# P25 & FP – **Design and feasibility of a multicentric study assessing blood microbiota and diet in relation to adenoma and colorectal cancer risk: a three-year project funded by AIRC**

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**Background:** Inflammation and immunity are inextricably linked to all phases of colorectal cancer (CRC) development. Gut inflammation leads to loss of epithelial barrier function, driving to the bacterial translocation from the gastrointestinal tract to bloodstream. In this context, an overrepresentation of bacterial cells in blood has been proposed as an indicator or a predictor of intestinal adenoma (IA) and/or CRC.

**Objective:** We designed a study to investigate whether bacterial translocation from gastrointestinal tract to bloodstream is associated to the risk of IA and/or CRC using an innovative metagenomic approach on blood samples. Diet will also be investigated in relation to bacterial translocation and to the risk of IA and/or CRC, with the aim to define dietary guidelines associated to a CRC risk reduction.

**Methodology:** A case-control study including 100 incident cases of histological confirmed CRC, 100 IAs and 100 healthy controls is conducted. Participants are enrolled at hospital by involving outpatient or inpatient eligible subjects who have a colonoscopy appointment. Healthy controls and IAs are matched with CRC cases (1:1 by age +/- 5 years and sex). An interview is performed by trained interviewers through a valid food frequency questionnaire collecting dietary and life-style habits, besides socio-demographic information and anthropometric measures. Blood samples will be also collected by a nurse before the colonoscopy.

**Results:** Project received ethical committee approval and data recruitment started in May 2017 in two hospitals of Milan, with involvement of CRC regional screening program. One hundred fifty-one subjects, 71 women and 89 men were recruited, with a total of 25 three matched trios have been recruited to date. In order to keep the signal to noise ratio optimal and to reduce technical variability, possibly overcoming the biological variation between groups, all samples will be analyzed in the same time, with the same reagents batches and by the same manipulator at the end of data recruitment to perform DNA extraction, qPCR quantification and Metagenomic Sequencing of all samples in the same experiment.

**Conclusions / Implications for practice:** The project is designed to contribute original information to the on-going international scientific debate on the causes of CRC and its prevention. It will allow to evaluate whether early diagnosis of CRC may be defined by mean of metagenomic microbiota profiling in blood, with relevant implications on a public health level, specifically related to CRC high risk subgroups.

**References**

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