CONSIDER FOR TALK

2025 SEA Symposium Abstract

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Using Oxford Nanopore Technologies (ONT) in the classroom to sequence Arthrobacter and Gordonia phages

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Advances in Oxford Nanopore Technologies (ONT) are transforming course-based undergraduate research experiences (CUREs) by making microbial genome sequencing more accessible. ONT offers a cost-effective and accurate (Q20+ or >99.0% raw reads) long-read DNA sequencing technology that can be used in the classroom for every student or group to sequence an isolate. For this study, eleven phages were isolated from soil using *Arthrobacter globiformis* B-2979 and *Gordonia rubripertincta* NRRL B-16540 as hosts and sequenced with a Nanopore MinION Mk1B using an R10.4.1 flow cell (FLO-MIN114). To assess the accuracy of the Nanopore assemblies, DNA from ten phages was pooled into three samples for Illumina sequencing. Genome sizes ranged from 38,515 bp (Glotell) to 195,163 bp (ReginaGlobina). A pairwise alignment of the Nanopore and Illumina assemblies showed that eight of the ten alignments were 100% identical, while the remaining two were 99.995% identical, differing by only two bp with no gaps. These phages belong to seven distinct clusters or subclusters (AO3, AP2, AS2, AS3, AY, DW, and FC). ONT empowers students to continue to take ownership of their research by sequencing their own isolates in the classroom, leading to the discovery of diverse phages.