Enhanced Th17 responses with intestinal dysbiosis in human allergic, inflammatory, and autoimmune diseases

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Abstract
Researchers have shown that gut microbiota contributed to immune-system maturation and the microbiota compositional changes affected intestinal immune responses. The excessive immune reaction was suggested to spread over the entire blood vessels and induce distant organ damage. We have shown that T helper 17 (Th17) cells increased and had already been activated in vivo in patients with Behcet’s disease (BD). We hypothesized that intestinal dysbiosis (unfavorable changes of microbiota) continuously induced Th17 responses in patients with BD.

A metagenomic analysis of patients with BD and normal individuals revealed that the family Lactobacillaceae, the genera Bifidobacterium and Eggerthella significantly increased in BD patients. The order Clostridiales and the genus Megamonas significantly increased in normal individuals. We suggest that lactate accumulation by Clostridiales species and low short chain fatty acid concentrations induced by depletion of the order Clostridiales in the intestine may closely relate to the skewed T cell responses of patients with BD.

In this review, we summarize recent advances in understanding of skewed T cell function and intestinal dysbiosis in human allergic, inflammatory, and autoimmune diseases.

Introduction
We have promoted personal hygiene and decreased pathogen exposure over the past several decades in Japan. Nonetheless, the ministry of Health, Labor, and Welfare in Japan reported that incidence rates of several allergic and autoimmune diseases have steadily increased. The hygiene hypothesis is based on the idea that frequent pathogen exposure in early life is important to develop adequate systemic immune function. Several researchers reported that children living on farms exposed to higher diversity of environmental microorganisms had lower prevalence of asthma and atopic dermatitis than control children [1].

Children delivered by cesarean section had lower abundance of gut microbes [2] and significantly increased risk of asthma, systemic connective tissue disorders, juvenile arthritis, inflammatory bowel disease, and leukemia compared with those with vaginal delivery [3].

These findings have been obtained by a new sequence based assessment of microbes, namely metagenomics, which is expected to facilitate the development of novel treatments for the immune diseases.

Using the technique, researchers explored whether unfavorable compositional and functional changes of gut microbiota, so called dysbiosis, exist in human allergic, inflammatory, and autoimmune diseases. The dysbiosis of gut microbiota was found in asthma, atopic dermatitis, inflammatory bowel disease, rheumatoid arthritis, psoriasis, multiple sclerosis, and Behcet’s disease (BD). Interestingly, hyperactivity of T helper 17 (Th17) cells were frequently observed in the same disease category as explained below.

We have shown that Th17 cells increased and had already been activated in vivo in patients with BD [4,5]. We demonstrated characteristic compositional changes of BD gut microbiota compared with that of normal individuals using a metagenomic analysis [6]. We suggest that the gut microbe compositional changes may be one type of BD dysbiosis and have a role in the skewed T cell responses in patients with BD.

Here, we review recent studies of Th17 cell function and gut microbiota composition in human allergic, inflammatory, and autoimmune diseases, and suggest a possible association between them.

Behcet’s disease (BD)
BD is a rare systemic inflammatory disorder of unknown etiology. Recurrent attacks of acute inflammation, such as uveitis, aphthous ulcers, genitor ulcers, skin erythema, colitis, vasculitis, and encephalitis characterize BD. Repeated attacks of uveitis can lead to blindness and gastrointestinal, central nervous system, and vascular involvement is associated with poor prognosis [7].

Studies of BD suggest that skewed T cell function, high prevalence of HLA-B51, and several microbial infection, such as Streptococcus sanguinis and Herpes simplex virus, may play a role in the pathogenesis of BD [7].

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Th17 cells produce a number of pro-inflammatory cytokines, including IL17, IL21 and IL22. Th17 cells proliferate in the presence of IL23 and respond to extracellular bacteria and fungi. In mouse experiments, commensal bacterium colonization of segmented filamentous bacteria potently induced Th17 cell differentiation [8]. The bacterial mono-colonization aggravated autoimmune arthritis and experimental autoimmune encephalomyelitis in mouse models [9].

