

Taxonomic Proposal to the ICTV Executive Committee

From the Bacterial SC

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

none

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

His 1 virus

Code[†] To designate the species
As the type species of the new genus*

Code[†] To create a new genus in the family[°]

Code[†] To name the new genus*

[†] Assigned by ICTV officers

[°] leave blank if inappropriate or in the case of an unassigned genus

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

Author(s) with email address(es) of the Taxonomic Proposal

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New Taxonomic Order

Order

Family

Genus *Salterprovirus*

Type Species *His 1 virus*

List of Species in the genus *His 1 virus*

List of Tentative Species in the Genus none

List of 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

His 1 virus

List of Tentative Species in the created genus

none

Argumentation to create a new genus:

The lemon-shaped virus **His1 virus** was originally thought to be closely related to the **SSV1** virus (Family *Fuselloviridae*, Genus *Fusellovirus*. Host *Sulfolobus solfataricus*). They are archaeal viruses of similar morphology (lemon or spindle shaped), and density, and contained dsDNA genomes of similar size (C. Bath and M. L. Dyll-Smith. 1998).

Since the 1998 publication, **His1 virus** has been studied in more detail and we now believe there is sufficient evidence to show that **His1 virus** and **SSV1** differ in a number of fundamental ways. **His1 virus** is lytic, whereas SSV1 is temperate. The **His1 virus** genome has been sequenced and is linear dsDNA of 14,462bp long, AT-rich (59%), and shows no similarity at the nucleotide or predicted amino acid level to **SSV1** or any other published virus. The **His1 virus** genome has inverted terminal repeats of 162 nt and protein attached at the termini. The largest ORF predicts a protein with significant amino acid similarity to family B DNA polymerases, specifically to the subset that use protein priming. The evidence indicates that **His1 virus** replicates its genome using its own DNA polymerase and the terminal proteins as primers. These characteristics are very different from **SSV1**, which does not appear to encode a DNA polymerase, has a circular dsDNA genome, and forms a prophage by integration at a specific site into its host genome.

Replication via terminal proteins is a common method among some bacteriophages and eukaryotic viruses (e.g. Adenovirus) but has not been described before among the known archaeal viruses. These fundamental differences show that His1 virus should be classified in a new genus, separate from that of **SSV1**. We are unsure of the criteria for membership of the Family *Fuselloviridae*. If it includes the genomic features of the genus *Fusellovirus* (circular dsDNA genome, gene organization, prophage state), then His1 virus cannot be placed there either.

We are in the process of publishing the new information on His1 virus and would like to state its official taxonomic status in the manuscript.

Origin of the proposed genus name

The proposed genus name *Salterprovirus* comes from the acronym of salt terminal protein, and reflects the characteristic replication method as well as the environment that the virus comes from

References

C. Bath and M. L. Dyll-Smith. 1998

C. Bath and M. L. Dyll-Smith. 1998. **His1**, an archaeal virus of the *Fuselloviridae* Family that infects *Haloarcula hispanica*. *J.Virol.*72: 9392-9395

Annexes: