

Bacteriophage observations and evolution

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Abstract

Bacteriophages are classified into one order and 13 families. Over 5100 phages have been examined in the electron microscope since 1959. At least 4950 phages (96%) are tailed. They constitute the order *Caudovirales* and three families. *Siphoviridae* or phages with long, noncontractile tails predominate (61% of tailed phages). Polyhedral, filamentous, and pleomorphic phages comprise less than 4% of bacterial viruses. Bacteriophages occur in over 140 bacterial or archaeal genera. Their distribution reflects their origin and bacterial phylogeny. Bacteriophages are polyphyletic, arose repeatedly in different hosts, and constitute 11 lines of descent. Tailed phages appear as monophyletic and as the oldest known virus group.

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1. Introduction

Bacterial viruses or bacteriophages, frequently called “phages”, were discovered twice at the beginning of the 20th century. Frederick William Twort, a British pathologist in London, described in 1915 the glassy transformation of “*Micrococcus*” colonies by a transmissible agent. He proposed several explanations, one of which was that the agent was viral in nature. Félix Hubert d’Hérelle, a French Canadian then working at the Pasteur Institute of Paris, observed the lysis of *Shigella* cultures in broth and described it in 1917. Twort did not pursue his discovery, but attempted for decades to propagate vertebrate viruses on inert media. D’Hérelle, on the contrary, clearly recognized the viral nature of his agent and devoted the rest of his scientific life to it. He coined the term “bacteriophage”, devised several techniques still in use, postulated the intracellular multiplication of viruses, and introduced phage therapy of infectious diseases [1]. The viral nature of bacteriophages, contested for a time, was definitely recognized in 1940 after the advent of the electron microscope [20].

2. Bacteriophage classification

For d’Hérelle [9], there was only one bacteriophage species with many races, the *Bacteriophagum intestinale*.

Holmes [12] classified phages as a suborder, a single family, and a single genus of the order *Virales*. His system, clearly premature in nature, classified viruses according to symptoms of disease and was soon forgotten. Lwoff, Horne, and Tournier [15] published a system of viruses based on morphology and nucleic acid type. They proposed the order *Urovirales* for tailed phages, the family *Inoviridae* for filamentous phages, and the family *Microviridae* for ϕ X-type phages, respectively. A further milestone was the recognition of six basic types: tailed phages, filamentous, phages, and cubic phages with ssDNA or dsDNA [7]. This simple scheme is still the basis of present phage classification.

In its first report, the ICTV or International Committee for Taxonomy of Viruses classified phages into six genera corresponding essentially to Bradley’s basic types. They included the T4, λ , ϕ X174, MS2, and fd phage groups and the newly described type PM2 [26]. New phage groups were added over time. The most recent development is the establishment of the order *Caudovirales* for tailed phages and of 15 tailed phage genera [2,16,24]. At the time of writing, an estimated 5300 bacterial viruses have been examined in the electron microscope. By comparison with other viruses [24], bacteriophages thus constitute the largest viral group in nature.

3. Phage classification today

The ICTV presently classifies viruses into three orders, 61 families, and 241 genera [24]. Bacteriophages constitute

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Table 1
Classification and basic properties of bacteriophages ^a

Shape	Nucleic acid	Order and families	Genera	Examples	Members	Characteristics
Tailed	DNA, ds, L	<i>Caudovirales</i>	15		4950	
		<i>Myoviridae</i>	6	T4	1243	Tail contractile
		<i>Siphoviridae</i>	6	λ	3011	Tail long, noncontractile
		<i>Podoviridae</i>	3	T7	696	Tail short
Polyhedral	DNA, ss, C	<i>Microviridae</i>	4	φX174	40	
		<i>Corticoviridae</i>	1	PM2	3?	Complex capsid, lipids
		<i>Tectiviridae</i>	1	PRD1	18	Internal lipoprotein vesicle
	RNA, ss, L	<i>Leviviridae</i>	2	MS2	39	
		<i>Cystoviridae</i>	1	φ6	1	Envelope, lipids
		<i>Inoviridae</i>	2	fd	57	Filaments or rods
Filamentous	DNA, ss, C	<i>Lipothrixviridae</i>	1	TTV1	6?	Envelope, lipids
		<i>Rudiviridae</i>	1	SIRV1	2	Resembles TMV
		<i>Plasmaviridae</i>	1	L2	6	Envelope, lipids, no capsid
Pleomorphic	DNA, ds, C, T	<i>Fuselloviridae</i>	1	SSV1	8?	Spindle-shaped, no capsid

