

PROPOSAL Prokaryote SC
New Genus 'φC31-like viruses'

- 2002.136B.02** to establish a new Genus, within the Family *Siphoviridae*, Order *Caudovirales*
- 2002.137B.02** to provisionally call this new genus 'φC31-like viruses'
- 2002.138B.02** to designate *Streptomyces bacteriophage φC31* (*φC31*) as the Type Species of the new Genus.
- 2002.139B.02** to designate *Streptomyces* phage φBT1, *Streptomyces* phage TG1, *Streptomyces* phage SEA, *Streptomyces* phage R4, *Streptomyces* phage VP5, *Streptomyces* phage RP2, and *Streptomyces* phage RP3 as Tentative Species of the new Genus.

Rationale

φC31 is probably the best studied virus infecting *Streptomyces*. Extensive genetic and biochemical studies over many years have established the major features of its temperate life style, including a complex and unique mechanism and organization of prophage repression. Recent determination of the genome sequence has significantly increased understanding of both general and specific features of the life style and established clear differences from the established Genera.

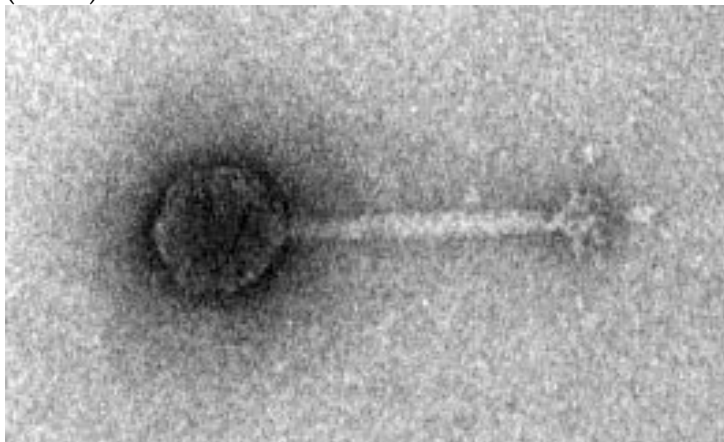
Distinguishing features

Phage DNA has cos ends, codes for a type A DNA polymerase and has a serine site-specific recombinase

Virion Properties

Morphology

Virions have isometric heads of about 53 nm in diameter and flexible tails of 100 nm long and 5 nm wide, a base plate of 15 nm (4) and 4 tail fibres with terminal knobs ('toes').



Physicochemical and physical properties

Bouyant density is 1.493g/cm³ (4). Chloroform sensitive.

Nucleic Acid

Genomes are about 43 kbp in size. Two genomes have been completely sequenced ϕ C31 and ϕ BT1 and are 41491 and 41832 bp respectively. G+C content is 63.6%.

Proteins

Virions contain 10 structural proteins, visible by Coomassie staining Mr approx 10 – 70 kDa.

Lipids

Not known

Carbohydrates

Not known

Genome organisation and replication

The genetic map is linear and related genes cluster together. The genome encodes 54 genes (ϕ C31) and has cohesive ends with 10 nucleotides protruding at the 3' end. Transcription of all except one gene is rightward. One tRNA gene is encoded. Mode of replication is unknown but contains a DNA polymerase, a phage P4-like primase-helicase, a D29 like dCMP deaminase and a T4-like nucleotide kinase. Head assembly genes most closely resemble those of *Pseudomonas* phage D3 and Enterobacteriophage HK97. Putative tail fibre gene contains collagen motif. Lytic growth occurs via transcription from multiple conserved promoters in the early region and a single operon in the late region. Repressor gene encodes three nested N-terminally different inframe proteins which bind to multiple highly conserved operators (6). The integrase belongs to the serine recombinase family of site-specific recombinases (5).

Biological properties

Phages are temperate and are specific for *Streptomyces* sp. Prophages integrate at specific site in the host genome and are not UV inducible. Phages homoimmune to ϕ C31 are susceptible to phage resistance mechanism (Pgl; phage growth limitation) in *S. coelicolor* A3(2) (2). Lytic growth switches off host transcription (1).

Species in the Genus

Streptomyces phage ϕ C31 [AJ006589]

Tentative species in the genus:

Streptomyces phage ϕ BT1

Streptomyces phage TG1

Streptomyces phage SEA

Streptomyces phage R4

Streptomyces phage VP5

Streptomyces phage RP2

Streptomyces phage RP3

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2. **Laity, C., K. F. Chater, C. G. Lewis, and M. J. Buttner** 1993. Genetic analysis of the phic31-specific phage growth limitation (Pgl) system of *Streptomyces coelicolor* A3(2). *Molecular Microbiology*. **7**:329-336.
3. **Smith, M. C. M., R. N. Burns, S. E. Wilson, and M. A. Gregory** 1999. The complete genome sequence of the *Streptomyces* temperate phage phi C31: evolutionary relationships to other viruses *Nucleic Acids Research*. **27**:2145-2155.
4. **Suarez, J. E., J. L. Caso, A. Rodriguez, and C. Hardisson** 1984. Structural characteristics of the *Streptomyces* bacteriophage phiC31 *FEMS Microbiol Letts*. **22**:113-117.
5. **Thorpe, H. M., and M. C. M. Smith** 1998. In vitro site-specific integration of bacteriophage DNA catalyzed by a recombinase of the resolvase/invertase family *Proc. Natl. Acad. Sci. USA*. **95**:5505-5510.
6. **Wilson, S. E., C. J. Ingham, I. S. Hunter, and M. C. M. Smith** 1995. Control of lytic development in the *Streptomyces* temperate phage phi-c31 *Molecular Microbiology*. **16**:131-143.