

**Three proposed new bacteriophage genera of staphylococcal phages:
“3alikevirus”, “77likevirus” and “Phietalikevirus”**

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Abstract

To date most members of the *Siphoviridae* family of bacteriophages remain unclassified, including the 46 staphylococcal phages for which the complete genome sequences have been deposited in public databases. Comparative nucleotide and protein sequence analysis, in addition to available data of phage morphology, allowed us to propose three new phage genera within the *Siphoviridae* family: “3alikevirus”, “77likevirus” and “Phietalikevirus”, which include related phages infecting *Staphylococcus aureus* and *Staphylococcus epidermidis*. However, six phages infecting *S. aureus*, *Staphylococcus pasteurii*, *Staphylococcus hominis* and *Staphylococcus capitis* strains remain to be classified (orphan phages). Overall, the former phages share morphological features and genome organization. The three groups have conserved domains containing peptidoglycan hydrolytic activities clearly identified as part of tape measure proteins (“3alikevirus” and “77likevirus”) or as individual virion-associated proteins (“Phietalikevirus”). In addition, bacteriophages belonging to the genus “3alikevirus” share closely related DNA-processing and packaging proteins, while bacteriophages included in the genus “Phietalikevirus” encode specific tail proteins for host interaction. These properties are considered as distinctive for these genera. Orphan phages seem to have a more divergent organization, yet shared with these genera.

Introduction

The recent increase in phage genome sequences available in public databases (828 in order *Caudovirales* as of June 20, 2013) along with the development of bioinformatic tools, have enabled the classification of bacteriophages on the basis of their genetic relationships. Recent approaches led to the creation of the *Autographivirinae* and

Picovirinae subfamilies in the family *Podoviridae* and the *Tevenvirinae* subfamily within the *Myoviridae* family [1-3]. To date, a large number of *Staphylococcus aureus* phages have been described, but a complete genetic and functional characterization has been performed only on a limited number. Previous attempts to classify *S. aureus* phages were based on genome sizes and resulted in three classes [4]. Class I included phages with a genome size <20-kb (P68, 66, and 44AHJD), class II 20 - 40-kb (42e, 3A, 47, 187, 69, 53, 85, 2638A, 77, 37, 96, 71, 55, 29, 52A, 88, 92, EW and X2), and class III 40 - 125-kb (Twort, K, and G1). Morphological differences among these classes were also observed. Class I phages belong to the *Podoviridae* family (C1 morphotype) with a short, non-contractile tail and an isometric head, whereas class II phages belong to the *Siphoviridae*. The majority of class II phages show a B1 morphotype with a long, non-contractile tail and an isometric head. In this group, phages 42e, 3A, and 47 display a B2 morphotype with a long, non-contractile tail and elongated head. Finally, the three phages from class III are structurally defined as members of the *Myoviridae*.

Recently, three novel temperate *Siphoviridae* phages (StB12, StB27, and StB20) from the coagulase-negative species (CoNS) *Staphylococcus hominis* and *Staphylococcus capitis* were isolated and characterized [5]. Based on the comparative analysis of these phages with prophage sequences, the authors proposed a novel classification for staphylococcal phages in nine different clusters.

The aim of the current work is to find a rational scheme for staphylococcal phage classification, which condenses the extensive data derived from genetic and proteomic studies, to give some clues in the evolutionary relationships among these phages. Thus, we propose the creation of three new siphovirus genera named “3alikevirus”, “77likevirus” and “Phietalikevirus”, in which 46 staphylococcal phages have been grouped.

Comparative genomics

Bioinformatic analyses of 46 staphylococcal phages indicated relatively minor differences in genome sizes and G+C content, which range between 40-45.8 kb and 33-38%, respectively. We first turned to comparative analyses employing BLASTN (<http://blast.ncbi.nlm.nih.gov/>); EMBOSS (http://www.ebi.ac.uk/Tools/psa/emboss_stretcher/) and Stretcher (<http://gel.ahabs.wisc.edu/mauve/>), along with protein content comparisons using CoreGenes 3.0 [6-8]. Before the global alignments could be performed, the genomes were manually colinearized, placing the arbitrary starting point for the sequence 150-bp in front of the gene for the small terminase subunit. The progressive-Mauve alignments reveal a similar organization of the phages in modules that fit to the general structure of most double-stranded DNA bacteriophages [9]. These modules include: packaging, structure/morphogenesis, host lysis, lysogeny and replication/regulation (Supplementary Figures 1-5). Taking into account phage morphology, genome size and organization, gene synteny and a shared protein content of 40%, three groupings can be described for which we propose status of genus, consistent with other *Caudovirales* groupings (Table 1): “3alikevirus” (3A, Φ 12, 47, phiIPLA35, Φ SLT and 42e), “77likevirus” (77, Φ PVL108 and Φ 13), and “Phietalikevirus” (Φ ETA, 52A, 80, 29, 71, 55, Φ MR11, Φ ETA3, 88, 92, X2, Φ NM4, 96, Φ ETA2, Φ 11, 53, 69, 80 α , 85, Φ MR25, Φ NM1, Φ NM2, phiIPLA88, 187, SAP-26). Phages 2638A, TEM123, SpaA1, StB12, StB20, and StB27 did not reveal a clear relationship with the others and remain as orphan phages. Using the Needleman-Wunsch rapid global alignment algorithm of EMBOSS Stretcher, nucleotide similarities with the type phage in each genus have been computed. Values over 53% of DNA identity were observed within each proposed genus (Table 1). Between genera these values were lower than 50% (data not shown). Focusing on the

Table 1. Features showed by “3alikevirus”, “77likevirus” and “Phietalikevirus” genera.

