Published in final edited form as:

Top Clin Nutr. 2019 ; 34(2): 153–160. doi:10.1097/TIN.0000000000000170.

Gut Microbiota and Cardiometabolic Risk Factors in Hemodialysis Patients: A Pilot Study

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Abstract

The gut microbiota has been implicated in the pathogenesis and progression of kidney disease. However, little is known about the gut microbiota in hemodialysis (HD) patients. We assessed the gut microbiota and its relationship with clinical variables in ten HD patients. We found that the *Firmicutes*-to-*Bacteroidetes* ratio was positively associated with traditional risk factors for cardiovascular disease. Furthermore, *Faecalibacterium* was positively associated with carbohydrate intake and negatively associated with arterial stiffness. Finally, endotoxemia was inversely associated with butyrate producers. Future studies should assess if targeting the gut microbiota result in a lower burden for cardiovascular disease in HD patients.

Keywords

Cardiovascular Disease; Gut microbiota; Hemodialysis; Nutrition; Kidney Disease

Introduction

The gut microbiota has been implicated in the pathogenesis of many chronic diseases, including kidney disease.¹ A unique gut microbiota has been described in chronic kidney disease (CKD) and end-stage renal disease (ESRD), including bacterial overgrowth in the duodenum and jejunum, overgrowth of some aerobic species, such as *Enterobacteria* and *Enterococci*, and a decrease in commensal bacteria genera, such as *Bifidobacteria*, leading to a dysbiotic environment.^{2,3}

In addition to the “dysbiotic” microbiota, a shift in the fermentation profile has been described. Particularly, an increase in protein fermentation byproducts, such as p-cresyl sulfate and indoxyl sulfate, has been observed. These protein fermentation metabolites are clinically important because they have been associated with cardiovascular disease and the

progression of CKD.^{4,5} Specifically, p-cresyl sulfate and indoxyl sulfate, which are products of the fermentation of tyrosine and tryptophan, respectively, have been associated with higher cardiovascular mortality, endothelial dysfunction, and mineral and bone disorder.^{5–9} Furthermore, trimethylamine N-oxide (TMAO), which is derived from the bacterial metabolite trimethylamine through the metabolism of choline, betaine, and carnitine, has also been associated with the progression of CKD.^{7,2} On the contrary, short-chain fatty acids (SCFA) derived from bacterial saccharolytic fermentation, particularly butyrate, have been associated with positive health outcomes, such as decreased inflammation and gut health.^{10,11} Importantly, diet is a main determinant of the gut microbiota and the modification of dietary intake by increasing the total dietary fiber intake may shift the fermentation profile towards the production of SCFA.² However, to date it remains controversial in the CKD and ESKD population.

In healthy individuals these metabolites are excreted in the urine, but due to the reduced or blunted ability to produce urine in ESRD patients, the concentrations of these bacterial metabolites are higher than in adults with preserved kidney function.^{12–14} However, little is known about the composition of the gut microbiota and its relationship with cardiometabolic risk factors in hemodialysis (HD) patients. Therefore, the objective of this pilot study was to examine the gut microbiota composition and its association with cardiometabolic risk factors in HD patients.

Methods

HD patients were recruited from local dialysis clinics in Illinois state. Patients were approached for recruitment if they received HD treatment 3 days/week, were age >30 years, did not have gastrointestinal disease (e.g., inflammatory bowel disease or celiac disease), did not take antibiotic treatment the month before testing, and had been receiving dialysis treatment for at least three months. Consent was obtained from each participant, and all protocols were approved by the University of Illinois Institutional Review Board in accordance with the Declaration of Helsinki. Subjects who qualified for the study and agreed to participate underwent a battery of tests on a single occasion on a non-dialysis day (18–24hr after a mid-week HD treatment):

Anthropometry, Bone, and Body Composition:

Barefoot standing height was measured to the nearest 0.1 cm with a stadiometer (Seca 222, Hamburg, Germany). Body weight was measured on a digital scale (Tanita BWB-800, Arlington Heights, IL) without shoes and outer garments. All measurements were taken in duplicate and averaged. Whole-body fat, lean, bone mass, and bone mineral density was measured by dual emission x-ray absorptiometry (DEXA) (Hologic QDR 4500A, Bedford, Massachusetts) following manufacturers protocol.

