Journal of Cell and Tissue Research Vol. 24(2): 7509-7518 (2024)
(Available online at www.tcrjournals.com)
ISSN: 0973-0028; E-ISSN: 0974-0910

Review Article

SYSTEMIC LUPUS ERYTHEMATOSUS MANAGED BY FAECAL MICROBIOTA TRANSFER TECHNOLOGY

PUSHKALA, K.[1] AND GUPTA, P. D.[2]*

[1]Former, Associate Professor, S.D.N.B. Vaishnav College for Women, Chromepet, Chennai, India. Former Director grade Scientist, Centre for Cellular and Molecular Biology, Hyderabad. India
E. mail: pdg2000@hotmail.com, Cell: 08072891356

Received: November 5, 2024: Accepted: November 19, 2024

Abstract: Systemic lupus erythematosus (SLE) is a chronic autoimmune disease causing many pathological disorders such as, lupus nephritis, seizures and memory problems, heart problems including scarring, pericarditis myocarditis, vasculitis, blood clots due to high levels of certain autoantibodies referred to as antiphospholipid antibodies, low blood cell counts, musculoskeletal problems hematologic problems, pleurisy, atherosclerosis and coronary artery disease. Etiology and management of this disease is still ill defined. However, recently developed FMT therapeutic technique showed promise in controlling SLE and its variants in animal as well human models.

Keywords: Systemic lupus erythematosus, FMT therapeutic .

INTRODUCTION

The etiology is still an enigma for systemic lupus erythematosus (SLE) but it is a chronic disease that causes inflammation in connective tissues, such as cartilage and the lining of blood vessels, which provide strength and flexibility to structures throughout the body. It is an autoimmune disorder involves many organs and systems, including the skin, joints, kidneys, lungs, central nervous system, and blood-forming (hematopoietic) systems. this chronic autoimmune disease is one of the causal factor for lupus nephritis, seizures and memory problems, heart problems including scarring, pericarditis myocarditis, vasculitis, blood clots due to high levels of certain autoantibodies referred to as antiphospholipid antibodies, low blood cell counts, musculoskeletal problems (eg, arthralgia, arthropathy, myalgia, frank arthritis, vascular necrosis), hematologic problems (e.g, cytopenias such as leukopenia, lymphopenia, anaemia or thrombocytopenia), pleurisy, atherosclerosis and coronary artery disease [1,2]. The signs and symptoms of SLE vary from patient to patient. It is a systemic autoimmune disease characterized due to over activation of lymphocyte and autoantibody production, featured by dysregulated immunity and production of antibodies targeting self-antigens. Environmental factors such as toxic chemicals and infections as well as susceptibility in born genetically, immune and inflammatory influences, hormonal, certain medicines are implicated to be responsible as causal factors for the development of though [1-5].

Variance of Systemic Lupus Erythematosus:

Paediatric systemic lupus erythematosus-us: Childhood-onset SLE (cSLE) is a rare disease

with an incidence of 0.3-0.9 per 100.000 children-years and a prevalence of 3.3-8.8 per 100.000 children. cSLE is a rare but severe autoimmune disease with multi-system involvement and wide heterogeneity of disease manifestations. Though diagnosis of cSLE is difficult, early recognition of the disease is important to limit adverse outcomes such as morbidity and lower survival rates [6].

Bullous systemic lupus erythematosus (BSLE): Bullous systemic lupus erythematosus (BSLE) is a rare cutaneous lesion that appear as tense, vesiculobullous eruptions with a predilection for the extremities, trunk, face, and neck, usually healing without scar or milia. Subepidermal blistering with a dense neutrophilic infiltration in the upper dermis concentrated on the papillary tip with the association of nuclear dust and fibrin is characteristic of BSLE. Involvement of Autoantibodies to type VII collagen is observed in the pathophysiology of the disease weakening the basement membrane-dermal adhesion, appearing as subepidermal blistering. A good distinguishing feature is the presence of large deposits of mucin in the reticular dermis from dermatitis herpetiformis [7].

Systemic lupus erythematosus (SLE) during pregnancy: Systemic lupus erythematosus (SLE) during pregnancy generally onsets in early adulthood, which means during fertile age. Pregnancies in these patients were considered high risk due to the potential disease flare-ups and unfavourable maternal–foetal outcomes. Several factors can negatively influence pregnancy in a woman with SLE, including disease activity, presence of some autoantibodies, pharmacological therapy, and comorbidities. In spite of advancements in medical care and a greater understanding of the pathophysiology of SLE pregnancy, adverse gestational events are still more frequent in women with SLE than in the general population [8].

