Improved sensitivity for bacterial community characterization in clinical samples

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Abstract

High-throughput sequencing of bacterial DNA samples allows for rapid analysis of bacterial communities from many samples at once. However, the utility of these methods is limited for samples with few bacteria, or a low bacterial load, or those with large amounts of DNA from non-bacterial sources, such as a host. Often, both limitations are a problem in analyzing clinical samples. A recent paper proposes a modified preparation protocol to increase sensitivity in samples with intermediate or low bacterial loads. To test a wide range of bacterial loads, the researchers used repeat tracheal aspirate samples from intubated pediatric patients. The modified protocol detected sequence data from over 30% more samples than the standard protocol. Where both protocols had results, they returned similar levels of community diversity, and the composition of those communities was also similar. These results suggest that this protocol modification allows for greater sensitivity without impacting the integrity of the results and could be a viable method for collecting more data about microbiomes in high-background, low-bacteria situations.