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Annotation of Phage McGalleon from Subcluster EA1 in Microbacterium foliorum

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This project highlights the genome annotation of the siphoviridae bacteriophage McGalleon (MG). McGalleon is a lytic phage isolated using *Microbacterium foliorum*, and is a member of cluster EA, subcluster EA1. McGalleon has a genome length of 42,562 bp, and a 63.70%, currently the longest genome of the EA cluster and the highest GC% of the subcluster. Annotation utilized the bioinformatics tools DNAMaster, Glimmer, Genemark, PhagesDB BLAST, NCBI BLAST, HHPred, and Phamerator. Of the 65 genes identified through auto-annotation, three genes were deleted due to lack of coding potential. Analysis supported assigning functions to 26 of the 62 annotated genes, and two previously unidentified regions were discovered during manual annotation: MG\_2 and MG\_52. MG\_2 is an insertion near the beginning of the genome. MG\_52 is located where two genes were predicted to be, based on their presence in most phage in the subcluster. However, MG\_52 lacks similarity to either of the missing genes normally found in the region surrounding MG\_52. McGalleon is missing a gene predicted to have phosphoesterase activity, which is found in 51 of 64 phage from EA1.