

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

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| **Code assigned:** | **2021.001F** |  |
| **Short title:** Create one new family *Fusariviridae* including three new genera (*Alphafusarivirus*, *Betafusarivirus* and *Gammafusarivirus*) and 34 new virus species (Durnavirales) | | |
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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) | 12-09-2021 |

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

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| **Comment:** Please address typos and other imprecisions observed in the Excel file. Additionally, clarify language concerning species demarcation criteria.  **Response:** Done |

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

**Name of accompanying Excel module**

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| 2021.001F.R.Fusariviridae\_1newfam.xlsx |

**Abstract**

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| After the discovery of Fusarium graminearum dsRNA virus 1 in 2007 and of Rosellinia necatrix fusarivirus 1 in 2014, the latter authors informally proposed a new family with the name “*Fusariviridae*” to classify these viruses. Since then, a number of related viruses with similar genomic organization and similar putative taxonomic assignment were described from different fungal hosts, some of which were characterized in depth molecularly and biologically. It is therefore time to officially recognize this new group of viruses as a new family for which we propose the original name *Fusariviridae.* Members of the proposed family are related but clearly distinct from the viruses in the family *Hypoviridae*. The 38 published coding-complete sequences currently available in the public databases (NCBI/GenBank) are classified in 34 new species, grouped in the three new genera (*Alphafusarivirus*, *Betafusarivirus* and *Gammafusarivirus*) included in the newly proposed family *Fusariviridae*. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | **HYSTORICAL BACKGROUND**  In 2007 a new virus with unique properties, named Fusarium graminearum virus-DK21, was characterized in *Fusarium graminearum* strain DK21 [7]. Several years later, a related virus, named Rosellinia necatrix fusarivirus1, was thoroughly characterized from *Rosellinia necatrix* and proposed to be a member of a new family named *Fusariviridae* [17]. The two viruses share similar evolutionary history of the polyproteins encoded by the largest ORF but have a slightly different genome organization (Figure 1). Both viruses were distantly related, and distinct, from those of the family *Hypoviridae*. Since then, a number of papers have provided the full length sequence or coding-complete sequences of a number of new viruses that would fit in this proposed family [1-6, 8-14, 16, 18, 19]. Here we propose establishment of a new family *Fusariviridae* composed of three genera to classify 38 previously unclassified viruses in 34 new species (Table 1).  **Genome organization:**  Viruses considered to belong to the proposed family have non-segmented RNA genome varying in length between 5.9 kb to 8.4 kb, with the exception of two viruses from *Rhizoctonia solani* which have a genome size exceeding 10 kb [15].  In the vast majority of cases these RNAs encodes two ORFs. The most 5’ proximal codes for a polyprotein with identifiable helicase and RdRP motifs; the protein encoded by the second ORF has no known function yet. The 3’ is generally polyadenylated. In analogy with members of the family *Hypoviridae*, these viruses are thought to be ssRNA viruses “with dsRNA lifestyle”, as abundant dsRNA can be purified from infected fungi.  Representative genome organization of some members are depicted in Fig. 1.  These viruses are thought to be capsidless since no virion could be purified on a sucrose density gradient.  **Phylogenetic relationships**:  A reliable tree with sufficient amino-acid conservation can be derived from ORF1 alignments with MAFFT program (Fig. 2). Including members of the *Hypoviridae* (Fig. 2) as an outgroup, all currently known fusarivirids form a well-supported monophyletic clade supporting the establishment of the *Fusariviridae* family. The phylogenetic tree also suggests splitting the proposed new family in three genera, *Alphafusarivirus*, *Betafusarivirus* and *Gammafusarivirus* (Fig. 2) with 22, 11 and 1 species, respectively.  Both, *Fusariviridae* and *Hypoviridae* families are assigned in the order *Durnavirales*, Phylum *Pisuviricota*, and share closest evolutionary relationships in their RdRPs with *bona fide* dsRNA viruses included in the families *Partitiviridae, Amalgaviridae, Picobirnaviridae or Curvulaviridae*.  In Fig. 3 we report the heatmap of the pairwise percentage identity matrix that includes all 38 sequences taken in consideration for this proposal. As four pairs of sequences share % identity in the aligned ORF1 greater than 80% (proposed as species demarcation criterion) we propose creation and classification of a total of 34 new species in the family.  **Species demarcation criteria**: We propose an arbitrary demarcation threshold of less than 80% identity in the amino acid sequences of ORF1-encoded polyprotein between viruses belonging to distinct species.  Accordingly, some of characterized fusariviruses do not meet these criteria and are assigned to same species. The list of viruses assigned to the same species is displayed in Table 2.  Etymology of the newly proposed taxon: The name *Fusariviridae* derives from the abbreviated name of original host of the first virus characterized of this family (*Fusarium graminearum*). | |