Systemic lupus erythematosus (SLE) genetics: Early studies of genetic linkage in multiplex lupus families and more recent studies of genome-wide genetic association have revealed numerous genetic risk factors for the development of SLE and specific disease manifestations. A list of genetic risk factors for SLE now contains at least gene 183 loci revealed a spectrum of genetic factors that include monogenic routes to disease that are more common in childhood onset SLE and polygenic in addition to environmental routes that are more common with SLE onset later in life [9]. Inflammation, and in some cases permanent tissue damage, affecting the skin, joints, heart, lung, kidneys, circulating blood cells, and brain is the expression of this disease. Lupus flares can be mild to serious, and they are unpredictable regarding the severity and frequency of the symptoms.

Symptoms include, arthritis, fevers, fatigue or feeling tired often, a malar or "butterfly" rash, round scaly rashes, rash due to sensitivity to the sun , hair loss, pain less sores in the nose and mouth (most often on the roof of the mouth), Raynaud's phenomenon, swollen glands, swelling in the legs or around the eyes, pain during breathing deeply or lying down, from inflammation of the lining around the lungs or heart, headaches, dizziness, depression, confusion, or seizures and abdominal pain.

Management great heterogeneity in clinical manifestations along with intricate underlying pathogenesis impedes the development of lupus treatment. A disparity also exists in the phenotypic manifestations caused by gut microbiota in SLE. For example, intestinal commensal *Enterococcus* commensal *Enterococcus gallinarum* can translocation to the liver and cause autoimmune hepatitis in patients with SLE [10].

The current treatments are limited and less progress in drug discovery for the last few decades with respect to SLE. However, no specific medicine has been identified with definite and general effects. Till now, the glucocorticoids and unselective immunosuppressors have been serving as the primary treatments and under such circumstances, alternative therapies through multiple pathways is essential.

The treatment often depends on the individual patient's disease severity and disease manifestations. Pharmacotherapy antimalarials (e.g, hydroxychloroquine), corticosteroids, nonbiologic

disease-modifying antirheumatic drugs (DMARDs), Nonsteroidal anti-inflammatory drugs (NSAIDS; eg, ibuprofen, naproxen, diclofenac), including the approved belimumab and anifrolumab. Biologic DMARDs, and/or IV immune globulin [2,3].

Mechanism of action of gut microbiota: Various mechanisms operated by gut microbiome to exert influence on immunity are through gut metabolites, molecular mimicry, microbiota translocation, and epigenetic regulation are few to mention. Among numerous gut metabolites, short chain fatty acids (SCFAs) play the most important role in intestinal immune maintaining homeostasis [3, 11] in their pilot clinical trial in active SLE patients study showed a significant enrichment of SCFAs-producing bacterial taxa and reduction of inflammation-related bacterial taxa after FMT treatment, in addition to the increased production of SCFAs in the gut.

High-salt diet plays an important role in the pathogenesis of gut microbiota dysbiosis in autoimmune diseases. A recent randomized controlled trial demonstrated that a low-salt diet increased circulating SCFAs and decreased blood pressures by affecting the gut microbiota in humans. Hence less dietary salt intake or targeting salt-sensitive associated protein may be a new therapeutic strategy for SLE treatment that could be a focus in therapeutics. But this strategy still needs to be confirmed by further studies [12). Some bacteria including Bacteroides up-regulate expression of genes for mucus production in goblet cells by producing high-level- acetate [13].

Molecular mimicry describes the sequence similarity between foreign (peptides from microorganisms) and self peptides (the host's antigen). Hosts with genetic backgrounds susceptible to autoimmunity can be triggered by some microbial antigens. Bacterial antigens inducing antibodies can recognize self-antigens and contribute to the development of autoimmune diseases. For example, *Burkholderia* spp causes lupus symptoms due to molecular mimicry. Similarly, there are several signatures found to be involved in SLE pathogenesis by molecular mimicry [3,14]. reported a partial purified antigen of *Burkholderia* and transcriptional regulatory peptide RAGTDEGFG could bind to dsDNA antibodies in sera from patients with SLE suggesting that the production of anti-dsDNA antibodies in patients with SLE is associated with *Burkholderia* bacterial molecular mimicry. Autoantibodies production is possible due to molecular mimicry caused by different bacterial infections in SLE. For example recent studies showed that peptides producedby *Odoribactersplanchnicus* and *Akkermansiamuciniphila* bacteria are highly similar to Sm antigen and Fas antigen epitopes.

More importantly, peptides from these bacteria can activate CD4+ T cells or B cells to produce autoantibodies [15]. However, the data from 1,046 healthy individuals suggested that environmental factors are more important than host genetics in shaping the human gut microbiota. In the past decades, the rising incidence of autoimmune diseases has been associated with environmental factors, including a high-salt diet (HSD) discussed earlier [12].