Phage name	Host	Shared protein content with phage type (%) ^a	Shared DNA identity with type phage (%) ^b	Reference	Accession number
3alikevirus					
3A	<i>S. aureus</i>	100	100	[4]	NC_007053
phiIPLA35	<i>S. aureus</i>	68.7	86.4	[14]	NC_011612
ΦSLT	<i>S. aureus</i>	56.7	77.1	[22]	NC_002661
47	<i>S. aureus</i>	77.6	85.4	[4]	NC_007054
Φ12	<i>S. aureus</i>	65.7	88.6	[23]	NC_004616
42e	<i>S. aureus</i>	61.2	74.7	[4]	NC_007052
77likevirus					
77	<i>S. aureus</i>	100	100	[4]	NC_005356
PVL108	<i>S. aureus</i>	52.2	60.5	[41]	NC_008689
Φ13	<i>S. aureus</i>	46.4	61.4	[23]	NC_004617
Phietalikevirus					
Subgroup 1					
ΦETA	<i>S. aureus</i>	100	100	[42]	NC_003288
52A	<i>S. aureus</i>	65.2	74.2	[4]	NC_007062
80	<i>S. aureus</i>	66.7	76.3	[43]	DQ908929
29	<i>S. aureus</i>	66.7	76.3	[4]	NC_007061
71	<i>S. aureus</i>	80.3	78.5	[4]	NC_007059
55	<i>S. aureus</i>	80.3	79.8	[4]	NC_007060
ΦMR11	<i>S. aureus</i>	66.7	75.3	[44]	NC_010147
ΦETA3	<i>S. aureus</i>	63.6	72.6	[42]	NC_008799
88	<i>S. aureus</i>	69.7	74.8	[4]	NC_007063
92	<i>S. aureus</i>	68.2	73.9	[4]	NC_007064
X2	<i>S. aureus</i>	66.7	70.8	[4]	NC_007065
ΦNM4	<i>S. aureus</i>	74.2	68.6	[45]	DQ530362
96	<i>S. aureus</i>	68.2	66.8	[4]	NC_007057
Subgroup 2					
ΦETA2	<i>S. aureus</i>	60.6	67.5	[42]	NC_008798
11	<i>S. aureus</i>	50.0	60.4	[23]	NC_004615
53	<i>S. aureus</i>	53	60.5	[4]	NC_007049
69	<i>S. aureus</i>	56.1	62.5	[4]	NC_007048
80α	<i>S. aureus</i>	56.1	60.8	[43]	NC_009526
85	<i>S. aureus</i>	48.5	60.1	[4]	NC_007050
ΦMR25	<i>S. aureus</i>	57.6	61.0	[46]	NC_010808
ΦNM1	<i>S. aureus</i>	60.6	63.7	[45]	NC_008583
ΦNM2	<i>S. aureus</i>	53.0	60.9	[45]	DQ530360
phiIPLA88	<i>S. aureus</i>	51.5	57.6	[21]	NC_011614
187	<i>S. aureus</i>	45.5	53.3	[4]	NC_007047
SAP-26	<i>S. aureus</i>	53.1	62.6	Unpublished	NC_014460
Subgroup 3					

37	<i>S. aureus</i>	42.4	53.5	[4]	NC_007055
EW	<i>S. aureus</i>	45.5	54.5	[4]	NC_007056
CNPH82	<i>S. epidermidis</i>	51.5	55.5	[47]	NC_008722
PH15	<i>S. epidermidis</i>	47.0	54.7	[47]	NC_008723
phiIPLA5	<i>S. epidermidis</i>	47.0	55	[39]	NC_018281
phiIPLA7	<i>S. epidermidis</i>	43.9	56.2	[39]	NC_018284
Orphan phages					
TEM123	<i>S. aureus</i>	NA	NA	Unpublished	NC_017968
2638A	<i>S. aureus</i>	NA	NA	[4]	NC_007051
SpaA1	<i>S. pasteurii</i>	NA	NA	[48]	NC_018277
StB20	<i>S. capitis</i>	NA	NA	[5]	JN700521
StB12	<i>S. hominis</i>	NA	NA	[5]	JN700520
StB27	<i>S. hominis</i>	NA	NA	[5]	JN700519

^a calculated with CoreGenes 3.0

^b calculated with EMBOSS Stretcher

percentage of shared proteins with phage type, values over 42% were observed within each genus, while lower values were determined between genera (data not shown).

