

Table 1. Changes of gut microbiota composition in renal diseases

Subject	Changes in gut microbiota			Functional effects and/or relevance	Reference
	Phylum level	Family level	Genus/Species level		
Mice with diabetic nephropathy	<i>Actinobacteria</i> ↑	Unknown	<i>Prevotella</i> ↓, <i>Rikenella</i> ↓, <i>Bifidobacterium</i> ↓, <i>Ruminococcus</i> ↓, <i>Bacteroides acidifaciens</i> ↓	Related to SCFAs production	15
Rats with diabetic nephropathy	<i>Actinobacteria</i> ↑ <i>Firmicutes</i> ↓ <i>Proteobacteria</i> ↓	<i>S24-7</i> ↓	<i>Turicibacter</i> ↑, <i>Coprobacillus</i> ↑ <i>Prevotella</i> ↓, <i>Clostridium</i> ↓ <i>Ruminococcus</i> ↓, <i>Oscillospira</i> ↓	Associated with the progression of diabetic nephropathy	19
14 T2DM patients with diabetic nephropathy	Unknown	<i>Coriobacteriaceae</i> ↑, <i>Prevotellaceae</i> ↓	<i>Escherichia-Shigella</i> ↑ <i>Prevotella_9</i> ↓	Contributed to the physiopathological diagnosis of DN from DM	20
Mice with diabetic nephropathy	<i>Firmicutes</i> ↓	Unknown	<i>Anaerospobacter</i> ↑ <i>Allobaculum</i> ↑, <i>Blautia</i> ↓	Gut flora may contribute to the heterogeneity of the induced response	21
Rats with diabetic nephropathy	Unknown	<i>Coriobacteriaceae</i> ↑ <i>Erysipelotrichaceae</i> ↑	<i>Adlercreutzia</i> ↑	Related to proteinuria in diabetic nephropathy	22
Rats with diabetic nephropathy	Unknown	<i>Peptostreptococcaceae</i> ↑ <i>Rikenellaceae</i> ↓, <i>Ruminococacceae</i> ↓	<i>Turicibacter</i> ↑, <i>Desulfovibrio</i> ↑ <i>SMB53</i> ↑, <i>Clostridium</i> ↓ <i>Lactobacillus</i> ↓	Related to the metabolic disorder of diabetic nephropathy	45

24 patients with ESRD and uremic animals	<i>Actinobacteria</i> ↑ <i>Firmicutes</i> ↑ <i>Proteobacteria</i> ↑	<i>Brachybacterium</i> ↑ <i>Enterobacteriaceae</i> ↑, <i>Halomonadaceae</i> ↑, <i>Lactobacillaceae</i> ↓, <i>Prevotellaceae</i> ↓	<i>Thiothrix</i> ↑ <i>Nesterenkonia</i> ↑	Unknown	Changes in the biochemical environment caused by uremia and its therapeutic intervention	24
Mice with bilateral I/R injury	Unknown	<i>Enterobacteriaceae</i> ↑ <i>Ruminococcaceae</i> ↓		<i>Lactobacilli</i> ↓	The hallmarks of I/R induced dysbiosis, associated with SCFAs reduction and intestinal inflammation	46
Mice with unilateral I/R injury	Unknown	Unknown		<i>Clostridium</i> ↑, <i>Bifidobacterium</i> ↓, <i>TM7</i> ↓	Related to D-Serine/L-Serine level and tubular damage/tubular cell proliferation	47
855 individuals with early renal function decline	Unknown	<i>Christensenellaceae</i> ↑ <i>Ruminococcaceae</i> ↑, <i>Lachnospiraceae</i> ↑		Unknown	Related to circulating metabolites derived from bacterial protein fermentation and eGFR	48
65 patients with CKD	Unknown	Unknown		<i>Roseburia</i> spp.↓ <i>Faecalibacterium prausnitzii</i> ↓	Butyrate-producing bacteria are negatively associated with renal function	49
892 adults with kidney disease/52 patients with ESRD	<i>Proteobacteria</i> ↑ <i>Verrucomicrobia</i> ↑ <i>Actinobacteria</i> ↓	<i>Enterobacteriaceae</i> ↑ <i>Streptococcaceae</i> ↑, <i>Prevotellaceae</i> ↓		<i>Streptococcus</i> ↑, <i>Prevotella</i> ↓, <i>Prevotella</i> 9↓, <i>Faecalibacterium</i> ↓, <i>Clostridium</i> ↓, <i>Coprococcus</i> ↓	Uremic toxin generation in adults with kidney disease at the expense of producing less butyrate	50, 51

