Template for Taxonomic Proposal to the ICTV Executive Committee
To create a new Genus in an existing Family

Code[†] 2005.160B To create a new genus in the family* ***Myoviridae***

Code[†] 2005.161B To name the new genus* **”phiKZ-like viruses”**

Code[†] 2005.163B To create as type species in the new genus the species named* **Pseudomonas phage phiKZ**

Code[†] 2005.164B To designate the following as species of the new genus*:

*Pseudomonas phage **phiK**Z*
Pseudomonas phage Lin68
Pseudomonas phage 201phi2-1

Code[†] To designate the following as tentative species in the new genus*:

[†] Assigned by ICTV officers
* repeat these lines and the corresponding arguments for each genus created in the family

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Order
Family
Genus
Type Species
Species in the Genus
Tentative Species in the Genus
Unassigned Species in the family

New Taxonomic Order

Order
Family
Genus
Type Species
Species in the Genus
Tentative Species in the Genus

Unassigned Species in the family

ICTV-EC comments and response of the SG

Accepted. Move to 04

Argumentation to choose the type species in the genus

Phage phiZ is the best-known species of the genus and the first sequenced.

Species demarcation criteria in the genus

Species differ in DNA homology, restriction endonuclease patterns, and N-terminal sequences of the major capsid protein The DNA of phiKZ is over 280 kb in size and has 306 ORFs, most of which are unrelated to any known proteins, while EL contains 201 ORFs within its 211 kb genome. These two phages and Pseudomonas phage Lin68 have recently been proposed as part of a genus ‘‘phiKZ viruses’’. We now consider that the differences (number of ORFs, mol%G+C, protein homologs) between phiKZ and EL exclude EL from membership in the same genus, although a relationship at a possible future subfamily level can be envisioned. Indeed, the recent analysis of novel *Pseudomonas* phage 201phi2-1 showed this phage to have a strong correlation to φKZ (167 similar proteins), showing that it is a true member of the “phiKZ-like virusses” (Figures 2 and 3).

List of Species in the created genus

Pseudomonas phage phiKZ
Pseudomonas phage Lin68
Pseudomonas phage 201phi2-1

List of Tentative Species in the created genus

Argumentation to create a new genus:

Virions are very large (heads 120 nm in diameter, tails 184 nm long) and have tails surrrounded by fibers. Heads contain a proteinic inner body as shown for 201phi2-1 in Figure 1.

Origin of the proposed genus name

Name of type species

References

Ackermann H-W, Cartier C, Slopek S, Vieu J-F. 1988. Morphology of *Pseudomonas aeruginosa* typing phages of the Lindberg set. Ann Inst Pasteur/Virol 139:389-404

Bourkaltseva MV, Krylov VN, Pleteneva EA, Shaburova OV, Krylov SV, Volkart G, Sykilinda NN, Kurochkina LP, Mesyanzhinov VV. 2002. Phenogenetic characterization of a group of giant ϕKZ-like bacteriophages of *Pseudomonas aeruginosa.* Genetika 38:1470-1479; Russ J Genet 1242–1250

Campbell JIA, Albrechtsen M, Sørensen J. 1995. Large *Pseudomonas* phages iolated from barley rhizosphere. FEMS Microbial Ecol 18:63-74

Hertveldt K, Lavigne R, Pleteneva E, Sernova N, Kurochkina L, Korchevskii R et al.: Genome comparison of Pseudomonas aeruginosa large phages. Journal of Molecular Biology 2005, 354: 536-545.

Krylov VN, Smirnova TA, Minenkova IB, Plotnikova TG, Zhazikov IZ, Khrenova EA. 1984. *Pseudomonas* bacteriophage ϕKZ contains an inner body in its capsid. Can J Microbiol 30:758-762

Krylov VN, Tolmachova TO, Akhverdyan VZ. 1993. DNA homology in species of bacteriophages active on *P4eudomonas aeruginosa.* Arch Virol 131:141–151

Krylov VN, Dela Cruz DM, Hertveldt K, Ackermann H-W: "phiKZ-like viruses", a proposed new genus of myovirus bacteriophages. Archives of Virology 2007, 152: 1955-1959.

