

A single cell, spatial map of healthy and diseased colon made with CosMx™ SMI identifies a unique population of inflammatory macrophages

Background

The molecular basis for the heterogeneity of ulcerative colitis (UC) and Crohn's Disease (CD) remains uncharacterized and there is remarkable variability in disease severity, progression, and treatment response

Research Question

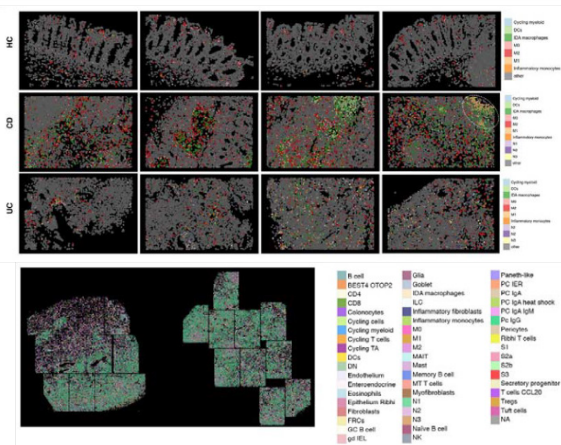
What is the cellular distribution and gene signature makeup of normal and inflamed colon tissue?

Experimental Setup

Instrument	CosMx™ SMI
Sample Type	FFPE
Tissue Type	Human Colon
Assay	Universal Cell Characterization RNA Panel
Analyte	RNA

"...Available sc-RNA-seq datasets lack information on tissue distribution and spatially relevant cell-to-cell interactions. To fill this critical gap, highly multiplexed spatial technologies are rapidly evolving. Our study is the first to provide combined sc-RNA-seq data with spatial transcriptomics at single-cell resolution to start unraveling patient-dependent disease mechanisms."

-Garrido-Trigo et al.



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Results & Conclusions

- Resident M0 and M2 macrophages as well as activated macrophages such as classical M1 and new inflammation-dependent alternative (IDA) types were found in IBD samples. M0 macrophages have never been described before in the intestine.
- Intestinal neutrophils were found in three transcriptional states.
- Subepithelial IDA macrophages expressed NRG1, which promotes epithelial differentiation, whereas NRG1^{low} IDA macrophages were found within the submucosa and in granulomas, close to inflammatory fibroblasts, which may promote macrophage activation.
- Macrophages can adopt diverse transcriptional signatures that are heterogenous between patients and associate with different types of cells such as fibroblasts.
- This is the first single cell, spatial map of healthy and diseased colon made by integrated scRNA-seq data with CosMx SMI data

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For more information, please visit nanosttring.com/cosmx

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