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Droplet Microfluidics for Virus Discovery ASSAF ROTEM, Department of Physics and SEAS Harvard University, SHELLEY COCKRELL, Department of Biological Sciences University of Pittsburgh, MIRA GUO, Department of Physics and SEAS Harvard University, JAMES PIPAS, Department of Biological Sciences University of Pittsburgh, DAVID WEITZ, Department of Physics and SEAS Harvard University, WEITZ LAB TEAM, PIPAS LAB TEAM — The ability to detect, isolate, and characterize an infectious agent is important for diagnosing and curing infectious diseases. Detecting new viral diseases is a challenge because the number of virus particles is often low and/or localized to a small subset of cells. Even if a new virus is detected, it is difficult to isolate it from clinical or environmental samples where multiple viruses are present each with very different properties. Isolation is crucial for whole genome sequencing because reconstructing a genome from fragments of many different genomes is practically impossible. We present a Droplet Microfluidics platform that can detect, isolate and sequence single viral genomes from complex samples containing mixtures of many viruses. We use metagenomic information about the sample of mixed viruses to select a short genomic sequence whose genome we are interested in characterizing. We then encapsulate single virions from the same sample in picoliter volume droplets and screen for successful PCR amplification of the sequence of interest. The selected drops are pooled and their contents sequenced to reconstruct the genome of interest. This method provides a general tool for detecting, isolating and sequencing genetic elements in clinical and environmental samples.

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