For example, infusion of the competitive ligands ibuprofen and furosemide led to doubling of indoxyl sulfate and indole-3 acetic acid clearance from plasma in an in vitro haemodialysis system¹⁵³. Although an attractive concept, the translation of this technique to the clinical realm is contingent on the identification of an inert and safe displacer, deciphering the off-target effects of the displacer once bound to HSA (for example, effects on hormones and drugs), and the fate of the displacer itself.

Gastrointestinal dialysis

In low-resource settings or situations in which traditional dialysis is not readily available, protocols have been developed for repetitive oral administration of cathartic compounds to promote the excretion of uraemic toxins and excess fluids — methods that are collectively referred to as 'gastrointestinal dialysis'. Although terminated prematurely, an open-label, randomized, controlled trial of oral magnesium oxide (MgO; a cathartic), and the oral carbon adsorbent AST-120 found that MgO, but not AST-120, may be effective in slowing progression of coronary artery calcification in patients with stages 3–4 CKD. However, the MgO group suffered from a dropout rate of 27%, primarily due to diarrhea¹⁵⁴.

Pharmacological interventions

Whereas non-pharmacological interventions are aimed at reducing the generation or improving the clearance of uraemic toxins, pharmacological interventions are



Fig. 5 | **Consequences of indoxyl sulfate binding to albumin. a** | Indoxyl sulfate interacts with human serum albumin at drug-binding site 2. Indoxyl sulfate is shown as a stick representation with a semi-transparent van der Waals surface (magenta). Selected side chains are shown as sticks color-coded by atom type; yellow dashed lines indicate hydrogen bonds. **b** | Indoxyl sulfate is a highly protein-bound uraemic toxin, and only ~10% exists in its free form. Indoxyl sulfate bound to albumin cannot be removed by dialysis; however, infusion of a ligand that can displace the uraemic toxin from the binding cavity of albumin is likely to increase the proportion of free indoxyl sulfate, enabling its removal in the dialysate outflow. Part **a** reprinted with permission from REF.¹⁴⁸, Elsevier.

Xenobiotic

A chemical substance found within an organism that is not naturally produced or expected to be present within the organism or in an ecological system. generally aimed at reducing the downstream intracellular effects of uraemic toxins without altering their concentrations. The ideal pharmacological regimen is scalable, sustainable over a long period of time and can be targeted to a specific disease manifestation induced by a particular uraemic toxin or a group of uraemic toxins.

Klotho

Klotho is a membrane-bound protein that is highly expressed in kidney tubules but also exists as a secreted form¹⁵⁵. Membrane-bound Klotho is a coreceptor for FGF23 and modulates FGF23 signal transduction. Soluble Klotho is found in the blood, urine, cerebrospinal fluid and is involved in processes such as aging, energy metabolism, Wnt signalling, anti-oxidation, ion transport and in the regulation of parathyroid hormone, the renin-angiotensin-aldosterone system and 1,25(OH)₂VD₃ production¹⁵⁵. Klotho has also demonstrated anti-senescent properties in several organ systems including aortic valve¹⁵⁶, regenerating muscle¹⁵⁷ and even adipose-derived stem cells158. Transgenic overexpression of Klotho expression in mouse models of CKD reduces vascular calcification, whereas Klotho haploinsufficiency has the opposite effect¹⁵⁹. CKD is a state of Klotho deficiency¹⁶⁰ and PB uraemic toxins directly influence Klotho expression. Both indoxyl sulfate and *p*-cresyl sulfate hypermethylate the promoter of *Kl*, which results in downregulation of Klotho, exacerbation of renal fibrosis and deterioration of renal function in mice¹⁶¹.