^aModified from reference [4]. With permission of John Libbey-Eurotext. Phage numbers are from reference [3]. C, circular; L, linear; S, segmented; T, superhelical; 1, single-stranded; 2, double-stranded.

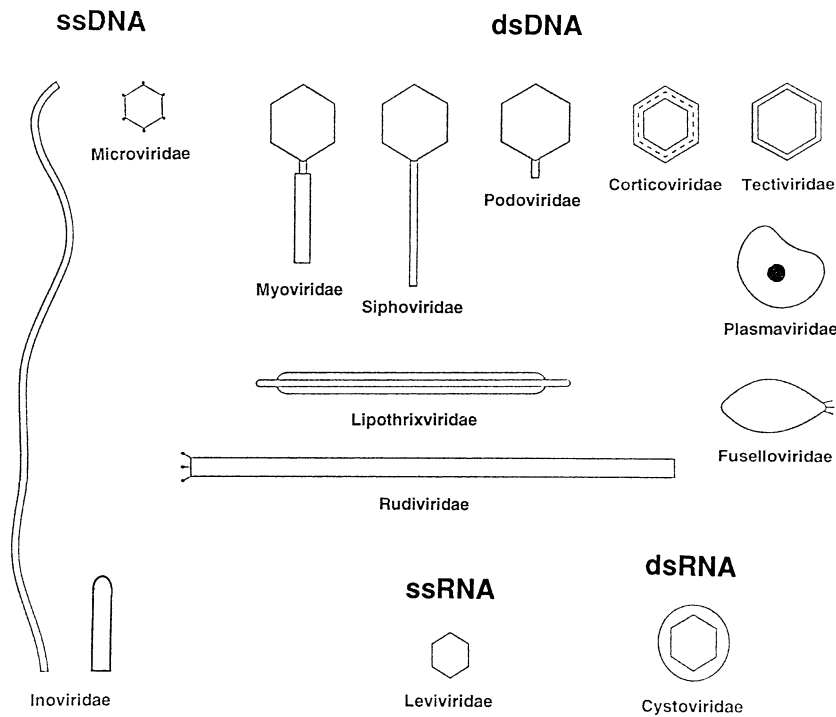


Fig. 1. Schematic representation of major phage groups.

one order, 13 families, and 30 genera (Table 1). Bacteriophage virions are tailed, polyhedral, filamentous, or pleomorphic (Fig. 1). Most phages contain dsDNA, but there are small phage groups with ssDNA, ssRNA, or dsRNA. A few types have lipid-containing envelopes or contain lipids as part of the particle wall. According to the latest phage count, tailed phages comprise at least 4950 viruses [3]. They are classified into the order *Caudovirales* and three large, phylogenetically related families.

Polyhedral, filamentous, and pleomorphic (PFP) phages comprise about 190 viruses only. They are classified into 10 small families which differ by their most basic properties and seem to constitute as many independent phylogenetic

groups or lines of descent. Capsids with cubic symmetry are icosahedra or related bodies. Particles are enveloped or not. The presence of lipids is accompanied by low buoyant density and high sensitivity to chloroform and ether.

As elsewhere in virology, families are chiefly defined by nature of nucleic acid and particle morphology. There are no universal criteria for genera and species. The ICTV uses every available property for classification and has adopted the “polythetic species concept”, meaning that a species is defined by set of properties, some of which may be absent in a given member [23]. Taxonomic names of orders, families, and genera are typically constructed from Latin or Greek roots and end in *-virales*, *-viridae*, and

-virus, respectively. Most genera of “cubic”, filamentous, and pleomorphic phages have latinized names. So far, tailed phage genera have vernacular names only (e.g., “T4-like viruses”).

