Virus capture facilitates a sensitive viral diagnosis for pathogens including SARS-CoV-2

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Abstract

When new viruses emerge, early detection is critical, but the detection of pathogens in clinical and environmental samples using high-throughput sequencing is often hampered by large amounts of background material. Enormous sequencing depth can be necessary to gain sufficient information to identify a certain pathogen. Now, a study demonstrates a new method to improve the sensitivity of viral diagnosis. Combining high-throughput sequencing with in-solution virus capture, researchers compiled a virus genome dataset for the design of a RNA-baits panel. The panel, called VirBaits, consists of about 178,000 RNA-baits based on over 18,000 complete viral genomes, targeting 35 epizootic and zoonotic viruses, including SARS-CoV-2. In a test of complex samples, viruses with both DNA and RNA genomes were enriched by anywhere from 10-fold to 10,000-fold, with enriched viruses having at least 72% overall identity shared with the viruses in the bait set. Although the cost and risk of cross-contamination remain concerns for this method, the VirBaits approach represents a promising technique for improving the sensitivity of viral diagnosis in complex samples, enabling the rapid detection of emerging pathogens.