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2021 SEA Symposium Abstract

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Genome sequence of cluster A6 phage Hoot and cluster G1 phage Jolene, from Las Vegas, Nevada

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The Phage Discovery course at the University of Nevada Las Vegas is currently in its fourth year. This year, phages were isolated from the UNLV Community Gardens. As in previous years, Mycobacterium smegmatis mc2 155 was used as the host. Nine phages were isolated, two of which were sequenced. Here, we report on the genomes of the sequenced phages, Hoot and Jolene. Hoot is a cluster A6 phage; its genome is 50,006 bp long, with 98 genes, of which 3 are tRNA genes. Jolene placed in cluster G1; its genome is 32,305 bp long, with 63 genes. About half of the genes in both phages had predicted function. The genomes were annotated with a novel in-house app named Phage Commander, which greatly facilitated the annotation process.