The ability to track signaling dynamics of single cells and then correlate to gene transcripts is extremely important for understanding stochasticity in gene expression relevant to cell-to-cell variability. In the context of immune cells this variability can have pathological consequences. For example, NFκB regulates transcription of pro-inflammatory, tumorigenesis and apoptotic genes. We present an integrated high-throughput, microfluidic platform for live-cell imaging and single-molecule Fluorescence *In-Situ* Hybridization (smFISH) in the same cells to enable correlation of early time events to mRNA transcriptional levels. smFISH is a quantitative method to characterize mRNA transcripts in cells; it uses multiple short, complementary oligonucleotides, and therefore is accurate to single transcript level(*1*, *2*). Conventional smFISH assays are done on cover slips that suffer from significant cell loss especially with suspension cells and require a substantial amount of reagents. While significant efforts have been devoted to developing robust probes for specific mRNA identification, there has been a large lag in developing tools for handling cells.

We have employed microfluidic technology to develop a method for performing cell stimulation, live-cell imaging and smFISH providing transcriptomic data at a single cell resolution for hundreds of cells in a single device with reduced reagent use. Our device holds about 900 cells on a $1mm^2$ footprint device, and utilizes 100-fold less reagents compared to the conventional assay. In addition, the platform consists of cell trapping microstructures that confine individual cells in defined positions allowing cell dynamics to be analyzed at a single-cell level through time. Because smFISH is a fluorescence-based technique, the number of transcripts we can simultaneously quantify is theoretically unlimited as long as they are spectrally separated. Therefore, this technique will contribute greatly to systems understanding of gene transcription under system perturbations such as immunological cell response to viral transcription in infected hosts. Our design provides a tool for studying stochasticity underlying gene expression, and will enable advancement in single-cell transcriptomics.

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