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Isolation of bacteriophage from soils that have experienced wildland fires

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Wildland fires kill trees, destroy homes and the heat can easily destroy power cables and data cables buried 2 to 4 feet in the ground. Wildfires not only change the vegetation, but they also change the microbial communities; this includes bacteriophage and their host bacteria. The purpose of this research is to compare the genomes of bacteriophage collected after wildland fires using Arthrobacter globiformis as a host to the genomes of previously isolated bacteriophage. The first aim of this research is to isolate bacteriophages from two different wildland fires that occurred in northwestern Colorado. The second aim was to compare the genome of the bacteriophage collected after the fires to the genome of the bacteriophage from the previously collected bacteriophage. Four soil samples were taken from burned soil by wildland fires. From those soil samples, four bacteriophages were isolated using enriched isolation methods. DNA from these bacteriophages was isolated, sequenced, and assembled. BLAST analysis revealed that those were contaminants and the original bacteriophage had been lost. Two new soil samples were obtained from two wildland fires outside Lyons, CO in October of 2022. One bacteriophage has been successfully isolated and purified from one of the samples, while another one is still being purified. Plaques formed by these two new isolates are small in size (less than 2 mm in diameter), which facilitates spotting any contamination from other phage in our laboratory. DNA has been extracted from these bacteriophages and sent off to North Carolina State University Sequencing Center for genome sequencing.