Mesyanzhinov VV, Robben J, Grymonprez B, Kostyuchenko VA, Bourkaltseva MV, Sykilinda NN, Krylov VN, Volckaert G. 2002. The genome of bacteriophage ϕKZ of *Pseudomonas aeruginosa*. J Mol Biol 317:1-19

Serwer P, Hayes SJ, Zaman S, Lieman K, Rolando M, Hardies SC. 2004. Improved isolation of undersampled bacteriophages: finding of distant terminase genes. Virology 239:412-424

Thomas JA, Rolando MR, Carroll CA, Shen PS, Belnap DM, Weintraub ST et al.: Characterization of Pseudomonas chlororaphis myovirus 201varphi2-1 via genomic sequencing, mass spectrometry, and electron microscopy. Virology 2008, 376: 330-338.

Annexes:

PhiKZ (original name ϕKZ)

Background

The ***Myoviridae*** family of tailed phages has 6 genera named after their type species: P1, P2, Mu, T4 (enterics), SPO1 *(Bacillus),* phiH1 *(Halobacterium).* These phages comprise no more than a small part of the known myoviruses and differ in every respect from phiKZ. In turn, phiKZ and its relatives do not resemble any other tailed phages (except very superficially in size).

Proposals

1. To establish a new genus within the family *Myoviridae*.
2. To name this genus 'phiKZ-like viruses.'
3. To designate *Pseudomonas* phage phiK as the type species of this genus.
4. To designate *Pseudomonas* phage phiKZ as the type virus of this species.
5. To establish two more species, named Lin68 and 201phi2-1, within the genus.
6. To designate *Pseudomonas* phages Lin68 and 201phi2-1 as type viruses of these species.

GENUS "phiKZ-LIKE VIRUSES"

Type Species Pseudomonas phage phiKZ

Distinguishing Features

Virions are very large and have tails surrrounded by fibers. Heads contain a proteinic inner body and a genome of 280 kb that differs from any myovirus genome known.

Virion Properties

Morphology

Heads are icosahedra of 120 nm in diameter. Extended tails measure 184 x 20 nm and have a large collar, a base plate, and a fibrous network extending from the base plate and wrapped around the tail sheath. Heads contain a spring-like protein cyclinder in addition to DNA.

Physicochemical and Physical Properties

Infectivity is chloroform-resistant.

Nucleic Acid

Genomes are ~280,000 bp in size, have a G+C content of 37%, and consist of 306 ORFs and 6 tRNAs. Unusual bases are absent. The genome of phage phiKZ has been fully sequenced. It contains many elements from other bacteriophages, eukaryote viruses, bacteria, and eukaryotic organisms.

Proteins

Virions contain at least 40 proteins, five of which are strongly homologous collagen.

Lipids None known.
Carbohydrates None known.

Genome Organization and Replication

Genomes are circularly permuted and terminally redundant and have a mosaic structure.

Antigenic Properties **No group antigens are reported.**

Biological Properties

Phages are virulent general transductants and specific for *Pseudomonas* bacteria. Most were isolated from soil. Plaques are extremely small (0.1 mm in diameter). Representatives have been found in many countries (USA, Russia, Georgia, Iran, Philippines).

List of Species Demarkation Criteria in the Genus

Species differ in DNA homology, restriction endonuclease patterns, and N-terminal sequences of the major capsid protein. Species LU11 has spiral fibers laying along the tail shaft and particles sometimes present a double collar.

