

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

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| **Code assigned:** | **2020.003F** |  |
| **Short title:** Create six new species in the genus *Alphachrysovirus* (*Ghabrivirales*: *Chrysoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Chrysoviridae* SG |

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

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**Submission dates**

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| Date first submitted to SC Chair |  |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2020.003F.R.Chrysoviridae.xls |

**Abstract**

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| The family *Chrysoviridae* currently includes two genera, *Alphachrysovirus* accommodating 17 species and *Betachrysovirus* accommodating 8 species. Here we propose the addition of 6 new species to the family *Chrysoviridae*, 3 to the genus *Alphachrysovirus* and 3 to the genus *Betachrysovirus*. |

**Text of proposal**

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| |  | | --- | | Currently there are 25 species in the family *Chrysoviridae*, 17 belonging to genus *Alphachrysovirus* and 8 belonging to genus *Betachrysovirus* (Kotta-Loizou *et al*., 2020). The genomic organization of Penicillium chrysogenum virus (PcV) and Botryosphaeria dothidea chrysovirus 1 (BdCV1), respectively exemplars of the type species of the genera *Alphachrysovirus* and *Betachrysovirus* is depicted in Fig. 1.  The recent discoveries of new viruses related to chrysoviruses have led to a proposed revision of the family organization as follows (Table 1):   1. Assignment of three additional species to the genus *Alphachrysovirus*. 2. Assignment of three additional species to the genus *Betachrysovirus*.   Members of the family *Chrysoviridae* have 3-7 dsRNA genomic segments and are therefore informally designated as trichrysoviruses (3 genomic segments), cinquechrysoviruses (5 genomic segments) and settechrysoviruses (7 genomic segments), in addition to the ‘traditional’ chrysoviruses with 4 genomic segments. Each dsRNA segment is individually encapsidated in a separate particle; dsRNA 1 usually encodes the RNA-dependent RNA polymerase (RdRP), another dsRNA (often dsRNA 2) encodes the capsid protein and the rest encode proteins of unknown function. The overall size of the genome ranges from 8.9 to 16.0 kbp. Chrysoviruses mostly infect fungi, ascomycetes and basidiomycetes, but also plants and insects.  As described in previous ICTV reports, the criteria to differentiate species within the family *Chrysoviridae* are:   * host of isolation * amino acid sequence data (≤ 70% aa sequence identity in the RdRP) * size of dsRNA segments * length of 5′-UTR * serological relationships   As evident by the phylogenetic analysis (Fig. 2), there are currently 12 fully sequenced viruses with publicly available accession numbers that belong to the family *Chrysoviridae*, 8 in the genus *Alphachrysovirus* and 4 in the genus *Betachrysovirus*. Based on BLAST alignments (Altschul *et al*., 1997) and a pairwise distance matrix (Fig. 3), 6 of these viruses have an evolutionary distance larger than 0.3 from exemplars of officially recognized species. Therefore 6 new species are proposed to accommodate these viruses.  Information on the exemplars representing the proposed species in the genera *Alphachrysovirus* and *Betachrysovirus*, together with the other new viruses, can be found in Table 2 and Table 3, respectively. | |

**Supporting evidence**



**Figure 1:** Schematic representation of the genomic organization of Penicillium chrysogenum virus (left panel) and Botryosphaeria dothidea chrysovirus 1 (right panel), exemplar viruses for the type species of genera *Alphachrysovirus* and *Betachrysovirus*. Each genome consists of four dsRNAs, each containing one ORF (coloured boxes) flanked by 5’- and 3’-UTRs (black double lines). The light coloured box in dsRNA 1 represents the RdRP\_4 motif (PF00680; Finn *et al.*, 2014); the dark coloured box in dsRNA 1 represents an independent P-loop NTPase domain predicted by HHpred (Zimmermann *et al*., 2017); the grey coloured thick lines represent a region of homology between the proteins encoded by dsRNAs 1 and 3 as detected by PSI-BLAST (Altschul *et al*., 1997).

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**Figure 2:** Maximum likelihood phylogenetic tree created based on the RdRP sequences of chrysoviruses and related viruses. The sequences were aligned with MUSCLE as implemented by MEGA 6 (Tamura *et al*., 2013), all positions with less than 30% site coverage were eliminated and the LG+G+I+F substitution model was used. At the end of the branches, established members of the family *Chrysoviridae* have shapes filled with dark colour; proposed members belonging to proposed new species have shapes filled with bright colour; proposed members belonging to established species have shape outlines. Blue squares indicate that the virus infects fungi; green circles indicate that the virus infects or is associated with plants; purple triangles indicate that the virus infects or is associated with insects. The number in brackets after the virus name indicates the number of dsRNA genomic segments. GenBank accession numbers of viruses used to construct the tree are presented in the legend of figure 3.



**Figure 3:** Pairwise distance matrix created based on the RdRP sequences of chrysoviruses and related viruses. The sequences were aligned with MUSCLE as implemented by MEGA 6 (Tamura *et al*., 2013), all positions with less than 30% site coverage were eliminated and the p-distance substitution method was used. Red background indicates high conservation while green background indicates low conservation.

