

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

Code[†] **2007.110B** To create a new genus in the family* ***Podoviridae***

Code[†] **2007.111B** To name the new genus* **“*phiKMV-like viruses*”**

Code[†] **2007.112B** To designate as type species the species named*
Enterobacteria phage phiKMV

Code[†] **2007.113B** To create and assign as species of the new genus*:
Enterobacteria phage phiKMV
Enterobacteria phage LKA1

[†] Assigned by ICTV officers

* repeat these lines and the corresponding arguments for each genus created in the family

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Old Taxonomic Order

| | |
|----------------------------------|------------------------------------|
| Order | Caudovirales |
| Family | Podoviridae |
| Genus | T7-like viruses |
| Type Species | <i>Enterobacteria phage phiKMV</i> |
| Species in the Genus | 9 |
| Tentative Species in the Genus | 11 |
| Unassigned Species in the family | 7 |

New Taxonomic Order

| | |
|----------------------------------|------------------------------------|
| Order | Caudovirales |
| Family | Podoviridae |
| Genus | phiKMV-like viruses |
| Type Species | <i>Enterobacteria phage phiKMV</i> |
| Species in the Genus | 6 |
| Tentative Species in the Genus | 0 |
| Unassigned Species in the Family | 0 |

ICTV-EC comments and response of the SG

Argumentation to choose the type species in the genus

Bacteriophage phiKMV is more intensely studied than the recently sequenced bacteriophages LKD16 and LKA1 (Ceysens *et al.*, 2006) and LUZ19. The structural proteins are identified (Lavigne *et al.*, 2006), its DNA ligase and its lytic proteins are characterized (Lavigne *et al.*, 2004; Lavigne *et al.*, 2005; Briers *et al.*, 2006) while its early genes and transcription scheme are currently under investigation.

Species demarcation criteria in the genus

Based on DNA sequence analysis, phages phiKMV, LKD16, phikF77 and LUZ19 are clearly related. Although LKD16 is closely related to phiKMV and shows strong similarity in 90% of its predicted open reading frames, differences in host range and infectivity parameters have been shown, albeit insufficient to warrant the establishment as different species (Ceysens *et al.*, 2006). Phage LKA1 is more distantly related and has an extremely narrow host spectrum, and has minimal DNA homology. However, similarity in 45% of its gene products is observed and genome organization is conserved compared to the other phages of the proposed subgenus.

Bacteriophages PT2 & PT5 are fully sequenced phages from the Eliava institute and show minimal mutational differences compared to phiKMV (A.M. Kropinski, personal communication) and a complete conservation of the genome organization. Genome accession numbers include:

NC_011107 Pseudomonas phage PT2
NC_011105 Pseudomonas phage PT5
NC_009936 Pseudomonas phage LKA1
NC_009935 Pseudomonas phage LKD16
NC_005045 Pseudomonas phage phiKMV
NC_012418 Pseudomonas phage phikF77

List of Species in the created genus

Enterobacteria phage phiKMV
Enterobacteria phage LKA1

List of Tentative Species in the created genus

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Argumentation to create a new genus:

This genus contains three recently isolated and sequenced phages, initially classified as 'T7-like Podoviridae'. However, homology to phage T7 is limited. Using the CoreGenes algorithm (<http://binf.gmu.edu:8080/coregenes2.0/>), only 9 homologue gene products can be detected for phiKMV and T7. The fact that phiKMV is not a genetic orphan was recently supported by the sequencing of phages LKD16 and LKA1. Additional evidence of the worldwide environmental distribution of this type of lytic phages was recently provided by the isolation of several phages from various Russian environmental samples, which were annotated as "phiKMV-like viruses" based on Southern hybridization experiments, including PRA1 (Burkal'tseva *et al.*, 2006).

Partial /complete genome sequencing on bacteriophages LUZ19, LKD16, phikF77, PT2, PT5 and PS028, MMA1, MMA2, FMV, PBK, LUZ24 show these six phages are also close DNA homologues of phiKMV.

In contrast to other members of the T7-like phages, phiKMV and LKA1 carry a single-subunit RNA polymerase gene adjacent to the structural genome region instead of in the early region, and they lack conserved phage promoters. These features suggest major differences in the transcription scheme for phiKMV-like phages.

Therefore, phages from the proposed phiKMV genus may have evolved separately from the 'sensu strictu' T7-like phages (T7, T3, gh-1, phiA1122, phiYeO3-12 and VP4) from a common ancestor. From this perspective the T7-like and phiKMV-like phages can be considered as members of the same subfamily.

Origin of the proposed genus name

phiKMV-like phages is named after its hallmark member bacteriophage phiKMV.

References

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