

Adaptations to extreme environments can provide insight toward understanding many biochemical functions. Antarctica poses several environmental challenges (e.g., extreme cold, desiccation, high ultraviolet radiation). The purpose of this research is to sequence the genomes of three different environmental isolates of Antarctic bacteria and to learn about the functional characteristics associated with each of these. We completed several microbiology tests for each isolate including gram-staining, catalase testing, physiological profiling of carbon sources, and biofilm formation.

Initial sequencing of the 16S rRNA gene showed that two isolates are very similar to previously described and sequenced bacteria, while the third was marginally similar to bacteria in three different genera but differs morphologically from these groups. Specifically, the closest related genera were *Rugamonas*, *Janthinobacterium*, and *Duganella*, all of which are known for producing various pigments. However, our isolate produces no pigment, even though pigmentation is often protective under high UV exposure.

To learn more about this unknown isolate and the biochemical pathways it possesses, we are sequencing the genome from lab cultures. The Nanopore MinION sequencer is currently being used by undergraduate researchers to sequence the genome, and progress of genomic sequencing will be discussed along with use in a primarily undergraduate institution. Genomic analysis will include identification and annotation of functional genes to inform future pathway analysis and wet-lab functional tests.