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# A STRUCTURAL AND GENOMIC INVESTIGATION OF NOVEL BACTERIOPHAGE KROMP

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The novel bacteriophage Kromp was isolated from a sample of rotting moss as part of the SEA Phages undergraduate research program. The sample was collected on September 4, 2017 in Forest Park, at 38.6409 °N, 90.2992 °W. It was then enriched in a bacterial broth before initial plating in a *Streptomyces lividans* bacterial lawn; after several rounds of purification, a high-titer lysate of  $1.0 \times 10^{11}$  plaque forming units (pfu)/mL was produced. Kromp creates an atypical plaque morphology in which surviving bacterial cells populate cloudy plaques and produce red pigmentation. Through electron microscopy, Kromp was determined to have a head with an average width of 66 nm and height of 63 nm, and a tail length of 230 nm. Many of its outward characteristics, such as its small, icosahedral head and long, striated tail, are prototypical of *Streptomyces* phages; however, Kromp also expresses a number of unique qualities that make it a bioinformatically interesting topic of study. The Kromp genome is 58268 base pairs in size and contains 96 protein-coding genes, a single tRNA-coding gene, and an unusually high GC content of 71.4%. Certain areas of the genome possess previously unobserved qualities, such as gene cluster 65-67, where evidence suggests that there are fully overlapping genes in multiple reading frames. Gene 17 spans an open reading frame (ORF) of 4815 bp, comprising 8.3% of Kromp's total genome size, making it nearly three times as long as the second-largest Kromp gene. Studying the genomic characteristics of novel bacteriophage such as Kromp contributes to a deeper understanding of phage genetic diversity, evolution, and functionality.