

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Rename the existing genus *Platrhavirus* (as *Alphaplatrhavirus*) and create 12 new species in the renamed genus, create the new genus *Betaplatrhavirus* including 12 new species, and create the new genus *Gammaplatrhavirus* including 6 new species (*Mononegavirales*: *Rhabdoviridae*) | |
| **Code assigned:** | 2024.014.Ac.v3.Platrhavirus\_2ng\_30nsp |

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**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:** |
| *Rhabdoviridae* SG |

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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** |
| *Rhabdoviridae* SG | 15 | 0 | 0 |
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| **Submission date:** | 09/06/2024 |

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

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept | **X** |
| 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| W - Withdrawn |  |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:** |
| Please Include renaming the existing 6 species in the genus to the newly proposed genus name. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
| The species have been renamed and included in the excel module.  Version 3 contains a typographical correction to the epithet nodulosus. |

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| **Revision date:** | 24/08/2024 |

**Part 2:** **GENERAL PROPOSAL**

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| **Abstract for General Proposal:** |

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

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| **Name of accompanying Excel module:** |
| 2024.014.Ac.v3.Platrhavirus\_2ng\_30nsp.xlsx |

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon | **X** | 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 X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Genus and species (*Mononegavirales*: *Rhabdoviridae*)  *Description of current taxonomy*:  The family *Rhabdoviridae* currently comprises four subfamilies and one additional genus (*Platrhavirus*) including 6 species.  *Proposed* *taxonomic change(s):*  Rename the existing genus *Platrhavirus* (as *Alphaplatrhavirus*) and create 12 new species in the renamed genus, and create two new genera (*Betaplatrhavirus* and *Gammaplatrhavirus*) including 18 new species for viruses detected by metagenomic sequencing in cestode or trematode worms (Platyhelminthes) or in the feces or visceral organs of animals (mammals, fish or crustaceans) that appear to have been infested with worms.  *Justification*:  The viruses cluster phylogenetically with others in the existing or proposed genera in ML trees inferred using L protein sequences. All new species in existing genera meet established demarcation criteria. The proposed renamed and new genera for viruses are well-separated phylogenetically from each other and from other rhabdoviruses. |

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| **Text of Taxonomy proposal:**   1. **Rename the genus *Platrhavirus* (as *Alphaplatrhavirus*)**   The genus *Platrhavirus* comprises six species for viruses detected by metagenomic sequencing in flat worms (Platyhelminthes) of various species, or in the feces of a fox (*Vulpes vulpes*) [1, 2]. The worms in which platrhaviruses have been detected include trematodes (class Trematoda) and cestodes (class Cestoda) that are known to infest various mammals and fish. It is now evident that rhabdoviruses from two other phylogenetically diverse clades have also been detected in platyhelminths, or in animals (mammals, fish or crustaceans) that appear to have been infested with platyhelminths. We propose to rename the genus *Platrhavirus* as *Alphaplatrhavirus* to accommodate the taxonomic classification of two other genera (*Betaplatrhavirus* and *Gammaplatrhavirus*) for rhabdoviruses from these diverse clades (**Figure 1**).   1. **Create 12 new species in the renamed genus *Alphaplatrhavirus***   Two novel viruses that have recently been detected by metagenomic sequencing of platyhelminths are proposed for classification in the genus *Alphaplatrhavirus*. Dicrocoilium rhabdo-like virus 2 (DicRLV2; strain XJ) was detected in the lanceatum body of lancet liver flukes (*Dicrocoelium dendriticum*) collected in Xinjiang Autonomous Region, China, in 2021. Schistocephalus solidus rhabdovirus (SsolRV; strain SSRVAE) was detected in coracidia of tapeworms (*Schistocephalus solidus*) laboratory-bred in Alaska, USA, in 2018 [3]. These parasites use mollusks or crustaceans as intermediate hosts and infest the visceral organs of the definitive host.  Eight other novel viruses detected by metagenomic sequencing of samples of various visceral organs of bats and shrew collected in China during the winter and early spring of 2016-17 are also proposed for classification in the genus *Alphaplatrhavirus*. Wufeng shrew rhabdovirus 5 (WfSRV5; strain WF\_Ch.smithii\_rhabdo\_1), Wufeng shrew rhabdovirus 7 (WfSRV7; strain WF\_Ch.smithii\_rhabdo\_3), Wufeng shrew rhabdovirus 8 (WfSRV8; strain WF\_Ch.smithii\_rhabdo\_4), and Wufeng shrew rhabdovirus 9 (WfSRV9; strain WF\_Ch.smithii\_rhabdo\_5) were each detected in Smith’s shrew (*Chodsigoa smithii*) collected in Hubei Province [4]. Jingmen bat rhabdovoirus 1 (JmBRV1; strain JM\_My.chinensis\_rhabdo\_1) was detected in a large myotis bat (*Myotis chinensis*) and Jingmen bat rhabdovirus 2 (JmBRV2: strain JM\_My.ricketti\_rhabdo\_1) was detected in a Ricket’s big-footed bat (*Myotis ricketti*), each also collected in Hubei Province [4]. Wenzhou bat rhabdovirus 1 (WzBRV1; strain WZ\_My.laniger\_rhabdo\_1) and Wenzhou bat rhabdovirus 3 (WzBRV3; strain WZ\_My.laniger\_rhabdo\_2) were each detected in Chinese water myotis bats (*Myotis laniger*) collected in Zhejiang Province.  Two other novel viruses detected by metagenomic sequencing of bats and finfish from China are also proposed for classification in the genus *Alphaplatrhavirus*. Rhabdovirus sp. HLGXC14/3 (HLGXCRV) was detected in the intestine of an intermediate roundleaf bat (*Hipposideros larvatus*) collected in Guangxi Autonomous Region, in 2014. Wenling dimarhabdovirus 8 (WlDRV8; strain DHBYCGS131) was detected in a pool of gut liver and gill tissue from a sharpspine skate (*Okamejei acutispina*) collected in Zhejiang Province [5].  We propose that these viruses be assigned to the following new species in the genus *Alphaplatrhavirus:*  *Alphaplatrhavirus dendriticum* (DicRLV2)  *Alphaplatrhavirus solidus* (SsolRV)  *Alphaplatrhavirus wufeng* (WfSRV5)  *Alphaplatrhavirus smithii* (WfSRV7)  *Alphaplatrhavirus chodsigoa* (WfSRV8)  *Alphaplatrhavirus hubei* (WfSRV9)  *Alphaplatrhavirus jingmen* (JmBRV1)  *Alphaplatrhavirus ricketti* (JmBRV2)  *Alphaplatrhavirus wenzhou* (WzBRV1)  *Alphaplatrhavirus langier* (WzBRV3)  *Alphaplatrhavirus larvatus* (HLGXCRV)  *Alphaplatrhavirus acutispina* (WlDRV8)  Genome organizations  The complete genome coding sequences all these viruses have been reported, lacking only extreme 3’ and 5’ termini (**Figure 2**). The genomes range in length from 11,353 nt (JmBRV2) to 14,994 nt (WlDRV8). Although there is some structural variation, all but one (JmBRV2) contain the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*) and include at least one additional gene in the region between the *G* and *L* genes. In JmBRV2, there is no *G* gene and no additional gene preceding the *L* gene. In most cases, one additional gene between *G* and *L* encodes a protein with the structural characteristics of a class I viroporin. The *G* genes encode class I transmembrane glycoproteins that are homologous with the G protein of vesicular stomatitis Indiana virus (VSIV; species *Vesiculovirus* *indiana*), sharing 10 of the 12 cysteine residues that form disulphide bridges (**Figure 3**). The G protein of fox fecal rhabdovirus (FFRV) lacks cysteine residue CIII but, as the paired cysteine residue (CV) is present, this may well be a sequencing error. All alphaplatrhaviruses share four additional cysteine residues that are likely to form two additional disulphide bridges in the folded proteins (**Figure 3**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, all 12 viruses proposed for assignment cluster with the 6 viruses already assigned to the genus, forming a distinct and well-supported monophyletic clade (**Figure 1**). Viruses detected directly by metagenomic sequencing of platyhelminths are scattered throughout the entire clade, as are viruses identified by metagenomic sequencing of vertebrates.  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments for all viruses in the genus indicated that WfSRV8 and WzBRV1 are most closely related (78.9% identity in N; 78.2% identity in L; 66.9% identity in G). (**Tables 1-3**).  Species demarcation criteria  The species demarcation criteria will be as for the existing genus *Platrhavirus* (to be renamed as *Alphaplatrhavirus*) which are that viruses assigned to different species within the genus have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) significant differences in genome organisation as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralization tests; and F) occupy different ecological niches as evidenced by differences in hosts and/or vectors.  All members of the proposed new genus meet criteria A, B and C. The genome organisations, although similar in overall structure, display significant differences (criterion D). No neutralization test data are yet available as there are currently no isolates of the viruses (criterion E). The viruses were detected in platyhelminths (trematodes and cestodes) of different genera in different geographic locations as well as in vertebrates of several species that appear to have been infested with platyhelminths (criterion F).  **NOTE:** Although occupying a distinct monophyletic clade and apparently sharing the unique ecology of association with platyhelminth hosts, these viruses are very diverse in genome sequence. As such, the possible discovery of additional related viruses in the future may necessitate the splitting of the genus, and possibly elevation to the taxonomic rank to subfamily.  Derivation of the names of new taxa  The species epithets for the new species were derived as follows:   |  |  | | --- | --- | | *Alphaplatrhavirus dendriticum* | adopted from the species epithet of the trematode parasite (*Dicrocoelium dendriticum*) that was the source of the virus sequence | | *Alphaplatrhavirus solidus* | adopted from the species epithet of the cestode parasite (*Schistocephalus solidus*) that was the source of the virus sequence | | *Alphaplatrhavirus wufeng* | derived from the Chinese city (Wufeng) from which the source shrew sample was collected for virus metagenomic sequencing | | *Alphaplatrhavirus smithii* | adopted from the species epithet of the source shrew sample (*Chodsigoa smithii*) that was collected for virus metagenomic sequencing | | *Alphaplatrhavirus chodsigoa* | adopted from the genus name of the source shrew sample (*Chodsigoa smithii*) that was collected for virus metagenomic sequencing | | *Alphaplatrhavirus hubei* | derived from the Chinese province (Hubei) from which the source shrew sample was collected for virus metagenomic sequencing | | *Alphaplatrhavirus jingmen* | derived from the Chinese city (Jingmen) from which the source bat sample was collected for virus metagenomic sequencing | | *Alphaplatrhavirus ricketti* | adopted from the species epithet of the source bat sample (*Myotis ricketti*) that was collected for virus metagenomic sequencing | | *Alphaplatrhavirus wenzhou* | derived from the Chinese city (Wenzhou) from which the source bat sample that was collected for virus metagenomic sequencing | | *Alphaplatrhavirus langier* | adopted from the species epithet of the source bat sample (*Myotis laniger*) that was collected for virus metagenomic sequencing | | *Alphaplatrhavirus larvatus* | adopted from the species epithet of the source bat sample (*Hipposideros larvatus*) was collected for virus metagenomic sequencing | | *Alphaplatrhavirus acutispina* | adopted from the species epithet of the source fish sample (*Okamejei acutispina*) was collected for virus metagenomic sequencing |  1. **Create the new genus *Betaplatrhavirus* including 12 new species**     Six novel viruses that have been discovered in platyhelminth parasites are proposed for classification in the new genus *Betaplatrhavirus*. Five were discovered by mining of high-throughput RNA-Seq libraries that are deposited in the Sequence Read Archive (SRA) database [2]. Triaenorhabdovirus 2 (TriRV2; strain TN1) was discovered in a library derived from the cestode parasite of fish, *Triaenophorus nodulosus*; psilorhabdovirus 1 (PsiRV1; strain PS2) and psilorhabdovirus 2 (PsiRV2; strain PS6) were discovered in libraries derived from trematode parasite of waterfowl, *Psilotrema simillimum*; sphaeridiorhabdovirus 2 (SphRV2; strain SP3-SP4-SP5) and sphaeridiorhabdovirus 3 (SphRV3; strain SP3) were discovered in libraries derived from the trematode parasite of waterfowl, *Sphaeridiotrema pseudoglobulus*. Himastelon rhabdovirus (HIMRV; strain wsk-h1) was discovered by metagenomic sequencing of the trematode parasite of waterbirds, *Himasthla elongata* [6]. These parasites use mollusks or crustaceans as intermediate hosts and infest the visceral organs of the definitive host.  Six other novel viruses that been discovered ­­­by metagenomic sequencing of vertebrate hosts are also proposed for classification in the new genus *Betaplatrhavirus*. Beihai dimarhabdovirus 1 (BhDRV1; strain BHFishS58819) was detected in gill tissue from an unidentified ray-finned fish (Actinopterygii) collected in Guangxi Province, China [5]. Wenling dimarhabdovirus 1 (WlDRV1; strain XYHYC188111) was detected in the gut of an unidentified ray-finned fish (Actinopterygii) collected in Zhejiang Province, China [5]. Fujian dimarhabdovirus (FjDRV; strain BHNC4885) was detected in the gut of the spotted paddle-tail newt (*Pachytriton brevipes*) collected in Fujian Province, China [5]. Eptesicus fuscus rhabdovirus (EfusRV; strain 20-12206) was detected in a big brown bat (*Eptesicus fuscus*) collected in South Dakota, USA, in 2020. Bat-associated rhabdovirus 2 (BaRV2; strain JX2020) was detected in a “swab” from the Japanese house bat (*Pipistrellus abramus*) collected in China, in 2020. Rhabdovirus HAGXC131516/2 (HAGXCRV) was detected in the intestine of a great roundleaf bat (*Hipposideros armiger*) collected in Guangxi Province, China.  We propose that these viruses be assigned to the following new species in the genus *Betaplatrhavirus:*  *Betaplatrhavirus nodulosus* (TriRV2)  *Betaplatrhavirus psilotrema* (PsiRV1)  *Betaplatrhavirus simillimum* (PsiRV2)  *Betaplatrhavirus sphaeridiotrema* (SphRV2)  *Betaplatrhavirus pseudoglobulus* (SphRV3)  *Betaplatrhavirus himastelon* (HIMRV)  *Betaplatrhavirus beihai* (BhDRV1)  *Betaplatrhavirus wenling* (WlDRV1)  *Betaplatrhavirus fujian* (FjDRV)  *Betaplatrhavirus fuscus* (EfusRV))  *Betaplatrhavirus abramus* (BaRV2)  *Betaplatrhavirus armiger* (HAGXCRV)  Genome organizations  The complete genome coding sequences all these viruses have been reported, lacking only extreme 3’ and 5’ termini (**Figure 2**). The genomes range in length from 9,449 nt (BhDRV1) to 12,600 nt (EfusRV). There is some structural variation amongst the genomes. All contain four of the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* and *L*) but only five of the 12 viruses have a *G* gene and one of the viruses (EfusRV) has an additional gene between the *G* and *L* genes. In one of the viruses (FjDRV), there is an alternative ORF of moderate length (298 nt) near the start of the *N* gene but it is not known if it is expressed. The *G* genes of five viruses encode class I transmembrane glycoproteins that are homologous with the G protein of vesicular stomatitis Indiana virus (VSIV; species *Vesiculovirus* *indiana*), containing all 12 cysteine residues that form disulphide bridges and two additional cysteine residues that are likely to form an additional disulphide bridge in the folded proteins (**Figure 4**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, all 12 viruses proposed for assignment form a distinct and well-supported monophyletic clade (**Figure 1**). Viruses detected directly in platyhelminths are scattered throughout the entire clade as are viruses identified by metagenomic sequencing of vertebrates.  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments for all viruses in the genus indicated that HAGXCRV and BaRV2 are most closely related in N (82.0% identity) and L (77.6% identity), and HAGXCRV and SphRV2 are most closely related in G (45.6% identity). (**Tables 4-6**).  Species demarcation criteria  The species demarcation criteria for the genus *Betaplatrhavirus* are that viruses assigned to different species within the genus have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) significant differences in genome organisation as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralization tests; and F) occupy different ecological niches as evidenced by differences in hosts and/or vectors.  All members of the proposed new genus meet criteria A and B. Those members that encode a G protein also meet criterion C. There are significant differences in genome organization between some members of the genus (criterion D). No neutralization test data are yet available as there are currently no isolates of the viruses (criterion E). The viruses were detected in platyhelminths (trematodes and cestodes) of different genera in different geographic locations as well as in vertebrates of several species that appear to have been infested with platyhelminths (criterion F).  **NOTE:** Although occupying a distinct monophyletic clade and sharing the unique ecology of association with platyhelminth hosts, these viruses are very diverse in genome sequence. As such, the possible discovery of additional related viruses in the future may necessitate the splitting of the genus and possibly elevation to the taxonomic rank to subfamily.  Derivation of the names of new taxa  The species epithets for the new species were derived as follows:   |  |  | | --- | --- | | *Betaplatrhavirus nodulosus* | adopted from the species epithet of the cestode parasite (*Triaenophorus nodulosus*) that was the source of the virus sequence | | *Betaplatrhavirus psilotrema* | adopted from the genus name of the trematode parasite (*Psilotrema simillimum*) that was the source of the virus sequence | | *Betaplatrhavirus simillimum* | adopted from the species epithet of the trematode parasite (*Psilotrema simillimum*) that was the source of the virus sequence | | *Betaplatrhavirus sphaeridiotrema* | adopted from the genus name of the trematode parasite (*Sphaeridiotrema pseudoglobulus*) that was the source of the virus sequence | | *Betaplatrhavirus pseudoglobulus* | adopted from the species epithet of the trematode parasite (*Sphaeridiotrema pseudoglobulus*) that was the source of the virus sequence | | *Betaplatrhavirus himastelon* | adopted from the virus name which is an acronym derived from the species name of the trematode parasite (*Himasthla elongata*) that was the source of the virus sequence | | *Betaplatrhavirus beihai* | derived from the Chinese city (Behai) from which the source bat sample was collected for virus metagenomic sequencing | | *Betaplatrhavirus wenling* | derived from the Chinese city (Wenling) from which the source bat sample was collected for virus metagenomic sequencing | | *Betaplatrhavirus fujian* | derived from the Chinese province (Fujian) from which the source bat sample was collected for virus metagenomic sequencing | | *Betaplatrhavirus fuscus* | adopted from the species epithet of the source bat sample (*Eptesticus fuscus*) that was collected for virus metagenomic sequencing | | *Betaplatrhavirus abramus* | adopted from the species epithet of the source bat sample (*Pipistrellus abramus*) that was collected for virus metagenomic sequencing | | *Betaplatrhavirus armiger* | adopted from the species epithet of the source bat sample (*Hipposideros armiger*) that was collected for virus metagenomic sequencing |  1. **Create the new genus *Gammaplatrhavirus* including 6 new species**   Three novel viruses that have been discovered in platyhelminth parasites are proposed for classification in the new genus *Gammaplatrhavirus*. Dicrocoilium rhabdo-like virus 1 (DicRLV1; strain XJ) was detected by metagenomic sequencing in a lancet liver fluke (*Dicrocoelium dendriticum*) collected in Xinjiang Autonomous Region, China, in 2021. Metorhabdovirus 1 (MetRV1; strain MO1) and clonorhabdovirus 1 (CloRV1; strain CS1-CS5-CS6-CS7-CS8) were each discovered by mining of high-throughput RNA-Seq libraries that are deposited in the Sequence Read Archive (SRA) database [2]. MetRV1 was discovered in a library derived from the trematode parasite of waterfowl, *Metorchis orientalis*; CloRV1 was discovered in a library derived from the Chinese river fluke (*Clonorchis sinensis*), a trematode parasite of fish and mammals. These parasites use mollusks or crustaceans as intermediate hosts and infest the visceral organs of the definitive host.  Three other novel viruses that been discovered ­­­by metagenomic sequencing of invertebrate or vertebrate hosts are also proposed for classification in the new genus *Betaplatrhavirus*. Beihai barnacle virus 7 (BhBV7; strain BHTH16013) was detected in a pool of unidentified barnacles (Crustacea) collected in Guangxi Province, China, in 2014 [7]. Barnaclevirus sp. (BarnV; strain VSYSC20/1) was detected in the intestine of an Asian particolored bat (*Vespertilio sinensis*) collected in Jilin Province, China, in 2020. Wenzhou bat rhabdovirus 2 (WzBRV2; strain WZ\_Mi.schreibersii\_rhabdo\_1) was detected in a common bent-wing bat (*Miniopterus schreibersii*) collected in Zhejiang Province, China during the winter and early spring of 2016-17 [4].  We propose that these viruses be assigned to the following new species in the genus *Gammaplatrhavirus dendriticum* (DicRLV1)  *Gammaplatrhavirus orientalis* (MetRV1)  *Gammaplatrhavirus sinensis* (CloRV1)  *Gammaplatrhavirus beihai* (BhBV7)  *Gammaplatrhavirus jilin* (BarnV)  *Gammaplatrhavirus wenzhou* (WzBRV2)  Genome organizations  The complete genome coding sequences all these viruses have been reported, lacking only extreme 3’ and 5’ termini (**Figure 2**). The genomes range in length from 10,791 nt (WzBRV2) to 11,778 nt (DicRLV1). The genomes all have a very similar structural organisation, containing the five canonical rhabdovirus structural protein genes (*N*, *P*, *M,* *G* and *L*) and an additional gene between the *G* and *L* genes encoding a protein with the structural characteristics of a class I viroporin. The *G* genes of the 6 viruses encode class I transmembrane glycoproteins that are homologous with the G protein of vesicular stomatitis Indiana virus (VSIV; species *Vesiculovirus* *indiana*), containing 8 of the 12 cysteine residues that form disulphide bridges and two additional cysteine residues that are likely to form an additional disulphide bridge in the folded protein (**Figure 5**).  Phylogenetic analysis  Based on ML trees generated from complete L protein sequences, all 6 viruses proposed for assignment form a distinct and well-supported monophyletic clade (**Figure 1**). Viruses detected directly in platyhelminths form a sub-clade to which the viruses detected in bats and the barnacle are ancestral.  Amino acid sequence identities  Pairwise sequence identities (p-distances) calculated in MEGAX from ClustalW amino acid sequence alignments for all viruses in the genus indicated that MetRV1 and BCloRV1 are most closely related in N (75.3% identity), L (70.9% identity) and G (74.3% identity) (**Tables 7-9**).  Species demarcation criteria  The species demarcation criteria for the genus *Gammaplatrhavirus* are that viruses assigned to different species within the genus have several of the following characteristics: A) minimum amino acid sequence divergence of 10% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) significant differences in genome organisation as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralization tests; and F) occupy different ecological niches as evidenced by differences in hosts and/or vectors.  All members of the proposed new genus meet criteria A, B and C. The genome organisations of the proposed members are all very similar (criterion D). No neutralization test data are yet available as there are currently no isolates of the viruses (criterion E). The viruses were detected in platyhelminths (trematodes and cestodes) of different genera in different geographic locations as well as in vertebrates and crustaceans that appear to have been infested with platyhelminths (criterion F).  Derivation of the names of new taxa  The species epithets for the new species were derived as follows:   |  |  | | --- | --- | | *Gammaplatrhavirus*  *dendriticum* | adopted from the species epithet of the trematode parasite (*Dicrocoelium dendriticum* ) that was the source of the virus sequence | | *Gammaplatrhavirus orientalis* (MetRV1) | adopted from the genus name of the trematode parasite (*Metorchis orientalis*) that was the source of the virus sequence | | *Gammaplatrhavirus sinensis* (CloRV1) | adopted from the species epithet of the trematode parasite (*Clonorchis sinensis*) that was the source of the virus sequence | | *Gammaplatrhavirus beihai* (BhBV7) | derived from the Chinese city (Beihai) from which the source barnacle sample was collected for virus metagenomic sequencing | | *Gammaplatrhavirus jilin* (BarnV) | derived from the Chinese province (Jilin) from which the source bat sample was collected for virus metagenomic sequencing | | *Gammaplatrhavirus wenzhou* (WzBRV2) | derived from the Chinese city (Wenzhou) from which the source bat sample was collected for virus metagenomic sequencing | |
|  |
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| **Tables, Figures:** below    **Figure 1 (above).** The evolutionary history was inferred from a multiple sequence alignment of complete L protein sequences of 428 rhabdoviruses that are currently assigned to species in the family *Rhabdoviridae* as well as 30 viruses proposed to be assigned to one renamed genus (*Alphaplatrhavirus*) and two new genera (*Betaplatrhavirus* and *Gammaplatrhavirus*) in the family. The alignment was constructed in MAFFT using the E-INS-I iterative refinement method. Phylogenetically informative sites were selected from the alignment using TrimAl, resulting in 933 positions in the final dataset. The tree was inferred in MEGA11 by using the Maximum Likelihood method based on the best-fit Le and Gascuel model with gamma distribution of evolutionary rates and invariable sites. The tree with the highest log likelihood (-404883.56) 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-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log-likelihood values. 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.    **Figure 2 (above).** Schematic scale illustration of the genome organisations of alphaplatrhaviruses, betaplatrhaviruses and gammaplatrhaviruses. Arrows represent long open reading frames (ORFs). ORFs encoding proteins with the structural characteristics of class I viroporins are shown in yellow.    **Figure 3 (above).** Clustal Omega multiple sequence alignment of the central folded domain of alphaplatrhavirus G proteins and the vesicular stomatitis Indiana virus (VSIV) G protein, for which disulphide bridges have been determined in the structural model informed by X-ray crystallography [8]. The 12 VSIV cysteine residues (CI-CXII) that form 6 disulphide bonds are shown. Other conserved cysteine residues in alphaplatrhaviruses are also shown with those which appear to form disulphide bridges shown in the same colour. The four additional cysteine residues shared by all alphaplatrhaviruses are shown in aqua. Other highly conserved residues are shown in grey.  **CI CII CIII**  VSIV\_G LAFLFIGVNCKFTIVFPHNQKGNWKNVPSNYHYCPSSS---DLNWHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGPKYITHSIRS  WlDRV1\_MG600014 HSSKLSTSLVNGNINIPVKALTPWDNISPIKIECSFTTPIIDKT--SSTLVYL----NDDQRSTTEVESTMCTAWNLKVNCQTSFLGYKNITKTKQY  EfusRV\_MT732687 WGY---SAGGQYSITVPTKMIKEPTPINFDQLECHVSIQDSTKVWSEKISAYF----FTADRLDPSEKTLLCTGWEYVTRCYEYWYGGVDVTHIRRP  PsiRV2\_BK059746 WITTSTSLKIGNKLGLPTRLLTKWHPINPRQISCHYSDYDSAKWHGGEHVVYL----FSADKVESHEKVKLCSAWELVTSCYEHWYFSTDVVHTRRP  SphRV2\_BK059663 LVLNIQGESQYLLPGFPSSLLTPWHRITPTQINCRFSGHDASTYSTNYYDVEL----FSVDKVKSEEKVYLCSAWELVTSCYEHWYFTSEVIHIKRP  HAGXCRV\_OR869044 SLISPVQSGSYIHPGFPSSRKTNWHNIHPKQISCQFTGGDASTYSTSTYDVSF----FDNQKVVDSEEVTLCSIWTFETECYEHWYLSTDITHIRRP  .\* : \* : .: . :\* . \* : : : :  **CIV CV CVI CVII CXIII**  VSIV\_G FTPSVEQCKESIEQTKQG----TWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYTGEWVDSQFIDGKCSNDICPTVHNSTTWHSDYKVKGLC  WlDRV1\_MG600014 EPITYQECLKTMNKSIIESIFDLKDDGLFPPTRCKWYSSETVEKSVITRNPVTADYDPFTDSLRHGLLNPEFCKGRCCDTKLPNSVMCPNKEAKTIC  EfusRV\_MT732687 AKPDLAKCTETYAQNTI--FPDEQAADEYSPPECHWLRSHDVVKKVNHAHTVYLKYDFYDRKVKDERLVAGECEADICPCVATNQVIFRPEIKHPEC  PsiRV2\_BK059746 VKIEPSECLSAWRSNEA--SLDDLPSDDFPDPSCYWLKTQDATKRVIHMQEIEMRFDYYSNAIVDDRLVNGKCQTHFCYGAQDNFIIIRTPNYQSKC  SphRV2\_BK059663 ATLSVSECKGVIAQGLL--RFTDLPTDPYPDPNCYWLRTVDTIKRVIHVQEIELNFDFYTNSLVDNRLLTGFCSQEVCKGTSENFLIIRKPDYKEHC  HAGXCRV\_OR869044 MHVRLNDCITEITNGEI--SVSRLPDENYPDPECYWLKKYTTSRKVVHLEKIKIHFDYYTNSLVDHRLLTGKCNKKYCEGTSDNVLIVRHEDYESHC  .\* . : \* : . : \* : . : \*. \* . . \*  **CIX CX CXI**  VSIV\_G DSNLISMDITFFSEDGELSSLGKEGTGFRSNYFAYETGDKACKMQYCKHWGVRLPSGVWFEMADKDLF-AAARFPECPEGSSISAPSQTSVDVS--L  WlDRV1\_MG600014 SSWKAIHVYT--SFY-GI--------QIEDS-DVSIPFADSCCFRYCGFPARRLIGGGVVVIKNHDGVGPIGCDTWCHDIHEVNTKADNSRVVSLT-  EfusRV\_MT732687 SQWKQDMIQY--RGH-EV--------WASSE-DAYYILKRSCDVKLCGRVGKIVDPGIFISLDKEQEIGPFAKTIPCANDVNVTT-AFTALIHQ-QE  PsiRV2\_BK059746 DHWVRRNVMI--SDH-SL--------KFVDT-DGLMYVSSKCDIEFCGHRGKRIGYGLFVAVPSESRIAALSEAPLCSVDKGLIA-ESPSRVLALSV  SphRV2\_BK059663 DHWVKKKVKI--SEH-MI--------QFEDS-KEDYFVSSQCDLKFCGKVGKRIGHGLFISVPDGSANWALARTSTCPTGSVNVS-SSPMTVLKLNF  HAGXCRV\_OR869044 NSWKKEKVHI--SDH-MI--------KVSGS-NVEYYIDQTCDLTFCGKMGKRLSHGLFIHVPDTSAYWALKRTVSCHGADATVS-SNPVISRELNL  . : . \* . \* . : \* . : . . \* :  **CXII**  VSIV\_G IQDVERILDYSLCQETWSKIRAGLPISPVDLSYLAPKNPG--TGPAFTIINGTLKYFETRYIRVEIAAPILSRMVGMISGTTT--ERELWD--DWA-  WlDRV1\_MG600014 ---ELETRQSERCMDARDLIVATGSVSTHTLSKLAPVINSGI-LPIYRISKGKLQRRLAIYEKASAFSYHPERLCATLAADST-KTWCLYSDSDSVF  EfusRV\_MT732687 LYRETDLLFYEQCMSALDLAKSTHKVTLHMYQALSPSIANGRIGPVYSLRDGKLYAGLAQYQAIQYVLEDTKGACVSINS----LRYCLARD-KDLF  PsiRV2\_BK059746 DNDRAAFDAYQRCLTSRDIIISTQQVTPHMLAQIAPLRSSGTVGEIYRFKNNTLEVATGVYSSVKNFTDDSTKGCAIVDDADTYSRRCFNFK-TWIY  SphRV2\_BK059663 DIEKIAYDAYQECMLARDIIISTGRVTPHLLAQIAPLKSGYVTGEIYRYVNGSLEVSTGQYRTISLYPDNSDRGCLKGDT----ETRCFDFK-GWVF  HAGXCRV\_OR869044 EGDKEGFMAYRDCLEAKDIIVISGQVTSHLLSQIAPMRAWYLKGDVYRFANNSLQVATGSYRTLDEFPPTSPQGCLKGGG----QIRCFSFS-SWVF  \* : . :: ::\* : ...\* \* . :    VSIV\_G -PYEDVEI-------------GPNGVLRTSSG  WlDRV1\_MG600014 ELTTGSQRDKNNIRSDMKETSLINGVHNGDDG  EfusRV\_MT732687 VPTSGFELR---RVGEKGIVPLTNGIYMDSKN  PsiRV2\_BK059746 DSETFPVIP---GSVRNAAAMLTNGLTVNQHG  SphRV2\_BK059663 NGTEPPQVP---YLLRTRGAMLINGITLLEGG  HAGXCRV\_OR869044 DALEPQPIP---PSLKNKTTLLINGIVLSQRG  \*\*: . .  **Figure 4 (above).** Clustal Omega multiple sequence alignment of the central folded domain of betaplatrhavirus G proteins and the vesicular stomatitis Indiana virus (VSIV) G protein, for which disulphide bridges have been determined in the structural model informed by X-ray crystallography [8]. The 12 VSIV cysteine residues (CI-CXII) that form 6 disulphide bonds are shown. Two additional conserved cysteine residues in betaplatrhaviruses which appear to form an additional disulphide bridge are also shown (green). Other highly conserved residues are shown in grey.  **CI CII CIII CIV**  VSIV\_G KFTIVFPHNQKG-NWKNVPSN--YHYCPSSSDLNWHNDLIGTALQVKMPKSHKAIQADGWMCHASKWVTTCDFRWYGPKYITHSIRSFTPSVEQCK  WzBV2\_OQ715697 LELGPFPIHICGANRRPTPFALPSNECRHSH---RINQPEHVGKLSLLTRANIAIPLSAYRCHAVISYASCMEWFLGVKDVRYWTEGDIVSKEECM  BarnV\_OR871063 IKVGPFPIHLCGANRRPTPYALPLTLCNPST---SGLSVEKQGPLNIMTRAHLSIPIDAYKCHSIISYASCMEWFLGVKDVKYWTEGDIVTLEECK  BhBV7\_KX884411 SESNYFDIHVCGGSSVPSPLPLPGIMCNIAP--TATQQPLRNGELDIITAMSSIFPVTVYRCHTVRKTSYCYKHFWGVPERMSWSSPVNDTLSSCQ  DicRLV1\_OP548620 RVDTPFAVYICGGTSVPSPNPLPGIQCVLED--YQDDEPVFNVTLKYLSGGTSLQPIDIYKCHRITTTKHCYIWWTGAKDISKDAAPSPIPKSVCT  CloRV1\_BK059698 APETPFPIFLCGANQQPVPTPLQGITCDTPP--EPSDRFLGTASINYFTGTSAKAPIEIYKCYRITTFAECFVWFLGVKDRTRWSKPGVAELEPCT  MetRV1\_BK059675 GAETPFPIFLCGANQQPIPTPLQGITCESLP--EPADRYLGQASINYFTGTSAKAPVEVYKCHRVITFAECFVWFLGVKDKTRWSKPGVAQLEQCT  \* \* . \* \* : : \*: \* : \* . \*  **CV**  VSIV\_G ESIEQTKQG-TWLNPGFPPQSCGYATVTDAEAVIVQVTPHHVLVDEYT------GE-----WV-------DSQ----FI-----------------  WzBV2\_OQ715697 SSI-QYTSS-TPSHLKSPRAKCIWWGNNTRQLRQVILEPVTVFANILTDAIVLPGHNST--WYFLNESWHFSDAEYYYLNEDSKHIYELRHRASEI  BarnV\_OR871063 ALY-NSTQGRAFTDILNPTPKCIWWGNNTLKSRNILIEPVTLFADILTDSVTLPGHNSS--WFFLEEEWHYADASYFVIPAMSTRVYSLKHNSASK  BhBV7\_KX884411 DRQVRSTSGSQFLSVVTPPYSCSWMREVSESTDSPLFEEDLAYYELLQDMIHIKGVGSFSTWA--NVSWYPSSGGYYFLPPESQARIRAYRLHSTH  DicRLV1\_OP548620 DMIIGHERGKQYTEIRESWEDCYYVQERQTATHNDLFEPQVAFYNAISDTIHLSGTTES--WN-SSTSMFDHKDNWYWVPPTTSKKILDYQQSLLR  CloRV1\_BK059698 KLVLTHVKGAYSNTISYPDYYCYWLQTNTLHRQNDLFEPTTAYYDILTDAIKVPGSDRI--WN-ITDELFFHEDSYYWIPESTRRSIDSYRRQHTK  MetRV1\_BK059675 TLVLSHVKGSTSNTITYPDYYCYWLQTNTRHIDNDLFEPTTAYYDILTDTVKIPGSDRI--WN-ISKELFFQEDAYYWIPDTTRKIIESYRRQHTK  . \* : . : \* \* . :  **CVI CVII CVIII CIX CX**  VSIV\_G DGKCS----NDICPTVHNSTTWHSDYKVKG-LCDSNLISMDITFFSEDGEL-SSLGKEGTGFRSNYFAYETGDKACKMQYCKHWGVRLPSGVWFEM  WzBV2\_OQ715697 EVECQVSTHRVVCPS-EAITFWLEDLTHKT-IKGKSYYEISPSLYMKHDLASWLMIN-----TSLKTLQEHRQGDPTIQYVLMRTNEVREGLLNMQ  BarnV\_OR871063 TIDCFATSHRVTCPE-EAITFWMEDLKPIM-IKKRQYYEVTPSLYIKRDFDAARLLN-----LSLQYLSHNRRGDPTIQYLLTRLDEIRSAMLVLE  BhBV7\_KX884411 STLCEVYVDRVRCPY-LAITVWLSDLKKTKIINNERYWSVSEGVYISRNHKWDRL-V-----ETKK--RTRRGAALQLQYVMDSLNMMTRAADRTA  DicRLV1\_OP548620 SVTCFIFENRIRCPE-AAVTFXHQDAHPVN-LNGRALLKVAPGFHILADKNWMKI-T-----TYYYQPRRTKRSVPQLNYIFDRLGSLERRSKTTF  CloRV1\_BK059698 TAKCQVYEQRIRCPR-EAVTIWMHELIDVE-LNGNRYLKAAEGFYIANDLLYEDL-L------RLQSPRRTRRQTLHLQYVLDLLKSTEFNIFKAV  MetRV1\_BK059675 VATCEVYERRIRCPH-EAVTIWMHELVDIE-LNTHHYMRAAEGFYIAKDHLYEDL-L------KMQNPKRVKRQTLHIQYLLDLIRSTELNVFKAI  \* . \*\* \* : : .. . : ::\*  **CXI CXII**  VSIV\_G ADKDLFAAARFPECPEGSSISAPSQTSVDVSLI---QDV----------ERILDYSLCQETW-SKIRAG--LPISPVDLSYLAPKNPGTGPAFT  WzBV2\_OQ715697 ENLGCALNN-------FKKMTALAIAPINPVMAGMIYLGERQPGVSISQGGLIKYA-CSRVTHWEIDSNQ-HGFKDLPIKYLLP--TYETVMTG  BarnV\_OR871063 QSHVCEISN-------LRKTTALAMASLNPVMAAMVYFGERYPGVSISQGGVIKYS-CTQITDWEIDSSR-YGYRDLPIKYMLP--LYRGDLTG  BhBV7\_KX884411 QSLRCEIKR-------LRRLTALAVASLSPALAAEIELGRRVAGVELTPAGLIKYS-CQKVFSWKLQSPASSTHTEVPIVYQLY--SSSSPVIG  DicRLV1\_OP548620 DYLDCAARL-------LRREIALGFSVISPTLAAQIEFQRFIPGVSLTPAGVVKHT-CQQIAIWTLRNDT-SPYSQIPITYAVY--PGTTPIEG  CloRV1\_BK059698 RQIQCEARQ-------NRRIVALAIAAVSPSLAAEIEFGKQFPGVSLTPAGLVKFS-CQEVYSWRLRVTN-EKVVQIPITYMPF--SGTSEING  MetRV1\_BK059675 RQVQCEARQ-------SRRIIALALASVSPALAAEIEFGQQLPGVSLTPAGLVKYS-CQEIHSWRLRSTS-EKVIQIPVTYTPF--PGTSEIHG  \* . : :. : ::..: \* . : : : \*  **Figure 5 (above).** Clustal Omega multiple sequence alignment of the central folded domain of gammaplatrhavirus G proteins and the vesicular stomatitis Indiana virus (VSIV) G protein, for which disulphide bridges have been determined the structural model informed by X-ray crystallography [8]. The 12 VSIV cysteine residues (CI-CXII) that form 6 disulphide bonds are shown. In gammaplatrhaviruses, four VSIV cysteine residues which form two disulphide bridges (CVIII-CX and CIX-CXI) are absent and two additional conserved cysteine residues (olive green) are available to form a new disulphide bridge. Other highly conserved residues are shown in grey. |

