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Commentary

A Novel Approach to Tumour Associated Microbiota in Cancer

Samuel Sussan*

Department of Oncology, Shengjing Hospital of China Medical University, Shenyang, China

DESCRIPTION

Across all kinds of human cancer, the tumor-associated microbiota is an integral part of the tumor microenvironment. Studies on the intra tumoral host microbiota have generally relied on bulk tissue analysis, which hides the microbiome's spatial dispersion and targeted impact within tumors. Here, they identify spatial, cellular, and molecular host-microbe interactions in oral squamous cell carcinoma and colorectal cancer using spatial-profiling technologies and single-cell RNA sequencing. To identify and pinpoint the location of intra tumoral microbial populations within patient tissues, they modified Visium Spatial (VS) transcriptomics. By using GeoMx digital spatial profiling, they demonstrate that bacterial communities are more prevalent in microniches that are immunosuppressive, less vascularized, and linked with malignant cells that have lower levels of Ki-67 than parts of the tumor that lack bacteria.

Cancer patients' tumors contain a complex network of non-malignant cells that, depending on their cell type and number, may have pro- or anti-tumorigenic effects around the malignant cells. Bacteria in the tumor-associated microbiota appear to play a role in cancer growth, metastasis, immune surveillance, and chemo resistance and preclinical animal models. At least 33 main cancer types have strong molecular evidence of an intra tumoral microbiota, and imaging findings demonstrate that pan-bacterial markers co-localize with immune and epithelial cell targets, indicating that the intra tumoral microbiota may also be intracellular. These cell-associated organisms' precise identities and the particular host cell types with which they interact in patient tumors are still unknown.

Historically, the intrinsic genetic changes that occurred in cancer cells during clonal proliferation were the only explanation for tumor heterogeneity. Extrinsic variables originating from the TME play a significant influence in carcinogenesis, according to studies conducted in the 1990s. In the TME, interactions between cancer cells and non-cancerous cell groups such fibroblasts, endothelium, and immune cells are known to promote transcriptome changes in transformed cells as the cancer progresses. They are learning more about the TME and the factors that influence tumor heterogeneity at the same time. Studies using genomic data have demonstrated that the majority of common kinds of human cancer have an intra tumoral microbiome.

Specific bacteria can influence the development and spread of cancer, the way in which patients react to treatment, and ultimately their chance of survival. These microbial populations differ depending on the type of cancer. However, the inherent variety of the situation has made it challenging to comprehend the interactions between various TME components, such as bacteria-host interactions in the setting of native tissue. The effect of the intra tumoral microbiota in the TME has far been ignored, despite the development of spatial transcriptomics and scRNA-seq technologies, which have made it possible to study eukaryotic components of the TME. They draw the conclusion that the intra tumoral microbiota is heterogeneously distributed across human tumors in this study by adapting and using these technologies.

The 33 major cancer forms that have so far been shown to possess an intra tumoral microbiome might be studied using the tools and technology they describe, even if their focus here was on two cancer types at the extremes of the gastrointestinal tract. In order to find molecular and cellular targets for the prevention and treatment of such cancers, analyses must transcend beyond correlative connections of the microbiota with human cancers and evaluate the functional impact of the intra tumoral microbiota. This body of research demonstrates that the intra tumoral microbiota is highly organized in microniches with immune and epithelial cell functions that support cancer progression, rather than being distributed in a random manner within patient tumors.

Correspondence to: Samuel Sussan, Department of Oncology, Shengjing Hospital of China Medical University, Shenyang, China, E-mail: samuelsussan@chi.cn

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