Wave Reflection and Arterial Stiffness:

Blood pressure was measured in duplicate using an automated cuff following a 10-minute quiet rest in the supine position (Omron IntelliSense HEM-907XL, Lake Forest, IL). Radial wave forms were then collected via tonometry and were used to estimate central pressures

using a validated transfer function (SphygmoCor, AtCor Medical, Sydney, Australia). Aortic pulse wave velocity (PWV) was determined by tonometry (SphygmoCor, AtCor Medical, Sydney, Australia).¹⁵

Physical Function:

Average walking speed (m/s) over a 10-m course was measured in triplicate and averaged. A validated incremental shuttle-walk test was performed to assess physical performance.¹⁶ Participants completed the 8ft up-and-go test to assess functional fitness.¹⁷

Dietary Intake:

Dietary recalls covering the 48 hours prior to collection of the fecal sample were collected by a trained researcher using the modified version of the USDA 5-pass method¹⁸ and analyzed using Nutrition Data System for Research (NDSR 2014 version, University of Minnesota, Minneapolis, MN).

Fecal Sample Collection:

Participants were asked to collect a complete fecal sample (Commode Specimen Collection System Sage Products, Crystal Lake, IL). Samples were stored at -80°C within 30 minutes of collection. DNA was extracted (Powerlyzer PowerSoil DNA Isolation Kit MO BIO, Carlsbad, CA). Primers targeting the V4 hypervariable region of the bacterial 16S rRNA gene were used to create amplicons of 250bp as described previously.¹⁹ Sequencing was performed using Illumina Mi-seq and V3 reagents. Relative changes in bacterial diversity (α -diversity) and taxonomical changes were analyzed using QIIME 1.9.1. "Sequences were clustered into operational taxonomic units (OTU) using closed-reference against the Greengenes 13_8 reference with a 97% similarity threshold."^{20p5} Since it was a cross-sectional study without a control group, α -diversity, or within-sample diversity was assessed through phylogenetic metrics (e.g., phylogenetic distance) and non-phylogenetic metrics (e.g., OTU count and Chao1).²¹

Blood Chemistry:

Plasma samples were collected in lithium-heparin coated tubes (BD vacutainer, Franklin Lakes, NJ) at the start of HD treatment immediately after the fecal sample collection. A renal function panel was measured (Piccolo Xpress, Abaxis Inc., Union City, CA).

Lipopolysaccharide-Binding Protein (LBP):

Plasma LBP was determined by a commercially-available enzyme-linked immunosorbent assay (ELISA) kit (Cell Sciences, Canton, MA). Inter-assay coefficient variation (CV) was 9.8–17.8%, while the intra-assay CV was 6.1%. The effective range of the assay was 5–50 ng/ml. All standards, blank, and samples were performed in triplicate and averaged.

Statistical Analysis

Data were analyzed using SPSS 24 (IBM Corporation, Armonk, NY). Data are presented as the mean $\pm$ standard error of the mean (SEM), unless otherwise indicated. Spearman correlations were used to compare gut microbiota OTUs (representative of 1% of total

bacterial population) and variables of interest. For all statistical tests, significance was considered as $P = 0.05$.

Results

Patient characteristics are described in Table 1. For the fecal microbiota, a total of 308,536 bacterial 16S rRNA sequences were obtained, with a median of 31,199 (range 25,056–35,617) sequences per sample. For diversity and species richness, the data were rarified to 25,056 sequences/sample. For α -diversity analysis (or within sample analysis), we observed a mean species richness (Chao1) of 339 ± 66 species, which was inversely associated with age ($\rho = -0.806$; $P = 0.005$) (Figure 1). Since this was a cross-sectional study, β -diversity (or between samples analysis) was not performed.

At the phyla level (Figure 2), Firmicutes and Bacteroidetes were the most abundant, followed by *Proteobacteria* and *Verrucomicrobia*. There was a Firmicutes-to-Bacteroidetes ratio of 1.40 ± 0.11 , which was positively associated with traditional risk factors for cardiovascular disease, such as resting brachial and aortic systolic blood pressures ($\rho = 0.648$ and 0.636 , respectively; $P < 0.05$). Additionally, this ratio was positively associated with dietary intake of total fat, saturated fat, and meat ($\rho = 0.667$, 0.636 , 0.661 , respectively; $P < 0.05$).