Recently, it was reported that Th17 cells were frequently found in the lesion and peripheral blood of patients in human allergic, inflammatory, and autoimmune diseases, though the numbers of infiltrating cells were limited [4,5,10-20]. The blockades of IL17 and IL23 remarkably ameliorated arthritis and colitis of patients with rheumatoid arthritis and inflammatory bowel disease, respectively [21]. We summarize recent literature demonstrating increased IL17/IL23 expressions in the lesion of patients with allergic, inflammatory, and autoimmune diseases in Table 1.

Table 1. Human allergic, inflammatory, and autoimmune diseases characterized by increased IL17/IL23 expressions, Th1/Th17 cell emergence, and intestinal dysbiosis.

| Increased IL17/IL23 expressions | Th1/Th17 cell emergence | Intestinal dysbiosis |
|---------------------------------|-------------------------|----------------------|
| Asthma [11-13]                  | Asthma [11-13]          | Asthma [30,31,33,34]  |
| Atopic dermatitis [14]          | Multiple sclerosis [15] | Atopic dermatitis [32,33] |
| Inflammatory bowel disease [15]| Multiple sclerosis [16] | Inflammatory bowel disease [39-42] |
| Multiple sclerosis [16]         | Psoriasis [18]          | Multiple sclerosis [43] |
| Rheumatoid arthritis [17]      | Psoriasis [18]          | Rheumatoid arthritis [44] |
| Systemic lupus erythematosus [18]| Behcet’s disease [5,6]  | Psoriatic arthritis [45] |
| Psoriasis [18]                  | Behcet’s disease [5,6]  | Psoriatic arthritis [45] |

We hypothesized that BD mucosal immunity with the gut microbiota continuously provided systemic Th17 responses through overproduction of several pro-inflammatory cytokines.

Intestinal dysbiosis in human allergic, inflammatory, and autoimmune diseases

In the past decade, there has been an increase in the number of publications which reported intestinal dysbiosis of patients with allergic, inflammatory, and autoimmune diseases.

In general, intestinal microbe composition is influenced by aging. The development of intestinal microbiota is begun with exposure of neonates to the member microbes in the birth canal and the amount of bacteria rapidly increases [29]. After breast-feeding, *Bifidobacterium* gradually emerges during about 3 days after the delivery and becomes one of the most abundant bacteria within one week. During the weaning period, the bacterial composition resembles that of adult which consists of predominant anaerobic gram-negative rods. *Bifidobacterium* disappears and *Clostridium perfringens* markedly increases in number in elderly individuals [29].

Several authors have recognized intestinal dysbiosis was observed in infancy with several allergic diseases, such as asthma [30,31] and atopic dermatitis [32]. The patterns of bacterial compositional alteration varied probably because of the bacterial compositional succession in early life, as mentioned above [33]. The presence of siblings, raising of dogs, growing in the farm, non-pasteurized milk intake, and breast-feeding are suggested to be effective on the frequent exposure to pathogens and reduce the disease risk [33,34]. Gut microbiota composition has been suggested to be associated with respiratory microbiota [34] and to regulate respiratory infection [35,36], and subsequent development of asthma [37,38]. These results suggest a new approach to the studies of “the hygiene hypothesis” and the concept of “common mucosal immune system” [34].

In human inflammatory/autoimmune diseases, dysbiosis of patients with inflammatory bowel disease was repeatedly assessed using metagenomics over the past decade [39]. Relative abundance of the phylum *Firmicutes* significantly decreased and that of the phylum *Bacteroides* significantly increased in patients with inflammatory bowel disease compared with those in normal individuals [39]. Furthermore, recent studies have demonstrated that intestinal dysbiosis was found in several human inflammatory/autoimmune diseases [Table 1] [40-46].

Table 2 summarizes bacterial compositional alteration patterns shown in patients with diseases displayed in Table 1.

