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No lysogeny here: the strictly lytic lifestyle of bacteriophage Horseradish

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Bacteriophages are the most abundant biological entities, with an estimated 1031 phages in the world. Research on bacteriophages provides insight into the biology of viruses and their bacterial hosts and opportunities for applications in human health, bioremediation and biotechnology. Bacteriophage Horseradish was isolated from composted soil collected from Roger’s Farm at the University of Maine, Orono, ME using an enrichment technique with the actinobacterial host Gordonia terrae 3612. Horseradish has a strictly lytic lifestyle and belongs to cluster CT. Its genome is 45,764 bp in length, has a GC content of 60%, and encodes 71 predicted protein coding genes. Beginning with the small and large terminase subunits (gp1 and gp4), the left arm encodes forward-transcribed structural and assembly genes (gp1 to gp28). The right arm of the genome encodes mainly reverse-oriented genes (gp29 to gp32 and gp36 to gp58), which are disrupted by three forward-transcribed genes, gp33 to gp35, including a MerR-like helix-turn-helix DNA binding domain gp33, and followed by twelve forward-transcribed genes (gp59 to gp71). The genome lacks genes required for lysogeny, such as an integrase and an immunity repressor. Future research steps involve testing the host range of Horseradish on other species of bacteria.