

# Genome Sequence of *Gordonia* Phage Yvonnetastic

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***Gordonia* bacteriophage Yvonnetastic was isolated from soil in Pittsburgh, PA, using *Gordonia terrae* 3612 as a host. Yvonnetastic has siphoviral morphology and a genome of 98,136 bp, with 198 predicted protein-coding genes and five tRNA genes. Yvonnetastic does not share substantial sequence similarity with other sequenced bacteriophage genomes.**

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*Gordonia* spp. are implicated in foaming of wastewater in treatment plants (1–3) and are associated with opportunistic infections in hospital catheters (4, 5). Seventeen bacteriophages of *Gordonia* have been isolated, sequenced, and deposited in GenBank (6–9), and although these represent several different genome types, it is unclear whether the overall genomic diversity of the *Gordonia* phage population is similar to that reported for mycobacteriophages (10–15). The Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science (SEA-PHAGES) is a course-based research experience in which undergraduates perform authentic research through isolation and characterization of viruses using hosts of the phylum *Actinobacteria*, and it provides an opportunity for isolation and characterization of *Gordonia* phages (16).

Yvonnetastic was isolated from soil through direct plating of a filtered soil extract on lawns of *Gordonia terrae* 3612. Its morphology is siphoviral, with an isometric head and a tail of 400 nm in length. After purification and amplification, DNA was extracted and sequenced using an Illumina MiSeq platform with 140-bp single-end reads. Reads were assembled using Newbler into one major contig of 98,136 bp with discrete ends and 10-base single-stranded 3' extensions with the sequence 5'-CGCGAAGCTC. Protein-coding genes were predicted using Glimmer (17), GeneMark (18), DNA Master, and Phamerator (19), and tRNAs were predicted using Aragorn version 1.3 (20); functional assignments were made using BLAST (21) and HHpred (22) against the publically available databases GenBank, the Protein Database, and pFamA. Yvonnetastic's genome has 59.7% G+C content, somewhat lower than that of its host (67.8%), and it contains 198 predicted protein-coding genes and five tRNA genes. Functional assignments were made to 42 (21%) of the protein-coding genes. The majority of the Yvonnetastic genes are transcribed left to right, with the exception of genes in the leftmost 3 kbp and rightmost 10 kbp of the genome.

Yvonnetastic shows little similarity to currently sequenced phage genomes in its nucleotide sequence, and of the 198 pre-

dicted protein-coding gene products, <50% have amino acid similarity to genes encoded in ~1,500 sequenced phages of actinobacterial hosts. Those that do primarily match gene products encoded in other *Gordonia* phages and in mycobacteriophages. Among the putative predicted gene functions are the virion structure and assembly proteins, two glycosyltransferases, five HNH endonucleases, a RecET recombination system, an endonuclease VII, and an exonuclease VII.

The Yvonnetastic genome is unusual in that a lysis cassette including L-alanyl-D-glutamate peptidase, glycoside hydrolase, and holin genes is located amid the minor tail protein genes, and a putative lysin B gene is located near the right end of the genome, separated by >50 kbp from the other lysis genes. We also note that the putative integrase gene (95) is embedded within a long operon of closely linked rightwards-transcribed genes, and we have not been able to identify a putative *attP* site or predict a chromosomal *attB* site for phage integration. We have also been unable to identify putative immunity repressor gene, and the only predicted regulatory protein is the 67-residue gp109, which contains a predicted helix-turn-helix DNA binding motif.

**Nucleotide sequence accession number.** The Yvonnetastic genome is available from GenBank under the accession no. [KU963248](https://www.ncbi.nlm.nih.gov/nuclot/KU963248).

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