

# Taxonomic Proposal to the ICTV Executive Committee

## Creating species in an existing genus

Code<sup>†</sup> **2007.123P.04** To designate the following as species in the genus:

*Tombusvirus*

belonging to the family<sup>°</sup> :

*Tombusviridae*

*Limonium flower distortion virus*  
*Pelargonium necrotic spot virus*

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

<sup>°</sup> 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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### Old Taxonomic Order

Order

Family *Tombusviridae*

Genus *Tombusvirus*

Type Species *Tomato bushy stunt virus*

Species in the Genus: 16

### New Taxonomic Order

Order

Family *Tombusviridae*

Genus *Tombusvirus*

Type Species *Tomato bushy stunt virus*

Species in the Genus: 18 (less 1 to be removed)

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

## Species demarcation criteria in the genus

- 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.

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

The coat proteins of both proposed species fall clearly within the genus *Tombusvirus* in phylogenetic analysis (see Annex, Fig. 1).

### ***Limonium flower distortion virus***

The CP gene has been sequenced (AY500882) and shows 72% aa identity to that of *Neckar river virus*, the serologically closest species, satisfying the criteria for a new species in the genus.

### ***Pelargonium necrotic spot virus***

Convincing molecular and ultrastructural evidence is provided in Heinze et al., (2004) that this virus is a member of the family *Tombusviridae*. On the basis of the complete sequence (AJ607402) the authors concluded that the virus is a recombinant between a tombus- and an aureusvirus, because its coat protein shares 60%, 57% and 34% amino acid sequence identity, respectively, with two *Pothos latent virus* isolates and *Cucumber leaf spot virus*. This conclusion is not convincing because the *Pelargonium necrotic spot virus* coat protein also shares 53% amino acid sequence identity with CymRSV, a true tombusvirus. Phylogenetic analyses of both the CP (Annex, Fig. 1) and the joined polymerase-mp-cp peptide sequences (Annex, Fig. 2) both place it clearly within the genus *Tombusvirus*. CymRSV has the most closely related CP and thus PNSV clearly satisfies the criteria for a new species in the genus.

## List of created Species in the genus

<i>Limonium flower distortion virus</i>		
Limonium flower distortion virus	(LFDV)	AY500882
<i>Pelargonium necrotic spot virus</i>		
Pelargonium necrotic spot virus	(PNSV)	AJ607402

## References

Heinze, C., Wobbe, V., Lesemann, D.-E., Zhang, D. Y., Willingmann, P., Adam, G. (2004). Pelargonium necrotic spot virus: a new member of the genus *Tombusvirus*. Arch. Virol. 149:1527-1539

Koenig R., Verhoeven J.T., Fribourg C.E., 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