In general, gut bacterial composition and function are suggested to be regulated by two major mechanisms involving gene function, namely...
the microbe capabilities for utilizing bacterial metabolites, such as short chain fatty acids, and the microbe tolerance to gut environments, such as pH and bile salt concentrations [47]. *Bifidobacterium* and *Lactobacillus* are the most prevalent lactic acid producing and pH regulating bacteria under the utilization of sugars. *Coriobacterium* species are lactic acid producing bacteria, too.

Several genera of the order **Clostridiales** are able to consume lactate and produce short chain fatty acids, such as butyrate and propionate. Short chain fatty acid production of the bacteria was remarkably reduced by lowering the environmental pH [47]. It was reported that oral administration of short chain fatty acids [48,49] and butyrate-producing bacteria, especially *Faecalibacterium prausnitzii* in *Clostridia* [50-52], effectively increased regulatory T cell differentiation. These results suggest that low pH and low short chain fatty acid concentrations of the intestinal lumen may induce a vicious cycle of unbalanced T cell differentiation. In fact, low butyrate concentrations and/or low frequencies of butyrate-producing bacteria in the intestine were observed in patients with inflammatory bowel disease [40-42] and BD [46]. Furthermore, other intestinal immune cell and bacterial metabolites, such as retinoic acid [53] and polysaccharide A [54], were suggested to play a role in T cell differentiation. Thus, the roles of intestinal dysbiosis in the skewed T cell differentiation of human diseases are expected to be elucidated with greater accuracy in terms of metagenomic analyses.

**Characteristic BD intestinal bacterial compositional alterations**

We hypothesized that dysbiosis of BD gut microbiota continuously provides Th17 type stimulation to peripheral blood lymphocytes. We conducted a metagenomic analysis of gut microbes [6].

The sequencing data showed that the family *Lactobacillaceae*, the genera *Bifidobacterium* and *Eggerthella* increased significantly in patients with BD (Table 3). The order *Clostridiales* and the genus *Megamonas* significantly increased in normal individuals (Table 3). Fecal secretory IgA concentrations increased significantly in BD patients compared with those in normal individuals [6]. Alpha diversity is defined as the species richness in each individual. Alpha diversity indexes of the bacterial taxa were comparable between BD patients and normal individuals [6]. Beta diversity is defined as the distance (difference) between two or more groups of plots, where each plot representing a patient/normal subject, calculated from individual species composition data. An exploratory analysis showed a significant difference between BD patients and normal individuals in beta diversity [6]. We suggest that the compositional changes of gut microbiota observed in BD patients may have a relationship with the pathogenesis of BD as one type of dysbiosis. The skewed T cell differentiation of BD patients may be caused by dysregulated bacterial metabolites, such as excessive lactate production and short chain fatty acid depletion, as a result of gut microbe compositional changes.

Further, BD dysbiosis shown in our study shared some common features with that of multiple sclerosis (Tables 2 and 3) [43]. From the point of view of intestinal dysbiosis, the two diseases may be classified into the same subcategory of human immune diseases.

**Perspectives**

This review article discussed a relationship between Th17 cell differentiation and intestinal dysbiosis in human allergic, inflammatory, and autoimmune diseases. We suggest that peripheral blood Th17 cell function may reflect the compositional and functional features of whole commensal bacteria colonizing the intestinal, genital, respiratory, and oral mucosa [55].

We suggest that accurate cut-off values for the assays of Th17 cell frequency and related gene expressions may establish an evaluation method for the status of commensal microbiota. It may be possible for us to define “normal” Th17 cell function and, after comparing the data with metagenomics, to define “healthy” microbiota of normal individuals and “stable” microbiota of patients.

