This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2008.012P***	(to be completed by ICTV officers)

Short title: 1 new species in the genus Ampelovirus
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply): **1** ☐ **2** ☐ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐

Author(s) with e-mail address(es) of the proposer:

G.P. Martelli (martelli@agr.uniba.it) on behalf of the Closteroviridae SG

ICTV-EC or Study Group comments and response of the proposer:

MODULE 5: **NEW SPECIES**

Code	***2008.012P***	(assigned by ICTV officers)

To create one new species assigned as follows:

Genus:	***Ampelovirus***
Subfamily:	
Family:	***Closteroviridae***
Order:	

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Plum bark necrosis stem pitting-associated virus

Argument to justify the creation of the new species:
If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

The criteria demarcating species in the genus in the 8th Report are:

- Particle size,
- Size of CP, as determined by deduced amino acid sequence data,
- Serological specificity using discriminatory monoclonal or polyclonal antibodies,
- Genome structure and organization (number and relative location of the ORFs),
- Amino acid sequence of relevant gene products (CP, CPm, HSP70h) differing

Argument to justify the creation of the new species:

by more than 10%,

- Vector species and specificity,
- Magnitude and specificity of natural and experimental host range,
- Cytopathological features (i.e., aspect of inclusion bodies and origin of cytoplasmic vesicles),

Plum bark necrosis-stem pitting disease was first recognized in California in *Prunus salicina* cv. Black Beaut (Uyemoto and Teviotdale, 1996) and was transmitted by grafting to almond, sweet cherry, Japanese flowering cherry, and several prune and plum varieties (Marini *et al*., 2002). A similar disease had been observed a year earlier in southern Italy in apricot cv. Tyrinthos (Di Terlizzi and Savino, 1995). In both cases symptomatic plants contained dsRNAs 15-17 kbp in size (Abou Ghanen *et al*., 2001; Marini *et al*., 2002; Al Rwahanih *et al*., 2007) which belonged to a putative closterovirus denoted Plum bark necrosis stem pitting-associated virus (PBNSPaV). The same virus was later found in Italy in naturally infected almond, peach, sweet cherry, apricot and plum trees with stem pitting symptoms (Amenduni *et al.*, 2005). The HSP70h gene of the virus was sequenced by Marini *et al*. (2002) (AF195501) and the complete genome sequence was more recently obtained (Al Rwahnih *et al*., 2007). PBNSPaV is currently listed as a tentative species in the genus *Ampelovirus* (8th ICTV Report).

PBNSPaV properties

(i) Virus particles: filamentous with distinct cross-banding, up to 1500 nm long
(ii) dsRNAs: multiple bands, the largest about 15 kbp in size
(iii) CP: 35.9 kDa (determined from deduced sequence data)
(iv) Nucleic acid: single molecule of ssRNA 14,214 nt in size
(v) Genome: monopartite, containing 7 ORFs (accession No. EF546442) and with structure comparable to that of member of the genus *Ampelovirus.*
(vi) Phylogenetic relationships: PBNSPaV groups with members of the genus *Ampelovirus* in trees constructed with HSP70h sequences. In particular, it clusters in a clade comprising *Pineapple melaybug wilt-associated virus 1* (PMWaV-1), *Grapevine leafroll-associated virus 5* (GLRaV-5), and Grapevine leafroll-associated virus 9 (GLRaV-9) (see Annex). At the amino acid level, none of the genome-encoded proteins has identity higher than 40% with comparable genome products of a reprentative each of the genera *Closterovirus* (CTV) and *Crinivirus* (LIYV) and four representatives of the genus *Ampelovirus* (GLRaV-5. GLRaV-9, PMWaV-1 and PMWaV-2).
(vii) Serological relationships: an antiserun to an Italian isolate of PBNSPaV recognized the California isolate of the same virus. No serological tests with other ampeloviruses have been done.
(viii) Mechanical transmission: negative
(ix) Transmission by vectors: no data
(x) Cytopathology: no data
(xi) Natural host range: several stone fruit species

The above data seem to justify upgrading of PBNSPaV from the status of tentative species to that of definitive species in the genus *Ampelovirus.*

References:

Abou Ghanen-Sabanadzovic N., Mahboubi M., Di Terlizzi B., Sabanadzovic S., Savino V., Uyemoto J.K. and Martelli G.P., 2001. Molecular detection of a closterovirus associated with apricot stem pitting in southern Italy. *Journal of Plant Pathology* **83**: 125-132.

