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The Remarkably Homogenous EA2 Subcluster of Microbacterium foliorum Phages

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The EA2 subcluster of bacteriophages is notable because of how remarkably similar the eight members of the subcluster are. Considering they were isolated from various locations around the nation from the Carolinas, Texas, and Maryland to Utah, this homogeneity is remarkable. All members of this subcluster infect Microbacterium foliorum. In this subcluster, the GC percentage is ~62%. The length of all eight genomes is within the range of 40224bp to 40494bp meaning that the maximum difference is less than 300 base pairs. There are no orphams in any of the members of the subcluster. Following the established pattern for EA bacteriophages all members of the EA2 subcluster have genes going in a left direction and the other oriented right. On the rightward genes, they are the same with only minor differences detected in the tape measure protein. While the homogeneity of the members of this subcluster is striking, they are not identical. It is the reverse-oriented genes where the few small differences between the members are found. These differences include the absence of a gene in Mcubed and Saratos which is found in the other members of the subcluster. Some variations in the nucleotide sequences between noncoding regions was also detected, and Sansa contained a gene belonging to pham number 18734 that is not present in any other EA2 subcluster bacteriophage genome. Despite these few differences the members of the EA2 subcluster are remarkably similar which is astounding for bacteriophages separated by incredible geographical differences and isolated in different climates and soil types.