The Role of the gut microbiome in immunotherapy response

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In recent years, a noteworthy alternative approach to cancer treatment has emerged. Immunotherapy, specifically, monoclonal antibodies targeting immune checkpoints such as the programmed death 1 (PD-1) have transformed the management of a variety of advanced cancers. The role of the gut microbiome in shaping the response to immunotherapy has been identified. The human microbiome, subject to influences from environmental factors, the host's lifestyle, and geographical location, plays a pivotal role in this regard. It is imperative to undertake efforts aimed at understanding the influence of the microbiome on cancer immunotherapy at a local scale. We recruited 26 cancer patients and we aimed to characterize the microbial population. Utilizing Hi-C technology, we profiled the microbial composition. Hi-C sets a new standard in microbiome research, offering a detailed community composition profile with enhanced insights into bacterial gene content and mobile genetic elements compared to conventional metagenomics. Using a healthy cohort as a reference (n = 21) which were also analyzed, we compared the relative abundance of microbial populations, plasmid and antibiotic resistance genes (AMR), and examined phages linked to the bacteria. The microbial composition of the oncologic cohort differs from that of the healthy control. Our results show higher relative abundance of *Alistipes shahii* and *Bifidobacterium longum* in the gut of oncologic patients as compared to healthy individuals. Furthermore, a notable prevalence of Tetracycline resistance genes was observed in bacteria prevalent in oncologic patients. We speculate that these results can be used in the future to fuel the development of new clinical interventions.