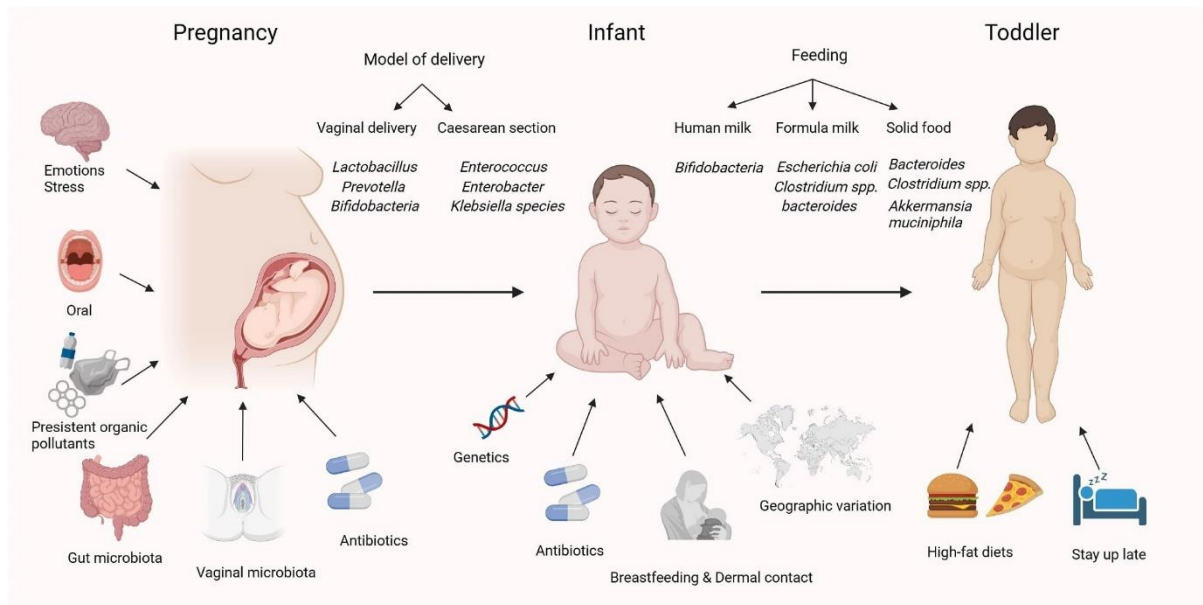


# How gut microbiota impacts childhood obesity

*Insights into how gut microbes impact childhood obesity reveal promising ways to restore balance and tackle the global epidemic*



*Factors shaping the gut microbiota of infants and young children. During pregnancy, exposure to persistent organic pollutants would impact infant lipid homeostasis in the blood and liver postnatally, and periodontitis or vaginal infections can lead to bacterial invasion into the uterine environment, while emotions can indirectly impact fetal development through the gut-brain axis. The administration of antibiotics during pregnancy and infancy can impede the ability of the dominant microbiota to colonize the skin surface of the newborn.*

*The mode of delivery determines the initial colonization of the infant gut microbiota. Postnatal factors, including antibiotic usage, feeding practices (e.g., breastfeeding, formula feeding, and introduction of solid foods), geographic variation, genetics, and environmental exposures, further contribute to the microbiota configuration during early life. As children age and their diets and environments diversify, the gut microbiota gradually transitions to an adult-like composition, typically by age 3.*

In a recent review published in the journal *Advances in Nutrition*, a team of researchers explored the role of *gut microbiota* in childhood obesity, focusing on its impact, underlying mechanisms, and potential therapeutic strategies.

## Background

Childhood obesity has reached epidemic levels globally, with nearly 340 million children and adolescents aged 5-19 years classified as overweight or obese, according to data from the

World Health Organization (WHO) and the World Obesity Federation. Once confined to high-income countries, obesity rates are now rising in low- and middle-income regions, with nearly half of overweight children under five residing in Asia.

Obesity significantly increases the risk of type 2 diabetes mellitus (T2DM), cardiovascular diseases, nonalcoholic fatty liver disease (NAFLD), and certain cancers. Dysbiosis in *gut microbiota*, characterized by an imbalance in *Firmicutes* and *Bacteroidetes*, is strongly linked to obesity, necessitating further research into personalized therapeutic approaches targeting *gut microbiota*. Recent studies also indicate that *gut microbiota* alterations are influenced by factors such as genetics, mode of delivery, and maternal health, contributing to obesity risk early in life.

## **Intestinal microecology and childhood obesity**

The gut is home to the body's most complex and dense microbial ecosystem, comprising bacteria, viruses, fungi, and their metabolites. Recent findings link changes in *gut microecology* to the progression of obesity.