Features of the bacteriophages belonging to the proposed genus “3alikevirus”

The “3alikevirus” genus includes six of the staphylococcal phages. All these viruses were reported to possess a prolate capsid (siphovirus B2 morphotype), 100 nm long and 50 nm wide, and a tail of 300-400 nm (for references see Table 1). Comparative proteomic analyses using CoreGenes 3.0 and BLASTP indicates the presence of several group-specific proteins. Among the replication associated proteins there are a helicase-like protein and an A-type DNA polymerase. At the morphogenesis module, a unique capsid protein containing a pfam05065 motif (Phage capsid family) and a major_cap_HK97 (TIGR01554; phage major capsid protein, HK97 family) motif can be distinguished. The tail module contains two specific proteins; the first shows a Siphon_tail (pfam05709) motif, while the latter, corresponds to a predicted prophage

endopeptidase tail motif (pfam06605). Other protein exclusive of these phages is RinA, whereas the RinB homolog can be found in other phages.

Comparative analysis of DNA sequences using progressive-Mauve alignments also indicates a particularly high degree of conservation in a region spanning the DNA packaging proteins (small and large terminase subunits, portal and scaffolding proteins) (Supplementary Figure 1). In addition, all phages belonging to the genus “3alikevirus”, share a region encoding a putative nuclease (HNH superfamily).

A relevant characteristic of the “3alikevirus” genus is the presence of peptidoglycan hydrolytic domains included in their tape measure proteins (TMPs). Specifically, a lytic transglycosylase SLT domain and a peptidase_M23 domain are detected in all of them (Table 2).

Table 2. Peptidoglycan hydrolytic domains and tail proteins associated to staphylococcal phages. The presence (+) or absence (-) of catalytic domains and tail proteins were indicated. [+] Some members of the subgroup lacked this protein.

Phage name	TMP		Hyd		SGNH	Fiber
	Peptidase_M23	Transglycosylase SLT	CHAP	Glucosaminidase		
3alikevirus						
3A	+	+	-	-	-	-
phiIPLA35	+	+	-	-	-	-
ΦSLT	+	+	-	-	-	-
47	+	+	-	-	-	-
Φ12	+	+	-	-	-	-
42 ^e	+	+	-	-	-	-
77likevirus						
77	+	+	-	-	-	-
PVL108	+	+	-	-	-	-
Φ13	+	+	-	-	-	-
Orphan						
TEM123	-	-	+	+	+	+
2638A	+	-	-	-	-	-
SpaA1	-	-	-	-	-	-
StB20	+	+	+	-	-	+
StB12	-	-	-	+	-	-
StB27	-	-	+	+	+	+
Phietalikevirus						
Subgroup 1	-	-	+	+	+	+
Subgroup 2	-	-	+	+	+	(+)
Subgroup 3	-	-	+	+	+	(+)

Features of the bacteriophages belonging to the genus “77likevirus”

The “77likevirus” genus includes three *S. aureus* phages with a similar genome size and morphology (B1 morphotype). No data on the size of the viral particles has been published. These phages shared characteristics with the other genera (“3alikevirus” and “Phietalikevirus”), such as the presence of nucleases in phages 77 and Φ 13, similar to those from the “3alikevirus” genus, and a common morphotype with “Phietalikevirus”. Among the peptidoglycan hydrolase domains, a lytic transglycosylase SLT domain and a peptidase_M23 domain, similar to those found in “3alikevirus” were detected in the tail tape measure proteins (TMPs) of the three phages belonging to “77likevirus” genus (Table 2) (Supplementary Figure 2). No other structural proteins with peptidoglycan catalytic domains were detected in these phages.

Features of the bacteriophages belonging to the genus “Phietalikevirus”

The “Phietalikevirus” genus, that includes 31 staphylococcal phages, can theoretically be divided into three subgroups (Supplementary Figures 3-5), based on DNA similarity. Genome size of these phages is very similar among all of them. Virion morphology is nearly identical, with isometric heads of about 50 nm in diameter, and a tail of 175 nm long. All phages belonging to this genus show a B1 morphotype, with the exception of phage EW, which was described as having an A morphotype [4]. Due its high homology with B1-bacteriophages we conclude that this is incorrect.

A particularly interesting region of the “Phietalikevirus” phages is the sequence of genes in the tail morphogenesis module (Fig. 1). Five arrangements with small differences were observed. In most of the phages from subgroup 1 and subgroup 2 (Φ ETA, 52A, 80, 29, 71, 55, Φ MR11, Φ ETA3, 88, 92, X2, Φ NM4, 96, Φ ETA2, Φ 11,

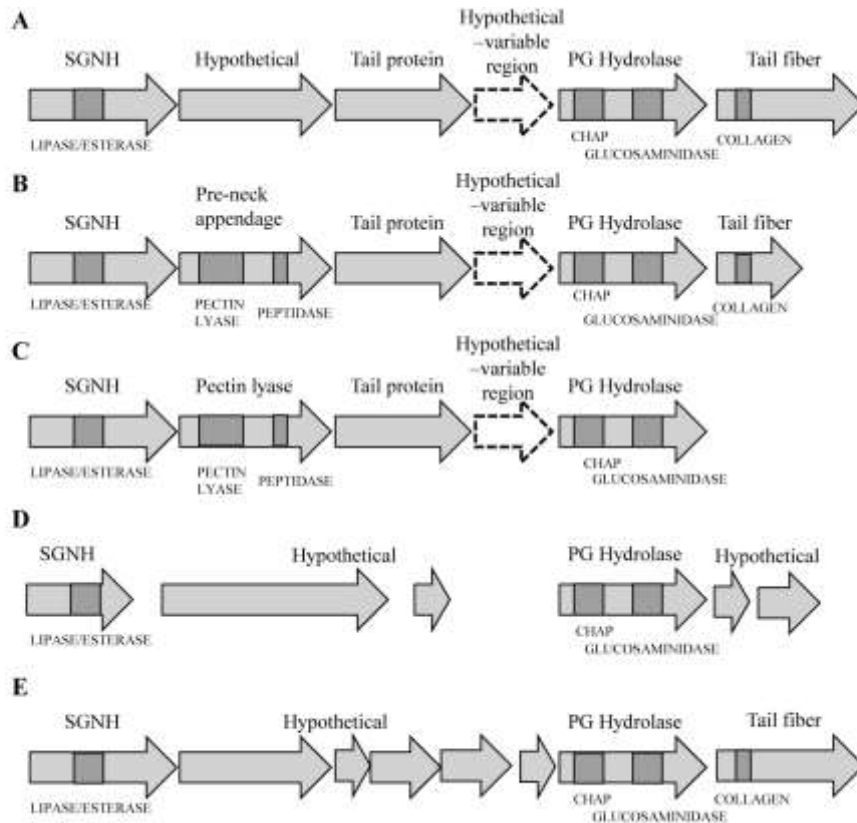


Figure 1. Morphogenetic tail region in the “Phietalikevirus” genus. (A) Structure for phages Φ ETA, 80, 52A, 29, 55, Φ MR11, Φ ETA3, Φ NM4, 96, Φ 11, Φ NM1, Φ NM2, 69, 80 α , 53, Φ ETA2, Φ MR25, 85, phiIPLA88, 92, X2, 88, 71. (B) Structure shared by phiIPLA5, CNPH82 and phage 37. (C) Structure for phiIPLA7 and PH15. (D) and (E) Structure for phages 187 and EW, respectively. Dashed arrow represents a region of variable number (from 3 to 5) conserved hypothetical proteins.

53, 69, 80 α , 85, Φ MR25, Φ NM1, Φ NM2, and phiIPLA88) this region is composed of a protein belonging to the SGNH hydrolase superfamily, a hypothetical protein, a tail protein, a virion-associated peptidoglycan hydrolase and a tail fiber protein (Fig. 1A). For most phages belonging to subgroup 3 (37, CNPH82, PH15, phiIPLA5 and phiIPLA7) a pectin lyase-encoding gene can be observed downstream of the SGNH protein (Fig. 1B and C). In all these phages, with the exception of phages phiIPLA7 and PH15, a tail protein is also present. Remarkable differences can be seen on the makeup of this region for phages 187 and EW, which lacks the pectin lyase. No tail protein

could be identified on 187 (Fig. 1D and E). The SGNH hydrolases containing lipase and esterase domains are present in all phages within the genus, including phage 187, which has a truncated protein (Fig. 1D). Moreover, peptidoglycan hydrolytic activities are present in all phages as virion-associated proteins containing two catalytic domains: a CHAP domain and a glucosaminidase domain (Fig. 1, Table 2). All phages, except phiIPLA7, PH15 and phage 187, encode tail fiber proteins with a collagen helix domain downstream from the peptidoglycan hydrolases. This domain consists of a triple helix formed by repetitions of the amino acid sequence glycine-X-Y. A shorter sequence of this protein is also observed for phages phiIPLA5 and CNPH82. The members of the subgroup 3, with the exception of phage 187 (Fig. 1B, C and D), have a pre-neck appendage protein between the SGNH hydrolase and the tail protein endowed with a pectin lyase and a peptidase domain.

Orphan phages infecting *Staphylococcus* within the *Siphoviridae* family

Six siphophages infecting *Staphylococcus* have no clear homology with the previous proposed genera. For instance, regarding the peptidoglycan hydrolytic activities specific to the other genera, the orphan phages, with the exception of 2638A and StB20, lack lytic domains associated with the TMPs. Phage 2638A had a TMP containing only the peptidase_M23 domain but not a transglycosylase SLT domain. An interesting structure can be observed in *S. capitis* phage StB20, which encodes TMP containing the peptidoglycan hydrolytic domains (a peptidase_M23 domain and a transglycosylase SLT domain), and additionally, a truncated virion-associated peptidoglycan hydrolase bearing a CHAP domain (Table 2). Complete peptidoglycan hydrolases are present in phages TEM123 and StB27. Other phages, like StB12, encode potentially truncated PG

hydrolases with a glucosaminidase domain. In phage SpaA1 no peptidoglycan lytic activities could be detected, either in the TMP or any other structural proteins.

