Osteoporosis

ASSOCIATION BETWEEN OSTEOPOROSIS AND DISRUPTION OF GUT MICROBIOTA: A META-ANALYSIS

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Background: Osteoporosis (OP) is a systemic disease of the skeleton characterized by decreased bone mineral density and the imbalance of bone, resulting in an increased risk of fragility fractures[1]. Gut microbiota has a mutually beneficial and symbiotic relationship with the host and plays a vital role in the host’s metabolism and immune regulation. An expanding body of studies asserts that gut microbiota has a role in bone metabolism and the pathogenesis of osteoporosis[2].

Objectives: This study aimed to confirm the changes of gut microbiota in osteoporosis through meta-analysis.

Methods: We searched PubMed, Embase, MEDLINE, Cochrane Library, CNKI, VIP, CBM, and Wanfang databases from the established to January 10 2023 on gut microbiota diversity in patients with OP. Standardized mean difference (SMD) and 95% confidence interval (CI) were used to evaluate the difference in microbial diversity compared with HCs.

Results: A total of 16 studies were included in this meta-analysis, including 517 OP and 714 HCs. The summary results showed that there was no significant difference in α diversity index compared with HCs (Simpson index: SMD=0.490, 95%CI(0.084~0.896), p<0.001; Chao1: SMD=0.000, 95%CI(-0.446~0.446), p<0.001; Observed_s: SMD=0.120, 95%CI(-0.031~0.271), p=0.049; Shannon index: SMD=-0.039, 95%CI(-0.284~0.206), p=0.001; ACE: SMD=0.029, 95%CI(-0.647~0.706), p<0.001; Chao1: SMD=0.000, 95%CI(-0.446~0.446), p<0.001; Observed_s: SMD=0.134, 95%CI(-0.049~0.317), p=0.198). To eliminate the heterogeneity caused by the difference of the observed species index by the sequencing method, we conducted a subgroup analysis of the observed species, and the results showed that the index obtained by high-throughput sequencing (Simpson=0.490, 95%CI(0.084~0.896), p=0.001) was higher than that of HCs.

Conclusion: This study suggested that changes in intestinal microbiology were related to OP. More studies should be conducted to explore the specific differences in gut microbiota in OP.

REFERENCES:
