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GENOME ANNOUNCEMENT

Genome Sequence of a Novel Actinophage PIS136 Isolated from a Strain of *Saccharomonospora* sp.

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A wide-host-range bacteriophage (phage) PIS136 was isolated from PA136, a strain of *Saccharomonospora* belonging to the group actinomycetes. Here, we present the genome sequence of the PIS136 phage, which is 94,870 bp long and contains 132 putative coding sequences and one tRNA gene. An IS element-like region with two genes for putative transposases was identified in the genome. The presence of IS element-like sequences suggests that PIS136 is still under active evolution.

Bacteriophages are the most abundant entities in any environment and can control the ecology of the system. However, their physical presence is difficult to ascertain unless a suitable host is found. A *Saccharomonospora* strain, PA136, was purified from a garden soil sample that produced diffusible green pigment. In tryptic soya agar/broth (TSA/TSB) medium, the PA136 strain underwent autolysis after 4 to 5 days of incubation at 30°C. A phage was purified from the lysate by the methods of Sambrook et al. (3). Electron microscopy of the cesium chloride-purified preparation showed the presence of a bacteriophage with a hexagonal icosahedral head and a long striated tail with tail fiber and was named PIS136. PIS136 has a wide host range within actinomycetes and a member of the family *Siphoviridae*. Initial characterization of the genome showed that PIS136 has a relatively large genome composed of GC-rich double-stranded circular DNA.

In the past, phages have been purified from thermophilic species of *Saccharomonospora* and were characterized by restriction analysis to show the differences between phages (4). However, the genome sequence of any of those phages or any other *Saccharomonospora* phage is not available. We report the genome sequence of this novel phage, PIS136. Genomic DNA was purified from the cesium chloride gradient-purified phage by the method of Sambrook et al. (3). The genome was sequenced using Illumina, which produced reads of 54 bases where the total number of reads was 23,034,944 with a *phred* score of >20. The total number of high-quality reads was 22,552,635, and the total number of high-quality bases was 1.24E+09. Sequence was assembled using a *De novo* assembly tool velvet_1.1.02, with a hash length of 35 to 71; the minimum contig length was 100, and an autocoverage cutoff was used. Randomly selected regions of the single contig were amplified by PCR to validate the assembly. The PIS136 genome is 94,870 bp long with a GC content of 65.88%. The open reading frames (ORFs) were predicted using FGENESV (SoftBerry, Inc., Mount Kisco, NY) and GeneMark (1). After manual curation, a total of 132 ORFs (61 ORFs on the positive strand and 71 on the negative strand) were annotated by using homology search at the nonredundant protein database of GenBank and Conserved Domain Database (NCBI). A single tRNA for cysteine was predicted by tRNAscan-SE (2).

Sequence analysis showed the presence of DNA polymerase, helicase, HNH endonuclease, DNA segregation ATPase, terminase, and many glycoproteins. The genome has four ORFs encoding putative transposases, where two of them are part of a region showing high homology to IS element IST*fu1* belonging to IS*200*/IS*605* from *Thermobifida fusca*. The presence of IS element-like sequences suggests that PIS136 is still under active evolution. To the best of our knowledge, this is a first report about the genome sequence of a phage from any species of *Saccharomonospora*.

Nucleotide sequence accession number. The draft sequence has been submitted to GenBank under accession number JX006077.

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