Alternaria alternata chrysovirus 1, LC350277; Amasya cherry disease associated chrysovirus, AJ781166; Anthurium mosaic-associated virus, FJ899675; Aspergillus fumigatus chrysovirus, FN178512; Aspergillus thermomutatus chrysovirus 1, MF045841; Beauveria bassiana chrysovirus 1, MK279433; Botryosphaeria dothidea chrysovirus 1, KF688736; Brassica campestris chrysovirus 1, KP782031; Chrysothrix chrysovirus 1, MN625832; Colletotrichum gloeosporioides chrysovirus 1, KT581957; Colletotrichum fructicola chrysovirus 1, MG425969; Coniothyrium diplodiella chrysovirus 1, MK584812; Cryphonectria nitschkei chrysovirus 1, GQ290649; Fusarium graminearum dsRNA mycovirus 2, HQ343295; Fusarium oxysporum f. sp. dianthi virus, KP876629; Fusarium oxysporum chrysovirus 1, EF152346; Fusarium sacchari chrysovirus 1, MN295964; Helminthosporium victoriae virus 145S, AF297176; Hubei chryso-like virus 1, MF176309; Isaria javanica chrysovirus 1, KX898416; Macrophomina phaseolina chrysovirus 1, KP900886; Magnaporthe oryzae chrysovirus 1-A, AB560761; Neofusicoccum parvum chrysovirus 1, MK584816; Penicillium chrysogenum virus, AF296439; Penicillium italicum chrysovirus, MK214380; Penicillium janczewskii chrysovirus 1, KT601115; Penicillium janczewskii chrysovirus 2, KT950836; Penicillium raistrickii chrysovirus 1, MK279429; Penicillium roseopurpureum chrysovirus 1, MG887760; Persea americana chrysovirus, KJ418374; Raphanus sativus chrysovirus 1, JQ045335; Saccharomyces cerevisiae virus L-A, AAA50508; Salado virus, MN661047; Shuangao chryso-like virus, MF176340; Verticillium dahliae chrysovirus 1, HM004067; Zea mays chrysovirus 1, MH931196.

