

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

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

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| ICTV *Paramyxoviridae* Study Group |

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

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| The ICTV *Paramyxoviridae* Study Group has seen and discussed this proposal and agreed to its submission to the ICTV Executive Committee based on majority vote. |

**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Paramyxoviridae* Study Group | 7 | 0 | 0 |

**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 |

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

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 23, 2023 |
| 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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| N/A |

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

**Name of accompanying Excel module**

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| 2023.018M.N.v1.Paramyxoviridae\_reorg.xlsx |

**Abstract**

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| The family *Paramyxoviridae* has not undergone a significant update for several years. However, during this time, numerous newly discovered sequences depicting potential paramyxovirid species have become available. To reevaluate the taxonomy, we employed Bayesian phylogeny and DEmARC analysis. As a result, we propose to establish five new subfamilies, six new genera, and 71 new species. |

**Text of proposal**

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| We used DEmARC, a computational approach introduced by Chris Lauber and Alexander Gorbalenya (Lauber and Gorbalenya, 2012a; Lauber and Gorbalenya, 2012b) to hierarchically classify the family *Paramyxoviridae* by relying solely on genetic data. Briefly, in DEmARC, or ‘DivErsity pArtitioning by hierarchical Clustering’, virus clusters are delimited by devising a threshold on the maximum intra-cluster (intra-taxon) divergence of virus sequences. This is done separately for each level of the hierarchical classification, all of which are selected using a cost function that measures the quality of virus clustering. The approach was extensively evaluated in a case study of picornavirids (Lauber and Gorbalenya, 2012b) and filovirids (Lauber and Gorbalenya, 2012a) and is the current method of choice for classification of all viruses in order *Nidovirales*.  Briefly, all publicly available coding-complete paramyxovirid genome sequences (last update 11 May 2023) were downloaded from NCBI GenBank, after which cd-hit (Li and Godzik, 2006) was used to cluster sequences with <5% nucleotide sequence divergence. For a representative sequence of each cluster, the six major paramyxovirid protein (N, P, M, F, RBP, and L) amino acid sequences were deduced and used to construct a concatenated multiple alignment. For this, the sequences of each of the proteins were seperately aligned with MAFFT v7.453 (Katoh and Standley, 2013) and trimmed with TrimAl v1.4.rev15 (Capella-Gutièrrez et al, 2009), after which the six multiple sequence alignments were concatenated. Bayesian phylogenetic analyses were inferred in BEAST v.1.10.4 (Suchard et al, 2018) using the LG+G4+I substitution model (Le and Gascuel, 2008) and employing MCMC with a chain length of 100,000,000 generations using the concatenated (N-P-M-F-RBP-L) alignment. The Markov chain Monte Carlo analysis was run until an effective samples size higher than 200 was obtained (allowing a burn-in period of 10%). A consensus tree was built with TreeAnnotator v1.10.4 using the maximum clase credibility method. This consensus tree was used as input for DEmARC to calculate a pairwise patristic distance matrix. This matrix was than used to calculate subfamily, genus, and species demarcations.  Finally, the DEmARC results were used to make and test a simplified method to demarcate paramyxovirid sequences:   1. Do an NCBI BLASTp search with the complete large (L) protein sequence of your virus of interest (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Proteins). 2. Using the top hit (highest overall score and full-length) of this BLASTp analysis, do a one-on-one BLASTp comparison of the other five major paramyxovirid proteins (N, P, M, F, and RBP) against this top hit sequence and calculate the average of all six BLASTp percentages.    1. If the average BLASTp identity for these six proteins is <85%, the sequence is considered to represent a new paramyxovirid species    2. If the average BLASTp identity is 85–90%, it will still be considered as a representative of a new paramyxovirid species if the specific BLASTp identity of the L protein is <90%. This second criterion ensures added weight is given to the L protein, the largest and most-conserved protein, in borderline cases.  * A few ‘borderline’ examples:   + The BLASTp top hit of **Lángyá** **virus** (OM101125) is Mòjiāng virus (KF278639), with an L protein identity of 90.11%. The average shared identity of the six major proteins is 84.45%. This sequence represents a separate species as the overall (average) identity is below 85%. For this sequence, a new species is proposed (species *Parahenipavirus langyaense*, subfamily *Orthoparamyxovirinae).*   + The BLASTp top hit of **chamois respirovirus** (MT180123) is ovine parainfluenzavirus 3 (MT756864), with an identity of the L protein of 89.31%. The overall identity is 85.46%. According to the newly defined demarcation rules, this sequence represents a new paramyxovirid species (proposed *Respirovirus rupicaprae*, subfamily *Feraresvirinae*).   + The BLASTp top hit of **feline morbillivirus type 1** (JQ411014) is feline morbillivirus type 2 (MK182089), with an identity of the L protein of 90.92%. The average shared identity of the six major proteins is 87.49%. This sequence does not represent a new paramyxovirid species, but belongs to the established species *Morbillivirus felis* (subfamily *Orthoparamyxovirinae*).   + The BLASTp top hit of Alston virus (MH972568), belonging to the previously established paramyxovirid species *Orthorubulavirus alstonvillense*, is parainfluenza virus 5 (JQ743324), with an identity of the L protein of 91.84%. The overall identity is 88.27%. In accordance with the new demarcation criteria, Alston virus belongs to the same species as parainfluenza virus 5, *Orthorubulavirus mammalis* (subfamily *Rubulavirinae*). Consequently, the species *Orthorubulavirus alstonvillense* is proposed to be abolished.   In conclusion, 71 new paramyxovirid species are proposed to be created using the above defined criteria and four recognized species are proposed to be abolished: one species, *Orthorubulavirus alstonvillense,* because it does not meet the newly defined demarcation criteria and three species (*Jeilongvirus anhuiense*, *Jeilongvirus felis*, and *Jeilongvirus murinae*) because no coding-complete genome sequence is publically available (we considered a sequence as coding-complete when the entire coding region of the genome, spanning from the start codon of the N gene until the stop codon of the L gene, is available; furthermore, the number of ambiguous (Y, R, S, W, K, M, B, D, H, V) or unknown (N) nucleotides may not result in stretches of more than 10 consecutive ambiguous (B, J, X, Z) amino acids or more than 20 ambiguous amino acids overall in the deduced protein sequences).  Based on distinct clustering in the Bayesian maximum clade credibility summary tree (using all available coding-complete concatenated protein sequences of the six major paramyxovirid proteins, see also **Figure 1**):   * Six new genera are proposed to be created:   + ***Hippocavirus***, to harbor the proposed species *Hippocavirus hippocampi*, containing the newly discovered Hippocampus erectus paramyxovirus 1 (OQ030201), whose branch length exceeds the current cut-off for minimal intergenus and even intersubfamily divergence (see Figure 1).   + ***Tupaivirus***, to harbor the established (now proposed to be renamed) species *Tupaivirus tupaiae* containing Tupaia paramyxovirus (AF079780), whose branch length exceeds the current cut-off for minimal intergenus divergence (see Figure 1).   + ***Bovinavirus***, to harbor the proposed species *Bovinavirus bovis*, containing the newly discovered bovine narmovirus 1 (ON861830), whose branch length exceeds the current cut-off for minimal intergenus divergence (see Figure 1).   + ***Parajeilongvirus***, to create a separation of the distinct rodent-/shrew-borne and bat-borne clades within the established genus *Jeilongvirus*. Although the branch lengths of these two clades do not meet the current cut-off for minimal intergenus divergence (see Figure 1), the clades are monophyletic and members of the two clades can be distinguished from each other by their host association as well as differences in genome organization. Members of the rodent-/shrew-borne clade are characterized by expanded RBP ORFs preceded by a TM gene and an optional SH gene. Members of the bat-borne clade, now proposed as the genus *Parajeilongvirus*, also have a TM gene but no RBP expansion. In some cases, an additional transmembrane protein is encoded by an extra gene preceding the TM. This gene is sometimes referred to as SH but differs from the SH of jeilongviruses both in length and sequence composition. The newly proposed genus *Parajeilongvirus* includes the established (now proposed to be renamed) species *Parajeilongvirus miniopteri*, *Parajeilongvirus madagascarense*, *Parajeilongvirus comorosense* and *Parajeilongvirus erinacei*, as well as 14 newly proposed species (see Table 1, Figure 1). The creation of a separate genus to harbor the bat-borne jeilongviruses is also in accordance with previous suggestions to create a new paramyxovirid genus ‘*Shaanvirus’* (Wu et al, 2016; Noh et al, 2018; Jang et al, 2020; Wells et al, 2022)   + ***Parahenipavirus***, in analogy with the genus *Parajeilongvirus*, proposed to be created to separate the distinct rodent-/shrew-borne and bat-borne clades within the genus *Henipavirus*. The branch lengths of these two clades, albeit longer than those of the genera *Jeilongvirus* and *Parajeilongvirus*, also do not meet the current cut-off for minimal intergenus divergence (see Figure 1). However, the clades are monophyletic and members of the two clades can be distinguished from each other by their host association as well as differences in genome organization. Specifically, members of the rodent-/shrew-borne clade, now recognized as the genus *Parahenipavirus*, have an extra ORF contained within the F gene that encodes a transmembrane protein. The newly proposed genus *Parahenipavirus* is proposed to include the established species *Parahenipavirus* *mojiangense* as well as 10 new species (see Table 1, Figure 1).   + ***Paramorbillivirus***, in analogy with the genera *Parajeilongvirus* and *Parahenipavirus*, proposed to be created to separate the distinct rodent-borne clade from the rest of the *Morbillivirus* genus. Although the branch length of this clade also fails to meet the current cut-off for minimal intergenus divergence (see Figure 1), it exceeds that of the genus *Parajeilongvirus*. Furthermore, the clade is monophyletic, has the same host association as the genera *Parahenipavirus* and *Jeilongvirus* and some, but not all, of its members are characterized by the presence of an additional ORF encoding a transmembrane protein. The newly proposed genus *Paramorbillivirus* would include four new species (see Table 1, Figure 1). * Five new subfamilies are proposed to be created:   + To harbor the three currently unassigned fish-associated genera (*Cynoglossusvirus*, *Hoplichthysvirus,* and *Scoliodonvirus*): ***Glossavirinae***, ***Ichthysvirinae***, and ***Skoliovirinae*** respectively.   + ***Kamposvirinae***, to harbor the newly proposed genus *Hippocavirus* (see above).   + ***Feraresvirinae***, to harbor the distinct genera *Respirovirus*, *Ferlavirus*, and *Aquaparamyxovirus*, not only based on branch lengths but also on shared pathological signs caused by the different viruses within this subfamily.   For a list of the newly proposed subfamilies, genera and species, please refer to **Table 1** and **Figure 1**. |

