

# TAXONOMIC PROPOSALS FROM THE *HERPESVIRIDAE* STUDY GROUP

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## THE *HERPESVIRIDAE* STUDY GROUP (2003-2005)

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## LIST OF PROPOSALS

- 2005.020V.04      To remove the following species from the genus *Rhadinovirus* of the subfamily *Gammaherpesvirinae* in the family *Herpesviridae*:  
*Alcelaphine herpesvirus 1*  
*Alcelaphine herpesvirus 2*  
*Equid herpesvirus 2*  
*Equid herpesvirus 5*  
*Equid herpesvirus 7*  
*Hippotragine herpesvirus 1*  
*Mustelid herpesvirus 1*  
*Ovine herpesvirus 2*
- 2005.021V.04      To remove the following unassigned viruses from the family *Herpesviridae*:  
*Acipenserid herpesvirus 1*  
*Acipenserid herpesvirus 2*  
*Anguillid herpesvirus 1*  
*Cyprinid herpesvirus 1*  
*Cyprinid herpesvirus 2*  
*Esocid herpesvirus 1*  
*Percid herpesvirus 1*  
*Pleuronectid herpesvirus 1*  
*Ranid herpesvirus 1*  
*Ranid herpesvirus 2*  
*Salmonid herpesvirus 1*  
*Salmonid herpesvirus 2*  
*Ostreid herpesvirus 1*  
*Ateline herpesvirus 3*  
*Columbid herpesvirus 1*  
*Elephantid herpesvirus 1*  
*Suid herpesvirus 2*

## Order *Herpesvirales*

- 2005.022V.04      To create a new order in the dsDNA viruses
- 2005.023V.04      To name the order *Herpesvirales*
- 2005.024V.04      To designate the following family in the order *Herpesvirales* *Herpesviridae*

**Family *Alloherpesviridae***

- 2005.025V.04 To create a new family in the order *Herpesvirales*
- 2005.026V.04 To name the family *Alloherpesviridae*
- 2005.027V.04 To designate the following genus in the family *Alloherpesviridae*  
*Ictalurivirus*
- 2005.028V.04 To designate the following unassigned viruses in the family *Alloherpesviridae*  
*Acipenserid herpesvirus 1*  
*Acipenserid herpesvirus 2*  
*Anguillid herpesvirus 1*  
*Cyprinid herpesvirus 1*  
*Cyprinid herpesvirus 2*  
*Esocid herpesvirus 1*  
*Percid herpesvirus 1*  
*Pleuronectid herpesvirus 1*  
*Ranid herpesvirus 1*  
*Ranid herpesvirus 2*  
*Salmonid herpesvirus 1*  
*Salmonid herpesvirus 2*
- 2005.029V.04 To create the following unassigned species in the family *Alloherpesviridae*  
*Cyprinid herpesvirus 3*

**Family *Malacoherpesviridae***

- 2005.030V.04 To create a new family in the order *Herpesvirales*
- 2005.031V.04 To name the family *Malacoherpesviridae*
- 2005.032V.04 To create a new genus in the family *Malacoherpesviridae*
- 2005.033V.04 To name the genus *Ostreavirus*
- 2005.034V.04 To designate *Ostreid herpesvirus 1* the type species of the genus *Ostreavirus*
- 2005.035V.04 To create the following species in the genus *Ostreavirus* *Ostreid herpesvirus 1*

**Family *Herpesviridae***

- 2005.036V.04 To create a new genus in the subfamily *Gammaherpesvirinae* of the family *Herpesviridae*
- 2005.037V.04 To name the genus *Macavirus*
- 2005.038V.04 To designate *Alcelaphine herpesvirus 1* the type species of the genus *Macavirus*
- 2005.039V.04 To designate the following species in the genus *Macavirus*  
*Alcelaphine herpesvirus 1*  
*Alcelaphine herpesvirus 2*  
*Hippotragine herpesvirus 1*  
*Ovine herpesvirus 2*
- 2005.040V.04 To create the following species in the genus *Macavirus*  
*Bovine herpesvirus 6*  
*Caprine herpesvirus 2*
- 2005.041V.04 To create the following species in the genus *Macavirus*  
*Suid herpesvirus 3*

2005.042V.04	To create the following species in the genus <i>Macavirus</i>	<i>Suid herpesvirus 4</i>
2005.043V.04	To create the following species in the genus <i>Macavirus</i>	<i>Suid herpesvirus 5</i>
2005.044V.04	To create a new genus in the subfamily <i>Gammaherpesvirinae</i> of the family <i>Herpesviridae</i>	
2005.045V.04	To name the genus	<i>Percavirus</i>
2005.046V.04	To designate the species <i>Equid herpesvirus 2</i> the type species of the genus <i>Percavirus</i>	
2005.047V.04	To designate the following species in the genus <i>Percavirus</i>	<i>Equid herpesvirus 2</i> <i>Equid herpesvirus 5</i> <i>Mustelid herpesvirus 1</i>
2005.048V.04	To create the following species in the subfamily <i>Gammaherpesvirinae</i>	<i>Equid herpesvirus 7</i>
2005.049V.04	To create a new genus in the subfamily <i>Betaherpesvirinae</i> of the family <i>Herpesviridae</i>	
2005.050V.04	To name the genus	<i>Proboscivirus</i>
2005.051V.04	To designate the species <i>Elephantid herpesvirus 1</i> the type species of the genus <i>Proboscivirus</i>	
2005.052V.04	To create the following species in the genus <i>Proboscivirus</i>	<i>Elephantid herpesvirus 1</i>
2005.053V.04	To create the following species in the genus <i>Mardivirus</i> in the subfamily <i>Alphaherpesvirinae</i> of the family <i>Herpesviridae</i>	<i>Columbid herpesvirus 1</i>
2005.054V.04	To designate the following species in the genus <i>Iltovirus</i> in the subfamily <i>Alphaherpesvirinae</i> of the family <i>Herpesviridae</i>	<i>Psittacid herpesvirus 1</i>
2005.055V.04	To create the following species of the genus <i>Rhadinovirus</i> in the subfamily <i>Gammaherpesvirinae</i> of the family <i>Herpesviridae</i>	<i>Ateline herpesvirus 3</i>
2005.056V.04	To create the following unassigned species in the subfamily <i>Betaherpesvirinae</i> of the family <i>Herpesviridae</i>	<i>Suid herpesvirus 2</i>
2005.057V.04	To create the following unassigned species in the subfamily <i>Alphaherpesvirinae</i> of the family <i>Herpesviridae</i>	<i>Chelonid herpesvirus 5</i>
2005.058V.04	To create the following unassigned species in the subfamily <i>Alphaherpesvirinae</i> of the family <i>Herpesviridae</i>	<i>Chelonid herpesvirus 6</i>
2005.059V.04	To create the following unassigned species in the subfamily <i>Gammaherpesvirinae</i> of the family <i>Herpesviridae</i>	<i>Phocid herpesvirus 2</i>
2005.060V.04	To create the following unassigned species in the family <i>Herpesviridae</i>	<i>Iguanid herpesvirus 2</i>

### Changes to species names

2005.061V.04	To rename <i>Cercopithecine herpesvirus 1</i> in the genus <i>Simplexvirus</i> of the family <i>Herpesviridae</i> as	<i>Macacine herpesvirus 1</i>
2005.062V.04	To rename <i>Cercopithecine herpesvirus 16</i> in the genus <i>Simplexvirus</i> of the family <i>Herpesviridae</i> as	<i>Papiine herpesvirus 2</i>

2005.063V.04	To rename <i>Cercopithecine herpesvirus 8</i> in the genus <i>Cytomegalovirus</i> of the family <i>Herpesviridae</i> as <i>Macacine herpesvirus 3</i>
2005.064V.04	To rename <i>Pongine herpesvirus 4</i> in the genus <i>Cytomegalovirus</i> of the family <i>Herpesviridae</i> as <i>Panine herpesvirus 2</i>
2005.065V.04	To rename <i>Cercopithecine herpesvirus 12</i> in the genus <i>Lymphocryptovirus</i> of the family <i>Herpesviridae</i> as <i>Papiine herpesvirus 1</i>
2005.066V.04	To rename <i>Cercopithecine herpesvirus 15</i> in the genus <i>Lymphocryptovirus</i> of the family <i>Herpesviridae</i> as <i>Macacine herpesvirus 4</i>
2005.067V.04	To rename <i>Pongine herpesvirus 1</i> in the genus <i>Lymphocryptovirus</i> of the family <i>Herpesviridae</i> as <i>Panine herpesvirus 1</i>
2005.068V.04	To rename <i>Pongine herpesvirus 3</i> in the genus <i>Lymphocryptovirus</i> of the family <i>Herpesviridae</i> as <i>Gorilline herpesvirus 1</i>
2005.069V.04	To rename <i>Cercopithecine herpesvirus 17</i> in the genus <i>Rhadinovirus</i> of the family <i>Herpesviridae</i> as <i>Macacine herpesvirus 5</i>
2005.070V.04	To rename <i>Cercopithecine herpesvirus 10</i> unassigned in the family <i>Herpesviridae</i> as <i>Macacine herpesvirus 6</i>
2005.071V.04	To rename <i>Cercopithecine herpesvirus 13</i> unassigned in the family <i>Herpesviridae</i> as <i>Macacine herpesvirus 7</i>
2005.072V.04	To rename <i>Callitrichine herpesvirus 1</i> unassigned in the subfamily <i>Gammaherpesvirinae</i> of the family <i>Herpesviridae</i> as <i>Saguinine herpesvirus 1</i>

## NEW TAXONOMIC ORDER

<b>Order</b>	<b>HERPESVIRALES</b>
<b>Family</b>	<b>Herpesviridae</b>
<b>Subfamily</b>	<b>Alphaherpesvirinae</b>
<b>Genus</b>	<b>Simplexvirus</b>
<b>Type Species</b>	<i>Human herpesvirus 1</i>
<b>Species in the genus</b>	<i>Ateline herpesvirus 1</i> <i>Bovine herpesvirus 2</i> <i>Cercopithecine herpesvirus 2</i> <i>Human herpesvirus 1</i> <i>Human herpesvirus 2</i> <i>Macacine herpesvirus 1</i> (previously <i>Cercopithecine herpesvirus 1</i> ) <i>Macropodid herpesvirus 1</i> <i>Macropodid herpesvirus 2</i> <i>Papiine herpesvirus 2</i> (previously <i>Cercopithecine herpesvirus 16</i> ) <i>Saimiriine herpesvirus 1</i>
<b>Genus</b>	<b>Varicellovirus</b>
<b>Type Species</b>	<i>Human herpesvirus 3</i>
<b>Species in the genus</b>	<i>Bovine herpesvirus 1</i> <i>Bovine herpesvirus 5</i> <i>Bubaline herpesvirus 1</i> <i>Canid herpesvirus 1</i> <i>Caprine herpesvirus 1</i> <i>Cercopithecine herpesvirus 9</i> <i>Cervid herpesvirus 1</i>

	<i>Cervid herpesvirus 2</i>
	<i>Equid herpesvirus 1</i>
	<i>Equid herpesvirus 3</i>
	<i>Equid herpesvirus 4</i>
	<i>Equid herpesvirus 8</i>
	<i>Equid herpesvirus 9</i>
	<i>Felid herpesvirus 1</i>
	<i>Human herpesvirus 3</i>
	<i>Phocid herpesvirus 1</i>
	<i>Suid herpesvirus 1</i>
	<i>Equid herpesvirus 6</i>
<b>Unassigned virus in the genus</b>	
<b>Genus</b>	<b><i>Mardivirus</i></b>
<b>Type Species</b>	<i>Gallid herpesvirus 2</i>
<b>Species in the genus</b>	<i>Columbid herpesvirus 1</i>
	<i>Gallid herpesvirus 2</i>
	<i>Gallid herpesvirus 3</i>
	<i>Meleagrid herpesvirus 1</i>
<b>Genus</b>	<b><i>Iltovirus</i></b>
<b>Type Species</b>	<i>Gallid herpesvirus 1</i>
<b>Species in the genus</b>	<i>Gallid herpesvirus 1</i>
	<i>Psittacid herpesvirus 1</i>
<b>Unassigned species in the subfamily</b>	<i>Chelonid herpesvirus 5</i>
	<i>Chelonid herpesvirus 6</i>
<b>Subfamily</b>	<b><i>Betaherpesvirinae</i></b>
<b>Genus</b>	<b><i>Cytomegalovirus</i></b>
<b>Type Species</b>	<i>Human herpesvirus 5</i>
<b>Species in the genus</b>	<i>Cercopithecine herpesvirus 5</i>
	<i>Human herpesvirus 5</i>
	<i>Macacine herpesvirus 3</i> (previously <i>Cercopithecine herpesvirus 8</i> )
	<i>Panine herpesvirus 2</i> (previously <i>Pongine herpesvirus 4</i> )
<b>Unassigned viruses in the genus</b>	<i>Aotine herpesvirus 1</i>
	<i>Aotine herpesvirus 3</i>
<b>Genus</b>	<b><i>Muromegalovirus</i></b>
<b>Type Species</b>	<i>Murid herpesvirus 1</i>
<b>Species in the genus</b>	<i>Murid herpesvirus 1</i>
	<i>Murid herpesvirus 2</i>
<b>Genus</b>	<b><i>Roseolovirus</i></b>
<b>Type Species</b>	<i>Human herpesvirus 6</i>
<b>Species in the genus</b>	<i>Human herpesvirus 6</i>
	<i>Human herpesvirus 7</i>
<b>Genus</b>	<b><i>Proboscivirus</i></b>
<b>Type Species</b>	<i>Elephantid herpesvirus 1</i>
<b>Species in the genus</b>	<i>Elephantid herpesvirus 1</i>
<b>Unassigned species in the subfamily</b>	<i>Caviid herpesvirus 2</i>
	<i>Suid herpesvirus 2</i>
	<i>Tupaïid herpesvirus 1</i>
<b>Subfamily</b>	<b><i>Gammaherpesvirinae</i></b>
<b>Genus</b>	<b><i>Lymphocryptovirus</i></b>
<b>Type Species</b>	<i>Human herpesvirus 4</i>
<b>Species in the genus</b>	<i>Callitrichine herpesvirus 3</i>
	<i>Cercopithecine herpesvirus 14</i>
	<i>Gorilline herpesvirus 1</i> (previously <i>Pongine herpesvirus 3</i> )
	<i>Human herpesvirus 4</i>
	<i>Macacine herpesvirus 4</i> (previously <i>Cercopithecine herpesvirus 15</i> )
	<i>Panine herpesvirus 1</i> (previously <i>Pongine herpesvirus 1</i> )
	<i>Papiine herpesvirus 1</i> (previously <i>Cercopithecine herpesvirus 12</i> )
	<i>Pongine herpesvirus 2</i>
<b>Genus</b>	<b><i>Rhadinivirus</i></b>

