to understand the role of gut microbiome in myasthenia gravis (MG) development, as well as obtaining clues on the regulation of gut microbiome to modulate the disease.

Methods A systematic search was conducted using predefined MeSH terms 'myasthenia gravis' and 'gut microbiome' or 'microbiota' in three databases (Pubmed, Ovid Medline, Scopus; from database inception to December 2019). All the journal titles and abstracts were screened based on inclusion and exclusion criteria. Studies reporting gut microbiome data in relation to gut microbiome effects were included. Studies without myasthenia gravis and/or gut microbiome data were excluded along with conference abstracts, reviews, systematic reviews, meta-analyses, and comments.

Results The systematic search identified 19 articles based on the MeSH term. The duplicate records were removed and 13 articles were accessed. Three studies were eligible for the qualitative analysis according to the inclusion criteria. All the studies reported changes in the microbiota composition as compared to control groups, with significantly lower in phyla Firmicutes and Actinobacteria. MG patients were found to harbour increased of the phylum Bacteroidetes and the family of Desulfovibrionaceae. The ratio of Firmicutes/Bacteroidetes in MG patients describes an inflammatory microbiota which might cause damage to the intestinal epithelium, subsequently trigger an immune response that contributes to the immunological imbalance characteristic of autoimmune disorder. It is reported that some of these microbes were linked with acetylcholine receptor (AchR) antibody, suggesting the gut microbiome influence the onset of myasthenia gravis through classical pathogenic pathways.

Conclusions These findings provide vital insight and knowledge on MG gut microbiome that could enhance the potential for future microbial-based therapies to improve the clinical outcome of MG. Figure 1 illustrates the dysbiosis of the gut microbiome in myasthenia gravis patients.

IDDF2020-ABS-0115 A MOULDING GAME: THE ROLE OF GUT MICROBIOME IN OSTEOPOROSIS

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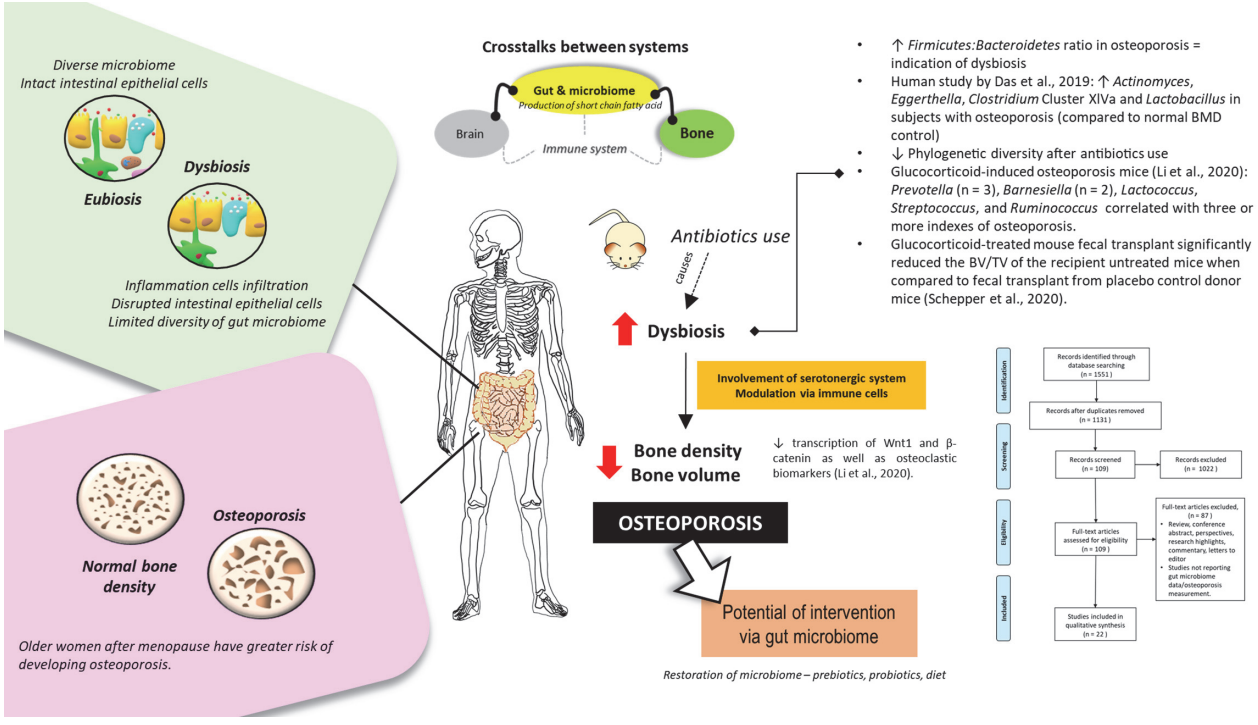
10.1136/gutjnl-2020-IDDF.24

