

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

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| **Code assigned:** | ***2023.020M*** |  |
| **Short title:** Create one new species in genus *Mechlorovirus* and three new species in genus *Tenuivirus* (family *Phenuiviridae*, order *Bunyavirales*) |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Phenuiviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Phenuiviridae* Study Group | 9 | 0 | 0 |

**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)** |
| N/A | N/A | N/A |

**Submission dates**

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| Date first submitted to SC Chair | June 23, 2023 |
| Date of this revision (if different to above) |  |

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

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| N/A |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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| N/A |

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

**Name of accompanying Excel module**

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| 2023.020M.N.v1.Phenuiviridae\_4nsp.xlsx |

**Abstract**

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| We propose the classification of 4 newly discovered phenuivirids into 1 new species in genus *Mechlorovirus* and 3 new species in genus *Tenuivirus*. |

**Text of proposal**

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| The bunyaviral family *Phenuiviridae* currently includes 22 genera (*Bandavirus*, *Beidivirus*, *Citricivirus*, *Coguvirus*, *Entovirus*, *Goukovirus*, *Horwuvirus*, *Hudivirus*, *Hudovirus*, *Ixovirus*, *Laulavirus*, *Lentinuvirus*, *Mechlorovirus*, *Mobuvirus*, *Phasivirus*, *Phlebovirus*, *Pidchovirus*, *Rubodvirus*, *Tanzavirus*, *Tenuivirus*, *Uukuvirus*, and *Wenrivirus*). In 2021, the ICTV *Phenuiviridae* Study Group established a species demarcation criterion of <95% identity in the amino acid sequence of the phenuivirid RNA-directed RNA polymerase (RdRp) (TaxoProp 2020.029M). **Novel mechlorovirus species:**Ramu stunt virus (RmSV) was discovered by HTS in sugarcane (panicoideaen *Saccharum officinarum* L.) in cultivar Ragnar with stunting symptoms collected in Ramu Madang Province, Papua New Guinea [2]. RmSV is a negative-sense RNA virus with a hexasegmented RNA genome. The negative-sense RNA1 encodes the putative RdRp, and the negative-sense or ambisense RNA2–6 encode two putative nucleocapsid proteins (NPs) and five non-structural proteins of unknown function. This genomic organization is similar to that reported previously for melon chlorotic spot virus (MeCSV), the single member of phenuivirid genus *Mechlorovirus* (Fig. 1A). A maximum likelihood phylogenetic tree was generated using amino acid sequences of the putative RdRp encoded by RmSV and representative members of all the genera of the *Phenuiviridae* family. RmSV is in the same clade with MeCSV, and the high bootstrap values in the phylogenetic tree strongly support the classification of RmSV in the genus *Mechlorovirus* (Fig. 2). The amino acid identity of the putative RdRp between MeCSV and RmSV is 44.1%, which is below the phenuivirid species demarcation criterion (<95% identity). For these reasons, we propose to classify RmSV as a member of a novel species, named *Mechlorovirus* *ramuense.***Origin of the name of the species:** *ramuense* is named after Ramu Madang Province, Papua New Guinea, where RmSV was first discovered.**Novel tenuivirus species:**Festuca stripe-associated virus (FSaV) was discovered by HTS in meadow fescue ([poaceae](https://en.wikipedia.org/wiki/Poaceae)n *Festuca pratensis* Huds.) showing chlorotic stripes and occasional necrotic dashes on the leaves collected in Saxony-Anhalt, Germany [1]. FSaV is a negative-sense RNA virus with a four-segmented RNA genome. The negative-sense RNA1 encodes the putative RdRp, and the ambisense RNA2–4 encode the putative movement protein (MP), the putative NP, the putative viral suppressor of RNA silencing (VSR), and three non-structural proteins of unknown function, respectively. This genomic organization is similar to that reported previously for members of phenuivirid genus *Tenuivirus* (Fig. 1B). A maximum likelihood phylogenetic tree was generated using amino acid sequences of the putative RdRp encoded by FSaV and representative members of the genera of the *Phenuiviridae* family. FSaV clusters with tenuiviruses, and the high bootstrap values in the phylogenetic tree strongly support the classification of FSaV in the genus *Tenuivirus* (Fig. 2). The putative RdRp of FSaV has amino acid identity ranging from 30.0% to 78.5% with the RdRps of classified tenuiviruses, and the highest identity value obtained with the RdRp encoded by rice hoja blanca virus is below the phenuivirid species demarcation criterion (<95% identity) (Fig. 3). For these reasons, we propose to classify FSaV as a member of a novel species, named *Tenuivirus festucae.***Origin of the name of the species**: *festucae* is named after plant host genus *Festuca*, in which FSaV was first discovered.**Novel tenuivirus species:**Wheat white spike virus (WWSV) was discovered by HTS in common wheat ([poaceae](https://en.wikipedia.org/wiki/Poaceae)n *Triticum aestivum* L.) showing pale yellowing, chlorotic streaks, and leaf mosaic collected in Ponta Grossa, Paraná State, Brazil [3]. WWSV is a negative-strand RNA virus with a five-segmented RNA genome. The negative-sense RNA1 encodes the putative RdRp, and the ambisense or the negative-sense RNA2–5 encode the putative MP, the putative NP, the putative VSR, and three non-structural proteins of unknown function. This genomic organization is similar to that reported previously for members of phenuivirid genus *Tenuivirus* (Fig. 1C). A maximum likelihood phylogenetic tree was generated using amino acid sequences of the RdRp encoded by WWSV and representative members of the genera of the *Phenuiviridae* family. WWSV clusters with tenuiviruses, and the high bootstrap values in the phylogenetic tree strongly support the classification of WWSV in the genus *Tenuivirus* (Fig. 2). The putative RdRp of WWSV has amino acid identity ranging from 30.3% to 80.4% with the RdRp of classified tenuiviruses, and the highest identity value was obtained with the RdRp encoded by rice hoja blanca virus, which is below the phenuivirid species demarcation criterion (<95% identity) (Fig. 3). For these reasons, we propose to classify WWSV as a member of a novel species, named *Tenuivirus pontaense.***Origin of the name of the species:** *pontaense* is named after Ponta Grossa, Paraná State, Brazil, where WWSV was first observed.**Novel tenuivirus species:**Wheat yellow virus (WhYV) was discovered by HTS in common wheat showing stunting and leaf chlorosis collected in KwaZulu-Natal province, South Africa [4]. WhYVis a negative-sense RNA virus with a four-segmented RNA genome. The negative-sense RNA1 encodes the putative RdRp, and the ambisense RNA2–4 encode the putative MP, the putative NP, and four non-structural proteins of unknown function. This genomic organization is similar to that reported previously for members of phenuivirid genus *Tenuivirus* (Fig. 1D). A maximum likelihood phylogenetic tree was generated using amino acid sequences of the putative RdRp encoded by WhYV and representative members of the genera of the *Phenuiviridae* family. In such a tree, WhYV clusters with tenuiviruses, and the high bootstrap values in the phylogenetic tree strongly support the classification of WhYV in the genus *Tenuivirus* (Fig. 2). The putative RdRp of WhYV has amino acid identity ranging from 30.2% to 79.8% with the RdRp of classified tenuiviruses, and the highest identity value was obtained with the RdRp encoded by rice stripe virus, which is below the phenuivirid species demarcation criterion (<95% identity) (Fig. 3). For these reasons, we propose to classify WhYV as a member of a novel species, named *Tenuivirus kwazuluense.***Origin of the name of the species**: *kwazuluense* is named after KwaZulu-Natal province, South Africa, where WhYV was first discovered. |

