

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Abolish one genus and create three new genera to include 98 new species in the subfamily *Betarhabdovirinae* (*Mononegavirales: Rhabdoviridae*) | |
| **Code assigned:** | 2024.015P.A.v1.Rhabdoviridae\_Cytorhabdovirus\_splitgen |

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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 | **X** |
| 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* study group |

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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** |
| *Rhabdovridae* SG | 10 | 0 | 4 |
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| **Submission date:** | 10/06/2024 |

**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 | **X** |
| 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| W - Withdrawn |  |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 change “abolish genus” to “split genus” in the spreadsheet |

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

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| **Response of proposer:** |
| The change has been included both in the word file and in the spreadsheet. |

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| **Revision date:** | 03/10/2024 |

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

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| **Name of accompanying Excel module:** |
| 2024.015P.A.v1.Rhabdoviridae\_Cytorhabdovirus\_splitgen.xlsx |

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

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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  ***Description of current taxonomy***: Viruses classified in the genus *Cytorhabdovirus* infect a wide range of plants, and the assignment of viruses to this genus is based on the placement of the viruses on Maximum Likelihood tree inferred from complete L protein sequences.  ***Proposed* *taxonomic change(s)****:* Split and abolish the genus *Cytorhabdovirus*, creating three new genera (*Alphacytorhabdovirus*, *Betacytorhabdovirus*, and *Gammacytorhabdovirus*) including 98 new species in the subfamily *Betarhabdovirinae* (*Mononegavirales*: *Rhabdoviridae),* and reassign current *Cytorhabdovirus* species to the new genera. Also, we propose to abolish four cytorhabdovirus species.  ***Justification***: Recently, 98 new putative cytorhabdoviruses were discovered. The phylogenetic relationships of the now significantly expanded number of known cytorhabdoviruses provide support for splitting the genus *Cytorhabdovirus* to establish three genera that represent distinct evolutionary lineages, which we propose to name *Alphacytorhabdovirus*, *Betacytorhabdovirus* and *Gammacytorhabdovirus*. Also, we propose to abolish four cytorhabdovirus species due to the lack of sequence data for the four viruses. |

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| **Text of Taxonomy proposal:** |
| ***Taxonomic rank(s) affected***: Genus and species    ***Description of current taxonomy***: Viruses classified in the genus *Cytorhabdovirus* infect a wide range of plants, and the assignment of viruses to this genus is based on the placement of the viruses on Maximum Likelihood tree inferred from complete L protein sequence.  ***Proposed* *taxonomic change(s)*:** Split and abolish the genus *Cytorhabdovirus*, creating three new genera (*Alphacytorhabdovirus*, *Betacytorhabdovirus*, and *Gammacytorhabdovirus*) including 98 new species in the subfamily *Betarhabdovirinae* (*Mononegavirales*: *Rhabdoviridae*) and reassign current *Cytorhabdovirus* species to the new genera. Also, we propose to abolish four cytorhabdovirus species.  ***Demarcation criteria****:*  **1)** We propose that viruses assigned to different species within the proposed genus *Alphacytorhabdovirus*, have several of the following characteristics:  A) nucleotide sequence identity less than 75% for the complete coding genome sequence  B) amino acid sequence identity less than 86% in proteins encoded by all the cognate open reading frames  **2)** We propose that viruses assigned to different species within the proposed genus *Betacytorhabdovirus*, have several of the following characteristics:  A) nucleotide sequence identity less than 75% for the complete coding genome sequence  B) amino acid sequence identity less than 86% in proteins encoded by all the cognate open reading frames  **3)** We propose that viruses assigned to different species within the proposed genus *Gammacytorhabdovirus*, have several of the following characteristics:  A) nucleotide sequence identity less than 75% for the complete coding genome sequence  B) amino acid sequence identity less than 86% in proteins encoded by all the cognate open reading frames  ***Justification***:  Recently, 98 putative new cytorhabdoviruses were discovered [1, 2, 3, 4, 5, 6, 7, 8]. The phylogenetic relationships of the now significantly expanded number of known cytorhabdoviruses provide support for splitting the genus *Cytorhabdovirus* to establish three genera that represent distinct evolutionary lineages, which we propose to name *Alphacytorhabdovirus*, *Betacytorhabdovirus* and *Gammacytorhabdovirus* [1] (**Figure 1**). Of the 51 established species within the genus *Cytorhabdovirus*, 30 will be accommodated in the genus *Alphacytorhabdovirus,* 19 in the genus *Betacytorhabdovirus*, and two in the genus *Gammacytorhabdovirus.* Moreover, the 98 cytorhabdoviruses members recently discovered will be assigned to the proposed three genera, where 41 will be accommodated in the genus *Alphacytorhabdovirus,* 41 in the genus *Betacytorhabdovirus*, and 16 in the genus *Gammacytorhabdovirus.*  **Genus *Alphacytorhabdovirus***  The genomic organization of the alphacytorhabdoviruses is quite similar, with few exceptions (**Figure 2B**); where all but one alphacytorhabdovirus identified so far have at least the six basic plant rhabdovirus genes N, P, P3, M, G and L reported for cytorhabdoviruses. The exception was one virus associated with the host Pogostemon, known as “patchouly chlorosis-associated cytorhabdovirus”, which was found to have a truncated G gene [1]. One distinctive feature of alphacytorhabdoviruses is the presence of an overlapping ORF within the P-encoding ORF, named P’ in most of their proposed members [1]. Moreover, the observed phylogenetic relationships suggest a common evolutionary history for alphacytorhabdoviruses, with four major clades observed (**Figure 2A**) [1].  Most of the alphacytorhabdoviruses have herbaceous dicots as associated host plants. Thus, these viruses likely have a host adaptation trajectory leading to preferentially infecting herbaceous dicots during their evolution [1]. Furthermore, the consensus gene junction sequences among the alphacytorhabdoviruses are highly similar, likely indicating a common evolutionary history for this group of viruses [1].  Alphacytorhabdoviruses have been shown to be aphid-transmitted, except for patchouly chlorosis-associated cytorhabdovirus, which was speculated to be vertically transmitted due to its truncated G protein. We, therefore, predict that the alphacytorhabdoviruses are likely aphid-transmitted [1].  