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Abstract

The gut microbiome, a diverse community of microorganisms, is emerging as a key driver of chronic diseases, including autoimmune, metabolic, neurodegenerative disorders, and cancer. These microorganisms produce a wide range of molecules, most of which remain unidentified and cannot be studied using traditional methods. Recently, small open reading frames (smORFs) have been discovered, with 30% predicted to be involved in cell-cell communication. Understanding the full scope of these molecules is a major scientific challenge.

Our project bridges basic science and clinical application by studying the gut microbiome's role in modulating responses to immune checkpoint inhibitors (ICIs), which have revolutionized cancer treatment but are only effective in a subset of patients. Using advanced multi-omics and machine learning, we aim to identify microbiome-derived molecules that influence the immune response to ICIs, potentially uncovering biomarkers to predict patient responses and developing new therapeutic strategies to enhance ICI efficacy, improving outcomes for a wider range of cancer patients