

Connection between Gut Biome and MS Pathophysiology?

Gut biome affects CNS through multiple mechanisms

- Connection between autonomic nervous system, enteric nervous system, and hypothalamic-pituitary-adrenal axis
- Immune system
- Neuroendocrine pathways

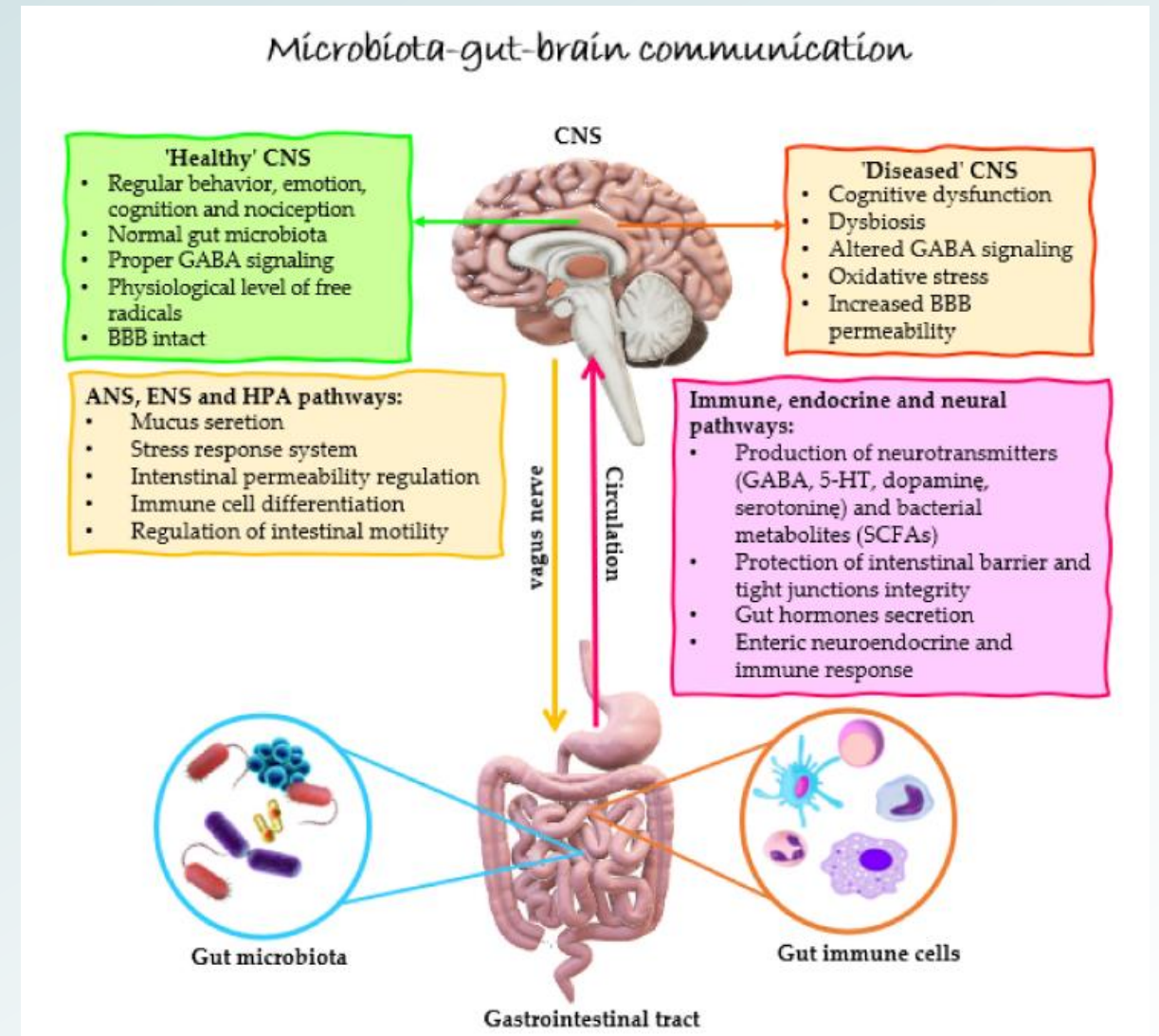
In CNS, circulating microbes, microbial products, and inflammatory factors, can lead to

