

Project: INterplay Between Lifestyle and blood micrObiome in colon rectal cancer prevention: a new Metagenomic perspective (InBLOOM)

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Colorectal cancer (CRC) is one of the most common types of cancer in the world. Over 90% CRCs derive from genetic alterations involving the transition from normal mucosa to pre-malignant lesions with progression to intestinal adenomas (IA) and invasive cancer. The etiology of CRC has been linked to several lifestyle factors, including diet, genetic mutations, and inflammatory processes, but the causes of a large proportion of CRC remain controversial. Recent demonstrations showed a substantial connection between gut dysbiosis and CRC, with some sequencing studies that have revealed changes in the gut microbiome of patients with CRC, and a disruption of the gut barrier that can facilitate the transit of microbes and microbial components (e.g. metabolites, protein, DNA) in blood. However, no single causative microorganism or microbiome directly and biologically related to CRC were found.

In this context, the InBLOOM project aims at evaluating the contribution of blood microbiome (i.e. the microbial DNA circulating into the blood flow) to CRC etiology, also in a translational perspective for the earlier diagnosis of CRC. Indeed, the translocation of microbial materials in blood led to a general mounting evidence of a role of the blood microbiome in the pathogenesis of non-infectious diseases. The project is based on a case-control study on 100 incident, histological confirmed CRCs, 100 IAs and 100 healthy controls. Preliminary analysis on blood samples using 16S rRNA samples were already performed together with the collection of information on sociodemographic status, lifestyle habits, past and recent diet, using a food frequency questionnaire from each recruited subject.

The candidate will be involved in a national research network and will have to contribute to data collection and management of the research project in a multidisciplinary context. The candidate will be involved in all wet lab activities necessary to characterize complex microbial communities using shotgun metagenomics. The candidate will also be involved in the bioinformatic analysis of the sequences as well as the statistical analysis, integrating the results with the available covariates.