<b>Type Species</b>	<i>Saimiriine herpesvirus 2</i>
<b>Species in the genus</b>	<i>Ateline herpesvirus 2</i> <i>Ateline herpesvirus 3</i> <i>Bovine herpesvirus 4</i> <i>Human herpesvirus 8</i> <i>Macacine herpesvirus 5</i> (previously <i>Cercopithecine herpesvirus 17</i> ) <i>Murid herpesvirus 4</i> <i>Saimiriine herpesvirus 2</i>
<b>Unassigned viruses in the genus</b>	Leporid herpesvirus 1 Leporid herpesvirus 2 Leporid herpesvirus 3 Marmosid herpesvirus 1
<b>Genus</b>	<i>Macavirus</i>
<b>Type Species</b>	<i>Alcelaphine herpesvirus 1</i>
<b>Species in the genus</b>	<i>Alcelaphine herpesvirus 1</i> <i>Alcelaphine herpesvirus 2</i> <i>Bovine herpesvirus 6</i> <i>Caprine herpesvirus 2</i> <i>Hippotragine herpesvirus 1</i> <i>Ovine herpesvirus 2</i> <i>Suid herpesvirus 3</i> <i>Suid herpesvirus 4</i> <i>Suid herpesvirus 5</i>
<b>Genus</b>	<i>Percavirus</i>
<b>Type Species</b>	<i>Equid herpesvirus 2</i>
<b>Species in the genus</b>	<i>Equid herpesvirus 2</i> <i>Equid herpesvirus 5</i> <i>Mustelid herpesvirus 1</i>
<b>Unassigned species in the subfamily</b>	<i>Equid herpesvirus 7</i> <i>Phocid herpesvirus 2</i> <i>Saguinine herpesvirus 1</i> (previously <i>Callitrichine herpesvirus 1</i> )
<b>Unassigned species in the family</b>	<i>Iguanid herpesvirus 2</i>
<b>Unassigned viruses in the family</b>	Accipitrid herpesvirus 1 Anatid herpesvirus 1 Boid herpesvirus 1 Callitrichine herpesvirus 2 Caviid herpesvirus 1 Caviid herpesvirus 3 Cebine herpesvirus 1 Cebine herpesvirus 2 Cercopithecine herpesvirus 3 Cercopithecine herpesvirus 4 Chelonid herpesvirus 1 Chelonid herpesvirus 2 Chelonid herpesvirus 3 Chelonid herpesvirus 4 Ciconiid herpesvirus 1 Cricetid herpesvirus Elapid herpesvirus 1 Erinaceid herpesvirus 1 Falconid herpesvirus 1 Gruid herpesvirus 1 Iguanid herpesvirus 1 Lacertid herpesvirus Lorisine herpesvirus 1 Macacine herpesvirus 6 (previously <i>Cercopithecine herpesvirus 10</i> ) Macacine herpesvirus 7 (previously <i>Cercopithecine herpesvirus 13</i> ) Murid herpesvirus 3

	Murid herpesvirus 5
	Murid herpesvirus 6
	Ovine herpesvirus 1
	Perdacid herpesvirus 1
	Phalacrocoracid herpesvirus 1
	Sciurid herpesvirus 1
	Sciurid herpesvirus 2
	Sphenicid herpesvirus 1
	Strigid herpesvirus 1
<b>Family</b>	<i>Alloherpesviridae</i>
<b>Genus</b>	<i>Ictalurivirus</i>
<b>Type Species</b>	<i>Ictalurid herpesvirus 1</i>
<b>Species in the genus</b>	<i>Ictalurid herpesvirus 1</i>
<b>Unassigned species in the family</b>	<i>Cyprinid herpesvirus 3</i>
<b>Unassigned viruses in the family</b>	Acipenserid herpesvirus 1
	Acipenserid herpesvirus 2
	Anguillid herpesvirus 1
	Cyprinid herpesvirus 1
	Cyprinid herpesvirus 2
	Esocid herpesvirus 1
	Percid herpesvirus 1
	Pleuronectid herpesvirus 1
	Ranid herpesvirus 1
	Ranid herpesvirus 2
	Salmonid herpesvirus 1
	Salmonid herpesvirus 2
<b>Family</b>	<i>Malacoherpesviridae</i>
<b>Genus</b>	<i>Ostreavirus</i>
<b>Type Species</b>	<i>Ostreid herpesvirus 1</i>
<b>Species in the genus</b>	<i>Ostreid herpesvirus 1</i>

## DEMARCATIION CRITERIA FOR SPECIES

Related herpesviruses are classified as distinct species if (a) their nucleotide sequences differ in a readily assayable and distinctive manner across the entire genome and (b) they occupy different ecological niches by virtue of their distinct epidemiology and pathogenesis or their distinct natural hosts. A paradigm is provided by HHV-1 and HHV-2, which differ in their sequence throughout the genome, tend to infect different epithelial surfaces and exhibit distinct epidemiological characteristics. These two viruses recombine readily in culture, but despite the fact that they can infect the same sites in the host, no recombinants have been isolated in nature, and the two viruses appear to have evolved independently for millions of years.

## DEMARCATIION CRITERIA FOR SUBFAMILIES AND GENERA

Nucleotide or predicted amino acid sequences of members of a subfamily or genus form a distinct lineage.

## ARGUMENTATION

022V All herpesviruses share the same overall morphology, in which a large linear dsDNA genome is contained within at T=16 capsid, which is surrounded by a proteinaceous tegument and then by a lipid envelope containing a variety of membrane-associated proteins. Phylogenetically, herpesviruses fall into three distinct classes. Herpesviruses of mammals, birds and reptiles share extensive genetic relationships detectable by amino acid sequence comparisons. Herpesviruses of fish and amphibians are also clearly related to each other, but are related only very marginally to those of mammals, birds and reptiles. Similarly, the single known invertebrate herpesvirus (of oyster) is tenuously related to the other two classes. No herpesvirus-specific gene is detectably conserved between the classes. However, one gene, which encodes the putative ATPase subunit

of a DNA-packaging terminase, is conserved among all herpesviruses and more distantly with T4-like bacteriophages.

If classification of herpesviruses is to reflect evolutionary pathways deduced from sequenced-based phylogeny, the three classes must be separated into three taxa of equivalent rank. Since all the available taxonomic levels from family downwards are occupied in the current family *Herpesviridae*, the distinction has to be made at the level of family. This necessitates encompassing the three classes of herpesvirus as families under an Order, whose coherence would rest largely on virion morphology.

#### References

Toward a comprehensive phylogeny for mammalian and avian herpesviruses: McGeoch et al., *J Virol* 74:10401-6 (2000)

Channel catfish virus: a new type of herpesvirus: Davison, *Virology* 186:9-14 (1992)

The capsid architecture of channel catfish virus, an evolutionarily distant herpesvirus, is largely conserved in the absence of discernible sequence homology with herpes simplex virus: Booy et al., *Virology* 215:134-41 (1996)

The genome of salmonid herpesvirus 1: Davison, *J Virol* 72:1974-82 (1998)

Genomic studies of the Lucke tumor herpesvirus (RaHV-1): Davison et al., *J Cancer Res Clin Oncol* 125:232-8 (1999)

Evolution of the herpesviruses: Davison, *Vet Microbiol* 86:69-88 (2002)

A novel class of herpesvirus with bivalve hosts: Davison et al., *J Gen Virol* 86: 41-53 (2005)

- 023V The proposed name has an obvious derivation from 'herpesvirus'.
- 024V See 022V.
- 025V See 022V.
- 026V The proposed family name prefix is derived from 'allo', meaning 'other'.
- 027V The genus *Ictalurivirus* contains the only fish herpesvirus (*Ictalurid herpesvirus 1*) for which a complete genome sequence is available.
- 028V Since membership of the three proposed families correlates with the type of host (mammals/bird/reptiles, amphibians/fish, bivalves), it is proposed to transfer unassigned members of the present family *Herpesviridae* that have fish or amphibian hosts to the family *Alloherpesviridae*. Supporting sequence data are available for some of these viruses (see references in 022V and literature cited therein).
- 029V Addition of the previously unclassified *Cyprinid herpesvirus 3* (koi herpesvirus) is supported by close sequence relationships to Cyprinid herpesviruses 1 and 2 and by relationships to several genes in *Ictalurid herpesvirus 1*.

#### Reference

Koi herpesvirus represents a third cyprinid herpesvirus (CyHV-3) in the family *Herpesviridae*: Waltzek et al., *J Gen Virol* 86:1659-67 (2005)

- 030V See 022V.
- 031V The proposed family name prefix is derived from 'malaco', meaning 'soft' and used in zoology to denote molluscs.
- 032V *Ostreid herpesvirus 1* would be the sole species in the family *Malacoherpesviridae*.
- 033V The proposed genus name is derived from 'ostrea', meaning 'oyster'.
- 034V See 032V.
- 035V See 032V.

