

P49 – Microbial and Immune characterization of human colorectal cancer

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Background: Colorectal cancer (CRC) is the third most frequent tumor worldwide and its development is influenced by dietary patterns, environmental conditions, host immunity, and microbial adhesion (Russo E et al., 2016). In detail, some studies suggested a potential dysbiosis of gut microbiota (GM) in CRC patients.

Objective:

- To define the CRC “core” microbiota both in gut area (stool and cancer tissue) and oral cavity.
- To characterize the immune T cell response (intra-tumoral and systemic) in CRC patients.

Methodology: Tumor-infiltrating lymphocytes (TILs) were isolated from 30 CRC patients and subsequently cloned (Amedei A et., 2009) and characterized by cytofluorimetric analysis, ELISA test and cytotoxic assay. Peripheral blood mononuclear cells were also isolated in order to characterize circulating T cell subsets by FACS analysis. Also, Bacterial signatures from saliva, stools, and colon biopsies of 10 CRC patients and 10 healthy controls were detected using next-generation sequencing (NGS) approach. DNA was extracted from each sample and used for Illumina NGS and species-level analysis was performed.

Results: NGS and bioinformatic analysis showed significant differences in bacterial population composition between control and cancer groups. In details: a) control and CRC patients had different gut microbiota compositions, b) immunological analysis revealed that in CRC patients increases the number of intratumoral T cells with a “not effector” profile, such as regulatory T cells (Tregs), c) Data shows a higher percentage of preoperative circulating Tregs in CRC patients that in healthy volunteers that goes down one week after surgery (Nicolai et al. 2017).

Conclusions / Implications for practice: the microbiota affects the immune response and some bacteria and their metabolites can influence the immune system and in particular the number of Tregs. For these reason further and deepened analysis will be necessary.

References

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