

# Template for Taxonomic Proposal to the ICTV Executive Committee

## Creating Species in an existing genus

Code<sup>†</sup>  To designate the following as species in the genus:

*Hantavirus*

belonging to the family<sup>°</sup> : *Bunyaviridae*

*Saaremaa virus*

Saaremaa virus – 160V (SAAV-160) **AJ410618**

<sup>†</sup> Assigned by ICTV officers

<sup>°</sup> leave blank if inappropriate or in the case of an unassigned genus

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### Old Taxonomic Order

Order

Family *Bunyaviridae*

Genus *Hantavirus*

Type Species *Hantaan virus*

Species in the Genus 22 altogether

Tentative Species in the Genus none identified

Unassigned Species in the family none identified

### New Taxonomic Order

Order

Family *Bunyaviridae*

Genus *Hantavirus*

Type Species *Hantaan virus*

Species in the Genus 23 altogether (SAAV included)

Tentative Species in the Genus none identified

Unassigned Species in the family none identified

### ICTV-EC comments and response of the SG

## Species demarcation criteria in the genus

Hantavirus species (from the VIIIth report of ICTV):

- (1) are found in a unique ecological niche, i.e. in a different primary rodent reservoir species or subspecies;
- (2) exhibit at least a 7% difference in aa identity on comparison of the complete GPC and N protein sequences;
- (3) show at least a 4-fold difference in two-way cross-neutralization tests; and
- (4) do not naturally form reassortants with other hantavirus species

## Argumentation to justify the designation of new species in the genus

When **Saaremaa virus** (SAAV) was identified and subsequently isolated from the striped field mouse (*Apodemus agrarius*) trapped on Saaremaa island, Estonia, it was regarded as an *A. agrarius* -carried variant of *Dobrava virus* DOBV [1,2]. Later it was observed that SAAV and DOBV are sympatric: in Slovenia [3] and Slovakia [4] these hantaviruses were found to be steadily maintained in their respective hosts, field and yellow-necked mice, that inhabited the same localities. The findings were interpreted as evidence of a reproductive isolation of SAAV from DOBV [5]. Serological study revealed 4-fold or higher cross-neutralization titers to DOBV or SAAV in the majority of human sera from Estonia and the Balkans, thus proving that they represent distinct hantavirus serotypes [6].

To summarize, SAAV fulfills the species demarcation criteria 1, 3 and 4 and comes close to the ARBITRARY SELECTED cutoff level of 7% in the aa identity of the GPC (6.1%) [5].

Notably, the two hantaviruses seem to possess different pathogenicity for humans and laboratory mice. In humans, DOBV causes severe HFRS with a case fatality rate of 8-12% [7, 8] while SAAV has not so far been associated with fatal HFRS (and in some areas the seroprevalence is higher than 3% [9]). In suckling mice, DOBV infection is lethal while SAAV infection is not [10].

In our opinion, we are dealing here with a case of host switching, which occurred in the evolution of these hantaviruses [11]. Phylogenetic analysis revealed a discrepancy in the relationships of DOBV, SAAV and Hantaan virus and their respective rodent hosts. This discrepancy is consistent with the transmission of (pre)DOBV/SAAV between *A. flavicollis* and *A. agrarius*, which resulted in the establishing of SAAV *via* its ecological and reproductive isolation from DOBV. Crucially, the estimated time-point of the host switching, 2.7-4.0 MYA, was closer to the present than the expected time of split between the two *Apodemus* species (<6.5MYA).

## List of created Species in the genus

*Saaremaa virus*

## References

1. **Plyusnin et al.** Dobrava hantavirus in Estonia: does the virus exist throughout Europe? *Lancet* **349**:1369-1370, 1997.
2. **Nemirov et al.** Isolation and characterization of Dobrava hantavirus carried by the striped field mouse (*Apodemus agrarius*) in Estonia. *J. Gen. Virol.*, 80:371-379, 1999.
3. **Avsic-Zupanc et al.** Genetic analysis of wild-type Dobrava hantavirus in Slovenia: co-existence of two distinct lineages within the same natural foci. *J Gen Virol* 81:1747-1755, 2000.
4. **Sibold et al.** Dobrava hantavirus causes hemorrhagic fever with renal syndrome in central Europe and is carried by two different *Apodemus* mice species. *J Med Virol* 63:158-167, 2001
5. **Plyusnin A.** 2002. Genetics of hantaviruses: implications to taxonomy (review). *Arch Virol*, 147:665-682.
6. **Brus-Sjölander et al.** Serological divergence of Dobrava and Saaremaa hantaviruses: evidence for two distinct serotypes. *J. Epidemiol. Infect.* **128**:99-103, 2002.
7. **Papa et al.** Retrospective serological and genetic study of the distribution of hantaviruses in Greece. *J Med Virol* 55:321-327, 1998.
8. **Avzic-Zupanc et al.** Hemorrhagic fever with renal syndrome in the Dolenjska region of Slovenia - a ten-year survey. *Clin Infect Dis* 28:860-865, 1999.
9. **Golovljova et al.** Hantaviruses in Estonia. *J. Med. Virol.* **68**:589-598, 2002.
10. **Klingström J,** Hantaviruses - animal models, immunology and pathogenesis. PhD Thesis, Karolinska Institute, 2004.
11. **Nemirov et al.** Phylogenetic evidence for host switching in the evolution of hantaviruses carried by *Apodemus* mice. *Virus Res.* **90**: 207-215, 2002 (Corrigendum: *Virus Res.* 92:125-126, 2003).

## Annexes: