Exploring the functional impacts of the intratumoral cancer microbiome and its relationship with immunotherapy response

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Abstract:

We and others have shown that bacteria are ubiquitous in and different between most major human cancers. Analogous to how the tumor microenvironment is spatially organized, intratumoral microbes must also have spatial organization. Herein, we describe a comprehensive and yet readily feasible approach to dissect the spatial distribution of microbes in non-small cell lung cancer through the lens of intratumor hypoxic gradients, which exist in roughly half of all known solid tumors. The data gathered by our digital spatial transcriptomic approach and selection of patients with immunotherapy response data will further enable the analysis of which microbes are most (and least) associated with antitumor immunity. We lastly propose a method to sort and unbiasedly sequence the entire transcriptome of 'infected' cancer cells with intracellular microbes while simultaneously characterizing the landscape of known intracellular bacteria. We believe that this proposal, if successful, will fundamentally change how we understand the role of bacteria in the tumor microenvironment and have important implications for immunotherapy, providing improved diagnostics of predicted patient response in the short-term and better patient outcomes in the long-term.