At the genera level, *Bacteroides spp.* was the most abundant genus in all patients, with a mean of $33.59 \pm 1.81\%$ of total sequences. Meanwhile, *Faecalibacterium spp.* was variably represented between subjects (mean $9.08 \pm 2.3\%$; range 0.10 – 23.17% of total sequences) and was positively associated with total carbohydrate intake ($\rho = 0.636$; $P = 0.048$) and negatively associated with carotid-femoral pulse wave velocity ($\rho = -0.867$, $P = 0.001$) (Figure 3). Finally, LBP was positively associated with *Bilophila spp.* ($\rho = 0.644$, $P = 0.044$), and inversely correlated with *Ruminococcus spp.* and *Oscillospira spp.* ($\rho = -0.733$, -0.697 , $P = 0.016$, 0.025 , respectively).

Discussion

In this cross-sectional study, we assessed the relationship between the gut microbiota composition and cardiometabolic risk factors in ten HD patients. First, we observed that bacterial richness was inversely associated with age. At the phylum level, the Firmicutes-to-Bacteroidetes ratio was positively associated with traditional risk factors for cardiovascular disease, such as resting brachial and arterial systolic blood pressure, total fat and saturated fat intake, and meat intake. Moreover, plasma concentration of LBP, a marker of bacterial translocation, was positively associated with *Bilophila spp.*, and negatively associated with the known butyrate producing bacterial phyla *Roseburia spp.* and *Oscillospira spp.*, but not *Faecalibacterium spp.* Finally, we observed that *Faecalibacterium spp.*, a known butyrate producer with potential anti-inflammatory properties, was negatively associated with aortic PWV, a surrogate of arterial stiffness.

Bacterial species richness (alpha-diversity) has been suggested as an important factor in the gut microbiota of healthy individuals.²² We observed a mean species richness of 339 ± 66 (Chao1), which is below what has been reported in healthy adults and healthy elderly

populations.²³ Additionally, we found that species richness was inversely associated with age (Figure 1). These data support previous findings suggesting reduced species richness with age, including patients undergoing HD.⁹ Previous studies have reported that species richness is lower in obesity.²⁴ However, we did not find an association between species richness and BMI or any other anthropometric measures, such as weight, whole-body fat, or waist-to-hip ratio.

The ratio of Firmicutes-to-Bacteroidetes is commonly assessed in both healthy and clinical populations since these two phyla are the most abundant in the gut.²⁵ In our study, Firmicutes were represented by $54.02 \pm 1.53\%$ of the total sequences, while Bacteroidetes by $40.07 \pm 2.19\%$ of the total sequences, accounting for 94.09% of the total sequences. The Firmicutes-to-Bacteroidetes ratio and its relationship with obesity as a result of increased capacity for energy harvest remains inconclusive.^{26,27} In our study, we found a positive association between this ratio and intakes of total fat, saturated fat, and meat. This was somewhat surprising because a higher abundance of *Bacteroides spp.*, the most abundant genus within the *Bacteroidetes*, has been associated with an animal-based diet, which is usually higher in total and saturated fat.²⁸ Additionally, we did not find an association between Bacteroidetes and meat, total fat, and saturated fat intake. Finally, we found no associations with other bacteria genera that traditionally have been associated with a higher consumption of animal-based products, such as *Desulfovibrio spp.* and *Bilophila spp.* Larger scale studies should aim to assess the relationship between dietary patterns across CKD and changes in the gut microbiota composition and function.