The Human Microbiome Project identified over 2,000 species in the gut, with *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, and *Proteobacteria* accounting for over 93% of the microbiota. These microorganisms influence nutrient metabolism, inflammation, and even behavior through the gut-brain axis (GBA). In addition to bacteria, fungi, and bacteriophages also play a critical role in shaping *gut microbiota* composition. Disruptions in this ecosystem can lead to diseases like inflammatory bowel disease (IBD), cancers, and obesity.

## **Bacteriophages and obesity**

Bacteriophages, an essential component of the gut microbiota, play a significant role in maintaining microbial balance. However, environmental factors such as diet and antibiotics can disrupt their ratios, contributing to obesity.

Research shows that children with obesity exhibit decreased stability in *crAssphage* populations, with shifts from protective subfamilies to those linked to metabolic syndrome. Studies have also found correlations between specific bacteriophage species and bacterial communities, such as *Collinsella aerofaciens*, which is associated with obesity. These changes affect interactions between specific bacterial species and phages, further exacerbating dysbiosis.

Studies suggest that therapeutic manipulation of bacteriophages may help restore balance, offering the potential for obesity management.

## **Gut fungi and obesity**

Intestinal fungi, although less studied, play critical roles in metabolism and obesity. Research demonstrates that fungal diversity in infancy correlates with early body mass index (BMI) changes.

Specific species like *Candida*, *Saccharomyces*, and *Rhodotorula* influence obesity risk, often linked to maternal BMI, diet, and antibiotic use. For example, an increase in *Candida parapsilosis* has been linked to high-fat diet (HFD)- induced obesity in animal models.

Further research on the interplay between fungi and bacteria in the gut could unlock novel strategies to prevent obesity.

## **Dysbiosis in childhood obesity**

Compared to their normal-weight counterparts, obese children exhibit reduced gut microbial diversity and altered bacterial community structures. Studies reveal increased *Firmicutes* and decreased *Bacteroidetes* levels in obese children, alongside specific genera like *Escherichia coli* and *Shigella*, linked to inflammation and insulin resistance. Conversely, beneficial bacteria like *Bifidobacterium* and *Akkermansia muciniphila* are reduced in obese children. *Akkermansia muciniphila*, in particular, has shown promise in improving gut barrier function and regulating metabolism.

## **Mechanisms underlying gut microbiota's role in obesity**

### ***Energy absorption and short-chain fatty acids***

Gut microbiota regulate energy metabolism through short-chain fatty acids (SCFAs) like acetate, butyrate, and propionate, which are products of fiber fermentation. While butyrate promotes insulin sensitivity and reduces inflammation, propionate may trigger overeating. Dysregulated SCFA production can contribute to obesity by enhancing energy absorption, disrupting appetite regulation, and promoting fat accumulation. Recent findings suggest that modulating SCFA production through dietary interventions can help regulate energy balance and improve metabolic health. Maintaining SCFA balance through diet or microbial modulation holds promise for obesity management.

### ***Metabolic pathways and bile acids***

Metabolites like lipopolysaccharides (LPS) and bile acids significantly affect metabolism. LPS from Gram-negative bacteria can induce systemic inflammation and insulin resistance, while bile acids regulate lipid digestion and energy homeostasis. Bile acid signaling through receptors like Farnesoid X Receptor (FXR) and Takeda G Protein-Coupled Receptor 5 (TGR5) can influence fat utilization and thermogenesis, highlighting their potential as obesity treatment targets.