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| |  |  | | --- | --- | | **Table 1:** Current and proposed organization of the family *Chrysoviridae* | | | **current organization** | **proposed organization** | | **Genus: *Alphachrysovirus*** | **Genus: *Alphachrysovirus*** | | *Amasya cherry disease associated chrysovirus* | *Amasya cherry disease associated chrysovirus* | | *Anthurium mosaic-associated virus* | *Anthurium mosaic-associated virus* | | *Aspergillus fumigatus chrysovirus* | *Aspergillus fumigatus chrysovirus* | | *Brassica campestris chrysovirus* | *Brassica campestris chrysovirus* | |  | Chrysothrix chrysovirus 1 | | *Colletotrichum gloeosporioides chrysovirus* | *Colletotrichum gloeosporioides chrysovirus* | | *Cryphonectria nitschkei chrysovirus 1* | *Cryphonectria nitschkei chrysovirus 1* | | *Fusarium oxysporum chrysovirus 1* | *Fusarium oxysporum chrysovirus 1* | | *Helminthosporium victoriae 145S virus* | *Helminthosporium victoriae 145S virus* | | *Isaria javanica chrysovirus* | *Isaria javanica chrysovirus* | | *Macrophomina phaseolina chrysovirus* | *Macrophomina phaseolina chrysovirus* | | *Penicillium brevicompactum virus* | *Penicillium brevicompactum virus* | | *Penicillium chrysogenum virus (type species)* | *Penicillium chrysogenum virus (type species)* | | *Penicillium cyaneofulvum virus* | *Penicillium cyaneofulvum virus* | | *Persea americana chrysovirus* | *Persea americana chrysovirus* | | *Raphanus sativus chrysovirus* | *Raphanus sativus chrysovirus* | |  | Salado virus | | *Shuangao insect-associated chrysovirus* | *Shuangao insect-associated chrysovirus* | | *Verticillium dahliae chrysovirus* | *Verticillium dahliae chrysovirus* | |  | Zea mays chrysovirus 1 | |  |  | | **Genus: *Betachrysovirus*** | **Genus: *Betachrysovirus*** | | *Alternaria alternata chrysovirus* | *Alternaria alternata chrysovirus* | |  | Aspergillus thermomutatus chrysovirus 1 | | *Botryosphaeria dothidea chrysovirus* | *Botryosphaeria dothidea chrysovirus* | | *Colletotrichum fructicola chrysovirus* | *Colletotrichum fructicola chrysovirus* | |  | Coniothyrium diplodiella chrysovirus 1 | | *Fusarium graminearum chrysovirus* | *Fusarium graminearum chrysovirus* |  | | *Fusarium oxysporum chrysovirus 2* | *Fusarium oxysporum chrysovirus 2* |  | | *Magnaporthe oryzae chrysovirus* | *Magnaporthe oryzae chrysovirus* |  | |  | Neofusicoccum parvum chrysovirus 1 |  | | *Penicillium janczewskii chrysovirus 1* | *Penicillium janczewskii chrysovirus 1* |  | | *Penicillium janczewskii chrysovirus 2* | *Penicillium janczewskii chrysovirus 2* |  | |  |  |  |   **Table 2:** New viruses in genus *Alphachrysovirus* | | | | |
| **virus name & abbreviation** | | **accession number & size** | | **Reference** |
| Beauveria bassiana chrysovirus 1 | | dsRNA 1: MK279433 (3478 bp) | | Gilbert *et al.,* 2019 |
| (BbCV1) | | dsRNA 2: MK279434 (3143 bp) | |  |
|  | | dsRNA 3: MK279435 (3069 bp)  dsRNA 4: MK279436 (2770 bp) | |  |
| Chrysothrix chrysovirus 1 | | dsRNA 1: MN625832 (3552 bp) | | Petrzik *et al.,* 2019 |
| (CCV1) | | dsRNA 2: MN625833 (3191 bp) | |  |
|  | | dsRNA 3: MN625834 (2879 bp)  dsRNA 4: MN625835 (2760 bp) | |  |
| Hubei chryso-like virus 1 | | dsRNA 1: MF176309 (3544 bp) | | Shi *et al*., 2017 |
| (HCV1) | | dsRNA 2: MF176310 (3197 bp) | |  |
|  | | dsRNA 3: MF176311 (3154 bp)  dsRNA 4: MF176312 (3145 bp) | |  |
| Penicillium italicum chrysovirus | | dsRNA 1: MK214380 (3570 bp) | | Zhang *et al.,* 2020 |
| (PiCV) | | dsRNA 2: MK214381 (3189 bp) | |  |
|  | | dsRNA 3: MK214382 (2975 bp) | |  |
|  | | dsRNA 4: MK214383 (2857 bp) | |  |
| Penicillium raistrickii chrysovirus 1 | | dsRNA 1: MK279429 (3501 bp) | | Gilbert *et al.,* 2019 |
| (PrCV1) | | dsRNA 2: MK279430 (3120 bp) | |  |
|  | | dsRNA 3: MK279431 (2955 bp)  dsRNA 4: MK279432 (2980 bp) | |  |
| Penicillium roseopurpureum chrysovirus 1 | | dsRNA 1: MG887760 (3565 bp) | | Nerva *et al.*, 2019 |
| (PrCV1) | | dsRNA 2: MG887761 (2859 bp) | |  |
|  | | dsRNA 3: MG887762 (2917 bp)  dsRNA 4: MH271211 (2833 bp) | |  |
| Salado virus | | dsRNA 1: MN661047 (3490 bp) | | Nitsche *et al.,* 2019 |
| (SV) | | dsRNA 2: MN661048 (3166bp) | | (unpublished) |
|  | | dsRNA 3: MN661049 (2964 bp)  dsRNA 4: MN661050 (3063 bp) | |  |
| Zea mays chrysovirus 1 | | dsRNA 1: MH931195 (4220 bp) | | Peyambari *et al.*, 2019 |
| (ZmCV1) | | dsRNA 2: MH931196 (3713 bp) | |  |
|  | | dsRNA 3: MH931197 (3373 bp) | |  |
| **Table 3:** New viruses in genus *Betachrysovirus* | | | | |
| **virus name & abbreviation** | **accession number & size** | | **Reference** | |
| Aspergillus thermomutatus chrysovirus 1 | dsRNA 1: MF045841 (3589 bp) | | Ejmal *et al*., 2018 | |
| (AtCV1) | dsRNA 2: MF045842 (2772 bp) | |  | |
|  | dsRNA 3: MF045843 (2676 bp) | |  | |
|  | dsRNA 4: MF045844 (2514 bp) | |  | |
| Coniothyrium diplodiella chrysovirus 1 | dsRNA 1: MK584812 (3625 bp) | | Nerva *et al*., 2019 | |
| (CdCV1) | dsRNA 2: MK584813 (2703 bp) | |  | |
|  | dsRNA 3: MK584814 (2676 bp) | |  | |
|  | dsRNA 4: MK584815 (2505 bp) | |  | |
| Fusarium sacchari chrysovirus 1  (FsCV1) | dsRNA 1: MN295964 (3518 bp) | | Yao *et al.*, 2020 | |
| dsRNA 2: MN295965 (2796 bp) | |
| dsRNA 3: MN295966 (2779 bp) | |
| dsRNA 4: MN295967 (2569 bp) | |
| Neofusicoccum parvum chrysovirus 1 | dsRNA 1: MK584816 (3461 bp) | | Nerva *et al.*, 2019 | |
| (NpCV1) | dsRNA 2: MK584817 (3039 bp) | |  | |
|  | dsRNA 3: MK584818 (3069 bp) | |  | |
|  | dsRNA 4: MK584819 (2883 bp) | |  | |

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