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Two new Microbacterium foliorum bacteriophages, Belthelas (EE) and Lupine (ED1)

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In Miami University's first efforts at discovering phages that infect Microbacterium foliorum, 10 students out of 20 successfully isolated phages from samples of soil and leafy organisms. All 10 phages had morphology typical of Siphoviridae. Two lytic phages, Belthelas and Lupine, were submitted for genome sequencing and subjected to annotation. In agreement with predictions from DNA analysis, Belthelas was found to be a cluster EE phage with a typical small genome of 17,502 bp and 25 predicted genes. The gene content, more or less identical to most other cluster EE phages, confirms the low diversity within this phylogenetic cluster, which is well-represented in the Actinobacteriophage Database. Lupine, in contrast, was a member of the much less commonly described subcluster ED1, with a genome of 62,533 bp. Preliminary annotation suggests approximately 110 genes plus 7 present in a second copy on the 3,260-bp terminal repeat region of the linearized genome. Analysis of these genes suggests substantial diversity within subcluster ED1, with an assortment of genes not assigned to any pham and some others that, although assigned to phams, have no BLAST hits above the threshold of significance. None of these novel genes could be assigned likely functions. We conclude that whereas the phages of cluster EE, frequently encountered and bearing low diversity, have arrived at a highly successful strategy for propagation, the highly diverse phages of subcluster ED1 are rather dynamic in terms of evolution.