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The Cancer microbiome research: understanding the host-microbe interactions to treat cancer

Gnanendra Shanmugam

Yeungnam University, South Korea

Our body is surrounded by trillions of microbes, among these, majority are bacteria, while we also host fungi, virus and archaea. The gene content of these microbes all together is collectively termed as microbiome or microbiota. However, humans show 99% similarity in their genetic makeup, they show 80-90% variation in terms of microbiome. In this scenario, microbiome research can facilitate understanding of the significance, for the human, of the microbes, and of the interactions among them. The change in the microbiome configuration has been associated with a number of diseases, including obesity, inflammatory bowel disease, arthritis, autism, asthma and cancer. Thus cataloguing the required and appropriate sets of health-supporting microbiome features and their normal ranges in healthy humans is an essential step in identifying and correcting disease-implicated microbial configurations. Also, exploring the features that broadly distinguish healthy from unhealthy microbiomes will help in the detection of microbiome-related diseases and may potentially offer new ways of preventing disease onset or enhancing prognosis.

Biography:

Dr. Gnanendra Shanmugam is currently an Assistant Professor (Research Professor) in the Department of Biotechnology at Yeungnam University, Gyeongsan, South Korea. He received his PhD degree in Bioinformatics from Bharathiar University, Coimbatore, India in 2014. After completing his PhD, he continued to have training as postdoctoral fellow (2016-2018) in Microbial genomics laboratory in the department of Biotechnology at Yeungnam University, Gyeongsan, South Korea. In 2018, he accepted the Assistant Professor position in the same university. He is a bioinformatician with keen research interests in deciphering the molecular mechanisms and pathways towards the novel lead discovery for various diseases. His research focuses is focused on Next generation sequencing analysis and he loves to develop machine learning, data mining algorithms with potential applications in predicting protein structure and functions. He has published over 25 peer-reviewed research articles.