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**Supporting evidence**

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**Figure 1**. Genome organizations of RmSV, FSaV, WWSV, and WhYV. The vcRNAs are depicted in 3′→5′ direction and mRNAs are depicted in a 5′→3′ direction. Boxes on the mRNAs depict ORFs that encode L (RdRp), putative large protein (RNA-directed RNA polymerase); MP, putative movement protein NP; putative nucleocapsid protein; VSR, putative viral suppressor of RNA silencing, NSvc2–6, non-structural proteins of unknown function on each virus-complimentary (vc)RNA; and NSv2–4, non-structural proteins of unknown function on each virus-sense (v)RNA.

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**Figure 2.** Neighbor-joining phylogenetic tree of RNA-directed RNA polymerase (RdRp) amino acids of bunyavirals and the four proposed viruses. GENETYX and MEGA7 was used to align the sequences and to generate phylogenetic tree. Numbers on branches are bootstrap values (%) obtained from 1,000 replicates. Tree branches are proportional to genetic distances between sequences and the scale bars at the top indicate substitutions per amino acid. For all taxa shown here, the complete genome or complete coding sequence is available at the GenBank nucleotide sequence database. Accession numbers are shown next to the respective virus.



**Figure 3**. Amino acid identity (%) matrix of the RdRp protein of three analyzed viruses (FSaV, WWSV, WhYV) and the current members of the genus *Tenuivirus*.

**References**

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