

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

**Part 1a: Details of taxonomy proposals**

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| **Title:**  | Create two new species (*Rotavirus kappagastroenteritidis*, *Rotavirus lambdagastroenteritidis*) in the genus *Rotavirus* (Family *Sedoreoviridae*) |
| **Code assigned:**  | 2024.015M.Rotavirus\_2nsp  |

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| **Author(s), affiliation and email address(es):**  |
| **Name**  | **Affiliation**  | **Email address**  | **Corresponding author(s)**  |
| Johne R | Federal Institute for Risk Assessment, Berlin, Germany [RJ]  | Reimar.Johne@bfr.bund.de | X |

**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee** |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses | **X** | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
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| **Optional – complete only if formally voted on by an ICTV Study Group:**  |
| **Study Group** | **Number of members** |
| **Votes in support** | **Votes against** | **No vote** |
| Sedoreoviridae group | 9 | 0 |  |
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| **Submission date:** |  14/06/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:**  |
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| **Revision date:** |  DD/MM/YYYY |

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

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| **Name of accompanying Excel module:**  |
| 2024.015M.Rotavirus\_2nsp.xlsx |

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| **Taxonomic changes proposed** |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Is any taxon name used here derived from that of a living person:**  |  **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached**  |

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| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*: The genus *Rotavirus* *Description of current taxonomy*: Currently, the 9 different rotavirus species *Rotavirus alphagastroenteritidis*, *Rotavirus aspergastroenteritidis, Rotavirus betagastroenteritidis, Rotavirus deltagastroenteritidis, Rotavirus gammagastroenteritidis, Rotavirus iotagastroenteritidis, Rotavirus jotagastroenteritidis, Rotavirus phigastroenteritidis, and Rotavirus tritogastroenteritidis* are existing. Their exemplar members are: rotavirus A (RVA), RVH, RVB, RVD, RVG, RVI, RVJ, RVF, and RVC, respectively.*Proposed* *taxonomic change(s):* Two new rotavirus species (*Rotavirus kappagastroenteritidis* and *Rotavirus lambdagastroenteritidis* should be created.*Justification*:Evolutionary analysis of complete coding regions of the recently reported rotavirus K (RVK) and rotavirus L (RVL) genomes using phylogenetic trees indicate a separate branching of all genome segments from that of the representative members (RVA-RVD and RVF-RVJ) of the established rotavirus species. In addition, the maximum identities of deduced amino acid sequence for VP6 with that of established rotavirus species reference strains are 51% for RVK and 47% for RVL, which are lower than the cut-off value (53%) for definition of new rotavirus species.  |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: The genus *Rotavirus* *Description of current taxonomy*: Currently, the 9 different rotavirus species *Rotavirus alphagastroenteritidis, Rotavirus betagastroenteritidis, Rotavirus tritogastroenteritidis, Rotavirus deltagastroenteritidis, Rotavirus phiagastroenteritidis, Rotavirus gammagastroenteritidis, Rotavirus aspergastroenteritidis, Rotavirus iotagastroenteritidis and Rotavirus jotagastreenteritidis* are existing.*Proposed* *taxonomic change(s)*: Two new rotavirus species (*Rotavirus kappagastroenteritidis* and *Rotavirus lambdagastroenteritidis* ~~[~~should be created.*Demarcation criteria:*% amino acids sequence identity of VP6 (<53%) and separate branching in phylogenetic trees.*Justification*: The exemplar strains of the proposed *Rotavirus kappagastroenteritidis* (RVK) and *Rotavirus lambdagastroenteritidis* (RVL) ~~strains~~ have been first identified in intestinal contents of common shrews (*Sorex araneus*) from Germany (Johne et al., 2019). The nearly complete genome sequence (complete ORFs, missing most 5’ and 3’-terminal non-coding sequences) of a ~~putative~~ RVK reference strain (RVK/shrew-wt/GER/KS14–0241/2013) was determined in 2023 (GenBank acc.-nos: OQ934016-OQ934026; Johne et al., 2023). The complete genome sequence of a ~~putative~~ RVL reference strain (RVL/shrew-wt/GER/KS14–0241/2013) was determined in 2022 (GenBank acc.-nos: OM101015-OM101025; Johne et al., 2022). Please note that both reference strains originate from the same animal, which was co-infected with RVK and RVL. The deduced amino acid sequence identities for the encoded virus proteins as compared to the reference strains, RVA-RVD and RVF-RVJ, of the established rotavirus species are shown in Table 1. Most notable, maximum identities of VP6 are 51% for RVK and 47% for RVL, which are lower than the cut-off value (53%) for definition of new rotavirus species (Matthijnssens et al., 2012, 2021, 2022). Phylogenetic trees for the distinct proteins (Figure 1) or all proteins concatenated (Figure 2) show separate branching for RVK and RVL compared to the exemplar members of the established rotavirus species. The sequences at the genome segment termini of RVL are conserved and similar to that of RVB, RVG, RVH, RVI and RVJ (Johne et al., 2022), which is in accordance with the clustering of these rotaviruses within the RVB-like clade in phylogenetic trees (Fig. 2). Additional partial genome sequences from other RVK and RVL strains have been identified in common shrews indicating continued circulation of these viruses in this host species (data not shown, see Johne et al., 2022, 2023).  |

