Streptomyces coelicolor is a model system for the study of Streptomyces, a genus of bacteria responsible for the production of many clinically important antibiotics. Here we report the genome sequence of φCAM, a new S. coelicolor generalized transducing bacteriophage, isolated from a soil sample originating from Lincolnshire, United Kingdom. Many open reading frames within φCAM shared high levels of similarity to a prophage from Salinispora tropica and a putative prophage in Streptomyces sp. strain C.

Streptomyces coelicolor, a Gram-positive bacterium, has been isolated from soil samples around the world, and it is a model organism for the study of bacterial differentiation, glycopeptide resistance, and secondary metabolite production (3, 4). The genus Streptomyces is also notable, as many of its species produce useful antibiotics, such as chloramphenicol (S. venezuelae) and neomycin (S. fradiae) (4). Other streptomycetes cause agriculturally important plant infections (S. scabies) and produce antifungal compounds, such as amphotericin B (S. nodosus).

The S. coelicolor bacteriophage φC31 is the most widely studied streptomycte phage, and its genome sequence has been reported (7). Other bacteriophages infecting S. coelicolor have been reported, although to date, no transducing phage for S. coelicolor has been sequenced. Here we report the sequence of the S. coelicolor generalized transducing phage, φCAM. φCAM was isolated from an enriched soil sample from Lincolnshire, United Kingdom. Its complete genome sequence was determined using a combination of 454 and Sanger sequencing (Department of Biochemistry, DNA Sequencing Facility, University of Cambridge). Putative open reading frames (ORFs) within φCAM were identified manually and confirmed by comparison with all other predicted ORFs within NCBI by PSI-BLAST (1). Any conserved protein domains were identified using the NCBI Conserved Domain Database and Pfam (6). The φCAM genome was scanned for putative tRNAs using tRNAscan-SE, but no putative tRNAs were identified (5).

The sequence of φCAM is 50,348 bp in length and contains 72 putative ORFs. The G+C content (65.59%) of φCAM was similar to the well-characterized S. coelicolor phage φC31 (G+C content, 63.8%), though notably different from S. coelicolor (G+C content, 72.1%) (2, 7). Many of the putative ORFs within φCAM were highly similar to those found in prophage I from the marine bacterium Salinispora tropica and a putative prophage from Streptomyces sp. strain C, an uncharacterized strain isolated from a Chinese soil sample (8). Salinispora tropica, like S. coelicolor, is a member of the order Actinomycetales and is a prolific producer of secondary metabolites. However, these bacteria are primarily found in two different niches: S. tropica is found in water, and S. coelicolor is found in soil.

Though 19 putative ORFs in prophage I of S. tropica and φCAM were similar, the integrase from prophage I was not found in φCAM. Furthermore, the putative endolysin and holin found in φCAM shared high levels of similarity with well-characterized proteins from other Streptomyces phages, such as φC31 and φBT1, but were not identified within prophage I (7). Despite the similarity of most φCAM ORFs with other phage proteins, many of their functions could not be predicted. However, the genomic sequence of φCAM will assist in the study of S. coelicolor and also aid our understanding of the role played by bacteriophages in the genomic evolution of Actinomycetes.

Nucleotide sequence accession number. The genome sequence of φCAM has been deposited in GenBank under the accession number JX889246.

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