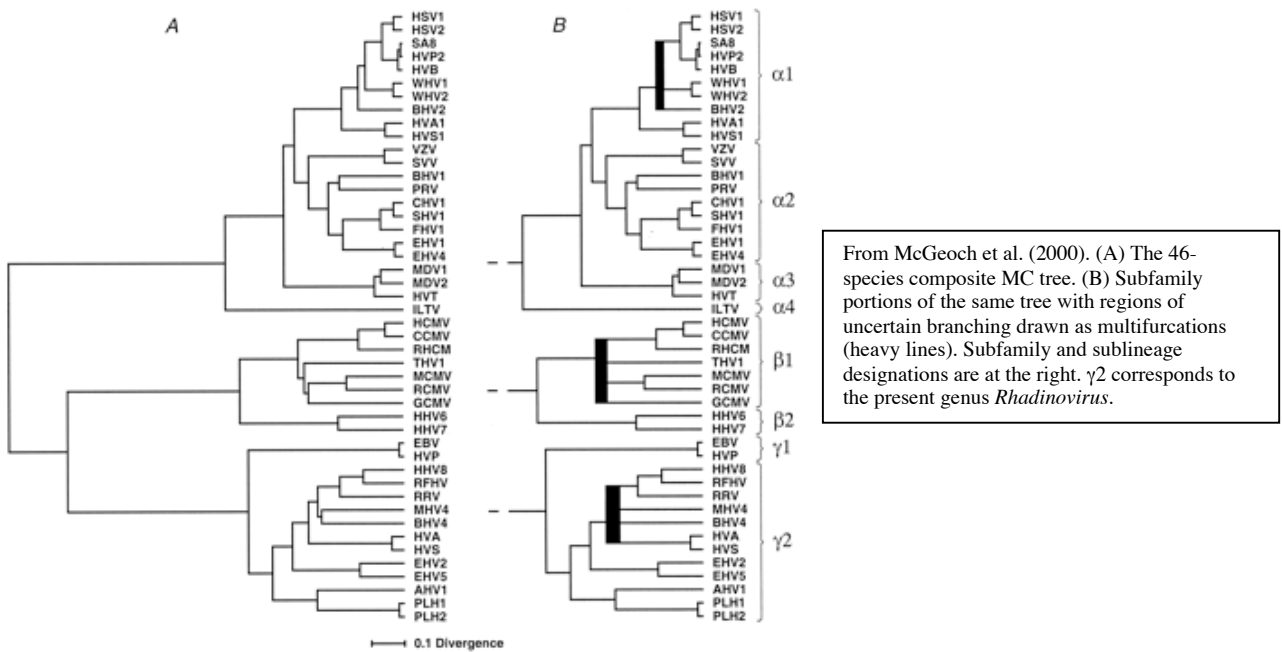


036V Phylogenetic trees based on a selection of genes show that certain species currently in the genus *Rhadinovirus*, plus several unclassified viruses, belong to a separate lineage within the subfamily *Gammaherpesvirinae*. The proposed new genus is represented in the tree below by *Alcelaphine herpesvirus 1* (AHV1) and two unclassified porcine lymphotropic herpesviruses (PLH1 and PLH2).

*References*

Toward a comprehensive phylogeny for mammalian and avian herpesviruses: McGeoch et al., *J Virol* 74:10401-6 (2000)

On phylogenetic relationships among major lineages of the *Gammaherpesvirinae*: McGeoch et al., *J Gen Virol* 86:307-16 (2005)



037V The proposed genus name is derived from a sigla from malignant catarrhal fever, the disease caused by the proposed type species.

038V Alcelaphine herpesvirus 1 is the most fully characterized virus in the proposed genus. The genome has been sequenced.

039V These species are currently in the genus *Rhadinovirus*.

a. Limited DNA sequence data show that *Alcelaphine herpesvirus 2* is a close relative of *Alcelaphine herpesvirus 1*.

*Reference*

Malignant catarrhal fever-like disease in Barbary red deer (*Cervus elaphus barbarus*) naturally infected with a virus resembling alcelaphine herpesvirus 2: Klieforth et al., *J Clin Microbiol* 40:3381-90 (2002)

b. Serological and DNA hybridization data show that *Hippotragine herpesvirus 1* is a close relative of *Alcelaphine herpesvirus 1*.

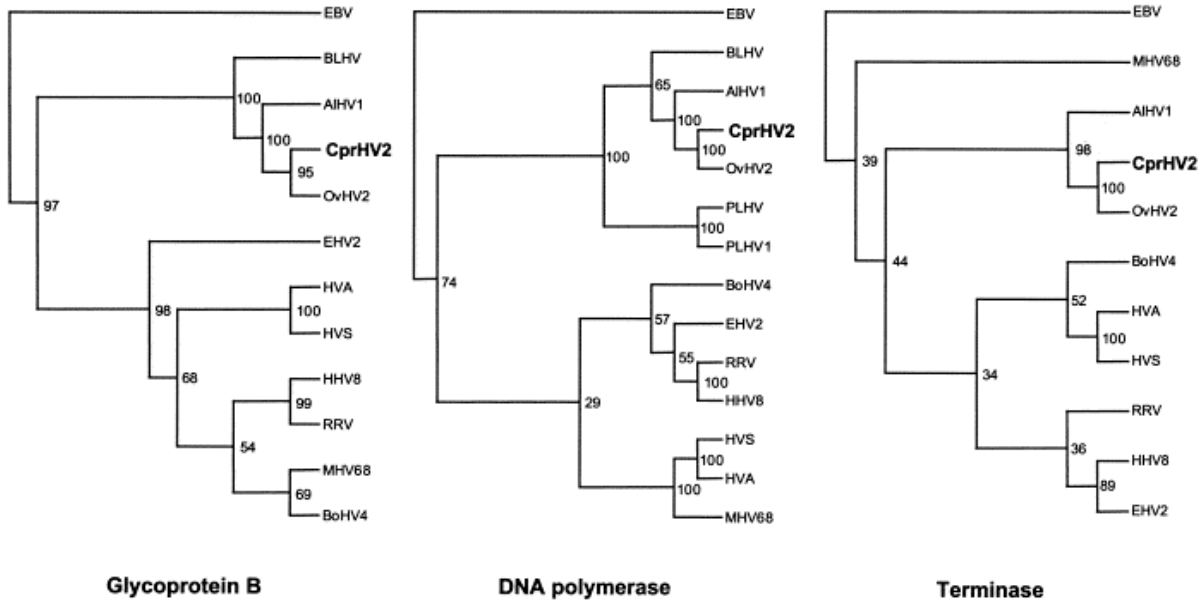
*Reference*

Recovery of a herpesvirus from a roan antelope (*Hippotragus equinus*): Reid & Bridgen, *Vet Microbiol* 28:269-78 (1991)

c. Phylogenetic analysis of parts of the glycoprotein B, DNA polymerase and terminase genes shows that *Ovine herpesvirus 2* belongs to the proposed genus.

*Reference*

Detection and multigenic characterization of a novel gammaherpesvirus in goats: Chmielewicz et al., *Virus Research* 75:87-94 (2001)



From Chmielewicz et al. (2001). Phylogenetic analyses of CprHV-2 and other gammaherpesviruses. OvHV2=ovine herpesvirus 2; CprHV2=caprine herpesvirus 2; BLHV=bovine lymphotropic herpesvirus.

- 040V Phylogenetic analysis of parts of the glycoprotein B and DNA polymerase genes shows that *Bovine herpesvirus 6* (bovine lymphotropic herpesvirus) belongs to the proposed genus. See the tree in 039V.

*Reference*

Detection and multigenic characterization of a novel gammaherpesvirus in goats: Chmielewicz et al., *Virus Research* 75:87-94 (2001)

Phylogenetic analysis of parts of the glycoprotein B, DNA polymerase genes and terminase genes show that *Caprine herpesvirus 2* belongs to the proposed genus. See the tree in 039V.

