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Outis: The Serial Bacterial Killer

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According to the CDC, 2.8 million antibiotic resistant infections occur each year. In recent years, the Actinobacteria, which includes the *Mycobacteria* that are responsible for serious human infections, have shown an alarming prevalence of antibiotic resistance. Bacteriophage (phage), viruses that infect bacteria, are a promising research front as a potential solution, because of their ability to lyse host bacteria. By studying Actinobacteriophage and their genomes, we learn about how they interact with their host, which can be applied to applications such as phage therapy. The recently identified phage, Outis, was isolated in Orono, Maine on the Actinobacteria host *Gordonia terrae* through enriched isolation. Genome sequencing of Outis revealed it belongs to cluster CR2 and is a lytic phage. The genome has 68,128 nucleotides that encodes no tRNAs and 94 protein-coding genes including 4 orphams and a HicA-like Toxin. Electron microscopy indicated a Siphoviridae morphology. Analysis of lytic phage like Outis brings opportunities to learn more about lytic phage and potentially discover antibacterial genes to improve the development of alternative treatments to bacterial infections.