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| **Table 1:** List with newly proposed species and etymology. | | | | |
| **Subfamily** | **Genus** | **New species** | **Name Origin** | **Virus** |
| *Avulavirinae* | *Metaavulavirus* | *Metaavulavirus calidris* | Named using the singular genitive of the genus name *Calidris* | avian metaavulavirus 6 |
| *Avulavirinae* | *Metaavulavirus* | *Metaavulavirus bangorense* | Named after the city Bangor, Northern Ireland | avian paramyxovirus 2 |
| *Avulavirinae* | *Metaavulavirus* | *Metaavulavirus procarduelis* | Named using the singular genitive of the genus name *Procarduelis* | avian metaavulavirus 2 |
| *Avulavirinae* | *Orthoavulavirus* | *Orthoavulavirus taiwanense* | Named after Taiwan | avian orthoavulavirus 12 |
| *Avulavirinae* | *Orthoavulavirus* | *Orthoavulavirus arenariae* | Named using the singular genitive of the genus name *Arenaria* | orthoavulavirus sp. |
| *Avulavirinae* | *Paraavulavirus* | *Paraavulavirus neophemae* | Named using the singular genitive of the genus name *Neophema* | avian paramyxovirus 3 |
| *Feraresvirinae* | *Respirovirus* | *Respirovirus rupicaprae* | Named using the singular genitive of the genus name *Rupicapra* | chamois respirovirus |
| *Feraresvirinae* | *Respirovirus* | *Respirovirus henanense* | Named after the province Hénán, China | porcine respirovirus 2 |
| *Kamposvirinae* | *Hippocavirus* | *Hippocavirus hippocampi* | Named using the singular genitive of the genus name *Hippocampus* | Hippocampus erectus paramyxovirus 1 |
| *Orthoparamyxovirinae* | *Bovinavirus* | *Bovinavirus bovis* | Named using the singular genitive of the genus name *Bos* | bovine narmovirus 1 |
| *Orthoparamyxovirinae* | *Henipavirus* | *Henipavirus angavokelyense* | Named after mount Angavokely, Madagascar | Angavokely henipavirus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus pajuense* | Named after the city Paju, South Korea | Paju Apodemus paramyxovirus 1 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus yeoncheonense* | Named after the county Yeoncheon, South Korea | Paju Apodemus paramyxovirus 2 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus oujiangense* | Named after the river Oujiang flowing through the city of Wēnzhōu, China | Wēnzhōu Rattus norvegicus jeilongvirus 1 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus niviventris* | Named using the singular genitive of the genus name *Niviventer* | Lóngquán Niviventer niviventer jeilongvirus 1 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus longquanense* | Named after the city Lóngquán, China | Lóngquán Niviventer fulvescens jeilongvirus 1 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus lishuiense* | Named after the prefecture-level city Líshǔi, China | Lóngquán Niviventer fulvescens jeilongvirus 2 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus taichungense* | Named after the city Taichung, Taiwan | Wǔfēng Rattus nitidus jeilongvirus 1 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus chaetodipodis* | Named using the singular genitive of the genus name *Chaetodipus* | Paramyxoviridae sp. virus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus neotomae* | Named using the singular genitive of the genus name *Neotoma* | Paramyxoviridae sp. virus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus microti* | Named using the singular genitive of the genus name *Microtus* | Ninove microtus virus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus nzerekorense* | Named after the Nzérékoré region, Guinea | Méliandou mastomys virus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus praomysis* | Named using the singular genitive of the genus name *Praomys* | Méliandou praomys virus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus gueckedouense* | Named after the Guéckédou prefecture, Guinea | Memana virus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus meliandouense* | Named after the town Méliandou, Guinea | Méliandou lophuromys virus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus merionis* | Named using the singular genitive of the genus name *Meriones* | gerbil paramyxovirus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus eothenomysis* | Named using the singular genitive of the genus name *Eothenomys* | Wǔfēng Eothenomys melanogaster jeilongvirus 1 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus typhlomysis* | Named using the singular genitive of the genus name *Typhlomys* | Wǔfēng Typhlomys cinereus jeilongvirus 1 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus wufengense* | Named after the district Wǔfēng, China | Wǔfēng Apodemus chevrieri jeilongvirus 1 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus ratti* | Named using the singular genitive of the genus name *Rattus* | Wēnzhōu Rattus losea jeilongvirus 2 |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus ochotonae* | Named using the singular genitive of the genus name *Ochotona* | Ochotona cansus jeilongvirus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus sichuanense* | Named after the province Sìchuān, China | Eothenomys eva jeilongvirus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus ninovense* | Named after the town Ninove, Belgium | ninapo virus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus winnikense* | Named after the Belgian town Denderwindeke, also known as 'Winnik' in the local dialect | denotus virus |
| *Orthoparamyxovirinae* | *Jeilongvirus* | *Jeilongvirus mastomysis* | Named using the singular genitive of the genus name *Mastomys* | ninomys virus |
| *Orthoparamyxovirinae* | *Morbillivirus* | *Morbillivirus suis* | Named using the singular genitive of the genus name *Sus* | porcine morbillivirus |