Leaky Gut has an influence on intestinal barrier function, since growing evidence suggests that the impaired intestinal barrier may be one of the essential factors responsible for the aggravation as well as progression of the disease due to increases the intestinal translocation of endotoxins or other organic molecules, thereby promoting apoptosis. The implication of leaky gut as one of the causal factor for the prognosis of many diseases have been suggested earlier [16-21].

The intestinal mucosa needs the intestinal barrier function to defend against the invasion of foreign antigens, such as food antigens, bacteria, and toxins. As previously mentioned, a leaky gut was observed in patients with SLE and in mice. Consistent increase in IgG and a higher level of calprotectin in the faecal sample of SLE patients implies impaired gut barrier function in SLE patients [22]. Another example to substantiate impaired gut barrier function is the detection of *E. gallinarum* in liver biopsy samples from both lupus and autoimmune hepatitis patients [23].

A recently study indicated that impaired intestinal barrier function is associated with intestinal oxidative stress in MRL/lpr lupus mice. After the treatment with antibiotics, probiotics, or dietary interventions in lupus mice, impaired gut barrier function and lupus were significantly ameliorated. In addition leaky gut allows symbiotic bacteria or their contents to leak out of the intestinal lumen, which may be related to intestinal oxidative stress. Translocated gut bacteria or bacterial components can promote the production of autoantibodies through molecular mimicry in addition leading to the deposition of immune complexes aggravating SLE progression. Certain components in bacterial biofilms such as curli and curli-DNA complexes were found to cross-react with autoantigens and induce the production of autoantibodies, resulting in SLE pathogenesis or disease aggravation [24].

Pan et al. [24] has discussed the specific pathogenic infections of the gut such as *Enterococcus gallinarum, Ruminococcusgnavus* is of great significance to study the mechanism of action in patients. *E. gallinarum* could be very easily translocated into systemic organs by disrupting the intestinal barrier promoting Th17 and Tfh cell proliferation and autoantibody production in addition to directly inducing autoantigens, ERV proteins, and other substances to promote autoimmune processes. Though *R. gnavus* may affect disease progression in SLE, but the causal relationship remains unresolved.

SLE is more common in women than men by nearly 10 to 1 though gender and age no bar for the development of SLE . However, it appears most often in young women between the ages of 15 and 44 are affected. Estrogen has the capability to alter gut microbiota and promote type I interferon response and autoantibody production to aggravate SLE progression on the other hand androgen plays a protective role. These observations substantiate that estrogen may account for gender bias in gut microbiota dysbiosis [25,26] in SLE, but the underlying mechanism remains to be clarified [24].

SLE managed by FMT: Gut microbiota is a term used to describe the collection of bacteria, archaea, and eukaryotes colonizing the gastrointestinal tract. The two dominant phyla in the gut microbiota are Firmicutes and Bacteroidetes, representing 90% of the gut microbiota. Actinobacteria, Proteobacteria, Synergistetes, Verrucomicrobia, and Fusobacteria phyla are also present but to a lesser extent [27].

The Firmicutes phylum is composed of more than 200 different genera, such as *Lactobacillus*, *Bacillus*, *Enterococcus*, *Ruminococcus*, and *Clostridium* which alone represents 95% of the Firmicutes phylum. However, the Bacteroidetes phylum consists of two predominant genera, *Bacteroides* and *Prevotella* [28].

Gut dysbiosis has been found both in patients and murine models with SLE. The diversity and richness of gut microbiota in patients with SLE have decreased compared with healthy controls, especially in patients with high SLE disease activity. Currently, however the enigma is whether changes in the gut microbiota occurred after the onset of lupus disease and whether gut microbiota dysbiosis is the cause or consequence of SLE. In recent years, with the application of metagenomic sequencing and 16sRNA sequencing technology, multiple reports have pointed out that the diversity of gut microbiota in SLE decreased comparing to healthy. Host and gut microbiota have co-evolved to form a reciprocal relationship, and gut microbiota and host immunity interact in a complex, dynamic, and context-dependent manner. Reconstruction of the gut microbiota normalizes the development of the immune system and immune response [29].

Short-term antibiotics exposure (following 1 week after antibiotics exposure) was observed to aggravate lupus severity by depleting beneficial gut microbiota for lupus, such as *Lactobacillus* and *Bifidobacterium*, and enriching harmful gut microbiota for lupus, such as *Klebsiella* and *Proteus*. In 9 to 13 weeks old of MRL/lpr mice short-term antibiotics or FMT before onset inhibited the therapeutic efficiency of prednisone on lupus. This observation implies that the gut microbiota before onset is important for lupus severity, progression and treatment. The short-term antibiotics exposure resulted in the reduction as well as the

significant change in the overall compositions of gut microbiota. Zhang, et al. [4] observed the influence of antibiotics to deplete in Firmicutes and Bacteroidetes. On the other hand, significant increases in *Proteobacteria* and *Verrucomicrobia* at phylum level. At the genus level, antibiotics significantly downregulated 17 genera, including *Bifidobacterium*, *Bacteroides*, and *Lactobacillus*, and only two genera (*Klebsi-ella* and *Proteus*) were upregulated by antibiotics. FMT could resort to the abundance alpha diversity and abundances of Firmicutes and Bacteroidetes and 10 genera changed by antibiotics, such as *Bifidobacterium*, *Adlercreutzia*, *Bacteroides*, *Klebsiella*, and *Proteus*. Weakening the therapeutic efficiency of prednisone might be due to the decreases in the abundance of *Allobaculum*, *Bifidobacterium*, and *Adlercreutzia*, which were all negatively correlated with lupus activity and reported to be capable of immunoregulatory in the intestines. Conclusion could b drawn that short-term changes of gut microbiota before onset affected not only therapeutic efficiency of prednisone but also the targeted gut microbiota of prednisone. In addition this observation implies that, gut microbiota could play a direct role in treating SLE or an auxiliary role in improving the efficiency of drugs on lupus [4].

Ma. et al.[30]reported from their study Lactobacillus reuteri was significantly enriched in both SLE patients and recipient mice. L. reuteri has been anticipated to become translocated from gut to the peripheral organs resulting in systemic immune activation; and it can drive autoimmunity in a Toll-like receptor 7-dependent mouse model of SLE [30]. In lupus-prone mice model Mu et al.[31] reported a significant reduction of Lactobacillus and supplementation with a mixture of Lactobacillus strains (L.oris, L.rhamnosus, L.reuteri, L.johnsonii, and L. gasseri) reversed leaky gut, contributed to an anti-inflammatory intestinal environment, and the survival value was elevated [31]. Marked depletion of *Lactobacillus* and an increase in *Lachnospiraceae* was observed in a study by Zhang et al. in murine lupus model [32,33]. Ruminococcusgnavus (of the family Lachnnospiraceae), which represents a symbiont within the healthy human intestinal microbiota, was significantly different between the groups of recipient mice model. In mice that received SLE faecal microbiota R. gnavus species showed a modest enrichment. High disease activity, especially in patients with lupus nephritis due to R. gnavus [11, 34]. Another study Azzouz et al. [22] showed that the Ruminococcusgnavus was 5-fold greater abundant in SLE patients compared to healthy controls and correlated directly with SLE disease activity [22]. Metabolism of histidine was significantly altered in GF mice treated with SLE patient faeces, as compared to those which received healthy faecal transplants.

Huang et al. [11] performed a single-arm pilot clinical trial between August 23, 2020, and June 28, 2021, 24 patients with active SLE were screened, of whom 20 were enrolled and received a full dose of FMT treatment; (ChiCTR2000036352) of oral encapsulated fecal microbiome clinical trial to explore and ascertain the efficacy and safety for 12 weeks. Their pilot study proved that a significant enrichment of SCFAs-producing bacterial taxa, reduction of inflammation-related bacterial taxa along with increased production of SCFAs in the gut and reduced levels of IL-6 and CD4+ memory/naïve ratio in the peripheral blood. This first signature on active SLE patients provide promising evidence for the feasibility, safety, and potentially effective therapy in SLE patients by modifying the gut microbiome and its metabolic profile. Gut microbiota dysbiosis in SLE, which is associated with the reduced intestinal microbial diversity and the decreased *Firmicutes/Bacteroidetes* ratio, displaying disease-specific patterns of dysbiosis correlated with the activity of SLE, has been demonstrated in several studies [3,22,30]. At the phylum level, FMT altered the relative abundance of *Firmicutestes* and *Bacteroidota*. After FMT, *Firmicutes* was significantly increased at week 4 , *Bacteroidota* were gradually decreased and correspondingly the ratio of *Firmicutes* to *Bacteroidota* increased gradually over time. To their surprise most of the significantly abundant taxa in post-FMT samples belonged to the phylum *Firmicutes,* including *Eubacterium hallii group*, *Dorea*, *Marvinbryantia*, and *Papillibacter*, which were reported to be SCFA-

producing genera. Other enriched taxa in post-FMT samples included *Porphyromonas*, *Pseudomonas* genera and *Alphaproteobacteria* class.

