

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2021.006F** |  |
| **Short title:** Create 35 new species and eight new genera, abolish one genus (*Hypovirus*) and rename four existing species (*Durnavirales*: *Hypoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Hypoviridae* Study Group |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | 21-05-2021 |
| Date of this revision (if different to above) | 15-09-2021 |

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

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| **EC Comments:** Numerous errors observed in the Excel file. Please address, along with minor suggestions for style improvement.  **Response:** Done. |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2021.006F.R.Hypoviridae\_8newgen\_35newsp.xlsx |

**Abstract**

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| Currently, the family *Hypoviridae* includes only a single genus (*Hypovirus*) with four species: *Cryphonectria hypovirus 1*, 2, *3*, and *4*. In the last twenty years, a number of hypovirid-like sequences were characterized, but none are officially classified yet. Phylogenetic analysis reveals a complex framework for these viruses, indicating the need for taxonomic updates.  Here we propose to revamp the taxonomy of these viruses by abolishing genus *Hypovirus* and reassigning the four recognized species to two new genera, *Alphahypovirus* and *Betahypovirus*. Furthermore, we propose creation of 35 novel species to classify 40 new viruses known from sequences and to create six additional new genera. In summary, an updated family *Hypoviridae* is proposed to comprise a total of eight genera in the family: *Alphahypovirus*, *Betahypovirus, Gammahypovirus, Deltahypovirus, Epsilonhypovirus, Zetahypovirus, Thetahypovirus, Etahypovirus*. |