- Increased BBB permeability
- Demyelination, axonal damage, and neurodegeneration

5-HT, serotonin; ANS, autonomic nervous system; BBB, blood-brain barrier; CNS, central nervous system; ENS, enteric nervous system; GABA, gamma-aminobutyric acid; GBA, gut-brain axis; HPA, hypothalamic-pituitary-adrenal; SCFAs, short-chain fatty acids.

Dziedzic A et al. *Int J Mol Sci.* 2022;23:14478. (CC BY 4.0);

Ullah H et al. *Curr Neuropharmacol.* 2021;19:1966-1983.



Gut Biome and MS

Altered Gut Biome with MS

Identical twin studies

- ↑ *Akkermansia*, *Acinetobacter*, *Methanobrevibacter*
- ↓ *Parabacteriodes*, *Butyricimonas*

Consistent changes across other studies:

- ↓ Bacteroidaceae family, *Faecalibacterium*, *Clostridium*, and *Prevotella*

Altered Levels of Microbial Metabolites

- ↓ **SCFAs**:
Gut – SCFAs maintain intestinal barrier, ↓ inflammation
Brain – cross BBB, modulate immune homeostasis
- ↓ **Propionate**, resulting in ↓ in SCFAs and Treg and ↑ in IL-17 producing T cell proportion in blood
- ↑ **Acetate**: ↑ IL-17 producing CD8⁺ cell proportion
- ↓ **Bile acid metabolites**, which modulate microglial and myeloid cell activation; neuroprotective role in CNS^{1,2}

Impaired Intestinal Barrier

- MS associated with impaired intestinal permeability
- MS associated with ↑ concentration of *A. muciniphila*, which are known to degrade the intestinal mucosal lining

Probiotics and MS Symptoms and Disease Severity

Major findings from small, preliminary, placebo-controlled trials in patients with MS

Probiotics	N		Key Outcomes (Probiotics relative to placebo)
	Probiotic	Placebo	
<i>L. acidophilus</i> , <i>L. casei</i> , <i>B. bifidum</i> , <i>L. fermentum</i>	20	20	Down-regulated gene expression of IL-8 and TNF- α in PBMCs
<i>L. acidophilus</i> , <i>L. casei</i> , <i>B. bifidum</i> , <i>L. fermentum</i>	30	30	Improved EDSS and physical and mental health scales, \downarrow serum insulin, \uparrow insulin sensitivity and HDL levels, \downarrow hs-CRP, NO metabolites, MDA
Visibiome blend of <i>Lactobacillus spp</i> , <i>Bifidobacterium spp</i> , <i>S. thermophilus</i>	9	13	\downarrow CD14 ⁺ CD16 ⁺ , CD45 ⁺ /LIN ⁻ /CD11c ⁺ , \uparrow CD8 ⁺ T cells
<i>B. infantis</i> , <i>B. lactis</i> , <i>L. reuteri</i> , <i>L. casei</i> , <i>L. plantarum</i> , <i>L. fermentum</i>	24	24	\uparrow mental health parameters, \downarrow EDSS, improved insulin resistance and lipid metabolism, \downarrow hs-CRP, NO, and MDA
Blend of <i>Lactobacillus spp</i> , <i>Bifidobacterium spp</i> , <i>S. thermophilus</i>	35	35	\uparrow mental health parameters

EDSS, expanded disability status scale; HDL, high-density lipoprotein; Hs-CRP, high sensitivity C-reactive protein; IL, interleukin; MDA, malondialdehyde; NO, nitric oxide; PBMCs, peripheral blood mononuclear cells; TNF- α , tumor necrosis factor α .

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