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Discovery of a recently described mobile element in novel Mycobacteriophage Camri

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Mycobacteriophages are genetically diverse viruses that infect bacteria in the Mycobacterium genus, which includes both *Mycobacterium tuberculosis* and *M. smegmatis*. Due to the continued increase of antibiotic resistance, researchers across the globe are revisiting old practices, such as phage therapy, to treat pathogenic bacterial infections. Understanding bacteriophage genetics is crucial in the development of these phage therapy treatments. The precise functions of the genes must be known in order to select the best phages to target each strain of bacteria. The aim of the SEA-PHAGES program is to discover and characterize novel bacteriophages using basic laboratory techniques and bioinformatic analyses to determine gene functions and find novel features within each genome. The goal of this project was to annotate the genome of novel bacteriophage Camri. Camri belongs to the G1 Subcluster and contains a unique genetic element only recently discovered in a small number of mycobacteriophages. Camri’s genome contains a transposable element, better known as an ultra-small Mycobacteriophage Mobile Element (MPME), in the latter section where recombination typically occurs. The MPME in Camri’s genome is relatively small in length and matches the MPME1 subcategory described in related phages. At this time, not much is known as to how these MPMEs specifically affect mycobacteriophage genomes, but they have been shown to alter gene regulation and expression in other organisms.