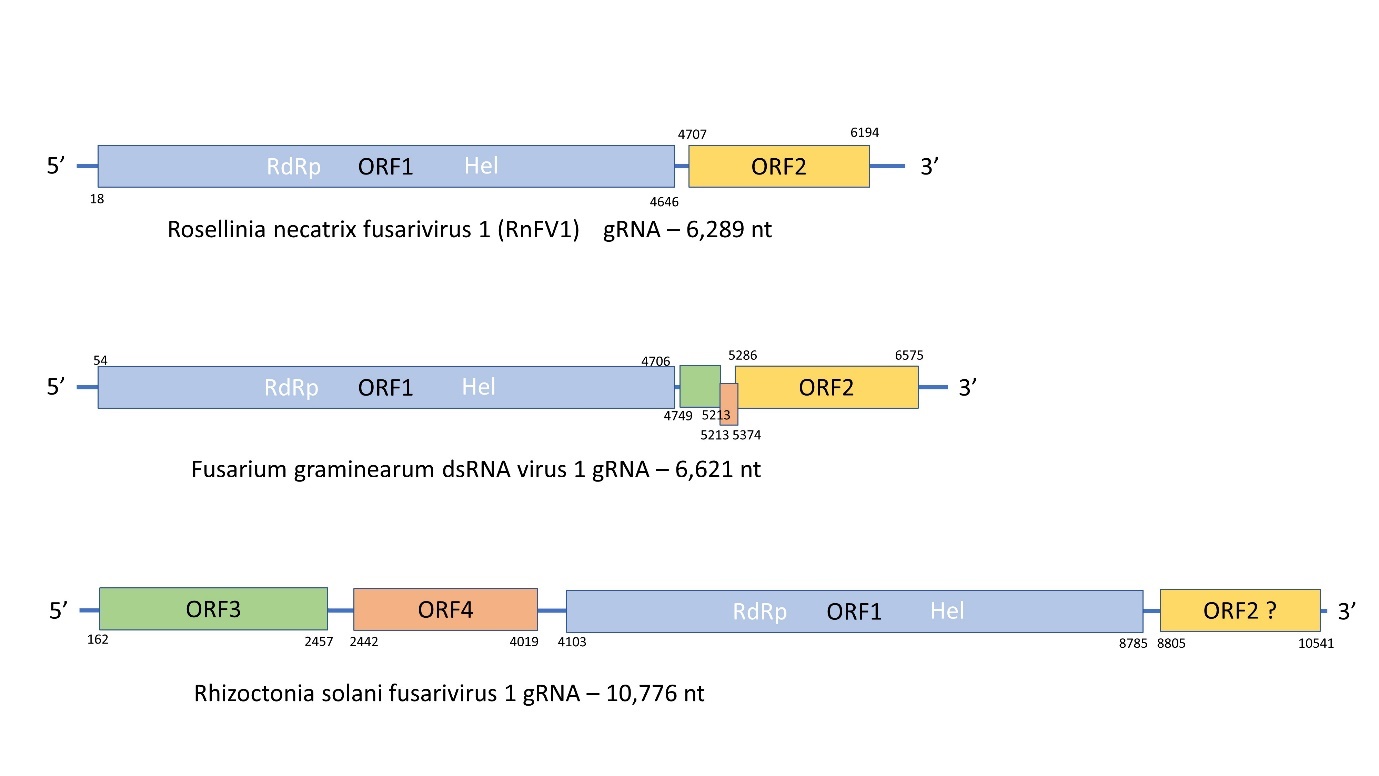
**Supporting evidence**

**Table 1:** Virus species and corresponding exemplar virus names in the proposed new family *Fusariviridae* along with their main features.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Genus | Species Name | Virus Name | Acronym | Lenght | NuclAcc | Isolate | References |
| *Alphafusarivirus* | ***Alphafusarivirus agarici*** | **Agaricus bisporus virus 10** | **AbV10** | **7033** | **KY357495.1** | **AbV10-003** | **2** |
| *Alphafusarivirus* | ***Alphafusarivirus portobelli*** | **Agaricus bisporus virus 11** | **AbV11** | **6981** | **KY357496.1** | **AbV11-003** | **2** |
| *Alphafusarivirus* | ***Alphafusarivirus aspergilli*** | **Aspergillus ellipticus fusarivirus 1** | **AeFV1** | **6253** | **MK279500.1** | **AeFv1CBS 707.79** | **3** |
| *Alphafusarivirus* | ***Alphafusarivirus auriculariae*** | **Auricularia heimuer fusarivirus 1** | **AhFV1** | **7127** | **MT232758.1** | **CCMJ1296** | **8** |
| *Alphafusarivirus* | ***Alphafusarivirus botryospheriae*** | **Botryosphaeria dothidea fusarivirus 1** | **BdFV1** | **6179** | **MN560974.1** | **SDAU11-86** | **10** |
| *Alphafusarivirus* | ***Alphafusarivirus botrytidis*** | **Botrytis cinerea fusarivirus 5** | **BcFV5** | **6313** | **MN617764** | **BCS3\_DN2128** | **16** |
| *Alphafusarivirus* | ***Alphafusarivirus fusarii*** | **Fusarium graminearum dsRNA mycovirus-1** | **FgDV1** | **6621** | **AY533037.2** | **DK-21** | **7** |
| *Alphafusarivirus* | ***Alphafusarivirus ioaponiae*** | **Fusarium poae fusarivirus 1** | **FpFV1** | **6379** | **LC150611** | **MAFF 240374** | **14** |
| *Alphafusarivirus* | ***Alphafusarivirus macrophominae*** | **Macrophomina phaseolina single-stranded RNA virus 1** | **MpFV1** | **6356** | **KP900890.1** | **Tn408** | [**12**](https://jvi.asm.org/content/90/15/6846.short) |
| *Alphafusarivirus* | ***Alphafusarivirus neofusicocci*** | **Neofusicoccum luteum fusarivirus 1** | **NlFV1** | **6244** | **KY906214.1** | **CBS110299** | **11** |