| *Orthoparamyxovirinae* | *Morbillivirus* | *Morbillivirus myotis* | Named using the singular genitive of the genus name *Myotis* | Myotis bat morbillivirus |
| *Orthoparamyxovirinae* | *Morbillivirus* | *Morbillivirus phyllostomi* | Named using the singular genitive of the genus name *Phyllostomus* | Phyllostomus bat morbillivirus |
| *Orthoparamyxovirinae* | *Narmovirus* | *Narmovirus ninovense* | Named after the town Ninove, Belgium | denestis virus |
| *Orthoparamyxovirinae* | *Narmovirus* | *Narmovirus microti* | Named using the singular genitive of the genus name *Microtus* | denalis virus |
| *Orthoparamyxovirinae* | *Narmovirus* | *Narmovirus meliandouense* | Named after the town Meliandou, Guinea | meleucus virus |
| *Orthoparamyxovirinae* | *Parahenipavirus* | *Parahenipavirus wenzhouense* | Named after the city Wenzhou, China | Wēnzhōu Apodemus agrarius henipavirus 1 |
| *Orthoparamyxovirinae* | *Parahenipavirus* | *Parahenipavirus gamakense* | Named after Kamak Mountain [Gamaksan], South Korea | Gamak virus |
| *Orthoparamyxovirinae* | *Parahenipavirus* | *Parahenipavirus daeryongense* | Named after Daeryong Mountain, South Korea | Daeryong virus, Jīngmén Crocidura shantungensis henipavirus 2 |
| *Orthoparamyxovirinae* | *Parahenipavirus* | *Parahenipavirus meliandouense* | Named after the town Méliandou, Guinea | melian virus |
| *Orthoparamyxovirinae* | *Parahenipavirus* | *Parahenipavirus winnikense* | Named after the Belgian town Denderwindeke, also known as 'Winnik' in the local dialect | denwin virus |
| *Orthoparamyxovirinae* | *Parahenipavirus* | *Parahenipavirus jingmenense* | Named after the city Jīngmén, China | Jīngmén Crocidura shantungensis henipavirus 1 |
| *Orthoparamyxovirinae* | *Parahenipavirus* | *Parahenipavirus chodsigoae* | Named using the singular genitive of the genus name *Chodsigoa* | Wǔfēng Chodsigoa smithii henipavirus 1 |
| *Orthoparamyxovirinae* | *Parahenipavirus* | *Parahenipavirus crocidurae* | Named using the singular genitive of the genus name *Crocidura* | Wǔfēng Crocidura attenuata henipavirus 1, Crocidura tanakae henipavirus |
| *Orthoparamyxovirinae* | *Parahenipavirus* | *Parahenipavirus langyaense* | Named after the historical LángyáCommandery, China | Lángyá virus |
| *Orthoparamyxovirinae* | *Parahenipavirus* | *Parahenipavirus soricis* | Named using the singular genitive of the genus name *Sorex* | ninorex virus |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus carolliae* | Named using the singular genitive of the genus name *Carollia* | Carollia bat paramyxovirus |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus hipposideri* | Named using the singular genitive of the genus name *Hipposideros* | Hipposideros bat paramyxovirus |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus diaemi* | Named using the singular genitive of the genus name *Diaemus* | Diaemus bat paramyxovirus |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus brazilense* | Named after Brazil | Diaemus bat paramyxovirus |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus hubeiense* | Named after the province Húběi, China | Jīngmén Miniopterus schreibersii paramyxovirus 1 |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus rhinolophi* | Named using the singular genitive of the genus name *Rhinolophus* | Wǔfēng Rhinolophus pearsonii paramyxovirus 1 |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus desmodi* | Named using the singular genitive of the genus name *Desmodus* | Boe paramyxovirus |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus hainanense* | Named after the province Hǎinán, China | bat paramyxovirus |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus myotis* | Named using the singular genitive of the genus name Myotis | Wǔfēng Myotis altarium paramyxovirus 1 |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus jingmenense* | Named after the city Jīngmén, China | Jīngmén Myotis davidii paramyxovirus 1 |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus wenzhouense* | Named after the city Wēnzhō, China | Wēnzhōu Myotis davidii paramyxovirus 1 |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus zhejiangense* | Named after the province Zhèjiāng, China | WēnzhōuMyotis laniger paramyxovirus 2 |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus pipistrelli* | Named using the singular genitive of the genus name *Pipistrellus* | piparella virus |
| *Orthoparamyxovirinae* | *Parajeilongvirus* | *Parajeilongvirus plecoti* | Named using the singular genitive of the genus name *Plecotus* | plecomyxo virus |
| *Orthoparamyxovirinae* | *Paramorbillivirus* | *Paramorbillivirus pueyrredonense* | Named after Lago Pueyrredón, Argentina | Raton olivaceo morbillivirus |
| *Orthoparamyxovirinae* | *Paramorbillivirus* | *Paramorbillivirus berylmysis* | Named using the singular genitive of the genus name *Berylmys* | Lóngquán Berylmys bowersi morbillivirus 1 |
| *Orthoparamyxovirinae* | *Paramorbillivirus* | *Paramorbillivirus niviventris* | Named using the singular genitive of the genus name *Niviventer* | Wǔfēng Niviventer fulvescens morbillivirus 1 |
| *Orthoparamyxovirinae* | *Paramorbillivirus* | *Paramorbillivirus gierlense* | Named after the town Gierle, Belgium | Gierle apodemus virus |
| *Rubulavirinae* | *Orthorubulavirus* | *Orthorubulavirus rhinolophi* | Named using the singular genitive of the genus name *Rhinolophus* | Wǔfēng Rhinolophus sinicus rubulavirus 1 |
| *Rubulavirinae* | *Pararubulavirus* | *Pararubulavirus eidoli* | Named using the singular genitive of the genus name *Eidolon* | Achimota pararubulavirus 3 |

