Date: June 27, 2002
From: *Astroviridae* Study Group

2002.V064.04:   to remove the unique genus *Astrovirus* from the family *Astroviridae*

2002.V065.04:   to create two new genera in the family *Astroviridae*

2002.V066.04:   to name the first genus *Mamastrovirus*

2002.V067.04:   to assign *Human astrovirus* (HAstV) as the type species of the genus created in
2002.V065.04:

2002.V068.04:   to assign all the astroviruses infecting mammals in the genus *Mamastrovirus*
including: *Bovine astrovirus* (BAstV), *Feline astrovirus* (FAstV), *Human
astrovirus* (HAstV), *Ovine astrovirus* (OAstV), and *Porcine astrovirus*
(PAstV).

2002.V069.04:   to name the second genus *Avastrovirus*

2002.V070.04:   to assign *Turkey astrovirus* (TAstV) as the type species of the genus created in
2002.V069.04:

2002.V071.04:   to assign all the astroviruses infecting avians in the genus *Avastrovirus*
including: *Duck astrovirus* (DAstV), *Turkey astrovirus* (TAstV), and *Avian
nephritis virus* (ANV).

Rational of the proposals

1. Proposal: Establishment of new taxa, two genera within the Family *Astroviridae*.

We propose that the Family *Astroviridae* be subdivided into two genera, *Mamastrovirus*
and *Avastrovirus*, on the basis of phylogenetic clustering of capsid sequence, host of
origin and target organs.

Mamastrovirus would include astroviruses that infect mammals and primarily cause
gastroenteritis.

Avastrovirus would include astroviruses that infect avian species and may cause intestinal
as well as extraintestinal illness.

2. Purpose

Since the previous report, a large number of sequences, representing a broad spectrum of
astroviruses, have become available. Complete genomic sequences of four serotypes of

human astrovirus, ovine astrovirus, turkey astrovirus and chicken astrovirus (avian nephritis virus) are now available in GenBank. A larger number of complete capsid sequences are available (eight serotypes of human astrovirus, feline astrovirus, porcine astrovirus, ovine astrovirus, two strains of turkey astrovirus and avian nephritis virus) and were analyzed for phylogenetic relatedness.

When the maximum likelihood algorithm, a comprehensive method for characterizing phylogenetic distances (reference below), was applied, two distinct clusters were evident: mammalian astroviruses (including all known human, feline, porcine, and ovine species) and avian astroviruses (including turkey and avian nephritis virus). The phylogenetic distances (expected number of nucleotide substitutions per site) between the two clusters in the complete capsid region are comparable to distances between genera of *Picornaviridae* and *Caliciviridae*. The minimal distance for astrovirus is 2.04 (turkey astrovirus to ovine astrovirus), compared to 1.59-3.29 for *Picornaviridae* and 0.94-3.94 for *Caliciviridae*.

The two clusters also differ in the host of origin, with mammalian astroviruses in one cluster and avian astroviruses in another cluster.

In addition, the two clusters differ in the organs involved in infection. Mammalian astroviruses primarily infect the gastrointestinal tract and cause a self-limiting gastroenteritis, whereas avian astroviruses have been reported to cause extraintestinal disease involving the liver, kidney and immune system.

3. Summary of the new taxonomic situation within the Family *Astroviridae*

The family would now consist of the following genera:

Genus: *Mamastrovirus*
Type Species: Human astrovirus (HAstV)

Genus: *Avastrovirus*.
Type Species: Turkey astrovirus (TastV)

4. Derivation of names proposed

Mamastrovirus has the stem "astro" from the family name, linked to "mam" (from Latin *mamma*, "breast") to designate mammalian astroviruses

Avastrovirus has the stem "astro" from the family name, linked to "av" (from Latin *avis*, "bird") to designate avian astroviruses

5. New literature references

Berke, T., and Matson, D.O. (2000). Reclassification of the *Caliciviridae* into distinct genera and exclusion of hepatitis E virus from the family on the basis of comparative phylogenetic analysis. *Arch. Virol.*, **145**, 1-16.

Table 1. Phylogenetic distances between genra of *Picornaviridae*, *Caliciviridae* and *Astroviridae*
(complete capsid sequences, maximum likelihood method)

Picornaviridae	Enterovirus	Rhinovirus	Cardiovirus	Aphtovirus	Hepatovirus
Enterovirus					
Rhinovirus	0.94				
Cardiovirus	1.63	1.75			
Aphtovirus	2.45	2.57	2.35		
Hepatovirus	3.81	3.94	3.71	3.65	

Caliciviridae	Norwalk-like	Sapporo-like	Lagovirus	Vesivirus
Norwalk-like				
Sapporo-like	2.08			
Lagovirus	2.19	1.76		
Vesivirus	2.1	1.66	1.59	

