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Isolation and genome annotation of the novel actinobacterial phage Eddiemania.

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Bacteriophages are the most abundant lifeforms on Earth with an estimated population of 1031 - 1034 virions. With this practically limitless biodiversity, phages have a vast range of potential in numerous applications including bioremediation, food safety, biocontrol, and treatment of antimicrobial resistant bacterial infections. These viruses tend to have a narrow host range and infect only one type of bacterial species, necessitating the creation of vast phage libraries to fully exploit their potential. To this end, Eddiemania was discovered by utilizing the actinobacterial host Gordonia rubripertincta NRRL B-16540, from a soil sample obtained in Southern Nevada. After purifying, amplifying, and electron microscopy, Eddiemania was shown to be a Siphoviridae forming small, clear, plaques consistent with a lytic replication strategy. The genome was extracted, sequenced, and annotated using the bioinformatics tools: DNA Master, Starterator, Phamerator, GeneMark, Blast, HHpred, ExPASY, and TMHMM. Eddiemania contains only forward reading frames and has a genome length of 61,427 base pairs with a 51.6% GC content, consistent with the DJ cluster’s average of 51.5%. In total, there were 91 genes with no genes novel to the DJ cluster. Additionally, no tRNA’s or frameshifts were found. Bacteriophage discovery has the potential to solve a wide variety of practical problems, ranging from antibiotic resistance to food biosecurity. As contributions such as this to the phage database continues to grow said database, so too does our understanding of how phages function and how we can apply them.