**Table 1.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of alphaplatrhavirus N protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | SphRV1 | **DicRLV2** | **WfSRV7** | SchRV | MicRV | **JmBRV2** | **WfSRV5** | FFRV | **HLGXCRV** | TriRV1 | **WfSRV8** | **WzBRV1** | **WzBRV3** | MetRV2 | **WlDRV8** | **JmBRV1** | **SsolRV** | **WfSRV9** |
| SphRV1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **DicRLV2** | 41.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **WfSRV7** | 40.5 | 47.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SchRV | 28.4 | 32.4 | 30.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MicRV | 10.3 | 11.3 | 10.0 | 7.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **JmBRV2** | 10.3 | 7.5 | 10.0 | 8.7 | 7.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **WfSRV5** | 10.4 | 11.5 | 11.8 | 11.7 | 7.2 | 34.5 |  |  |  |  |  |  |  |  |  |  |  |  |
| FFRV | 10.9 | 9.9 | 8.9 | 10.6 | 12.8 | 17.3 | 15.8 |  |  |  |  |  |  |  |  |  |  |  |
| **HLGXCRV** | 9.6 | 9.2 | 7.7 | 9.3 | 9.6 | 15.6 | 12.3 | 16.7 |  |  |  |  |  |  |  |  |  |  |
| TriRV1 | 11.7 | 8.7 | 12.3 | 11.9 | 9.0 | 9.6 | 7.5 | 9.1 | 9.3 |  |  |  |  |  |  |  |  |  |
| **WfSRV8** | 14.5 | 17.8 | 17.1 | 17.0 | 10.9 | 6.7 | 10.8 | 9.4 | 9.5 | 6.1 |  |  |  |  |  |  |  |  |
| **WzBRV1** | 15.5 | 16.4 | 15.6 | 17.0 | 11.2 | 7.9 | 11.0 | 9.4 | 10.6 | 7.7 | 78.9 |  |  |  |  |  |  |  |
| **WzBRV3** | 16.4 | 13.5 | 12.7 | 12.8 | 10.8 | 8.0 | 6.6 | 10.2 | 7.6 | 9.2 | 23.1 | 22.0 |  |  |  |  |  |  |
| MetRV2 | 11.8 | 12.8 | 10.9 | 13.6 | 11.0 | 9.0 | 9.2 | 10.8 | 10.1 | 10.3 | 12.8 | 11.6 | 11.1 |  |  |  |  |  |
| **WlDRV8** | 10.5 | 9.5 | 9.6 | 11.1 | 13.4 | 9.7 | 10.9 | 12.1 | 7.2 | 8.7 | 13.9 | 14.9 | 12.0 | 7.8 |  |  |  |  |
| **JmBRV1** | 13.9 | 9.3 | 12.1 | 9.4 | 12.4 | 11.8 | 11.0 | 13.3 | 12.1 | 11.1 | 12.8 | 13.7 | 10.5 | 9.9 | 15.0 |  |  |  |
| **SsolRV** | 12.0 | 10.2 | 13.6 | 12.7 | 13.1 | 10.3 | 10.8 | 11.2 | 12.9 | 12.3 | 10.8 | 12.0 | 10.6 | 11.4 | 15.1 | 45.3 |  |  |
| **WfSRV9** | 11.8 | 11.3 | 12.2 | 12.3 | 11.8 | 11.6 | 10.9 | 9.4 | 13.5 | 11.0 | 10.9 | 12.6 | 9.3 | 10.5 | 11.8 | 43.2 | 55.9 |  |