| *Alphafusarivirus* | ***Alphafusarivirus neurosporae*** | **Neurospora discreta fusarivirus 1** | **NdFV1** | **6648** | **MK279503.1** | **NdFv1FGSC8579** | **3** |
| *Alphafusarivirus* | ***Alphafusarivirus penicilli*** | **Penicillium aurantiogriseum fusarivirus 1** | **PaFV1** | **6139** | **KT601099.1** | **MUT4330-a** | **13** |
| *Alphafusarivirus* | ***Alphafusarivirus roqueforti*** | **Penicillium roqueforti ssRNA mycovirus 1** | **PrFV1** | **6002** | **KJ817266.1** | **PRG42-7** | **Not available** |
| *Alphafusarivirus* | ***Alphafusarivirus plasmoparae*** | **Plasmopara viticola lesion associated fusarivirus 1** | **PvlaFV1** | **6643** | **MN551102.1** | **DMG-B-DN53634** | **1** |
| *Alphafusarivirus* | ***Alphafusarivirus italiae*** | **Plasmopara viticola lesion associated fusarivirus 2** | **PvlaFV2** | **6222** | **MN551105.1** | **DMG-A-DN22538** | **1** |
| *Alphafusarivirus* | ***Alphafusarivirus pleosporae*** | **Pleospora typhicola fusarivirus 1** | **PtFV1** | **6733** | **KT601107.1** | **MUT4379** | **14** |
| *Alphafusarivirus* | ***Alphafusarivirus rhizoctoniae*** | **Rhizoctonia solani fusarivirus 3** | **RsFV3** | **5959** | **MK558258.1** | **BR19** | **15** |
| *Alphafusarivirus* | ***Alphafusarivirus roselliniae*** | **Rosellinia necatrix fusarivirus 1** | **RnFV1** | **6286** | **AB915829.1** | **NW10** | **17** |
| *Alphafusarivirus* | ***Alphafusarivirus rutstroemiae*** | **Rutstroemia firma fusarivirus 1** | **RfFV1** | **6641** | **MK279504.1** | **RfFv1CBS 115.86** | **3** |
| *Alphafusarivirus* | ***Alphafusarivirus sclerotii*** | **Sclerotium rolfsii fusarivirus 1** | **SrFV1** | **7301** | **MH766491.1** | **BLH-1-10** | **19** |
| *Alphafusarivirus* | ***Alphafusarivirus rolfsii*** | **Sclerotium rolfsii fusarivirus 2** | **SrFV2** | **7281** | **MH766492.1** | **BLH-1-11** | **19** |
| *Alphafusarivirus* | ***Alphafusarivirus zymoseptoriae*** | **Zymoseptoria tritici fusarivirus 1** | **ZtFV1** | **5969** | **MK279506.1** | **ZtFv1IPO323** | **3** |
