This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

## MODULE 1: TITLE, AUTHORS, etc

| | | |
|---|---|---|
| **Code assigned:** | ***2015.003a,bF*** | (to be completed by ICTV officers) |

**Short title:** Four new species in the family *Partitiviridae*
(e.g. 6 new species in the genus *Zetavirus*)

| | | | | | |
|---|---|---|---|---|---|
| **Modules attached**<br>(modules 1 and 10 are required) | **1** ☒ | **2** ☒ | **3** ☐ | **4** ☐ | **5** ☐ |
| | **6** ☐ | **7** ☐ | **8** ☐ | **9** ☐ | **10** ☒ |

**Author(s):**

Vainio, E. J.; Kashif, M.; Hyder, R.; Hantula, J.

**Corresponding author with e-mail address:**

Eeva Vainio (eeva.vainio@luke.fi)

**List the ICTV study group(s) that have seen this proposal:**

| | |
|---|---|
| A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses) | Partitiviridae SG |

**ICTV Study Group comments (if any) and response of the proposer:**

SG: 1. Add statements justifying assignment of each new species to particular genus. 2. Add phylograms providing support for those assignments.
Proposer: Changes made as requested.

| | |
|---|---|
| Date first submitted to ICTV: | May 25, 2015 |
| Date of this revision (if different to above): | June 8, 2015 |

**ICTV-EC comments and response of the proposer:**

Fungal and Protist Viruses Subcommittee Chair: Revised proposal approved for submission.

MODULE 2.1: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

| | | |
|---|---|---|
| Code | ***2015.003aF*** | (assigned by ICTV officers) |

**To create 3 new species within:**

| | |
|---|---|
| Genus: | ***Alphapartitivirus*** |
| Subfamily: | |
| Family: | ***Partitiviridae*** |
| Order: | |

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

| **Name of new species:** | **Representative isolate: (only 1 per species please)** | **GenBank sequence accession number(s)** |
|---|---|---|
| *Heterobasidion partitivirus 12* | HetPV12-an1 | KF963175, KF963176 |
| *Heterobasidion partitivirus 13* | HetPV13-an1 | KF963177, KF963178 |
| *Heterobasidion partitivirus 15* | HetPV15-pa1 | KF963186, KF963187 |

**Reasons to justify the creation and assignment of the new species:**

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

The species demarcation criteria within genus *Alphapartitivirus* are:
$\leq$ 90% aa-sequence identity in the RdRp, and/or
$\leq$ 80% aa-sequence identity in the CP
The three *Alphapartitivirus* species listed here share less than 70% (53.3-67.6%) aa-sequence identity in the RdRp and less than 75% (27.6-73.7%) aa-sequence identity in the CP as compared to each other and most closely related sequences available in GenBank, which include Heterobasidion partitiviruses (HetPV3, HetPV14) and Helicobasidium mompa partitivirus V70 (see Table S5 in Kashif et al., 2015; doi: 10.1016/j.virusres.2014.09.002).

HetPV12, HetPV13 and HetPV15 should not be assigned to another genus in the family because they share only ~13-29% RdRp aa sequence identity and ~7-11% CP aa sequence identity with other genera of family *Partitiviridae* (see reference trees and BlastP results in Annex).

## MODULE 2.2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

| | | |
|---|---|---|
| Code | ***2015.003bF*** | (assigned by ICTV officers) |

**To create 3 new species within:**

| | |
|---|---|
| Genus: | ***Betapartitivirus*** |
| Subfamily: | |
| Family: | ***Partitiviridae*** |
| Order: | |

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write “**(new)**” after its proposed name.
- If no genus is specified, enter “**unassigned**” in the genus box.

| **Name of new species:** | **Representative isolate:** (only 1 per species please) | **GenBank sequence accession number(s)** |
|---|---|---|
| *Heterobasidion partitivirus 7* | HetPV7-pa1 | JN606091, JN606090 |

**Reasons to justify the creation and assignment of the new species:**

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

The species demarcation criteria within genus *Betapartitivirus* are:
≤ 90% aa-sequence identity in the RdRp, and/or
≤ 80% aa-sequence identity in the CP
HetPV7 shares ca. 66% and 60% aa-sequence identity in the RdRp and CP with HetPV2, which is the most closely related virus available in GenBank (see Vainio et al., 2015); doi:10.1038/ismej.2014.145).

HetPV7 should not be assigned to another genus in the family because it shares only ~12-29% RdRp aa sequence identity and ~5-8% CP aa sequence identity with other genera of family *Partitiviridae* (see reference trees and BlastP results in Annex).