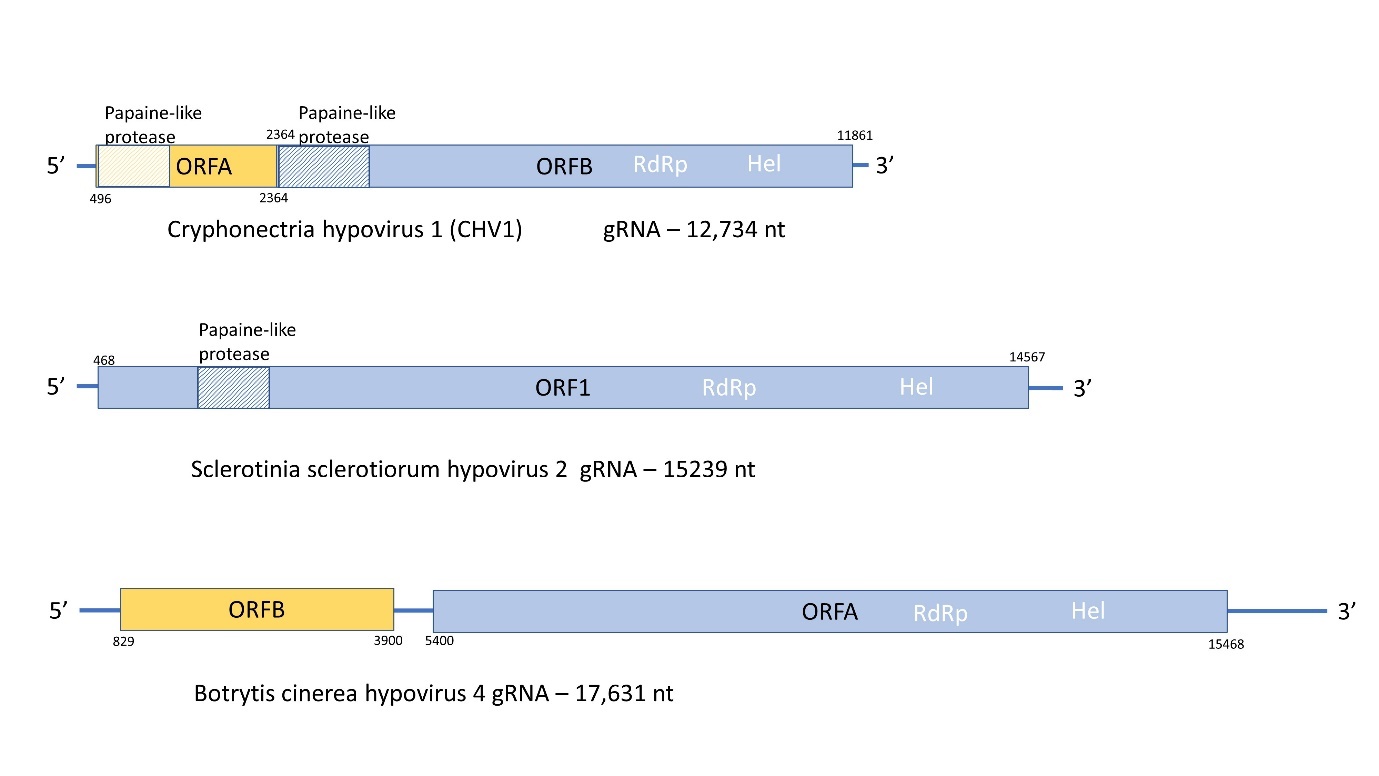
**Text of proposal**

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| |  | | --- | | **HYSTORICAL BACKGROUND**  Currently, the family *Hypoviridae* includes only a single genus (*Hypovirus*) with four species: *Cryphonectria hypovirus 1*, 2, *3*, and *4*. These four species have been established for viruses that infect the ascomycete *Cryphonectria parasitica*, and of which the last was characterized and classified more than 15 years ago [6, 13, 21, 23]. Since then, a great number of hypovirid-like virus genomes were characterized through traditional cloning procedures or by HTS approaches [1, 3-5, 7, 9-12, 14, 16-18, 20, 22, 24, 25, 27-31]. Here we propose the classification of 40 new viruses into 35 new species, whereas four established species are renamed and moved into new genera (Table 1).  **Genome organization:**  The accepted hypovirus species and the ones we here propose have member viruses with a monosegmented RNA genome of positive sense orientation. Contrary to *bona fide* dsRNA viruses, hypoviruses are infectious as plus strand RNA transcripts [2, 15]. Genome length generally ranges from 9 to 13 kb, with exception of Sclerotinia sclerotiorum hypovirus 6 (7.3 kb) and a number of members of the proposed *Thetahypovirus* genus with genomes exceeding 15 kb in length [5, 19, 20, 31].  Most hypovirid-like sequences contain a single ORF that encodes a polyprotein with identifiable RdRp and helicase domains. Additionally, a third, papain-like protease domain is also present in the same polypeptide. Some members of the family *Hypoviridae* have more than a single ORF, mostly upstream of the polyprotein carrying Hel and RdRp domains. In the case of Cryphonectria hypovirus 1 (CHV1) such an accessory ORF encodes a second papain-like protease. Recently a long bicistronic hypovirid-like genome was also described in a virus reported from *Botrytis cinerea* (Botrytis cinerea hypovirus 4). Representative genome organizations in the family are described in Fig. 1.  **Phylogenetic relationships**:  Previous phylogenetic analysis has assigned the members of the family *Hypoviridae* to phylum *Pisuviricota*, and, with less robust statistical support, to class *Duploviricetes* of order *Durnavirales* [8, 26]. Here, using a phylogenetic analysis that uses the MAFFT alignment of the whole polyprotein of a total of 44 recognized and proposed hypovirids, we show that they indeed form a monophyletic lineage that can be subdivided in eight distinct clades corresponding to eight new genera (Fig. 2).  Furthermore, a pairwise identity matrix from the same alignment (Fig. 3) shows that Rosellinia nectrix hypovirus 2, Fusarium graminearum hypovirus 2, Botrytis cinerea hypovirus 5, Macrophomina phaseolina hypovirus 2 and Botrytis cinerea hypovirus 3 are members, respectively, of *Epsilonhypovirus entoleucae*, *Epsilonhypovirus fusarii*, *Thetahypovirus sclerotiniae*, *Alphahypovirus macrophominae* and *Betahypovirus sinensis* which includes as exemplar isolates Entoleuca hypovirus 1, Fusarium poae hypovirus 1, Sclerotinia sclerotiorum hypovirus 2, Macrophomina phaseolina hypovirus 1 and sclerotinia sclerotiorum hypovirus 1, respectively. Therefore, five proposed species comprise closely related viruses reported from different hosts.  **Species demarcation criteria**: Less than 80 % identity in the amino acid content of the polyprotein carrying the RdRp domain is the threshold proposed to distinguish viruses belonging to distinct species.  **Etymology of the newly proposed taxa:** The term *Hypoviridae* comes from the term hypovirulence, the phenomenon caused by the most studied virus in this family. Names of new genera contain prefixes consisting of spelled Greek alphabet letters, alpha, beta, gamma, etc., followed by a suffix “hypovirus” (for example: *Alphahypovirus*, *Betahypoviris*, etc.). | |