**Supporting evidence**

**Figure 1**: Overview of the revised *Paramyxoviridae* taxonomy matched with a Bayesian maximum clade credibility summary tree. Numbers next to selected nodes indicate the posterior support, which can be interpreted as the probability of the clade being true given the data, the model and the parameter priors. Only posterior values lower than 1 are shown.The tree is drawn to scale, with branch lengths expressed in the number of substitutions per site.

**Afbeelding met tekst, diagram, Plan, ontwerp

Automatisch gegenereerde beschrijving**

**Table 2:** NCBI BLASTp top hit identities (in %) for the viruses of each of the paramyxovirid species.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Query** | **Best Hit** | **N** | **P** | **M** | **F** | **RBP** | **L** | **Average** |
| JN689227.1 | MZ328277.1 | 85.632 | 78.024 | 94.706 | 92.164 | 85.831 | **89.319** | 87.613 |
| MZ328277.1 | DQ100461.1 | 83.525 | 75.514 | 92.059 | 88.419 | 86.649 | **89.912** | 86.013 |
| OM030314.1 | OM030317.1 | 85.366 | 68.601 | 97.941 | 91.681 | 83.703 | **88.158** | 85.908 |
| OM030317.1 | OM030314.1 | 85.366 | 68.601 | 97.941 | 91.681 | 83.703 | **88.158** | 85.908 |
| DQ100461.1 | MZ328277.1 | 83.525 | 74.597 | 92.059 | 88.419 | 86.649 | **89.912** | 85.860 |
| MT180123.1 | KT215610.1 | 89.126 | 72.819 | 92.000 | 84.815 | 83.624 | **89.217** | 85.267 |
| MZ574407.1 | OM030317.1 | 84.991 | 64.505 | 95.882 | 91.327 | 85.918 | **87.167** | 84.965 |
| HM159995.1 | KT071755.1 | 93.873 | 69.136 | 91.057 | 85.955 | 85.962 | **82.087** | 84.678 |
| KF278639.1 | OM101125.1 | 85.714 | 64.183 | 90.294 | 90.353 | 86.035 | **90.110** | 84.448 |
| OM101125.1 | KF278639.1 | 85.714 | 64.183 | 90.294 | 90.353 | 86.035 | **90.110** | 84.448 |
| EF569970.1 | AB759118.1 | 94.409 | 63.927 | 90.984 | 87.619 | 81.077 | **86.236** | 84.042 |
| AF212302.2 | AF017149.3 | 92.105 | 66.064 | 91.520 | 89.179 | 78.738 | **86.586** | 84.032 |
| AF017149.3 | AF212302.2 | 92.105 | 66.064 | 91.520 | 89.179 | 78.738 | **86.586** | 84.032 |
| JX857409.1 | OK044775.1 | 82.510 | 75.610 | 90.751 | 75.583 | 93.576 | **85.727** | 83.960 |
| OK044775.1 | JX857409.1 | 82.510 | 75.610 | 90.751 | 75.583 | 93.576 | **85.727** | 83.960 |
| AB759118.1 | EF569970.1 | 94.409 | 63.927 | 90.984 | 85.662 | 81.077 | **86.236** | 83.716 |
| KT215610.1 | MT180123.1 | 89.126 | 58.479 | 92.000 | 84.815 | 83.624 | **89.217** | 82.877 |
| AF014953.1 | KC802221.1 | 85.660 | 76.680 | 91.940 | 77.349 | 74.172 | **89.968** | 82.628 |
| KC802221.1 | AF014953.1 | 85.660 | 76.680 | 91.940 | 77.349 | 74.172 | **89.968** | 82.628 |
| KY370098.1 | OQ438284.1 | 83.774 | 77.049 | 94.118 | 88.376 | 59.687 | **91.205** | 82.368 |
| OQ438284.1 | KY370098.1 | 83.774 | 77.049 | 94.118 | 88.376 | 59.687 | **91.205** | 82.368 |
| KP271124.1 | AF298895.2 | 90.173 | 71.948 | 91.467 | 85.907 | 73.187 | **79.595** | 82.046 |
| AF298895.2 | KP271124.1 | 90.173 | 71.948 | 91.467 | 85.907 | 73.187 | **79.568** | 82.042 |
| EU326526.1 | AF178654.1 | 85.631 | 63.773 | 92.308 | 83.015 | 76.748 | **89.028** | 81.751 |
| MZ328283.1 | MZ328277.1 | 78.178 | 66.734 | 92.059 | 85.978 | 82.378 | **83.678** | 81.501 |
| AF178654.1 | EU326526.1 | 85.631 | 63.773 | 92.308 | 81.447 | 76.748 | **89.028** | 81.489 |
| OQ438285.1 | OK623355.1 | 79.811 | 65.577 | 90.882 | 86.852 | 79.283 | **85.153** | 81.260 |
| OK623355.1 | OQ438285.1 | 79.811 | 65.326 | 90.882 | 86.852 | 79.283 | **85.153** | 81.218 |
| OM030335.1 | OM030336.1 | 91.160 | 67.901 | 89.706 | 78.887 | 70.994 | **85.695** | 80.724 |
| OM030336.1 | OM030335.1 | 91.160 | 67.901 | 89.706 | 78.887 | 70.994 | **85.695** | 80.724 |
| MG203877.1 | MG203878.1 | 87.976 | 61.155 | 91.667 | 80.916 | 74.329 | **87.159** | 80.534 |
| MG203878.1 | MG203877.1 | 86.693 | 61.155 | 91.667 | 78.467 | 74.329 | **87.159** | 79.912 |
