Introduction

The human microbiome (totality of all microorganisms) has become the focus of scientific interest over the past ten years. Alterations in the gut microbiota have been linked repeatedly to pathological states including overweight, asthma, colon cancer, graft-versus-host disease or inflammatory bowel disease (IBD).

The human microbiome is a metabolically active organ that generates more than 1000 metabolic products. This creates important metabolites, such as secondary bile acids or short-chain fatty acids, which exert local and systemic functions.

Objectives

- Develop and establish a method for sample collection, preservation and storage that allow the preservation of the metabolites of interest in fecal sample;
- Develop and validate analytical methods to analyze metabolites related to microbiome in stool samples by Mass spectrometry based platform, covering initially the following metabolites: Bile acids, amino acids, free fat acids, polar lipids (acil carnitines, diacyl-phosphatidylcholines, acyl-alkyl-phosphatidylcholines, sphingomyelines, acyl-, alkyl-lysophosphatidylcholines and sum of hexoses) and metabolites involved in the TCA cicle.
- Apply the methodology to analyze, at least, 50 samples of health subjects (children and adolescents ranging 6 to 17 years old) to be used as an internal reference.
- Apply the methodology developed to clinical studies to better understand metabolic changes due disorders such as, but not limited to, IBD and the response of exclusive nutritional therapy treatment as well as *H. pylori* infection and the metabolic response to antibiotic and supplementation with *lactobacillus*.