

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

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| **Code assigned:** | **2020.008M** |  |
| **Short title:**  Create one new species (*Dillard sunrhavirus*) in the genus *Sunrhavirus* (*Mononegavirales*: *Rhabdoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Rhabdoviridae* Study Group |

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

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| Approved by all responding SG members (10 of 14) with minor revisions. |

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

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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 | 26 July 2020 |
| Date of this revision (if different to above) |  |

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

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

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2020.008M.R.Sunrhavirus\_1nsp |

**Abstract**

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| The new species *Dillard sunrhavirus* is proposed for Dillard’s Draw virus. The virus clusters phylogenetically with members of the genus *Sunrhavirus* and is most closely related to Oak Vale virus. Dillard’s Draw virus meets demarcation criteria for assignment to a new species in the genus. |

**Text of proposal**

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| |  | | --- | | Dillard’s Draw virus (DDRV; strain DDrV-2015) was detected in mosquitoes (*Culex tarsalis*) collected in 2015 in New Mexico, USA [1]. The near-complete genome sequence (11,124 nt) has been determined, including complete coding sequences but incomplete 3' and 5' termini [1]. We propose to assign Dillard’s Draw virus to a new species *Dillard sunrhavirus* in the genus *Sunrhavirus*.  **Genome organization**  The DDRV genome is similar in organisation to those of other sunrhaviruses, containing the five canonical rhabdovirus structural protein genes (N, P, M, G and L) and an additional gene between the M and G genes encoding a small hydrophobic protein (U1) (**Figure 1**). The DDRV U1 protein displays moderate amino acid sequence identity with the U1 proteins of Oak Vale virus (OVV; species *Oakvale sunrhavirus*) and Kwatta virus (KWAV; species *Kwatta sunrhavirus*) (**Figure 2**). Like other sunrhaviruses, DDRV also has an alternative open reading frame (Px) that commences near the start of the P gene; the DDRV Px protein displays moderate amino acid sequence identity with the Px proteins of OVV and KWAV, and it is similar in size to the OVV Px protein (**Figure 3**).  Based on ML trees generated from complete L protein sequences DDRV falls within the sunrhavirus clade and is most closely related to OVV (**Figure 4**). Amino acid sequence divergence between DDRV and OVV in pair-wise alignments (p-distances) is 28.8 % in the N proteins, 25.3 % in the G proteins and 27.8 % in the L proteins (**Tables 1-3**).  **Ecology**  Sunrhaviruses have been isolated from birds, mosquitoes or biting midges. Like DDRV, OVV and KWAV have each been isolated from mosquitoes (*Culex* spp.); OVV was isolated in Australia and KWAV in Surinam.    **Species demarcation criteria**  Viruses assigned to different species within the genus *Sunrhavirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N; B) minimum amino acid sequence divergence of 10% in L; C) minimum amino acid sequence divergence of 15% in G; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralisation tests; and F) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.  DDRV meets demarcation criteria A, B and C. DDRV has a similar genome organization to OVV (criterion D). Neutralisation tests (criterion E) have not been conducted using DDRV as no virus isolate is currently available. DDRV appears to have similar ecology to OVV and KWAV but has been isolated from a geographically distant location (criterion F). | |

**Supporting evidence**

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**Figure 1.** Sunrhavirus genome organisations. Open arrows indicate the locations of long open reading frames (ORFs) N, P, M, G and L represent ORFs encoding the canonical rhabdovirus structural protein genes. The U1 ORFs (shaded blue or green) also occur in independent transcriptional units and encode small hydrophobic proteins of unknown function. The HARDV U2 ORF (shaded orange) also occurs as an independent transcriptional unit and encodes a very small protein (2.38 kDa) of unknown function. Alternative ORFs (shaded purple, green and brown) occur near the start of each of the P genes. Colours indicate sets of proteins that share obvious amino acid sequence identity.

OVV\_U1 M--FWKVFFALVLFSYWNNPD-VASRTATTIFDMM-LLA--TRYIASYILPASACPPCPEVHAPFP

DDRV\_U1 MSAFWKVFFALVLFSYWNNPE-VASKTATTLFDMI-IGV--MRYILAYIFPKGSCPPCPEVKSPYP

KWAV\_U1 M-AGWKLLFVLLIVLYWHNPEGVTSLMKSSLNIMETILAEPIRKVVSFFTPP--CPPCPQCLVKTP

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**Figure 2.** Clustal X amino acid sequence alignment of the OVV, KWAV and DDRV U1 proteins.