Administration of recombinant α-Klotho protein reduced kidney and cardiac fibrosis, attenuated cardiac remodelling and improved cardiac function in a mouse model of CKD¹⁶². In vitro and in vivo studies have shown that Klotho also protects against indoxyl sulfate-associated cardiac toxicity and left ventricular hypertrophy, with Klotho-deficient mice showing an exaggerated response to indoxyl sulfate¹⁶³. In patients with CKD, lower serum Klotho levels were associated with arterial stiffness even after correcting for confounding factors¹⁶⁴. By contrast, a 2.6-year follow-up study of patients with CKD stages 2–4 found that FGF23, but not Klotho itself, was associated with decompensated heart failure, although neither marker predicted development of atherosclerosis¹⁶⁵.

The link between Klotho and uraemic solutes remains poorly explored. Daily intraperitoneal injection of indoxyl sulfate for 8 weeks induced ventricular hypertrophy in mice — an effect that was more pronounced in Klotho-haplodeficient mice¹⁶³. This ventricular hypertrophy was attenuated by administration of Klotho through inhibition of indoxyl sulfate-induced p38 and ROS signalling¹⁶³.

Ongoing clinical trials are aimed at assessing the value of serum Klotho as a predictor of cardiovascular calcification in patients with CKD¹⁶⁶. It is conceivable that Klotho supplementation or use of a peptide-based approach may have beneficial effects in patients with CKD, including on the progression of kidney disease and cardiomyopathy¹⁶². However, additional studies are warranted to assess the beneficial effects of Klotho on uraemic toxin levels and CVD outcomes in patients with CKD.

Aryl hydrocarbon receptor inhibitors

AHR signalling is a well-known xenobiotic pathway associated with chemical carcinogenesis. AHR is a receptor that is ubiquitously expressed in the cytosol of cells, which upon ligand binding undergoes nuclear translocation to induce the transcription of genes such as those encoding specific members of the cytochrome P450 family of microsomal enzymes (FIG. 4). A wealth of studies in rodents have uncovered a role for AHR signalling in cardiovascular functions, including cardiac myocyte function^{167,168}, angiogenesis (that is, vessel development from the existing vascular bed) and neovascularization (that is, vessel development from a naive bed)^{169,170}, blood pressure regulation^{171,172}, atherosclerosis⁷⁸, myocardial ischaemia–reperfusion injury and post-ischaemic conditioning¹⁷³, and stroke¹⁰⁹.

Mounting evidence also implicates AHR signalling as an important mediator of uraemic toxicity by a set of uraemic toxins that are particularly cardio- and vasculotoxic. Uraemic toxins derived from tryptophan amino acids, including indoxyl sulfate, indoxyl acetate, kynurenine, kynurenic acid, are all AHR ligands^{174,175}. Several mouse and human studies have implicated CKD as a global state of AHR activation with particular involvement of the myocardium and vasculature^{175,176}. As described earlier, indoxyl sulfate and kynurenine bind to the ligand-binding domain of AHR, leading to increased levels of tissue factor in ECs and VSMCs, while simultaneously AHR binds tissue factor to prevent its degradation⁷⁴ (FIG. 4). This bimodal action increases levels of tissue factor, which promotes thrombosis, upon spontaneous rupture of plaque, thus augmenting the risk of adverse cardiovascular events. The central role of AHR in cardiovascular functions, as well as its activation by uraemic toxins, provides a strong mechanistic rationale for therapeutic targeting of AHR in CKD. A number of AHR inhibitors are already in pre-clinical development. We have assessed the effects of AHR inhibitors in mouse models of vascular injury-associated thrombosis in mice with adenine-induced CKD and in mouse models of uraemic toxicity induced by exposure to indoxyl sulfate or kynurenine73,77. Emulating features seen in patients with CKD, these mouse models exhibited increased levels of tissue factor in the aorta and heightened thrombosis at baseline as demonstrated by a shortened time to occlusion of carotid blood flow following ferric chloride-induced vascular injury as a model of occlusive thrombosis; administration of AHR inhibitors downregulated tissue factor expression and suppressed thrombosis.