| MG573140.1 | OK623364.1 | 77.620 | 66.255 | 91.716 | 81.648 | 71.406 | **85.872** | 79.086 |
| MZ328279.1 | MZ328280.1 | 75.514 | 66.258 | 90.588 | 85.531 | 70.264 | **85.492** | 78.941 |
| MT823459.1 | OM030332.1 | 83.902 | 61.237 | 92.059 | 81.296 | 71.108 | **83.044** | 78.774 |
| MT511667.1 | MZ312422.1 | 78.967 | 66.469 | 92.239 | 80.519 | 66.998 | **86.441** | 78.606 |
| MZ312422.1 | MT511667.1 | 78.967 | 66.469 | 92.239 | 80.519 | 66.998 | **86.441** | 78.606 |
| AB195968.1 | LS992584.1 | 83.689 | 56.294 | 89.080 | 77.941 | 75.393 | **87.551** | 78.325 |
| LS992584.1 | AB195968.1 | 83.626 | 56.294 | 89.080 | 77.941 | 75.393 | **87.551** | 78.314 |
| EU403085.1 | EU782025.1 | 89.640 | 58.205 | 93.333 | 70.943 | 72.743 | **83.106** | 77.995 |
| EU338414.1 | KT071755.1 | 89.278 | 56.204 | 84.011 | 81.538 | 78.201 | **78.402** | 77.939 |
| KT071755.1 | EU338414.1 | 89.278 | 56.204 | 84.011 | 81.538 | 78.201 | **78.402** | 77.939 |
| OK623353.1 | OK623354.1 | 81.468 | 57.450 | 93.235 | 79.623 | 69.094 | **86.626** | 77.916 |
| OK623354.1 | OK623353.1 | 81.468 | 57.450 | 93.235 | 79.623 | 69.094 | **86.626** | 77.916 |
| EU782025.1 | EU403085.1 | 88.621 | 58.205 | 93.333 | 70.943 | 72.743 | **83.203** | 77.841 |
| OK623364.1 | MG573140.1 | 77.620 | 66.255 | 91.716 | 82.792 | 60.266 | **85.872** | 77.420 |
| OQ438287.1 | MZ328279.1 | 68.078 | 67.004 | 87.647 | 81.404 | 71.646 | **84.141** | 76.653 |
| AF457102.1 | AB195968.1 | 85.294 | 55.017 | 86.494 | 70.888 | 73.171 | **86.594** | 76.243 |
| OM030332.1 | MT823459.1 | 83.902 | 61.237 | 92.059 | 81.296 | 50.867 | **83.044** | 75.401 |
| MZ328275.1 | OM101125.1 | 76.449 | 49.570 | 89.706 | 79.284 | 71.959 | **81.994** | 74.827 |
| MZ328280.1 | MZ328279.1 | 75.514 | 66.258 | 90.588 | 85.531 | 42.286 | **85.492** | 74.278 |
| AB016162.1 | X98291.3 | 75.238 | 61.188 | 88.955 | 79.596 | 58.746 | **81.677** | 74.233 |
| X98291.3 | AB016162.1 | 75.238 | 61.188 | 88.955 | 79.596 | 58.746 | **81.677** | 74.233 |
| KC333050.1 | MZ802804.1 | 79.919 | 53.125 | 84.615 | 75.143 | 69.707 | **73.512** | 72.670 |
| MZ802804.1 | KC333050.1 | 79.919 | 53.125 | 84.615 | 75.143 | 69.707 | **73.512** | 72.670 |
| MZ574409.1 | OK623354.1 | 74.128 | 45.302 | 90.588 | 76.667 | 64.848 | **83.187** | 72.453 |
| AY562991.1 | KY511044.1 | 78.004 | 54.831 | 76.099 | 76.336 | 70.388 | **76.821** | 72.080 |
| OK623360.1 | OK623359.1 | 79.159 | 58.453 | 90.294 | 66.605 | 57.369 | **78.978** | 71.810 |
| OK623359.1 | OK623360.1 | 79.159 | 59.025 | 90.294 | 65.818 | 57.369 | **78.978** | 71.774 |
| KY511044.1 | AY562991.1 | 77.800 | 54.831 | 76.099 | 74.677 | 70.388 | **76.821** | 71.769 |
| MF594598.1 | EU910942.1 | 81.838 | 52.703 | 77.473 | 71.538 | 69.788 | **72.480** | 70.970 |
| EU910942.1 | MF594598.1 | 80.368 | 52.477 | 77.473 | 71.538 | 69.788 | **72.480** | 70.687 |
| MT823463.1 | MG573140.1 | 74.880 | 60.700 | 86.647 | 75.287 | 46.207 | **79.751** | 70.579 |
| MZ753810.1 | MZ312426.1 | 77.843 | 44.715 | 89.855 | 74.904 | 65.210 | **70.816** | 70.557 |
| OQ236153.1 | OQ438285.1 | 72.494 | 48.868 | 82.353 | 76.753 | 66.304 | **76.398** | 70.528 |
| MF943130.1 | OK623359.1 | 77.863 | 53.805 | 88.824 | 63.904 | 60.480 | **78.155** | 70.505 |
| MZ926778.1 | AY562991.1 | 79.108 | 54.791 | 74.725 | 72.137 | 66.451 | **75.511** | 70.454 |
| OK623362.1 | OK623361.1 | 66.788 | 51.919 | 84.706 | 78.598 | 61.979 | **78.192** | 70.364 |
| MZ328288.1 | MG203877.1 | 78.599 | 49.098 | 86.325 | 69.541 | 58.632 | **79.945** | 70.357 |
| MZ312426.1 | MZ753810.1 | 77.843 | 44.715 | 89.855 | 73.234 | 65.210 | **70.816** | 70.279 |
| OK623361.1 | OK623362.1 | 66.788 | 51.919 | 84.706 | 77.022 | 62.172 | **78.207** | 70.136 |
| MG516455.1 | OK623355.1 | 78.555 | 57.714 | 80.000 | 77.509 | 45.695 | **78.473** | 69.658 |
| KY452443.1 | KY452442.1 | 81.377 | 53.191 | 75.068 | 66.795 | 66.438 | **74.784** | 69.609 |