List of Species in the Genus

Official virus species names are in italics. Tentative virus species names, alternative names (), strains, or serotypes are not italicized. Virus names, genome sequence accession numbers [], and assigned abbreviations are:

SPECIES IN THE GENUS

Pseudomonas phage phiKZ		
Pseudomonas phage phiKZ	[AF399001]	(phiKZ)
Pseudomonas phage Lin21		
Pseudomonas phage NN		
Pseudomonas phage PTB80		
Pseudomonas phage Lin68		
Pseudomonas phage Lin68		(Lin68)
Pseudomonas phage LBG22		
Pseudomonas phage 201phi2-1		
Pseudomonas phage *201phi2-1*	[AJ697969	(EL)

Similarity to Other Taxa **Not reported.**

References

Ackermann H-W, Cartier C, Slopek S, Vieu J-F. 1988. Morphology of *Pseudomonas aeruginosa* typing phages of the Lindberg set. Ann Inst Pasteur/Virol 139:389-404

Bourkaltseva MV, Krylov VN, Pleteneva EA, Shaburova OV, Krylov SV, Volkart G, Sykilinda NN, Kurochkina LP, Mesyanzhinov VV. 2002. Phenogenetic characterization of a group of giant ϕKZ-like bacteriophages of *Pseudomonas aeruginosa.* Genetika 38:1470-1479; Russ J Genet 1242–1250

Campbell JIA, Albrechtsen M, Sørensen J. 1995. Large *Pseudomonas* phages iolated from barley rhizosphere. FEMS Microbial Ecol 18:63-74

Krylov VN, Dela Cruz DM, Hertveldt K, Ackermann H-W. 2007. "ϕKZ-like viruses, a proposed new genus of myovirus bacteriophages. Arch Virol DOI 10.1007/soo705-1037-7

Krylov VN, Smirnova TA, Minenkova IB, Plotnikova TG, Zhazikov IZ, Khrenova EA. 1984. *Pseudomonas* bacteriophage ϕKZ contains an inner body in its capsid. Can J Microbiol 30:758-762

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Serwer P, Hayes SJ, Zaman S, Lieman K, Rolando M, Hardies SC. 2004. Improved isolation of undersampled bacteriophages: finding of distant terminase genes. Virology 239:412-424

COMMENTS

1. A G+C content of 48% that was reported in early work (1978 and 1980). This has been superseded by sequence data and is not cited.

2. I do not mention ϕKZ-like phages that were mentioned somewherein the literature and then disappeared (ϕNZ, PMN17, see refs. Krylov et al., 1993; Sharibjanova, 1992; Sharibjanova et al., 1992) or which are as yet unpublished (phage 1615 or Ph-1615; Shaburova et al.).

3. The group was already called a genus (Bourkaltseva et al., 2002; Krylov et al., 2003)

SUPPORTING MATERIAL

Dimensions

References	Phage	Head, nm	Tail, nm
Ackermann 1988	21, 68	124	184 x 19
Krylov 1984	phiKZ	120	180 x 20
Krylov 1978	phiKZ	120	180 x 20
Adamia 1999	phiST-1	140	240 x 30
Campbell 1995	Psp3	130	197
Serwer	201phi2-1	140	200 (Figure 1)

