Gut microbiome in animal health

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•Abstract

All metazoan guts have evolved to form a strategic alliance with indigenous microbiota. This evolutionarily-conserved mutualistic phenomenon has long-believed to be achieved by fine-tuned molecular interactions between the host and its microbiota. A corollary to the necessity of a commensal microbiota for host physiological homeostasis is that failure to achieve balanced host-microbe interactions may result in pathophysiological consequences for the host. In fact, it has been observed that altered community structure of gut microbiota is likely to be associated with metabolic and/or inflammatory diseases such as obesity, diabetes, and inflammatory bowel diseases. However, the lack of understanding of critical genes in the microbiome and host genomes makes it difficult to explain the exact mechanism by which the gut microbiota impacts host health. The research on this issue has been hampered mainly by technical difficulties associated with in-depth integrated genetic analysis of both the microbes and host. To overcome these limitations, we have developed the combination of *Drosophila* and its commensal microbiotaas a genetic model of host-microbe interaction which enabled us to perform a simultaneous genetic analysis of both host and microbe in an *in vivo* interacting condition. Using this Drosophila-microbiota in vivo interacting model system, we could identify commensal microbiomes involved in host development as well as bacterial microbiome involved in gut inflammation. The straightforward simplicity of *Drosophila*-microbiota model system will provide a novel insight into the underlying mechanistic events to advance our knowledge in more complex vertebrate models, which will hopefully elucidate the unexpected roles of the microbiome in animal health and diseases.