Marian et al. [35] demonstrated for the first time in twenty Egyptian SLE patients Firmicutes/Bacteroidetes (F/B) ratio in SLE patients (mean ratio: 0.66%) compared to healthy subjects (mean ratio: 1.79%) (female/male = 18/2) with a mean age of 25.6 ± 6.3 years at the time of diagnosis, as well as twenty healthy subjects (female/male = 16/4) with a mean age of 29.9 ± 6.6 years. The low ratio was found to be ethnicity independent. This study also demonstrated a significant alteration in the fecal microbiota profile in recently diagnosed treatment-naive SLE Egyptian patients with lowering in both Firmicutes/Bacteroidetes ratio and *Lactobacillus* abundance compared to healthy controls which was negatively correlated to disease activity [35]. This result comes in agreement with Hevia et al.[32], who studied the gut dysbiosis associated with SLE patients in Spain and reported a significantly lower F/B ratio in SLE patients (median ratio: 1.97) than in healthy subjects (median ratio: 4.86; $p < 0.002$).

Hevia et al. [32] reported that compared with healthy controls, patients with SLE suffered from intestinal dysbiosis and had a significantly lower ratio of *Firmicutes*/*Bacteroidetes* (F/B)[32]. which was confirmed by subsequent studies. Significantly, *Firmicutes* are inversely correlated with the SLE disease activity index (SLEDAI score), confiming that *Firmicutes* can delay lupus progression as well as reduced F/B ratio is an important manifestation of gut microbiota dysbiosis in patients with SLE. An analysis of stool samples from 117 untreated patients with SLE had a pro-inflammatory and autoimmune profile compared to healthy controls [36]. Notably, Li et al.[37] demonstrated that genera *Streptococcus*, *Campylobacter*, and *Veillonella* were positively associated with lupus activity, while *Bifidobacterium* was negatively correlated with disease activity. while the genus Bifidobacterium was inversely correlated with the disease activity [37]. The genera *Prevotella* and *Veillonella*, as well as the *Burkholderiales* order, which were associated with increased systemic inflammation which were abundant in pre-FMT samples, but decreased after FMT is of therapeutic value in treatment. 42.12% of patients reached the SRI-4 primary outcome by week 12 when clinical observation ended. Clinical observations show the limited diversity of certain gut bacterial taxa FMT to SLE patients may represent a promising approach to restore a healthy repertoire of intestinal microbiota. They concluded that this pilot trial provides sufficient evidence for a randomized, double-blind, placebo-controlled, multicenter clinical study to evaluate the long-term safety and effectiveness of FMT in SLE patients. Huang et al. [11] identified a combination of 14 important species in the baseline faecal microbiota, achieving good identification accuracy in distinguishing SRI-4 responders from non-responders (AUC: 0.89, 95% CI:0.74–1), with a sensitivity of 0.875 and a specificity of 0.8. In this regard, higher intestinal levels of *Anaerobutyricumhallii*, and lower abundance of *unclassified Lachnospiraceae, unclassified Parabacteroides and Senega-limassilia* stood out as most differentiating microbes at baseline between responders and non- responders. Further they indicated that specific bacterial taxa in post-FMT gut microbiota were related to clinical response of FMT, with the presence of *Bifidobacterium longum*, *Bifidobacteriumbifidum*, *Bifidobacteriumbreve* and *unclassified ifidobacterium* were associated with therapeutic benefit. Huang et al. observed that post-FMT *increased* with most stool SCFAs including acetic acid, butyric acid, valeric acid, isovaleric acid, hexanoic acid, octanoic acid, and heptanoic acid, while reduced nonanoic acid and decanoic acid. Huang, et al. [11]. Notably, Li et al. [37] demonstrated that the genera Streptococcus, Campylobacter, and Veillonella were positively associated with lupus activity, while the genus Bifidobacterium was inversely correlated with the disease activity [37]. Another study from Azzouz et al.[22] showed that the *Ruminococcusgnavus* was 5-fold greater abundant in SLE patients compared to healthy controls and correlated directly with SLE disease activity [22]. Mu et al.[31] observed a significant reduction of Lactobacillus in lupus-prone mice, and supplementation with a mixture of Lactobacillus

strains (*L.oris, L.rhamnosus, L.reuteri, L.johnsonii,* and *L. gasseri*) reversed leaky gut, contributed to an anti-inflammatory intestinal environment, and prolonged their survival [31]. Subsequantly, Ciccia and Gandolfo [38] from their similar first FMT trial in SLE patients and provides supportive evidence that FMT appears to be a safe, feasible and potentially effective treatment modality in SLE [38].