**Table 2.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of alphaplatrhavirus L protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | SphRV1 | **DicRLV2** | **WfSRV7** | SchRV | MicRV | **JmBRV2** | **WfSRV5** | FFRV | **HLGXCRV** | TriRV1 | **WfSRV8** | **WzBRV1** | **WzBRV3** | MetRV2 | **WlDRV8** | **JmBRV1** | **SsolRV** | **WfSRV9** |
| SphRV1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **DicRLV2** | 51.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **WfSRV7** | 52.3 | 52.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SchRV | 45.4 | 46.0 | 46.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MicRV | 22.7 | 22.5 | 22.6 | 22.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **JmBRV2** | 23.3 | 22.4 | 23.0 | 21.9 | 19.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **WfSRV5** | 22.5 | 22.9 | 22.1 | 21.0 | 20.6 | 46.4 |  |  |  |  |  |  |  |  |  |  |  |  |
| FFRV | 22.4 | 23.0 | 23.0 | 22.3 | 20.6 | 28.3 | 27.9 |  |  |  |  |  |  |  |  |  |  |  |
| **HLGXCRV** | 23.1 | 22.2 | 22.1 | 21.9 | 20.3 | 25.9 | 25.2 | 25.7 |  |  |  |  |  |  |  |  |  |  |
| TriRV1 | 21.3 | 20.6 | 20.5 | 20.1 | 20.5 | 20.3 | 20.5 | 22.3 | 21.7 |  |  |  |  |  |  |  |  |  |
| **WfSRV8** | 24.4 | 24.6 | 25.4 | 24.7 | 21.6 | 22.6 | 23.5 | 22.0 | 23.8 | 22.7 |  |  |  |  |  |  |  |  |
| **WzBRV1** | 24.6 | 24.6 | 25.3 | 24.3 | 21.6 | 22.9 | 23.6 | 21.8 | 23.5 | 22.8 | 78.2 |  |  |  |  |  |  |  |
| **WzBRV3** | 24.7 | 24.9 | 24.5 | 24.7 | 21.9 | 22.5 | 22.2 | 21.0 | 23.6 | 21.2 | 41.7 | 41.3 |  |  |  |  |  |  |
| MetRV2 | 24.5 | 24.7 | 24.4 | 24.1 | 22.7 | 24.4 | 23.1 | 22.9 | 24.3 | 22.4 | 28.3 | 28.3 | 27.2 |  |  |  |  |  |
| **WlDRV8** | 26.1 | 25.9 | 26.4 | 24.8 | 21.1 | 23.9 | 22.9 | 22.7 | 24.2 | 22.3 | 25.7 | 25.0 | 25.2 | 25.4 |  |  |  |  |
| **JmBRV1** | 25.8 | 23.8 | 25.0 | 24.3 | 21.7 | 23.5 | 23.6 | 23.2 | 24.0 | 22.4 | 24.7 | 24.7 | 23.3 | 26.6 | 32.5 |  |  |  |
| **SsolRV** | 23.9 | 23.6 | 24.1 | 23.5 | 20.3 | 23.7 | 23.4 | 22.0 | 23.3 | 20.4 | 25.4 | 24.9 | 24.0 | 26.0 | 31.7 | 49.4 |  |  |
| **WfSRV9** | 24.5 | 23.7 | 24.2 | 24.6 | 21.3 | 23.2 | 23.1 | 22.8 | 23.7 | 21.5 | 26.4 | 26.0 | 24.7 | 26.2 | 32.3 | 48.9 | 63.2 |  |

