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GENOME ANNOUNCEMENT

Genome Sequence of a New *Streptomyces coelicolor* Generalized Transducing Bacteriophage, ϕCAM

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***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 streptomycete 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 *Acintomycetales* 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 ϕBTI, 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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We declare that we have no competing conflicts of interest.

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