Further mechanistic probing of the AHR-tissue factor-thrombosis axis showed that ligand-activated AHR regulates TF and thrombosis through the regulation of STUB1 (also known as CHIP)⁷³ — a U-box-containing E3 ligase that ubiquitinates several substrate proteins¹⁷⁷. Genetic manipulation of *STUB1* in VSMCs showed that loss of STUB1 activity reduced tissue factor ubiquitination and increased thrombosis⁷³. YL-109, an analogue of 2-(4-amino-3-methylphenyl)benzothiazole, has been assessed in preclinical studies owing to its proposed tumour-suppressing properties. It is a partial AHR inhibitor and upregulates *STUB1* transcription¹⁷⁸.

An increase in STUB1 protein levels induced degradation of tissue factor and suppressed thrombosis in a flow loop system⁷³. Importantly, the activation of STUB1 by YL-109 did not augment the risk of bleeding⁷³. These studies suggest support of the pharmacological rationale for suppressing the AHR-STUB1 axis to downregulate tissue factor and thrombosis in patients with CKD.

At least three AHR inhibitors, including CH223191 and CB7993113, have been assessed in models of CKD, illustrating a number of intriguing points. First, AHR inhibitors effectively extended the time to occlusion in CKD mice to that observed in non-CKD mice following ferric chloride-induced vascular injury73. Notably, inhibition of AHR did not increase the bleeding time of CKD mice as this manipulation did not alter physiological haemostatic mechanisms⁷³. By contrast, the antithrombotic actions of heparin are accompanied by substantially prolonged bleeding time in CKD mice, because agents such as heparin or oral anticoagulants perturb the haemostatic machinery in blood as part of their action⁷³. These findings in mice corroborate observations in patients with CKD. Estimates suggest that every 30-ml/min decrease in creatinine clearance is associated with a 50% increase in the risk of major and minor bleeding¹⁷⁹. Thus, AHR seems to represent a safe and CKD-specific antithrombotic target in uraemic mice⁷³. The finding that this approach can lower the thrombotic risk induced by the CKD milieu to a range seen in non-CKD models is encouraging. Second, the finding that AHR inhibitors antagonize the effects of indoxyl sulfate to downregulate TF in VSMCs72 encourages the exploration of uraemic toxins as biomarkers to guide AHR inhibitor therapy in patients with CKD⁷².

Adverse and off-target effects of AHR. Examination of potential adverse effects is important when considering any protein target, as is an understanding of the limitations of rodent models for studying AHR biology, as rodent and human AHR exhibit different ligand selectivity and gene regulation^{180,181}. For example, mouse AHR demonstrated 10-fold higher binding affinity for typical AHR ligands such as 2,3,7,8 tetrachlorodibenzo-p-dioxin than human AHR, whereas human AHR had higher binding for indirubin¹⁸⁰. In the same vein, genes identified as differentially expressed between mouse and human AHR are known to be involved in a number of biological pathways, including cell proliferation and the inflammatory response181. These studies underscore a need to exercise caution in extrapolating mouse data to humans for AHR studies. Global Ahr-knockout mice are viable and fertile¹⁸² but show vascular defects (patent ductus venosus) in liver183 and a 24% reduction in platelet counts, illustrating the importance of AHR expression in certain organ or cell types¹⁸⁴. As mentioned earlier, members of the cytochrome P450 system of microsomal enzymes are direct transcriptional targets of AHR¹⁸⁵. These enzymes catalyse the first step in the metabolism of lipophilic xenobiotics or drugs to generate more water-soluble intermediate compounds that can be readily excreted, suggesting that AHR inhibitors could induce undesirable drug-drug interactions. In addition, AHR regulates the expression of other metabolic