**Table 3.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of alphaplatrhavirus G protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | SphRV1 | **DicRLV2** | **WfSRV7** | SchRV | MicRV | **WfSRV5** | FFRV | **HLGXCRV** | TriRV1 | **WfSRV8** | **WzBRV1** | **WzBRV3** | MetRV2 | **WlDRV8** | **JmBRV1** | **SsolRV** | **WfSRV9** |
| SphRV1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **DicRLV2** | 25.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **WfSRV7** | 27.3 | 28.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SchRV | 23.4 | 22.1 | 21.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| MicRV | 13.3 | 13.5 | 13.8 | 12.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **WfSRV5** | 11.3 | 13.1 | 13.5 | 10.4 | 17.0 |  |  |  |  |  |  |  |  |  |  |  |  |
| FFRV | 11.7 | 13.6 | 13.7 | 10.7 | 14.5 | 16.9 |  |  |  |  |  |  |  |  |  |  |  |
| **HLGXCRV** | 9.2 | 13.7 | 12.4 | 9.3 | 14.5 | 14.6 | 15.6 |  |  |  |  |  |  |  |  |  |  |
| TriRV1 | 12.7 | 14.1 | 11.8 | 11.6 | 17.5 | 16.6 | 17.7 | 15.9 |  |  |  |  |  |  |  |  |  |
| **WfSRV8** | 12.1 | 11.6 | 13.1 | 9.4 | 18.4 | 17.9 | 15.8 | 14.7 | 18.1 |  |  |  |  |  |  |  |  |
| **WzBRV1** | 11.1 | 11.2 | 12.8 | 10.4 | 18.4 | 18.3 | 15.3 | 12.5 | 16.7 | 66.9 |  |  |  |  |  |  |  |
| **WzBRV3** | 13.8 | 13.4 | 13.8 | 13.3 | 18.3 | 17.4 | 16.0 | 15.1 | 18.0 | 40.0 | 39.5 |  |  |  |  |  |  |
| MetRV2 | 12.3 | 14.5 | 12.7 | 12.5 | 17.7 | 16.8 | 16.0 | 13.3 | 18.2 | 18.9 | 19.8 | 20.4 |  |  |  |  |  |
| **WlDRV8** | 13.1 | 12.1 | 13.1 | 14.5 | 16.5 | 15.7 | 15.2 | 15.2 | 17.7 | 18.8 | 19.9 | 20.8 | 18.9 |  |  |  |  |
| **JmBRV1** | 14.5 | 14.6 | 12.2 | 13.2 | 15.9 | 15.8 | 16.7 | 13.3 | 17.7 | 17.8 | 16.7 | 19.3 | 18.4 | 22.5 |  |  |  |
| **SsolRV** | 13.4 | 13.5 | 12.6 | 14.1 | 15.5 | 14.9 | 16.2 | 14.7 | 16.3 | 16.2 | 16.9 | 18.0 | 18.3 | 19.5 | 41.2 |  |  |
| **WfSRV9** | 12.5 | 12.8 | 13.2 | 15.0 | 16.2 | 13.6 | 16.6 | 13.7 | 16.4 | 16.1 | 16.6 | 19.2 | 16.0 | 21.6 | 41.9 | 52.3 |  |

**Table 4.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of betaplatrhavirus N protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **BhDRV1** | **TriRV2** | **WlDRV1** | **HIMRV1** | **FjDRV** | **EfusRV** | **PsiRV1** | **SphRV3** | **PsiRV2** | **SphRV2** | **HAGXCRV** | **BaRV2** |
| **BhDRV1** |  |  |  |  |  |  |  |  |  |  |  |  |
| **TriRV2** | 14.2 |  |  |  |  |  |  |  |  |  |  |  |
| **WlDRV1** | 8.9 | 6.7 |  |  |  |  |  |  |  |  |  |  |
| **HIMRV1** | 9.4 | 10.2 | 17.8 |  |  |  |  |  |  |  |  |  |
| **FjDRV** | 10.2 | 9.2 | 18.9 | 29.9 |  |  |  |  |  |  |  |  |
| **EfusRV** | 8.8 | 11.6 | 18.8 | 25.9 | 35.3 |  |  |  |  |  |  |  |
| **PsiRV1** | 10.5 | 9.6 | 19.6 | 28.3 | 34.2 | 30.5 |  |  |  |  |  |  |
| **SphRV3** | 8.2 | 9.2 | 18.0 | 28.0 | 32.3 | 30.9 | 43.6 |  |  |  |  |  |
| **PsiRV2** | 10.6 | 9.4 | 19.4 | 26.5 | 37.8 | 36.8 | 39.5 | 37.4 |  |  |  |  |
| **SphRV2** | 10.1 | 11.8 | 19.2 | 27.3 | 34.6 | 33.3 | 37.7 | 37.7 | 63.1 |  |  |  |
| **HAGXCRV** | 9.1 | 10.5 | 18.3 | 26.0 | 36.4 | 32.8 | 38.4 | 35.4 | 52.5 | 54.9 |  |  |
| **BaRV2** | 8.7 | 10.1 | 18.3 | 24.9 | 36.7 | 33.0 | 38.0 | 34.3 | 52.5 | 54.4 | 82.0 |  |

