UC San Diego
MOORES CANCER CENTER

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Illuminating host-microbiome relationships in triple-negative breast cancer using spatial transcriptomics and long-read metagenomics

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Scientific Abstract:

The human microbiome is highly diverse compared to human cells, and microbial genes account for 99% of the unique genes found in the body. Prior work has shown the existence of tumor microbiomes, and that microbes can influence carcinogenesis (for ex: genotoxic byproducts) and resistance to therapy (for ex: metabolism of chemotherapeutics). Tumor microbiomes are vastly unexplored in this regard, but the application of novel microbiome approaches, such as long-read metagenomics and bacterial spatial transcriptomics, has the potential to identify specific microbes and their expressed genes. MpTNBC is a rare chemoresistant subtype of triple-negative breast cancer that is associated with high recurrence risk and low survival rates. Uncovering links between the tumor microbiome and clinical outcomes will open possibilities for prognostic/ predictive biomarkers and potential novel therapies for this difficult-to-treat cancer. We will accomplish this by first comparing long-read metagenomic sequencing of metaplastic and non-metaplastic TNBC tumors to assess unique microbes or abundances, then we will stain for these microbes in conjunction with spatial transcriptomics technology. The results will be analyzed with bioinformatics approaches specifically applied for microbiome applications.

Lay Abstract:

The human microbiome is a collection of diverse microorganisms that live in and on our bodies, with roughly the same number of cells as our own. These tiny organisms carry a huge number of unique genes, encoding proteins and other molecules that affect our health, many times more than our own cells. Recent studies have found that there are specific microbial communities associated with tumors, known as tumor microbiomes. These microbes can play a role in the development of cancer by producing harmful substances that damage our DNA, potentially leading to cancerous growth. They can also affect how well cancer treatments work by altering the way our bodies process chemotherapy drugs. Understanding these interactions could have a big impact on cancer treatment, helping us develop better therapies and possibly even ways to prevent cancer from developing in the first place. In the short term, this research might lead to more personalized treatments that take into account a person's unique microbiome. In the long term, it could revolutionize how we approach cancer prevention and diagnosis, including with the use of engineered microbes to deliver therapies, potentially saving countless lives.