3.1. Tailed phages (Caudovirales)

Particles consist of a head with cubic symmetry and a “helical” tail and are said to have binary symmetry [15]. They possess no envelope and usually consist of protein and DNA only. The head-tail structure is unique in virology. Although tail-like structures occur in a few other viruses, for example in tectiviruses (see below) and some algal viruses, they are inconstant and do not compare with the permanent, regular tails of tailed phages [2]. Heads are icosahedra or elongated derivatives thereof. Isometric heads prevail in all tailed phage families (85%). Capsomers are rarely visible. Tails are helical or consist of stacked disks and carry in most cases terminal fixation structures such as base plates, spikes, or fibers.

The DNA is a single linear, double-stranded filament. Its composition generally reflects that of the host bacterium, but some DNAs contain unusual bases such as 5-hydroxymethylcytosine. Genetic maps are complex and include about 290 genes in phage T4 (possibly more in larger phages). Genes for related functions cluster together. Replicating DNA tends to form large branched intermediates or “concatemers”. The DNA is then cut to size and fills pre-formed capsids. Maturation is complex and comprises separate pathways for heads and tails, which are joined together.

Many morphological or physiological properties indicate thus that tailed phages constitute a monophyletic evolutionary group. At the same time, tailed phages are extremely varied in DNA content and composition, dimensions and fine structure, and physiology; for example, DNA sizes vary between 17 and over 700 kb and tail lengths range from 10 to 800 nm. Indeed, tailed phages constitute probably the most diversified of all virus groups. Tailed phage are divided into three families.

- *Myoviridae* with contractile tails consisting of a sheath and a central tube (25% of tailed phages).
- *Siphoviridae*, long, noncontractile tails (61%).
- *Podoviridae*, short tails (14%).

Fifteen genera have been defined by genome structure (presence or absence of *cos*- or *pac*-sites, terminal redundancies and circular permutations), concatemer formation, presence or absence of unusual bases and DNA or RNA polymerase genes, and DNA sequence. The 15 genera correspond to phage groups with vernacular names derived from those of the type species:

- *Myoviridae* (groups T4, P1, P2, Mu, Mu, SPO1, ΦH).
- *Siphoviridae* (groups, T1, T5, L5, c2, ψM).
- *Podoviridae* (groups T7, P22, φ29).

This classification into genera [16,24] is still at its beginnings. Many more tailed phage genera are likely to be individualized in the future. The present genera may be seen as crystallization points for phages awaiting classification. About 250 species are presently recognizable, mostly on the basis of morphology, DNA–DNA hybridization and sequencing, and serology.

3.2. Polyhedral DNA phages

3.2.1. Microviridae (*ssDNA*)

Virions are small, have no envelope and contain a single piece of circular *ssDNA*. Phages infect very different hosts (enterobacteria, *Bdellovibrio*, *Chlamydia*, *Spiroplasma*) and are classified into four genera. Microviruses of enterobacteria have conspicuous capsomers. Infecting phage DNA replicates as a double-stranded replicative form (RF) following the rolling-circle model.

3.2.2. Corticoviridae (*dsDNA*)

The family has a single member, maritime phage PM2. Its capsid consists of two protein shells and a lipid bilayer sandwiched in-between. Two similar phages were isolated from seawater, but are little known.

3.2.3. Tectiviridae (*dsDNA*)

Phages have a rigid protein capsid which surrounds a thick, flexible lipoprotein vesicle. Upon adsorption to bacteria or chloroform treatment, this vesicle becomes a tail-like tube of about 60 nm in length, thus a nucleic acid ejection device [5]. Tectiviruses of bacilli have apical spikes. Despite their apparent rarity, tectiviruses have an extremely wide host range (Table 4).

3.3. Polyhedral RNA phages

3.3.1. Leviviridae (*ssRNA*)

Virions resemble polioviruses and have no morphological particulars. However, the coat protein of levivirus MS2 has no structural similarity to that of other known RNA viruses [22]. Most known leviviruses are plasmid-specific coliphages that adsorb to F or sex pili. They have been divided, by serology and other criteria, into two genera. Several not yet classified leviviruses occur outside of the enterobacteria family. Levivirus RNA acts as mRNA and needs no translation.

4. Cystoviridae (*dsRNA*)

This family has a single official member, but two related viruses have recently been found [18]. Viruses are unique among bacteriophages because they contain three molecules of *dsRNA* and RNA polymerase. Capsids are surrounded by lipid-containing envelopes and contain a dodecahedral RNA polymerase complex [6]. Infecting cystoviruses lose

their envelopes and their capsids enter the space between cell wall and cytoplasmic membrane. Host range is limited to *Pseudomonas syringae*, a phytopathogen.

4.1. Filamentous phages

4.1.1. Inoviridae (ssDNA)

The family consists of two genera with very different host ranges. After infection, phage DNA is converted to double-stranded RF DNA and replicates via a rolling-circle mechanism. This similarity in replication seems to derive from the nature of phage DNA rather than from a common origin of the two genera. The *Inovirus* genus includes 42 phages that are long, rigid or flexible filaments and have been classified into 29 species. They occur in enterobacteria and their relatives and also in *Clostridium* [14] and *Propionibacterium* [10]. Viruses are sensitive to chloroform and sonication and very resistant to heat. The *Plectrovirus* genus includes 15 isolates. Phages are short, straight rods and occur in mycoplasmas only. Progeny inoviruses are extruded from host cells. The latter are not lysed and may produce phages indefinitely.

4.1.2. Lipothrixviridae (dsDNA)

This family includes four viruses of the archaeobacterial genus *Thermoproteus*. Particles are characterized by the combination of a lipoprotein envelope and rod-like shape. Contrary to inoviruses, novel virions are released by lysis.

4.1.3. Rudiviridae (dsDNA)

This family includes two viruses of different length isolated from extremely thermophilic archaeobacteria. Particles are straight, rigid rods without envelopes and resemble the tobacco mosaic virus.

4.2. Pleomorphic phages

4.2.1. Plasmaviridae (dsDNA)

Only one member is known, *Acholeplasma* virus MVL2 or L2. Particles have no capsid and consist of an envelope and a dense nucleoprotein granule. Five similar isolates have been found, but are poorly known and cannot be classified with certainty. Plasmaviruses infect their hosts by fusion of the viral envelope with the mycoplasmal cell membrane. Viruses are released by budding.

4.2.2. Fuselloviridae (dsDNA)

This family too has only one certain member, SSV1, which is harbored in the archaeobacterium *Sulfolobus shibatae* as a plasmid and as an integrated prophage. SSV1 is inducible, but has not been propagated for absence of a suitable host. Particles are lemon-shaped with short spikes at one end. The coat consists of two hydrophobic proteins and host lipids and is disrupted by chloroform. A possibly related droplet-shaped virus, named *Guttavirus*, has been found in *Sulfolobus* [21]. Fuselloviruses are liberated by extrusion.

Remarkably, lysogeny is not limited to tailed phages, but also occurs in the *Fuselloviridae*, *Inoviridae*, *Lipothrixviridae*, and *Plasmaviridae* families. Tailed phages exhibit three types of lysogeny: (i) the λ type with integrase-mediated integration of phage DNA at preferred sites, (ii) the P1 type with persistence of phage DNA as a plasmid, and (iii) the Mu type with random integration mediated by a transposase. Integrase-mediated lysogeny also occurs in the *Fuselloviridae* and *Plasmaviridae* families [2]. The type of lysogeny used by the *Lipothrixviridae* is unknown.

Note added in proof:

Filamentous inoviruses of *Vibrio cholerae* integrate by means of host recombinases [28].

5. Evolutionary implications of host range

Phages are known in over 140 bacterial genera. They occur in archaea and eubacteria, in cyanobacteria, in exospore and endospore formers, spirochetes, mycoplasmas and chlamydias, in aerobes, anaerobes, budding, gliding, ramified, sheathed, or stalked bacteria (Table 2). Podovirus particles have even been found within bacterial endosymbionts of paramecia. Of particular significance is the occurrence of a typical myovirus in the archaeon, *Halobacterium halobium*. The phage, named Φ H, has the morphology of coliphage P2 and its prophage DNA behaves as a plasmid like that of coliphage P1 [27]. However, tailed phages observed in *Chlorella* and *Penicillium* cultures are probably laboratory contaminants.

