

# Diet and the Intestinal Microbiome: Associations, Functions, and Implications for Health and Disease

Lindsey G. Albenberg<sup>1</sup>Gary D. Wu<sup>2</sup>

<sup>1</sup>Division of Gastroenterology, Hepatology, and Nutrition, The Children's Hospital of Philadelphia, Philadelphia, Pennsylvania; and <sup>2</sup>Division of Gastroenterology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania

Therapeutic Modification  
of the Gut Microbiome

**The mutual relationship between the intestinal microbiota and its mammalian host is influenced by diet. Consumption of various nutrients affects the structure of the microbial community and provides substrates for microbial metabolism. The microbiota can produce small molecules that are absorbed by the host and affect many important physiological processes. Age-dependent and societal differences in the intestinal microbiota could result from differences in diet. Examples include differences in the intestinal microbiota of breastfed vs formula-fed infants or differences in microbial richness in people who consume an agrarian plant-based vs a Western diet, which is high in meat and fat. We review how diet affects the structure and metabolome of the human intestinal microbiome and may contribute to health or the pathogenesis of disorders such as coronary vascular disease and inflammatory bowel disease.**

**Keywords:** Intestine; Microbiota; Diet; Inflammation.

A healthy human fetus develops in an environment that is believed to be largely sterile.<sup>1</sup> Significant colonization of the gut begins immediately after delivery, although, remarkably, bacteria can be found in an infant's first meconium.<sup>2</sup> The initial intestinal colonization pattern depends on the mode of delivery.<sup>1</sup> Infants born vaginally are initially colonized by bacterial taxa found in the vagina, such as *Lactobacillus* and *Prevotella*, whereas infants born by cesarean section are initially colonized by bacteria found in the skin microbiota.<sup>2</sup> After this primary inoculation, infants are regularly exposed to microbes, and diversity increases rapidly.<sup>3</sup> The early colonization pattern is believed to be chaotic, and a growing body of literature has shown that environmental exposures early in life, including diet, are responsible for these fluctuations (Figure 1). Characterization of the intestinal microbiota in a single infant over 2.5 years showed how the bacterial taxa change with life events such as illnesses, dietary changes, and antibiotic treatment.

Interestingly, the greatest change in the composition of the infant's intestinal microbiota occurred with the introduction of solid foods. There was also a shift toward a more stable, adult-like microbiota with weaning.<sup>3</sup> Ultimately, the intestinal microbiota of the young resemble that of the adult by approximately 3 years of age<sup>4</sup> (Figure 1).

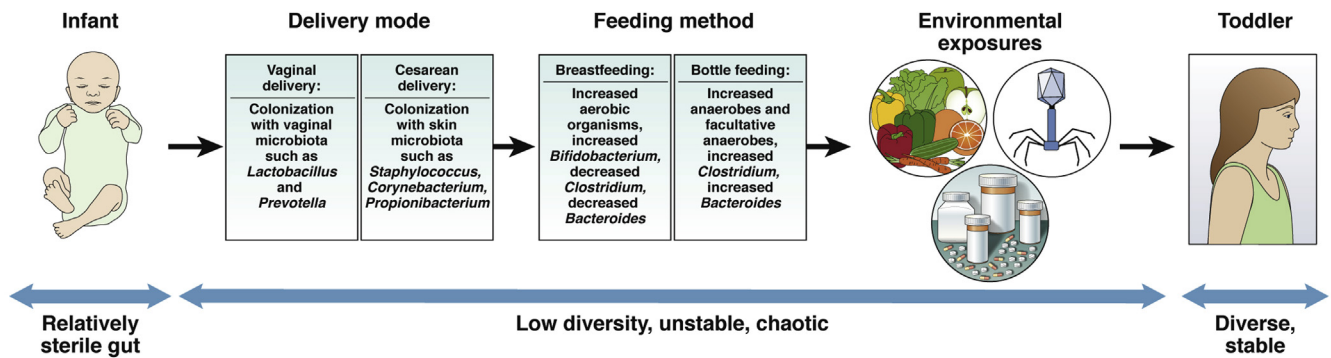
Within the first year of life, there are significant inter-individual differences in the composition of the intestinal microbiota, yet some similarities exist. Similarities among individual infants can be attributed to the major taxonomic groups associated with the infant diet. Multiple studies have established differences in the composition of the intestinal microbiota based on whether infants are breastfed or formula fed.<sup>5–7</sup> Indeed, this introduces the concept of a potential association between the infant diet, the composition of the intestinal microbiota, and health (Figure 1).

Breast milk is the ideal food for infants, because it meets all their nutritional and physiological demands. Over the years, there have been improvements in our understanding of the composition of human milk and, subsequently, complex formulas have been developed that have a similar nutrient value. For mothers who are unable to breastfeed, infant formulas are now considered to be acceptable alternatives to breast milk. However, formula is not a perfect substitute for human milk. For example, there are important bioactive compounds in human milk that contribute to physiological functions such as absorption and digestion of nutrients, immune protection, and defense against potentially pathogenic gut microbes.<sup>8,9</sup> The effects of these bioactive compounds are difficult to replicate.

