

The Role of Host Genetic Variability in the Development and Establishment of Human Gut Microbiome Diversity

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Abstract

Studies have shown that human microbiome plays important roles in physiology, from food digestion to mental diseases. Since the gut microbiome composes the highest number of microbial cells outnumbering even our own cell counts, it is expected that the gut microbiome would affect a great deal of human biological functions. This makes the gut microbiome key to maintain homeostasis in the various biological levels where there are constant and active interactions between microbes, tissue, cells and molecules. The structure of the gut microbiota is shaped by many factors, including host genetics. Understanding how these factors determine the microbiome during the development and establishment of the gut microbiota at early stages of human life is crucial to infer biological and pathological microbiome composition. The purpose of this study is to apply tools of bioinformatics to process and analyse data samples of feces of triplet babies in order to verify host genetic associations with gut microbiome during the first 3 years of the babies lives

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Biography

Larissa Matos graduated in biomedicine (2010) and master in biology applied to health (2013) from the Federal University of Pernambuco - UFPE. She is PhD in science (2017) from the University of São Paulo - USP (Program of Experimental Epidemiology Applied to Zoonoses). She has experience in the areas of microbiology, molecular biology, carcinogenesis and molecular probes, with a focus on microbiome, bacterial

pathogenesis (leptospirosis), NGS sequencing, bioinformatics, cloning, expression and purification of recombinant proteins, electrophoresis, chromatography, ELISA, western blotting, chemiluminescence and diagnosis. She is currently a postdoc researcher at the Center for Research on the Human Genome and Stem Cells (CEGH-IB/USP), working mainly with the microbiome-host