**Table 5.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of betaplatrhavirus L protein sequences.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **BhDRV1** | **TriRV2** | **WlDRV1** | **HIMRV1** | **FjDRV** | **EfusRV** | **PsiRV1** | **SphRV3** | **PsiRV2** | **SphRV2** | **HAGXCRV** | **BaRV2** |
| **BhDRV1** |  |  |  |  |  |  |  |  |  |  |  |  |
| **TriRV2** | 34.5 |  |  |  |  |  |  |  |  |  |  |  |
| **WlDRV1** | 26.7 | 28.5 |  |  |  |  |  |  |  |  |  |  |
| **HIMRV1** | 26.5 | 31.1 | 34.4 |  |  |  |  |  |  |  |  |  |
| **FjDRV** | 27.1 | 31.1 | 34.6 | 41.8 |  |  |  |  |  |  |  |  |
| **EfusRV** | 27.9 | 29.5 | 34.6 | 42.6 | 41.9 |  |  |  |  |  |  |  |
| **PsiRV1** | 26.8 | 30.1 | 34.6 | 42.7 | 45.0 | 45.4 |  |  |  |  |  |  |
| **SphRV3** | 27.4 | 29.5 | 34.4 | 43.0 | 44.8 | 44.6 | 55.7 |  |  |  |  |  |
| **PsiRV2** | 27.6 | 31.0 | 35.6 | 43.8 | 44.9 | 45.7 | 50.9 | 51.6 |  |  |  |  |
| **SphRV2** | 27.6 | 30.3 | 36.0 | 43.5 | 45.6 | 47.0 | 49.5 | 50.7 | 64.8 |  |  |  |
| **HAGXCRV** | 28.0 | 30.3 | 35.6 | 41.8 | 44.4 | 45.7 | 49.2 | 50.0 | 56.8 | 57.4 |  |  |
| **BaRV2** | 28.3 | 30.4 | 35.6 | 41.8 | 43.6 | 45.1 | 48.5 | 49.6 | 57.9 | 57.9 | 77.6 |  |