**Abbreviations used in this paper:** CD, Crohn's disease; EEN, exclusive enteral nutrition; IBD, inflammatory bowel disease; MOS, milk oligosaccharides; TMA, trimethylamine; TMAO, trimethylamine oxide; TPN, total parenteral nutrition; UC, ulcerative colitis.

© 2014 by the AGA Institute  
0016-5085/\$36.00

<http://dx.doi.org/10.1053/j.gastro.2014.01.058>



**Figure 1.** Development of the human intestinal microbiota and the effects of environmental exposures. Colonization of the early intestinal microbiota depends on multiple environmental exposures. The taxa that colonize the relatively sterile newborn intestine are largely determined by the mode of delivery. The intestinal microbiota also develops differently determined by differences in infant feeding (breastfeeding vs formula feeding). Throughout infancy and early childhood, the microbiota changes with dietary alterations, infections, and exposure to antibiotics. The intestinal microbiota of the infant is characterized by instability and low levels of diversity. However, by the toddler years, the intestinal microbiota is similar in diversity and stability to that of adults.

Human milk oligosaccharides (MOS) are bioactive compounds that are the third largest component of human milk.<sup>10</sup> MOS are indigestible glycans that remain whole as they travel through the intestinal tract to the colon, where they nourish specific colonic bacteria. It is believed that MOS benefit the infant by functioning as prebiotics and selectively promoting growth of members of the genus *Bifidobacterium*. Some of the differences in the composition of the intestinal microbiota in breastfed vs formula-fed infants are believed to be secondary to the effects of MOS on these bacteria; many studies have shown an increased proportion of bifidobacteria in breastfed infants<sup>6,7,11</sup> compared with formula-fed infants. An increased proportion of bifidobacteria in the microbiota of breastfed infants may be associated with health. For example, these bacteria have been linked to fortification of the gut mucosal barrier through activities against pathogens.<sup>12,13</sup> Bifidobacteria are also believed to modulate the intestinal immune system and have been shown to increase the production of immunoglobulin A.<sup>14</sup> Many aspects of the mechanisms by which bifidobacteria produce these effects are yet to be determined, and more research is needed in this area. Recent studies have shown that select strains of bifidobacteria possess specialized enzymes capable of metabolizing MOS glycans.<sup>15–17</sup> Genome sequencing of numerous strains, particularly *Bifidobacterium longum* subsp *infantis*, has confirmed the presence of genes that allow these organisms to metabolize mammalian carbohydrates.<sup>18</sup>

Another difference in the composition of the intestinal microbiota in breastfed vs formula-fed infants is that aerobic organisms seem to be more prevalent in the feces of breastfed infants, whereas anaerobic and facultative anaerobic organisms, which preferentially use anaerobic glycolysis, are more commonly found in the feces of formula-fed infants.<sup>6</sup> In terms of taxonomy, multiple studies have shown a decrease in clostridia colonization of breastfed infants,<sup>19,20</sup> including colonization with *Clostridium difficile*.<sup>21</sup> *Bacteroides* are also present in a lower concentration in breastfed infants.<sup>7,20</sup> This is particularly interesting

because certain *Bacteroides* strains are able to digest MOS,<sup>22</sup> suggesting a potential competitive relationship between *Bifidobacterium* and *Bacteroides* in breastfed infants.

Given the health benefits associated with breastfeeding, there are ongoing attempts to develop infant formulas that are more similar in composition and function to breast milk. Oligosaccharide-enriched formulas have been developed, and infants fed these specialized formulas have been shown to harbor greater numbers of bifidobacteria in the feces.<sup>5,23</sup> Breast milk also differs from formula in the type and quantity of protein and other nutrients. Interestingly, in a recent examination of the intestinal microbiota of healthy infants, a formula that was more similar to breast milk in terms of protein composition and the amount of phosphate was found to increase proportions of *Bifidobacterium* similar to that of a formula that was supplemented with these bacteria.<sup>24</sup> Ultimately, alterations in infant formulas that lead to a more “breastfed-like” composition of the intestinal microbiota may be beneficial, although additional evidence is needed.<sup>25</sup> Recent technologies to assess the structure and function of the infant intestinal microbiome will allow a deeper understanding of the relationship between diet, early intestinal colonization patterns, and health. This may be particularly important given the belief that early environmental exposures affect predisposition to immune-mediated diseases later in life.<sup>26,27</sup>

## Diet Helps Shape the Composition of the Intestinal Microbiota

The coevolution of humans and our intestinal microbiota has led to our interdependent, mutualistic relationship. Food sources have guided the evolution of *Homo sapiens*. A comparison of the intestinal microbiota between different primates and mammals found that humans clustered more closely with other primates than nonprimates. Interestingly, diet was the most important determinant when human microbiota samples were most similar to samples from omnivorous primate species.<sup>28</sup> The variety of foods in an

Download English Version:

<https://daneshyari.com/en/article/3292302>

Download Persian Version:

<https://daneshyari.com/article/3292302>

[Daneshyari.com](https://daneshyari.com)