

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

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| **Code assigned:** | **2022.003P** |  |
| **Short title:** Create one new species (*Waikavirus rosae*) in the genus *Waikavirus* (*Picornavirales*: *Secoviridae*) |
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**Author(s) and email address(es)**

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| Jeremy Thompson |

**List the ICTV Study Group(s) that have seen this proposal**

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| *Secoviridae* Study Group |

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

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| Most members of the *Secoviridae* Study Group are supportive of the proposal |

**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| *Secoviridae* Study Group | 6 | 1 |  |
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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 | May 20, 2022 |
| Date of this revision (if different to above) | May 27, 2022 |

**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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| 2022.003P.N.v1.Secoviridae\_1ns.xlsx |

**Abstract**

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| The complete genome sequence of a novel virus infecting sweetbriar rose (*Rosa rubiginosa*) was assembled using high-throughput sequencing combined with RACE-PCR. The identified monopartite single-stranded positive-sense RNA genome of 13.2 kb contains a single large ORF. The virus is tentatively named sweetbriar rose curly top-associated virus (SRCTaV). The genome structure, together with the homology of waikavirus proteins, clearly indicate that the detected virus is a novel member of the genus *Waikavirus*. The name of the species *Waikavirus rosae* is proposed. |

**Text of proposal**

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| A novel waikavirus was identified in sweetbriar rose (*Rosa rubiginosa*) plants showing symptoms of leaf curling of upper leaves and shortening of the terminal internodes, using high-throughput sequencing (MiSeq, Illumina), with the residual 5’ terminus of the genome determined by RACE-PCR and 3’ terminus resolved from an RT-PCR-derived fragment using Oligo-(d)T and virus-specific primers. The genome sequence of the novel waikavirus was determined to be 13,184 nt in length excluding the 3’ poly(A) tail. A single large ORF of 11,328 nt in size is flanked by the 5’ and 3’ UTR, 520 nt and 1,336 nt in length, respectively. Six putative cleavage sites of the 426 kDa polyprotein (3775 aa) were predicted from ClustalW-aligned aa sequences of known waikaviruses producing a hypothetical protein (protein 1), three capsid proteins (CPs), a putative NTP-binding protein (NTB), a 3C-like proteinase (Pro) and a RdRP. Phylogenetic analysis in both the conserved Pro-Pol and CP regions showed that the novel virus is clearly located in a clade containing all other members, recognised or tentative, of the genus *Waikavirus*. Further, the amino acid sequences of conserved Pro-Pol region and CP region of SRCTaV share 37.3% - 53.7% and 24.3% - 37.8% identity, respectively, to all currently known waikaviruses. Based on the genome structure, phylogenetic analyses, percentage aa sequence identities, Considering the species demarcation criteria for the family *Secoviridae* of less than 75% amino acid sequence in the CP and/or less than 80% amino acid sequence in the conserved Pro-Pol region (Karasev et al. 2019, Sanfaçon et al. 2019, Thompson et al. 2017), we propose to classify sweetbriar rose curly-top associated virus (SRCTaV) as a member of a novel species named *Waikavirus rosae* in the genus *Waikavirus* of the family *Secoviridae.* |

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**Supporting evidence**

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**Figure 1.** The genome structure of sweetbriar rose curly top associated virus (SRCTaV). Boxes represent open reading frames, blue terminal lines untranslated regions (UTR). Predicted cleavage sites and their positions are marked by arrows above the predicted cleavage residues. The calculated length and molecular mass for each protein is shown under its name. P1, hypothetical protein (protein 1); CP, capsid protein; NTB, putative NTP-binding protein; Pro, 3C-like proteinase; RdRP, RNA-dependent RNA polymerase.

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**Figure 2.** Phylogenetic trees of members of the genus *Waikavirus* and representative members of the family *Secoviridae* based on an alignment of the amino acid sequences of the CG-GDD region (A) and coat protein region (B). The trees were produced by PhyML [12] in TOPALi v2.5 using WAG+I+G evolutionary model. Results are presented as a rooted tree. Bootstrap values (right) (1000 bootstrap replicates) greater than 50% and percentage posterior probabilities (left) (as obtained using MrBayes) are shown at the corresponding branches. Dash (-) indicates less than 50% support. Virus genera are shown on the right with waikavirus and sequivirus clades marked with shade. PVY (potato virus Y) = outgroup. The position of sweetbriar rose curly top-associated virus (SRCTaV) is highlighted by the rectangle box. Bar on the left represents the genetic distance. All analysed sequences are labelled with the virus acronym and accession number. AYV1, Actinidia yellowing virus 1; BBWV2, broad bean wilt virus 2; BCWVA, blackcurrant waikavirus A; BnRV1, Brassica napus RNA virus 1; BVCV, bellflower vein chlorosis virus; CNDV, carrot necrotic dieback virus; CPMV, cowpea severe mosaic virus; CRLV, cherry rasp leaf virus; GFLV, grapevine fanleaf virus; LWaiV1, lettuce waikavirus 1; MCDV, maize chlorotic dwarf virus; PoLV1, Poaceae Liege virus 1; PWaiV, persimmon waikavirus; PYFV, parsnip yellow fleck virus; RCaV1, red clover-associated virus 1; RTSV, rice tungro spherical virus; SDV, satsuma dwarf virus; ToTV, tomato torrado virus.

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| **Table 1**. Comparison of identity (%) of whole genome nucleotide (nt) sequences, and amino acid (aa) sequences of selected regions, for definitive and tentative members of *Waikavirus* |
| **Virus/GenBank accession** | **Whole genome (nt)** | **Whole coding region (aa)** | **Polymerase CG-GDD region (aa)** | **Coat proteins (aa)** |
| AYV1\_MN180070 | 40.57 | 21.72 | 37.26 | 24.28 |
| BCWVA\_QMU95531 | 44.54 | 28.76 | 53.65 | 32.63 |
| BnRV1\_NC\_040586 | 46.04 | 30.61 | 49.89 | 37.81 |
| BVCV\_NC\_027915 | 46.07 | 29.61 | 51.19 | 36.08 |
| LWaiV1\_MT348710 | 45.25 | 29.80 | 47.85 | 35.50 |
| MCDV\_NC\_003626 | 43.85 | 28.13 | 49.68 | 33.89 |
| PoLV1\_MW289237 | 41.59 | 23.74 | 40.42 | 27.13 |
| PWaiV\_LC488189 | 41.82 | 22.59 | 39.96 | 25.80 |
| RCaV1\_MH325329 | 46.15 | 29.32 | 51.18 | 33.74 |
| RTSV\_NC\_001632 | 44.10 | 27.50 | 48.50 | 32.25 |

**References**

Tang J, Delmiglio C, Ward L, Thompson J (2022) Complete nucleotide sequence of sweetbriar rose curly-top associated virus, a tentative member of the genus *Waikavirus*.Arch Virol https://doi.org/10.1007/s00705-021-05337-y