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Q Cluster Mycobacteriophage, Gancho, shares high genome similarity to Mycobacterium vulneris, most notably in RecET-like genes, implying lateral gene transfer through the RecET recombination pathway

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Bacteriophage are viruses that infect bacteria. These entities are highly diverse and can be grouped into clusters based on genome identity. Phage genomes exhibit mosaicism, having acquired an array of genes through lateral gene transfer between host or other phage genomes. The Q cluster mycobacteriophage, Gancho, contains 54,250 base pairs with 86 genes, many with unknown functions. The Gancho genome contains a RecET recombination system, shared among all of the Q cluster phages, and found to be essential in Giles, a closely related Q mycobacteriophage. Further analysis reveals 63% of the entire Gancho genome shares significant similarity to genes in *Mycobacterium vulneris*, a subset of the *Mycobacterium avium* complex. This suggests an expanded host range for Gancho with the RecET recombination system potentially playing an essential role in acquiring those genes via lateral gene transfer.