Recently, researchers reported that oral administration of Chinese herbal medicine Qing-Dai was effective in the treatment of patients

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**Table 2. Intestinal dysbiosis observed in human allergic, inflammatory, and autoimmune diseases.**

| Human immune diseases | Prevalent bacterial taxa in patients | Prevalent bacterial taxa in normal individuals | α diversity in patients | metabolites and gene function in patients |
|-----------------------|------------------------------------|---------------------------------------------|------------------------|------------------------------------------|
| Asthma [30,31,33,34]   | *Clostridium, Enterococci*         | *Veillonella, Faecalibacterium*              | Decreased              | Decreased acetate concentration          |
| Atopic dermatitis [32,33] | *Clostridium*               | *Bacteroides*                             | Decreased              |                                          |
| Inflammatory bowel disease [39-42] | *Gammaproteobacteria*        | *Clostridia, Ruminococcaceae, Bifidobacterium, Lactobacillus* | Decreased              | Decreased butyrate concentration         |
| Multiple sclerosis [43] | *Eggerthella*                  | *Megamonas, Prevotella*                    | Comparable            |                                          |
| Rheumatoid arthritis [44] | *Prevotella*                   | *Bacteroides*                             | Decreased              | Low abundance of vitamin metabolism gene |
| Postratic arthritis [45] | None                          | *Clostridia*                             | Decreased              | Decreased heptanoate and hexanoate concentration |
| BD [46]               | *Bacteroidales*                | *Roseburia, Subdoligranulum*              | Decreased              | Decreased butyrate concentration         |

**Table 3. BD intestinal dysbiosis observed in our study [6].**

| Prevalent bacterial taxa in BD patients | Prevalent bacterial taxa in normal individuals |
|----------------------------------------|---------------------------------------------|
| **Order** | **Family** | **Genus** | **Order** | **Family** | **Genus** |
| *Bifidobacteriales* | *Bifidobacteriaceae* | *Bifidobacterium* | *Clostridiales* | *Veillonellaceae* | *Megamonas* |
| *Coriobacteriales* | *Coriobacteriaceae* | *Eggerthella* | *Prevotellaceae* | *Paraprevotellaceae* | *Phascolarctobacterium* |
| *Bacillales* | *Peptostreptococcaceae* | *Filifactor* | *Prevotellaceae* | *Slaskia* |
| CW940 | *Lactobacillaceae* | *Coprobbacillus* | | *Prevotella* |
| | | | Enterobacter | |
| | | | Atopobium | |
| | | | Orbibacterium | |
with ulcerative colitis [56,57]. They suggest that Qing-Dai reduces disease activity possibly by inhibiting Th17 cell differentiation through aryl hydrocarbon receptor (AhR). AhR is a member of the basic helix-loop-helix superfamily of transcription factors and is reported to be activated by ligands, including Qing-Dai [56,58]. The ubiquitous and highly conserved protein AhR recognizes a lot of herbal extracts and modulates the expression of a set of genes [59]. Intestinal microbes are able to produce AhR ligands, such as indole-3-aldehyde (3-IAld) and indole-3-acetaldehyde, both of which are intermediates in tryptophan metabolism [56,59]. AhR and the ligand interactions are thought to be essential for the adequate maintenance of the intestine [59]. Daily food intake plays a role in the metabolic interaction including tryptophan [59].

Lactobacilli were reported to become abundant in tryptophan-rich environment of gastrointestinal tract and the bacteria generated 3-IAld [60]. The AhR ligand activated innate lymphocytes to produce IL22 and contributed to mucosal resistance against Candida albicans through the lymphocyte activation [60,61]. The IL22 expressing lymphocytes regulated colonization of segmented filamentous bacteria, the Th17 cell inducing gut commensal bacteria, too. The inhibitory effect of IL22 expressing cells was suggested to indicate a negative feedback loop for controlling excessive activation of Th17 cells [61]. Protective effects of 3-IAld on the local immunity was found in the vaginal mucosa [60].

10% of patients treated with Qing-Die developed mild liver dysfunction [56]. These data support that probiotics and prebiotics, even food ingredients, have variable effects on the intestinal immune system and we need to clarify the relationship among them.

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