Over 5100 phages have been studied in the electron microscope since the introduction of negative staining in 1959. This number excludes mutants, particulate “bacteriocins” and other defective phages, phage-like particles in rumen or seawater without known hosts, shadowed phages, and unpublished phages from congress reports. A tabulation published in 2001 lists 4650 tailed phages (96%) and only 186 (3.6%) polyhedral, filamentous, or pleomorphic phages [3]. Polyhedral or filamentous phages often adsorb to sides or tips of plasmid-specified pili, namely tectiviruses, leviviruses, cystoviruses, and filamentous inoviruses. This has evident consequences for host ranges.

Bacteriophages occur in bacteria of nearly all sections of Bergey’s Manual [13] (Table 2). However, arrangement of phages according to phylogenetic groups of bacteria [25] (Table 3) reveals that most major bacterial phyla are, so far, without phages. This suggests that many more phages may be found in the future. Most phages have been found in easily grown and medically or industrially important bacteria:

1. Firmicutes with high G + C (coryneforms, listerias, mycobacteria, streptomycetes),
2. Firmicutes with low G + C (bacilli, lactobacilli, clostridia, staphylococci, lactococci, streptococci).

Table 2
Frequency of phages in traditional host groups^a

Bergey section ^b	Group	Myoviridae	Siphoviridae	Podoviridae	PFP ^c	Total
	Gram-negative eubacteria					
1	Spirochetes	10	1			11
2	Spirilla and vibrioids	26	14		9	49
4	Rods and cocci, aerobic	303	323	230	22	878
5	Rods, facultatively anerobic	440	340	300	93	1173
6	Rods, anaerobic	4	21	5		30
7	Sulfate and sulfur reducers	1	1			2
8	Anaerobic cocci		2	2		4
9	Rickettsias and chlamydias		1	1	2	4
11	Endosymbionts			2		2
18	Anoxygenic phototrophs	3	6	3		12
19	Cyanobacteria	22	6	16		44
20	Chemolithotrophs	1	1			2
21	Budding and/or appendaged bacteria	8	90	14	8	120
22	Sheathed bacteria			1		1
23	Nonfruiting gliding bacteria	30	2		2	34
24	Myxobacteria	11		5		16
	Gram-positive eubacteria					
10	Mycoplasmas	1	2	14	21?	38
12	Cocci	44	1144	29		1217
13	Endospore producers	257	317	51	10	635
14	Nonsporing regular rods	71	213	2		286
15	Nonsporing pleomorphic rods		183	13	1	197
16	Mycobacteria	1	77			78
17, 26	Nocardioforms	1	95	1		97
28	Actinoplanes	1	4			5
29	Streptomyces	2	121	8		131
30	Maduromycetes		3			3
31	Thermomonosporae		27			27
32	Thermoactinomycetes		3	1		4
33	Other actinomycetes		6			6
	Archaea (section 25)	7	7		18	32
Total		1243	3011	696	186	5139

^aModified from reference [4]. With permission of John Libbey-Eurotext. Phage numbers are from reference [3].

^bBergey's Manual of Determinative Bacteriology [13].

^cPolyhedral, filamentous, and pleomorphic phages.

Table 3
Frequency of phages in bacterial phylogenetic divisions^a

Division or subdivision	Important host groups or genera	Tailed phages	PFP ^b
Archaea			
Euryarchaeota	<i>Halobacterium</i> , <i>Methanobacterium</i>	14	4
Crenarchaeota	<i>Sulfolobus</i> , <i>Thermoproteus</i>		14
Eubacteria			
<i>Bacteroides</i> and relatives	<i>Cytophaga</i> , <i>Flavobacterium</i>	59	2
Chlamydiales			2
Cyanobacteria	<i>Anabaena</i> , <i>Synechococcus</i>	44	
<i>Deinococcus-Thermus</i>		14	4
Firmicutes: high G + C branch	Actinomycetes, mycobacteria, nocardioforms, streptomycetes	506	1
low G + C branch	Bacilli, lactobacilli, clostridia, Gram- positive cocci, <i>Listeria</i> , mycoplasmas	1757	31
Fusobacteria		5	
Proteobacteria	<i>Aeromonas</i> , enterobacteria, pseudomonads, rhizobia, vibrios	2022	128
Spirochetes		11	
Total		4427	186