We found an inverse association between the genus *Faecalibacterium* and carotid-femoral pulse wave velocity, a surrogate of arterial stiffness. Within the genus *Faecalibacterium*, *Faecalibacterium prausnitzii* is a known butyrate producer.^{10,29} Interestingly, there have not been any reports of a direct relationship between the relative abundance of *Faecalibacterium prausnitzii* and cardiovascular disease. One possible explanation that may be driving this relationship is the inverse correlation between butyrate production and systemic inflammation.²⁹ Unfortunately, we were not able to measure inflammation in the current study and this should be explored in future studies. Additionally, we did not find a relationship between dietary fiber intake and the fecal relative abundance of *Faecalibacterium*. Therefore, further studies should explore the relationship between *Faecalibacterium prausnitzii*, interventions targeting the gut microbiota, and cardiovascular disease in CKD and ESRD.

Endotoxemia, or increased concentrations of lipopolysaccharide in blood due to bacterial translocation, has been shown to be prevalent in CKD patients, including those on HD.³⁰ This may be in part due to the direct effect of uremia on the intestinal tight-junction proteins, increasing the risk of bacterial translocation from the intestinal lumen to the bloodstream.³¹ Moreover, endotoxemia contributes to the increased systemic inflammation in HD patients.³² In our study, LBP concentration was $32.35 \pm 4.05 \mu\text{g/ml}$, which is higher than what has been reported in healthy subjects, but similar to other studies in CKD, ESRD, and kidney transplant subjects.^{30,33} LBP was inversely associated with *Ruminococcus spp.* and *Roseburia spp.*, genera that are known butyrate producers, but not *Faecalibacterium spp.* or other genera containing known butyrate producers. Furthermore, we observed a positive

correlation between LBP and *Bilophila spp.*, which is a genus that has been associated with a dietary pattern high in animal products, such as meat.²⁸ However, we did not find an association between LBP and any nutrient intake or food group consumption. Because of this possible relationship, future studies should aim to assess if interventions that increase butyrate production decrease endotoxemia and inflammation in HD patients.

There are several limitations in our study. First, this was a cross-sectional study with a small sample size. Second, we did not have a control group to compare our variables against. Lastly, our patients were recruited from only one clinic in Central Illinois state and cannot be generalized to other HD patients. Although the gut microbiota assessment may not be clinically available, we believe this study offers clear rationale to further explore the gut microbiota and cardiometabolic risk factors in HD patients and to develop targeted interventions to assess if changes in the gut microbiota result in better outcomes in HD patients. Further investigation is important due to the association between the gut microbiota and cardiovascular disease, which is the main cause of mortality in HD patients.

Conclusion

We found several associations between the gut microbiota composition and cardiometabolic risk factors. Importantly, we found that the genus *Faecalibacterium* was inversely associated with arterial stiffness, a predictor of cardiovascular mortality in HD patients. Future studies should aim to assess if interventions that increase the production of short-chain fatty acids (e.g., fermentable dietary fiber), particularly butyrate, reduce arterial stiffness in HD patients.

Acknowledgements

We would like to thank the patients and staff of the Champaign-Urbana Dialysis units for their continuous support. We thank Tzu-Wen Liu Cross for her input with the gut microbiota analyses.

Support and Financial Disclosures:

AB was funded by a Predoctoral Fellowship from CONACyT (Mexico's Council of Science and Technology) and received research funding from the Renal Research Institute. **PJF** has received funding from the Renal Research Institute and American College of Sports Medicine. **KRW** has received funding from the National Institutes of Health and the Renal Research Institute. **JMA, BMK, JHJ, and KSS** have no relevant financial relationships to disclose.

References

1. Sekirov I, Russell SL, Antunes LCM, Finlay BB. Gut microbiota in health and disease. *Physiol Rev* 2010;90(3):859–904. 10.1152/physrev.00045.2009. [PubMed: 20664075]
2. Ramezani A, Massy ZA, Meijers B, Evenepoel P, Vanholder R, Raj DS. Role of the Gut Microbiome in Uremia: A Potential Therapeutic Target. *Am J Kidney Dis* 2016;67(3):483–498. 10.1053/j.ajkd.2015.09.027. [PubMed: 26590448]
3. Vaziri ND, Wong J, Pahl M, et al. Chronic kidney disease alters intestinal microbial flora. *Kidney Int* 2013;83(2):308–315. 10.1038/ki.2012.345. [PubMed: 22992469]
4. Missailidis C, Hällqvist J, Qureshi AR, et al. Serum Trimethylamine-N-Oxide Is Strongly Related to Renal Function and Predicts Outcome in Chronic Kidney Disease. *PLoS One* 2016;11(1):e0141738 10.1371/journal.pone.0141738. [PubMed: 26751065]

