February 19, 2002

From the *Retroviridae* Study Group

2002.V043.04: To create two subfamilies within the family *Retroviridae*, the first one would contain the six genera as previously defined: *Alpharetrovirus*, *Betaretrovirus*, *Gammaretrovirus*, *Deltaretrovirus*, *Epsilonretrovirus* and *Lentivirus*. The second one would contain a single genus, *Spumavirus*.

2002.V044.04: to name the first subfamily *Orthoretrovirinae*

2002.V045.04: to name the second subfamily *Spumaretrovirinae*.

2002.V046.04: To incorporate the genera *Alpharetrovirus*, *Betaretrovirus*, *Gammaretrovirus*, *Deltaretrovirus*, *Epsilonretrovirus* and *Lentivirus,* currently genera of the family *Retroviridae*, within the new subfamily *Spumaretrovirinae*.

2002.V047.04: To incorporate the genus *Spumavirus,* currently a genus of the family *Retroviridae*, within the new subfamily *Spumaretrovirinae*.

2002.V048.04: To designate *Simian foamy virus* as the new type species of the genus *Spumavirus* instead of Champazee foamy virus, now a strain of the species *Simian foamy virus*.

2002.V049.04: To incorporate in the species *Simian foamy virus,* the new type species of the genus *Spumavirus* the strains Chimpanzee foamy virus, Simian foamy virus 1 and Simian foamy virus 3, previously listed as species in the *Spumavirus* genus

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2002.V044.04: to name the first subfamily *Orthoretrovirinae*

2002.V045.04: to name the second subfamily *Spumaretrovirinae*.

Background: The background of this proposal is as follows: The Retroviridae Study Group had proposed in the past to separate the family *Retroviridae* into two subfamilies, to be called *Orthoretrovirinae* and the *Spumaretrovirinae*.

> **The EC made the following comments for the proposal in May 2001. The EC had reservations about this proposal and requested clarification. The EC questioned whether the *Spumaretrovirinae* really represents a subfamily or if these viruses should be moved to a new family. The EC said the SG would need to consider how the family will be described in the future if the two subfamilies are retained. Is the genome of the viruses in this family RNA or DNA or both? The EC also asked the SG to consider how creation of this proposed new subfamily will be related to the pararetroviruses of plants.**

The Retroviridae Study Group renewed discussion about the questions from the EC and unanimously retains their desire to create the two subfamilies. Answers to clarify the EC questions are as follows: First, because of the genome structure (three genes, gag, pol and env), the phylogenetic relatedness of the pol genes in all the retroviruses, the mechanism of reverse transcription (use of a tRNA primer etc.) all the viruses in the proposed two subfamilies clearly belong in the same family. There is no problem about having both subfamilies in the same family, *Retroviridae*. What distinguishes them are details of their replicative cycle. Second, all of these viruses encapsidate RNA and have a DNA proviral form in the cell. The difference is timing of reverse transcription. For the *Orthovirinae*, reverse transcription predominantly occurs after a particle with an RNA genome enters a cell and is uncoated. For the *Spumaretrovirinae*, reverse transcriptase also occurs as the virus is budded and matures, so that a large amount of full length DNA is found in virions. For at least one member of the *Spumaretrovirinae* subfamily, the functional genome has been shown to be DNA, but the Study Group strongly argues that this is not a property that should remove it from the *Retroviridae.*

The Study Group does not think this proposed change to create a new subfamily with the *Retroviridae* will have any impact on the pararetroviruses. The pararetroviruses don't integrate and they use a different mechanism of RT compared to the retroviruses so they do not belong in the *Retroviridae* family or in either of the two proposed subfamilies within the *Retroviridae*.

Purpose: Recent results have indicated that the foamy viruses share characteristics amongst themselves, which are highly divergent from other members of the *Retroviridae*. These include a DNA genome, a spliced Pol mRNA, requirement for Env proteins for budding, and a second promoter located in the *env* gene. No members of this group have been shown to cause disease in natural or accidental hosts. Subfamilies allow for a more complex hierarchy of taxa, in keeping with the apparent intrinsic complexity of the relationships among member viruses. Since the foamy viruses are so different from viruses in the other six genera within the *Retroviridae* in their replication strategy, a subfamily is appropriate in accordance of the recommendations of the International Committee on Taxonomy of Viruses (ICTV).

The foamy viruses contain both RNA and DNA. Full length genomic RNA of ca. 12-13 kB has not been detected in virions. A large percent of virions contain ca. 13 kB double stranded DNA of unknown structure. For the type species, DNA extracted from virions has infectivity. Evidence that the infectious genome is DNA sets these viruses apart from the other genera.