## **Therapeutic strategies targeting gut microbiota**

### ***Dietary and lifestyle interventions***

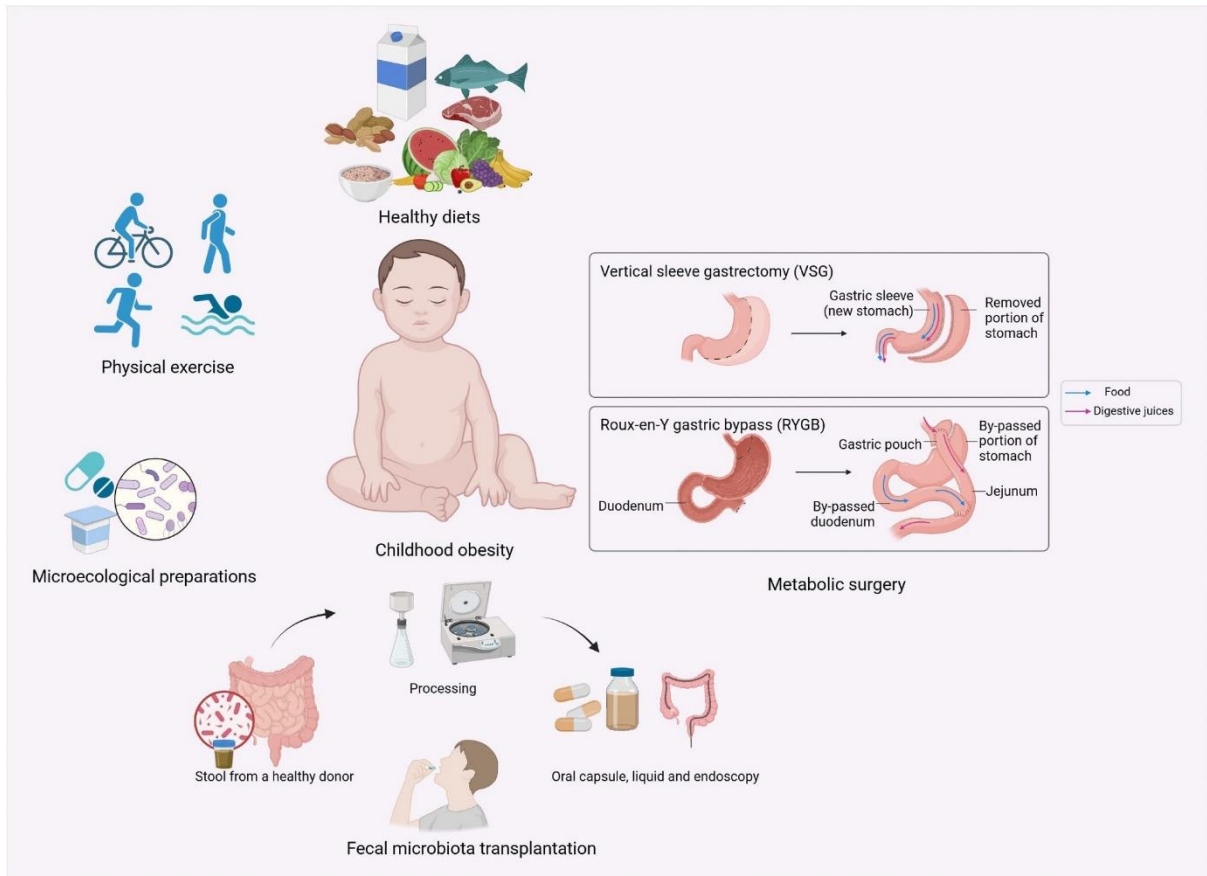
A balanced diet rich in fiber and regular exercise enhances microbial diversity and reduces inflammation. For example, the Mediterranean diet, characterized by a high intake of vegetables, whole grains, and healthy fats, has been shown to increase *Bifidobacterium* levels and reduce markers of inflammation. Reducing HFD and sugar consumption while promoting structured meal times can mitigate obesity risk.

### ***Probiotics, prebiotics, and synbiotics***

Probiotics like *Bifidobacterium* and *Lactobacillus* improve gut barrier function, reduce inflammation, and regulate lipid metabolism. Prebiotics, including inulin and galacto-oligosaccharides, stimulate beneficial bacteria and SCFA production. Synbiotics, combining probiotics and prebiotics, offer a synergistic effect in restoring microbial balance and enhancing metabolic health.

### ***Fecal microbiota transplantation (FMT)***

FMT introduces microbiota from healthy donors to restore microbial diversity and function in recipients. While promising, its efficacy in managing obesity remains inconclusive due to variability in donor selection and long-term outcomes. Personalized approaches in FMT could improve outcomes by tailoring treatments based on individual gut microbiota profiles.



*Treatment of childhood obesity from the perspective of gut microbiota. Healthy diets and regular physical exercise can reduce fat accumulation and enhance gut microbial diversity. Moreover, using microecologic preparations such as probiotics, prebiotics, and symbiotics plays a significant role in ameliorating childhood obesity by restoring the gut microbiome and improving metabolic dysregulation. Fecal microbiota transplantation refers to administering bacterial fluids containing fecal extracts from healthy donors into the recipients' intestines through oral capsules, nasal feeding, or endoscopy to alter chronic low-grade inflammatory responses and establish an optimal ratio of gut microbiota. Moreover, metabolic surgery is acknowledged as an effective approach for the treatment of severe obesity. Currently prevalent surgical procedures encompass vertical sleeve gastrectomy (VSG) and Roux-en-Y gastric bypass (RYGB).*

## Conclusions

To summarize, the study emphasizes the intricate role of gut microbiota in childhood obesity, highlighting mechanisms such as energy absorption, metabolic regulation, and inflammation. Variations in microbial composition influenced by genetics, delivery mode, diet, and early-life factors contribute significantly to obesity risk. Innovative approaches like dietary interventions, probiotics, and fecal microbiota transplantation hold promise for modulating microbiota and managing obesity. -[www.news-medical.net](http://www.news-medical.net), January 21, 2025

**Journal reference:**

- Luo, Y., Li, M., Luo, D., & Tang, B. (2025). Gut Microbiota: An Important Participant in Childhood Obesity. *Advances in Nutrition*, 16(2), 100362. DOI:10.1016/j.advnut.2024.100362, <https://www.sciencedirect.com/science/article/pii/S2161831324001960>