Understanding the gut ecosystem: bugs, drugs & diseases

Vich Vila, Arnau

DOI:
10.33612/diss.102587978

Propositions

The gut microbiota of patients with inflammatory bowel disease (IBD) is characterized by a decreased abundance of obligate anaerobes and a “blooming” of pathobionts. (This thesis)

Intestinal surgeries and disease location greatly influence the microbiome composition in patients with IBD. (This thesis)

The fecal microbiome has great potential as a biomarker and could be used to help distinguish patients with IBD from patients with irritable bowel syndrome. (This thesis)

IBD sub-phenotypes are related not only to changes in bacterial composition, but also to changes in absolute bacterial abundance. (This thesis)

The effects of environmental factors on gut microbiota composition dominate over the effects of genetics. None-the-less, the study of IBD cohorts can help reveal associations between host genetics and gut microbial composition. (This thesis)

Commonly used medication affects the gut microbiota. (This thesis)

In the future, the combination of sequencing data with quantitative measurements of the gut microbiota will help to improve the comparability of different microbiome studies.

Studies involving the perturbation of the gut microbiota and the estimation of the ecosystem resilience are needed in order to identify the key characteristics of a “healthy” microbiota.

The gut microbiota is not an organ: it is an ecosystem. This notion is essential for designing therapeutic strategies that modify the gut microbiota.