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Orono ME

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Pharb song: you’re K3, you’re lysogenic, and you’re plain.

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Opportunistic Mycobacterium abscessus infections are increasingly dangerous in the United States due to multi- or total-drug resistance. Long-term mortality from nontuberculous mycobacterial (NTM) pulmonary disease is as high as 50% over 15 years. Bacteriophages, viruses that exclusively infect bacterial hosts, offer promising new opportunities to combat antibiotic resistance. However, for phage therapy to be a viable option, novel phages must be isolated and characterized. Novel Mycobacterium phage, Pharb, was isolated from a soil sample taken in Orono, ME. Pharb is a temperate, cluster K3 mycobacteriophage belonging to the Siphoviridae family. The genome length, 60,827 bp, is the shortest of cluster K3 phages and has a 67.3% GC content. It encodes 95 protein-coding genes and no tRNA genes. Pharb’s host range was tested on NTMs, including M. chelonae, M. abscessus, M. marinum, and M. salmoniphilum strains. While other cluster K3 phages are known to infect pathogenic mycobacteria, Pharb only infected the isolation strain, M. smegmatis. Differences in minor tail proteins may play a critical role in host specificity. Pharb\_26, a minor tail protein, differs in protein sequence at the C-terminal end compared to Keshu and Shedlockholmes, two cluster K3 phages with broad host ranges. Pharb’s genome is the only cluster K3 genome missing Pham 4511, a small gene within the minor tail proteins of cluster K2, K3, K6, and A3 genomes. Pharb’s host range should be tested on other strains of Mycobacteria.