

Microbiome and type 2 diabetes mellitus: The need-to-know population variability in Latin American populations



Microbioma y diabetes mellitus tipo 2: la necesidad de conocer la variabilidad poblacional en poblaciones latinoamericanas

Dear Editor,

In a recent article in the journal Science, Ju-Sheng Zheng¹ raises the need for countries to delve deeper into researching the human microbiome. The author is a cofounder of the Westlake Gut Project epidemiological consortium (WeGut). In total, WeGut has microbiome data from more than 30,000 participants from seven cohorts, covering 17 provinces and megacities across China.

Precedents for projects such as the aforementioned author are the Human Microbiome Project (HMP), funded by the US National Institutes of Health, and its continuation, the Integrative Human Microbiome Project (iHMP), which increased our understanding of how the microbiome affects human health. These projects have contributed to disease prevention and prediction, as well as precision treatment, and are likely to become even more prominent in future therapies.

Of particular note is the association of the gut microbiome with various nutritional and metabolic diseases, especially type 2 diabetes mellitus (DM2). For example, there is ample evidence on treatments with the plant *Astragalus* which acts on the microbiome by improving intestinal barrier function and immunity, acting on the intestinal microbiome to treat DM2.² On the other hand, interactions between hypoglycemic drugs and the gut microbiome have been found in patients with DM2.³ However, these findings are limited to specific populations and complex socio-cultural factors which, if integrated, would allow progress towards precision nutrition strategies to address risk factors for obesity and DM2.

The gut microbiome is involved in complex networks of metabolism, being thus associated with diseases of diverse nature, as is the case of the interaction of glycation and the gut microbiome in the pathogenesis of DM2, Alzheimer's disease, and Parkinson's disease⁴, the role of the gut microbiome and its metabolites in diabetic nephropathy,⁵ or in hepatic regulation in general.⁶

Association studies between gut microbiome and DM2 still cover a small fraction of the population diversity globally, focusing on the United States, Europe and, to a lesser extent East Asia. Baseline studies on the variability of the gut microbiome in other populations are of great value, such as those performed in African populations.⁷ Such knowledge, in integration with other genetic and epigenetic factors, will contribute to understanding the role of the gut microbiome in DM2 and therapies targeting the leaky gut.⁸

Latin American populations are still very underrepresented in association studies between microbiome and DM2. A systematic review by Elena RIM et al.⁹ identified nine scientific articles, concluding an effect of the gut microbiome on obesity and DM2, with no concrete evidence about the underlying pathophysiological mechanisms.

The pattern of miscegenation in Latin America since the European conquest, where women were predominantly Native Americans, imprinted genetic signatures in current populations: high contribution of Native American genetic ancestry for the mitochondrial genome and the X chromosome, and the inverse for the Y chromosome. Similarly, a high contribution from the Native American, and subsequently East Asian, lineages on the microbiome charge is expected in this populations, considering the high contribution of mothers through pregnancy to early infancy.¹⁰ That allows to infer that association between gut microbiome and diseases, like DM2, in integration with other epigenetic factors, would occur in a particular way. Zheng's proposal¹ would, therefore, be of great impact if applied in this subcontinent.

We believe that LatinBiota (latinbiota.net) is currently the closest initiative to meet the needs discussed here, in relation to the variability of the microbiome and type 2 diabetes mellitus (and other pathologies) in Latin American populations. However, a public, open access and disease-oriented platform, available for research under ethical standards, as is the case of several "biobanks" around the world, is what is required, and towards which efforts in this subcontinent will undoubtedly converge.

Funding

There are not founding sources associated to this study.

Conflict of interest

The authors declare that they have no conflicts of interest.

Bibliografía

1. Zheng JS. Mapping the Chinese microbiome: it's time for a united effort. *Nature*. 2023. <https://doi.org/10.1038/d41586-023-01843-y> [published online].
2. Su M, Tang T, Tang W, Long Y, Wang L, Liu M. *Astragalus* improves intestinal barrier function and immunity by acting on intestinal microbiota to treat T2DM: a research review. *Front Immunol*. 2023;14:1243834. <https://doi.org/10.3389/fimmu.2023.1243834>.
3. Li R, Shokri F, Rincon AL, Rivadeneira F, Medina-Gomez C, Ahmadizar F. Bi-directional interactions between glucose-lowering medications and gut microbiome in patients with type 2 diabetes mellitus: a systematic review. *Genes (Basel)*. 2023;14. <https://doi.org/10.3390/genes14081572>.
4. Patil RS, Tupe RS. Communal interaction of glycation and gut microbes in diabetes mellitus Alzheimer's disease, and Parkinson's disease pathogenesis. *Med Res Rev*. 2023. <https://doi.org/10.1002/med.21987> [published online].
5. Zhao H, Yang CE, Liu T, Zhang MX, Niu Y, Wang M, et al. The roles of gut microbiota and its metabolites in diabetic nephropathy. *Front Microbiol*. 2023;14:1207132. <https://doi.org/10.3389/fmicb.2023.1207132>.
6. Colella M, Charitos IA, Ballini A, Cafiero C, Topi S, Palmirotta R, et al. Microbiota revolution: how gut microbes regulate our lives. *World J Gastroenterol*. 2023;29:4368–83. <https://doi.org/10.3748/wjg.v29.i28.4368>.
7. Pheeha SM, Tamuzi JL, Chale-Matsau B, Manda S, Nyasulu PS. A scoping review evaluating the current state of gut microbiota research in Africa. *Microorganisms*. 2023;11. <https://doi.org/10.3390/microorganisms11082118>.
8. Sadagopan A, Mahmoud A, Begg M, Tarhuni M, Fotso M, González NA, et al. Understanding the role of the gut microbiome in diabetes and therapeutics targeting leaky gut: a systematic review. *Cureus*. 2023;15:e41559. <https://doi.org/10.7759/cureus.41559>.
9. Elena RIM, Gabriela GD, Arnulfo GC, Enrique CA. Studying the gut microbiome of Latin America and Hispanic/Latino populations Insight into obesity and diabetes: systematic review. *Curr Diabetes Rev*. 2019;15:294–301. <https://doi.org/10.2174/157339981466618073012481710>.
10. Mesa MD, Loureiro B, Iglesia I, Fernández-González S, Llubra-Olivé E, García-Algar O, et al. The evolving microbiome from pregnancy to early infancy: a comprehensive review. *Nutrients*. 2020;12:133. <https://doi.org/10.3390/nu12010133>.

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<https://doi.org/10.1016/j.eimc.2023.10.008>

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