| *Betafusarivirus* | ***Betafusarivirus alternariae*** | **Alternaria brassicicola fusarivirus 1** | **AbFV1** | **6656** | **KT581960** | **817-14** | **18** |
| *Betafusarivirus* | ***Betafusarivirus sinensis*** | **Botrytis cinerea fusarivirus 1** | **BcFV1** | **8448** | **MG554633** | **HBtom-372** | **5** |
| *Betafusarivirus* | ***Betafusarivirus hispaniae*** | **Botrytis cinerea fusarivirus 3** | **BcFV3** | **8354** | **MN617762** | **BCS15\_DN2871** | **16** |
| *Betafusarivirus* | ***Betafusarivirus iberiae*** | **Botrytis cinerea fusarivirus 4** | **BcFV4** | **8349** | **MN617763** | **BCI12\_DN9205** | **16** |
| *Betafusarivirus* | ***Betafusarivirus botrytidis*** | **Botrytis cinerea fusarivirus 7** | **BcFV7** | **7881** | **MN617766** | **BCS13\_13** | **16** |
| *Betafusarivirus* | ***Betafusarivirus crassae*** | **Neurospora crassa fusarivirus 1** | **NcFV1** | **7794** | **LC530175.1** | **JW60** | **6** |
| *Betafusarivirus* | ***Betafusarivirus neurosporae*** | **Neurospora discreta fusarivirus 2** | **NdFV2** | **7506** | **LC586030.1** | **NdFV2-W683** | **6** |
| *Betafusarivirus* | ***Betafusarivirus rhizoctoniae*** | **Rhizoctonia solani fusarivirus 1** | **RsFV1** | **10776** | **MK558257.1** | **BR18** | **15** |
| *Betafusarivirus* | ***Betafusarivirus brasiliensis*** | **Rhizoctonia solani fusarivirus 2** | **RsFV2** | **10710** | **MK558256.1** | **BR17** | **15** |
| *Betafusarivirus* | ***Betafusarivirus homeocarpa*** | **Sclerotinia homoeocarpa fusarivirus 1** | **ShFV1** | **7171** | **MK279505.1** | **ShFvLT11** | **3** |
| *Betafusarivirus* | ***Betafusarivirus sclerotiniae*** | **Sclerotinia sclerotiorum fusarivirus 1** | **SsFV1** | **7769** | **KP842791.1** | **JMTJ14** | **9** |
| *Gammafusarivirus* | ***Gammafusarivirus lentinulae*** | **Lentinula edodes fusarivirus 1** | **LeFV1** | **6271** | **MN744720** | **Le14HNZMD** | **4** |

