This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.005D*** | | | | (to be completed by ICTV officers) |
| **Short title:** Proposal for a new virus species in family *Iridoviridae*, genus *Ranavirus* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Bernardo Saucedo Garnica; Jolianne M Rijks | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Bernardo Saucedo Garnica, [b.saucedogarnica@uu.nl](mailto:b.saucedogarnica@uu.nl) | | | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | Iridoviridae Study Group | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 15, 2017 | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.005D.N.v1.Ranavirus\_sp |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

|  |
| --- |
| **References:** |
| Balsiero A, Dalton KP, del Cerro A, Marquez I, Cunningham AA, Parra F, et al. Pathology, isolation and molecular characterisation of a ranavirus from the common midwife toad *Alytes obstretricans* on the Iberian Peninsula. Dis Aquat Organ. 2009; 84: 95–104. doi: 10.3354/dao02032 PMID: 19476279  van Beurden SJ, Hughes J, Saucedo B, Rijks J, Kik M, Haenen OLM, et al. Complete genome sequence of a common midwife toad virus-like ranavirus associated with mass mortalities in wild amphibians in the Netherlands. Genome Announc. 2014; 2:e01293–14. doi: 10.1128/genomeA.01293-14 PMID: 25540340  Price SJ, Garner TWJ, Nichols RA, Balloux F, Ayres C, Mora-Cabello de Alba A, et al. Collapse of amphibian communities due to an introduced ranavirus. Curr Biol. 2014; 24: 2586–2591. doi: 10.1016/j. cub.2014.09.028 PMID: 25438946  Rijks JM, Saucedo B, Spitzen-van der Sluijs A, Wilkie GS, van Asten AJ, van den Broek J, Boonyarittichaikij R, Stege M, van der Sterren F, Martel A, Pasmans F, Hughes J, Gröne A, van Beurden SJ, Kik MJ. [Investigation of amphibian mortality events in wildlife reveals an on-going ranavirus epidemic in the North of the Netherlands.](https://www-ncbi-nlm-nih-gov.proxy.library.uu.nl/pubmed/27315226) PLoS One. 2016 Jun 17;11(6):e0157473. doi: 10.1371/journal.pone.0157473  Price SJ. Comparative genomics of amphibian-like ranaviruses, nucleocytoplasmic large DNA viruses of poikilotherms. Evolutionary Bioinformatics 2016; 11 (S2) 71–78 |

|  |
| --- |
| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria:** Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteria have previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa:**    + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the origin of names assigned to new taxa at genus level and above.   + For each new genus a type species must be designated to represent it. Please explain your choice. * **Supporting evidence:** The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.     We propose common midwife toad virus as a member of a new species of the genus *Ranavirus,* within the sub-family *Alphairidovirinae,* family *Iridoviridae*. The virus was first reported in 2008 as the cause of a massive die-off of larval stages from *Alytes obstetricans* and *Messotriton alpestris* (Balsiero *et al*., 2009) and has since been found in various sites throughout continental Europe causing severe mortality events in both wild and captive amphibian populations (*Pelophylax* spp*., Rana temporaria, Alytes obstetricans, Messotriton alpestris, Lissotriton vulgaris*, etc.) (van Beurden *et al., 2013*; Price *et al*., 2014; Rijks *et al.,* 2016). The virus causes distinct clinical signs such as edema and widespread hemorrhages, and microscopically necrosis in multiple organs and presence of intracytoplasmic inclusions which correspond to virus assembly sites are characteristic.  Next generation sequencing has allowed complete genome sequencing of various viruses belonging to the tentative Common midwife toad virus species; these include common midwife toad virus (CMTV-E) from Spain, common midwife toad virus Netherlands (CMTV-NL), Andrias davidinus ranavirus, Testudo hermanni ranavirus and pike perch iridovirus. The genomes of all ranaviruses belonging to the tentative new species Common midwife toad virus share a unique medium sized inversion (30 kp in length) that dissects an opening reading at the end of the genome from another ranavirus species, *Ambystoma tigrinum virus* (Price, 2016). The unique genome structure of common midwife toad virus, as well as its more or less restricted distribution in the wild throughout Continental Europe and the classical clinical signs and pathological changes in affected hosts, are the reasons we propose common midwife toad virus as new species of the genus *Ranavirus*.  The proposed taxonomic change is based on the unique genomic structure, pathological changes, spreading patterns and severe population impacts that have characterized the proposed virus species (Common midwife toad virus) for almost 10 years since strains of the proposed virus were originally described.  **Species demarcation criteria:**  The majority of ranaviruses show a high nucleotide similarity among themselves. The attached phylogeny clearly depicts the phylogenetic difference between the proposed members of the new proposed species and the other ranavirus species. The overall nucleotide similarity between the members of the proposed Common midwife toad virus and other ranavirus species varies between 94-98%, this seemingly low variation in nucleotide similarity is not unlike that which exists between two already characterized species of the genus: *European catfish virus* and *Epizootic hematopoietic necrosis virus* (approximately 96%).  All proposed members of the newly proposed species, Common midwife toad virus, possess genome lengths ranging from 107-108 kbp, 102 putative opening reading frames, and a G+C content of approximately 55%. All these genomes share a unique medium sized inversion (30 kp in length) that dissects an opening reading at the end of the genome from another ranavirus species *Ambystoma tigrinum virus* (Price et al., 2016).  **Origin of name:**  The name was formulated based on the English name of the host species in which the virus was originally detected. This host species was the common midwife toad (*Alytes obstetricans*) (Balseiro et al., 2009).  **Supporting evidence:**  We enclose the figure of the Maximum likelihood phylogeny (1000 replicates) of the common midwife toad virus from our PLoS ONE 2016 publication to highlight the position of these viruses within the Ranavirus genus. To reconstruct the phylogeny of the fully sequenced Dutch isolate, (GenBank no.NL\_KP056312), twenty-six core protein sequences from 17 full genomes from members of the family *Iridoviridae* were extracted from GenBank. These were aligned with the isolate’s 26 core iridovirus proteins using MAFFT version 7 to produce a protein alignment for each gene. The core set of genes was concatenated and the best protein substitution models for each gene partition were selected using PartitionFinder. The maximum likelihood phylogeny was reconstructed using 1000 bootstrap replicates using RAxML (version 8). The attached figure corresponds to our PloS ONE 2016 publication (modified to indicate proposed and existing virus species).  Further support is provided by references to previously published papers by Price (2016), Balseiro et al. (2009) and van Beurden et al. (2014). |

