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Researchers track how microbiome bacteria adapt to humans via transmission

Date: August 4, 2021

Source: Wellcome Trust Sanger Institute

Summary: New research has shed light on how transmission of gut bacteria influences its evolution and functions.

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FULL STORY

Beneficial bacteria in the gut microbiome use different means to transmit from one person to another which impacts their abundance in the gut and the functions they provide, new research has found.

This novel research, by scientists at the Wellcome Sanger Institute, used genetic sequencing to shed new light on the evolution, colonisation and transmission of gut bacteria, which play a large role in human health.

The study, published today (5 August 2021) in *Genome Biology*, provides a deeper understanding of the evolution of bacteria in the human microbiome. It could also inform the development of microbiome-based therapeutics where key bacteria could be selected to treat different intestinal-associated illnesses.

Humans are populated by an extremely large amount of microorganisms, called a microbiome, which include bacteria, viruses, archaea and fungi. Beneficial bacteria in the body roughly match human cells one to one* and in the gut, this collection of bacteria has been found to play an important role in human health. The makeup of the gut microbiome affects the immune system, prevents infections and supports the body by breaking down some carbohydrates that human cells cannot do alone.

In order for bacterial species in the gut to survive, they have to be able to transmit from one person to another. Gut bacteria are mainly anaerobic, meaning they cannot survive in oxygen. To spread, some produce spores, which are sometimes likened to seeds and can lie dormant until they encounter the right conditions to grow.

This research, from the Wellcome Sanger Institute, investigated the group of bacteria known as the Firmicutes, which are dominant in the human microbiome and produce spores. The researchers analysed the genomes of 1,358 Firmicutes and tracked the evolution of certain characteristics, including spore production. They observed that gut bacteria that form spores were found at lower abundances in the gut, and had larger genomes compared to those that had lost the ability to produce spores (sporulate). Within their genomes, they also had more genes associated with carbohydrate metabolism and vitamin biosynthesis, which suggests that they have important metabolic functions.

Firmicutes bacteria that could no longer form spores had smaller genomes, but were present at higher abundances in the gut and had a more specialised metabolism based on genome analysis. They were also less prevalent in the general population, meaning they were found in a smaller number of individuals, suggesting loss of sporulation limits their ability to transmit widely.

Smaller genomes and more specialised metabolism indicate that bacteria that have lost the ability to sporulate are becoming more adapted to their human host which could allow them to colonise to higher levels in the gut. On the other hand, bacteria that still produce spores appear less adapted to humans based on their larger genomes which could explain why they are not as abundant in the gut.

These differences show that that transmission is an important process that shapes the evolution of gut bacteria and further research is now needed to continue to learn more about the link between transmission of gut bacteria and the roles they play in human health. Understanding these processes could help inform therapeutics, such as investigating whether specific bacteria could be given to people based on their ability to colonise and how the differing metabolism of these bacteria could impact health conditions and treatments.

Dr Hilary Browne, first author and Staff Scientist at the Wellcome Sanger Institute, said: "Even though transmission of gut bacteria between humans is essential for their survival, the genetic and biological features of the bacteria that allows them to do this, is still poorly understood. This research starts to unravel some of this mystery by analysing the genomes and finding that the ability of bacteria to produce spores has been lost multiple times, impacting their evolution and function. It is necessary to continue looking at the genetic detail of the microbiome to help understand the roles of specific bacteria, and how lacking these might impact human health."

Dr Trevor Lawley, senior author and Senior Group Leader at the Wellcome Sanger Institute, said: "The microbiome plays an essential role in human health and development, and influences a wide range of physiological functions in the body. Understanding more about the bacteria that inhabit us and how they are adapted to living in humans through their metabolism will be important for the development of new therapeutics and diagnostics for microbiome-mediated diseases."

Story Source:

Materials provided by **Wellcome Trust Sanger Institute**. *Note: Content may be edited for style and length.*

Journal Reference:

1. Hilary P. Browne, Alexandre Almeida, Nitin Kumar, Kevin Vervier, Anne T. Adoum, Elisa Viciani, Nicholas J. R. Dawson, Samuel C. Forster, Claire Cormie, David Goulding, Trevor D. Lawley. **Host adaptation in gut Firmicutes is associated with sporulation loss and altered transmission cycle**. *Genome Biology*, 2021; 22 (1) DOI: 10.1186/s13059-021-02428-6
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