

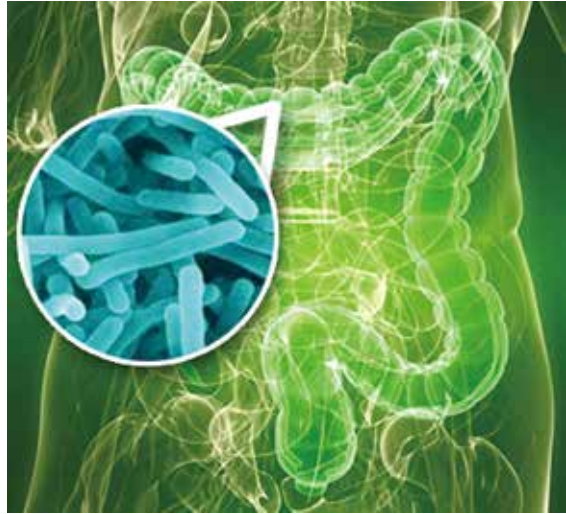


# Understanding How Gut Bacteria Is Related to Type II Diabetes

The gut microbiota has been recognized as a key contributor to human health. Various chronic diseases, including type II diabetes, are connected with the dysbiosis of the intestinal microbiota. Bacteriophages are the killers of gut bacteria by infecting and lysing their hosts, and are thought to be the most abundant biological entities in the human gut. However, gut phage studies remain challenging due to the extremely high diversity of gut phages.

A research group led by MA Yingfei and LIU Chenli from the Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences reported an interesting study which correlated gut phages with type II diabetes, which substantially expanded our understanding of human gut phages through large-scale genome wide analysis by using bioinformatic pipeline developed in-house.

Their study revealed that instead of a reciprocal relationship of phage specific to its bacterial host, there is actually a complex core interaction among bacteria and phages. They found that the alteration of gut phages is significantly specific to T2D, and the T2D-associated changes in the phage community cannot simply be explained as co-variation with their altered bacterial hosts. Bacteriophages likely play roles in intestinal physiology that are far more important than the alteration of bacterial communities via killing their bacterial hosts.



The study suggested that scientists need to pay more attention to the role of the bacterial "killers" in human microbiome.

Their paper entitled "A human gut phage catalog correlates the gut phageome with type 2 diabetes" has been published in *Microbiome* in February 2018. The research was supported by the National Nature Science Foundation of China, the National Basic Research Program, the Science and Technology Program of Shenzhen, and the Peacock Innovation Project of Shenzhen.