or low bone mineral density (BMD). Additionally, some studies (n = 7) showed that broad-spectrum antibiotics reduced BMD and bone volume in mice. Even if microbial repopulation was allowed after antibiotics treatment, gut microbiome still reflected to be dysbiotic, marked with higher bone resorption and lower bone formation activity compared to control. Besides that, the modulatory action of the gut microbiome on bone formation can be exerted via the immune system and serotonergic system.

Conclusions With the advancement in sequencing technologies, the changes of gut microbiome are worthwhile to be investigated, given its potential to be developed as a disease biomarker for metabolic diseases like osteoporosis. summarizing the findings from previous literature, it is highly possible that the restoration of gut microflora - whether by the use of prebiotics, probiotics or diet, can improve osteoporosis conditions.

IDDF2020-ABS-0116 | THE ROLE OF GUT MICROBIOME IN TRADITIONAL CHINESE MEDICINE SYNDROMES: FOCUSING ON THE SPLEEN **DEFICIENCY SYNDROME**

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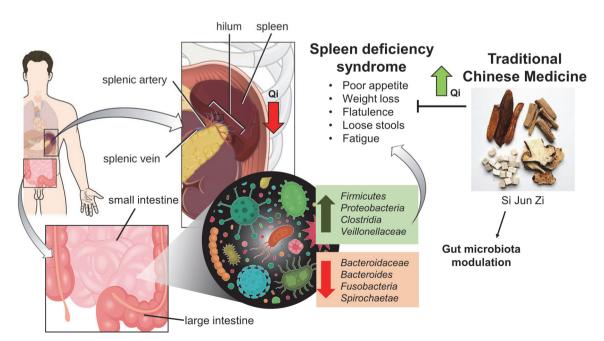
10.1136/gutinl-2020-IDDF.25

Background According to TCM theory, 'Spleen' is associated with the functions of digestion, absorption and nutrition, differs from the function as an immune organ in modern medicine context. Being as one of the most common TCM syndromes, spleen deficiency syndrome (SDS) is a multi-system functional impairment which manifests multiple symptoms includes inappetence, flatulence, fatigue, pale complexion, weight loss and loose stools. The gut microbiome has been shown to be associated with health promotion and development of different gastrointestinal diseases. Thus, this review aims to explore the interactions of gut microbiome on the development of SDS and the modulation of gut microbiota by TCM as a strategy for patients with TCM syndromes.

Methods Based on the PRISMA guidelines, several databases (PubMed, Web of Science, EBSCOhost) were accessed to perform systematic literature searches using 'Spleen deficiency' AND 'microbiome' as the MeSH terms. Studies reporting on the relationship between the gut microbiome and SDS were included. Meanwhile, studies reporting on the SDS without the involvement of gut microbiome were excluded, along with reviews, conference proceedings and commentaries.

Results Twelve studies which accordance to the inclusion criteria out of 175 articles were selected for qualitative analysis. Three studies profiled the gut microbiota composition in patients with SDS, while the remaining studies explored the modulation of gut microbiota in SDS-induced animal models with TCM interventions. The human studies demonstrated differential abundance and functional pathways of the gut microbiome in SDS patients as compared to the healthy subjects. Firmicutes, Proteobacteria, Clostridia, Clostridiales, Veillonellaceae are the several prominent taxa found to be significantly increased in abundance but reduced in the taxa of Bacteroidaceae, Bacteroides, Fusobacteria, Spirochaetae among SDS patients and animals. Jianpi Buqi, Atractylodis rhizoma, Si Junzi and Buzhong Yiqi decoctions, were the TCM preparations shown to promote recovery of animals with SDS by gut microbiota modulation (figure 1).

Conclusions A potential connection can be drawn between gut dysbiosis and spleen deficiency syndrome, which possibly mediated via the perturbation on the metabolite pathways related to carbohydrate, lipid and tryptophan metabolisms. These findings also provide further insights on a potential therapy for SDS by gut microbiota modulation via TCM interventions.



Abstract IDDF2020-ABS-0116 Figure 1 The role of gut microbiome in spleen deficiency syndrome and modulation of gut microbiota by TCM

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