Bacteriophage TEM123 shares characteristics with the “Phietalikevirus” genus, such as the presence of structural proteins related with host interaction (SGNH and tail fiber protein) but lacks of an overall homology with this genus (Table 2). Phage 2638A seems to be more related to “3alikevirus” sharing nuclease and helicase proteins (data not shown). Phages StB20 and StB27 may have a putative relation to “Phietalikevirus” due to the presence of host interaction proteins; StB27 has SGNH hydrolase and tail fiber protein and StB20 also shows a tail fiber protein in the structural module (Table 2).

Phylogeny

Typing of microbial pathogens is often performed using multi-locus sequence typing, in which fragments of several housekeeping genes are sequenced; concatenated and phylogenetic trees are constructed [10]. In this regard, by using ClustalX [11] we have aligned the complete, colinearized genomes of all phages and generated a phylogenetic tree that was visualized with FigTree (<http://tree.bio.ed.ac.uk/software/figtree/>). Figure 2 shows the whole genome tree of the staphylococcal phages, and clearly reveals the three proposed genera, “3alikevirus”, “77likevirus” and “Phietalikevirus”, along with the three subgroups belonging to the latter genus being also recognizable. This tree also shows that phage TEM123 is related to the Phietalikeviruses, and shares over 40% proteins with members of subgroup 2 of the genus (data not shown), in spite of the shared protein content with Φ ETA its homology is only 28.8% as calculated with CoreGenes. For these particular phages, the method of whole genome phylogenetic tree building corroborates the previously performed comparative genomic analyses and can be a good tool in phage taxonomy.

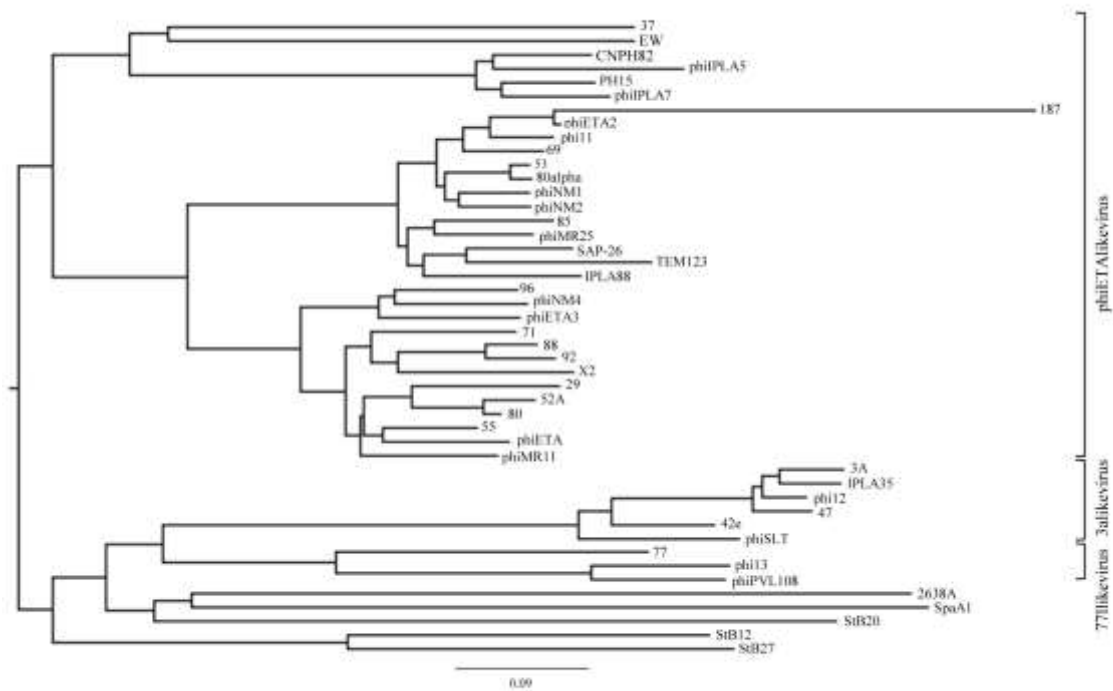


Figure 2. Phylogenetic tree of the complete genome sequences of the staphylococcal phages, aligned with ClustalX and drawn with FigTree. Genomes that were re-oriented to start with the small terminase subunit gene have been designated as _RO.

Phylogenetic analysis of some conserved proteins was also carried out. Homology between phage large terminase subunits was previously shown as indicative of different functional classes [12]. We determined that there is a high sequence identity between large terminase subunits in genus “3alikevirus”. This protein possesses the typical domains from the “Terminase_1 superfamily,” which are shared by 2638A, StB20, and phages belonging to the “77likevirus” genus (Fig. 3A). Phages belonging to “Phietalikevirus” (with the exception of phage SAP-26) and the orphan phages SpaA1, StB12, StB27 and TEM123, show large terminase subunits associated with the “Terminase_3 superfamily.” These data indicate a different packaging mechanism in phages of the different genera, which would further support the proposed clustering.

This grouping is further supported by phylogenetic analysis of the major head proteins. In fact, it shows a clear correlation between the proposed staphylococcal genera and even a higher homology to those belonging to the “Phietalikevirus” genus (Fig. 3B). Similar results were observed using head and tail proteins, such as portal protein and TMP (data not shown).

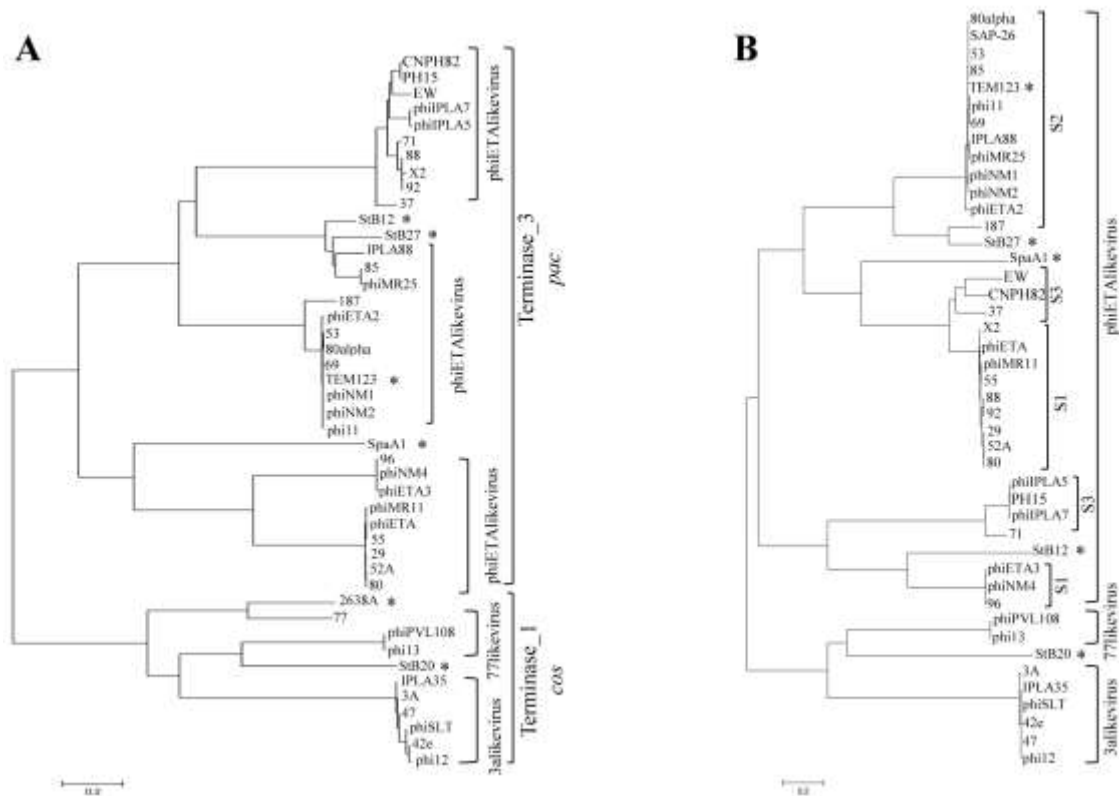


Figure 3. Neighbor-joining tree of (A) large terminase subunit amino acid sequences encoded by staphylococcal phages and (B) major head protein encoded by staphylococcal phages. (*) Orphan phages. S1, subgroup 1; S2, subgroup 2; S3, subgroup 3.

Discussion

The current phage taxonomy, as laid out by the International Committee on Taxonomy of Viruses (ICTV), is based on a multitude of phenotypical and genotypical parameters, including morphology, infectivity and genome organization. Several proposals for