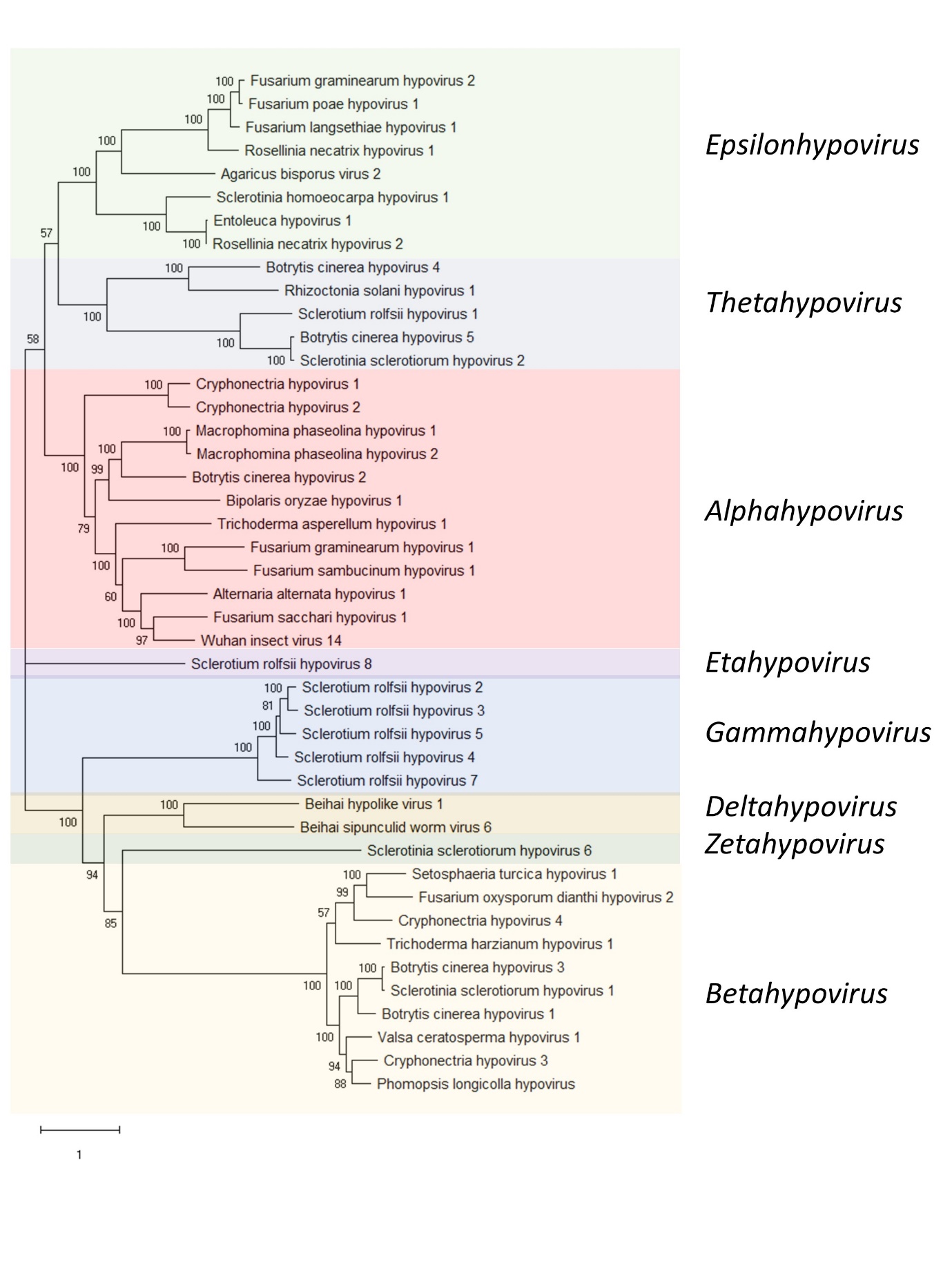
**Supporting evidence**

**Table 1:**  List of proposed new taxonomic organization of the family *Hypoviridae* with some features of member viruses.

