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Annotation of Microbacterium Phage MrWorldwide, a Member of the EA1 Subcluster

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Bacteriophages are the most numerous microbes in the biome and display massive genetic diversity. Microbacterium Phage MrWorldwide is capable of replication in *Microbacterium foliorum NRRL B-24224* and was isolated without enrichment in Philadelphia, PA by Kayla Sweeny and Will Grillo at The University of Sciences in Philadelphia. MrWorldwide was sequenced by the Pittsburgh Bacteriophage Institute and its sequence revealed that it is a novel bacteriophage. MrWorldwide has a circular permuted genome that is 41,810 bp in length and has a GC content of 63.6%. The genome lacks any lysogeny-associated genes which is consistent with other members of the EA1 subcluster.