*Reference*

Detection and multigenic characterization of a novel gammaherpesvirus in goats: Chmielewicz et al., *Virus Research* 75:87-94 (2001)

- 041V Phylogenetic analysis of the glycoprotein and DNA polymerase genes shows that *Suid herpesvirus 3* (porcine lymphotropic herpesvirus 1) belongs to the proposed genus. About 73 kbp of the genome has been sequenced.

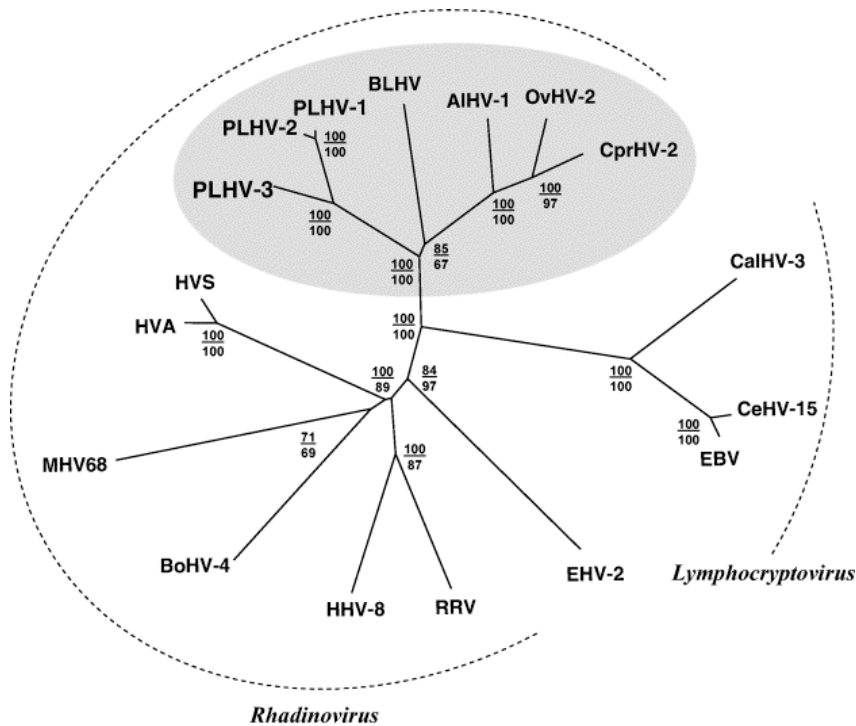
*References*

Characterization of the DNA polymerase loci of the novel porcine lymphotropic herpesviruses 1 and 2 in domestic and feral pigs: Ulrich et al. *J Gen Virol* 80:3199-205 (1999)

Characterization of the DNA polymerase loci of porcine cytomegaloviruses from diverse geographic origins: Goltz et al., *Virus Genes* 21:249-55 (2000)

Toward a comprehensive phylogeny for mammalian and avian herpesviruses: McGeoch et al., *J Virol* 74:10401-6 (2000)

A novel porcine gammaherpesvirus: Chmielewicz et al., *Virology* 308:317-29 (2003)



From Chmielewicz et al. (2003). Phylogenetic relatedness of PLHV-3. A phylogenetic tree was constructed with the neighbor-joining method, using concatenated multiple amino acid sequence alignments of conserved regions of gB and DPOL. PLHV=porcine lymphotropic herpesvirus. Also see the tree in (15).

042V Phylogenetic analysis of the DNA polymerase gene shows that *Suid herpesvirus 4* (porcine lymphotropic herpesvirus 2) belongs to the proposed genus. About 60 kbp of the genome has been sequenced. See the tree in 041V.

*References*

- Characterization of the DNA polymerase loci of the novel porcine lymphotropic herpesviruses 1 and 2 in domestic and feral pigs: Ulrich et al. *J Gen Virol* 80:3199-205 (1999)
- Characterization of the DNA polymerase loci of porcine cytomegaloviruses from diverse geographic origins: Goltz et al., *Virus Genes* 21:249-55 (2000)
- Toward a comprehensive phylogeny for mammalian and avian herpesviruses: McGeoch et al., *J Virol* 74:10401-6 (2000)
- A novel porcine gammaherpesvirus: Chmielewicz et al., *Virology* 308:317-29 (2003)

043V Phylogenetic analysis of the glycoprotein B and DNA polymerase genes shows that *Suid herpesvirus 5* (porcine lymphotropic herpesvirus 3) belongs to the proposed genus. About 60 kbp of the genome has been sequenced. See the tree in 041V.

*Reference*

- A novel porcine gammaherpesvirus: Chmielewicz et al., *Virology* 308:317-29 (2003)

044V See 036V. Phylogenetic trees based on a selection of genes show that several species currently in the genus *Rhadinovirus* belong to a separate lineage within the subfamily *Gammaherpesvirinae*. The proposed new genus is represented in the tree in 036V by *Equid herpesvirus 2* (EHV2) and *Equid herpesvirus 5* (EHV5).

045V The proposed genus name is derived from a sigla from perissodactyl and carnivore, the relevant current host types. The name is not so obvious as to seem ill-judged should other host types be identified in future.

046V Equid herpesvirus 2 is the most fully characterized member of the proposed genus. The genome has been sequenced.

047V These species are currently in the genus *Rhadinovirus*.

- a. Sequence analysis shows that *Equid herpesvirus 5* is a close relative of *Equid herpesvirus 2*. Phylogenetic

analysis shows that this virus belongs to the proposed genus. See the tree in 036V.

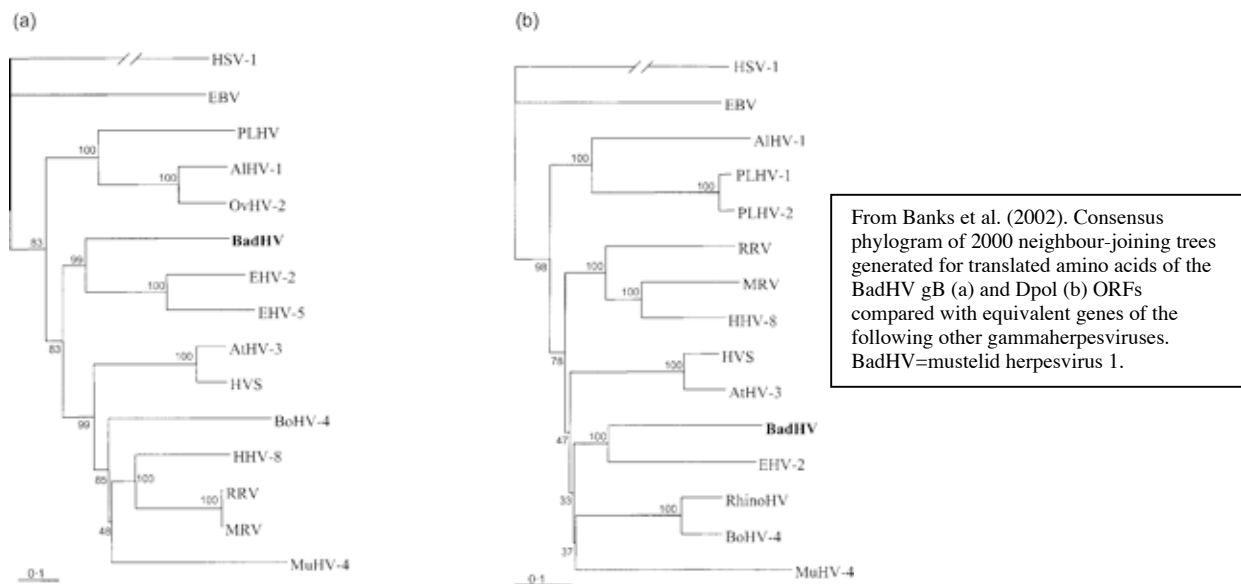
### References

Equine herpesviruses 2 and 5 are gamma-herpesviruses: Telford et al., *Virology* 195:492-9 (1993)  
Identification, sequence analysis and characterisation of equine herpesvirus 5 glycoprotein B: Holloway et al., *Arch Virol* 144:287-307 (1999)  
Toward a comprehensive phylogeny for mammalian and avian herpesviruses: McGeoch et al., *J Virol* 74:10401-6 (2000)

b. Phylogenetic analysis of the glycoprotein B and DNA polymerase genes shows that *Mustelid herpesvirus 1* belongs to the proposed genus.