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| **References:**  |
| Johne, R., Tausch, S. H., Grützke, J., Falkenhagen, A., Patzina-Mehling, C., Beer, M., Höper, D., Ulrich, R. G., 2019. Distantly Related Rotaviruses in Common Shrews, Germany, 2004-2014. Emerg. Inf. Dis. 25(12), 2310–2314.Johne, R., Schilling-Loeffler, K., Ulrich, R. G., Tausch, S. H., 2022. Whole Genome Sequence Analysis of a Prototype Strain of the Novel Putative Rotavirus Species L. Viruses 14(3), 462. Johne, R., Tausch, S.H., Ulrich, R.G., Schilling-Loeffler, K., 2023. Genome analysis of the novel putative rotavirus species K. Virus Res., 334, 199171.Matthijnssens, J., Otto, P. H., Ciarlet, M., Desselberger, U., Van Ranst, M., Johne, R., 2012. VP6-sequence-based cutoff values as a criterion for rotavirus species demarcation. Arch. Virol. 157(6), 1177–1182. Matthijnssens, J., Attoui, H., Bányai, K., Brussaard, C.P.D., Pranav Danthi, P., del Vas, M., Dermody, T.S., Duncan, R., Fang, Q., Johne, R., et al., 2021. *Reoviridae*. Virus Taxonomy: 2020 Release. International Committee on Taxonomy of Viruses. Available online: https://talk.ictvonline.org/ictv-reports/ictv\_online\_report/dsrna-viruses/w/reoviridae (accessed on 19 March 2023).Matthijnssens, J., Attoui, H., Bányai, K., Brussaard, C. P. D., Danthi, P., Del Vas, M., Dermody, T. S., Duncan, R., Fāng Q., Johne, R., Mertens, P. P. C., Mohd Jaafar, F., Patton, J. T., Sasaya, T., Suzuki, N., Wei, T., 2022. ICTV Virus Taxonomy Profile: *Sedoreoviridae* 2022. J. Gen. Virol. 103(10), 10.1099/jgv.0.001782.   |

**Table 1:**

Identity of deduced amino acid sequences of RVK strain RVK/shrew-wt/GER/

KS14–0241/2013 and RVL strain RVL/shrew-wt/GER/KS14–0241/2013 to the reference strains of the established rotavirus species (RVA-RVD, RVF-RVJ, see Johne et al., 2023, for strain designations and GenBank acc.-nos.). Identities for VP6 are marked in bold face.

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|  | % amino acid sequence identity for RVK | % amino acid sequence identity for RVL |
| VP1 | 21 - 59 | 21 - 64 |
| VP2 | 11 - 63 | 12 - 63 |
| VP3 | 11 - 49 | 12 - 52 |
| VP4 | 9 - 34 | 10 - 36 |
| **VP6** | **9 - 51** | **10 - 47** |
| VP7 | 11 - 46 | 11 - 37 |
| NSP1\* | 5 - 21 | 6 - 22 |
| NSP2 | 11 - 49 | 12 - 49 |
| NSP3 | 11 - 53 | 8 - 29 |
| NSP4 | 2 - 13 | 3 - 15 |
| NSP5 | 5 - 24 | 7 - 37 |

\* for RVB, RVG and RVI, which encode two forms of NSP1 (NSP1–1 and NSP1–2), identities with NSP1–2 are shown. Adapted from Johne et al., 2022 and Johne et al., 2023.

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**Figure 1: Phylogenetic relationship of RVK and RVL proteins VP1-VP4, VP6-VP7 and NSP1-NSP5 with that of the other rotavirus species.** The complete deduced amino acid sequences of the encoded proteins of RVK and RVL were compared with those of reference strains of the other rotavirus species by the Maximum Likelihood method using MEGA X. RVK and RVL are marked in red and bootstrap values > 50% are shown. Scaled in amino acid substitutions per site. Rotavirus species belonging to the evolutionary RVA-like clade are shaded in orange, whereas those of the RVB-like clade are shaded in blue. For RVB, RVG and RVI, which encode two forms of NSP1 (NSP1-1 and NSP1-2), only NSP1-2 was used in the NSP1 tree. Adapted from Johne et al., 2023.

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**Figure 2:** **Phylogenetic relationship of rotavirus species based on the concatenated amino acid sequences of VP1-VP4, VP6-VP7 and NSP1-NSP5.** The concatenated amino acid sequences of proteins of RVK and RVL were compared with that of reference strains of the other rotavirus species by the Maximum Likelihood method using MEGA X, and a radiated tree was constructed. Bootstrap values > 50% are shown. Scaled in amino acid substitutions per site. Rotavirus species belonging to the evolutionary RVA-like clade are shaded in orange, whereas those of the RVB-like clade are shaded in blue. Adapted from Johne et al., 2023.

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