Cancer-triggered gut dysbiosis in a uruguayan cohort

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Abstract

Human gut microbiome is highly influenced by environmental factors, the host lifestyle and the geographic region. Efforts to understand the role of the gut microbiome in cancer on a local scale are needed to incorporate this knowledge in the clinic. We recruited 25 patients (melanoma, renal cell carcinoma, non-small cell lung cancer, and head and neck squamous cell carcinoma) and we aimed to characterize the diversity of the microbiota. Using shotgun metagenomics and culture-based tools we profiled the microbial composition of our uruguayan cohort. We compared the taxonomic diversity, gene families and metabolic pathways of our oncologic cohort with a healthy reference (n = 68). The microbial composition of the oncologic cohort differs from that of the healthy control. Our results show higher relative abundance of *Enterococcus faecium* and *Klebsiella pneumoniae* as compared to healthy individuals. Using culture-based techniques, we began the first Uruguayan microbial biobank from the gut microbiome.