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

Code[†] 2005.012P.04 To designate the following as species in the genus:

belonging to the family° :

Tombusvirus

Tombusviridae

Havel River virus
Havel River virus – S (HRV-S)
AY370535

[†] 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

R. Koenig: r.koenig@bba.de
G.P. Martelli : martelli@agr.uniba.it

Old Taxonomic Order

Order: None
Family: *Tombusviridae*
Genus: *Tombusvirus*
Type Species: *Tomato bushy stunt virus*
Species in the Genus: 15
Tentative Species in the Genus: 1
Unassigned Species in the family: None

New Taxonomic Order

Order: None
Family: *Tombusviridae*
Genus: *Tombusvirus*
Type Species: *Tomato bushy stunt virus*
Species in the Genus: 16
Tentative Species in the Genus: 1
Unassigned Species in the family: none

ICTV-EC comments and response of the SG

Species demarcation criteria in the genus

The criteria demarcating species in the genus are:

- Extent of serological relationship as determined by immunodiffusion usually not below 3, and/or ELISA,
- Extent of sequence identity between relevant gene products,
  - Less than 87% aa sequence identity of the CP,
  - Less than 96% aa sequence identity of the polymerase,
- Size of the CP,
- Differential cytopathological features; organelles from which multivesicular bodies arise,
- Natural host range,
- Artificial host range reactions.

A critical evaluation of these criteria has been published by Koenig et al. 2004 (reference 2). Molecular data seem to be more reliable for species demarcation than the results of serological and host range studies

Argumentation to justify the designation of new species in the genus

Molecular, serological and host range data suggest that this virus is a distinct species in the genus tombusvirus. The only other tombusvirus to which it is serologically distantly related is Cucumber necrosis virus. Its coat protein shares 70% amino acid sequence identity with that of Cucumber necrosis virus. The average percentages of coat protein amino acid sequence identities with other tombusviruses are below 40% (see anex). The amino acid sequences of the movement proteins and the ORF 4 proteins (PTGS suppressors?) are similar to those of other tombusviruses (reference 1).

List of created Species in the genus

Havel River virus

References

1. Koenig R, Pfeilstetter E, Kegler H, Lesemann D-E (2004) Isolation of two strains of a new Tombusvirus (*Havel river virus*; HaRV) from surface waters in Germany. European Journal of Plant Pathology 110, 429-433

2. Koenig R, Verhoeven JThJ, Fribourg CE, Pfeilstetter E, Lesemann D-E (2004) Evaluation of various species demarcation criteria in attempts to classify ten new tombusvirus isolates. Arch Virol 149: 1733-1744

ANNEX

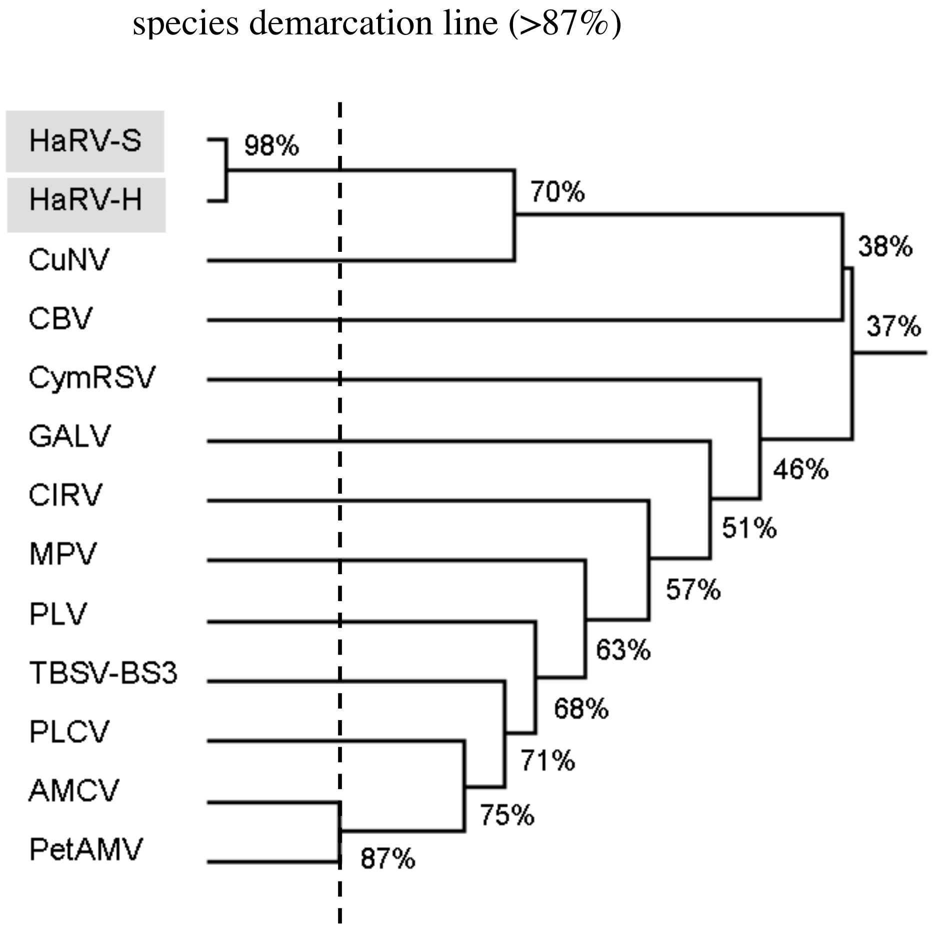

Fig 1. Tree based on the average percentages of amino acid sequence identities between the coat proteins of all tombusviruses analysed so far. The coat proteins of the two isolates of HaRV (HaRV-S and HaRV-H) are only very distantly related to those of other tombusviruses. The closest relationship with 70% amino acid sequence identity is with the coat protein of Cucumber necrosis virus. This percentage is far below the 87% suggested for species demarcation in the genus tombusvirus.