phage classification based on sequence information have been made, sometimes with conflicting views. Rohwer and Edwards [13] built a tree based on pairwise dissimilarities between the complete bacteriophage proteomes, Pride and colleagues [14] proposed a phylogeny based on tetranucleotide usage patterns, and Lima-Méndez and colleagues [15] published a framework for a reticulate classification of phages based on gene content, which incorporates more elements of mosaicism and horizontal exchange [16-18]. More disruptive is the non-hierarchical model proposed by Lawrence and colleagues [19], which is not based in viral lineages, but the creation of reticulate groups that more accurately represent biological relationships among these phages. Phages could belong to several groups and phages within a group would share a particular module or phenotypic characteristics, reflecting their mosaic nature. In this work, we confirm the validity of the CoreGenes approach to create coherent phage groups as well as the identification of individual phages with special properties. Thus, a detailed analysis of staphylococcal phages within the *Siphoviridae* family allowed us to propose three genera based on a close genetic similarity and on the presence of specific proteins involved in DNA packaging and host interaction. In addition to the high sequence identity across the structural module [20], we have also observed gene synteny in the region comprising the DNA packaging proteins of phages grouped as “3alikevirus”. This feature was previously described for phages 3A, 47 and 42e by Kwan and colleagues [4]. Furthermore, phylogenetic analysis of both the terminase large subunit and the major head protein clearly substantiate and support the establishment of the “3alikevirus” genus. In addition, the predicted DNA packaging mechanism used by “3alikevirus” is mediated by cohesive ends and a specific large terminase subunit (*terminase_1*) and differs from the “Phi2alikevirus” genus. Phages belonging to the genera “3alikevirus” and “77likevirus” are likely to use a *cos*

packaging mechanism as it was previously suggested for phage phiIPLA35 and phage Φ SLT [21, 22]. By contrast, phietalikeviruses appear to use a *pac* site to package DNA into capsids, as it was suggested for some phages such as phiIPLA88 and Φ 11 [21, 23]. Clearly, the homology among large terminase subunits with similar enzymatic end-generating functions matched with staphylococcal phage genera.

The presence of HNH superfamily (homing) nucleases seems to be specific to the “3alikevirus”. It has been proposed that the presence of endonuclease genes in phage genomes can be considered analogous to insertion or transposon elements in bacterial genomes [24, 25], which could explain their presence in phages infecting other different genera than *Staphylococcus* as well as for orphan phages (StB20 and 2638A) and some “77likeviruses” (data not shown). Moreover, highly conserved helicase proteins (DEAD-like helicases superfamily) found in “3alikevirus” are also present in phage 2638A.

Close examination of the differences between phage genera reveals two distinct arrangements in the peptidoglycan hydrolytic domains. Genomes of bacteriophages belonging to the “3alikevirus” and “77likevirus” genera encode peptidoglycan hydrolytic domains (peptidase_M23 and transglycosylase (SLT), as part of TMPs), whereas “Phietalikevirus” individual genes encode for CHAP and glucosaminidase domains located in virion-associated peptidoglycan hydrolases. Previous analyses have revealed that phage TMPs frequently contain a soluble lytic transglycosylase domain [26, 27], and lytic transglycosylases have been proposed to be involved in phage DNA entry during early stages of infection [28, 29]. Similar catalytic domains were previously described in TMPs from several mycobacteriophages where they play an essential role in the infection of stationary-phase cells [30]. In other phages, such as

phage T5, these catalytic domains are included in a TMP that also carries fusogenic activities [31].

Phages of the “Phieta-likevirus” genus have a peptidoglycan hydrolytic activity also associated with the phage particle, but as an independent protein. Virion-associated peptidoglycan hydrolases facilitate the entry of phage DNA across the bacterial cell envelope during infection [32]. They are also responsible for “lysis from without,” a phenomenon caused by some phages when adsorbed onto the host cell at very high numbers [33, 34]. Activity of these proteins against peptidoglycan was confirmed for those encoded by phages phiIPLA88 and Φ MR11 [35, 36]. Although the peptidoglycan hydrolase activity of these proteins has been demonstrated, its function in the phage lytic cycle is not clear. Likewise, PRD1 and T7 mutant phages without virion-associated peptidoglycan hydrolase activity are able to infect host cells although the process was significantly delayed [32, 37].

The “Phieta-likevirus” genus division is also supported by a more complex host interaction machinery, including a SGNH protein, a pectin lyase, a tail protein and a tail fiber protein. These proteins are probably implicated in degradation of extracellular or capsular material facilitating phage infection. SGNH proteins are involved in the hydrolysis of wide variety of substrates, including fatty acids, aromatic esters, and amino acid derivatives [38]. Pectin lyase proteins have been described as a putative hydrolases against extracellular components from bacterial biofilms [39]. They are comprised of two domains, including a pectin/lyase that shares a right-handed beta helical folds identified in carbohydrate depolymerizing enzymes [40]. These relationships suggest that these proteins might interact with the bacterial cell envelope and therefore might be related to the bacterial receptor interaction.

It is interesting to highlight the structure of the orphan phages 2638A, StB12 and StB20. These phages are not clearly related to any proposed genera on the basis of DNA and protein homology. They show truncated peptidoglycan hydrolytic domains (2638A and StB12) or “duplicate” domains (StB20) that could be seen as intermediaries in phage exchange of these catalytic domains.

Overall, our results are in accordance with previous attempts at staphylococcal phages and prophage classification [4, 5]. The comparative nucleotide and protein sequence analyses performed have allowed us to define three novel genera in which phages previously grouped [4] have been included. Of note is the fact that the clusters proposed in the recent classification provided by Deghorain et al. [5] match, with a few exceptions, our classification in genera and subgroups supporting its validity.