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

## References:

Kashif M, Hyder R, De Vega Perez D, Hantula J, Vainio EJ (2015). *Heterobasidion* wood decay fungi host diverse and globally distributed viruses related to *Helicobasidium mompa* partitivirus V70. Virus Research 195:119–123. doi: 10.1016/j.virusres.2014.09.002

Vainio EJ, Müller MM, Korhonen K, Piri T, Hantula J. (2015). Viruses accumulate in aging infection centers of a fungal forest pathogen. The ISME Journal 9, 497–507. doi:10.1038/ismej.2014.145

## Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

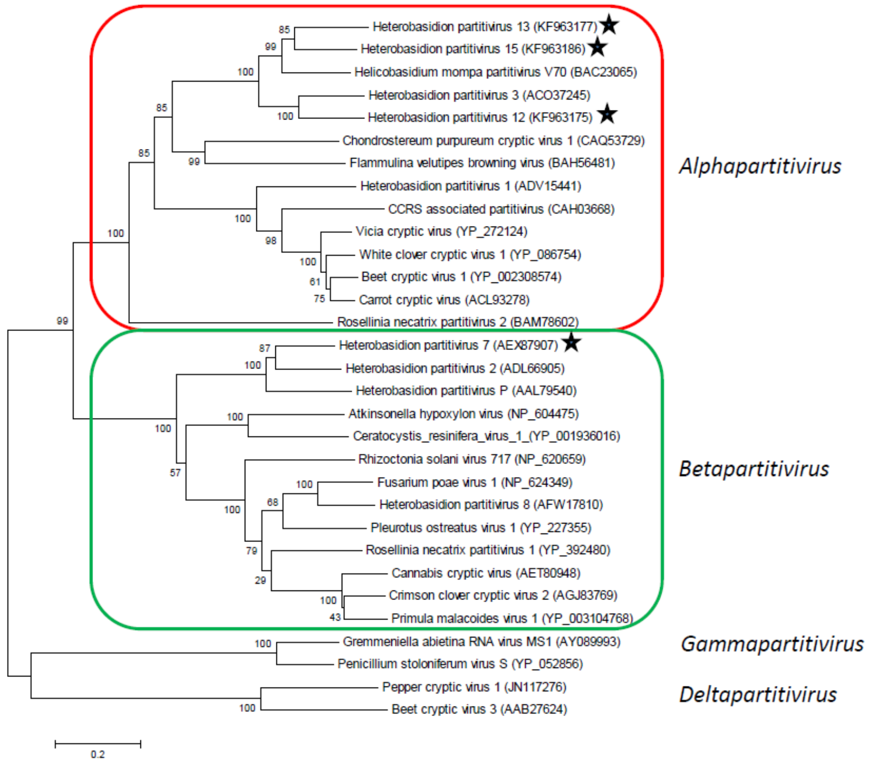

**Figure 1.** Neighbor-Joining dendrogram with complete RdRp amino acid sequences. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of aa substitutions per site. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA5.

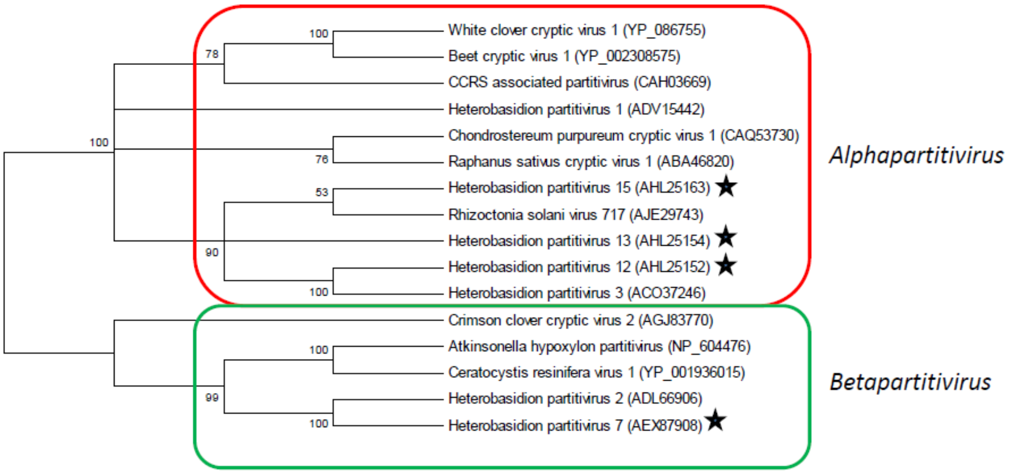

**Figure 2.** Neighbor-Joining dendrogram with complete CP amino acid sequences. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. Branches with < 50% bootstrap support were collapsed. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of aa substitutions per site. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA5.

**Table 1.** BlastP results for HetPV12 (protein lengths are 585 aa for the RdRp and 520 aa for the CP, respectively)

| Virus species | Genus | Size (aa) | | Identity % | | Query cover % | | E-value | | Accessions | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | RdRp | CP | RdRp | CP | RdRp | CP | RdRp | CP | RdRp | CP |
| Heterobasidion partitivirus 3 | *Alphapartitivirus* | 585 | 521 | 65 | 74 | 99 | 100 | 0.0 | 0.0 | ACO37245 | ACO37246 |
| Rhizoctonia solani virus 717 | *Alphapartitivirus* | 578 | 548 | 61 | 26 | 96 | 98 | 0.0 | $1^{-26}$ | AJE29742 | AJE29743 |
| Heterobasidion partitivirus 13 | *Alphapartitivirus* | 581 | 509 | 58 | 30 | 98 | 97 | 0.0 | $3^{-44}$ | AHL25153 | AHL25154 |
| Heterobasidion partitivirus 15 | *Alphapartitivirus* | 581 | 512 | 57 | 29 | 99 | 99 | 0.0 | $5^{-45}$ | AHL25162 | AHL25163 |
| Helicobasidium mompa partitivirus | *Alphapartitivirus* | 598 | - | 57 | - | 92 | - | 0.0 | - | BAC23065 | Not available |
| White clover cryptic virus 1[a] | *Alphapartitivirus* | 616 | 487 | 35 | 26 | 84 | 62 | $6^{-84}$ | $2^{-8}$ | YP_086754 | YP_086755 |
| Atkinsonella hypoxylon virus[b] | *Betapartitivirus* | 665 | 652 | 28 | ~8[c] | 75 | - | $3^{-33}$ | - | NP_604475 | NP_604476 |
| Heterobasidion partitivirus 7 | *Betapartitivirus* | 724 | 654 | 28 | ~9[c] | 67 | - | $7^{-31}$ | - | AEX87907 | AEX87908 |
| Penicillium stoloniferum virus S | *Gammapartitivirus* | 539 | 434 | ~14[c] | ~10[c] | - | - | - | - | YP_052856 | YP_052857 |
| Pepper cryptic virus 1 | *Deltapartitivirus* | 479 | 412 | ~13[c] | ~11[c] | - | - | - | - | AEJ07890 | AEJ07891 |

[a] Type species of *Alphapartitivirus*

[b] Most similar member of genus *Betapartitivirus*

[c] Value based on full sequence alignment with MAFFT (not detected by BlastP)

**Table 2**. BlastP results for HetPV13 (protein lengths are 581 aa for the RdRp and 509 aa for the CP, respectively)

| Virus species | Genus | Size (aa) | | Identity % | | Query cover % | | E-value | | Accessions | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | RdRp | CP | RdRp | CP | RdRp | CP | RdRp | CP | RdRp | CP |
| Heterobasidion partitivirus 3 | *Alphapartitivirus* | 585 | 521 | 55 | 29 | 96 | 96 | 0.0 | 5-50 | ACO37245 | ACO37246 |
| Rhizoctonia solani virus 717 | *Alphapartitivirus* | 578 | 548 | 55 | 25 | 98 | 79 | 0.0 | 5-20 | AJE29742 | AJE29743 |
| Heterobasidion partitivirus 12 | *Alphapartitivirus* | 585 | 520 | 58 | 30 | 99 | 96 | 0.0 | 2-47 | AHL25151 | AHL25152 |
| Heterobasidion partitivirus 15 | *Alphapartitivirus* | 581 | 512 | 70 | 29 | 96 | 99 | 0.0 | 4-54 | AHL25162 | AHL25163 |
| Helicobasidion mompa partitivirus | *Alphapartitivirus* | 598 | - | 66 | - | 94 | - | 0.0 | - | BAC23065 | Not available |
| White clover cryptic virus 1[a] | *Alphapartitivirus* | 616 | 487 | 33 | 25 | 91 | 58 | $2^{-81}$ | 6-11 | YP_086754 | YP_086755 |
| Atkinsonella hypoxylon virus | *Betapartitivirus* | 665 | 652 | 25 | ~7[c] | 74 | - | $1^{-21}$ | - | NP_604475 | NP_604476 |
| Heterobasidion partitivirus 7[b] | *Betapartitivirus* | 724 | 654 | 29 | ~8[c] | 67 | - | $6^{-32}$ | - | AEX87907 | AEX87908 |
| Penicillium stoloniferum virus S | *Gammapartitivirus* | 539 | 434 | ~14[c] | ~8[c] | - | - | - | - | YP_052856 | YP_052857 |
| Pepper cryptic virus 1 | *Deltapartitivirus* | 479 | 412 | ~14[c] | ~11[c] | - | - | - | - | AEJ07890 | AEJ07891 |

[a] Type species of *Alphapartitivirus*

[b] Most similar member of genus *Betapartitivirus*

[c] Value based on full sequence alignment with MAFFT (not detected by BlastP)

**Table 3**. BlastP results for HetPV15 (protein lengths are 581 aa for the RdRp and 512 aa for the CP, respectively)

| Virus species | Genus | Size (aa) | | Identity % | | Query cover % | | E-value | | Accessions | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | RdRp | CP | RdRp | CP | RdRp | CP | RdRp | CP | RdRp | CP |
| Heterobasidion partitivirus 3 | *Alphapartitivirus* | 585 | 521 | 57 | 29 | 6 | 96 | 0.0 | $5^{-43}$ | ACO37245 | ACO37246 |
| Rhizoctonia solani virus 717 | *Alphapartitivirus* | 578 | 548 | 56 | 28 | 97 | 98 | 0.0 | $9^{-36}$ | AJE29742 | AJE29743 |
| Heterobasidion partitivirus 12 | *Alphapartitivirus* | 585 | 520 | 57 | 29 | 99 | 96 | 0.0 | $5^{-45}$ | AHL25151 | AHL25152 |
| Heterobasidion partitivirus 13 | *Alphapartitivirus* | 581 | 509 | 70 | 29 | 96 | 99 | 0.0 | $1^{-51}$ | AHL25153 | AHL25154 |
| Helicobasidium mompa partitivirus | *Alphapartitivirus* | 598 | - | 67 | - | 94 | - | 0.0 | - | BAC23065 | Not available |
| White clover cryptic virus 1[a] | *Alphapartitivirus* | 616 | 487 | 31 | 31 | 90 | 28 | $7^{-74}$ | $1^{-6}$ | YP_086754 | YP_086755 |
| Atkinsonella hypoxylon virus | *Betapartitivirus* | 665 | 652 | 26 | ~7[c] | 74 | - | $4^{-24}$ | - | NP_604475 | NP_604476 |
| Heterobasidion partitivirus 7[b] | *Betapartitivirus* | 724 | 654 | 26 | ~9[c] | 80 | - | $6^{-31}$ | - | AEX87907 | AEX87908 |
| Penicillium stoloniferum virus S | *Gammapartitivirus* | 539 | 434 | ~14[c] | ~9[c] | - | - | - | - | YP_052856 | YP_052857 |
| Pepper cryptic virus 1 | *Deltapartitivirus* | 479 | 412 | ~14[c] | ~10[c] | - | - | - | - | AEJ07890 | AEJ07891 |

[a] Type species of *Alphapartitivirus*

[b] Most similar member of genus *Betapartitivirus*

[c] Value based on full sequence alignment with MAFFT (not detected by BlastP)

**Table 4**. BlastP results for HetPV7 (protein lengths are 724 aa for the RdRp and 654 aa for the CP, respectively)

| Virus species | Genus | Size (aa) | | Identity % | | Query cover % | | E-value | | Accessions | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | RdRp | CP | RdRp | CP | RdRp | CP | RdRp | CP | RdRp | CP |
| Heterobasidion partitivirus 2 | *Betapartitivirus* | 722 | 659 | 66 | 60 | 100 | 98 | 0.0 | 0.0 | ADL66905 | ADL66906 |
| Heterobasidion partitivirus P | *Betapartitivirus* | 734 | - | 59 | - | 98 | - | 0.0 | - | AAL79540 | Not available |
| Atkinsonella hypoxylon virus[a] | *Betapartitivirus* | 665 | 652 | 42 | 26 | 78 | 97 | $2^{-143}$ | $2^{-44}$ | NP_604475 | NP_604476 |
| Ceratocystis resinifera virus 1 | *Betapartitivirus* | 663 | 661 | 38 | 26 | 88 | 76 | $1^{-136}$ | $8^{-35}$ | YP_001936016 | YP_001936015 |
| Crimson clover cryptic virus 2 | *Betapartitivirus* | 746 | 674 | 36 | 17 | 84 | 73 | $7^{-108}$ | $2^{-3}$ | AGJ83769 | AGJ83770 |
| Heterobasidion partitivirus 13 [b] | *Alphapartitivirus* | 581 | 509 | 29 | ~8[d] | 62 | - | $8^{-32}$ | - | AHL25153 | AHL25154 |
| White clover cryptic virus 1[c] | *Alphapartitivirus* | 616 | 487 | 27 | ~8[d] | 54 | - | $5^{-22}$ | - | YP_086754 | YP_086755 |
| Penicillium stoloniferum virus S | *Gammapartitivirus* | 539 | 434 | ~14[d] | ~6[d] | - | - | - | - | YP_052856 | YP_052857 |
| Pepper cryptic virus 1 | *Deltapartitivirus* | 479 | 412 | ~12[d] | ~5[d] | - | - | - | - | AEJ07890 | AEJ07891 |

[a] Type species of *Betapartitivirus*

[b] Most similar *Alphapartitivirus* with complete genome sequence

[c] Type species of *Alphapartitivirus*

[d] Value based on full sequence alignment with MAFFT (not detected by BlastP)