Xin, et al. [3] observed efficacy results turned out that 42.12% of the subjects reached the primary endpoint SLE Responder Index-4 (SRI-4) from A total of 20 patients were enrolled and accepted 3 doses of administration, 18 of whom completed the final follow-up at week 12. From their 16S rRNA gene sequencing analysis, the FMT regimen increased the gut microbiota abundance of the receptors significantly as well as the *Firmicutes/ Bacteroidota* ratio, suggesting that the microbiota composition of SLE patients got similar to the profiles of healthy donors a similar observation in patients by Ma et al. [30] In terms of the gut microbiota metabolism, most SCFAs have been increased by FMT. Microbiota profile of responders' baseline was featured by lower abundance of unclassified Parabacteroides, unclassified *Lachnospiraceae* and *Senegalimassilia faecalis,* and higher abundance of *Anaerobutyricumhallii* compared with the non-responders. In addition a significant increased abundance of Bifidobacterium compared with the baseline, which may play dominant roles in FMT therapy.

Together these results suggested that some special species may play pathogenetic roles in the pathogenesis of SLE. Earlier observations has shown that gut microbiota in SLE patients showed significantly different compared with healthy cohorts, the Firmicutes-to-Bacteroidetes ratio may be reduced or not significantly different and the diversity index of microbial communities are reduced in SLE. In addition the relative abundance of some species such as Lactobacillus differs from MRL/lpr or NZB/ W F1 mice [30].

Zheng, et al. [29] performed a single-cell RNA sequencing reveals main cell types and their changes in SLE patients before and after FMT treatment. Single-cell RNA sequencing on peripheral blood mononuclear cells (PBMCs) of patients who accepted FMT therapy and found a vital observation that important lymphocyte alterations in SLE following FMT treatment. Still, which specific microbiotas or their metabolites in FMT are responsible for the changes in immune cells need to be elucidated from further studies only. From their study, conclusion could be drawn that elaborate immune cells variations in SLE after FMT treatment, which helps us to better acknowledge the mechanism of FMT on SLE.

A meta-analysis including 11 case-control studies conducted in five countries and nine cities performed by Xiang et al.[39], found increased abundance in *Enterobacteriaceae* and *Enterococcaceae* and decreased abundance in *Ruminococcaceae* in the gut microbiota of patients with SLE. Furthermore, a two-sample mendelianr and omization study found that *Actinobacteria, Bacillales, Coprobacter* and *Lachnospira* were inversely correlated with the risk of SLE, and *Bacilli, Eggertella* and *Lactobacillales* might be the risk factors of SLE. More importantly, this study showed causal effects of gut microbiota on SLE [40].

CONCLUSION

FMT trials in animal models as well as Walking After Eating: Why It's a Great Idea Bhavesh B. Like Dislike Font Size: A+ A- Join Us Share Send to friends Many of us are familiar with the post-meal slump, that feeling of sluggishness that often follows a hearty lunch or dinner. After enjoying a satisfying meal, many of us are tempted to relax on the couch or take a nap. However, a simple habit like taking a short walk after eating can offer surprising health benefits that you might not expect. Like From boosting your mood to managing blood sugar levels, a post-meal stroll might be the secret ingredient to a healthier you. Let's explore the science behind this age-old practice. Related: walking 4,000 steps daily can save your life!

1. Improved digestion like walking after eating can help your body digest food better. A study in PLOS

One revealed that walking gets the stomach and intestines working, which helps move food through the digestive system faster. This can be especially helpful for people with irritable bowel syndrome, as it can reduce bloating. Bloating happens when gas builds up in the digestive tract from breaking down undigested food or when you swallow air while eating or drinking. Being active, like going for a walk, can help move that extra gas through your system.

2. Blood sugar regulation Like Taking a short walk after eating can help keep your blood sugar levels steady. A study found that people who walked after a meal had better blood sugar control than those who stayed seated. Even a quick walk of just a few minutes can make a difference. You should begin walking as soon as possible after eating a meal since blood sugar levels tend to spike between 60 and 90 minutes after eating. While you can walk after any meal, many people are less active in the evening, so an after-dinner walk is a good habit to start.

3. Walking can help lower your blood pressure. High blood pressure is linked to heart problems and strokes. Studies show that taking three short walks a day can help people with high blood pressure. You can easily do these walks after meals. People with more serious high blood pressure have seen even bigger improvements because of post-meal strolls.

4. To lose weight, 0ne needs to burn more calories than you eat. People often say you need to burn 3,500 calories to lose one pound. This means burning 500 calories extra each day for a week. But this isn't always an ironclad rule. Walking after eating can help you burn extra calories. If you weigh about 150 pounds, for example, you'll burn around 100 calories for every mile you walk at a normal pace. A 30-minute walk can burn up to 150 calories.