| KY452442.1 | KY452443.1 | 81.377 | 53.100 | 75.068 | 65.492 | 66.438 | **74.784** | 69.377 |
| MG230624.1 | MG203877.1 | 78.958 | 45.766 | 85.632 | 67.897 | 56.485 | **78.304** | 68.840 |
| X64275.1 | X57559.1 | 70.567 | 65.063 | 71.883 | 65.743 | 62.298 | **77.235** | 68.798 |
| X57559.1 | X64275.1 | 70.567 | 65.063 | 71.883 | 65.743 | 62.298 | **77.103** | 68.776 |
| GU128082.1 | KF774436.1 | 83.301 | 59.701 | 75.733 | 61.770 | 57.487 | **72.127** | 68.353 |
| KF774436.1 | GU128082.1 | 83.301 | 59.701 | 75.733 | 61.770 | 57.487 | **72.127** | 68.353 |
| JX112711.1 | AF298895.2 | 79.541 | 57.761 | 84.946 | 66.004 | 54.878 | **64.763** | 67.982 |
| OL409126.1 | JN689227.1 | 60.766 | 53.719 | 81.176 | 72.593 | 60.516 | **77.289** | 67.677 |
| OM030338.1 | MZ328278.1 | 69.965 | 57.637 | 83.086 | 67.593 | 51.261 | **75.409** | 67.492 |
| MZ328278.1 | OM030338.1 | 69.877 | 57.637 | 83.086 | 67.593 | 51.261 | **75.409** | 67.477 |
| OM030330.1 | OQ438285.1 | 72.261 | 50.095 | 82.059 | 77.905 | 42.305 | **79.452** | 67.346 |
| AJ849636.2 | AB016162.1 | 73.485 | 47.255 | 85.329 | 73.247 | 48.020 | **75.240** | 67.096 |
| OM030333.1 | OM030334.1 | 70.798 | 53.427 | 80.000 | 63.218 | 56.348 | **78.446** | 67.040 |
| AJ608288.1 | AB016162.1 | 74.102 | 48.450 | 84.478 | 74.259 | 44.372 | **73.984** | 66.608 |
| OM030334.1 | OM030333.1 | 67.836 | 53.427 | 80.000 | 63.218 | 56.348 | **78.446** | 66.546 |
| LC041132.1 | KC333050.1 | 74.648 | 50.856 | 73.626 | 69.674 | 59.935 | **65.860** | 65.767 |
| OK623363.1 | OM030338.1 | 72.331 | 52.419 | 81.306 | 62.774 | 49.399 | **73.844** | 65.346 |
| MG573141.1 | OK623361.1 | 62.222 | 46.421 | 83.529 | 69.187 | 55.946 | **73.488** | 65.132 |
| JX051319.1 | GU128081.1 | 76.864 | 54.478 | 74.734 | 61.034 | 49.828 | **69.934** | 64.479 |
| GU128081.1 | JX051319.1 | 76.864 | 54.478 | 74.734 | 59.693 | 49.828 | **69.934** | 64.255 |
| OQ438289.1 | OM030336.1 | 63.793 | 39.506 | 82.749 | 67.736 | 59.174 | **69.877** | 63.806 |
| AY900001.1 | KY370098.1 | 54.991 | 46.640 | 82.941 | 69.853 | 50.000 | **74.032** | 63.076 |
| JX051320.1 | MT062420.1 | 78.058 | 49.383 | 75.532 | 54.420 | 52.650 | **67.909** | 62.992 |
| MT062420.1 | JX051320.1 | 78.058 | 49.383 | 75.532 | 54.420 | 52.650 | **67.909** | 62.992 |
| OK623365.1 | AY286409.1 | 76.526 | 49.077 | 82.059 | 55.373 | 37.959 | **71.429** | 62.071 |
| AB543336.1 | MZ328287.1 | 81.182 | 40.334 | 65.526 | 60.846 | 46.384 | **69.865** | 60.690 |
| AY286409.1 | OK623365.1 | 67.126 | 48.897 | 82.059 | 55.373 | 37.959 | **71.429** | 60.474 |
| MZ328284.1 | OK623356.1 | 63.296 | 47.082 | 74.850 | 65.421 | 39.769 | **71.859** | 60.380 |
| OK623356.1 | MZ328284.1 | 63.296 | 47.082 | 74.850 | 65.056 | 39.769 | **71.859** | 60.319 |
| FJ231524.1 | MK677430.1 | 73.593 | 37.740 | 64.463 | 57.611 | 65.775 | **61.203** | 60.064 |
| MK677430.1 | FJ231524.1 | 71.908 | 37.740 | 64.463 | 57.663 | 65.775 | **61.203** | 59.792 |
| MZ328287.1 | AB543336.1 | 74.805 | 40.952 | 65.526 | 60.846 | 46.384 | **69.865** | 59.730 |
| MZ312424.1 | MZ753810.1 | 66.092 | 35.217 | 83.430 | 54.797 | 52.604 | **60.602** | 58.790 |
| KY452444.1 | KY452443.1 | 68.031 | 48.294 | 58.678 | 56.840 | 54.021 | **66.167** | 58.672 |
| MZ328290.1 | OQ438288.1 | 68.825 | 37.320 | 69.714 | 61.481 | 42.407 | **69.464** | 58.202 |
| MW557651.1 | AF014953.1 | 68.321 | 43.028 | 74.030 | 56.182 | 31.776 | **75.298** | 58.106 |
| MZ312421.1 | MG230624.1 | 59.725 | 39.499 | 77.937 | 57.524 | 43.937 | **68.679** | 57.884 |
| HM147142.3 | EU338414.1 | 74.187 | 39.667 | 56.369 | 62.619 | 51.521 | **61.054** | 57.570 |
| MH900516.1 | EU156171.1 | 48.491 | 34.561 | 68.588 | 62.637 | 56.437 | **74.490** | 57.534 |
| EU156171.1 | MH900516.1 | 48.399 | 34.380 | 68.588 | 62.637 | 56.690 | **74.490** | 57.531 |
