**Application of a novel instrument-free and microfluidics-free single-cell analysis technology (PIPseq) that is well suited for viral applications in resource constrained laboratories**

**Genomics**

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Introduction: Single cell RNA sequencing (scRNA-Seq) has made profound impacts in the study of cellular and molecular diversity in complex tissues. In the study of virology, this resolution of single-cell transcriptional changes in response to viral infection provides valuable insight into the mechanisms of infection and host response.

Materials and Methods: Current scRNA-Seq methods are not easily adopted in the virology lab as they are expensive, require complex instrumentation and consumables, and hence can be challenging to implement in a laboratory with limited resources and accessibility. Fluent BioSciences has developed a novel scRNA-Seq approach with Pre-templated Instant partitions (PIPseq) that enables the analysis of thousands of cells without requiring complex instrumentation and consumables. The small format and convenient workflow, with the lack of instrumentation, allows PIPseq to be easily implemented in high-containment laboratories.

Results: Using a GFP-expressing control virus, we have demonstrated simultaneous capture and barcoding of viral and cellular transcriptomes, identified cellular gene expression shifts in response to viral infection, and identified gene expression responses in non-infected cells from low MOI infected samples compared to mock controls. Furthermore, we have demonstrated that the PIPseq protocol is effective at inactivating residual virus in sequencing library samples, thus enabling convenient sample post-processing outside of the virology laboratory.

Conclusion: PIPseq is an effective method to study viral-host interactions at a single-cell resolution, and can be easily implemented in a core facility or resource constrained laboratories. The ongoing COVID-19 pandemic exemplifies the need for new tools and methods to elucidate the mechanisms of viral infection, pathogen-host responses, and diversity in cellular responses to infection.