Using PcyII-10, a clinical strain of *Pseudomonas aeruginosa*, as the host strain, two virulent bacteriophages were isolated in Orsay, France, in the year 2014. Phage vB_PaeP_PcyII-10_P3P1 (P3P1) was found in compost and produced large clear plaques, whereas phage vB_PaeM_PcyII-10_PII10A (PII10A) was isolated from wastewater and formed small clear plaques. PII10A and P3P1 could be propagated on nine and 10, respectively, out of 27 tested clinical strains representative of the *P. aeruginosa* diversity (1). They were not capable of forming plaques on three different mutants of the lipopolysaccharide (LPS) biosynthesis pathway (2). The morphology of phage virions was determined using transmission electron microscopy (TEM). TEM was performed at 80 kV in JEM-100B (JEOL) with use of negative contrast with 1% uranyl acetate. P3P1 showed a 74 ± 0.6-nm icosahedral capsid with a short tail, characteristic of *Podoviridae*, and PII10A showed a 70 ± 1-nm head and a 130 ± 3-nm nonflexible contractile tail characteristic of *Myoviridae*.

Phage DNA was sequenced in an Illumina MiSeq 300-bp paired-end run with a 900-bp insert library produced by mechanical shearing at the IMAGIF Sequencing facility. Quality-controlled trimmed reads were assembled, using Geneious R9, to a single linear contig at mean coverages of 2,932-fold for P3P1 and 2,447-fold for PII10A. The P3P1 genome was 72,778 bp long, with a G+C content of 56%. A 671-bp direct repeat was found at position 42576 in an intergenic region upstream of the Lit1virus genus of the *Pbunavirus* family. Their genomes are 72,778 bp and 65,712 bp long, containing 94 and 93 predicted open reading frames, respectively.

Complete Genome Sequences of *Pseudomonas aeruginosa* Phages vB_PaeP_PcyII-10_P3P1 and vB_PaeM_PcyII-10_PII10A

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vB_PaeP_PcyII-10_P3P1 and vB_PaeM_PcyII-10_PII10A are *Pseudomonas aeruginosa* bacteriophages belonging, respectively, to the Lit1virus genus of the *Podoviridae* family and the *Pbunavirus* genus of the *Myoviridae* family. Their genomes are 72,778 bp and 65,712 bp long, containing 94 and 93 predicted open reading frames, respectively.
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