

## **Microbiome in cancer and obesity**

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The human body provides habitat for over 30 trillion microorganisms collective known as microbiome. The development of culture-independent genomic techniques such as the next-generation-sequencing (NGS) has enabled us to look deep into these microbial communities, which has greatly advanced our understanding on their influences on our life. Disturbance of the microbiome or dysbiosis is associated with various diseases including cancer. Using NGS, we have studied the baseline microbiome composition in a cohort of gastritis patients with or without development into gastric cancer (GC) in order to identify possible microbiome signature that can be used to predicate the progression to GC. We identified a panel of discriminatory bacterial signature and gene functions which could be further validated for application as biomarkers for GC progression in patients. In the second part of my talk, I will focus on a molecule known as interferon regulatory factor 3 (IRF3). I will discuss about how this important innate immune regulator can also play an important role in the development of obesity, obesity-associated metabolic disorders, as well as it's possible regulation on gut microbiome during obesity development.