

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2023.023P** |  |
| **Short title:** Establish a new species in the genus *Nanovirus* (family *Nanoviridae*) | | |
|  | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
|  |  |
| Heydarnejad J, Gronenborn B, Varsani A, | [heydarnejad@uk.ac.ir](mailto:heydarnejad@uk.ac.ir);  [bgronenborn@gmail.com](mailto:bgronenborn@gmail.com);  [Arvind.varsani@asu,edu](mailto:Arvind.varsani@asu,edu) |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Department of Plant Protection, College of Agriculture, Shahid Bahonar University of Kerman, Kerman 7616914111, Iran [JH]  Im Broich 38, 50128 Bergheim-Fliesteden, Germany [BG]  The Biodesign Center of Fundamental and Applied Microbiomics, School of Life Sciences, Center for Evolution and Medicine, Arizona State University, 1001 S. McAllister Ave, Tempe, AZ 85287-5001, USA [AV] |

**Corresponding author**

|  |
| --- |
| A. Varsani (Arvind.Varsani@asu.edu) |

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

|  |
| --- |
| *Nanoviridae* SG |

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

|  |
| --- |
|  |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| Nanoviridae | 10/12 | 0/12 | 2/12 |
|  |  |  |  |

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

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | 19th June 2023 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
|  |

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

**Text of proposal**

|  |
| --- |
|  |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2023.023P.A.v1\_Nanovirus\_1nsp.xlsx |