enzymes, such as aldehyde dehydrogenases (specifically ALDH1A1 and ALDH3A1) and specific drug transporters, such as multidrug resistance-associated protein 4 (encoded by ABCC4) and P-glycoprotein¹⁸⁶. Available evidence suggests that uraemic toxins influence the expression of certain drug transporters, which can affect drug pharmacokinetics. For example, indoxyl sulfate upregulates the expression of P-glycoprotein in human hepatoma (HepG2) cells. The same study also demonstrated that of patients with CKD who underwent heart or kidney transplantation, those with higher serum levels of indoxyl sulfate required higher doses of ciclosporin (a P-glycoprotein substrate) to obtain the cyclosporin target blood concentration¹⁸⁷. Thus, the CKD milieu may influence the pharmacokinetics of various medications through modulation of AHR-mediated transcriptional processes¹⁸⁶ and AHR inhibitors may normalize this adverse effect of uraemic toxins on drug clearance mechanisms. However, the effect of AHR inhibitors on the pharmacokinetics of drugs and other endogenous compounds¹⁸⁸ and the potential for adverse drug-drug interactions require careful consideration.

Limitations of AHR inhibitors. So far, these inhibitors have been developed using either cell-based AHR activity assays (for example, the Bayer compound BAY218)¹⁸⁹, or by in silico screening or homology modelling (CH223191 and CB7993113)¹⁹⁰. In the absence of a crystal structure of human AHR, proof of their binding to the AHR is lacking. The absence of this information is notable given the increasing recognition that a number of drugs do not bind to their intended protein targets, but rather elicit biological activity through off-target effects¹⁹¹. The availability of this critical information will help to drive the development of highly selective AHR inhibitors and confirm their mechanism of action. Moreover, not all AHR inhibitors have been assessed in models of CKD.

AHR inhibitors can be classified as complete antagonists (such as CB7993113) or partial antagonists (such as YL109)¹⁹². On the basis of their ability to selectively regulate AHR signalling, AHR ligands are classified as either selective AHR modulators¹⁹³ (for example, 3',4'-dimethoxy- α -naphthoflavone¹⁹⁴ and 6,2',4'-trime thoxyflavone¹⁹⁵) or non-selective AHR modulators (for example, CH223191 and CB7993113). Several AHR inhibitors currently in cancer trials^{196,197} are complete AHR antagonists. Selective AHR modulators remain unexplored for therapeutic use in clinical studies. However, our current understanding of the integral role of AHR in cardiovascular biology, its activation by uraemic toxins, and its association with uraemic complications, suggests that this receptor is a tantalizing therapeutic target for CKD-associated CVD.

Kynureninase

The tryptophan metabolite kynureninase is associated with CVD in the general population^{60,198}, and has demonstrated pro-thrombotic properties in a mouse model of CKD⁷⁷. Accumulation of kynureninase is evident in early stages of CKD and progresses with CKD progression, reaching levels of 4.8–6.5 μ M (normal <2 μ M).

Aza-analogue

Chemical compounds in which a carbon atom is replaced by a nitrogen atom.

As mentioned earlier, kynurenine is generated by the catabolism of tryptophan by indoleamine 2,3-dioxygenase 1 (IDO1) or tryptophan 2,3-dioxygenase 2 (TDO2), and is further degraded by kynureninase⁴⁰. Therapeutic strategies to target kynurenine include suppression of its production or approaches to stimulating its degradation. IDO1 and kynurenine have been attributed immunosuppressive properties through the activation of AHR, leading to the production of immune-tolerant dendritic cells and regulatory T cells. Tumour cells produce excessive kynurenine to evade immune recognition and suppression of kynurenine production has therefore been considered as a clinical approach in the oncology field¹⁹⁹. Efforts to promote kynurenine degradation through use of pegylated-kynureninase have also been made²⁰⁰. However, caution is warranted with this agent, as kynureninase may increase levels of metabolites such as anthranilic acid and quinolinic acid (FIG. 1b). Both of these metabolites are uraemic toxins that are associated with augmented thrombosis in patients77, and contribute to other systemic toxic effects, such as neurocognitive diseases^{201,202}. Kynureninase supplementation has not been examined in models of CKD. Careful long-term pre-clinical CKD models and clinical studies involving patients with CKD are warranted to examine the risk-benefit profile of targeting kynureninase in CKD.

