Template for Taxonomic Proposal to the ICTV Executive Committee To create a new Unassigned Genus

Code [†] 2005.084B.04	To create a new genus*
Code [†] 2005.085B.04	To name the new genus* <i>Ampullavirus</i>
Code [†] 2005.086B.04	To designate the speciesAcidianus bottle-shaned virusAs the type species of the new genus*
Code [†] 2005.087B.04	To designate the following as species of the new genus*:
Code [†]	Acidianus bottle-shaped virus 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	
	address(es) of the Taxonomic Proposal
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Old Taxonomic Order	r

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

New Taxonomic Order

 Order

 Family

 Genus
 Ampullavirus

 Type Species
 Acidianus bottle-shaped virus

 Species in the Genus
 Acidianus bottle-shaped virus

 Tentative Species in the Genus
 none

 Unassigned Species in the family
 none

Argumentation to choose the type species in the genus

Only virus described

Species demarcation criteria in the genus

Not appropriate

List of Species in the created genus

Acidianus bottle-shaped virus (ABV)

List of Tentative Species in the created genus

none

Argumentation to create a new genus:

We propose classifying the *Acidianus bottle-shaped virus* as a first representative of a new genus because of the unique bottle-shaped morphology of the virion which, to our knowledge, has not previously been observed in the viral world. Moreover, the complex asymmetric virion, lacking elements with icosahedral or regular helical symmetry, with two completely different structures at each end and an envelope encasing a funnel-shaped core represents, as far as we can judge, represents a principally novel type of virus particle.

The funnel-shaped core of the enveloped virion consists of three distinct structural units: the "stopper", the nucleoprotein cone, consisting of double-stranded DNA and DNA-binding proteins, and the inner core. Electron microscopy evidence suggests that the "stopper" is a structural element involved in recognition of cellular receptors and adsorption, and it is the only component to which DNA is directly attached. The broad end of the virion exhibits an unusual structure with the 20 (\pm 2) thin filaments regularly distributed around, and inserted into, a disc or ring. TEM observations indicate that these filaments are not involved in adsorption and their function remains unclear.

NEW INFORMATION

The double-stranded, linear DNA genome of the virus ABV contains 23,794 bp including 580 bp inverted terminal repeats (ITR). No similarity was found to any gene/genomes in the public databases at the nucleotide sequence level while only three of the 59 identified ORFs yield limited amino acid sequence similarity (<40% identity) with proteins in public databases. They include a protein-primed DNA polymerase, a thymidylate kinase and a glycosyltransferase. The latter is the only ABV protein with homologs in other archaeal viruses.

Origin of the proposed genus name

From the Latin ampulla, for bottle

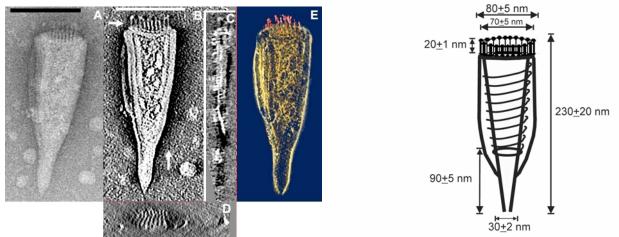
References

Häring, M., R. Rachel, X. Peng, R. A. Garrett, and D. Prangishvili (2005). Diverse viruses in hot springs of Pozzuoli, Italy, including a unique archaeal virus, *Acidianus* bottle-shaped virus, from a new family, the *Ampullaviridae*. J. Virol., vol. 79, No. 15, in press.

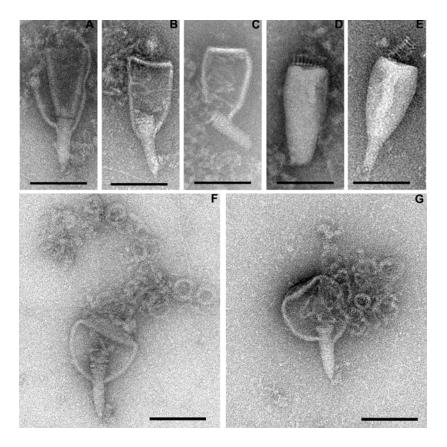
Häring M., R. Rachel, X. Peng, R. A. Garrett, and D. Prangishvili. 2005. Diverse viruses in hot springs of Pozzuoli, Italy, including a unique bottle-shaped archaeal virus ABV from a new family, the *Ampullaviridae*. J. Virol. 147, 2419-2429.

Peng, X., T. Basta, M. Haring, R. A. Garrett, and D. Prangishvili. 2007. Genome of *Acidianus* bottle-shaped virus and insights into the replication and packaging mechanisms. *Virology* 364, 237-243.

Annexes:



Electron micrograph and 3D reconstruction of ABV negatively stained with 3% uranyl acetate. (A) Original micrograph at 0 degree tilt. (B) Horizontal slice (0.7 nm) through the 3D data set of 3D reconstruction of ABV. (C) Vertical slice (YZ), (D) vertical slice (XZ) through the same data set. (C) and (D), the position of the slices are indicated by white arrows in B. (E) Color-coded representation of virions 3D structure. Bars: 100 nm. One the right side, a scheme of the structure of an ABV virion



Electron micrographs of partially disrupted particles of ABV negatively stained with 3% uranyl acetate. Bar, 100 nm.