We propose that the species *Cytorhabdovirus actinidiae, Cytorhabdovirus fragariae, Cytorhabdovirus alphatrifolii*, *Cytorhabdovirus alphawuhaninsectum*, *Cytorhabdovirus asclepiadis*, *Cytorhabdovirus bacopae*, *Cytorhabdovirus betafragariae*, *Cytorhabdovirus betatrifolii*, *Cytorhabdovirus betawuhaninsectum*, *Cytorhabdovirus brassicicolae*, *Cytorhabdovirus chrysanthemi*, *Cytorhabdovirus daphnis*, *Cytorhabdovirus fragariarugosus, Cytorhabdovirus gammawuhaninsectum*, *Cytorhabdovirus glehniae*, *Cytorhabdovirus hyptisis, Cytorhabdovirus kenyatuberosum*, *Cytorhabdovirus lactucamaculante, Cytorhabdovirus lactucanecante*, *Cytorhabdovirus lycopersici*, *Cytorhabdovirus medicagonis*, *Cytorhabdovirus nymphaeae*, *Cytorhabdovirus pastinacae, Cytorhabdovirus persimmon, Cytorhabdovirus pogostemi*, *Cytorhabdovirus ribes*, *Cytorhabdovirus rubus, Cytorhabdovirus sambuci, Cytorhabdovirus taraxaci* and *Cytorhabdovirus trichosanthei* shall be moved into the genus *Alphacytorhabdovirus* and be renamed *Alphacytorhabdovirus actinidiae, Alphacytorhabdovirus alphafragariae*, *Alphacytorhabdovirus alphatrifolii*, *Alphacytorhabdovirus alphawuhaninsectum*, *Alphacytorhabdovirus asclepiadis, Alphacytorhabdovirus bacopae*, *Alphacytorhabdovirus betafragariae, Alphacytorhabdovirus betatrifolii*, *Alphacytorhabdovirus betawuhaninsectum*, *Alphacytorhabdovirus brassicicolae*, *Alphacytorhabdovirus alphachrysanthemi*, *Alphacytorhabdovirus daphnis, Alphacytorhabdovirus fragariarugosus, Alphacytorhabdovirus gammawuhaninsectum*, *Alphacytorhabdovirus glehniae, Alphacytorhabdovirus hyptisis, Alphacytorhabdovirus kenyatuberosum, Alphacytorhabdovirus lactucamaculante, Alphacytorhabdovirus lactucanecante*, *Alphacytorhabdovirus lycopersici*, *Alphacytorhabdovirus alphamedicagonis*, *Alphacytorhabdovirus nymphaeae, Alphacytorhabdovirus pastinacae, Alphacytorhabdovirus persimmon*, *Alphacytorhabdovirus alphapogostemi*. *Alphacytorhabdovirus ribes, Alphacytorhabdovirus alpharubi, Alphacytorhabdovirus sambuci, Alphacytorhabdovirus taraxaci* and *Alphacytorhabdovirus trichosanthei*.  In addition to those reassigned species, we propose the creation of 41 new species within the genus *Alphacytorhabdovirus* to accommodate the following recently identified viruses:  **Arctium alphacytorhabdovirus 1 (ArcACRV1)** was identified from an in-silico analysis of transcriptome data of greater burdock (*Arctium lappa*) tissues from Dalian, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ArcACRV1 has 12,768 nucleotides (BK064262), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of ArcACRV1 has the highest sequence identity with that of Chrysanthemum alphacytorhabdovirus 1 (ChrACRV1; 68.7%), while the ArcACRV1 L protein amino acid sequence has the highest sequence identity with that of ChrACRV1 (80.1%) [1]. Based on ML tree generated from complete L protein sequences, ArcACRV1 is placed within a subclade of the alphacytorhabdoviruses, with ChrACRV1, and Wuhan insect virus 5 (**Figure 2A**).  **Artemisia alphacytorhabdovirus 1 (ArtACRV1)** was identified from an in-silico analysis of transcriptome data of silvery wormwood (*Artemisia argyi*) tissues from Anhui, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ArtACRV1 has 12,978 nucleotides (BK064263) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1], representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 2B**). The CCG nucleotide sequence of ArtACRV1 has the highest sequence identity with that of lettuce necrotic yellows virus (LNYV; 56.4%), while the ArtACRV1 L protein amino acid sequence has the highest sequence identity with that of LNYV (68.1%) [1]. Based on ML tree generated from complete L protein sequences, ArtACRV1 is placed within a subclade of the alphacytorhabdoviruses, with LNYV (**Figure 2A**).  **Artemisia alphacytorhabdovirus 2 (ArtACRV2)** was identified from an in-silico analysis of transcriptome data of common wormwood (*Artemisia montana*) tissues from Kyoto, Japan. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ArtACRV2 has 14,344 nucleotides (BK064264), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of ArtACRV2 has the highest sequence identity with that of Zea alphacytorhabdovirus 1 (ZeaACRV1; 63.6%), while the ArtACRV2 L protein amino acid sequence has the highest sequence identity with that of ZeaACRV1 (75.2%) [1]. Based on ML tree generated from complete L protein sequences, ArtACRV2 is placed within a subclade of the alphacytorhabdoviruses, with ZeaACRV1, and Artemisia alphacytorhabdovirus 3 (**Figure 2A**).  **Artemisia alphacytorhabdovirus 3 (ArtACRV3)** was identified from an in-silico analysis of transcriptome data of Sievers wormwood (*Artemisia sieversiana*) tissues from Inner Mongolia, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ArtACRV3 has 14,339 nucleotides (BK064265), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of ArtACRV3 has the highest sequence identity with that of Artemisia alphacytorhabdovirus 2 (ArtACRV2; 61.5%), while the ArtACRV3 L protein amino acid sequence has the highest sequence identity with that of ArtACRV2 (73.3%) [1]. Based on ML tree generated from complete L protein sequences, ArtACRV3 is placed within a subclade of the alphacytorhabdoviruses, with ArtACRV2, and Zea alphacytorhabdovirus 1 (**Figure 2A**).  **Baccharis alphacytorhabdovirus 1 (BacACRV1)** was identified from an in-silico analysis of transcriptome data of desert broom (*Baccharis sarothroides*) tissues from Sonora, Mexico. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of BacACRV1 has 13,581 nucleotides (BK064266), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of BacACRV1 has the highest sequence identity with that of Conopholis alphacytorhabdovirus 1 (ConACRV1; 56.9%), while the BacACRV1 L protein amino acid sequence has the highest sequence identity with that of ConACRV1 (68.7%) [1]. Based on ML tree generated from complete L protein sequences, BacACRV1 is placed within a subclade of the alphacytorhabdoviruses, with ConACRV1, and cabbage cytorhabdovirus (**Figure 2A**).  **Cardamine alphacytorhabdovirus 1 (CarACRV1)** was identified from an in-silico analysis of transcriptome data of large bittercress (*Cardamine amara*) tissues from Zurich, Switzerland. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CarACRV1 has 13,209 nucleotides (BK064267), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of CarACRV1 has the highest sequence identity with that of Pastinaca cytorhabdovirus 1 (PaCRV1; 66.6%), while the CarACRV1 L protein amino acid sequence has the highest sequence identity with that of PaCRV1 (78.3%) [1]. Based on ML tree generated from complete L protein sequences, CarACRV1 is placed within a subclade of the alphacytorhabdoviruses, with PaCRV1 (**Figure 2A**).  **Chelidonium yellow mottle associated virus (CheYMaV)** was identified in greater celandine (*Chelidonium majus*) plants collected in Liaoning, China. The complete genome (CG) sequence of CheYMaV has 12,121 nucleotides (OR290114), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [2] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CG nucleotide sequence of CheYMaV has the highest sequence identity with that of Trifolium pratense virus A (TpVA; 68.8%), while the CheYMaV L protein amino acid sequence has the highest sequence identity with that of TpVA (80.5%) [2]. Based on ML tree generated from complete L protein sequences, CheYMaV is placed within a subclade of the alphacytorhabdoviruses, with TpVA, and Glehnia littoralis virus 1 (**Figure 2A**).  **Chrysanthemum alphacytorhabdovirus 1 (ChrACRV1)** was identified from an in-silico analysis of transcriptome data of Indian chrysanthemum (*Chrysanthemum indicum*) tissues from Guangzhou, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ChrACRV1 has 12,715 nucleotides (BK064269), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of ChrACRV1 has the highest sequence identity with that of Arctium alphacytorhabdovirus 1 (ArcACRV1; 68.7%), while the ChrACRV1 L protein amino acid sequence has the highest sequence identity with that of ArcACRV1 (80.1%) [1]. Based on ML tree generated from complete L protein sequences, ChrACRV1 is placed within a subclade of the alphacytorhabdoviruses, with ArcACRV1, and Wuhan insect virus 5 (**Figure 2A**).  **Cnidium virus 2 (CnV2)** was identified in Senkyu root (*Cnidium officinale*) plants collected in Yeongyang-gun, South Korea. The complete genome (CG) sequence of CnV2 has 13,527 nucleotides (OQ442952), and contains eight ORFs in the order 3’-N-P´-P- P3-P4-M-G-L-5’ [3] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, an accessory protein P4 between the P3 and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CG nucleotide sequence of CnV2 has the highest sequence identity with that of Sambucus virus 1 (SaV1; 53.8%), while the CnV2 L protein amino acid sequence has the highest sequence identity with that of SaV1 (72.7%) [3]. Based on ML tree generated from complete L protein sequences, CnV2 is placed within a subclade of the alphacytorhabdoviruses, with SaV1, and Trichosanthes associated rhabdovirus virus 1 (**Figure 2A**).  **Conopholis alphacytorhabdovirus 1 (ConACRV1)** was identified from an in-silico analysis of transcriptome data of bear corn (*Conopholis americana*) tissues from China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ConACRV1 has 13,083 nucleotides (BK064270), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of ConACRV1 has the highest sequence identity with that of Baccharis alphacytorhabdovirus 1 (BacACRV1; 56.9%), while the ConACRV1 L protein amino acid sequence has the highest sequence identity with that of BacACRV1 (68.7%) [1]. Based on ML tree generated from complete L protein sequences, ConACRV1 is placed within a subclade of the alphacytorhabdoviruses, with BacACRV1, and cabbage cytorhabdovirus (**Figure 2A**).  **Coriander cytorhabdovirus 1 (CoCRV1)** was identified in coriander (*Coriandrum sativum*) plants collected in Santiago de Chile, Chile. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CoCRV1 has 14,180 nucleotides (OR536958), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [4] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of CoCRV1 has the highest sequence identity with that of Zea alphacytorhabdovirus 1 (ZeaACRV1; 57.7%), while the CoCRV1 L protein amino acid sequence has the highest sequence identity with that of ZeaACRV1 (69.6%) [4]. Based on ML tree generated from complete L protein sequences, CoCRV1 is placed within a subclade of the alphacytorhabdoviruses, with ZeaACRV1, Artemisia alphacytorhabdovirus 2, and Artemisia alphacytorhabdovirus 3 (**Figure 2A**).  **Cynara alphacytorhabdovirus 1 (CynACRV1)** was identified from an in-silico analysis of transcriptome data of cardoon (*Cynara cardunculus*) tissues from Sicily, Italy. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CynACRV1 has 13,726 nucleotides (BK064271), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of CynACRV1 has the highest sequence identity with that of Taraxacum cytorhabdovirus 1 (TCRV1; 70.5%), while the CynACRV1 L protein amino acid sequence has the highest sequence identity with that of TCRV1 (82.9%) [1]. Based on ML tree generated from complete L protein sequences, CynACRV1 is placed within a subclade of the alphacytorhabdoviruses, with TCRV1 (**Figure 2A**).  **Euphorbia alphacytorhabdovirus 1 (EupACRV1)** was identified from an in-silico analysis of transcriptome data of Fischer´s spurge (*Euphorbia fischeriana*) tissues from Inner Mongolia, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of EupACRV1 has 13,713 nucleotides (BK064272), and contains eight ORFs in the order 3’-N-P- P3-P4-M-G-P7-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, an accessory protein P4 between the P3 and M genes, and the accessory protein P7 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of EupACRV1 has the highest sequence identity with that of Persimmon virus A (PeVA; 57.6%), while the EupACRV1 L protein amino acid sequence has the highest sequence identity with that of PeVA (69.4%) [1]. Based on ML tree generated from complete L protein sequences, EupACRV1 is placed within a subclade of the alphacytorhabdoviruses, with PeVA, and wetland metagenome associated alphacytorhabdovirus 1 (**Figure 2A**).  **Ficus alphacytorhabdovirus 1 (FicACRV1)** was identified from an in-silico analysis of transcriptome data of Tikoua fig (*Ficus tikoua*) tissues from Guiyang, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of FicACRV1 has 13,839 nucleotides (BK064274), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of FicACRV1 has the highest sequence identity with that of strawberry crinkle virus (SCV; 48.6%), while the FicACRV1 L protein amino acid sequence has the highest sequence identity with that of SCV (60.4%) [1]. Based on ML tree generated from complete L protein sequences, FicACRV1 is placed within a subclade of the alphacytorhabdoviruses, with SCV (**Figure 2A**).  **Garlic alphacytorhabdovirus 1 (GarACRV1)** was identified from an in-silico analysis of transcriptome data of garlic (*Allium sativum*) tissues from Jilin, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of GarACRV1 has 13,400 nucleotides (BK064275), and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 2B**). The CCG nucleotide sequence of GarACRV1 has the highest sequence identity with that of Trifolium pratense virus B (TpVB; 47.4%), while the GarACRV1 L protein amino acid sequence has the highest sequence identity with that of TpVB (59.1%) [1]. Based on ML tree generated from complete L protein sequences, GarACRV1 is placed within a subclade of the alphacytorhabdoviruses, with TpVB, Artemisia alphacytorhabdovirus 1, lettuce necrotic yellows virus, lettuce yellow mottle virus and Primula alphacytorhabdovirus 1 (**Figure 2A**).  **Geum alphacytorhabdovirus 1 (GeuACRV1)** was identified from an in-silico analysis of transcriptome data of herb bennet (*Geum urbanum*) tissues from Priory wood, United Kingdom. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of GeuACRV1 has 12,756 nucleotides (BK064276), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of GeuACRV1 has the highest sequence identity with that of Hedera alphacytorhabdovirus 1 (HedACRV1; 72.9%), while the GeuACRV1 L protein amino acid sequence has the highest sequence identity with that of HedACRV1 (85.6%) [1]. Based on ML tree generated from complete L protein sequences, GeuACRV1 is placed within a subclade of the alphacytorhabdoviruses, with HedACRV1 (**Figure 2A**).  **Hedera alphacytorhabdovirus 1 (GeuACRV1)** was identified from an in-silico analysis of transcriptome data of English ivy (*Hedera helix*) tissues from China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of HedACRV1 has 12,588 nucleotides (BK064277), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of HedACRV1 has the highest sequence identity with that of Geum alphacytorhabdovirus 1 (GeuACRV1; 72.9%), while the HedACRV1 L protein amino acid sequence has the highest sequence identity with that of GeuACRV1 (85.6%) [1]. Based on ML tree generated from complete L protein sequences, HedACRV1 is placed within a subclade of the alphacytorhabdoviruses, with GeuACRV1 (**Figure 2A**).  **Ilex alphacytorhabdovirus 1 (IleACRV1)** was identified from an in-silico analysis of transcriptome data of plum-leaved holly (*Ilex asprella*) tissues from Hong Kong. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of IleACRV1 has 14,540 nucleotides (BK064278), and contains nine ORFs in the order 3’-N-P´-P-P3-M-G-P6-L-P8-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the accessory protein P6 between the G and L genes, an accessory protein P8 between the L gene and 5´trailer region, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of IleACRV1 has the highest sequence identity with that of Actinidia virus D (AcVD; 48.6%), while the IleACRV1 L protein amino acid sequence has the highest sequence identity with that of AcVD (60.4%) [1]. Based on ML tree generated from complete L protein sequences, IleACRV1 is placed within a subclade of the alphacytorhabdoviruses, with AcVD (**Figure 2A**).  **Medicago alphacytorhabdovirus 1 (MedACRV1)** was identified from an in-silico analysis of transcriptome data of alfalfa (*Medicago sativa*) tissues from Inner Mongolia, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of MedACRV1 has 13,586 nucleotides (BK064279), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of MedACRV1 has the highest sequence identity with that of strawberry virus 1 (StrV1; 55.6%), while the MedACRV1 L protein amino acid sequence has the highest sequence identity with that of StrV1 (67.8%) [1]. Based on ML tree generated from complete L protein sequences, MedACRV1 is placed within a subclade of the alphacytorhabdoviruses, with StrV1 and Pogostemom alphacytorhabdovirus 2 (**Figure 2A**).  **Mentha alphacytorhabdovirus 1 (MenACRV1)** was identified from an in-silico analysis of transcriptome data of horse mint (*Mentha longifolia*) tissues from Guangdong, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of MenACRV1 has 12,387 nucleotides (BK064280), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of MenACRV1 has the highest sequence identity with that of Trifolium pratense virus A (TpVA; 50.6%), while the MenACRV1 L protein amino acid sequence has the highest sequence identity with that of TpVA (62.8%) [1]. Based on ML tree generated from complete L protein sequences, MenACRV1 is placed within a subclade of the alphacytorhabdoviruses, with TpVA, Chelidonium yellow mottle associated virus, Glehnia littoralis virus 1, Pelargonium alphacytorhabdovirus1, Primula alphacytorhabdovirus 2, and rose alphacytorhabdovirus 2 (**Figure 2A**).  **Morinda alphacytorhabdovirus 1 (MorACRV1).** Two strains of this virus, named as MorACRV1\_Mor and MorACRV1\_Ile, were identified from an in-silico analysis of transcriptome data of Indian mulberry (*Morinda officinalis*) and Chinese holly (*Ilex cornuta*) tissues from Guandong and Jingzhou, China, respectively. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of MorACRV1\_Mor and MorACRV1\_Ile has 13,023 (BK064281) and 12,876 nucleotides (BK064282), respectively, and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence identity of both strains of MorACRV1 is 78.5%, while the L protein aa sequence of both strains is 89% identical. On the other hand, the CCG of both strains of MorACRV1 has the highest sequence identity with that of Pogostemom alphacytorhabdovirus 1 (PogACRV1; 51.9% and 51.8%), while the L protein amino acid sequence of both strains of MorACRV1 has the highest sequence identity with that of PogACRV1 (63.7% and 63.6%) [1]. Based on ML tree generated from complete L protein sequences, MorACRV1 is placed within a subclade of the alphacytorhabdoviruses, with PogACRV1 (**Figure 2A**).  **Oak alphacytorhabdovirus 1 (OakACRV1)** was identified from an in-silico analysis of transcriptome data of oak (*Quercus robur*) tissues from Atcham, United Kingdom. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of OakACRV1 has 12,817 nucleotides (BK064283), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of OakACRV1 has the highest sequence identity with that of Phyllostachys alphacytorhabdovirus 1 (PhyACRV1; 37.9%), while the OakACRV1 L protein amino acid sequence has the highest sequence identity with that of PhyACRV1 (46.6%) [1]. Based on ML tree generated from complete L protein sequences, OakACRV1 forms a well-supported clade with other alphacytorhabdoviruses (**Figure 2A**).  **Ocimum alphacytorhabdovirus 1 (OciACRV1)** was identified from an in-silico analysis of transcriptome data of holy basil (*Ocimum tenuiflorum*) tissues from Bangalore, India. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of OciACRV1 has 12,478 nucleotides (BK064284), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of OciACRV1 has the highest sequence identity with that of Kenyan potato cytorhabdovirus (KePCyV; 65.5%), while the OciACRV1 L protein amino acid sequence has the highest sequence identity with that of KePCyV (77.2%) [1]. Based on ML tree generated from complete L protein sequences, OciACRV1 is placed within a subclade of the alphacytorhabdoviruses, with KePCyV (**Figure 2A**).  **Pelargonium alphacytorhabdovirus 1 (PelACRV1)** was identified from an in-silico analysis of transcriptome data of scented pelargonium (*Pelargonium x hybrid*) tissues from Grasse, France. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PelACRV1 has 12,332 nucleotides (BK064285), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of PelACRV1 has the highest sequence identity with that of Primula alphacytorhabdovirus 2 (PriACRV2; 66.6%), while the PelACRV1 L protein amino acid sequence has the highest sequence identity with that of PriACRV2 (78.3%) [1]. Based on ML tree generated from complete L protein sequences, PelACRV1 is placed within a subclade of the alphacytorhabdoviruses, with PriACRV2 (**Figure 2A**).  **Phyllostachys alphacytorhabdovirus 1 (PhyACRV1)** was identified from an in-silico analysis of transcriptome data of moso bamboo (*Phyllostachys edulis*) tissues from Sichuan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PhyACRV1 has 12,947 nucleotides (BK064286), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of PhyACRV1 has the highest sequence identity with that of Strawberry virus 2 (StrV2; 46.4%), while the PhyACRV1 L protein amino acid sequence has the highest sequence identity with that of StrV2 (57.8%) [1]. Based on ML tree generated from complete L protein sequences, PhyACRV1 forms a well-supported clade with other alphacytorhabdoviruses (**Figure 2A**).  **Pinellia alphacytorhabdovirus 1 (PinACRV1)** was identified from an in-silico analysis of transcriptome data of Peltate green dragon (*Pinellia peltata*) tissues from Sichuan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PinACRV1 has 13,438 nucleotides (BK064287), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of PinACRV1 has the highest sequence identity with that of Triticum alphacytorhabdovirus 1 (TriACRV1; 57.3%), while the PinACRV1 L protein amino acid sequence has the highest sequence identity with that of TriACRV1 (68.9%) [1]. Based on ML tree generated from complete L protein sequences, PinACRV1 is placed within a subclade of the alphacytorhabdoviruses, with TriACRV1 and Rubus alphacytorhabdovirus 1 (**Figure 2A**).  **Plumbago necrotic spot associated virus (PNSaV)** was identified in scarlet leadwort (*Plumbago indica*) plants collected in Beijing, China. The complete genome (CG) sequence of PNSaV has 13,180 nucleotides (OR335651), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [5] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CG nucleotide sequence of PNSaV has the highest sequence identity with that of Cardamine alphacytorhabdovirus 1 (CarACRV1; 47.7%), while the PNSaV L protein amino acid sequence has the highest sequence identity with that of CarACRV1 (58.1%). Based on ML tree generated from complete L protein sequences, PNSaV is placed within a subclade of the alphacytorhabdoviruses, with CarACRV1, chrysanthemum yellow dwarf associated virus, Pastinaca cytorhabdovirus 1, and Utricularia alphacytorhabdovirus 1 (**Figure 2A**).  **Pogostemom alphacytorhabdovirus 1 (PogACRV1).** Three strains of this virus, named as PogALCRV1\_Pip, PogACRV1\_Pog and PogALCRV1\_Sol, were identified from an in-silico analysis of transcriptome data of black pepper (*Piper nigrum*), patchouli (*Pogostemom cablin*) and tropical soda apple (*Solanum viarum*) tissues from Agra, India, Hainan, China, and India, respectively. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PogALCRV1\_Pip, PogACRV1\_Pog and MorALCRV1\_Sol has 13,063 (BK064289), 13,171 (BK064288) and 13,138 nucleotides (BK064290), respectively, and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence identity of the three strains of PogACRV1 ranged from 82.5% to 84.3%, while the L protein aa sequence identity of the three strains of PogACRV1 ranged from 93% to 96.3%. On the other hand, the CCG of the three strains of PogACRV1 has the highest sequence identity with that of Morinda alphacytorhabdovirus 1 (MorACRV1; 51.9%, 51.8% and 51.6%), while the L protein amino acid sequence of both strains of PogACRV1 has the highest sequence identity with that of MorACRV1 (63.7%, 63.6% and 63.3%) [1]. Based on ML tree generated from complete L protein sequences, PogACRV1 is placed within a subclade of the alphacytorhabdoviruses, with MorACRV1 (**Figure 2A**).  **Pogostemom alphacytorhabdovirus 2 (PogACRV2)** was identified from an in-silico analysis of transcriptome data of patchouli (*Pogostemom cablin*) tissues from Hainan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PogACRV2 has 13,209 nucleotides (BK064291), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of PogACRV2 has the highest sequence identity with that of strawberry virus 1 (StrV1; 69.5%), while the PogACRV2 L protein amino acid sequence has the highest sequence identity with that of StrV1 (82%) [1]. Based on ML tree generated from complete L protein sequences, PogACRV2 is placed within a subclade of the alphacytorhabdoviruses, with StrV1 and Medicago alphacytorhabdovirus 1 (**Figure 2A**).  **Pogostemom alphacytorhabdovirus 3 (PogACRV3).** Two strains of this virus, named as PogALCRV3\_Lag and PogACRV3\_Pog, were identified from an in-silico analysis of transcriptome data of Indian crepe myrtle (*Lagerstroemia indica*) and patchouli (*Pogostemom cablin*) tissues from Jiangsu and Guangdong, China, respectively. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PogACRV3\_Lag and PogACRV3\_Pog has 13,149 (BK064293) and 13,252 nucleotides (BK064292), respectively, and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence identity of both strains of PogACRV3 is 81.5%, while the L protein aa sequence of both strains is 90.8% identical. On the other hand, the CCG of both strains of PogACRV3 has the highest sequence identity with that of Scutellaria alphacytorhabdovirus 1 (ScuACRV1; 69.7% and 69.9%), while the L protein amino acid sequence of both strains of PogACRV3 has the highest sequence identity with that of ScuACRV1 (80.1% and 80.3%) [1]. Based on ML tree generated from complete L protein sequences, PogACRV3 is placed within a subclade of the alphacytorhabdoviruses, with ScuACRV1 and Bacopa monnieri virus 1 (**Figure 2A**).  **Primula alphacytorhabdovirus 1 (PriACRV1)** was identified from an in-silico analysis of transcriptome data of candelabra primrose (*Primula chungensis*) tissues from Sichuan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PriACRV1 has 12,953 nucleotides (BK064294), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of PriACRV1 has the highest sequence identity with that of lettuce yellow mottle virus (LYMV; 62.6%), while the PriACRV1 L protein amino acid sequence has the highest sequence identity with that of LYMV (73.9%) [1]. Based on ML tree generated from complete L protein sequences, PriACRV1 is placed within a subclade of the alphacytorhabdoviruses, with LYMV and Trifolium pratense virus B (**Figure 2A**).  **Primula alphacytorhabdovirus 2 (PriACRV2)** was identified from an in-silico analysis of transcriptome data of glory primrose (*Primula oreodoxa*) tissues from Sichuan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PriACRV2 has 12,146 nucleotides (BK064295), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of PriACRV2 has the highest sequence identity with that of Pelargonium alphacytorhabdovirus 1 (PelACRV1; 66.6%), while the PriACRV2 L protein amino acid sequence has the highest sequence identity with that of PelACRV1 (78.3%) [1]. Based on ML tree generated from complete L protein sequences, PriACRV2 is placed within a subclade of the alphacytorhabdoviruses, with PelACRV1 (**Figure 2A**).  **Rose alphacytorhabdovirus 1 (RosACRV1)** was identified from an in-silico analysis of transcriptome data of beach rose (*Rosa rugosa*) tissues from Huazhong, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of MenACRV1 has 12,601 nucleotides (BK064296), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of RosACRV1 has the highest sequence identity with that of Trifolium pratense virus A (TpVA; 53.6%), while the RosACRV1 L protein amino acid sequence has the highest sequence identity with that of TpVA (64.9%) [1]. Based on ML tree generated from complete L protein sequences, RosACRV1 is placed within a subclade of the alphacytorhabdoviruses, with TpVA, Chelidonium yellow mottle associated virus, Glehnia littoralis virus 1, Pelargonium alphacytorhabdovirus1 and Primula alphacytorhabdovirus 2 (**Figure 2A**).  **Rubus alphacytorhabdovirus 1 (RubACRV1)** was identified from an in-silico analysis of transcriptome data of Korena bramble (*Rubus coreanus*) tissues from Sichuan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of RubACRV1 has 14,682 nucleotides (BK064297), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of RubACRV1 has the highest sequence identity with that of Triticum alphacytorhabdovirus 1 (TriACRV1; 41.3%), while the RubACRV1 L protein amino acid sequence has the highest sequence identity with that of TpVA (52.8%) [1]. Based on ML tree generated from complete L protein sequences, RubACRV1 is placed within a subclade of the alphacytorhabdoviruses, with TriACRV1, and Pinellia alphacytorhabdovirus 1 (**Figure 2A**).  **Scutellaria alphacytorhabdovirus 1 (ScuACRV1)** was identified from an in-silico analysis of transcriptome data of barbed skullcap (*Scutellaria barbata*) tissues from Shangai, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ScuACRV1 has 13,187 nucleotides (BK064298), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of ScuACRV1 has the highest sequence identity with that of Pogostemom alphacytorhabdovirus 3 (PogACRV3; 69.9%), while the ScuACRV1 L protein amino acid sequence has the highest sequence identity with that of PogACRV3 (80.3%) [1]. Based on ML tree generated from complete L protein sequences, ScuACRV1 is placed within a subclade of the alphacytorhabdoviruses, with PogACRV3 (**Figure 2A**).  **Tolmiea alphacytorhabdovirus 1 (TolACRV1)** was identified from an in-silico analysis of transcriptome data of piggyback plant (*Tolmiea menziesii*) tissues from Washington, USA. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of TolACRV1 has 12,746 nucleotides (BK064299), and contains seven ORFs in the order 3’-N-P´-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the overlapping ORF within the P-encoding ORF, which is named P´ (**Figure 2B**). The CCG nucleotide sequence of TolACRV1 has the highest sequence identity with that of blackcurrant rhabdovirus 2 (BCRV2; 65.6%), while the TolACRV1 L protein amino acid sequence has the highest sequence identity with that of BCRV2 (76.5%) [1]. Based on ML tree generated from complete L protein sequences, TolACRV1 is placed within a subclade of the alphacytorhabdoviruses, with BCRV2 (**Figure 2A**).  **Triticum alphacytorhabdovirus 1 (TriACRV1)** was identified from an in-silico analysis of transcriptome data of wheat (*Triticum aestivum*) tissues from Hebei, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of TriACRV1 has 13,955 nucleotides (BK064300), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of TriACRV1 has the highest sequence identity with that of Pinellia alphacytorhabdovirus 1 (PinACRV1; 57.3%), while the TriACRV1 L protein amino acid sequence has the highest sequence identity with that of PinACRV1 (68.9%) [1]. Based on ML tree generated from complete L protein sequences, TriACRV1 is placed within a subclade of the alphacytorhabdoviruses, with PinACRV1 and Rubus alphacytorhabdovirus 1 (**Figure 2A**).  **Utricularia alphacytorhabdovirus 1 (UtrACRV1)** was identified from an in-silico analysis of transcriptome data of long-leaved bladderwort (*Utricularia longifolia*) tissues from Nanjing, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of UtrACRV1 has 13,017 nucleotides (BK064301), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of UtrACRV1 has the highest sequence identity with that of Cardamine alphacytorhabdovirus 1 (CarACRV1; 48.8%), while the UtrACRV1 L protein amino acid sequence has the highest sequence identity with that of CarACRV1 (59.6%) [1]. Based on ML tree generated from complete L protein sequences, UtrACRV1 is placed within a subclade of the alphacytorhabdoviruses, with CarACRV1 and Pastinaca cytorhabdovirus 1 (**Figure 2A**).  **Wetland metagenome associated alphacytorhabdovirus 1 (WMaACRV1)** was identified from an in-silico analysis of transcriptome data of wetland freshwater samples from Ohio, USA. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of WMaACRV1 has 12,726 nucleotides (BK064302), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of WMaACRV1 has the highest sequence identity with that of Persimmon virus A (PeVA; 51.5%), while the WMaACRV1 L protein amino acid sequence has the highest sequence identity with that of PeVA (62.7%) [1]. Based on ML tree generated from complete L protein sequences, WMaACRV1 is placed within a subclade of the alphacytorhabdoviruses, with PeVA and Euphorbia alphacytorhabdovirus 1 (**Figure 2A**).  **Wurfbainia alphacytorhabdovirus 1 (WurACRV1)** was identified from an in-silico analysis of transcriptome data of Malabar cardamon (*Wurfbainia villosa*) tissues from Guangdong, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of WurACRV1 has 13,348nucleotides (BK064303), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of WurACRV1 has the highest sequence identity with that of Scutellaria alphacytorhabdovirus 1 (ScuACRV1; 46.5%), while the WurACRV1 L protein amino acid sequence has the highest sequence identity with that of ScuACRV1 (57.3%) [1]. Based on ML tree generated from complete L protein sequences, WurACRV1 is placed within a subclade of the alphacytorhabdoviruses, with ScuACRV1, Bacopa monnieri virus 1 and Pogostemom alphacytorhabdovirus 3 (**Figure 2A**).  **Zea alphacytorhabdovirus 1 (ZeaACRV1)** was identified from an in-silico analysis of transcriptome data of maize (*Zea mays*) tissues from Anhui, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ZeaACRV1 has 14,358 nucleotides (BK064304), and contains eight ORFs in the order 3’-N-P´-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the overlapping ORF within the P-encoding ORF, which is named P´, and the accessory protein P6 between the G and L genes (**Figure 2B**). The CCG nucleotide sequence of ZeaACRV1 has the highest sequence identity with that of Artemisia alphacytorhabdovirus 2 (ArtACRV2; 63.6%), while the ZeaACRV1 L protein amino acid sequence has the highest sequence identity with that of ArtACRV2 (75.2%) [1]. Based on ML tree generated from complete L protein sequences, ZeaACRV1 is placed within a subclade of the alphacytorhabdoviruses, with ArtACRV2, and Artemisia alphacytorhabdovirus 3 (**Figure 2A**).  ArcACRV1, ArtACRV1, ArtACRV2, ArtACRV3, BacACRV1, CarACRV1, CheYMaVACRV1, ChrACRV1, CnV2, ConACRV1, CoCRV1, CinACRV1, EupACRV1, FicACRV1, GarACRV1, GeuACRV1, HedACRV1, IleACRV1, MedACRV1, MenACRV1, MorACRV1, OakACRV1, OciACRV1, PelACRV1, PhyACRV1, PinACRV1, PNSaV, PogACRV1, PogACRV2, PogACRV3, PriACRV1, PriACRV2, RosACRV1, RubACRV1, ScuACRV1, TolACRV1, TriACRV1, UtrACRV1, WMaACRV1, WurACRV1 and ZeaACRV1 meet the demarcation criteria A and B. Thus, we propose to classify ArcACRV1, ArtACRV1, ArtACRV2, ArtACRV3, BacACRV1, CarACRV1, CheYMaVACRV1, ChrACRV1, CnV2, ConACRV1, CoCRV1, CinACRV1, EupACRV1, FicACRV1, GarACRV1, GeuACRV1, HedACRV1, IleACRV1, MedACRV1, MenACRV1, MorACRV1, OakACRV1, OciACRV1, PelACRV1, PhyACRV1, PinACRV1, PNSaV, PogACRV1, PogACRV2, PogACRV3, PriACRV1, PriACRV2, RosACRV1, RubACRV1, ScuACRV1, TolACRV1, TriACRV1, UtrACRV1, WMaACRV1, WurACRV1 and ZeaACRV1 in the new species *Alphacytorhabdovirus arctii*, *Alphacytorhabdovirus alphaartemisiae*, *Alphacytorhabdovirus betaartemisiae*, *Alphacytorhabdovirus gammaartemisiae*, *Alphacytorhabdovirus baccharis*, *Alphacytorhabdovirus cardaminis*, *Alphacytorhabdovirus chelidonii*, *Alphacytorhabdovirus betachrysanthemi*, *Alphacytorhabdovirus cnidii*, *Alphacytorhabdovirus conopholis*, *Alphacytorhabdovirus coriandri*, *Alphacytorhabdovirus cynarae*, *Alphacytorhabdovirus euphorbiae*, *Alphacytorhabdovirus fici*, *Alphacytorhabdovirus allii*, *Alphacytorhabdovirus gei*, *Alphacytorhabdovirus hederae*, *Alphacytorhabdovirus ilicis*, *Alphacytorhabdovirus betamedicagonis*, *Alphacytorhabdovirus menthae*, *Alphacytorhabdovirus morindae*, *Alphacytorhabdovirus querci*, *Alphacytorhabdovirus ocimi*, *Alphacytorhabdovirus pelargonii*, *Alphacytorhabdovirus phyllostachysis*, *Alphacytorhabdovirus pinelliae*, *Alphacytorhabdovirus plumbagonis*, *Alphacytorhabdovirus betapogostemi*, *Alphacytorhabdovirus gammapogostemi*, *Alphacytorhabdovirus deltapogostemi*, *Alphacytorhabdovirus alphaprimulae*, *Alphacytorhabdovirus betaprimulae*, *Alphacytorhabdovirus rosae*, *Alphacytorhabdovirus betarubi*, *Alphacytorhabdovirus scutellariae*, *Alphacytorhabdovirus tolmieae*, *Alphacytorhabdovirus tritici*, *Alphacytorhabdovirus utriculariae*, *Alphacytorhabdovirus paludis*, *Alphacytorhabdovirus wurfbainiae*, and *Alphacytorhabdovirus zeae*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*.  **Genus *Betacytorhabdovirus***  The genomic organization of betacytorhabdoviruses is quite diverse, with 16 distinct genomic organizations discernable among its putative members (**Figure 3B**) suggesting a complex evolutionary history [1]. Moreover, the observed phylogenetic relationships suggest a common evolutionary history for betacytorhabdoviruses, where several evolutionary clades could be distinguished (**Figure 3A**) [1].  Interestingly, many betacytorhabdoviruses have woody dicots as associated host plants. Thus, many betacytorhabdoviruses likely infect woody dicots, which may be a distinctive feature of this group of viruses. [1]. Furthermore, the consensus gene junction sequences among the betacytorhabdoviruses showed some variability, but there appears to be a correlation with the phylogenetic relationships thus supporting a common evolutionary history for these viruses [1].  