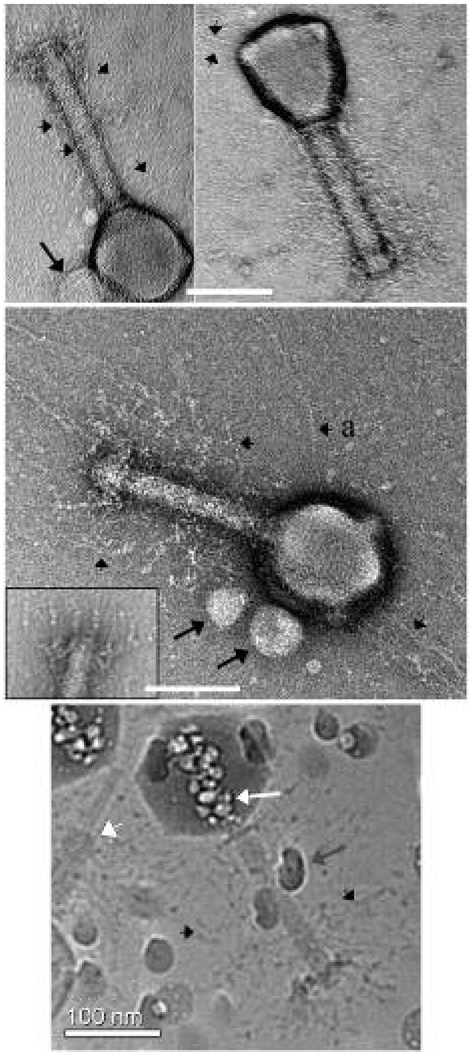

Figure 1: Electron micrographs of 201phi2-1. Black short tailed arrows in all panels highlight several fine fibers projecting from the tail sheaths or heads of 2012-1 virions. (Top panel) Two particles of purified 2012-1 that were treated with DNAase immediately prior to being negatively stained with uranyl acetate. (Middle panel) Negatively stained 2012-1 without prior DNAase treatment. The arrow marked “a” indicates a possible strand of DNA. The inset image highlights a well stained baseplate from a virion. (Bottom panel) Cryo-EM image of 2012-1, without DNAase treatment. The white short tailed arrow highlights a particle (at the image edge) that has a contracted tail sheath and an empty head. The large white arrow highlights gaseous bubbles which formed in the head despite the use of low-dose techniques (see text). In the top and middle rows, large black arrows highlight particles that co-purified with 2012-1 virions. In the bottom row, the large gray arrow highlights contamination on the cryo-EM specimen. All three scale bars = 100 nm.

