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CHANGES IN THE GUT MICROBIOTA OF GOUT PATIENTS: A SYSTEMATIC REVIEW AND META-ANALYSIS

Keywords: Gout

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Background: Gout is a crystal-related joint disease caused by the deposition of monosodium urate crystals in or around the joints[1][2]. Structural changes or imbalances in the gut microbiota could cause metabolic disorders and participate in the synthesis of purine-metabolizing enzymes and the release of inflammatory cytokines, which is closely related to the occurrence and development of metabolic, immune disease and gout.

Objectives: This study aimed to explore the disorders of intestinal microflora alpha diversity and microbial community composition in patients with gout through meta-analysis.

Methods: According to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA), we comprehensively searched the databases of PubMed, Web of Science, Embase, Cochrane Library, CNKI, VIP, CBM, and Wanfang database without language restrictions. We obtained data related to the alpha diversity index (Shannon index, Simpson index, ACE, Chao1, Observed species) and analyzed phylum and genus composition.

Results: Nine studies, including 423 gout patients and 458 healthy controls (HCs), were included in our analysis. The Simpson index of gout was significantly lower than that of HCs (SMD=−1.037, 95%CI=−1.959−0.115). There was no significant difference in other alpha diversity indexes between the two groups (Shannon index: SMD=−0.429, 95%CI=−0.900−0.441; ACE: SMD=0.102, 95%CI=0.918−1.122; Chao1: SMD=0.863, 95%CI=0.267−1.993; Observed species: SMD=−0.162, 95%CI=−5.011−1.088). We collected the relative abundance of 30 genera of gout and classified them according to the species affiliation. The results showed that the relative abundance of microflora in probiotics was significantly lower than that of HCs (SMD=−0.498, 95%CI=−0.911−0.086). However, the relative abundance of microflora in Fusobacteria (SMD=0.589, 95%CI=0.249−0.929), Actinobacteria (SMD=0.546, 95%CI=0.207−0.885), and Bacteroides (SMD=0.395, 95%CI=0.035−0.756) increased in gout patients. We did not observe significant changes in the gut microbes of Firmicutes (SMD=−0.210, 95%CI=−0.456−0.036).

Conclusion: This systematic evaluation and meta-analysis showed that the impact of gut microbiota was mainly observed at the level of phylum and genus, but limited to microbial diversity. It is necessary to further study the role and function of specific bacteria and their influence on the physiology and pathology of gout.

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Figure 1. Rate of sonographic deposits in AH across different definitions.

Conclusion: In a multidisciplinary sample of AH, the rates of sonographic deposits dramatically varied across the different classifications used, highlighting the need for an agreed and validated definition that facilitates further research in this setting.