Template for Taxonomic Proposal to the ICTV Executive Committee
To create a new Genus in an existing Family

Code† **2006.024V.04** To create a new genus in the family* *Poxviridae*

Code† **2006.025V.04** To name the new genus* *Cervidpoxvirus*

Code† **2006.026V.04** To designate the species *Deerpox virus W-848-83*
As the type species of the new genus:

Code† **2006.027V.01** To designate the following as species of the new genus*:

removed

Code† **2006.028V.01** To designate the following as unassigned isolate in the new genus*:

removed

† Assigned by ICTV officers
* repeat these lines and the corresponding arguments for each genus created in the family

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Old Taxonomic Order
Order
Family *Poxviridae*
Genus
Type Species
Species in the Genus
Tentative Species in the Genus

New Taxonomic Order
Order
Family *Poxviridae*
  Genus *Cervidpoxvirus*
  Type Species *Deerpox virus W-848-83*
Species in the Genus *Deerpox virus W-848-83*
  Unassigned isolates in the Genus Deerpox virus W-1170-84

ICTV-EC comments and response of the SG

The following changes to this proposal set were made following comments at the Kingston (June 2007) meeting of the EC:
1. **2006.027V** (to designate *Deerpox virus W-848-83* as a species in the new genus) is superfluous following **2006.026V**, and was therefore removed.
2. **2006.028V** (to designate **Deerpox virus W-1170-84** as an 'unassigned isolate' in the new genus; referred to in the argumentation as a tentative species) does not conform to current usage and was removed.

Argumentation to choose the type species in the genus

Only deerpox virus isolates W-848-83 and W-1170-84 were sequenced. We arbitrarily chose isolate W-848-83 as the representative isolate of the type species.

Species demarcation criteria in the genus

Based on recent analyses of poxvirus genomic sequence, poxvirus genera and species will have 40-77% and 78-99% percent identity at the DNA sequence level, respectively (Lefkowitz et al., 2006).

List of Species in the created genus

Deerpox virus W-848-83

List of Unassigned isolate in the created genus

Argumentation to create a new genus:

Deerpox viruses (DPVs) are poorly characterized viruses responsible for non-parapoxvirus-like infections in members of two subfamilies of cervids, American deer (*Odocoileinae*) and reindeer (Rangiferinae) (Barker *et al.*, 1980; Williams *et al.*, 1985). Until now there has been insufficient information available to classify these chordopoxviruses.

Recently Alfonso and colleagues sequenced the protein coding region of DPV isolate W-848-83 (W83) and W-1170-84 (W84) (Afonso *et al.*, 2005). DNA sequence comparisons of DPV-W83 with available genomic sequences of members of the subfamily *Chordopoxvirinae* indicate that DPV-W83 is most similar to members of capripoxvirus, suipoxvirus, leporipoxvirus and yatapoxvirus genera, yet the phylogenetic distance estimate between DPV-W83 and members of these genera is of a similar order of magnitude as the distance among the members of these genera. DPVs are also distinguished from members of these genera by the presence of 5 DPV-specific genes and an ortholog of VACV A31R that has so far been observed only in orthpoxviruses and avipoxviruses. The sum total of the data indicate that DPV-W83 isolate should be classified as the type species in the new (proposed *Cervidpoxvirus*) genera in the Subfamily *Chordopoxvirinae* of the Family *Poxviridae*.

The second DPV-W84 isolate shares with DPV-W83 only 88% amino acid identify of genes located in the terminal regions of the genomes, which generally vary to a greater extent among poxvirus species than the highly conserved central region. DPV-W84 lack 2 DPV-W83 genes and has an in-frame stop in a third. DPV-W83 lacks 3 genes present in DPV-W84. Whole genome maximum likelihood distances between DPV-W83 and DPV-W84 (0.042) are less than distances between *Lepoxripoxvirus* species myxoma and Shope fibroma virus (0.166), but greater than distances between sequenced capripoxvirus species sheepoxvirus, goatpoxvirus, and lumpy skin disease (0.023 to 0.034). These genomic differences support classification of W84 as a tentative species in the *Cervidpoxvirus* genus.

Origin of the proposed genus name

Suggested by D. L. Rock

References

1. Afonso, C.L., Delhon, G., Tulman, E.R., Lu, Z., Zsak, A., Becerra, V.M., Zsak, L., Kutish, G.F., and Rock, D.L. (2005). Genome of Deerpox Virus. *J. Virol*. 79: 966-977.

2. Barker, I.K., Mehren, K.G., Rapley, W.A., and Cagnon, A.N. 1980. Keratoconjunctivitis and oral cutaneous lesions associated with poxvirus infections in reindeer, p. 171-177. *In* R.J. Montali and G Migaki (ed.). The comparative pathology of zoo animals: proceeding of a symposium held at the National Zoological Park, Smithsonian Institution. Smithsonian Institution Press, Washington

3. Lefkowitz, E. J., C. Wang and C. Upton (2006). "Poxviruses: past, present and future." *Virus Research* 117, 115-118.

4. Williams, E.S., Becerra, V.M., Thorne, E.T., Graham, T.J., Owens, M.J., and Nunamarker, C.E. 1985. Spontaneous poxviral dermatitis and keratoconjunctivitis in free-ranging mule deer (*Odocoileus hemionus*) in Wyoming. *J. Wildl. Dis*. 21:430-433.

Annexe

Maximum Parsimony Branch-and-Bound Trees
Amino Acid Alignments