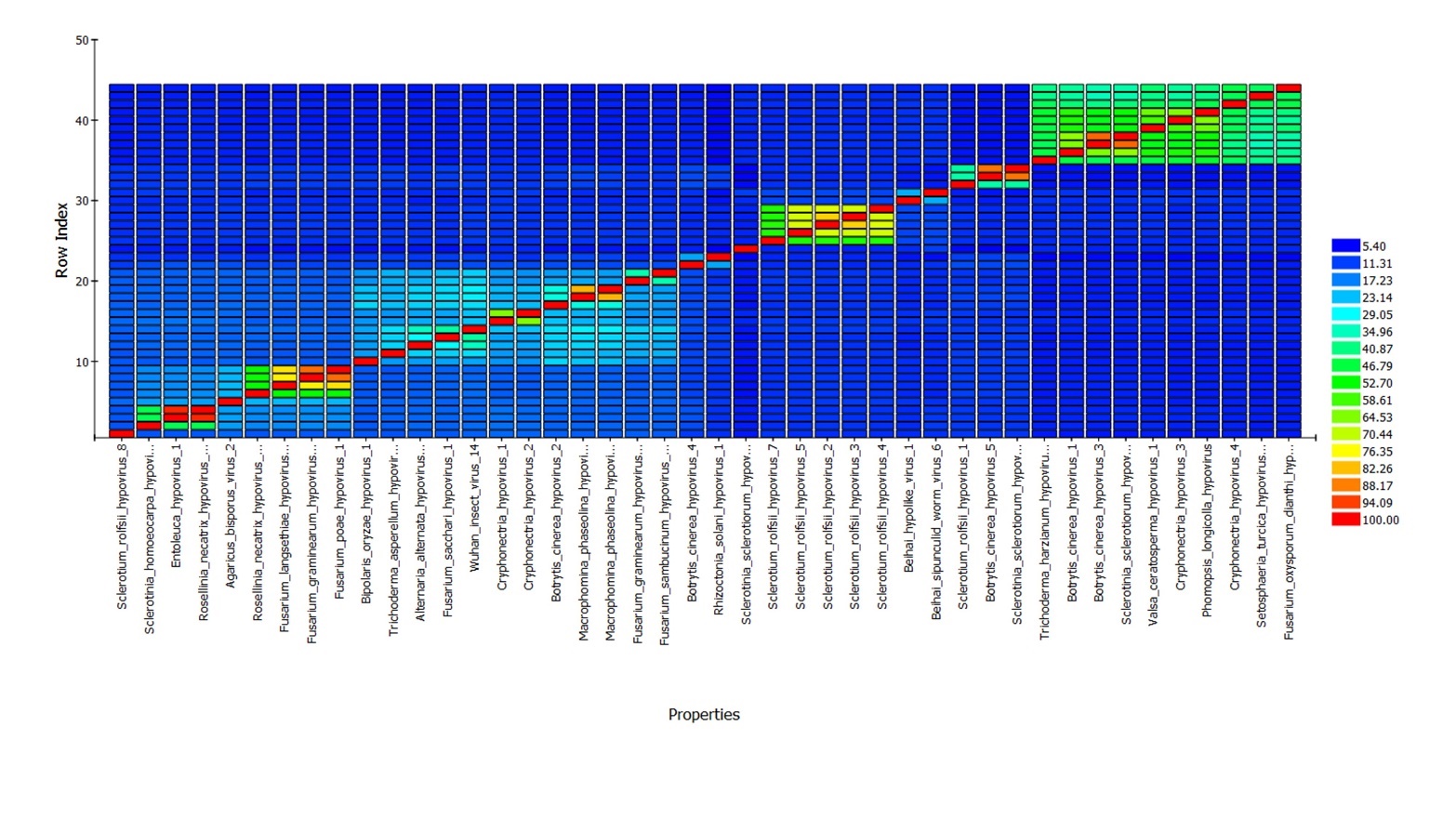
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| --- | --- | --- | --- | --- | --- | --- | --- |
| Genus | Species Name | Virus Name | Acronym | Lenght | NuclAcc | Isolate | References |
| *Alphahypovirus* | *Alphahypovirus alternariae* | Alternaria alternata hypovirus 1 | AaHV1 | 14102 | MK189193 | YL-3C | 9 |
| *Alphahypovirus* | *Alphahypovirus bipolaridis* | Bipolaris oryzae hypovirus 1 | BoHV1 | 13625 | MH316122.2 | ES35 | 12 |
| *Alphahypovirus* | *Alphahypovirus botrytidis* | Botrytis cinerea hypovirus 2 | BcHV2 | 13722 | MN617169.1 | BCS3\_DN9124 | 20 |
| *Alphahypovirus* | *Alphahypovirus cryphonectriae* | Cryphonectria hypovirus 1 | CHV1 | 12734 | M57938.1 | EP713 | 21 |
| *Alphahypovirus* | *Alphahypovirus americanum* | Cryphonectria hypovirus 2 | CHV2 | 12507 | L29010.1 | NB-58 | 6 |
| *Alphahypovirus* | *Alphahypovirus fusarii* | Fusarium graminearum hypovirus 1 | FgHV1 | 13035 | MK279472.1 | HN10 | 4 |
| *Alphahypovirus* | *Alphahypovirus sacchari* | Fusarium sacchari hypovirus 1 | FsHV1 | 13969 | MN295969.1 | F206 | 29 |
| *Alphahypovirus* | *Alphahypovirus japonicum* | Fusarium sambucinum hypovirus 1 | FsHV1 | 13120 | LC596823.1 | Fs1837h | 17 |
| *Alphahypovirus* | *Alphahypovirus macrophominae* | Macrophomina phaseolina hypovirus 1 | MpHV1 | 12468 | KP900893.1 | Mp2003b | 16 |
| *Alphahypovirus* | *Alphahypovirus macrophominae* | Macrophomina phaseolina hypovirus 2 | MpHV2 | 13299 | MT062425.1 | 2012-022 | 25 |
| *Alphahypovirus* | *Alphahypovirus trichodermae* | Trichoderma asperellum hypovirus 1 | TaHV1 | 14211 | MK279475.1 | CBS 1131938 | 4 |
| *Alphahypovirus* | *Alphahypovirus insecti* | Wuhan insect virus 14 | WHIV14 | 12473 | NC\_033473.1 | WHZM10168 | 22 |
| *Betahypovirus* | *Betahypovirus sinensis* | Botrytis cinerea hypovirus 1 | BcHV1 | 10252 | MG554632 | HBtom-372 | 5 |
| *Betahypovirus* | *Betahypovirus sinensis* | Botrytis cinerea hypovirus 3 | BcHV3 | 10863 | MN617170.1 | BCI1\_3 | 20 |
| *Betahypovirus* | *Betahypovirus cryphonectriae* | Cryphonectria hypovirus 3 | CHV3 | 9799 | AF188515.1 | WY | 23 |