Kinase inhibitors

Kinases are well-established mediators of almost all cellular functions and are validated targets, mostly in the field of cancer treatment. Tyrosine kinases (including both receptor and non-receptor kinases, such as Src kinases) and serine/threonine kinases (such as AKT) have been implicated in various kidney pathological conditions, such as liver fibrosis, glomerulonephritis and diabetic kidney disease^{203,204}, and are also considered to mediate several CVD pathological conditions, such as cardio-pulmonary fibrosis and ischaemia-reperfusion injury²⁰⁵. Despite these connections, little is known about the link between uraemic toxins and kinases. Indoxyl sulfate has been shown to induce the release of microparticles from human umbilical vein endothelial cells via upregulation of the p38-mitogen-activated protein kinase signalling pathway²⁰⁶, and such microparticles have been implicated in promoting thrombosis²⁰⁷. However, key questions as to the effect of uraemic toxins on kinases and the relevance to CKD-associated CVD remain unanswered. A variety of kinase inhibitors are under preclinical development and/or are FDA approved²⁰⁸, suggesting that these could be repurposed for therapeutic purposes for CKD pending the outcomes of appropriate studies.

TMAO inhibitors

TMAO is a metabolite of choline and L-carnitine, which are processed through specific enzymes in the gut microbiome (FIG. 2). In addition to dietary interventions and probiotics, investigators have assessed the ability of antibiotics to reduce the production of TMAO, and demonstrated beneficial effects on TMAO levels and aortic plaque development in mice fed with a high L-carnitine and/or choline diet²⁰⁹. However, this approach is likely to induce non-specific alterations in the gut microbiome. Meldonium is an aza-analogue of GBB — the quaternary amine bio-precursor of L-carnitine — and competes with L-carnitine and GBB for y-butyrobetaine hydroxylase and carnitine/organic cation transporter type 2 (OCTN2), which synthesizes TMAO²¹⁰. Treatment of rats with meldonium significantly decreased intestinal microbiota-dependent production of TMA and TMAO from L-carnitine but not from choline²¹¹. The administration of meldonium together with L-carnitine significantly increased GBB concentration in blood plasma and in isolated rat small intestine perfusates. Meldonium did not influence bacterial growth or bacterial uptake of L-carnitine but significantly decreased TMA production by K. pneumoniae. DMB is an inhibitor of choline lyase (FIG. 2). Mice fed a western diet with or without 1.0% DMB in drinking water for 8 weeks showed significantly reduced plasma TMAO levels and improved cardiac function compared with mice fed a western diet only¹¹⁶. DMB also prevented an increase in levels of proinflammatory cytokines and interstitial fibrosis in the hearts of these mice. However, DMB cannot completely eliminate TMAO synthesis. A 2018 study reported that enalapril lowered TMAO levels by increasing its excretion without affecting its production or the gut microbiome, suggesting that a combined approach to reducing TMAO production while promoting TMAO elimination might be more effective than either approach alone²¹². Although encouraging, studies to date have been preclinical and involved rodent models with normal kidney function; hence, the ability of these compounds to prevent CKD-associated CVD in experimental models and human patients through modulation of TMAO levels is yet to be established.

AST-120

The role of the gut flora in generating precursors for some uraemic toxins has generated interest in pharmacological agents that are enterally active. Of these, AST-120 is probably best known. AST-120 is an oral sorbent comprising porous spherical carbon particles that are capable of non-specifically adsorbing several low-molecular-weight molecules (100–10,000 kDa). Intestinal adsorption of intermediate metabolites of indoxyl sulfate, p-Cresol sulfate and other uraemic toxins by AST-120 reduces their availability to mediate toxic downstream effects²¹³. On the basis of this rationale, pre-clinical studies have been performed to assess the effects of AST-120 on various uraemic manifestations, including atherosclerosis, cardiac dysfunction and bone disease, as discussed elsewhere²¹⁴.

