



學術報告

Deciphering Functional Redundancy in the Human Microbiome



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Biography: Liang Tian is a research fellow in the Channing Division of Network Medicine at Brigham and Women's Hospital and Harvard Medical School, working with Dr. Yang-Yu Liu. Currently, he is working on percolation transitions on complex networks and also dynamics and functions of the human microbiome. His works have been published in Nature Communications, Physical Review E, Europhysics letter. Prior to joining the Yang lab, he completed his Ph.D. in theoretical physics at Nanjing University of Aeronautics and Astronautics and Hong Kong Baptist University. His dissertation work focused on statistics and dynamics of complex network.

The taxonomic composition of human microbiome varies across individuals. Although this redundancy is thought to underlie the stability and resilience of the human microbiome, its origin is elusive. We decipher the functional redundancy in the human microbiome by depicting its genomic content network. We find that this network exhibits several topological features. And the human gut microbiota displays a unique assembly pattern. This pattern and the associated high functional redundancy of the gut microbiota are gradually established during the first year of life in healthy infants. Acute disturbances abolish the assembly pattern and the functional redundancy weakens, but several chronic diseases do not markedly alter the assembly pattern and the functional redundancy of the gut microbiota. This result suggests that the functional redundancy can serve as a resilience indicator of diseased microbiota against compositional interventions.