### Reference

Partial characterization of a novel gammaherpesvirus isolated from a European badger (*Meles meles*): Banks et al., *J Gen Virol* 83:1325-30 (2002)



048V DNA hybridization experiments shows that Equid herpesvirus 7 (a donkey virus) is related to *Equid herpesvirus 2* and *Equid herpesvirus 5*. The precise order of relationships to genera is unknown, and placement in the subfamily *Gammaherpesvirinae* is appropriate.

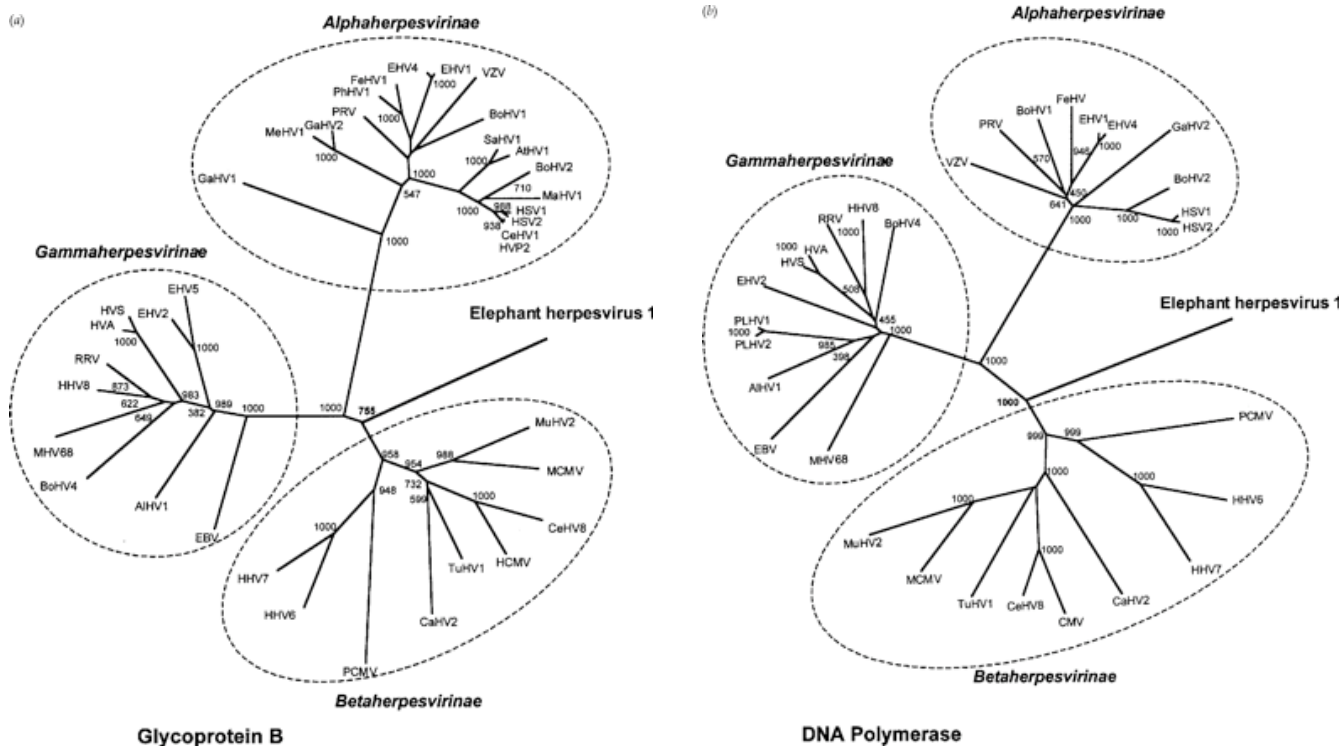
### Reference

Asinine herpesvirus genomes: comparison with those of the equine herpesviruses: Browning et al., *Arch Virol* 101:183 (1988)

049V Phylogenetic trees based on the DNA polymerase and glycoprotein gene B genes show that endotheliotropic elephant herpesvirus (EEHV) belongs to a distinct lineage of subfamily *Betaherpesvirinae* that is separate from other genera.

### References

Novel endotheliotropic herpesviruses fatal for Asian and African elephants: Richman et al., *Science* 283:1171-6 (1999)  
Genetic and ultrastructural characterization of a European isolate of the fatal endotheliotropic elephant herpesvirus: Ehlers et al., *J Gen Virol* 82:475-82 (2001)  
Integrating reptilian herpesviruses into the family *Herpesviridae*: McGeoch & Gatherer, *J Virol* 79:725-31 (2005)

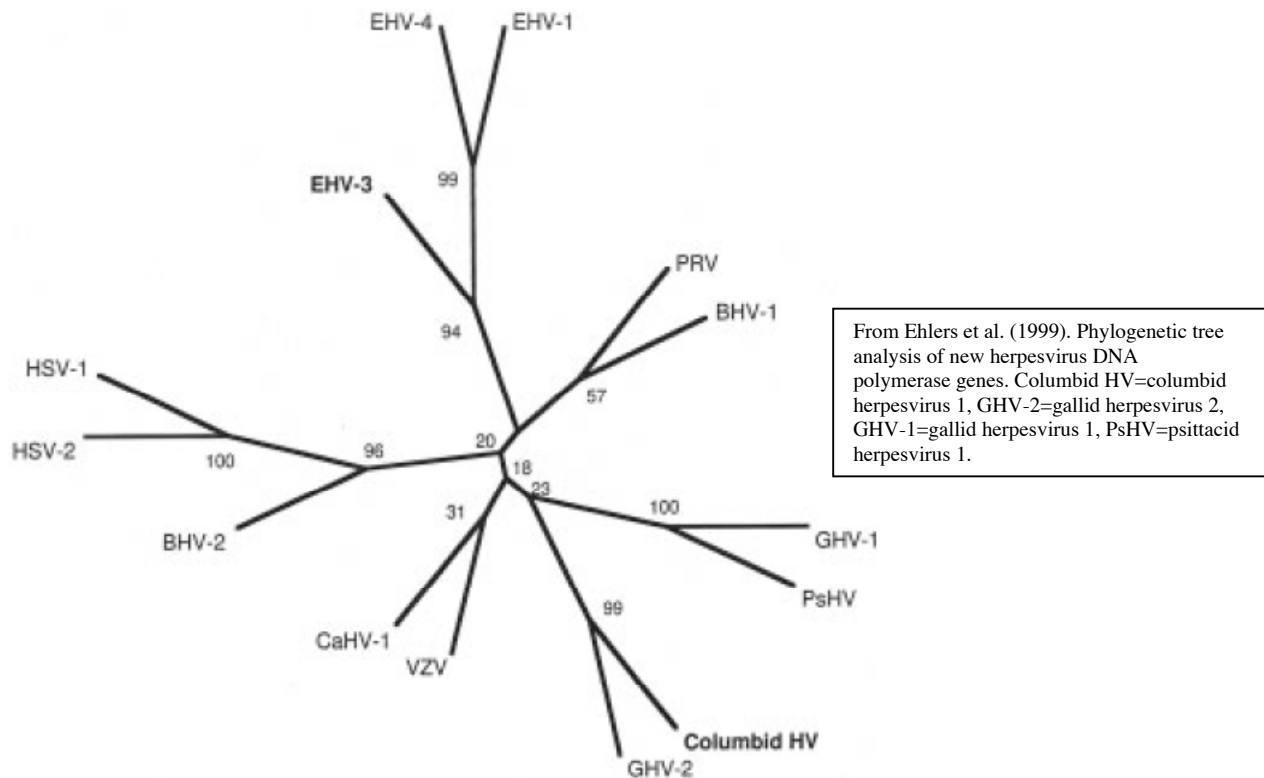


From Ehlers et al. (2001). Phylogenetic analysis of gB and DPOL of EIHV-1. Phylogenetic trees were constructed by the neighbour-joining method, using multiple amino acid sequence alignments of conserved regions of the gB (a) and DPOL (b) proteins. Also see the tree in (37).