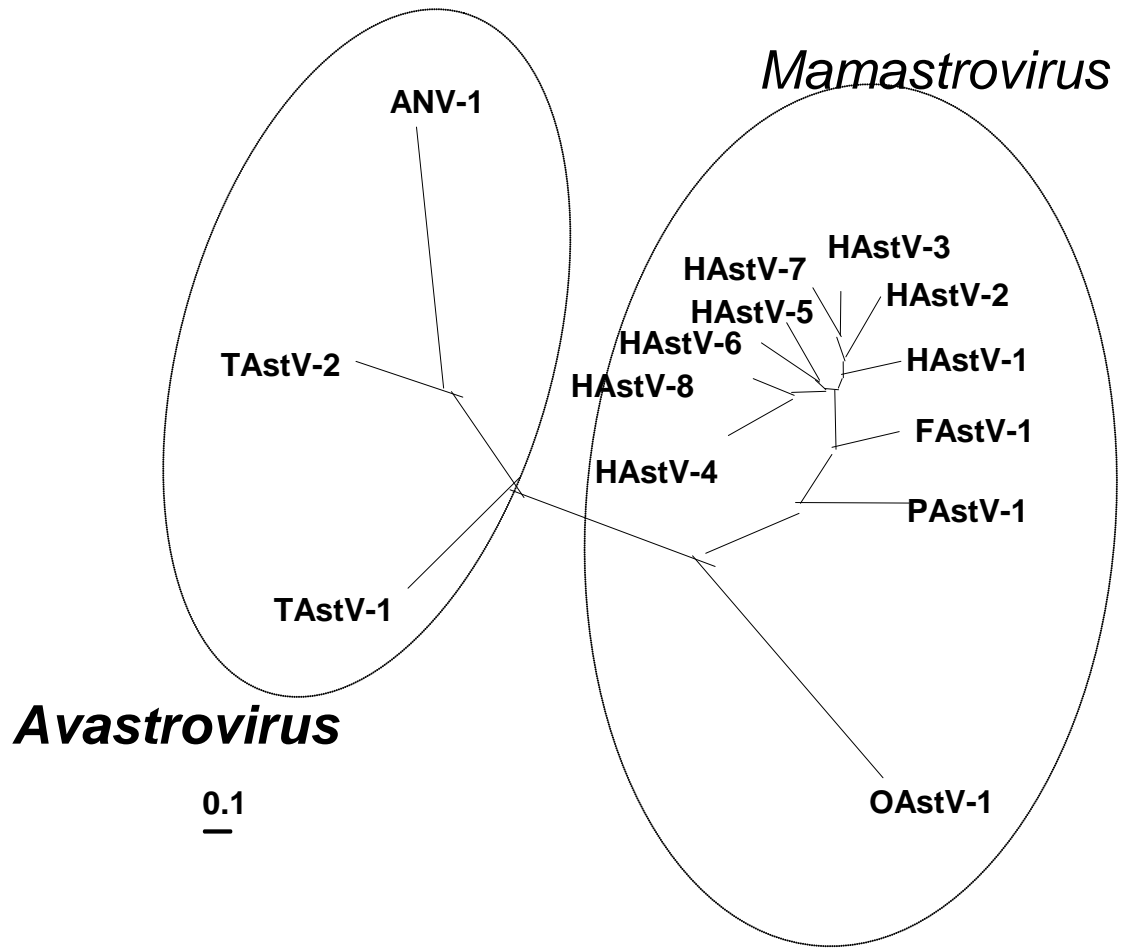| ***Astroviridae***	OAstV
TAstV-1	2.04

Figure 1. Phylogram demonstrating the two proposed genera within *Astroviridae*. Published (GenBank) HAstV capsid gene sequences used in the phylogenetic analyses included human astroviruses representing each of the eight known serotypes: HAstV-1 [L23513], HAstV-2 [L13745], HAstV-3 [AF117209], HAstV-4 [Z33883], HAstV-5 [U15136], HAstV-6 [Z46658], HAStV-7 [AF248738], HAstV-8 [Z66541], and animal astroviruses: feline [AF056197], porcine [Z66541], ovine [Y15937], turkey from Ohio [Y15936] and turkey from USDA [AF206663] and avian nephritis virus [AB033998]. Basic sequence manipulation and verification were performed using Omiga (v2.0; Oxford, Molecular Ltd, Madison, WI). ClustalW v1.7 was used to create multiple alignments of the amino acid sequences of the selected complete capsid sequences. The nucleic acid sequences were added and aligned by GeneDoc v2.3 using the corresponding amino acid sequences as template, resulting in a consensus length of 2577 nt terminating at the 3' end of ORF2. A phylogenetic tree was constructed from the nucleic acid sequence alignment using the maximum likelihood algorithm in the program DNAML of PHYLIP (v 3.52c) running in an UNIX environment.