5. Stress reduction Like Taking a walk after you have finished eating can help you feel better. Exercise lowers stress hormones like cortisol and boosts positive hormones like endorphins and oxytocin, known as the love hormone. These hormones improve your mood, help you fall asleep faster, and promote better sleep. It's important to note that walking after a meal doesn't have to be an all-or-nothing effort. Even a few minutes of walking is beneficial. The most important thing is to make walking after meals a habit. Improved gut health like walking appears to greatly affect the gut by controlling and altering bowel movements. Taking walks after meals regularly can help maintain regular bowel functions. More physical activity can enhance gut movement and reduce the likelihood of constipation. It is associated with healthier and more diverse gut bacteria, which promotes better gut health and prevents digestive disorders. Walking also helps with better nutrient absorption from the food you eat, enabling your body to absorb essential vitamins and minerals more efficiently when digestion is effective.

SLE patients significantly ameliorates disease in lupus by restoring the intestinal bacterial balance and intestinal barrier function however, donor stool screening must be improved to prevent infectious events. Performing FMT early in the onset of lupus suppresses the progression of lupus, but, at the same time, affects the therapeutic effect of glucocorticoid therapy so if patients with SLE are routinely treated with glucocorticoids, treatment with FMT should be carefully considered. There is a long way to go, but we are confident to set FMT as a new therapeutic option for SLE and look forward to the results of the ongoing in depth study the altered gut microbiota and its behaviour in the disease. However, in the present scenario evidences from studies show that limited diversity of certain gut bacterial taxa has been identified. Transfer of intestinal microbiota from healthy hosts to SLE patients may represent a promising approach to restore a healthy repertoire of intestinal microbiota.

REFERENCES

[1].Systemic Lupus Erythematosus (Lupus) - Who gets it? | NIAMS National Institutes of Health (NIH) .gov),https://www.niams.nih.gov › Health Topics

[2]. Systemic Lupus Erythematosus (SLE), Rheumatology (2024).

[3]. Xin, Y *et al.*, (2023). Fecal microbiota transplantation in the treatment of systemic lupus erythematosus:

What we learnt from the explorative clinical trial. *J Autoimmun* 11;103058.

[4]. Zhang, Y. *et al.,* (2020). Early and Short-Term Interventions in the Gut Microbiota Affects Lupus Severity, Progression, and Treatment in MRL/lpr Mice. *Front Microbiol.* 11: 628.

[5]. Kamen DL. (2014).Environmental influences on systemic lupus erythematosus expression. *Rheum Dis Clin North Am.* 40:3:401-12.

[6]. Levy, D.M. and Kamphuism S. (2012).Systemic lupus erythematosus in children and adolescents. *Pediatr Clin North Am.* 59: 2:345-64.

[7]. Odonwodo A, Vashisht P. (2024).Bullous Systemic Lupus Erythematosus. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; . Available from: https://www.ncbi.nlm.nih.gov/books/NBK557445/.

[8]. Gamba, A. *et al.,* (2024). Modern Management of Pregnancy in Systemic Lupus Erythematosus: From Prenatal Counseling to Postpartum Support. *J. Clin. Med.* 13: 3454.

[9]. Harley I.T.W and Sawalha A.H. (2022).Systemic lupus erythematosus as a genetic disease. *Clin Immunol.* 236:108953.

[10]. Manfredo Vieira S *et al.* (2018).Translocation of a Gut Pathobiont Drives Autoimmunity in Mice and Humans. *Science* .359:1156–61.

[11]. Huang, C. *et al.,* (2022). Safety and efficacy of faecal microbiota transplantation for treatment of systemic Lupus Erythematosus: An EXPLORER trial. *Autoimmun.* 130:102844.

[12]. Chen, L *et al.* (2020).Modest sodium reduction increases circulating short-chain fatty acids in untreated hypertensives: A randomized, double-blind, placebo-controlled trial. *Hypertension.* 76: 1:73-79.

[13].Wrzosek, L. *et al.* (2013). Bacteroides thetaiotaomicron and Faecalibacteriumprausnitzii influence the production of mucus glycans and the development of goblet cells in the colonic epithelium of a gnotobiotic model rodent. *BMC Biol* 11, 61 (2013). https://doi.org/10.1186/1741-7007-11-61.

[14].Zhang, W. and Reichlin M. (2008). A possible link between infection with burkholderia bacteria and systemic lupus erythematosus based on epitope mimicry. *Clin Dev Immunol.* 2008:683489.

[15]. Chen, BD. et al. (2021).AnAutoimmunogenic and Proinflammatory Profile Defined by the Gut Microbiota of Patients With Untreated Systemic Lupus Erythematosus. *Arthritis Rheumatol.* 73:232–43.

[16]. Pushkala, K. (2023).Faecal transplant technology in therapeutics of Alzheimer's. *J. Cell Tissue Res.*23:20:73-7325.