Table 2. Effects of diabetic drugs on gut microbiota and renal outcomes

Agents	Drugs	Effect on gut microbiota			Effect on renal outcomes	Reference	
		Phylum level	Family level	Genus/Species level			
GLP-1 receptor agonists	Exenatide	Unknown	Unknown	Unknown	Reduce albuminuria and pathological renal injury	121,122	
	Liraglutide	<i>Bacteroides</i> ↑ <i>Verrucomicrobia</i> ↑ <i>Proteobacteria</i> ↓ <i>Actinobacteria</i> ↓	<i>Rikenellaceae</i> ↑, <i>S24-7</i> ↑ <i>Erysipelotrichaceae</i> ↑ <i>Lachnospiraceae</i> ↓ <i>Peptostreptococcaceae</i> ↓	<i>Akkermansia</i> ↑, <i>Romboutsia</i> ↑ <i>Anaerotruncus</i> ↓, <i>Klebsiella</i> ↓ <i>Lachnospiraceae_UCG-001</i> ↓ <i>Lachnospiraceae_NK4A136_group</i> ↓ <i>Ruminiclostridium</i> ↓, <i>Desulfovibrio</i> ↓	Reduce the incidence of nephropathy and macroalbuminuria	125,127, 129, 130	
			Unknown	<i>Aerococcus</i> ↑, <i>Bacteroides</i> ↑, <i>Ruminococcus</i> ↑, <i>Coprobacillus</i> ↓	<i>Akkermansia</i> ↑ <i>Barnesiella</i> ↑ <i>Oscillibacter</i> ↑	Lower the incidence in new-onset large albuminuria and sustained decline of eGFR	131,133
			Unknown	Unknown	Unknown	Improve UACR	134,135

DPP-4 inhibitors	Linagliptin	<i>Bacteroides</i> ↑, <i>Actinobacteria</i> ↓ <i>Proteobacteria</i> ↓	Unknown	Unknown	Reduce proteinuria and improve renal injury	140,142,143
	Alogliptin	Unknown	Unknown	Unknown	Improve UACR and maintain eGFR	144
	Saxagliptin	<i>Firmicutes</i> ↑, <i>Bacteroides</i> ↓	<i>Erysipelotrichaceae</i> ↑, <i>Bacteroidaceae</i> ↓	<i>Lactobacillus</i> ↑, <i>Allobaculum</i> ↑ <i>Turicibacter</i> ↑, <i>Prevotella</i> ↓	Improve UACR	147,148
	Sitagliptin	<i>Bacteroides</i> ↑, <i>Proteobacteria</i> ↑ <i>Actinobacteria</i> ↑, <i>Firmicutes</i> ↓ <i>Tenericutes</i> ↓	<i>Ruminococcaceae</i> ↑	<i>Roseburia</i> ↑, <i>Bifidobacterium</i> ↑ <i>Blautia</i> ↓	Reduce urinary albumin levels	150,151
	Canagliflozin	<i>Actinobacteria</i> ↓, <i>TM-7</i> ↓	Unknown	<i>Alistipes</i> ↑, <i>Alloprevotella</i> ↑ <i>Olsenella</i> ↑, <i>Oscillospira</i> ↓ <i>Bifidobacterium</i> ↓, <i>Helicobacter</i> ↓ <i>Mucispirillum</i> ↓	Reduce plasma uremic toxins and lower UACR	155,157, 158
SGLT-2 inhibitors	Dapagliflozin	<i>Firmicutes</i> ↑, <i>Proteobacteria</i> ↑ <i>Bacteroides</i> ↓, <i>Actinobacteria</i> ↓	<i>Desulfovibrionaceae</i> ↑, <i>Lactobacillaceae</i> ↓	<i>Oscillospira</i> ↓, <i>Mucispirillum</i> ↓ <i>Barnesiella</i> ↓	Prevent progression of kidney disease	160–163
	Empagliflozin	<i>Bacteroides</i> ↑, <i>Firmicutes</i> ↓	Unknown	<i>Bacteroides</i> ↑, <i>Bifidobacterium</i> ↑ <i>Parabacteroides</i> ↑	Reduce the risk of nephropathy, proteinuria and serum creatinine	133,164, 165

Ertugliflozin

Unknown

Unknown

Unknown

Reduce the risk of renal
composite endpoint and 167,168
preserve eGFR and UACR
