Spatial Single Cell characterization of SIV reservoirs in lymphoid tissues and B cell follicles in rhesus macaques

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- reservoirs
- 5 Spatial context analysis on individual cells accurately reproduces the tissue architecture and immune neighborhoods of the lymph node. • First measurements of the microenvironment alterations surrounding individual SIV infected cells within the different lymph immune neighborhoods.

This spatial profiling provides insight beyond what is available from bulk analyses and shows the role of viral reservoirs in the context of their cellular immune neighborhoods. These results improve our understanding of NHPs as a model system for HIV and may lead to potential treatment options to eliminate the entirety of the viral reservoir in the infected individual.

SMI visualizes SIV genes in 3D

Subcellular localization of SIV RNA discriminates productive infection from virions trapped on follicular dendritic cells within B cell follicles

Retrovirus infection and reverse transcription

3D visualization of SIV transcripts indicates that a subset of

single cells have high viral gene content at the intracellular

location (vRNA+), while the others are located outside of

single cells (virions). Examples (Left) show productively

infected T cells (top) and uninfected follicular dendritic cell

networks (bottom).





ag pol nef env vif tat_rev_vpr_vpx Membrane

CosMx: Differential expression at single cell level within unique tissue niches



Sample and study design



SIV infection of rhesus macaques (RM) is important model of HIV infection of humans. RMs were placed into two study groups (as shown above), the day 56 (week 8) post SIV infection (and treatment) lymph nodes were used to make FFPE blocks. Serial 5 µm sections of FFPE lymph nodes were utilized for spatial transcriptomic analysis on two nanoString Technologies platforms; the GeoMx DSP and the CosMx SMI. Samples include 6 SIV infected lymph nodes where three had been treated with an αCD21 blocking antibody (red arrows) and three with an IgG (black arrows) control antibody. The SMI panel consisted of the RNA 1K-plex panel with a custom spike-in probe set for 9 SIV genes. The tissues were stained with a morphology kit including B2M/CD298, PanCK, CD45, and CD20 antibodies to help select applicable Field of Views (FOVs) for analysis.

Overview of the CosMx and GeoMx assays

GeoMx DSP spatial analysis of lymph tissue

Challenge:

Results:







fibroblast



Conclusions

• The CosMx Spatial Molecular Imager (SMI) is a single instrument solution for subcellular spatial analysis: SMI provides sub-cellular resolution of 1000+-plex transcriptomic information and SIV viral genes.

• Both GeoMx and CosMx SMI spatial platforms provide complementary spatial **information:** GeoMx DSP profiles up to the whole transcriptome, while CosMx SMI provides sub-cellular resolution of biological targets.



1000-Plex RNA Panel for Cell Typing and Cell-Cell Interaction Studies	
Applications	# of genes
Cell typing and mapping	243 genes
Cell state and function	269 genes
Cell-cell interaction (ligand-receptor)	435 genes
Hormone activities	46 genes



*short genes tat, rev, vpr, & vpx were combined in one probe set



A neighborhood matrix was calculated for each cell by identifying the cell types of all cells within a 100 μ m radius of it. Clustering was performed on this matrix to identify 3 distinct spatial neighborhoods which can be used to identify cells experiencing similar environments or niches.



• Sub-cellular resolution spatial transcriptomics enables discrimination of singleinfected cells from virions located in the extracellular space of single cells (reservoirs).

• Using single cell spatial transcriptomic analysis we performed the first characterization of SIV infection effects on BOTH the individual infected cells and their local microenvironment.



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