

Complete Genome Sequence of the *Streptomyces* Phage Nanodon

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***Streptomyces* phage Nanodon is a temperate double-stranded DNA *Siphoviridae* belonging to cluster BD1. It was isolated from soil collected in Kilauea, HI, using *Streptomyces griseus* subsp. *griseus* as a host.**

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Streptomyces spp. are Gram-positive, filamentous, and spore-forming members of the *Actinomycetaceae* family, from which two-thirds of antibiotics have been derived (1). Here, we present the genome of the double-stranded DNA bacteriophage Nanodon, a *Siphoviridae* isolated from volcanic soil collected in Kilauea, HI (22°10'28.6"N 159°26'08.3"W), which was then harvested and investigated using *Streptomyces griseus* subsp. *griseus* (ATCC 10137) (*S. griseus*) as a host by University of Maryland, Baltimore County (UMBC) undergraduate researchers, as described previously (2).

Nanodon produced variably sized clear plaques when incubated for 48 h on lawns of *S. griseus* grown on supplemented nutrient agar at 30°C (3). Nanodon has an icosahedral capsid ($d = 46$ nm) with a flexible noncontractile tail ($l = 151$ nm). Shotgun sequencing was carried out by the Pittsburgh Bacteriophage Institute to approximately 1,201-fold coverage by Illumina sequencing. Nanodon has a linear 50,082-bp genome with an 11-bp 3' sticky overhang and a 65.7% G+C content. Genomic analysis of Nanodon determined that the phage contains 75 protein-coding genes, of which 25 have been assigned predicted functions. Among these were both a serine integrase and an immunity repressor, suggesting that Nanodon is a temperate phage (4, 5).

Genomic comparison of Nanodon with the 69 *Streptomyces* phages sequenced to date by SEA-PHAGES participants (2) identified Nanodon as a member of cluster BD, one of nine established *Streptomyces* phage clusters (<http://phagesdb.org/>) and, specifically, as a member of subcluster BD1. Nanodon shares $84.4\% \pm 0.02\%$ average \pm standard deviation (SD) nucleotide identity (ANI) with other members of subcluster BD1 available in GenBank, and $71.5\% \pm 0.02\%$ ANI with phages in the other four current BD subclusters (6). A comparison of Nanodon by whole-genome alignment (7) and phylogenetic analysis using the terminase gene also demonstrated that Nanodon clusters with other members of the BD1 subcluster.

Codon usage bias (CUB) analysis using the *scnRCA* program (8) and reference sets derived from several *Firmicutes* and *Actinobacteria* genomes revealed that protein-coding sequences in the Nanodon genome are adapted for translational optimization on *Streptomyces* hosts, with capsid and tail assembly proteins showing the highest level of codon optimization. However, CUB patterns

revealed no specific optimization for *S. griseus* compared to other *Streptomyces* species, suggesting that Nanodon might have broad-range specificity within the *Streptomyces*, as seen previously for other temperate *Streptomyces* phages (9, 10).

Accession number(s). The complete genome sequence of the *Streptomyces* phage Nanodon is available in GenBank with the accession no. [KX344445](https://www.ncbi.nlm.nih.gov/nuclot/KX344445).

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The members of the 2015 UMBC Phage Hunters class are listed at <http://phages.umbc.edu/home/class-lists/2015-16/>.

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