Template for Taxonomic Proposal to the ICTV Executive Committee Species in an existing genus

Code [†] FT2003.044I.01	To designate the follow <i>Ranavirus</i>	ving viruses as species in the belonging to the family°	
	Bohle iridovirus Epizootic haematopoietic necrosis virus Ambystoma tigrinum virus Santee-Cooper ranavirus European catfish virus		

[†] Assigned by ICTV officers
° leave blank if inappropriate or in the case of an unassigned genus

Author(s) with email address(es) of the Taxonomic Proposal

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New Taxonomic Order

Order	
Family	Iridoviridae
Genus	Ranavirus
Type Species	Frog virus 3
List of Species	in the genus

Bohle iridovirus

Epizootic haematopoietic necrosis virus Ambystoma tigrinum virus Santee-Cooper ranavirus European catfish virus

List of Tentative Species in the Genus List of Unassigned Species in the Family

Argumentation to justify the designation of new species in the genus

Species demarcation criteria in the genus

Species are distinguished by several criteria: the percent common bands in RFLP profiles, size distribution of viral proteins (SDS-PAGE), percent amino acid/nucleotide sequence identity/similarity among key viral genes (e.g., major capsid protein, ATPase, etc.), and host range.

Species show

- 1. unique RFLP profiles, i.e., <70% bands held in common,
- 2. distinctive viral protein profiles,
- 3. <95% sequence identity/similarity between select viral genes,
- 4. a distinctive range of susceptible species.

Argumentation to justify the designation of new species in the genus

While ranaviruses cannot be distinguished from each other serologically, the different species can be demarcated based on the multiple criteria listed above. Moreover, although viruses within this genera can infect multiple animal species, it is becoming clear that some species are clearly more susceptible than others to infection with a given agent. By using the multiple criteria listed above (e.g., RFLP and protein profiles, amino acid/nucleotide sequence identity, and susceptible animal species) we can distinguish 6 species within the genus *Ranguirus*

List of created Species in the genus

Bohle iridovirus Epizootic haematopoietic necrosis virus Ambystoma tigrinum virus Santee-Cooper ranavirus European catfish virus

References

- Chinchar V.G. (2002). Ranaviruses (family *Iridoviridae*): Emerging cold-blooded killers. *Arch. Virol.* 147, 447 470.
- Essbauer S., Bremont M., Ahne W. (2001). Comparison of eIF-2 homologous proteins of seven ranaviruses (*Iridoviridae*). Virus Genes 23, 347 359.
- He JG, Lu L, Deng M, He HH, Weng SP, Wang XH, Zhou SY, Long QX, Wang XZ, and Chan SM (2002). Sequence analysis of the complete genome of an iridovirus isolated from the tiger frog. *Virology* 292, 185 197.
- He JG, Deng M, Weng SP, Li Z, Zhou SY, Long QX, Wang XZ, and Chan SM. (2001). Complete genome analysis of the mandarin fish infectious spleen and kidney necrosis iridovirus. *Virology* 291, 126 139.
- Hyatt A.D., Gould A.R., Zupanovic Z., Cunningham A.A., Hengstberger S., Whittington R.J., Kattenbelt J., and Coupar B.E.H. (2000). Comparative studies of piscine and amphibian iridoviruses. *Arch. Virol.* 145, 301 331 (2000).
- Jakob N.J., Muller K., Bahr U., and Darai G. (2001). Analysis of the first complete DNA sequence of an invertebrate iridovirus: Coding strategy of the genome of Chilo iridescent virus. *Virology* 286, 182 196.
- Martinez G., Christian P., Marina C., and Williams T. (2003). Sensitivity of *Invertebrate iridescent virus 6* to organic solvents, detergents, enzymes, and temperature treatment. *Virus Res.* 91, 249 254.
- Mao, J., Hedrick, R.P. and Chinchar, V.G. (1997). Molecular characterization, sequence analysis and taxonomic position of newly isolated fish iridoviruses. *Virology*, **229**, 212-220.
- Nakajima K, Inouye K., and Sorimachi M. (1998). Viral diseases in cultured marine fish in Japan. *Fish Pathol.* 33, 181 188.
- Stasiak K., Demattei M-V., Federici B.A., Bigot Y. (2000). Phylogenetic position of the *Diadromus pulchellus* ascovirus DNA polymerase among viruses with large double-stranded DNA genomes. *J. Gen Virol.* 81, 3059 – 3072.
- Sudthongkong C., Miyata M., and Miyazaki T. (2002). Viral DNA sequences of genes encoding the ATPase and the major capsid protein of tropical iridovirus isolates which are pathogenic to fishes in Japan, South China Sea, and Southeast Asian countries. *Arch. Virol.* 47, 2089 2109.
- Tidona, C.A. and Darai, G. (1997). The complete DNA sequence of lymphocystis disease virus. *Virology*, **230**, 207-216.
- Tidona, C.A., and Darai, G. (2000). Iridovirus homologues of cellular genes: Implications for the molecular evolution of large DNA viruses. *Virus Genes*, 21, 77 81.
- Webby, R., Kalmakoff, J. (1998). Sequence comparison of the major capsid protein gene from 18 diverse iridoviruses. *Arch. Virol.*, 143, 1949-1966.
- Williams, T. (1996). The iridoviruses. Adv. Virus Res., 46, 347-412.
- Williams, T. and Cory, J.S. (1994). Proposals for a new classification of iridescent viruses. J. Gen. Virol., 75, 1291-1301

Annexes: