# The Gut Microbiome on Health and Disease

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With the advent of powerful sequencing methods, the rapid development of computer technology and bioinformatics, we have come to appreciate the multi-system effects of the gut microbiome. Emerging evidence suggests that imprinting of the gut microbiota commences already *in utero* as bacterial DNA has been shown to be present in the feto-placental unit and in the newborn's first stool. As microbial DNA is a powerful ligand for innate toll-like receptor signaling, this provides a likely explanation how exposures in pregnancy may impact immune programming of the offspring. The human gut microbiome development occurs primarily in infancy and early childhood, resulting in a relatively stable community. Disturbed gut microbial colonization patterns and reduced microbial diversity in early life have now been observed to precede the development of inflammatory diseases, including allergic diseases and asthma. There is evidence from animal models and *in vitro* studies that gut microbiota modulate immune programming and can prevent the allergic phenotype, and recent studies suggest that reduced abundance of potentially immunemodulatory bacteria are associated with exagerrated innate immune responses with increased production of inflammatory mediators. Still, there are gaps in our knowledge of the optimal patterns of colonization for promoting immune tolerance. Even though powerful sequencing techniques have facilitated our understanding of the infant gut ecosystem, further mechanistic studies from microbiology, immunology and genetics need to be combined for a deeper understanding of how the early life microbiome influences development of allergic disease.

## References

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