



Systemic Biomarkers of Gut Dysbiosis and Metabolism in Vitiligo Patients

Kerstin Schlund*

Department of Dermatology, University of Vienna, Vienna, Austria

DESCRIPTION

Vitiligo affects approximately 0.5-2% of the global population and presents as acquired depigmentation of the skin due to selective loss of melanocytes. While its etiology involves autoimmunity, oxidative stress and genetic predisposition, a growing body of evidence suggests that systemic interactions particularly involving the gut microbiome and mental health play important roles in disease onset and progression.

Patients with vitiligo frequently experience emotional distress, including anxiety, low self-esteem and depression. These psychological states are not only outcomes of the disease's visible nature but may also contribute to systemic inflammation and immune dysregulation. Recent studies propose that emotional health, microbiota composition, and metabolic processes may be interconnected in vitiligo pathophysiology.

Gut-skin axis in autoimmune conditions

The gut-skin axis refers to the bidirectional communication between intestinal microbiota and skin health, mediated by immune signals, metabolites and the nervous system. In autoimmune and inflammatory skin diseases, such as psoriasis and atopic dermatitis, alterations in gut microbiota have been well documented.

In vitiligo, this connection is under active investigation. Disruptions in microbial diversity and changes in the abundance of specific bacterial taxa have been identified in affected individuals. These imbalances can alter gut permeability, immune cell priming, and cytokine profiles, all of which may influence melanocyte-targeted autoimmunity.

Microbiome alterations in vitiligo

Studies exploring gut microbial profiles in vitiligo patients have reported several consistent features.

Reduced alpha diversity: Alpha diversity reflects the number and evenness of microbial species in the gut. Vitiligo patients often show lower alpha diversity, indicating a less balanced microbial ecosystem.

Increased firmicutes-to-bacteroidetes ratio: This altered ratio is frequently observed in autoimmune diseases and may reflect metabolic and immunological imbalances.

Decreased abundance of beneficial bacteria: Bacteria such as *Faecalibacterium prausnitzii*, known for producing anti-inflammatory Short-Chain Fatty Acids (SCFAs), are found in lower numbers in vitiligo patients.

Elevated pathobionts: Overrepresentation of potentially inflammatory bacteria, including *Escherichia coli* and *Ruminococcus gnavus*, has been documented.

These changes may influence immune tolerance and barrier integrity, predisposing individuals to autoimmune activity against melanocytes.

Emotional distress and microbial dysregulation

Mental health and the gut microbiome are linked through the microbiota-gut-brain axis. Emotional distress can influence gut function, motility, secretion and microbial composition through both neural and hormonal pathways. Conversely, microbial imbalances can affect mood and behavior by altering neurotransmitter synthesis, modulating the *Hypothalamic-Pituitary-Adrenal (HPA)* axis and stimulating systemic inflammation.

Metabolic signatures in vitiligo

Beyond microbiota, the metabolic profile or metabolome of vitiligo patients is also altered. These metabolic shifts reflect immune activation, oxidative stress and mitochondrial dysfunction. Commonly reported metabolic features include.

Elevated homocysteine levels: Hyperhomocysteinemia has been reported in several studies on vitiligo and may impair melanocyte survival through oxidative stress and DNA damage.

Impaired tryptophan metabolism: Tryptophan metabolites are precursors for serotonin and kynurenine pathways. Disruptions in these pathways have been linked to both skin inflammation and mood disorders.

Correspondence to: Kerstin Schlund, Department of Dermatology, University of Vienna, Vienna, Austria, E-mail: Kerstin.schlund@tuwien.ac.at

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Changes in lipid profiles: Abnormalities in fatty acid metabolism, including reduced omega-3 levels and increased lipid peroxidation products, are observed in vitiligo patients, especially those with more extensive disease.

Vitiligo is increasingly recognized as a systemic condition influenced by more than cutaneous immunity alone. The interaction between gut microbiota, metabolic processes, and emotional health creates a complex landscape that may

influence disease onset, severity and progression. Patients with co-morbid emotional distress show distinct patterns in both microbial composition and metabolic function, suggesting an interconnected pathway of immune and neuroendocrine dysregulation. Recognizing and addressing these factors may open opportunities for more comprehensive vitiligo management and improved patient outcomes.