5. Tang WHW, Wang Z, Kennedy DJ, et al. Gut microbiota-dependent trimethylamine N-oxide (TMAO) pathway contributes to both development of renal insufficiency and mortality risk in chronic kidney disease. *Circ Res* 2015;116(3):448–455. 10.1161/CIRCRESAHA.116.305360. [PubMed: 25599331]
6. Meijers BKL, De Preter V, Verbeke K, Vanrenterghem Y, Evenepoel P. p-Cresyl sulfate serum concentrations in haemodialysis patients are reduced by the prebiotic oligofructose-enriched inulin. *Nephrol Dial Transplant* 2010;25(1):219–224. 10.1093/ndt/gfp414. [PubMed: 19692415]
7. Rossi M, Johnson DW, Xu H, et al. Dietary protein-fiber ratio associates with circulating levels of indoxyl sulfate and p-cresyl sulfate in chronic kidney disease patients. *Nutr Metab Cardiovasc Dis* 2015;25(9):860–865. 10.1016/j.numecd.2015.03.015. [PubMed: 26026209]
8. Lin C-J, Wu V, Wu P-C, Wu C-J. Meta-Analysis of the Associations of p-Cresyl Sulfate (PCS) and Indoxyl Sulfate (IS) with Cardiovascular Events and All-Cause Mortality in Patients with Chronic Renal Failure. *PLoS One* 2015;10(7):e0132589 10.1371/journal.pone.0132589. [PubMed: 26173073]
9. Barreto FC, Barreto DV, Canziani MEF, et al. Association between indoxyl sulfate and bone histomorphometry in pre-dialysis chronic kidney disease patients. *J Bras Nefrol* 2014;36(3):289–296. 10.5935/0101-2800.20140042. [PubMed: 25317610]
10. Louis P, Flint HJ. Diversity, metabolism and microbial ecology of butyrate-producing bacteria from the human large intestine. *FEMS Microbiol Lett* 2009;294(1):1–8. 10.1111/j.1574-6968.2009.01514.x. [PubMed: 19222573]
11. Macfarlane GT, Macfarlane S. Fermentation in the human large intestine: its physiologic consequences and the potential contribution of prebiotics. *J Clin Gastroenterol* 2011;45 Suppl:S120–7. 10.1097/MCG.0b013e31822fecfe. [PubMed: 21992950]
12. Leong S, Sirich T. Indoxyl Sulfate—Review of Toxicity and Therapeutic Strategies. *Toxins (Basel)* 2016;8(12):358 10.3390/toxins8120358.
13. Sirich TL, Meyer TW, Gondouin B, Brunet P, Niwa T. Protein-Bound Molecules: A Large Family With a Bad Character. *Semin Nephrol* 2014;34(2):106–117. 10.1016/j.semnephrol.2014.02.004. [PubMed: 24780467]
14. Evenepoel P, Meijers BKL, Bammens BRM, Verbeke K. Uremic toxins originating from colonic microbial metabolism. *Kidney Int* 2009;76(114):S12–S19. 10.1038/ki.2009.402.
15. Van Bortel LM, Duprez D, Starmans-Kool MJ, et al. Clinical applications of arterial stiffness, Task Force III: recommendations for user procedures. *Am J Hypertens* 2002;15(5):445–452. 10.1016/S0895-7061(01)02326-3. [PubMed: 12022247]
16. Win T, Jackson A, Groves AM, Sharples LD, Charman SC, Laroche CM. Comparison of shuttle walk with measured peak oxygen consumption in patients with operable lung cancer. *Thorax* 2006;61(1):57–60. 10.1136/thx.2005.043547. [PubMed: 16244091]
17. Rikli RE, Jones CJ. Development and validation of criterion-referenced clinically relevant fitness standards for maintaining physical independence in later years. *Gerontologist* 2013;53(2):255–267. 10.1093/geront/gns071. [PubMed: 22613940]
18. Murphy SP. Collection and Analysis of Intake Data from the Integrated Survey. *J Nutr* 2003;133(2):585S–589. <http://jn.nutrition.org/cgi/content/long/133/2/585S>. Accessed January 13, 2017. [PubMed: 12566508]
19. Caporaso JG, Lauber CL, Walters WA, et al. Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proc Natl Acad Sci U S A*. 2011;(Supplement 1):4516–4522. 10.1073/pnas.1000080107. [PubMed: 20534432]
20. DeSantis TZ, Hugenholtz P, Larsen N, et al. Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. *Appl Environ Microbiol* 2006;72(7):5069–5072. 10.1128/AEM.03006-05. [PubMed: 16820507]
21. Navas-Molina JA, Peralta-Sánchez JM, González A, et al. Advancing Our Understanding of the Human Microbiome Using QIIME Vol 531 1st ed. Elsevier Inc; 2013 10.1016/B978-0-12-407863-5.00019-8.
22. Heiman ML, Greenway FL. A healthy gastrointestinal microbiome is dependent on dietary diversity. *Mol Metab* 2016;5(5):317–320. 10.1016/j.molmet.2016.02.005. [PubMed: 27110483]