**Table 6.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of betaplatrhavirus G protein sequences.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **WlDRV1** | **EfusRV** | **PsiRV2** | **SphRV2** | **HAGXCRV** |
| **WlDRV1** |  |  |  |  |  |
| **EfusRV** | 18.2 |  |  |  |  |
| **PsiRV2** | 17.7 | 22.9 |  |  |  |
| **SphRV2** | 21.3 | 24.1 | 44.3 |  |  |
| **HAGXCRV** | 20.9 | 23.2 | 36.5 | 45.6 |  |

**Table 7.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of gammaplatrhavirus N protein sequences.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **WzBV2** | **BarnV** | **BhBV7** | **DicRLV1** | **MetRV1** | **CloRV1** |
| **WzBV2** |  |  |  |  |  |  |
| **BarnV** | 58.3 |  |  |  |  |  |
| **BhBV7** | 30.3 | 30.2 |  |  |  |  |
| **DicRLV1** | 28.4 | 32.5 | 31.9 |  |  |  |
| **MetRV1** | 33.2 | 33.4 | 36.0 | 34.6 |  |  |
| **CloRV1** | 32.9 | 32.9 | 36.0 | 35.1 | 75.3 |  |

**Table 8.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of gammaplatrhavirus L protein sequences.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **WzBV2** | **BarnV** | **BhBV7** | **DicRLV1** | **MetRV1** | **CloRV1** |
| **WzBV2** |  |  |  |  |  |  |
| **BarnV** | 58.6 |  |  |  |  |  |
| **BhBV7** | 39.0 | 37.9 |  |  |  |  |
| **DicRLV1** | 37.0 | 37.2 | 42.0 |  |  |  |
| **MetRV1** | 39.8 | 39.5 | 45.8 | 47.5 |  |  |
| **CloRV1** | 39.7 | 39.0 | 46.0 | 47.1 | 70.9 |  |

**Table 9.** Percentage amino acid identities (p-distance) of a CLUSTAL W alignment of gammaplatrhavirus G protein sequences.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **WzBV2** | **BarnV** | **BhBV7** | **DicRLV1** | **MetRV1** | **CloRV1** |
| **WzBV2** |  |  |  |  |  |  |
| **BarnV** | 56.5 |  |  |  |  |  |
| **BhBV7** | 25.0 | 26.1 |  |  |  |  |
| **DicRLV1** | 22.5 | 26.2 | 27.8 |  |  |  |
| **MetRV1** | 25.8 | 30.0 | 28.7 | 35.8 |  |  |
| **CloRV1** | 25.4 | 29.3 | 27.9 | 37.5 | 74.3 |  |