^aBased on the organism list of the National Center for Biotechnology Information (NCBI) database (<http://www.ncbi.nlm.nih.gov/taxonomy/>) [25] and on phage counts from reference [3]. Total phage numbers are lower than in Table 1 because rRNA data are unavailable for a number of phage hosts.

^bPolyhedral, filamentous, and pleomorphic phages.

3. Proteobacteria, especially of the γ subdivision. The latter includes enterobacteria (814 tailed and 76 polyhedral

or filamentous phages), acinetobacters, pseudomonads, and vibrios (Table 4).

Table 4
Host range of major phage groups

Phage group or family	Bacterial group or genus
<i>Caudovirales</i>	Eubacteria, Euryarchaeota (extreme halophiles and methanogens)
<i>Microviridae</i>	Enterobacteria, <i>Bdellovibrio</i> , <i>Chlamydia</i> , <i>Spiroplasma</i>
<i>Corticoviridae</i>	<i>Alteromonas</i>
<i>Tectiviridae</i>	(a) Enterics, <i>Acinetobacter</i> , <i>Pseudomonas</i> , <i>Thermus</i> , <i>Vibrio</i> (b) <i>Bacillus</i> , <i>Alicyclobacillus</i>
<i>Leviviridae</i>	Enterics, <i>Acinetobacter</i> , <i>Caulobacter</i> , <i>Pseudomonas</i>
<i>Cystoviridae</i>	<i>Pseudomonas</i>
<i>Inoviridae</i> :	
<i>Inovirus</i>	Enterics, <i>Pseudomonas</i> , <i>Thermus</i> , <i>Vibrio</i> , <i>Xanthomonas</i>
<i>Plectrovirus</i>	<i>Acholeplasma</i> , <i>Spiroplasma</i>
<i>Plasmaviridae</i>	<i>Acholeplasma</i>
<i>Lipothrixviridae</i>	Crenarchaeota: <i>Acidianus</i> , <i>Sulfolobus</i> , <i>Thermoproteus</i>
<i>Rudiviridae</i>	Crenarchaeota: <i>Sulfolobus</i>
<i>Fuselloviridae</i>	(a) Crenarchaeota: <i>Acidianus</i> , <i>Sulfolobus</i> (b) Euryarchaeota: <i>Methanococcus</i> , <i>Pyrococcus</i> ?

Close examination of phage host ranges reveals many oddities that shed light on the evolutionary history of phages:

1. Tailed phages predominate almost everywhere. They occur in both eubacteria and halophilic and methanogenic archaeobacteria (Euryarchaeota), but have not been found, so far, in the hyperthermophilic Crenarchaeota:
 - (a) *Siphoviridae* constitute about 61% of tailed phages; *Myoviridae* and *Podoviridae* are much rarer.
 - (b) *Siphoviridae* are particularly frequent in Firmicutes with high G + C content (actinomycetes and their relatives) and in streptococci and lactococci.
 - (c) Myoviruses and podoviruses are relatively frequent in γ proteobacteria and bacilli.
 - (d) Isometric heads predominate in all three tailed phage families (85%). Elongated heads occur in unrelated bacteria; for example, heads of the T4 type occur in enteric, *Bdellovibrio*, *Clostridium*, and spirochete phages [3].
2. Polyhedral, filamentous, and pleomorphic phages are relatively rare and have narrow host ranges:
 - (a) Tectiviruses occur in enterobacteria, bacilli, and the phylogenetically remote genus *Thermus*.
 - (b) Leviviruses are restricted to enterics and closely related bacteria.
 - (c) Cystoviruses are limited to a single *Pseudomonas* species.
 - (d) Filamentous inoviruses are mainly found in enterics and their relatives, but also occur in *Thermus*, *Clostridium*, and *Propionibacterium*.
 - (e) Rod-shaped inoviruses and plasmaviruses are restricted to mycoplasmas.
 - (f) Fuselloviruses, lipothrixviruses, and rudiviruses are restricted to archaea.