| *Betahypovirus* | *Betahypovirus americanum* | Cryphonectria hypovirus 4 | CHV4 | 9149 | AY307099.1 | SR2 | 13 |
| *Betahypovirus* | *Betahypovirus fusarii* | Fusarium oxysporum dianthi hypovirus 2 | FodHV2 | 9444 | MN176979.1 | **N.A** | **N.A.** |
| *Betahypovirus* | *Betahypovirus phomopsis* | Phomopsis longicolla hypovirus | PlHV1 | 9760 | KF537784 | ME711 | 7 |
| *Betahypovirus* | *Betahypovirus sclerotiniae* | Sclerotinia sclerotiorum hypovirus 1 | SsHV1 | 10438 | JF781304.1 | SZ-150 | 27 |
| *Betahypovirus* | *Betahypovirus setosphaeriae* | Setosphaeria turcica hypovirus 1 | StHV1 | 9069 | MK279474.1 | 128A | 4 |
| *Betahypovirus* | *Betahypovirus trichodermae* | Trichoderma harzianum hypovirus 1 | ThHV1 | 11251 | MN172262.1 | T-70 | 30 |
| *Betahypovirus* | *Betahypovirus valsae* | Valsa ceratosperma hypovirus 1 | VcHV1 | 9543 | AB690372 | MVC86 | 28 |
| *Deltahypovirus* | *Deltahypovirus sinicum* | Beihai hypo-like virus 1 | BH-LV1 | 9925 | KX883006 | BHZC36965 | 22 |
| *Deltahypovirus* | *Deltahypovirus sipunculidi* | Beihai sipunculid worm virus 6 | BHSWV6 | 8923 | KX883005 | BHNXC41400 | 22 |
| *Epsilonhypovirus* | *Epsilonhypovirus agarici* | Agaricus bisporus virus 2 | AbV2 | 13871 | KY357507.1 | C19-C1 | 3 |
| *Epsilonhypovirus* | *Epsilonhypovirus entoleucae* | Entoleuca hypovirus 1 | EnHV1 | 10920 | MF375885.1 | EnHV1-97-14 | 24 |
| *Epsilonhypovirus* | *Epsilonhypovirus fusarii* | Fusarium graminearum hypovirus 2 | FgHV2 | 12800 | KP208178.1 | JS16 | 10 |
| *Epsilonhypovirus* | *Epsilonhypovirus sinicum* | Fusarium langsethiae hypovirus 1 | FlHV1 | 12839 | KY120321 | AH32 | 11 |
| *Epsilonhypovirus* | *Epsilonhypovirus japonicum* | Fusarium poae hypovirus 1 | FpHV1 | 12795 | LC150612.1 | MAFF 240374 | 18 |
| *Epsilonhypovirus* | *Epsilonhypovirus roselliniae* | Rosellinia necatrix hypovirus 1 | RnHV1 | 13156 | LC318482 | Rn-Ca | 1 |
| *Epsilonhypovirus* | *Epsilonhypovirus entoleucae* | Rosellinia necatrix hypovirus 2 | RnHV2 | 14918 | LC333733.1 | Rn118-8 | 1 |
| *Epsilonhypovirus* | *Epsilonhypovirus sclerotiniae* | Sclerotinia homoeocarpa hypovirus 1 | ShHV1 | 12370 | MK279473.1 | LT11 | 4 |
