

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

Code[†] To create a new family*

Code[†] To name the new family*

Code[†] To designate the following genera as part of the new family*:

[†] Assigned by ICTV officers

[°] Leave blank is not appropriate

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

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Old Taxonomic Order

Order
Family
Genus *Bicaudavirus*
Type Species *Acidianus two-tailed virus*
Species in the Genus *Acidianus two-tailed virus*
Tentative Species in the Genus none
Unassigned Species in the family none

New Taxonomic Order

Order
Family *Bicaudaviridae*
Genus *Bicaudavirus*
Type Species *Acidianus two-tailed virus*
Species in the Genus *Acidianus two-tailed virus*
Tentative Species in the Genus none
Unassigned Species in the family none

ICTV-EC comments and response of the SG

Accepted. Move to 02.

Argumentation to create a new family:

We propose classifying the *Acidianus two-tailed virus* (ATV) as a first representative of a new family because of the unique morphology of the virion, its exceptional property to develop two tails outside and independently of the host cell, and specific genomic properties.

Virions of the *Acidianus two-tailed virus* are released from host cells as lemon-shaped particles and thereafter develop long tails, one at each of two pointed ends, which terminate in anchor-like structures. This major morphological development takes place specifically at temperatures above 75°C, close to that of the natural habitat, and it does not require the presence of the host cells, an exogenous energy source and any co-factors. Although in the viral world several examples of natural extracellular morphogenesis are known, these are triggered on a host-cell surface concurrently with the virus budding or adsorption. To our knowledge, ATV is the first example of a virus with a host-independent as well as extracellular functional activity.

The *Acidianus two-tailed virus* is the only known virus of hyperthermophilic acidophilic host causing lysis of the host cell. It is capable of two alternative developmental cycles: after infection, either ATV replication occurs and leads to lysis, or the infected cell is converted into a lysogene (in lysogens viral DNA is found integrated into the host chromosome) in which virus production can be induced by stress factors, e.g. UV-irradiation, decrease of temperature.

Among putative genes there are very few homologues to genes of characterized viruses. All of them are homologous to viruses of the hyperthermophilic archaeal hosts (genus *Acidianus* or the closely related genus *Sulfolobus*). These few similarities are compatible with horizontal gene transfer, rather than with common ancestry of the viruses.

Origin of the proposed family name

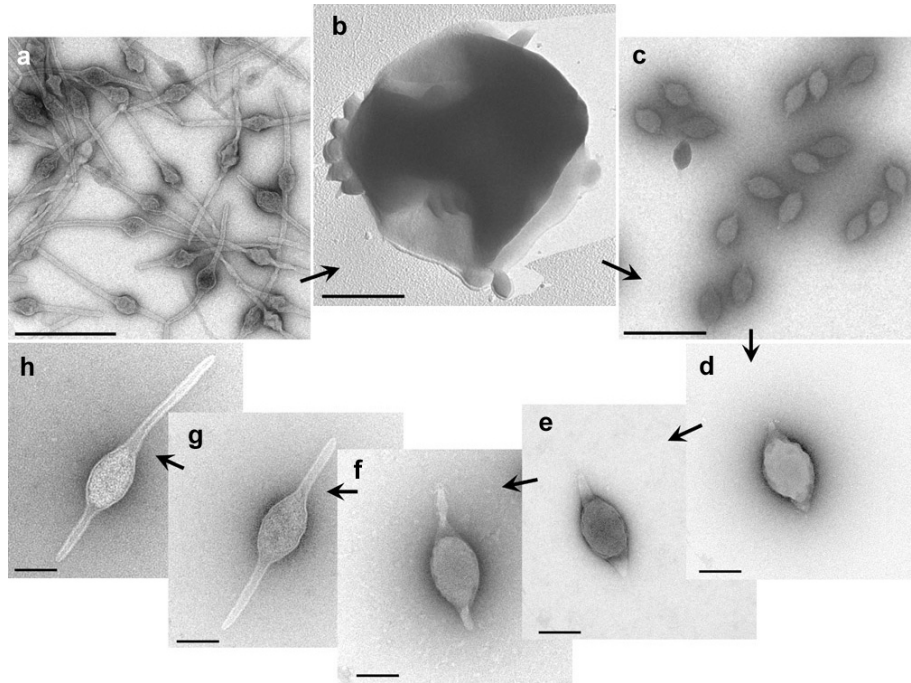
From the Latin *cauda*, for tail

References

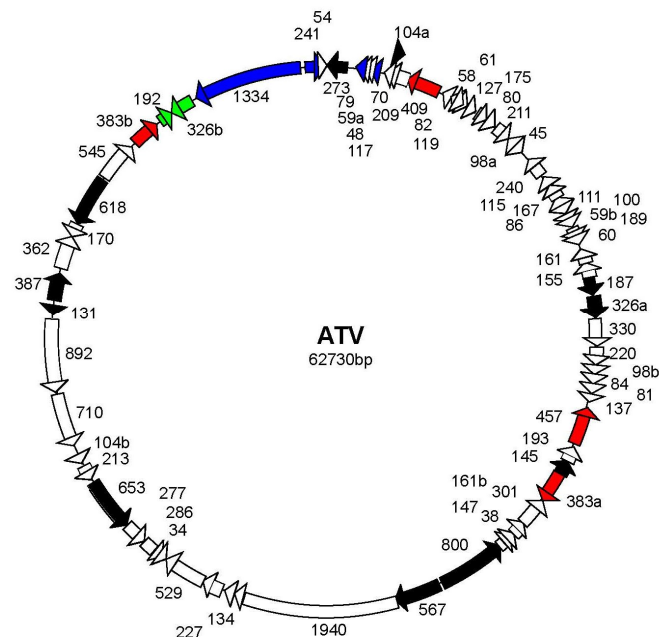
Häring, M., G. Vestergaard, R. Rachel, L. Chen, R. A. Garrett, and D. Prangishvili (2005). Independent virus development outside a host. *Nature* vol. 436, pp. 1101-1102.

Prangishvili, D., G. Vestergaard, M. Häring, R. Aramayo, T. Basta, R. Rachel, and R.A. Garrett (2006) Structural and genomic properties of the hyperthermophilic archaeal virus ATV with an extracellular stage of the reproductive cycle. *J. Mol. Biol.* 359, 1203-1216.

Annexes:



Electron micrographs of “*Acidianus convivator*” and different forms of ATV. **a**, Virions in an enriched environmental sample. **b**, Extrusion of virions from an ATV-infected cell of “*A. convivator*”. **c**, Virions in a growing culture of ATV-infected “*A. convivator*”, 2 days p.i.. **d**, As for **c**, but purified by CsCl density gradient. **e-h**, As for **d**, but incubated at 75°C for 2, 5, 6, and 7 days, respectively. All preparations were negatively stained with 3% uranyl acetate, except for **b**, which was platinum shadowed. Bars: **a** to **c** 0.5 μ m; **d** to **h** 0.1 μ m.



A gene map of the circular ATV genome. ORFs are represented by arrows and labelled according to the number of amino acids in the predicted proteins. Genes for putative AAA ATPases, transposases, integrase and highly coiled-coil proteins are indicated. Colour coded ORFs correspond to: black, virion proteins; blue - homologous ORFs present in other crenarchaeal hyperthermophilic viruses, green - homologous ORFs occurring in conjugative plasmids of *Sulfolobus*; red - transposases.