**Table 2:** Virus species with multiple member viruses and their main features

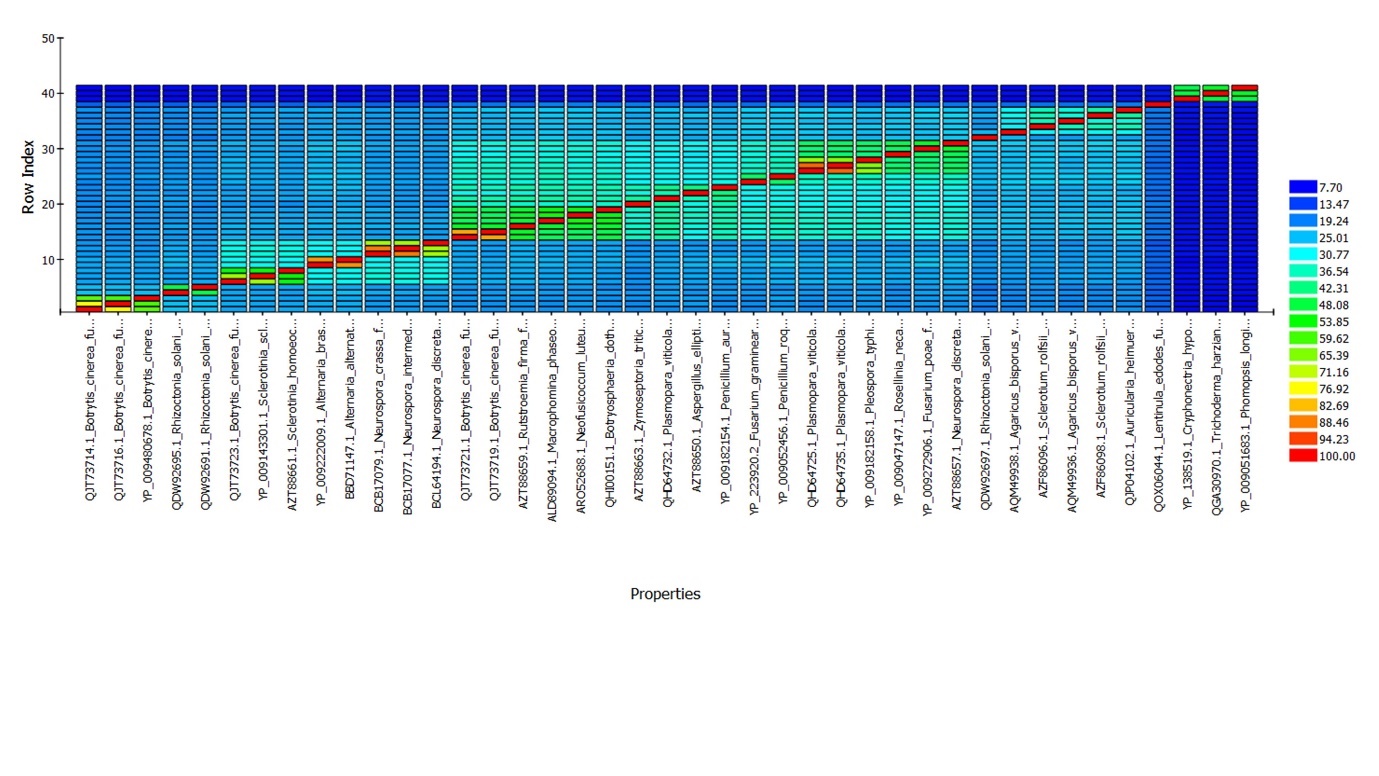
|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Virus Species | Virus Name | Acronym | Genome Length | GenBank | Strain |
| *Betafusarivirus alternariae* | Alternaria brassicicola fusarivirus 1 | AbFV1 | 6656 | KT581960 | 817-14 |
| Alternaria alternata fusarivirus 1 | AaFV1 | 6647 | LC209862.1 | T88-4 |
| *Alphafusarivirus plasmoparae* | Plasmopara viticola lesion associated fusarivirus 1 | PvlaFV1 | 6643 | MN551102.1 | DMG-B-DN53634 |
| Plasmopara viticola lesion associated fusarivirus 3 | PvlaFV3 | 6639 | MN551107.1 | DMG-B-DN52217 |
| *Betafusarivirus crassae* | Neurospora crassa fusarivirus 1 | NcFV1 | 7794 | LC530175.1 | JW60 |
| Neurospora intermedia fusarivirus 1 | NiFV1 | 7781 | LC530174.1 | FGSC 2559 |
| *Alphafusarivirus botrytidis* | Botrytis cinerea fusarivirus 5 | BcFV5 | 6313 | MN617764 | BCS3\_DN2128 |
| Botrytis cinerea fusarivirus 6 | BcFV6 | 6301 | MN617765 | BCS8\_DN9299 |

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

Immagine che contiene testo

Descrizione generata automaticamente**Figure 2**: Phylogenetic analysis of the alignment of 38 virus ORF1 with three hypovirus-like ORFB. Proteins were aligned with MAFFT software, whereas the phylogenetic tree was constructed with the Maximum Likelihood methodology implemented with the IQ-TREE software. The main existing and proposed taxa are shown. Virus names and corresponding GenBank accession numbers are reported.



**Figure 3**: Heatmap of pairwise alignment obtained with MAFFT software of ORF1-encoded polyproteins included in the phylogenetic tree.

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