Al Rawhnih M., Uyemoto J.K, Falk B.W and Rowhani A., 2007. Molecular characxtrization and detection of plum bark necrosis stem pitting-associated virus. *Archives of Virology* **152**: 2197-2206.

Amenduni T., Hobeika C., Minafra A., Boscia D., Castellano M.A., Savino V., 2005. Plum bark necrosis stem pitting-associated virus in different stone fruit species in Italy. *Journal of Plant Pathology* **87**: 131-134.

Marini D.B., Zhang Y.P., Rowhani A. and Uyemoto J.K, 2002. Etiology and host range of a closterovirus associated with plum bark necrosis-stem pitting disease. *Plant Disease* **86**: 415-417.

Uyemoto J.K. and Teviotdale B.L., 1996. Graft transmission of the causal agent of a bark necrosis-stem pitting disease of Black beaut plum (*Prunus salicina*). *Phytopathology* **86**: S111-S112.

Annexes:

Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.

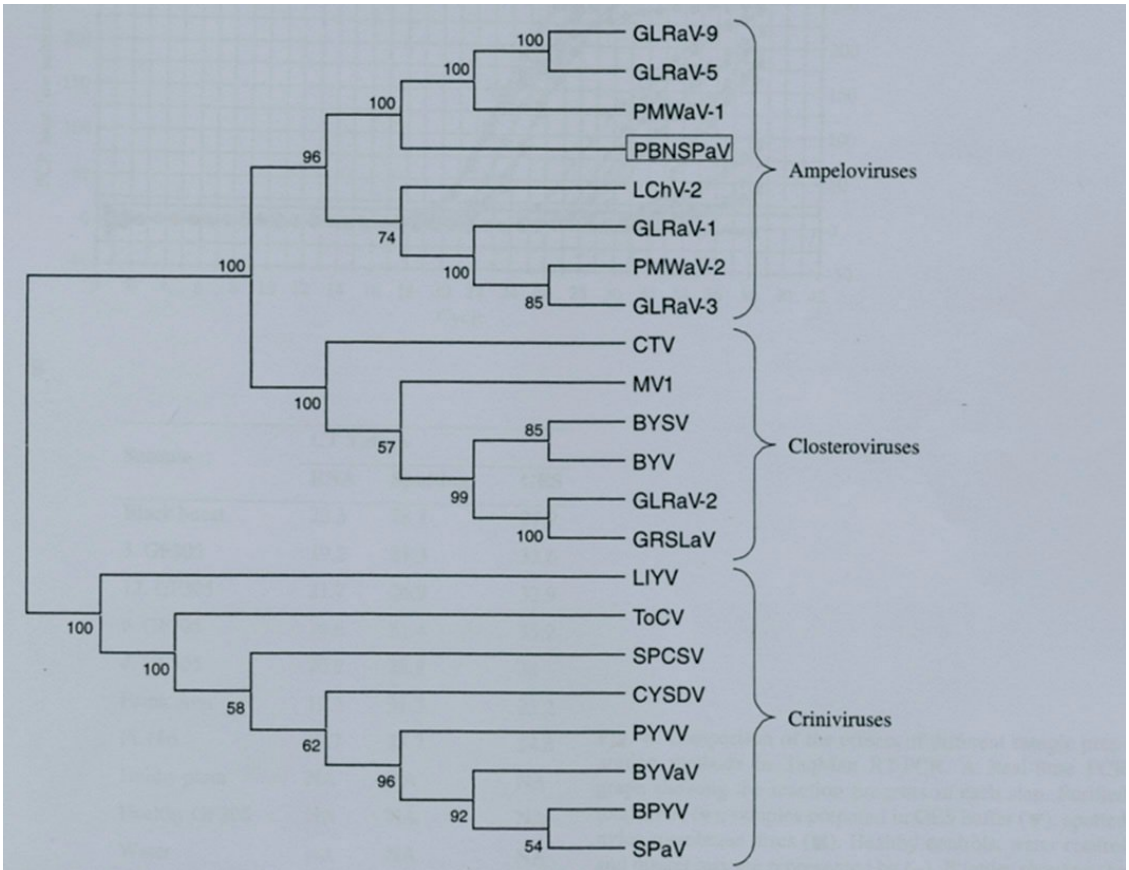

Fig. 3. Phylogenetic analysis of the HSP70h showing the relationship of PBNSPaV and other members of family *Closteroviridae* based on their amino acid sequences. Bootstrap values are shown as percentage values