Commentary: Causal effects of specific gut microbiota on bone mineral density: a two-sample Mendelian randomization study

Jiahao Chen†, Xiang Guo† and Hong Song*

School of Basic Medicine, Zhejiang Chinese Medical University, Hangzhou, Zhejiang, China

A Commentary on

Causal effects of specific gut microbiota on bone mineral density: a two-sample Mendelian randomization study

by Chen S, Zhou G, Han H, Jin J and Li Z (2023) *Front. Endocrinol.* 14:1178831. doi: 10.3389/fendo.2023.1178831

1 Introduction

Shuai Chen and his colleagues published a study titled "Causal effects of specific gut microbiota on bone mineral density: a two-sample Mendelian randomization study" in *Frontiers in Endocrinology* (1). The authors concluded, "Our MR analysis also found that the abundance of Prevotella9 and Prevotellaceae was associated with high BMD at different sites. Consistent directional effects for all analyses were observed in both MR-Egger and weighted median methods, which suggests that Prevotella might be a promising target for osteoporosis prevention." We support and appreciate the authors' work and agree with their conclusions. However, we have some concerns about their data and results. Here are some critical comments on these issues.

On the first line of Supplementary Table S1, the Effect allele and Other alleles were marked wrong. In the article of Qi Wang et al. (2–4), the Effect_allele of rs182549 was C, and Other_allele was T, while in the author's article, the Effect_allele of rs182549 was T, and Other_allele was C. In short, "Effect_allele" and "Other_allele" should switch places in the Supplementary Table S1.

Under the subheading of Causal effect of the gut microbiota on forearm bone mineral density, this article first describes "Genus Prevotella9 (β = 0.129, 95% CI: 0.007–0.251, P = 0.039) were negatively associated with FA-BMD (Figure 2)". Then, in *Discussion*, this article describes "which suggests that Prevotella might be a promising target for osteoporosis prevention." There is an apparent inconsistency between the two accounts. β is the beta value, and exposure factors and outcomes are positively correlated when β is >0 (5–7). Hence, Prevotella9 was positively correlated with FA-BMD, which is consistent with the study of Liang Zhuang et al., "Some short-chain fatty acids (SCFAs) producers,

including Lactobacillus, Akkermansia, Prevotella, Alistipes, and Butyricicoccus, were reduced in patients with lower bone mass (LBM) and PMO." (8).

The study by Chen and his colleagues has helped us better understand the relationship between specific gut microbiota and bone mineral density. Still, it needs to be written more accurately to demonstrate the causal relationship between the gut microbiota and the risk of osteoporosis.

Author contributions

JC: Writing – original draft, Investigation. XG: Investigation, Writing – original draft. HS: Writing – review & editing.

Funding

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

References

1. Chen S, Zhou G, Han H, Jin J, Li Z. Causal effects of specific gut microbiota on bone mineral density: a two-sample Mendelian randomization study. *Front Endocrinol.* (2023) 14:1178831. doi: 10.3389/fendo.2023.1178831

2. Wang Q, Dai H, Hou T, Hou Y, Wang T, Lin H, et al. Dissecting causal relationships between gut microbiota, blood metabolites, and stroke: A mendelian randomization study. *J Stroke.* (2023) 25:350–60. doi: 10.5853/jos.2023.00381

3. Xie L, Zhao H, Chen W. Relationship between gut microbiota and thyroid function: a two-sample Mendelian randomization study. *Front Endocrinol.* (2023) 14:1240752. doi: 10.3389/fendo.2023.1240752

4. Xu Q, Ni JJ, Han BX, Yan SS, Wei XT, Feng GJ, et al. Causal relationship between gut microbiota and autoimmune diseases: A two-sample mendelian randomization study. *Front Immunol.* (2022) 12:746998. doi: 10.3389/fimmu.2021.746998

5. Huang D, Lin S, He J, Wang Q, Zhan Y. Association between COVID-19 and telomere length: A bidirectional Mendelian randomization study. *J Med Virol.* (2022) 94:5345–53. doi: 10.1002/jmv.28008

6. Rosoff DB, Bell AS, Jung J, Wagner J, Mavromatis LA, Lohoff FW. Mendelian randomization study of PCSK9 and HMG-CoA reductase inhibition and cognitive function. *J Am Coll Cardiol.* (2022) 80:653–62. doi: 10.1016/j.jacc.2022.05.041.

7. Chen X, Kong J, Pan J, Huang K, Zhou W, Diao X, et al. Kidney damage causally affects the brain cortical structure: A Mendelian randomization study. *EBioMedicine.* (2021) 72:103592. doi: 10.1016/j.ebiom.2021.103592

8. Liang Z, Hao Y, Yang L, Yuan P, Kang W, Liang T, et al. The potential of Klebsiella and Escherichia-Shigella and amino acids metabolism to monitor patients with postmenopausal osteoporosis in northwest China. *BMC Microbiol.* (2023) 23:199. doi: 10.1186/s12866-023-02927-5