[17]. Pushkala, K and Gupta, P.D. (2023). Faecal microbiota therapy: A promising therapeutic tool for Autism spectrum disorder. *J. Brain and Neurological Disorders*, 6(6): DOI:10.31579/2692-9422/072.

[18]. Pushkala, K. and Gupta, P.D. Management of Huntington's disease by Faecal Microbiota Transplant (FMT) Technology.*J Infect Dise Treat.* 2023**.** 1(1): 1-3.

[19] . Pushkala, K and Gupta, P.D. (2023). Faecal microbiota transplantation (FMT): An effective therapeutic agent for Parkinson's disease. J New Medical Innovations and Research, 4(4);DOI:10.31579/2767-7370/052

[20]. Gupta, P.D. and K Pushkala,K. (2024). Efficacy of Faecal Transplant Therapy in Non-alcoholic Fatty Liver Disease, *J Thoracic Disease and Cardiothoracic Surgery*, 5(5); DOI:10.31579/2693-2156/099.

[21]. Pushkala,K. and Gupta, P.D. (2024), Promising role of Faecal transplant therapy on Sclerosis, *Clinical Trials and Case Studies*, 3(5); DOI:10.31579/2835-835X/070.

[22]. Azzouz, D. *et al.* (2019). Lupus nephritis is linked to disease-activity associated expansions and immunity to a gut commensal. *Ann. Rheum. Dis.* 78:7: 947–956.

[23]. Vieira S.M. *et al.* (2018). Translocation of a gut pathobiont drives autoimmunity in mice and humans. *Science: 359:1156–61.*

[24]. Pan, Q. *et al.* (2021). Gut microbiota dysbiosis in systemic Lupus Erythematosus: Novel

[25]. Pushkala, K. and Gupta, P.D. (2023). Polycystic Ovarian Syndrome Managed by Faecal Transplant Therapy. *J. Gyne Obste & MotherHealth.* 1:2: 01-04.

[26]. 13. Gupta, P.D. and K Pushkala, K. (2023). FMT as an effective therapeutic agent for Endometriosis. J. Clinical and Medical Case Reports and Reviews V(2)I(2).

[27]. Fujio-Vejar, S. et al., (2017).The Gut Microbiota of Healthy Chilean Subjects Reveals a High Abundance of the Phylum Verrucomicrobia. *Front Microbiol.* 8:1221.

[28]. Marian A. *et al.,* (2021). Altered Profile of Fecal Microbiota in Newly Diagnosed Systemic Lupus Erythematosus Egyptian Patients. *Int. J. Microbiology*, vol. 2021, Article ID 9934533,

[29]. Zheng, M. *et al.* (2023). A single-cell map of peripheral alterations after FMT treatment in patients with systemiclupus erythematosus. *Autoimmun 135:* 102989.

[30]. Ma, Y. *et al.,* (2021).Lupus Gut Microbiota Transplants Cause Autoimmunity and Inflammation. Clin Immunol.. 2021 233:108892.

[31]. Mu Q, *et al.,* (2017). Antibiotics ameliorate lupus-like symptoms in mice. *Sci Rep.* 7:1:13675.

[32]. *Hevia, A. et al.* (2014).*Intestinal Dysbiosis Associated With Systemic Lupus Erythematosus. mBio 5:*5:*e01548–14.*

[33]. Zhang H. *et al.,* (2014). Dynamics of gut microbiota in autoimmune lupus. *Appl Environ Microbiol* . 80:7551–60.

[34] de la Visitación N *et al.* (2021). Gut microbiota contributes to the development of hypertension in a genetic mouse model of systemic lupus erythematosus. *Br J Pharmacol.*178:18:3708-3729.

[35]. Marian A. *et al.* (2021). Altered Profile of Fecal Microbiota in Newly Diagnosed Systemic Lupus Erythematosus Egyptian Patients. *Int. J. Microbiology.* 9934533, 7 pages, 2021.

[36]. Zheng, D. *et al.* (2020). Interaction between microbiota and immunity in health and disease. *Cell Res.* 30:6: 492–506.

[37]. *Li Y. et al.,* (2019). *Disordered intestinal microbes are associated with the activity of systemic lupus erythematosus. Clinical Science. 133*: *7:821–838.*

[38]. C iccia, F and Gandolfo, S. (2022). Will fecal microbiota transplantation eventually be an effective therapeutic strategy for systemic lupus erythematosus? *Clin Immunol.* 242:109096.

[39]. Xiang, S. *et al.* (2022). Association between systemic lupus erythematosus and disruption of gut microbiota: a meta-analysis. *Lupus Sci Med* 9:e000599.

[40]. Xiang, K. *et al.*, (2021). . Causal effects of gut microbiome on systemic lupus erythematosus: a two-sample mendelian randomization study. *Front Immunol* 12:667097.