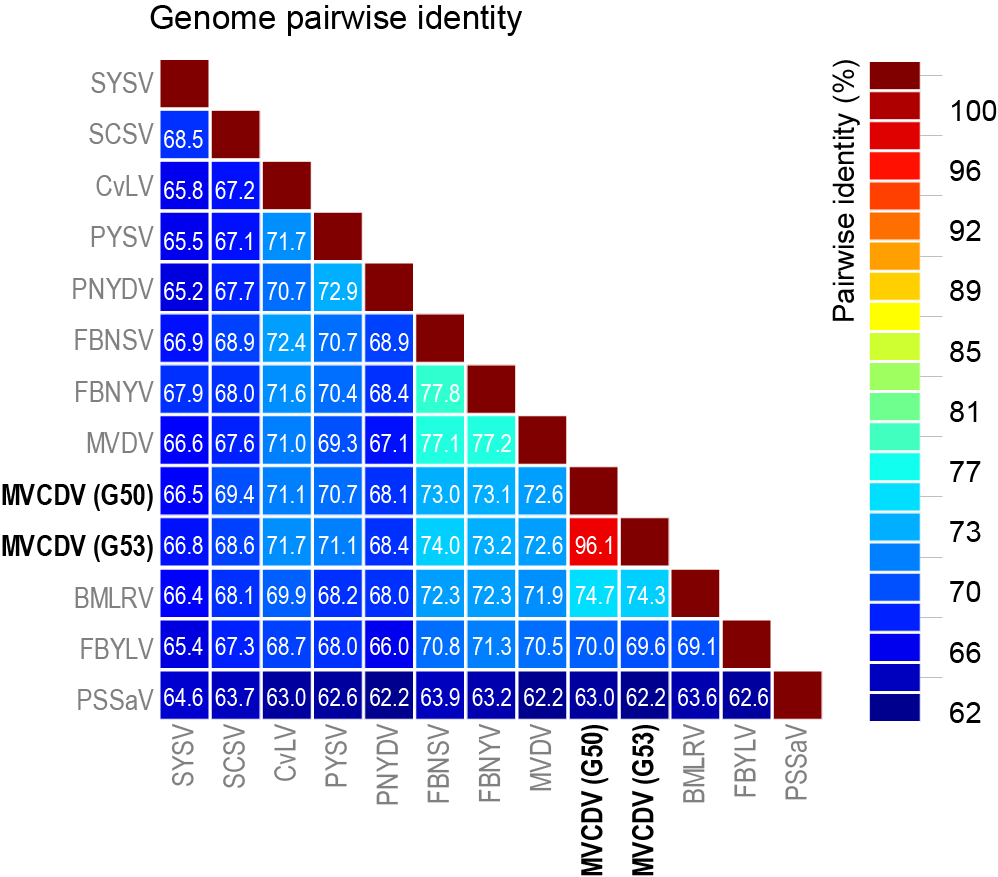
**Abstract**

|  |
| --- |
| Milk vetch chlorotic dwarf virus was identified in Iran from two symptomatic milk vetch (*Astragalus myriacanthus* Boiss.) samples (sample ID G50 and G53; sampled in 2018) showing marginal leaf chlorosis, reduced leaf size and dwarfing symptoms. These two nanoviruses represent a new species in the family *Nanoviridae*. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | A new nanovirus, milk vetch chlorotic dwarf virus (MVCDV), was identified in Iran from two symptomatic milk vetch (*Astragalus myriacanthus* Boiss.) samples (sample ID G50 and G5). These were sampled in 2018 from Nafech in Chaharmahal and Bakhtiari province of central Iran, and showed marginal leaf chlorosis, small leaves and dwarfing symptoms [1].  Each genome component of the G50 and G53 share 84.4 - 99.7% pairwise identity, determined using SDT v1.2 [2] with the counterpart component sequences. The genomes (concatenated component sequences) of MVCDV share 62.2-74.7% pairwise identity with all other nanoviruses (Figure 1). The CPs encoded by DNA-S of MVCDV share 78.6-85.0% amino acid sequence identity with those of black medic leaf roll virus (BMLRV) and 44-62% with those of all others nanovirus CPs.  The species demarcation threshold for nanoviruses proposed by the ICTV Nanoviridae Study group [3-4] is >15% divergence in the CP amino acid sequence and/or nucleotide pairwise identity of overall genomes <75% when compared to other nanoviruses.  The genome of MVCDV and that of BMLRV is close to 75% and the CP amino acid identity is <85%, both of which are close to the new species demarcation limits. The phylogenetic analysis (Figure 2) of the individual components coupled with the pairwise identity analysis supports the establishment of a new species to accommodate MVCDV.  To conform with the binominal species names [5], we propose the name ***Nanovirus astragalirani*** (epithet is a contraction of host genus name *Astragalus* and Iran). The exemplar virus in this new species is milk vetch chlorotic dwarf virus isolate G53 with the following accession numbers:  DNA-U4: MN273339  DNA-U2: MN273338  DNA-U1: MN273337  DNA-R: MN273336  DNA-N: MN273335  DNA-M: MN273334  DNA-S: MN273333  DNA-C: MN273332 | |

**Supporting evidence**

****

Black medic leaf roll virus – BMLRV

Cow vetch latent virus – CvLV

Faba bean necrotic stunt virus – FBNSV

Faba bean necrotic yellows virus – FBNY

Faba bean yellow leaf virus – FBYLV

Milk vetch chlorotic dwarf virus – MVCDV

Milk vetch dwarf virus – MVDV

Pea necrotic yellow dwarf virus, – PNYDV

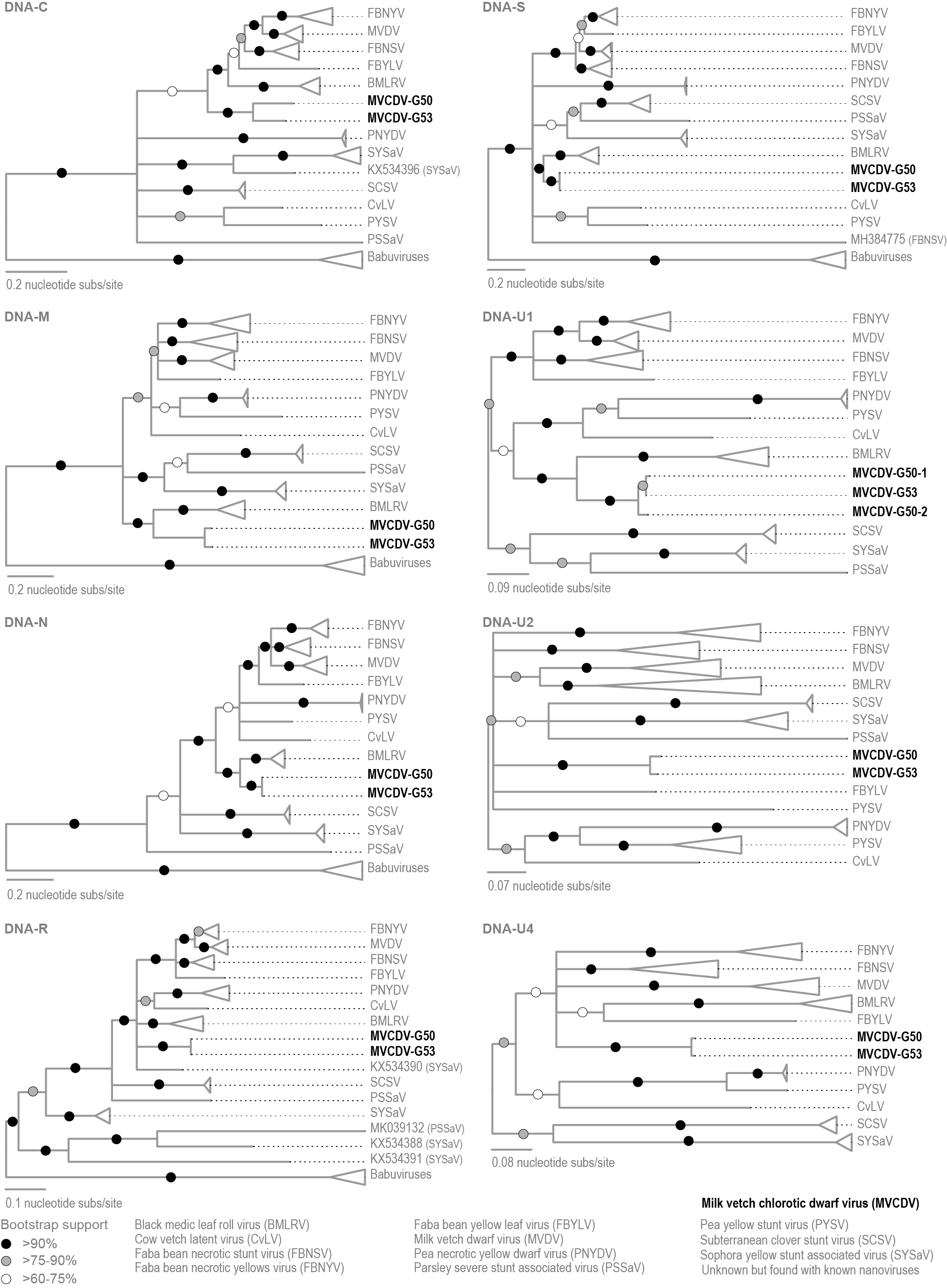
Parsley severe stunt associated virus – PSSaV

