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Interesting Genes in Moleficent, a New EK2 Subcluster Phage of Microbacterium foliorum

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Students in Miami University's MBI (Microbiology) 223 class in Fall 2022 isolated phages that infect Microbacterium foliorum. Two were selected for sequencing analysis, but only one yielded any sequence data. Moleficent, a podovirus in subcluster EK2, was subjected to analysis the subsequent semester in MBI 224 using the conventional SEA-PHAGES tools. At 54,452 base pairs with a total of 56 genes (preliminarily), its genome size is typical of subcluster EK2, as is its gene content. Like related phages, its genome appears to be divided into two replichore-like elements, the "left" component with genes on the bottom strand, and the "right" portion, which includes the capsomere-encoding genes, on the top strand. Gene 22, according to both Phamerator and BLAST, a gene of unknown function, is particularly divergent in sequence. Only a section of 36 out of 66 encoded amino acids aligned above DNA Master's default BLAST threshold level with the corresponding gene in only one other phage, Pabst. Other EK2 genomes have genes of a variety of sizes at this position, suggesting that this gene might be particularly important for adaptation. The amino acid sequence encoded by gene 45, which lies amid structural genes but whose homologs in other phages have no assigned functions, has high-probability HHpred hits to a variety of proteins with capsid-associated functions. It is likely that this gene encodes a capsid protein, but difficult to discern its role. Although subcluster EK2 phages are largely similar to one another, variations in a few genes might suggest new functions and alternative mechanisms of adaptation.