Proteome comparison

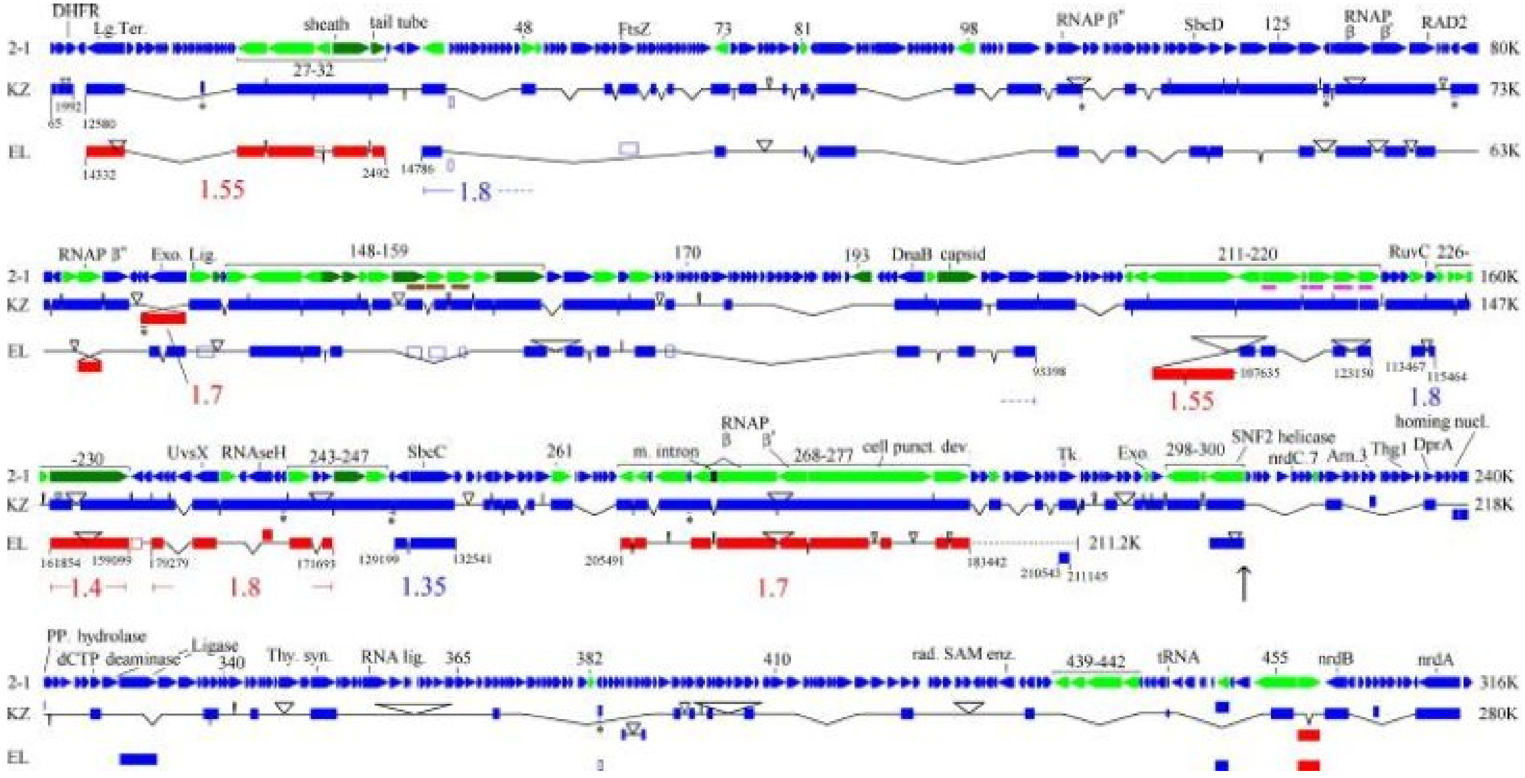

Figure 2: Genome map of 201phi2-1 in comparison to KZ and EL. Color coding in the 201phi2-1 track: green — gene product detected by MS (with abundant proteins in dark green); brown and magenta — two families of paralogues. Color coding in the KZ and EL tracks: blue — same orientation as the homologous 201phi2-1 gene, red — opposite orientation. Solid boxes are matching segments in the style of tblastx (see Materials and methods). An asterisk below an underlined section of a phiKZ match indicates protein sequence similarity within a newly predicted gene in KZ (Supplementary Table 1). Hollow boxes indicate similarity detection requiring a profile method. The names of individual phiKZ or EL genes found within the matching segments are in GenBank EU197055. The connectors between matching segments are inflected to indicate the amount of DNA inserted or deleted relative to 201phi2-1. Coordinates within the KZ or EL genomes are given at the ends of chains of matches. The average 201phi2-1:EL/201phi2-1:phiKZ divergence over segments delimited by inversion points is given in the same color as the chain of matches defining the segment and located below the EL track. The black dotted line for EL portrays the end of its genome relative to its rightmost major matching segment. Boxes not connected into chains map to uncorrelated positions in the different genomes. The vertical arrow indicates the beginning of the region discussed for its high rate of gene exchange in the text. Abbreviations are Lg. Ter (large subunit of terminase), RNAP (RNA polymerase), Exo. (exonuclease), Lig. (ligase), m. intron (mobile intron), Tk (thymidine kinase), Thy. syn. (thymidylate synthetase), rad. SAM enz. (radical SAM enzyme).