AST-120 has been approved for the treatment of uraemic symptoms and to delay progression of disease in CKD patients in Japan since 1991 (REF.²¹⁵). However, human studies have yielded conflicting results. Two multinational, randomized, double-blind, placebo-controlled trials that evaluated the effects of AST-120 on the progression of CKD in 2,035 adults with moderate to severe CKD²¹⁶ found no difference between the intervention and placebo groups in the time taken to reach the primary end point (a composite of dialysis initiation, kidney transplantation and doubling of the serum

creatinine level). Although clinical studies have primarily focused on the progression of CKD, a retrospective analysis of nearly 200 patients with non-dialysis-dependent CKD found significantly lower aortic calcification in those treated with AST-120 (REFS^{217,218}). Despite these beneficial effects, AST-120 has not been approved for use in the USA or Europe owing to concerns related to its non-specific binding to several low-molecular-weight molecules in the gut. Nonetheless, these studies have paved the way for the development of targeted binders of the uraemic toxin precursors in the gut.

Conclusions and future directions

Epidemiological studies indisputably identify CKD as an independent risk factor for various CVDs, implicating the existence of CKD-specific risk mediators. These mediators include uraemic toxins, such as indoxyl sulfate and kynurenine, AHR activation, immune dysfunction and gut dysbiosis, and hence a multipronged approach is warranted to target these processes. An increasing number of mechanistic studies demonstrate the existence of a causal link between uraemic toxins and CKD-associated CVD, and as our understanding of the pathogenic contribution of uraemic toxins to CVD unfolds, a parallel, comprehensive approach is needed to translate this knowledge to the clinical realm.

As the processes underlying CVD development begin in the early stages of CKD and CVD risk increases as CKD progresses, it stands to reason that early targeting of uraemic toxins should be considered. Conventional haemodialysis cannot efficiently remove vasculotoxic PTUBs, which may underlie the poor outcomes of patients with advanced CKD²¹⁹.

The unique environment of CKD demands a unique approach. A number of nodes have been identified through which the pathogenicity of uraemic toxins can potentially be targeted; however, further research into the cardiovascular benefits of these targeted approaches is needed. A multimodal approach is also likely to be needed, with adjustments according to the different stages of CKD. For example, levels of uraemic toxins could be regulated through nutrition and microbiota manipulations in early stages of CKD, whereas more aggressive manoeuvres to improve the clearance of uraemic toxins could be applied in patients with kidney failure through the use of selective dialyzers for uraemic toxins^{31,32,220}. The pharmacological targeting of cellular pathways affected by uraemic toxins could span all stages of CKD and could potentially be guided by biomarkers of CVD.

The successful translation of discoveries to the clinical realm will be contingent on overcoming bottlenecks such as the altered pharmacokinetics of patients with CKD, and will require careful evaluation of the cost–benefit ratio of protracted therapy, as well as consideration of primary end points for clinical studies. These and other challenges can be overcome by a coordinated effort by the nephrology community, biotechnology industry and regulatory agencies. Such an approach is needed to address the enormous CVD burden of patients with CKD.

Published online: 23 March 2021

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Acknowledgements

This work was funded by NIH grants R01 HL132325 and R21 DK119740-01 to V.C.C. We thank the Evans Center for Interdisciplinary Biomedical Research and the Department of Medicine at Boston University School of Medicine for their ongoing support of Affinity Research Collaboratives on Thrombosis and Hemostasis.

Author contributions

All authors contributed equally to writing and reviewing/ editing before submission.

Competing interests

The authors declare no competing interests.

Peer review information

Nature Reviews Nephrology thanks P. Evenepoel, J. Shapiro and the other, anonymous, reviewer(s) for their contribution to the peer review of this work.

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