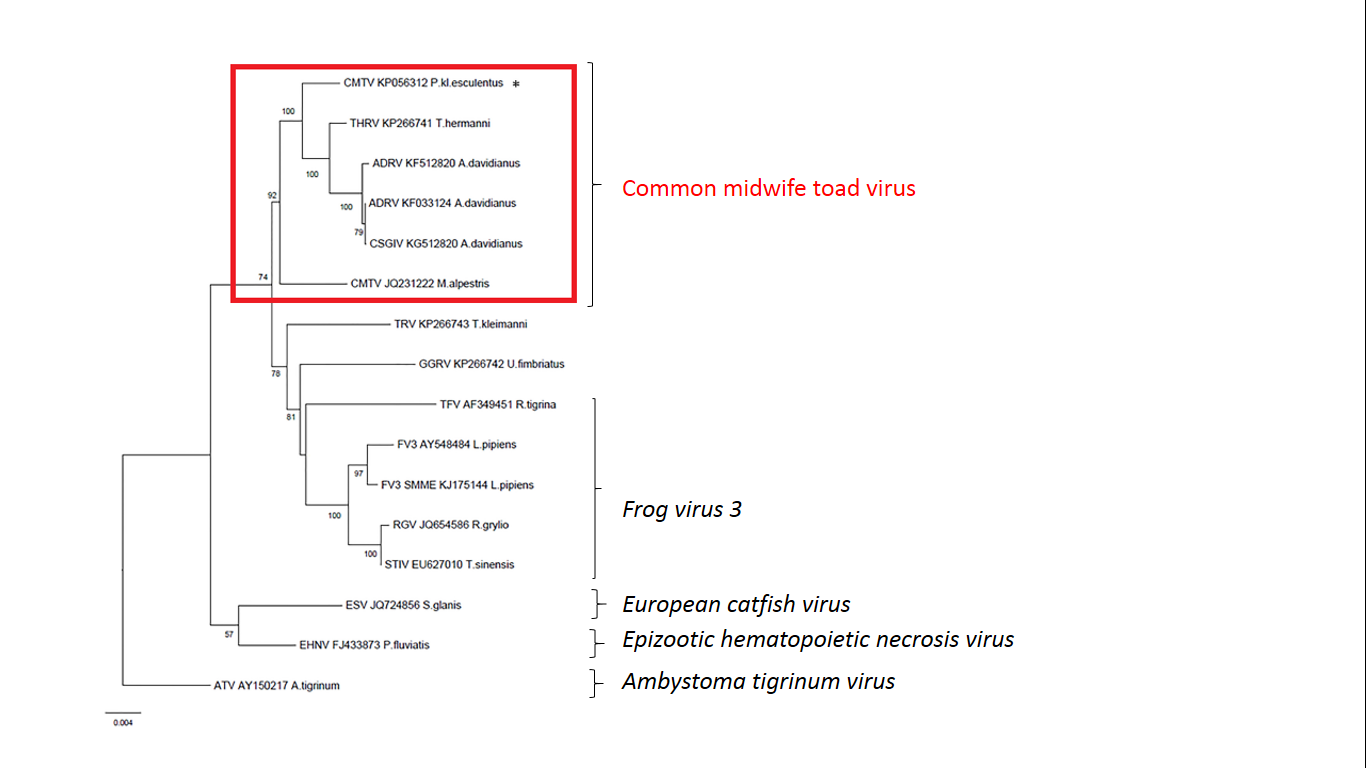


Fig 1. Phylogeny of ranaviruses (virus strains provided in the left / recognized virus species provided in the right). The figure was modified from Rijks *et al*. (2016) to highlight published strains (red square) belonging to the proposed Common midwife toad virus species (in red). Maximum likelihood phylogeny based on the 26 iridovirus core proteins of the fully sequenced Dutch ranavirus and other publicly available ranavirus genomes. The Singapore grouper iridovirus and Santee-Cooper ranavirus were used as an outgroup (not shown). The bootstrap support is shown at the nodes. Virus strains used include: common midwife toad virus-NL (CMTV GenBank no. KP056312), common midwife toad virus-E (CMTV GenBank no. JQ31222), Andrias davidianus ranavirus (ADRV GenBank no. KF512820), Andrias davidianus ranavirus (ADRV GenBank no. KF033124), Chinese giant salamander virus (GenBank no. KG512820), tortoise ranavirus (TRV GenBank no.KP266743), German gecko ranavirus (GGRV KP266742), frog virus 3 (GenBank no. AY548484), frog virus 3 (GenBank no. KJ175144), Rana grylio virus (RGV JQ654586), soft-shelled turtle iridovirus (STIV GenBank no. EU627010), European sheathfish virus (ESV), epizootic hematopoietic necrosis virus (EHNV GenBank no. FJ433873), and Ambystoma tigrinum virus (ATV, GenBank no. AY150217).