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Three new Microbacterium foliorum EE cluster phages, Octopus, BoomRoasted, and Aztec

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Microbacteriophages Octopus, BoomRoasted, and Aztec were extracted from host *Microbacterium foliorum* using enriched soil samples obtained from Gonzaga University’s campus in Spokane, Washington. These EE cluster phages were sequenced (Illumina) and annotated using established bioinformatics tools from the SEA-PHAGES program. Aztec with a genome length of 17368bp and 24 protein coding genes (preliminary estimates given for each phage), produced plaques that were round, clear, ranged in size from <1 to 3mm, and was of the siphoviridae morphotype. BoomRoasted was 17455bp in length with 26 protein coding genes with a siphoviridae morphotype; its plaques were also round and clear. Octopus was 17368bp in length with 25 protein coding genes; however, plaques and morphotype for this phage were not available. Octopus and Aztec were found to be 99.98% identical, while Octopus and BoomRoasted were found to be 93.33% in a BLASTn comparison. The current research goal is to resolve functions of proteins, and focus on comparisons of the frame shift tail assembly chaperone protein region, and differences in minor tail protein regions across EE phages. These regions are of interest because they contain substantial sequence diversity based on a preliminary comparison using Phamerator.