

Microbiome-Derived Metabolites as Therapeutic Targets in Autoimmune Diseases

Amina Diallo ¹

¹ Dr., Department of Immunopathology, Cheikh Anta Diop University, Dakar, Senegal

* **Corresponding Author:** amina.diallo@ucad.sn

ARTICLE INFO

Received: 10 Feb 2024

Accepted: 06 Apr 2024

ABSTRACT

Autoimmune diseases are chronic, debilitating conditions characterized by aberrant immune responses against self-antigens. In recent years, the human microbiome has emerged as a critical modulator of immune homeostasis, with increasing evidence pointing to microbiome-derived metabolites as pivotal agents influencing immune responses. This review explores the role of microbiome-derived metabolites in the pathogenesis and treatment of autoimmune diseases. Particular attention is paid to short-chain fatty acids (SCFAs), tryptophan catabolites, bile acid derivatives, and microbial polyamines. The therapeutic potential of targeting these metabolites is discussed in the context of diseases such as multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease, and systemic lupus erythematosus. The article concludes with a discussion on the translational challenges and future directions for microbiome-targeted therapies in autoimmune conditions.

Keywords: Microbiome, Autoimmune Diseases, Metabolites, Immunomodulation, Therapeutic Targets.

INTRODUCTION

Autoimmune diseases such as multiple sclerosis (MS), systemic lupus erythematosus (SLE), inflammatory bowel disease (IBD), and rheumatoid arthritis (RA) affect millions worldwide, often resulting in significant morbidity. While genetic susceptibility plays a role in their pathogenesis, environmental factors—particularly the composition and activity of the gut microbiota—have been increasingly recognized as crucial determinants of immune tolerance and dysregulation (Belkaid & Hand, 2014).

The human gut microbiome, composed of trillions of bacteria, archaea, viruses, and fungi, produces a vast array of bioactive metabolites that influence host physiology. These microbiome-derived metabolites can act locally in the gut or systemically through circulation, affecting immune cell activation, differentiation, and function (Lavelle & Sokol, 2020). Recent studies suggest that these microbial products may offer new avenues for therapeutic interventions in autoimmune diseases. This review synthesizes current knowledge of how specific microbiome-derived metabolites contribute to the immunopathology of autoimmune diseases and evaluates their potential as therapeutic targets.

THE ROLE OF THE GUT MICROBIOME IN AUTOIMMUNITY

The gut microbiome is instrumental in shaping immune development and function. Early colonization, microbial diversity, and metabolite production are all factors that influence the balance between immune tolerance and activation. Dysbiosis—an imbalance in microbial composition—has been implicated in numerous autoimmune conditions, often preceding clinical onset (Honda & Littman, 2016).

Importantly, it is not just the composition but also the metabolic activity of the microbiota that modulates immune responses. Microbial metabolites such as SCFAs, secondary bile acids, and amino acid

catabolites serve as signaling molecules that interact with host receptors to regulate inflammation and immune function (Nicholson et al., 2012).

Key Microbiome-Derived Metabolites in Autoimmune Regulation

Short-Chain Fatty Acids (SCFAs)

Produced by microbial fermentation of dietary fibers, SCFAs—especially acetate, propionate, and butyrate—have been shown to reinforce gut barrier function, promote regulatory T cell (Treg) differentiation, and suppress pro-inflammatory cytokines. Butyrate, in particular, is a histone deacetylase (HDAC) inhibitor that enhances Foxp3 expression, a key transcription factor for Tregs (Furusawa et al., 2013). In animal models of colitis and MS, SCFA supplementation has demonstrated protective effects (Trompette et al., 2014).

Tryptophan Metabolites

Tryptophan metabolism through microbial pathways yields indoles and kynurenines, which can bind the aryl hydrocarbon receptor (AhR), influencing T-cell polarization and intestinal homeostasis. In experimental autoimmune encephalomyelitis (EAE), an MS model, activation of AhR by indole derivatives from *Lactobacillus* spp. alleviated disease symptoms (Rothhammer et al., 2016).

Bile Acid Metabolites

Primary bile acids synthesized in the liver are modified by gut bacteria into secondary bile acids, which have immunoregulatory properties. For example, lithocholic acid derivatives have been shown to inhibit Th17 differentiation and enhance Treg induction via FXR and TGR5 receptor pathways (Hang et al., 2019). Dysregulation of bile acid metabolism has been linked to IBD pathogenesis.

Polyamines

Polyamines such as spermidine and putrescine are produced by both host and microbial cells. They are involved in cellular growth, apoptosis, and inflammation. Spermidine enhances autophagy and has shown anti-inflammatory properties in models of colitis and lupus, making it a promising target (Puleston et al., 2014).

MICROBIOME-METABOLITE PATHWAYS IN SPECIFIC AUTOIMMUNE DISEASES

Multiple Sclerosis

Patients with MS often display decreased levels of SCFAs and tryptophan-derived metabolites. SCFA supplementation and AhR activation have been proposed as strategies to restore immune tolerance in MS patients (Rothhammer & Quintana, 2019).

Rheumatoid Arthritis

RA patients show altered gut microbiota composition with reduced butyrate-producing bacteria. Recent trials using butyrate supplementation or probiotics that produce SCFAs have shown promise in reducing joint inflammation and pain (Chen et al., 2016).