Acknowledgments

This research study was supported by grants AGL2012-40194-C02-01 (Ministry of Science and Innovation, Spain) and bacteriophage network FAGOMA. D. G. is a fellow of the Ministry of Science and Innovation, Spain. R. L., P. G. and A. R. are members of the FWO Vlaanderen funded “Phagebiotics” research community (WO.022.09).

Competing interests

The authors declare that they have no competing interests.

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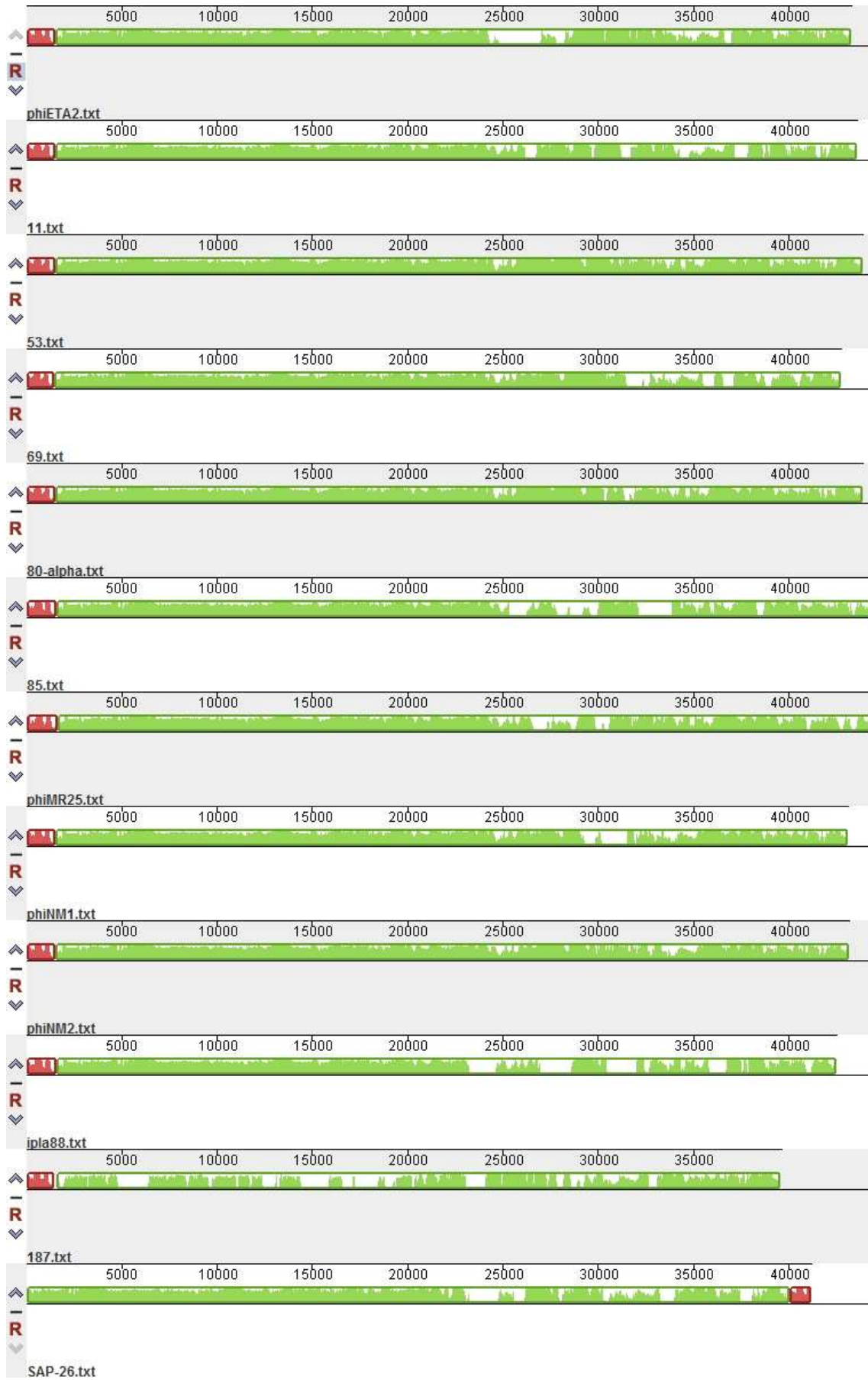
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Supplementary material. Alignments of the staphylococcal phage genomes belonging to *Siphoviridae* family, using the progressive-MAUVE software. Inside each block nucleotide sequence similarity is indicated by the height of the coloured bars, while regions that are dissimilar are in white. (1) Comparison of genomes of “3alikevirus”; (2) MAUVE analysis of “77likevirus”; (3) “Phietalikevirus” subgroup 1; (4) “Phietalikevirus” subgroup 2; (5) “Phietalikevirus” subgroup 3.



Supplementary Fig. 1



Supplementary Fig. 4



Supplementary Fig. 5