

Huahui Ren

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Educational and Working Experience:

- ✓ 2009.09-2013.08: BSc of Information and Computing Sciences, Institute of Mathematics, Shanxi University
 - ✓ 2013.09-2015.07: Master of Applied Statistics, School of Statistics, Dongbei University of Finance & Economics
 - ✓ 2015.07-2019.01: Bioinformatic Engineer, Institute of Metagenomics, BGI-Research
 - ✓ 2019.01-2023.10: PHD of Genomics, Institute of Biology, University of Copenhagen
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Self-assessment and Research Interest:

- ✓ 8-year experience in the field of metagenomics.
- ✓ Focusing on the effect of gut microbiota on metabolic diseases and the bidirectional association between gut microbiota and oral antibiotic drugs.
- ✓ Expert in multi-omics analysis, high-throughput sequencing data analysis, statistic and machine-learning methods.
- ✓ Familiar with project management and paper publication.

Main Projects:

1. **Project Title:** Multi-Omics Study of Suzhou Cohort

Main Contents: This project is based on a cross-sectional study including healthy controls, pre-diabetic and type 2 diabetic patients to comprehensively identify molecular markers of type II diabetes through the application of multi-omics techniques (metagenomics, metaproteomics and metabolomics).

Contributions: Processing and analysis of multi-omics data,

2. **Project Title:** A Series of Oral Antidiabetic Drugs (OADs) Interventions for Newly Diagnosed T2D Patients

Main Contents: Investigating OADs-Gut Microbiota interactions and OADs-mediated gut microbiota glucose-lowering mechanisms by analysis metagenomic and metabolomic data before and after interventions with acarbose, glipizide, vildagliptin and metformin.

Contributions: Project management, data analysis, academic writing.

3. **Project Title:** Mechanism and precision intervention of berberine and probiotics in the treatment of type II diabetes mellitus

Main Contents: Based on a large, multicenter, placebo-controlled clinical trial, a novel mechanism for lowering blood glucose and postprandial lipid levels in patients with type II diabetes mellitus was investigated with the combination of berberine and probiotics.

Contributions: Project management and multi-omics data analysis.

4. **Project Title:** A study of intra-tumor bacteria in colorectal cancer

Main Contents: Based on non-human WGS and RNA data from a large colorectal cancer study to reveal the composition of bacteria in tumor tissues, bacteria-host relationships, and bacterial prediction of clinical prognosis..

Contributions: Data analysis.

Professional Skills:

Programing Languages: R, Shell, Python, Perl

Operating Systems: Linux and Windows

Research Fields: Bioinformatics, Metagenomics, Data Mining, Statistics.

Language Skill:

English: Presentation and academic writing.

Publication:

1. Zhong H, Fang C, Fan Y, et al. Lipidomic profiling reveals distinct

- differences in plasma lipid composition in healthy, prediabetic, and type 2 diabetic individuals. *Gigascience*. 2017;6(7). doi:10.1093/gigascience/gix036
2. Gu Y, Wang X, Li J, et al. Analyses of gut microbiota and plasma bile acids enable stratification of patients for antidiabetic treatment. *Nat Commun*. 2017;8(1). doi:10.1038/s41467-017-01682-2
 3. Jie Z, Xia H, Zhong S-L, et al. The gut microbiome in atherosclerotic cardiovascular disease. *Nat Commun*. 2017;8(1). doi:10.1038/s41467-017-00900-1
 4. Zhong H, Penders J, Shi Z, **Ren H**, et al. Impact of early events and lifestyle on the gut microbiota and metabolic phenotypes in young school-age children. *Microbiome*. 2019;7(1). doi:10.1186/s40168-018-0608-z (**co-first**)
 5. Zhong H, **Ren H**, Lu Y, et al. Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. *EBioMedicine*. 2019;47. doi:10.1016/j.ebiom.2019.08.048(**co-first**)
 6. Zhang Y, Gu Y, **Ren H**, et al. Gut microbiome-related effects of berberine and probiotics on type 2 diabetes (the PREMOTÉ study). *Nat Commun*. 2020;11(1). doi:10.1038/s41467-020-18414-8 (**co-first**)
 7. Yang F, Sun J, Luo H, **Ren H** et al. Assessment of fecal DNA extraction protocols for metagenomic studies. *Gigascience*. 2020;9(7):1-12. doi:10.1093/gigascience/giaa071
 8. Zou H, Wang D, **Ren H**, Cai K, Chen P, Fang C. Effect of Caloric Restriction on BMI, Gut Microbiota, and Blood Amino Acid Levels in Non-Obese Adults. *Nutrients*. 2020;12(631):1-14. (**co-first**)
 9. Zhong H, Wang Y, Shi Z, Zhang L, **Ren H**, et al. Characterization of respiratory microbial dysbiosis in hospitalized COVID-19 patients. *Cell Discov*. 2021. doi:10.1038/s41421-021-00257-2 (**co-first**)
 10. Zhang X, Zhong H, Li Y, Shi Z, **Ren H**, et al. Sex- and age-related trajectories of the adult human gut microbiota shared across populations of different ethnicities. *Nat Aging*. 2021;1(January). doi:10.1038/s43587-020-00014-2
 11. Zhu J, **Ren H**, Zhong H, et al. An Expanded Gene Catalog of Mouse Gut Metagenomes. *mSphere*. 2021;6(1):1-12. (**co-first**)
 12. Wang S, **Ren H**, Zhong H, et al. Combined berberine and probiotic treatment as an effective regimen for improving postprandial hyperlipidemia in type 2 diabetes patients: a double blinded placebo controlled randomized study. *Gut Microbes*. 2022;14(1):2003176. doi:10.1080/19490976.2021.2003176 (**co-first**)
 13. Zhang X, **Ren H**, Zhao C, et al. Metagenomic analysis reveals crosstalk between gut microbiota and glucose-lowering drugs targeting the gastrointestinal tract in Chinese patients with type 2 diabetes: a 6 month, two-arm randomised trial. *Diabetologia*. 2022;65(10):1613-1626. doi:10.1007/s00125-022-05768-5 (**co-first**)
 14. Zhang M, Shi Z, Wu C, et al. Cushing's Syndrome is associated with Gut Microbial Dysbiosis and Cortisol-Degrading Bacteria. *J Clin Endocrinol Metab*. Published online December 29, 2023. doi:10.1210/clinem/dgad766

15. **Ren, Huahui**, Zhun Shi, Fangming Yang, et al. 2024. "Deciphering Unique and Shared Interactions Between the Human Gut Microbiota and Oral Antidiabetic Drugs." iMeta:e179. <https://doi.org/10.1002/imt2.179> (**First**)
16. Three research articles are under review (**Nature Medicine**, co-first; **Med**, co-first; **Cell host and microbe**)
17. Two patents.