23. Lakshminarayanan B, Stanton C, O'Toole PW, Ross RP. Compositional dynamics of the human intestinal microbiota with aging: Implications for health. *J Nutr Health Aging* 9 2014:1–14. 10.1007/s12603-014-0513-5.
24. Huttenhower C, Gevers D, Knight R, et al. Structure, function and diversity of the healthy human microbiome. *Nature* 2012;486(7402):207–214. 10.1038/nature11234. [PubMed: 22699609]
25. Ley RE, Turnbaugh PJ, Klein S, Gordon JI. Microbial ecology: Human gut microbes associated with obesity. *Nature* 2006;444(7122):1022–1023. 10.1038/4441022a. [PubMed: 17183309]
26. Turnbaugh PJ, Ley RE, Mahowald MA, Magrini V, Mardis ER, Gordon JI. An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature* 2006;444(7122):1027–1131. 10.1038/nature05414. [PubMed: 17183312]
27. Tilg H, Kaser A. Gut microbiome, obesity, and metabolic dysfunction. *J Clin Invest* 2011;121(6):2126–2132. 10.1172/JCI58109. [PubMed: 21633181]
28. David LA, Maurice CF, Carmody RN, et al. Diet rapidly and reproducibly alters the human gut microbiome. *Nature* 2013;505(7484):559–563. 10.1038/nature12820. [PubMed: 24336217]
29. Hippe B, Remely M, Aumueller E, Pointner A, Magnet U, Haslberger AG. Faecalibacterium prausnitzii phylotypes in type two diabetic, obese, and lean control subjects. *Benef Microbes* 2016;7(4):511–517. 10.3920/BM2015.0075. [PubMed: 27048834]
30. Lemesch S, Ribitsch W, Schilcher G, et al. Mode of renal replacement therapy determines endotoxemia and neutrophil dysfunction in chronic kidney disease. *Sci Rep* 2016;6:34534 10.1038/srep34534. [PubMed: 27698480]
31. Vaziri N, Zhao Y, Pahl M. Altered intestinal microbial flora and impaired epithelial barrier structure and function in CKD: the nature, mechanisms, consequences and potential treatment. *Nephrol Dial Transplant* 2015;0(0):1–10. 10.1093/ndt/gfv095.
32. Feroze U, Kalantar-Zadeh K, Sterling KA, et al. Examining Associations of Circulating Endotoxin With Nutritional Status, Inflammation, and Mortality in Hemodialysis Patients. *J Ren Nutr* 2012;22(3):317–326. 10.1053/j.jrn.2011.05.004. [PubMed: 21880509]
33. Umoh FI, Kato I, Ren J, et al. Markers of systemic exposures to products of intestinal bacteria in a dietary intervention study. *Eur J Nutr* 2016;55(2):793–798. 10.1007/s00394-015-0900-7. [PubMed: 25903259]

Figure 1. Age is inversely associated with species richness

Figure 2. *Firmicutes*-to-*Bacteroidetes* ratio in Hemodialysis patients

Figure 3. *Faecalibacterium* spp. is inversely associated with arterial stiffness

Table 1.

Patient characteristics

Variable	Mean $\pm$ SEM
<i>Demographics</i>	
Age (years)	50 $\pm$ 4
Sex (M/F)	7/3
Ethnicity (% African American)	80%
<i>Anthropometry, bone, and body composition</i>	
BMI (kg/m ²)	31.04 $\pm$ 7.4
Waist-to-hip circumference ratio	0.94 $\pm$ 0.014
Whole-body fat (%)	30.21 $\pm$ 3.37
Whole-body lean mass index (kg/m ²)	21.09 $\pm$ 1.22
Whole-body BMD (g/cm ²)	1.2 $\pm$ 0.03
<i>Cardiovascular</i>	
Brachial SBP (mmHg)	157.3 $\pm$ 8.39
Brachial DBP (mmHg)	82.3 $\pm$ 3.09
Aortic SBP (mmHg)	143.6 $\pm$ 8.38
Aortic DBP (mmHg)	84 $\pm$ 3.07
Augmentation Index @75bpm	28.3 $\pm$ 3.58
cfPWV (m/s)	9.21 $\pm$ 0.63
<i>Physical function</i>	
Gait speed (m/s)	8.69 $\pm$ 1.03
ISWT (s)	291.4 $\pm$ 44.05
8ft up-and-go (s)	3.86 $\pm$ 0.82
<i>Dietary intake</i>	
Energy (kcal/kg/d)	24.37 $\pm$ 2.77
Protein (g/kg/d)	0.86 $\pm$ 0.09
Total fat (% total kcal)	37.91 $\pm$ 2.39
Carbohydrates (% total kcal)	48.23 $\pm$ 2.53
Fiber (g/1000kcal)	6.24 $\pm$ 0.79
Protein-to-fiber ratio	6.39 $\pm$ 0.57
<i>Blood parameters</i>	
Albumin (g/dL)	4.05 $\pm$ 0.09
Phosphorus (mg/dL)	5.98 $\pm$ 0.58
Potassium (mg/dL)	4.95 $\pm$ 0.18
LBP (μ g/mL)	32.35 $\pm$ 4.05

SEM, standard error of the mean; M, male; F, female; BMI, body mass index; BMD, bone mineral density; SBP, systolic blood pressure; DBP, diastolic blood pressure; bpm, beats per minute; cfPWV, carotid-femoral pulse-wave velocity; ISWT, incremental shuttle-walk test; LBP, Lipopolysaccharide-binding protein.

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Table 2.

Relative abundance (% of total sequences) of bacteria (phyla and genera)

Bacteria Genera	Mean $\pm$ SEM
<i>Bacteroidetes</i>	40.07 $\pm$ 2.19
<i>Bacteroides</i>	33.59 $\pm$ 1.81
<i>Parabacteroides</i>	4.66 $\pm$ 1.14
<i>Firmicutes</i>	54.02 $\pm$ 1.53
<i>Faecalibacterium</i>	9.08 $\pm$ 2.30
<i>Undefined Lachnospiraceae</i>	5.80 $\pm$ 1.02
<i>Blautia</i>	5.79 $\pm$ 1.79
<i>Undefined Clostridiales</i>	5.12 $\pm$ 0.78
<i>Ruminococcus</i>	2.81 $\pm$ 1.01
<i>Dorea</i>	1.53 $\pm$ 0.45
<i>Eubacterium</i>	1.37 $\pm$ 0.27
<i>Streptococcus</i>	0.94 $\pm$ 0.014
<i>Roseburia</i>	0.81 $\pm$ 0.37
<i>Oscillospira</i>	0.59 $\pm$ 0.12
<i>Actinobacteria</i>	1.58 $\pm$ 0.42
<i>Bifidobacterium</i>	0.73 $\pm$ 0.31
<i>Proteobacteria</i>	2.63 $\pm$ 0.59
<i>Bilophila</i>	0.22 $\pm$ 1.09
<i>Verrucomicrobia</i>	1.63 $\pm$ 1.22
<i>Akkermansia</i>	1.63 $\pm$ 1.22

SEM, standard error of the mean.