Editorial: How Next Generation Sequencing has Transformed Microbial Ecology

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In recent years, biology has steadily become a more interdisciplinary field. Advances in technology have pioneered the development of many tools that allow concepts in physics, math, computer science, and chemistry to be applied to biological problems. As an example, next generation sequencing (NGS) technologies have been rapidly developed with these tools becoming more and more accessible to biologists. NGS is also known as high-throughput sequencing and is an all-inclusive term used to describe modern sequencing technologies including Illumina, 454, Ion torrent, and SOLiD sequencing that can generate billions of reads. With the advent of NGS and big data, many biological quandaries ranging from the microbiome to human population studies can now be explored in ways that were not previously possible.

In this issue, Dr. Lisa Boughner and Dr. Pallavi Singh, winner of the November 2016 Postdoc of the Month, from Michigan State University review the development of genetic tools used to study microorganism isolates progressing from restriction digest- and PCR-based approaches to the more current metagenomics and transcriptomics approaches. Dr. Boughner is a postdoctoral researcher who studies microorganisms that utilize toxic chlorinated dioxin compounds as their sole carbon source. Dr. Singh is a postdoctoral researcher who studies intestinal microbial communities of patients with enteric infections and uses whole genome assembly, genome mapping and comparative genomics to achieve these goals. Prior to the development of NGS technologies, these researchers may not be able to address their research interests in the high throughput and population-level fashion that is possible today.

Historically, microbiologists were limited to studying only cultivatable bacteria. There are approximately 2×10^6 and 4×10^6 total prokaryotic species in the ocean and soil, both of which are widely studied ecosystems in microbial ecology (Curtis *et al.*, 2002). However, current estimates approximate that only 1% of the total microbial population can be cultured (reviewed in (Pham and Kim, 2012)). Thus it is likely that billions of important microbial interactions are missed when only focusing on cultivatable bacteria (Whitman *et al.*, 1998). Accordingly, microbial ecologists have taken advantage of advances in NGS to study microbial communities as a whole; in theory the entire consortium can be evaluated allowing for novel biological processes to come to light.

Aside from the approaches mentioned by Dr. Boughner and Dr. Singh, there are many other developments in high throughput sequencing methodology including those that use microfluidics to sequence microbes on a single cell level. In single-cell sequencing, gene or protein expression levels can be examined within individual cells. One such example is Drop-Seq where individual cells are separated into droplets, RNA from each droplet is uniquely barcoded, and then sequenced en masse (Macosko *et al.*, 2015). Such single-cell experiments allow researchers to ask questions about variability within a population or to examine specific interactions between microbes.

Despite the excitement of NGS, we must not forget the importance of experiments based on bacterial cultivation. Cultivation permits us to genetically manipulate organisms and ask complementary biological questions informed by NGS. Though the launch of NGS technologies makes studying complex microbial communities possible, bacterial cultivation

remains important for verifying conclusions from NGS studies. While cultivation for many microbes is difficult today, NGS could provide insight on how to culture these organisms for the future allowing for the use of novel bacterial cultures in industrial processes or in basic science research.

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