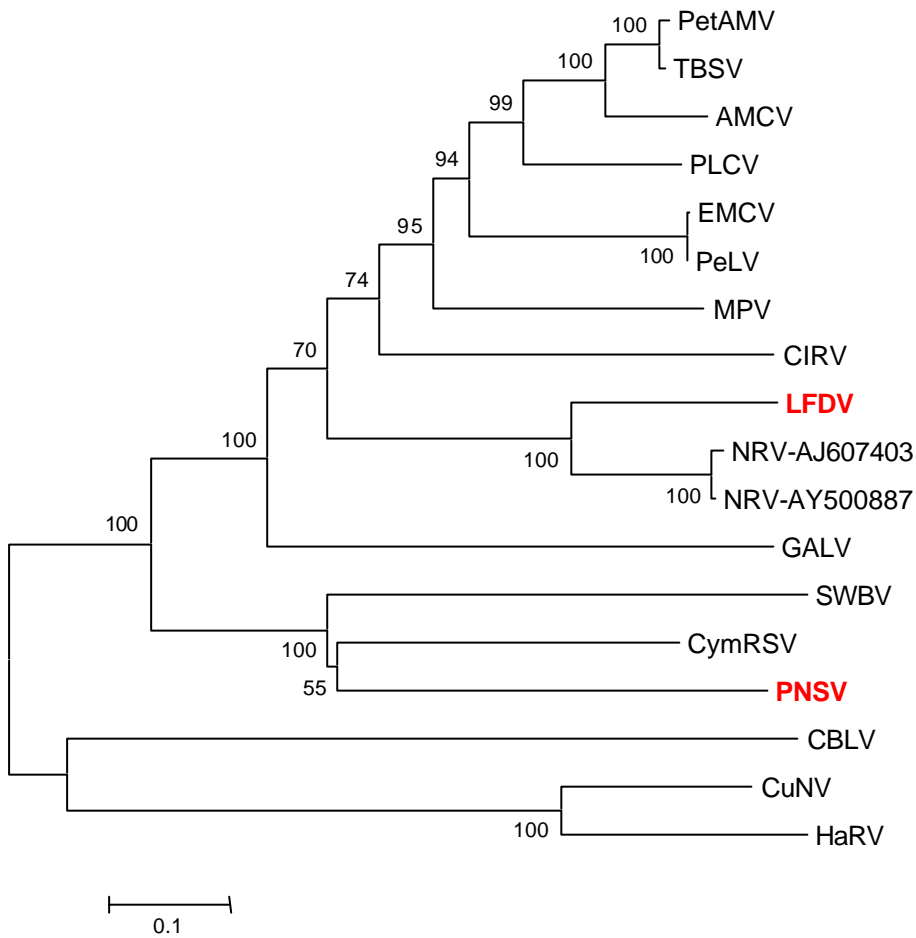


Fig. 1. Phylogenetic (Neighbor-joining) tree for the coat protein amino acid sequences of members of the genus *Tombusvirus*. Analysis in MEGA 3.1 used JTT distances and 1000 bootstrap replicates. The proposed new species are highlighted in red.

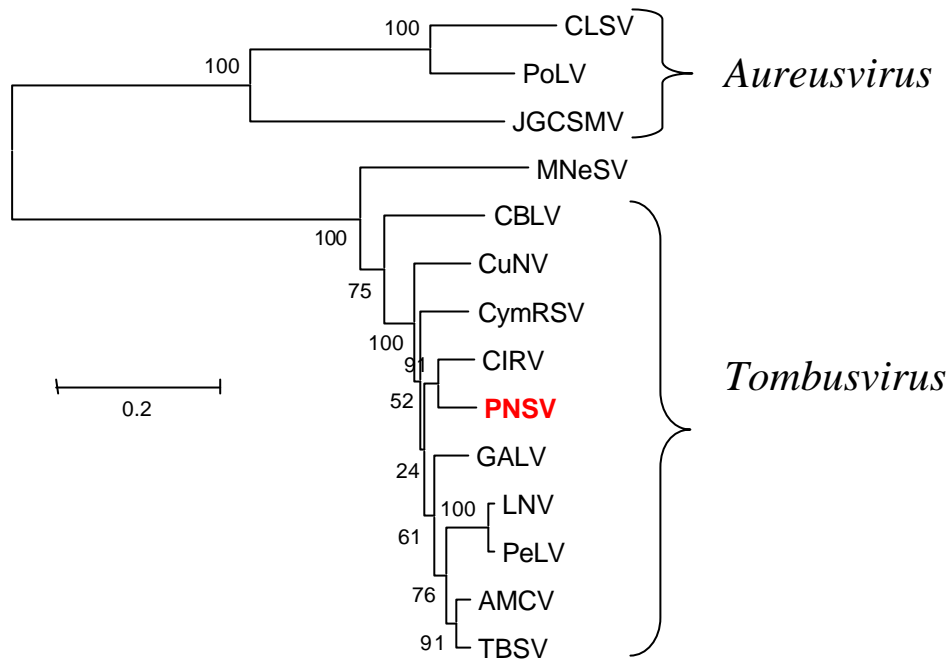


Fig. 2. Phylogenetic (Neighbor-joining) tree for members of the genus *Tombusvirus* and *Aureusvirus*, based on the joined polymerase-mp-cp peptide sequences. Analysis in MEGA 3.1 used JTT distances and 100 bootstrap replicates. Pelargonium necrotic spot virus (PNSV) is highlighted in red.