Inflammatory Bowel Disease

In IBD, reduced microbial diversity correlates with decreased SCFA and bile acid production. Fecal microbiota transplantation (FMT) and dietary fiber interventions have aimed to restore beneficial metabolite profiles, with mixed but encouraging results (Sartor & Wu, 2017).

Systemic Lupus Erythematosus

SLE patients often exhibit metabolic endotoxemia and disrupted tryptophan metabolism. Recent work suggests that modulating microbial kynurenine pathways may reduce autoantibody production and systemic inflammation (Zhao et al., 2019).

THERAPEUTIC STRATEGIES TARGETING MICROBIOME-DERIVED METABOLITES

Probiotics and Prebiotics

Supplementation with strains that produce SCFAs or tryptophan derivatives may help restore metabolic

balance. Prebiotics like inulin and resistant starch can increase endogenous SCFA production and improve immune tolerance.

Direct Metabolite Supplementation

Therapeutic delivery of butyrate, indole-3-aldehyde, or bile acid derivatives is under investigation. Formulation challenges remain due to metabolite instability and rapid absorption.

Enzyme Modulation

Targeting microbial enzymes involved in metabolite synthesis, such as tryptophanases or bile salt hydrolases, may offer selective ways to modulate metabolite output without broad microbial disruption.

Synthetic Biology

Engineered microbes designed to produce specific immunoregulatory metabolites are a promising frontier, enabling precise control over metabolite production in situ (Charbonneau et al., 2020).

CHALLENGES AND FUTURE DIRECTIONS

The complexity and individuality of the human microbiome present challenges for universal therapies. Inter-individual variability, diet, genetics, and environmental exposures all influence microbiota composition and function. Moreover, it remains difficult to determine causality versus correlation in many studies. Longitudinal and interventional trials with metabolomic profiling are essential to establish therapeutic efficacy.

Future work will need to integrate systems biology approaches, combining metagenomics, metabolomics, and immune phenotyping to personalize microbiome-based interventions. Ethical and regulatory considerations around FMT and engineered microbes must also be addressed.

CONCLUSION

Microbiome-derived metabolites offer a promising frontier for therapeutic innovation in autoimmune diseases. By targeting key microbial metabolic pathways, it may be possible to restore immune balance and alleviate disease symptoms. Although challenges remain, the convergence of microbiome science, immunology, and bioengineering provides an exciting path forward for personalized medicine.

REFERENCES

- Belkaid, Y., & Hand, T. W. (2014). Role of the microbiota in immunity and inflammation. *Cell*, *157*(1), 121–141. <https://doi.org/10.1016/j.cell.2014.03.011>
- Chen, J., Wright, K., Davis, J. M., Jeraldo, P., Marietta, E. V., Murray, J., ... & Taneja, V. (2016). An expansion of rare lineage intestinal microbes characterizes rheumatoid arthritis. *Genome Medicine*, *8*(1), 43. <https://doi.org/10.1186/s13073-016-0299-7>
- Furusawa, Y., Obata, Y., Fukuda, S., et al. (2013). Commensal microbe-derived butyrate induces the differentiation of colonic regulatory T cells. *Nature*, *504*(7480), 446–450. <https://doi.org/10.1038/nature12721>
- Hang, S., Paik, D., Yao, L., et al. (2019). Bile acid metabolites control TH17 and Treg cell differentiation. *Nature*, *576*(7785), 143–148. <https://doi.org/10.1038/s41586-019-1785-z>
- Honda, K., & Littman, D. R. (2016). The microbiota in adaptive immune homeostasis and disease. *Nature*, *535*(7610), 75–84. <https://doi.org/10.1038/nature18848>
- Lavelle, A., & Sokol, H. (2020). Gut microbiota-derived metabolites as key actors in inflammatory bowel disease. *Nature Reviews Gastroenterology & Hepatology*, *17*(4), 223–237. <https://doi.org/10.1038/s41575-019-0244-x>
- Nicholson, J. K., Holmes, E., Kinross, J., et al. (2012). Host-gut microbiota metabolic interactions. *Science*, *336*(6086), 1262–1267. <https://doi.org/10.1126/science.1223813>
- Puleston, D. J., Buck, M. D., Klein Geltink, R. I., et al. (2014). Polyamine metabolism is a central determinant of helper T cell lineage fidelity. *Cell*, *158*(3), 633–645. <https://doi.org/10.1016/j.cell.2014.06.043>
- Rothhammer, V., Mascanfroni, I. D., Bunse, L., et al. (2016). Type I interferons and microbial metabolites of tryptophan modulate astrocyte activity and central nervous system inflammation via the aryl hydrocarbon receptor. *Nature Medicine*, *22*(6), 586–597. <https://doi.org/10.1038/nm.4106>
- Rothhammer, V., & Quintana, F. J. (2019). The aryl hydrocarbon receptor: An environmental sensor integrating immune responses in health and disease. *Nature Reviews Immunology*, *19*(3), 184–197. <https://doi.org/10.1038/s41577-019-0125-8>
- Sartor, R. B., & Wu, G. D. (2017). Roles for intestinal bacteria, viruses, and fungi in pathogenesis of inflammatory bowel diseases and therapeutic approaches. *Gastroenterology*, *152*(2), 327–339. <https://doi.org/10.1053/j.gastro.2016.10.012>
- Zhao, L., Tang, H., & Huang, T. (2019). Tryptophan metabolism and gut-brain homeostasis: A new frontier for neurodegenerative diseases. *Frontiers in Immunology*, *10*, 515. <https://doi.org/10.3389/fimmu.2019.00515>