Background The importance of gut health and microbiome have been implicated in metabolic diseases like osteoporosis which occurs specifically in bone, leading to fragility fractures, bone deformities and serious disability. As much as diet and genetic factors contribute to the development of osteoporosis, dysbiosis can aggravate inflammation – an important risk factor that influences bone turnover. Thus, the current study aims to investigate the relationship between gut microbiome and osteoporosis, particularly how certain microbes influence bone formation and resorption.

Methods Searches were performed in three databases (PubMed, Medline, CENTRAL; database inception to 31st March 2020) using 'gut', 'microbiome' combined with 'osteoporosis' or 'bone' as MeSH terms (following PRISMA guidelines). All titles and abstracts retrieved were screened based on the inclusion and exclusion criteria. Studies reporting gut microbiome data in relation to osteoporosis were included in the current analysis but not those without gut microbiome data and/or evaluation on osteoporosis condition.

Results Twenty-two studies (animal = 19, human = 3) were selected for the qualitative analysis according to the inclusion and exclusion criteria (figure 1). Animal models for osteoporosis were induced by ovariectomy (n = 8), drugs (n = 3) or low-calcium diet (n = 1). In general, most studies observed the increase of Firmicutes:Bacteriodetes ratio (dysbiotic indication) in animals as well as human patients with osteoporosis



Abstract IDDF2020-ABS-0115 Figure 1 Potential importance of gut microbiome in osteoporosis

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. By 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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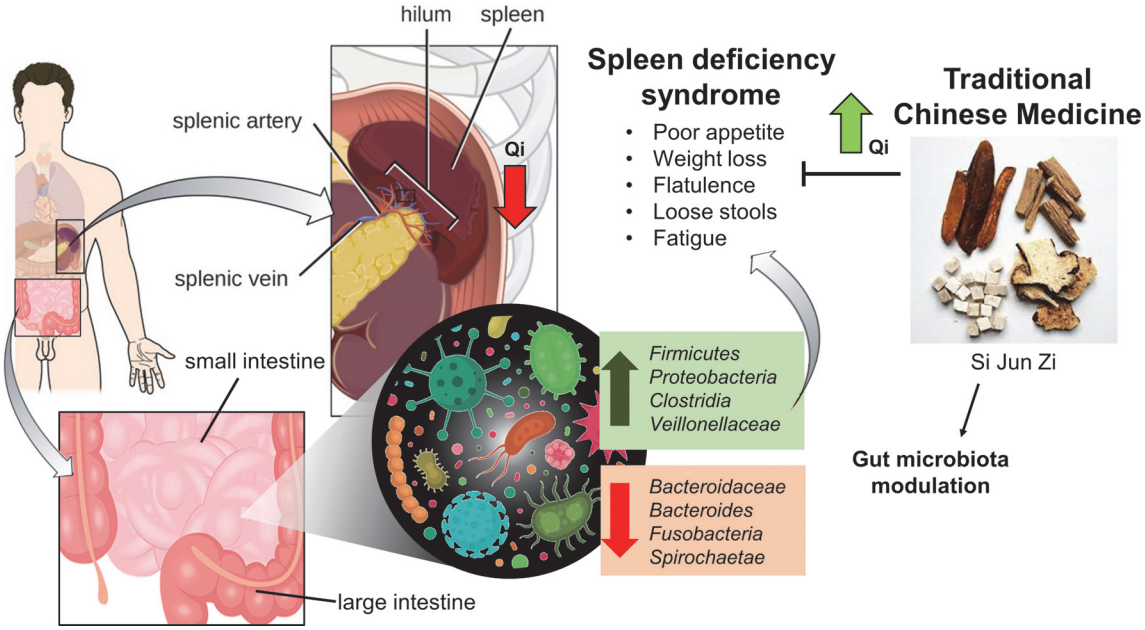
10.1136/gutjnl-2020-IDDF.25

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