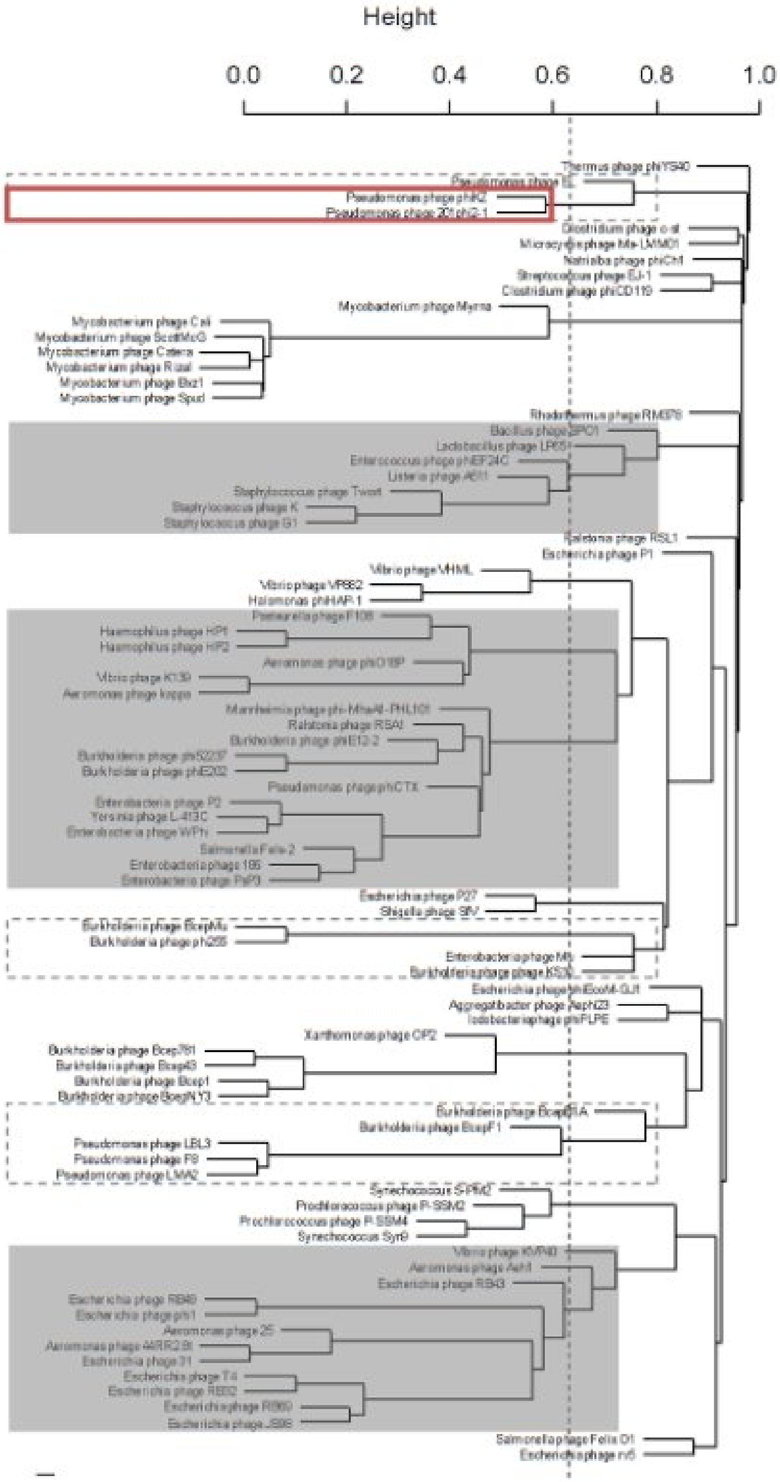

Figure 3: The relative dissimilarity between the phage proteomes (between 0.0 and 1.0) forms the basis for the proposed groupings. The dotted lines reflects the cut-off value used for the establishement of genera, used consistently for all Myoviridae and the previously defined Podoviridae (Lavigne et al., 2008). Subfamily and tentative subfamily groupings are indicated in the grey and dotted boxes, respectively. The “phiKZ-like viruses” are marked in red. Note the ‘proteomic divergence’ which excludes phage EL from this genus.

References not to be cited in the Report:

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Some physicochemical properties of bacteriophage ϕKZ. Mol Biol (SSSR) 14:802-805 (transl.)