Spatial proteomics of bacteria in the tumor microenvironment (TME) of oral cancer and colorectal cancer

Background

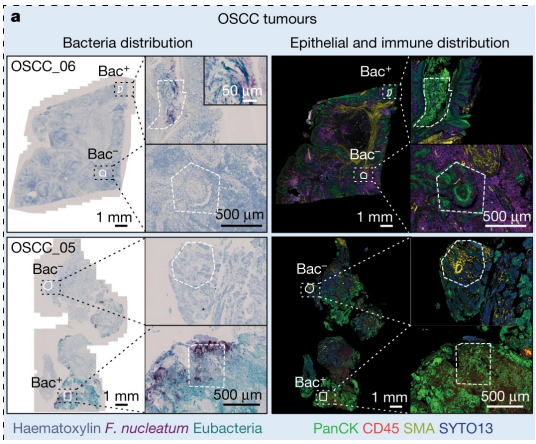
- Tumor-associated microbiota is an intrinsic component of the TME across human cancer types
- Identification of cell-associated microbiota and specific host cell types with which they interact in tumors are not known

Research Question

Are there any bacteria in colorectal and oral tumors and what (if any) is their effect on host cells?

Experimental Setup

Instrument	GeoMx® DSP
Sample Type	FFPE
Tissue Type	Oral mucosa and colon
Assay	Human Immuno-Oncology Protein Panel
Analyte	Protein
Readout	nCounter® Analysis System



Why GeoMx?

Spatial characterization of protein expression in the TME compartments infected with *Fusobacterium* species provided direct evidence of how bacteria may alter cells and hamper the immune response against cancer.

RNAScope CISH images show the distribution of *F. nucleatum* (dark red) and other bacterial communities (eubacteria probe: cyan) as well as ROI selection in the DSP image based on staining of PanCK, CD45, SMA, and SYTO13. Figure reproduced with permission from Galeano Niño JL et al. Nature. 2022 under the ***Creative Commons license.***

Results & Conclusions

- Within the CD45+ Immune Compartment:
  Bacteria reside in immunosuppressive microniches characterized by enrichment of myeloid cells and upregulation of ARG1 and CTLA4; PD-1 was overexpressed in bacteria-positive microniches with downregulation of T-cell markers in OSCC tumors.
- Data suggest that T cells are excluded in bacteria-colonized regions.
- Within the PanCK+ Epithelial Compartment:
  Regions were less vascularized than bacteria-negative regions and there was a significant reduction in wild-type P53 correlated with highly transformed cancer cells within the TME.
- High levels of JNK, ERK1, ERK2 and P38 reveal signaling pathways that are activated in response to bacteria. Reduced Ki-67 expression suggests there is lower proliferation in infected regions.

Galeano Niño JL et al. Effect of the intratumoral microbiota on spatial and cellular heterogeneity in cancer. Nature. 2022 Nov;611(7937):810-817
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