

Table 39-1. Properties of *Streptomyces* and *Saccharopolyspora* phages

Phage	Isolation host	Genome Size	% G+C	DNA ends	Phage-phage relationship	Phage-host interactions	Application	Reference
φC31 φC43 φC62 φBT1 φSEA	<i>S. lividans</i> 66 Broad host range	All around 41.5 kbp	63.6	Cohesive	All in the same immunity group. Similar at the DNA sequence level, but with additional DNA in some genomes and evidence of mosaicism. φC31 DNA cross-hybridises to that of TG1. TG1 & φA7 have similar genome organisation to φC31 & φBT1.	Temperate. φC31 anti-modification in <i>S. albus</i> . Sensitive to Pgl, Inhibits host rRNA synthesis in lytic growth. Receptor probably a glycoprotein.	Cloning & integration vectors; plasmid transduction	(17, 21, 23, 57, 65, 86, 87, 92)
TG1	<i>S. cattleya</i> Broad host range	41		Cohesive	Related to φC31 by DNA hybridisation, cross-reactivity with antisera and similar genome organisation.	Temperate	Phagemids; accommodate 8.5 kbp.	(33, 34)
φA7	<i>S. antibioticus</i> Broad host range	46.7		Cohesive	Similar genome organisation to φC31, φBT1 and TG1.	Temperate		(31, 32)
φA2, φA4, φA9	<i>S. antibioticus</i> Broad host range	43 49 53		Cohesive	Cross-hybridise with each other.	φA2 avoids <i>SalP1</i> restriction. φA4 avoids <i>Sac</i> restriction.		(32)
φHAU3	<i>S. hygrosopicus</i> Broad host range	51	66	Cohesive	-	Temperate. <i>S. lividans</i> resistance to φHAU3 is due to Ea59-like endonuclease	Phagemids	(107, 108)
φA5, φA6	<i>S. antibioticus</i> Fairly broad host range.	-		Terminally redundant	Cross-hybridise strongly to each other and faintly to φA8.	Temperate		(32)
R4, SH10	<i>S. albus</i> J1074 (R ^M) Broad host range	53.7	67	Cohesive	R4, SH10 have very similar restriction maps.	Temperate. Anti-modification in <i>S. albus</i> .	Cloning and integration vectors. Plasmid transduction.	(17, 20, 59, 68, 71)
SH10	<i>S. hygrosopicus</i> Broad host range	~41	68-73	Cohesive	Same immunity group as R4.	Temperate. Inducible by UV.		(59, 60)

VWB	<i>S. venezualae</i> (Narrow host range.)	43.7	69.3	Cohesive	Genome organisation similar to R4. Coat proteins distantly related to those of λ .	Temperate.	Cloning & integration vectors	(2, 3, 100)
ϕ A8	<i>S. antibioticus</i> Broad host range	50	-	Cohesive	Probably homoimmune with R4.	Temperate	-	(32)
SA1	<i>S. azureus</i>	~37	71	-	-	Temperate	-	(72)
RP2, RP3	<i>S. rimosus</i> Narrow host range	64.7 62.4	70	Cohesive	~400bp cross-hybridisation between RP2 and RP3.	Temperate.	Plasmid transduction, integration vectors.	(36, 58, 74)
SC623 SC681 SC347	<i>S. coelicolor</i> (Müller)	57	68-71		SC681 & 623 are homoimmune.	Temperate		(80)
FP43	<i>S. fradiae</i> , <i>S. griseofuscus</i> Broad host range	68		Terminally redundant	-	Temperate.	Plasmid transduction	(69)
ϕ A1	<i>S. antibioticus</i>	100		Discrete	-	-	-	(32)
FP22	<i>S. fradiae</i> , <i>S. griseofuscus</i> Broad host range	131	46	Discrete	Homoimmune with to P23, and cross hybridise	Temperate. Refractory to restriction.		(41)
ϕ SF1	<i>S. fradiae</i>	82		Terminally redundant		Prophage is a plasmid and can form pocks. Two prophage forms differ in their frequency of prophage induction.	Generalised transducing phage	(22)
ϕ SV1,3,9, 10-12	<i>S. venezualae</i> Narrow host range	45	-	Terminally redundant	SV1,9,11 are different immunity groups but cross-hybridise.	Temperate.	Generalised transducing phages	(94, 101)
DAH1, DAH2, DAH4 - DAH6	<i>S. coelicolor</i> A3(2) Also plaque on <i>S. avermitilis</i> and <i>S. lividans</i>	93-121	-	-	-	-	Generalised transducing phages	(12)
JHJ3, (JHJ1, JHJ2)	<i>Saccharopolyspora hirsuta</i> . JHJ1 & 2 are broad host range in the <i>Saccharopolyspora</i> genus.	41.1	70	Cohesive	JHJ1 & 2 are derivatives of JHJ3.	JHJ3 is temperate. JHJ1 is virulent. JHJ1, JHJ2 can form invasive plaques.	Plasmid shuttle vectors.	(37, 38, 42)
ϕ C69	<i>Saccharopolyspora</i>	40	-	Cohesive	-	Virulent.	-	(55)

	<i>a erythrae</i> Narrow host range					Displays 'lysis from without' in some <i>Saccharopolyspora</i> strains (eg NRRL2359)		
121, SE-3 SE-5	<i>Saccharopolyspora erythrae</i> Narrow host range	41.9 (121) 42.2 (SE-5)	57.5-62.5	Cohesive	Homoimmune and cross-hybridise strongly, except in central region. 121 cannot propagate on ϕ FR113/114 lysogens.	Virulent. SE-3 shows 'lysis from without' with NRRL2359		(78) (11, 93)
ϕ FR113/ ϕ FR114	<i>Saccharopolyspora rectivergula</i> (used to be <i>Faenia rectivergula</i>)	43 42		Cohesive	Homoimmune and cross-hybridise strongly, except in central region.			(79)