The present distribution of bacteriophages probably reflects their origin and evolution. It is unlikely that tailed phages originated more than once [2,11]. The same can be

postulated for other phage families, except the possibly heterogeneous inoviruses. On the other hand, it is conceivable that ancestral phage groups crossed bacterial boundaries in the past, either when these boundaries were still permeable or by plasmid transfer. It is also conceivable that established phage groups died out in some hosts. At the present state of knowledge, with the help of much speculation and considering that knowledge of archaeal viruses is very inadequate, the distribution and frequency of phages in the bacterial world may be explained as follows:

1. Tailed phages are the oldest viruses and originated before the separation of eubacteria and Euryarchaeota. They may be as old as 3.5 billions of year, close to the origin of life [2]. An old age of tailed phages is also suggested by their extraordinary diversification.
 - (a) Siphoviruses with isometric heads correspond, morphologically, to primordial tailed phages because of their overwhelming frequency. However, myoviruses must be nearly as old because they occur in eubacteria and the archaeon, *Halobacterium*.
 - (b) The relative frequency of tailed phage families is related to bacterial speciation, for example to the evolution of receptors or restriction endonucleases. This probably led to the disappearance or proliferation of some phage types in some bacterial hosts and could explain, for example, the high frequency of siphoviruses in streptomycetes.
 - (c) Elongated heads arose independently and repeatedly in unrelated phages.
2. Crenarchaeota constitute a distinct host domain characterized by the apparent absence of tailed phages and the presence of two types of filamentous phages.
3. The hosts of polyhedral, filamentous, and pleomorphic phages constitute ecological niches. Various phage types arose there independently and some of them spread via plasmid transfer [17].

- (a) Tectiviruses, filamentous inoviruses, and leviviruses arose in enterobacterial-like Gram-negatives and spread from there following plasmids.
- (b) Rod-shaped inoviruses and plasmaviruses arose in mycoplasmas and did not spread because of their dependence on the host plasma membrane for adsorption. Similarly, cystovirus $\phi 6$ remained confined to *Pseudomonas* bacteria because of its pilus-specificity.
- (c) *Fuselloviridae*, *Lipothrixviridae*, and *Rudiviridae* originated in archaea and did not spread to eubacteria. The last two families seem to be confined to Crenarchaeota.

There is no ready explanation for the odd distribution of microviruses, which occur in isolated genera of different phyla with nothing in-between. Relationships between phages and eukaryotic viruses remain conjectural and tenuous. Tectiviruses, podovirus $\phi 29$, and adenoviruses have type B (*Escherichia coli* Pol II) DNA polymerases and genomes with terminal proteins [5], but it remains to be seen whether this is an extraordinary case of horizontal gene transfer and or of vertical phylogenetic relationship. Cystovirus $\phi 6$ and vertebrate, plant, or fungal viruses with dsRNA, e.g., reoviruses, birnaviruses, or totiviruses, resemble each other by the presence of segmented RNA and RNA polymerase within the virion and may have a common origin [8], but phage $\phi 6$ differs from the other dsRNA viruses by presence of an envelope and number of RNA segments [24]. The archaeal *Rudiviridae*, despite gross morphological differences, resemble poxviruses, African swine fever virus, and phycodnaviruses of *Chlorella* by genome structure and replication machinery [19]. Furthermore, many (not all) tailed phages and herpesviruses share several features: similar capsid size and DNA molecular weight, circularization of infecting DNA, concatemer formation, procapsid formation using scaffolding proteins and proteolytic cleavage, DNA entering preformed capsids, and persistence of latent viral DNA either as plasmids or in integrated form [2]. This suggests that herpesviruses and tailed phages may have a common, though distant, ancestor.

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