OVV\_Px M-TKTVLQRRSLRAALSAKRCSHQTH-LTPRVKSWITSQVERVMDRLTRVLNGIILFLLEQVIRTTPGQEAVCQLLDQV

DDRV\_Px M-TKTVLRQRSLKNALSAKRCSHQTH-LTPKVKSWITSQVEKVMDNVTRALNGIILFFLERLLWTAPGQEAVCQLLDQI

KWAV\_Px MMTRKRLASGSIDRILQRKRCNHQSHQWTPQVSGWIHRQVG----KVTQAIHGVLCYLLEKILMTPVGIQVVCQILEGE

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OVV\_Px ELE--DQVDSSEEEVD---------------------------------------------------------------

DDRV\_Px EVE--DPEESLLC------------------------------------------------------------------

KWAV\_Px EVDEDDLPQSLRMESHRPIQVLEPENPRISPVEILGQDPKQVKEAQSPPLPPPRRSPTPPDPSPIPEREDHRRMDPHSQ

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**Figure 3.** Clustal X amino acid sequence alignment of the OVV, KWAV and DDRV Px proteins.



**Figure 4.** The evolutionary history was inferred from a Clustal W alignment of 169 complete L protein sequences of 168 animal rhabdoviruses currently assigned or recently proposed for assignment to species in other genera and Dillard’s Draw virus which we propose to be assigned to a new species in the genus *Sunrhavirus*. Phylogenetically informative sites were selected from the alignment using Gblocks resulting in 915 positions in the final dataset. The tree was inferred in MEGA7 by using the Maximum Likelihood method based on the Whelan and Goldman + Freq. model. The tree with the highest log likelihood (-127314.573) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Joining and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap values (100 iterations) are shown for each node.

**Table 1.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of sunrhavirus N proteins.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | SUNV | HARDV | WACV | GARV | KWAV | OVV | DDRV |
| SUNV |  |  |  |  |  |  |  |
| HARDV | 86.8 |  |  |  |  |  |  |
| WACV | 47.6 | 49.5 |  |  |  |  |  |
| GRAV | 37.7 | 38.0 | 39.2 |  |  |  |  |
| KWAV | 28.8 | 29.3 | 32.9 | 28.1 |  |  |  |
| OVV | 29.6 | 30.3 | 31.3 | 27.9 | 38.5 |  |  |
| DDRV | 30.0 | 30.3 | 30.5 | 27.6 | 36.3 | 71.2 |  |

**Table 2.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of sunrhavirus G proteins.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | SUNV | HARDV | WACV | GARV | KWAV | OVV | DDRV |
| SUNV |  |  |  |  |  |  |  |
| HARDV | 77.1 |  |  |  |  |  |  |
| WACV | 45.9 | 46.5 |  |  |  |  |  |
| GRAV | 35.9 | 35.7 | 34.5 |  |  |  |  |
| KWAV | 26.7 | 25.1 | 27.1 | 26.3 |  |  |  |
| OVV | 24.5 | 22.7 | 24.7 | 24.7 | 42.2 |  |  |
| DDRV | 25.3 | 23.1 | 25.3 | 24.1 | 44.7 | 74.7 |  |

**Table 3.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of sunrhavirus L proteins.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | SUNV | HARDV | WACV | GARV | KWAV | OVV | DDRV |
| SUNV |  |  |  |  |  |  |  |
| HARDV | 85.8 |  |  |  |  |  |  |
| WACV | 55.3 | 54.3 |  |  |  |  |  |
| GRAV | 54.4 | 54.6 | 51.6 |  |  |  |  |
| KWAV | 42.3 | 41.3 | 40.6 | 41.5 |  |  |  |
| OVV | 40.7 | 40.4 | 39.6 | 40.6 | 55.4 |  |  |
| DDRV | 41.8 | 40.9 | 39.7 | 40.3 | 54.7 | 72.2 |  |

**References**

1. Reeves WK, Miller MM, Gruner WE (2018) Two *Rhabdoviridae*: Dillard's Draw virus, aputative new virus, and Merida virus from *Culex tarsalis* (Diptera: Culicidae) in New Mexico, USA. Acta Virologica 62:326-329. PMID: **30160148** DOI: 10.4149/av\_2018\_226