- 050V The proposed genus name is derived from proboscis, meaning ‘elephant’s trunk’.
- 051V The proposed genus would contain a single member. EEHV was detected in Asian elephants that died from endothelial inclusion body disease, and also from benign dermal lesions on African elephants (including one from the Kruger National Park; see below). A related, but distinct, virus was detected in an African elephant that died from endothelial inclusion body disease. It was suggested that lethal disease may have resulted from transfer of a benign virus from African to Asian elephants, and vice versa, but evidence for this is lacking. The nomenclature for elephant herpesviruses is complicated by the fact that Elephantid herpesvirus 1 is an unassigned virus in the *Herpesviridae*. This virus was described in a single report concerning African elephants in the Kruger National Park that was published in 1971, and, as far as is known, is now unavailable. Although this is an unusual step, it is proposed that EEHV should assume the designation *Elephantid herpesvirus 1*; Ehlers et al. (2001) have already implemented this.
- 052V See 051V.
- 053V Phylogenetic analysis of a 1.6 kbp segment of the DNA polymerase gene shows that *Columbid herpesvirus 1* belongs to the genus *Mardivirus*.

*Reference*

Detection of new DNA polymerase genes of known and potentially novel herpesviruses by PCR with degenerate and deoxyinosine-substituted primers: Ehlers et al., *Virus Genes* 18:211-20 (1999)



054V Phylogenetic analysis of several genes of this virus from the complete genome sequence show that *Psittacid herpesvirus 1* belongs to the genus *Iltoivirus* (GenBank accession AY372243 analysed by D.J. McGeoch). See also the tree in 053V.

055V Phylogenetic analysis of several genes from the complete genome sequence show that *Ateline herpesvirus 3* belongs to the genus *Rhadinovirus*. See the tree in (15), where HVA is *Ateline herpesvirus 3*. This virus appears to be very closely related to *Ateline herpesvirus 2*, which is already in the genus *Rhadinovirus*, but there are insufficient sequence data from the latter to permit both to be reduced to a single species.

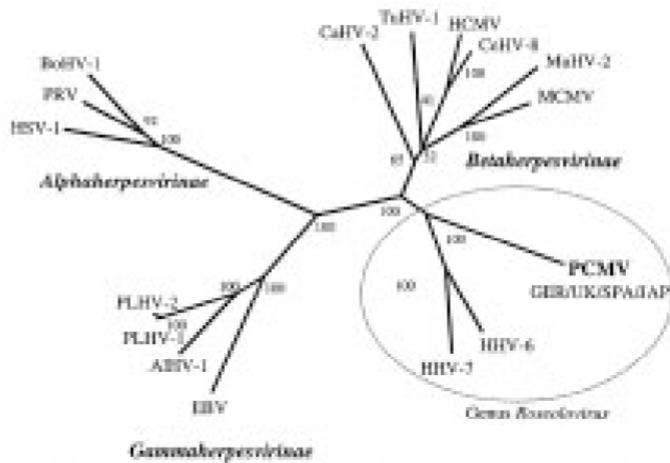
*Reference*

Toward a comprehensive phylogeny for mammalian and avian herpesviruses: McGeoch et al., *J Virol* 74:10401-6 (2000)

056V Phylogenetic analysis of the complete DNA polymerase gene shows that *Suid herpesvirus 2* belongs to the subfamily *Betaherpesvirinae*.

*Reference*

Characterization of the DNA polymerase loci of porcine cytomegaloviruses from diverse geographic origins: Goltz et al., *Virus Genes* 21:249-55 (2000)

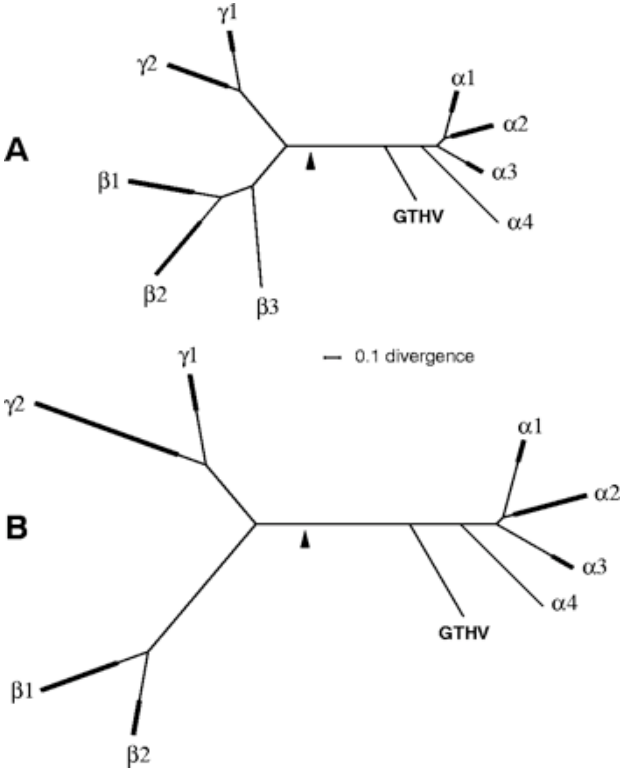


From Goltz et al. (2000). Phylogenetic analysis of the PCMV DNA polymerase. PCMV=suid herpesvirus 2.

057V Phylogenetic analysis of several genes shows that *Chelonid herpesvirus 5* (green turtle herpesvirus) belongs to subfamily *Alphaherpesvirinae*. About 44 kbp of the genome has been sequenced.

*References*

Rapid acquisition of entire DNA polymerase gene of a novel herpesvirus from green turtle fibropapilloma by a genomic walking technique: Yu et al., *J Virol Methods* 91:183-95 (2001)  
 Sequencing and characterization of the full-length gene encoding the single-stranded DNA binding protein of a novel Chelonian herpesvirus: Nigro et al., *Arch Virol* 149:337-47 (2004)  
 Tumor outbreaks in marine turtles are not due to recent herpesvirus mutations: Herbst et al., *Curr Biol* 14:R697-9 (2004)  
 Integrating reptilian herpesviruses into the family *Herpesviridae*: McGeoch & Gatherer, *J Virol* 79:725-31 (2005)



From McGeoch & Gatherer (2005). POL and DBP trees, including GTHV. The top-scoring trees are shown based on HV POL amino acid sequences (A) and HV DBP amino acid sequences (B). The trees are presented as unrooted and in a condensed format showing genus-level groupings rather than individual species, with the multiple-branch region of each genus-level clade represented by a single heavy line. In each tree, the estimated position of the root is indicated by a filled arrowhead, calculated as the midpoint of the distance from the mean positions of branch tips in the alpha subfamily to the mean positions of branch tips in the beta and gamma subfamilies. A common scale bar is indicated for divergence (i.e., substitutions per amino acid site). Genus-equivalent labels are as follows:  $\alpha$ 1, *Simplexvirus*;  $\alpha$ 2, *Varicellovirus*;  $\alpha$ 3, *Mardivirus*;  $\alpha$ 4, *Iltovirus*;  $\beta$ 1, *Cytomegalovirus* (including *Muromegalovirus* and *Tupaia HV*);  $\beta$ 2, *Roseolovirus* (including porcine cytomegalovirus);  $\beta$ 3, elephant endothelial HV;  $\gamma$ 1, *Lymphocryptovirus*;  $\gamma$ 2, *Rhadinovirus*. (A) The POL tree contains 44 species in addition to GTHV, distributed as follows:  $\alpha$ 1, 4 species;  $\alpha$ 2, 7 species;  $\alpha$ 3, 3 species;  $\alpha$ 4, 1 species;  $\beta$ 1, 8 species;  $\beta$ 2, 3 species;  $\beta$ 3, 1 species;  $\gamma$ 1, 3 species;  $\gamma$ 2, 14 species. (B) The DBP tree contains 35 species in addition to GTHV, distributed as follows:  $\alpha$ 1, 4 species;  $\alpha$ 2, 6 species;  $\alpha$ 3, 3 species;  $\alpha$ 4, 1 species;  $\beta$ 1, 7 species;  $\beta$ 2, 2 species;  $\gamma$ 1, 3 species;  $\gamma$ 2, 9 species. GTHV=chelonid herpesvirus 5.