There are three foamy virus envelope proteins encoded by the *env* gene, SU (surface), TM (transmembrane) and LP, the Env leader peptide which is cleaved from the Env precursor and is the only LP which is incorporated into virions. There are two non-glycosylated structural proteins encoded by the *gag* gene, incorporated with a stoichiometry of about 1:1. Further Gag proteolytic cleavage products MA, CA, and NC are not readily detected in infectious particles, unlike the other six genera.

Other distinct *Spumaretrovirinae* characteristics are that the *pol* mRNA is a spliced product using the 5' splice donor and a splice acceptor near the end of the *gag* gene. The resultant Pol protein does not contain Gag sequences. The viral genome contains a second promoter within the *env* gene, the internal promoter (IP) which is required for replication. Capsids assemble intracellularly and are released from the cell by a process of budding. The Env protein is required for viral budding through a specific interaction between the Gag protein and the Env leader peptide (LP). The packaging signal for viral genomic RNA does not appear to be located near the 5' end of the RNA. All of these characteristics are unique to foamy viruses.

Summary: The new subfamilies *Orthoretrovirinae* and *Spumaretrovirinae* would contain members with similar replication strategies. *Orthoretrovirinae* would contain the alpharetroviruses, betaretroviruses, gammaretroviruses, deltaretroviruses, epsilonretroviruses and lentiviruses. *Spumaretrovirinae* would contain the foamy viruses which have a divergent replication strategy.

Derivation of name: The *Orthoretrovirinae* is based on the *Hepadnaviridae* classification, where the mammalian viruses are considered *Orthohepadnavirinae* from the Latin, ortho = correct. The *Spumaretrovirinae* derive from the name previously given to the species, the Spumaviruses.

References:

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Leceilier, C.-H. and A. Saïb. Foamy viruses: between retroviruses and pararetroviruses. Virology 271:1-8, 2000.

Lindemann, D., T. Pietschmann, M. Picard-Mareau, A. Berg, M. Heinkelein, J. Thurow, P. Knaus, H. Zentgraf, and A. Rethwilm. A particle associated glycoprotein signal peptide essential for viral maturation and infectivity. J.Virol., in press, 2001.

2002.V047.04: To incorporate the genus *Spumavirus,* currently a genmus of the family *Retroviridae*, within the new subfamily *Spumaretrovirinae*.

Purpose: To retain the name of the *Spumavirus* genus as a genus within the new subfamily *Spumaretrovirinae*.

Taxonomic situation: The new subfamily *Spumaretrovirinae* would now consist of the genus *Spumavirus*.

Derivation of name: Latin, spuma = foamy.

References:

Rethwilm, A. Unexpected replication pathways of foamy viruses. J. of Acquired Immune Deficiency Syndromes and Human Retrovirology 13:1):S 248-S 253, 1996.

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Leceilier, C.-H. and A. Saïb. Foamy viruses: between retroviruses and pararetroviruses. Virology 271:1-8, 2000.

Linial, M.L. and Weiss, R.A. Other human and primate retroviruses. Chapter 62 In Fields Virology, Fourth edition, in press, 2001.

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2002.V049.04: To incorporate in the species *Simian foamy virus,* the new type species of the genus *Spumavirus* the strains Chimpanzee foamy virus, Simian foamy virus 1 and Simian foamy virus 3, previously listed as species in the *Spumavirus* genus

Background: The background of this proposal is as follows: The *Retroviridae* Study Group proposed in the spring of 2001 to separate the family into two subfamilies and to change the species names for the simian foamy viruses.

The current genus *Spumavirus* contains several listed species. These include *Bovine foamy virus*, *Chimpanzee foamy virus*, *Feline foamy virus* and *Simian foamy virus 1* and *Simian foamy virus 3*. The Study Group now proposes to make a unified naming for the species of simian foamy virus. This change will remove the species name Chimpanzee foamy virus and the strains Chimpanzee foamy virus, Simian foamy virus 1 and Simian foamy virus 3 will be listed under the new *Simian foamy virus* species.

Purpose: To make a change to unify the species name for the simian foamy virus. Currently, simian foamy virus 1 and simian foamy virus 3 are listed as separate species as is chimpanzee foamy virus. It is proposed to make a single species name for these viruses from monkeys and apes and the single species will be called simian foamy virus. The strains chimpanzee foamy virus, simian foamy virus 1 and simian foamy virus 3 will be listed under the new simian foamy virus species. This change will remove the current species name of Chimpanzee foamy virus.

Taxonomic situation: The to be approved subfamily *Spumaretrovirinae,* will contain one genus, *Spumavirus* with the type species *Simian foamy virus*.

Derivation of proposed names: not applicable

References:
Herchenroder, O., R. Renne, D. Loncar, E. K. Cobb, K. K. Murthy, J. Schneider, A. Mergia, and P. A. Luciw. Isolation, cloning, and sequencing of simian foamy viruses from chimpanzees (SFVcpz): high homology to human foamy virus (HFV). Virology 201:187-199, 1994.

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