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 \( \phi \)C31 and \( \phi \)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 (\( \phi \)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 phiC31 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 \( \phi \)C31 [AJ006589]

Tentative species in the genus:
Streptomyces phage \( \phi \)BT1
Streptomyces phage TG1
Streptomyces phage SEA
Streptomyces phage R4
Streptomyces phage VP5
Streptomyces phage RP2
Streptomyces phage RP3


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.