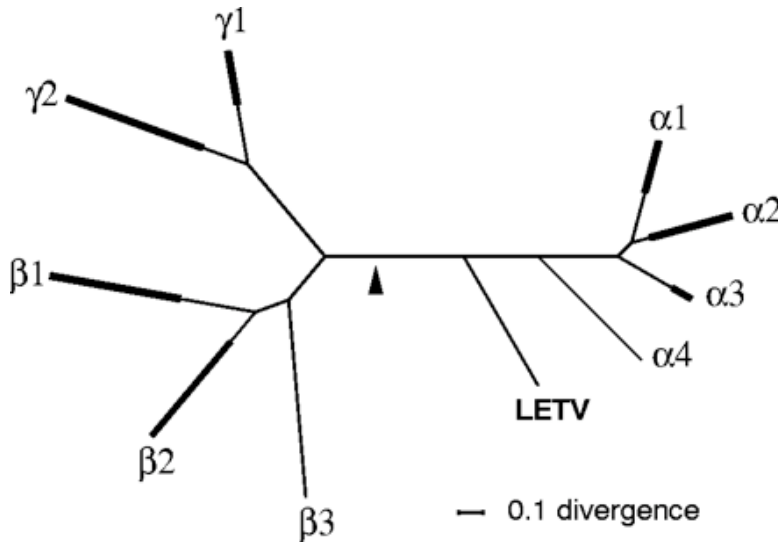
058V Phylogenetic analysis of the glycoprotein B and part of the scaffolding protein genes (1.7 kbp) shows that *Chelonid herpesvirus 6* (lung-eye-trachaea disease-associated herpesvirus of green turtle) belongs to the subfamily *Alphaherpesvirinae*.

*References*

Identification and expression of immunogenic proteins of a disease-associated marine turtle herpesvirus: Coberley et al., *J Virol* 76:10553-8 (2002)

Integrating reptilian herpesviruses into the family *Herpesviridae*: McGeoch & Gatherer, *J Virol* 79:725-31 (2005)

Four chelonid herpesviruses from other turtle species have been classified previously. Their relationships to the two newly characterized viruses of green turtle are unknown.



From McGeoch & Gatherer (2005). gB tree, including LETV. The top-scoring tree is shown based on HV gB amino acid sequences, obtained by two separate methods (Codeml and MrBayes). The format is as described for (37). LETV=chelonid herpesvirus 6.

059V Phylogenetic analysis of part of the UL52 gene (788 bp) shows that Phocid herpesvirus 2 belongs to the subfamily *Gammaherpesvirinae*. Sequences are available for substantial parts of three other genes, and show closest relationships to the subfamily *Gammaherpesvirinae*. This virus probably belongs to the proposed genus *Percavirus*, but the analysis is insufficiently developed at present.

*References*

Characterization of phocid herpesvirus-1 and -2 as putative alpha- and gammaherpesviruses of North American and European pinnipeds: Harder et al., *J Gen Virol* 77:27-35 (1996)

Seal gammaherpesviruses: identification, characterisation and epidemiology: Martina et al., *Virus Res* 94:25-31 (2003)

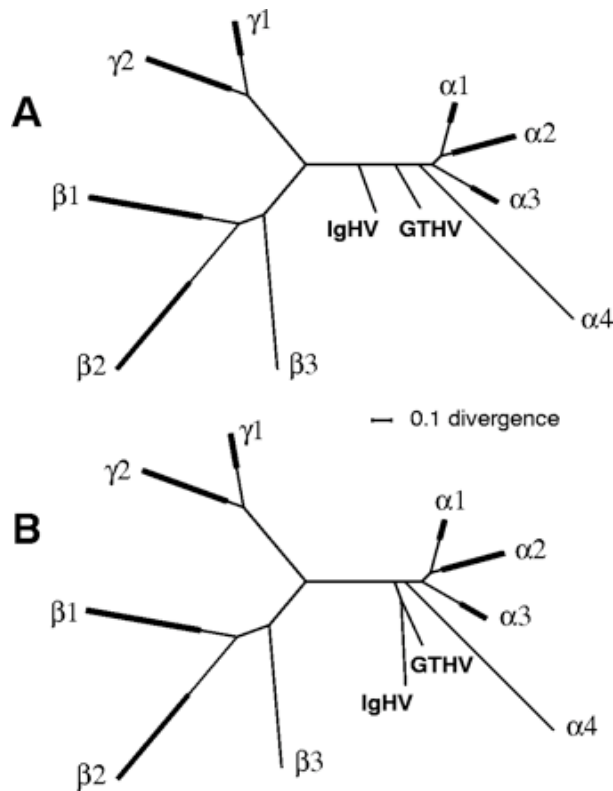
060V Phylogenetic analysis of part of the DNA polymerase gene (780 bp) shows that *Iguanid herpesvirus 2* belongs to family *Herpesviridae*. The relationship of this virus to Iguanid herpesvirus 1, which was classified many years ago and may no longer be available, is unknown.

*References*

A novel herpesvirus associated with hepatic necrosis in a San Esteban Chuckwalla: Wellehan et al., *J Herpetol Med Surg* 13:15-9 (2003)

Integrating reptilian herpesviruses into the family *Herpesviridae*: McGeoch & Gatherer, *J Virol* 79:725-31 (2005)





From McGeoch & Gatherer (2005). Trees based on a part of POL, including IgHV. The two top equal trees are shown based on a 226-amino-acid alignment of a section of POL. The alignment included 46 species: 45 as described for (36) plus IgHV. The format is as described for (37). IgHV=iguanid herpesvirus 2.

061V-072V The following argument applies to each of these proposals, and therefore these stand or fall as one.

There is a taxonomical discrepancy in that New World primate herpesviruses are named after the host genus, whereas Old World non-human primate herpesviruses are named after the family. This proposal entails renaming Old World non-human primate herpesvirus species after the host genus in order to resolve this discrepancy and divide the increasingly large number (~30) of cercopithecine herpesviruses. It would cause the species names of certain Old World non-human primate herpesviruses to change, although only the proposed *Macacine herpesvirus 1* and *Macacine herpesvirus 5* are studied to any significant extent, and informal names are used almost exclusively for these in the literature. Although some authorities in primate taxonomy have transferred the African green monkey from genus *Cercopithecus* to genus *Chlorocebus*, the older name is retained for the herpesviruses with this host in order to minimize the number of changes in nomenclature and to accommodate *Cercopithecine herpesvirus 9*, whose natural host species is unclear.

072V Renaming of the New World primate herpesvirus *Callitrichine herpesvirus 1* is necessary because it was isolated from *Saguinus oedipus*.

## ADDITIONAL AREAS FOR FUTURE DISCUSSION

### Improving the species definition

### Suppressing current species

Some viruses are no longer available and should be suppressed. The names should not be occupied by other viruses.

### Classifying viruses detected only by PCR

Many unclassified herpesviruses have been characterized only through sequencing of short PCR products. Their number is likely to increase. These viruses should be acknowledged in some formal way by ICTV, but must be distinguished from viruses that have been subjected to more extensive characterization. One possibility is to recognize the currently developing informal nomenclature, and to allow it to feed into the formal classification process.

**COMMENTS FROM THE ICTV**