| OQ438288.1 | OM030336.1 | 67.213 | 32.645 | 69.516 | 61.686 | 41.735 | **69.595** | 57.065 |
| MW579602.1 | OM030338.1 | 56.920 | 35.950 | 74.481 | 62.004 | 47.619 | **65.038** | 57.002 |
| OL630969.1 | MG203877.1 | 57.505 | 37.769 | 77.143 | 54.461 | 43.581 | **69.704** | 56.694 |
| MF033136.2 | EU338414.1 | 68.966 | 37.472 | 53.659 | 64.137 | 53.501 | **59.661** | 56.233 |
| FJ215863.2 | EU338414.1 | 71.552 | 37.713 | 52.304 | 64.015 | 48.944 | **59.332** | 55.643 |
| OK210080.1 | OK623363.1 | 63.575 | 31.377 | 74.481 | 56.415 | 39.394 | **63.182** | 54.737 |
| KU672593.1 | MT062420.1 | 78.824 | 45.161 | 61.580 | 48.752 | 32.620 | **60.771** | 54.618 |
| KX932454.2 | HM147142.3 | 71.397 | 38.283 | 52.011 | 59.735 | 45.739 | **60.352** | 54.586 |
| FJ362497.2 | AY286409.1 | 68.119 | 38.306 | 70.796 | 49.905 | 31.379 | **66.410** | 54.153 |
| OM030331.1 | MT823463.1 | 53.202 | 35.318 | 81.250 | 53.906 | 36.957 | **63.066** | 53.950 |
| EF095490.1 | BK005918.1 | 67.910 | 38.519 | 57.182 | 49.615 | 44.930 | **60.897** | 53.176 |
| OQ438286.1 | OM030316.1 | 58.929 | 32.474 | 74.706 | 54.064 | 29.412 | **68.536** | 53.020 |
| AF052755.1 | X57559.1 | 69.154 | 42.394 | 49.337 | 47.719 | 46.858 | **61.915** | 52.896 |
| OM030316.1 | OQ438286.1 | 58.929 | 29.448 | 74.706 | 53.137 | 30.000 | **68.536** | 52.459 |
| MZ312420.1 | OM030334.1 | 56.500 | 34.799 | 67.582 | 51.498 | 43.640 | **58.492** | 52.085 |
| GU206351.1 | EF569970.1 | 61.489 | 32.321 | 54.918 | 55.263 | 56.552 | **50.329** | 51.812 |
| MN561699.1 | OQ438288.1 | 58.087 | 34.917 | 64.957 | 54.120 | 33.877 | **62.206** | 51.361 |
| BK005918.1 | EF095490.1 | 56.410 | 38.575 | 57.182 | 49.615 | 44.930 | **60.897** | 51.268 |
| OK210078.1 | MG573140.1 | 54.028 | 38.348 | 70.145 | 51.257 | 29.403 | **62.305** | 50.914 |
| HQ660129.1 | AF017149.3 | 65.783 | 35.484 | 61.834 | 54.766 | 29.714 | **53.354** | 50.156 |
| GU128080.1 | MT062420.1 | 71.021 | 41.707 | 56.800 | 42.424 | 28.495 | **60.202** | 50.108 |
| OQ236117.1 | OK623363.1 | 61.347 | 30.816 | 66.469 | 48.211 | 31.894 | **58.193** | 49.488 |
| AB040874.1 | AF052755.1 | 63.825 | 37.626 | 42.162 | 47.579 | 44.621 | **58.554** | 49.061 |
| JQ001776.1 | AF017149.3 | 61.736 | 33.846 | 63.663 | 44.340 | 30.566 | **56.857** | 48.501 |
| BK061229.1 | MZ328284.1 | 54.675 | 31.481 | 63.772 | 52.015 | 24.286 | **62.810** | 48.173 |
| KX258200.1 | GU206351.1 | 57.634 | 30.425 | 49.311 | 48.790 | 52.951 | **48.652** | 47.961 |
| MZ328285.1 | MZ328284.1 | 51.016 | 35.119 | 55.828 | 54.579 | 21.990 | **60.555** | 46.515 |
| JQ411014.1 | MZ312422.1 | 54.512 | 33.981 | 60.119 | 44.492 | 21.483 | **56.825** | 45.235 |
| JQ886184.1 | EU338414.1 | 59.513 | 31.724 | 38.525 | 45.418 | 42.632 | **48.604** | 44.403 |
| ON613535.1 | OM030316.1 | 52.941 | 25.592 | 52.011 | 42.213 | 21.070 | **53.587** | 41.236 |
| ON861830.1 | OK623360.1 | 53.606 | 30.337 | 54.054 | 31.263 | 21.148 | **51.303** | 40.285 |
| EU877976.1 | EU403085.1 | 51.416 | 37.500 | 35.475 | 34.690 | 40.949 | **41.670** | 40.283 |
| AF079780.2 | AY286409.1 | 42.958 | 31.937 | 53.293 | 38.950 | 20.667 | **50.352** | 39.693 |
| JQ697837.1 | MZ328284.1 | 47.117 | 28.228 | 46.970 | 39.831 | 18.996 | **47.659** | 38.134 |
| AY141760.2 | EU156171.1 | 27.295 | 0\* | 36.735 | 41.805 | 42.127 | **43.521** | 31.914 |
| OQ030201.1 | OK623364.1 | 25.513 | 0\* | 32.698 | 35.271 | 29.032 | **41.826** | 27.390 |
| MG600058.1 | MG573141.1 | 24.280 | 0\* | 25.937 | 33.398 | 21.606 | **35.565** | 23.464 |
| MG600057.1 | OM030334.1 | 20.863 | 0\* | 0\* | 20.502 | 0\* | **32.179** | 12.257 |
| MG600059.1 | MG600058.1 | 0\* | 0\* | 0\* | 22.053 | 0\* | **30.285** | 8.723 |
| MG600062.1 | MG600059.1 | 0\* | 0\* | 0\* | 0\* | 0\* | **30.041** | 5.007 |

\*No significant similarity detected, values manually set to 0.

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