PROPOSALS FROM THE ADENOVIRIDAE STUDY GROUP

March 1, 2002

Proposals relating to a third genus in the Adenoviridae

2002.V050.04: To create species *Ovine adenovirus D* (OAdV-D) to contain ovine adenovirus 7 (OAdV-7, isolate OAV287).
Criteria:
1. More than 5% phylogenetic distinctness from other species based on distance matrix analysis performed on hexon amino acid sequences
2. The host is sheep or goat
3. Meets the criteria for Atadenovirus (see Proposal 2002.V054.04: below)

2002.V051.04: To create species *Bovine adenovirus D* to contain bovine adenovirus 4.
Criteria:
1. More than 5% phylogenetic distinctness from other species based on distance matrix analysis performed on hexon amino acid sequences
2. The host is cattle
3. Meets the criteria for Atadenovirus (see Proposal 2002.V054.04 below)

2002.V052.04: To create species *Possum adenovirus* to contain possum adenovirus 1 (PoAdV-1).
Criteria:
1. More than 5% phylogenetic distinctness from other species based on distance matrix analysis performed on hexon amino acid sequences
2. Marsupial host
3. Meets the criteria for Atadenovirus (see Proposal 2002.V054.04 below)

2002.V053.04: To create species *Duck adenovirus A* to contain duck adenovirus 1 (DAdV-1, syn. egg drop syndrome virus).
Criteria:
1. More than 10% phylogenetic distinctness from other species based on distance matrix analysis performed on hexon amino acid sequences
2. Avian host
3. Meets the criteria for Atadenovirus (see Proposal 2002.V054.04 below)

2002.V054.04: To create a new genus within the family *Adenoviridae*.
Criteria:
1. More than 15% phylogenetic distinctness from other genera (based on distance matrix analysis performed on amino acid sequences)
2. Avian, marsupial or ruminant host
3. GC content of 33-43%
4. Existence of precursor protein p32K
5. Existence of the gene E1B-55K homolog
6. Existence of the gene of 34K homolog
7. Lack of protein V and IX, E1A and E3 regions
8. No cross neutralization with members of other genera
6. No DNA hybridisation with members of other genera

2002.V055.04: To name the genus proposed in 2002.V054.04: *Atadenovirus*.
The name reflects the characteristic high AT content of the first studied members of the genus and is already widely used in the literature.

2002.V056.04: To assign species *Ovine adenovirus D, Bovine adenovirus D, Duck adenovirus A,* and *Possum adenovirus* to genus *Atadenovirus.*
They meet the criteria of the genus and seem to have a common evolutionary (supposed to be a reptilian one that was followed by three independent host switches to ruminants, marsupials and birds).

2002.V057.04: To designate *Ovine adenovirus D* (OAdV-7) to be the type species of the genus created in 2002.V054.04:.
This was the first fully sequenced member of the genus.

Proposals relating to a fourth genus in the Adenoviridae

2002.V058.04: To create species *Frog adenovirus* to contain frog adenovirus 1 (FrAdV-1).
Criteria:
1. More than 10% phylogenetic distinctness from other species based on distance matrix analysis performed on hexon amino acid sequences
2. Anura host
3. Meets the criteria for Siadenovirus (see Proposal 2002.V060.04 below)

2002.V059.04: To create species *Turkey adenovirus A* to contain turkey adenovirus 3 (TAdV-3, syn., hemorrhagic enteritis virus, marble spleen disease virus).
Criteria:
1. More than 10% phylogenetic distinctness from other species based on distance matrix analysis performed on hexon amino acid sequences
2. Avian host
3. Meets the criteria for Siadenovirus (see Proposal 2002.V060.04: below)

2002.V060.04: To create a new genus within the family *Adenoviridae*.
Criteria:
1. More than 15% phylogenetic distinctness from other genera (based on distance matrix analysis performed on hexon amino acid sequences)
2. Amphibian and avian hosts
3. GC content of 33-43%
4. Existence of sialidase gene homolog
5. Lack of protein V and IX, E1, E3, E4 regions, dUTPase or p32K genes.
8. No cross neutralization with members of other genera
6. No DNA hybridisation with members of other genera

2002.V061.04: To name the new genus created in 2002.V060.04: *Siadenovirus*.
Only adenovirus species in this genus have a sialidase homolog gene.

2002.V062.04: To assign species *Frog adenovirus* and *Turkey adenovirus A* to genus created in 2002.V060.04:.

They meet the criteria of the genus and seem to have a common evolutionary (a supposed reptilian one followed by host switch to birds).

2002.V063.04: To designate *Frog adenovirus* to be the type species of the genus created in 2002.V060.04:.
Siadenoviruses may have an amphibian origin thus frog adenovirus may reflect better the original amphibian characteristics than turkey adenovirus 3, that presumably has switched to the avian host.

Reasoning:
The original concept of the genus classification of adenoviruses was the host origin, on a class level. Thus, initially, two genera for the avian and mammalian isolates were created. Following this philosophy, the recently sequenced frog adenovirus should have been allocated to a third genus dedicated to amphibian adenoviruses. Indeed, the genome size and organisation of the frog adenovirus (including unique genes, like the sialidase) were as different from the two traditional genera, as they are from each other. The phylogenetic analysis of the frog virus revealed its close genetic relation to turkey haemorrhagic enteritis virus (THEV), which was an exception in the aviadenovirus genus. It seems to be reasonable to separate these two viruses into a new genus, and suppose that this sort of genome organisation represents the adenoviruses of amphibians.

Our preliminary data on the genome sequencing of a snake adenovirus isolate revealed, that the snake (and supposedly all reptilian) adenoviruses have a fourth type of genomic arrangement, which is shared by the members of the proposed atadenovirus genus. They all have the gene of p32K protein, and cluster together in phylogenetic calculations. We hypothesize that candidate members of this genus originated from reptiles and underwent several host switches to ruminant, marsupial and avian hosts.

Members of the two accepted and two proposed genera, show striking differences in their genome organisation (different gene sets). In phylogenetic calculations, the separation of four, clear-cut clusters is also obvious.