This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

Part 1: **TITLE, AUTHORS, etc**

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| **Code assigned:** | ***2017.006D*** | | | | (to be completed by ICTV officers) |
| **Short title: Taxonomic reorganization of the genus *Spumavirus*** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Arifa S. Khan  Jochen Bodem  Florence Buseyne  Antoine Gessain  Welkin Johnson  Jens H. Kuhn  Jacek Kuzmak  Dirk Lindemann  Maxine L. Linial  Martin Löchelt  Magdalena Materniak  Marcelo A. Soares  William M. Switzer | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Arifa S. Khan, [arifa.khan@fda.hhs.gov](mailto:arifa.khan@fda.hhs.gov) | | | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | **ICTV Retroviridae Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
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| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | | Sept 26, 2017 | |

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| **ICTV-EC comments and response of the proposer:** |
| Label Figure 1 with genus names.  Response: Done |

**Part 2**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.006D.U.v2.Spumaretrovirinae\_4gen |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| [1] A. Rethwilm, Molecular biology of foamy viruses, Med. Microbiol. Immunol. 199 (2010) 197–207. doi:10.1007/s00430-010-0158-x.  [2] A. Rethwilm, J. Bodem, Evolution of foamy viruses: the most ancient of all retroviruses, Viruses. 5 (2013) 2349–2374. doi:10.3390/v5102349.  [3] W.M. Switzer, M. Salemi, V. Shanmugam, F. Gao, M.-E. Cong, C. Kuiken, et al., Ancient co-speciation of simian foamy viruses and primates, Nature. 434 (2005) 376–380. doi:10.1038/nature03341.  [4] A. Katzourakis, P. Aiewsakun, H. Jia, N.D. Wolfe, M. LeBreton, A.D. Yoder, et al., Discovery of prosimian and afrotherian foamy viruses and potential cross species transmissions amidst stable and ancient mammalian co-evolution, Retrovirology. 11 (2014) 61. doi:10.1186/1742-4690-11-61.  [5] O.R.P. Bininda-Emonds, M. Cardillo, K.E. Jones, R.D.E. MacPhee, R.M.D. Beck, R. Grenyer, et al., The delayed rise of present-day mammals, Nature. 446 (2007) 507–512. doi:10.1038/nature05634.  [6] W. Heneine, M. Schweizer, P. Sandstrom, T. Folks, Human infection with foamy viruses, Curr. Top. Microbiol. Immunol. 277 (2003) 181–196. |

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| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

Foamy viruses display several shared features that distinguish them from other retroviruses [1, 2], and consequently comprise a subfamily within the *Retroviridae*, the *Spumaretrovirinae*. The current taxonomy includes a single genus, *Spumavirus*, with a small number of species listed. However, one of the most distinctive characteristics of the foamy viruses is an extraordinarily stable, long-term pattern of co-evolution and co-speciation with their respective hosts [2-4]; phylogenetic trees of the foamy virus lineage are topologically largely identical to the corresponding mammalian host trees [5], spanning millions of years of mammalian evolution, with high bootstrap support for the major nodes (which also correspond to major nodes on the host tree) (Fig. 1). Moreover, natural foamy virus infections are non-pathogenic [6], an expected consequence of long term virus−host coevolution. Although rare instances of ancient cross-species transmissions are revealed in such analyses, these are the exceptions rather than the rule [4]. In contrast, the pattern among retroviruses in the subfamily *Orthoretrovirinae* is often dominated by interspecies-transmission and emergence of new virus−host combinations.

Given the very long (millions of years) co-evolution of foamy viruses and their respective hosts, lack of evidence that spillover transmission leads to successful emergence, and the large taxonomic divergence between the respective hosts (in some cases reflecting hosts from different mammalian orders), we propose the creation of new genera within the subfamily *Spumaretrovirinae*, to be composed of species (existing and new) represented by well-defined foamy virus isolates representing each host. The new genera, which replace the genus *Spumavirus*, are: *Simiispumavirus* (simian foamy viruses), *Prosimiispumavirus* (foamy viruses of prosimians), *Bovispumavirus* (bovine foamy viruses), *Equispumavirus* (horse foamy viruses), and *Felispumavirus* (foamy viruses of domestic and wild cats). Currently, the most species-rich genus would be *Simiispumavirus*, which includes distinct viruses of old world monkeys, new world monkeys, and apes (Fig. 1).

In summary, the overall changes in classification are needed since FVs are ancient viruses that co-speciate with their hosts and therefore the viruses can be reliably classified according to the taxonomy of the host (genus and species). Furthermore, since FV genome sequences are highly stable, even upon cross-species transmission, it is easy to identify the host of origin (we have also included this situation in our nomenclature, i.e. species of origin vs species of isolation). Initially only a small number of viruses were available and therefore all were classified under one genus *Spumavirus*:  among these, most were simian foamy viruses and only one from other animal species. Now there are several strains isolated from representatives of different animal genera, including different orders of mammals. The new taxonomy is meant to allow for this ongoing expansion in foamy viruses, and to prevent confusion as the list of foamy virus isolates from different mammalian orders continues to expand.



**Figure 1. Spumaretrovirus phylogeny reflects long-term virus−host cospeciation.** The figure shows an unrooted maximum likelihood tree based on an alignment of the highly conserved *pol* gene of 23 foamy virus isolates representing hosts from five mammalian orders. Branch tips are labeled with the designation of the representative virus isolate from a host organism, followed by the viral species name and the proposed genus name. Some viruses not yet included in the current proposal are shown for completeness (such virus names are non-italicized except for host name). Nodes are labeled with bootstrap support values (out of 100 replicates). Tree was inferred by PhyML as implemented in Geneious 10.1.3. Similar trees and related discussion can be found in references 2-4.