Pea yellow stunt virus – PYSV

Subterranean clover stunt virus – SCSV

Sophora yellow stunt virus – SYSV

**Figure 1:** Pairwise identity matrix of the genome (concatenated component sequences) of representative nanoviruses determine using SDT v1.2 [2]. Figure adapted from Hassan-Sheikhi et al., [1].

****

**Figure 2:** Maximum likelihood phylogenetic trees, inferred using PhyML [6] of MVCDV component nucleotide sequences and rooted with babuvirus sequences except for those of DNA-U1, DNA-U2 and DNA-U4 which are midpoint rooted. Figure adapted from Hassan-Sheikhi et al. [1].

**References**

1. Hassan-Sheikhi P, Heydarnejad J, Massumi H, Kraberger S, Varsani A. 2020. Novel nanovirus and associated alphasatellites identified in milk vetch plants with chlorotic dwarf disease in Iran. Virus Res. 276: 197830. PMID: 31790775 DOI: 10.1016/j.virusres.2019.197830
2. Muhire BM, Varsani A, Martin DP (2014) SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One 9:e108277. PMID: 25259891; DOI: 10.1371/journal.pone.0108277
3. Thomas JE, Gronenborn B, Harding RM, Mandal B, Grigoras I, Randles JW, Sano Y, Timchenko T, Vetten HJ, Yeh H-H, Ziebell H, ICTV report consortium. (2021) ICTV virus taxonomy profile: Nanoviridae. Journal of General Virology, 102, 001544. PMID: 33433311 PMCID: PMC8515864 DOI: 10.1099/jgv.0.001544
4. Vetten HJ, Dale JL, Grigoras I, Gronenborn B, Harding R, Randles JW, Sano Y, Thomas JE, Timchenko T, Yeh HH, 2012. Nanoviridae. In: King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (Eds.), Virus Taxonomy. Elsevier, San Diego, pp. 395-404.
5. Siddell SG, Walker PJ, Lefkowitz EJ, Mushegian AR, Dutilh BE, Harrach B, Harrison RL, Junglen S, Knowles NJ, Kropinski AM, Krupovic M, Kuhn JH, Nibert ML, Rubino L, Sabanadzovic S, Simmonds P, Varsani A, Zerbini FM, Davison AJ (2020) Binomial nomenclature for virus species: a consultation. Arch Virol 165:519-525. PMID: 31797129; DOI: 10.1007/s00705-019-04477-6
6. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst Biol 59:307-321. PMID: 20525638; DOI: 10.1093/sysbio/syq010