| *Etahypovirus* | *Etahypovirus sclerotii* | Sclerotium rolfsii hypovirus 8 | SrHV8 | 12769 | MH766503.1 | BLH-1-3 | 31 |
| *Gammahypovirus* | *Gammahypovirus sclerotii* | Sclerotium rolfsii hypovirus 2 | SrHV2 | 11010 | MH766497.1 | BLH-1-17 | 31 |
| *Gammahypovirus* | *Gammahypovirus sinensis* | Sclerotium rolfsii hypovirus 3 | SrHV3 | 10739 | MH766498.1 | BLH-18 | 31 |
| *Gammahypovirus* | *Gammahypovirus atheliae* | Sclerotium rolfsii hypovirus 4 | SrHV4 | 11035 | MH766499.1 | BLH-19 | 31 |
| *Gammahypovirus* | *Gammahypovirus meridionalis* | Sclerotium rolfsii hypovirus 5 | SrHV5 | 10758 | MH766500.1 | BLH-1-20 | 31 |
| *Gammahypovirus* | *Gammahypovirus uredi* | Sclerotium rolfsii hypovirus 7 | SrHV7 | 10961 | MH766502.1 | BLH-1-2 | 31 |
| *Thetahypovirus* | *Thetahypovirus botrytidis* | Botrytis cinerea hypovirus 4 | BcHV4 | 17631 | MN617171.1 | BCS17\_DN134 | 20 |
| *Thetahypovirus* | *Thetahypovirus sclerotiniae* | Botrytis cinerea hypovirus 5 | BcHV5 | 15353 | MT157414.1 | BCI10\_DN5057 | 20 |
| *Thetahypovirus* | *Thetahypovirus rhizoctoniae* | Rhizoctonia solani hypovirus 1 | RsHV1 | 18371 | MK558259.1 | BR20 | 19 |
| *Thetahypovirus* | *Thetahypovirus sclerotiniae* | Sclerotinia sclerotiorum hypovirus 2 | SsHV2 | 15249 | MH347276.1 | HBStr-470 | 5 |
| *Thetahypovirus* | *Thetahypovirus sclerotii* | Sclerotium rolfsii hypovirus 1 | SrHV1 | 16113 | MH037014.1 | BLH-1 | 31 |
| *Zetahypovirus* | *Zetahypovirus sclerotiniae* | Sclerotinia sclerotiorum hypovirus 6 | SsHV6 | 7382 | MH766501.1 | BLH-1-1 | 31 |

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**Figure 1:** Genome organization of three representative members of the family *Hypoviridae*.



**Figure 2**: Phylogenetic analysis of the 44 polyproteins containing the RdRp domain encoded by representative hypoviruses. Proteins were aligned with MAFFT, whereas the phylogenetic tree was derived with the Maximum Likelihood methodology implemented with the IQ-TREE software. The eight new genera are shown by colored rectangles.



**Figure 3**: Heatmap of percentage identity of RdRp-encoding polyproteins included in the phylogenetic tree.

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