Some betacytorhabdoviruses have been shown to be transmitted by planthoppers, others by leafhoppers and others by whiteflies. We, therefore, predict that the potential vectors of the novel betacytorhabdoviruses may be whiteflies, planthoppers, leafhoppers and likely non-aphid arthropods, like psyllids. Those betacytorhabdoviruses that lack the G gene or with a shorter G gene are likely vertically transmitted [1].  We propose that the species *Cytorhabdovirus rosae, Cytorhabdovirus anthurii, Cytorhabdovirus bemisiae, Cytorhabdovirus betarosae* *Cytorhabdovirus broussonetiae*, *Cytorhabdovirus caricae*, *Cytorhabdovirus colocasiae*, *Cytorhabdovirus cucurbitae*, *Cytorhabdovirus flaviyerbamate, Cytorhabdovirus glycinis, Cytorhabdovirus gramineae*, *Cytorhabdovirus hordei*, *Cytorhabdovirus maydis*, *Cytorhabdovirus maysflavostriatis*, *Cytorhabdovirus oryzae*, *Cytorhabdovirus rudbeckiae, Cytorhabdovirus* *tagetis*, *Cytorhabdovirus tiliae* and *Cytorhabdovirus yerbamate* shall be moved into the genus *Betacytorhabdovirus* and be renamed *Betacytorhabdovirus alpharosae, Betacytorhabdovirus anthurii, Betacytorhabdovirus bemisiae, Betacytorhabdovirus betarosae,* *Betacytorhabdovirus broussonetiae*, *Betacytorhabdovirus caricae*, *Betacytorhabdovirus colocasiae*, *Betacytorhabdovirus alphacucurbitae*, *Betacytorhabdovirus flaviyerbamate, Betacytorhabdovirus glycinis, Betacytorhabdovirus gramineae*, *Betacytorhabdovirus hordei*, *Betacytorhabdovirus maydis*, *Betacytorhabdovirus maysflavostriatis*, *Betacytorhabdovirus oryzae*, *Betacytorhabdovirus rudbeckiae, Betacytorhabdovirus* *tagetis*, *Betacytorhabdovirus tiliae* and *Betacytorhabdovirus yerbamate*.  In addition to those reassigned species, we propose the creation of 41 new species within the genus *Betacytorhabdovirus* to accommodate the following recently identified viruses:  **Aristolochia associated cytorhabdovirus (AaCV)** was identified in Aristolochia (*Aristolochia gibertii*) plants collected in Sao Paulo, Brazil. The complete genome (CG) sequence of AaCV has 13,128 nucleotides (OR090884), and contains seven ORFs in the order 3’-N-P- P3-P4-M-G-L-5’ [6] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and an accessory protein P4 between the P3 and M genes (**Figure 3B**). The CG nucleotide sequence of AaCV has the highest sequence identity with that of yerba mate chlorosis-associated virus (YmCaV; 50.3%), while the AaCV L protein amino acid sequence has the highest sequence identity with that of YmCaV (54.9%) [6]. Based on ML tree generated from complete L protein sequences, AaCV is placed within a subclade of the betacytorhabdoviruses, with YmCaV (**Figure 3A**).  **Artemisia betacytorhabdovirus 1 (ArtBCRV1)** was identified from an in-silico analysis of transcriptome data of rock wormwood (*Artemisia rupestris*) tissues from Xinjiang, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ArtBCRV1 has 13,426 nucleotides (BK064305), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of ArtBCRV1 has the highest sequence identity with that of Chrysanthemum betacytorhabdovirus 1 (ChrBCRV1; 55.3%), while the ArtBCRV1 L protein amino acid sequence has the highest sequence identity with that of ChrBCRV1 (61.4%) [1]. Based on ML tree generated from complete L protein sequences, ArtBCRV1 is placed within a subclade of the betacytorhabdoviruses, with ChrBCRV1 (**Figure 3A**).  **Begonia betacytorhabdovirus 1 (BegBCRV1)** was identified from an in-silico analysis of transcriptome data of zip begonia (*Begonia conchifolia*) tissues from Edinburgh, United Kingdom. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of BegBCRV1 has 13,838 nucleotides (BK064306), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of BegBCRV1 has the highest sequence identity with that of Pentaphragma betacytorhabdovirus 1 (PenBCRV1; 44.3%), while the BegBCRV1 L protein amino acid sequence has the highest sequence identity with that of PenBCRV1 (48.9%) [1]. Based on ML tree generated from complete L protein sequences, BegBCRV1 is placed within a subclade of the betacytorhabdoviruses, with PenBCRV1 and Howea betacytorhabdovirus 1(**Figure 3A**).  **Betula betacytorhabdovirus 1 (BetBCRV1)** was identified from an in-silico analysis of transcriptome data of white birch (*Betula pendula*) tissues from Finland. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of BetBCRV1 has 14,744 nucleotides (BK064307), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of BetBCRV1 has the highest sequence identity with that of Betula betacytorhabdovirus 2 (BetBCRV2; 71.3%), while the BetBCRV1 L protein amino acid sequence has the highest sequence identity with that of BetBCRV2 (80%) [1]. Based on ML tree generated from complete L protein sequences, BetBCRV1 is placed within a subclade of the betacytorhabdoviruses, with BetBCRV2 and Corylus betacytorhabdovirus 1(**Figure 3A**).  **Betula betacytorhabdovirus 2 (BetBCRV2)** was identified from an in-silico analysis of transcriptome data of Himalayan birch (*Betula utilis*) tissues from India. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of BetBCRV2 has 15,147 nucleotides (BK064308), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of BetBCRV2 has the highest sequence identity with that of Betula betacytorhabdovirus 1 (BetBCRV1; 71.3%), while the BetBCRV2 L protein amino acid sequence has the highest sequence identity with that of BetBCRV1(80%) [1]. Based on ML tree generated from complete L protein sequences, BetBCRV2 is placed within a subclade of the betacytorhabdoviruses, with BetBCRV1 and Corylus betacytorhabdovirus 1(**Figure 3A**).  **Bouteloa betacytorhabdovirus 1 (BouBCRV1)** was identified from an in-silico analysis of transcriptome data of buffalo grass (*Bouteloa dactyloides*) tissues from Nebraska, USA. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of BouBCRV1 has 14,127 nucleotides (BK064309), and contains nine ORFs in the order 3’-N-P- P3-M-G-P6-P7-P8-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory proteins P6, P7 and P8 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of BouBCRV1 has the highest sequence identity with that of peat soil associated betacytorhabdovirus 2 (PSaBCRV2; 54.7%), while the BouBCRV1 L protein amino acid sequence has the highest sequence identity with that of PSaBCRV2 (60.3%) [1]. Based on ML tree generated from complete L protein sequences, BouBCRV1 is placed within a subclade of the betacytorhabdoviruses, with PSaBCRV2 (**Figure 3A**).  **Chrysanthemum betacytorhabdovirus 1 (ChrBCRV1)** was identified from an in-silico analysis of transcriptome data of hardy garden mum (*Chrysanthemum morifolium*) tissues from Hefei, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ChrBCRV1 has 13,309 nucleotides (BK064310), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of ChrBCRV1 has the highest sequence identity with that of Artemisia betacytorhabdovirus 1 (ArtBCRV1; 55.3%), while the ChrBCRV1 L protein amino acid sequence has the highest sequence identity with that of ArtBCRV1 (61.4%) [1]. Based on ML tree generated from complete L protein sequences, ChrBCRV1 is placed within a subclade of the betacytorhabdoviruses, with ArtBCRV1 (**Figure 3A**).  **Corylus betacytorhabdovirus 1 (CorBCRV1)** was identified from an in-silico analysis of transcriptome data of Siberian hazelnut (*Corylus heterophylla*) tissues from Liaoning, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CorBCRV1 has 15,228 nucleotides (BK064311), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of CorBCRV1 has the highest sequence identity with that of Betula betacytorhabdovirus 2 (BetBCRV2; 64.3%), while the CorBCRV1 L protein amino acid sequence has the highest sequence identity with that of BetBCRV2 (70.8%) [1]. Based on ML tree generated from complete L protein sequences, CorBCRV1 is placed within a subclade of the betacytorhabdoviruses, with BetBCRV2 and Betula betacytorhabdovirus 1 (**Figure 3A**).  **Cucurbita betacytorhabdovirus 1 (CucBCRV1)** was identified from an in-silico analysis of transcriptome data of buffalo gourd (*Cucurbita foetidissima*) tissues from California, USA. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CucBCRV1 has 12,969 nucleotides (BK064312), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of CucBCRV1 has the highest sequence identity with that of Chrysanthemum betacytorhabdovirus 1 (ChrBCRV1; 42.4%), while the CucBCRV1 L protein amino acid sequence has the highest sequence identity with that of ChrBCRV1 (49.6%) [1]. Based on ML tree generated from complete L protein sequences, CucBCRV1 is placed within a subclade of the betacytorhabdoviruses, with ChrBCRV1 and Artemisia betacytorhabdovirus 1 (**Figure 3A**).  **Cypripedium betacytorhabdovirus 1 (CypBCRV1)** was identified from an in-silico analysis of transcriptome data of slipper orchid (*Cypripedium flavum*) tissues from Sichuan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CypBCRV1 has 9,958 nucleotides (BK064313) and contains four ORFs in the order 3’-N-P-P3-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 between the P and L genes. Interestingly this virus genome lacked the M and G genes (**Figure 3B**). The CCG nucleotide sequence of CypBCRV1 has the highest sequence identity with that of mango betacytorhabdovirus 1 (ManBCRV1; 33.8%), while the CypBCRV1 L protein amino acid sequence has the highest sequence identity with that of ManBCRV1 (37.5%) [1]. Based on ML tree generated from complete L protein sequences, CypBCRV1 is placed within a subclade of the betacytorhabdoviruses, with ManBCRV1 (**Figure 3A**).  **Dryobalanops betacytorhabdovirus 1 (DryBCRV1)** was identified from an in-silico analysis of transcriptome data of keladan (*Dryobalanops oblongifolia*) tissues from Malaysia. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of DryBCRV1 has 14,393 nucleotides (BK064314) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus genome has a short G gene [1]. The CCG nucleotide sequence of DryBCRV1 has the highest sequence identity with that of Phellodendron betacytorhabdovirus 1 (PheBCRV1; 49.4%), while the DryBCRV1 L protein amino acid sequence has the highest sequence identity with that of PheBCRV1 (54.2%) [1]. Based on ML tree generated from complete L protein sequences, DryBCRV1 is placed within a subclade of the betacytorhabdoviruses, with PheBCRV1, within a well-supported clade with those betacytorhabdoviruses that have the shorter G gene (**Figure 3A**).  **Durio betacytorhabdovirus 1 (DurBCRV1)** was identified from an in-silico analysis of transcriptome data of durian (*Durio zibethinus*) tissues from Pahang, Malaysia. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of DurBCRV1 has 12,791 nucleotides (BK064315), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of DurBCRV1 has the highest sequence identity with that of Trifolium betacytorhabdovirus 1 (TriBCRV1; 52.4%), while the DurBCRV1 L protein amino acid sequence has the highest sequence identity with that of TriBCRV1 (57.3%) [1]. Based on ML tree generated from complete L protein sequences, DurBCRV1 is placed within a subclade of the betacytorhabdoviruses, with TriBCRV1 (**Figure 3A**).  **Gleditsia betacytorhabdovirus 1 (GleBCRV1)** was identified from an in-silico analysis of transcriptome data of littleleaf honey locust (*Gleditsia microphylla*) tissues from Hebei, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of GleBCRV1 has 13,339 nucleotides (BK064316) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus has a shorter G gene than most other betacytorhabdoviruses [1]. The CCG nucleotide sequence of GleBCRV1 has the highest sequence identity with that of Dryobalanops betacytorhabdovirus 1 (DryBCRV1; 41.4%), while the GleBCRV1 L protein amino acid sequence has the highest sequence identity with that of DryBCRV1 (45.7%) [1]. Based on ML tree generated from complete L protein sequences, GleBCRV1 forms a well-supported clade with those betacytorhabdoviruses that have the shorter G gene (**Figure 3A**).  **Glycyrrhiza betacytorhabdovirus 1 (GlyBCRV1)** was identified from an in-silico analysis of transcriptome data of Chinese licorice (*Glycyrrhiza inflata*) tissues from Guangzhou, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of GlyBCRV1 has 14,755 nucleotides (BK064317) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus genome has a shorter G gene than most other betacytorhabdoviruses [1]. The CCG nucleotide sequence of GlyBCRV1 has the highest sequence identity with that of goji cytorhabdovirus A (GCVA; 47.4%), while the GlyBCRV1 L protein amino acid sequence has the highest sequence identity with that of GCVA (52.8%) [1]. Based on ML tree generated from complete L protein sequences, GlyBCRV1 is placed within a subclade of the betacytorhabdoviruses, with GCVA and Sophora betacytorhabdovirus 1, within a well-supported clade with the betacytorhabdoviruses that have the shorter G gene (**Figure 3A**).  **Goji cytorhabdovirus A (GCVA)** was identified in goji (*Lycium barbarum*) plants collected in Ningxia, China. The complete genome (CG) sequence of GCVA has 14,812 nucleotides (OR489165), and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [7] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus genome has a shorter G gene [7]. The CG nucleotide sequence of GCVA has the highest sequence identity with that of Sophora betacytorhabdovirus 1 (SopBCRV1; 50.4%), while the GCVA L protein amino acid sequence has the highest sequence identity with that of SopBCRV1 (55.5%). Based on ML tree generated from complete L protein sequences, GCVA is placed within a subclade of the betacytorhabdoviruses, with SopBCRV1, within a well-supported clade with those betacytorhabdoviruses that have the shorter G gene (**Figure 3A**).  **Hepatica betacytorhabdovirus 1 (HepBCRV1)** was identified from an in-silico analysis of transcriptome data of pennywort (*Hepatica nobilis*) tissues from Japan. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of HepBCRV1 has 10,440 nucleotides (BK064318), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes. Interestingly this virus genome lacked a G gene (**Figure 3B**). The CCG nucleotide sequence of HepBCRV1 has the highest sequence identity with that of rose virus R (RVR; 43.8%), while the HepBCRV1 L protein amino acid sequence has the highest sequence identity with that of RVRV (48.5%) [1]. Based on ML tree generated from complete L protein sequences, HepBCRV1 is placed within a subclade of the betacytorhabdoviruses, with RVR (**Figure 3A**).  **Howea betacytorhabdovirus 1 (HowBCRV1)** was identified from an in-silico analysis of transcriptome data of kentia palm (*Howea forsteriana*) tissues from Lord Howe Island, Australia. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of HowBCRV1 has 13,727 nucleotides (BK064319), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of HowBCRV1 has the highest sequence identity with that of Begonia betacytorhabdovirus 1 (BegBCRV1; 40.4%), while the HowBCRV1 L protein amino acid sequence has the highest sequence identity with that of BegBCRV1 (45.5%) [1]. Based on ML tree generated from complete L protein sequences, HowBCRV1 is placed within a subclade of the betacytorhabdoviruses, with BegBCRV1 and Pentaphragma betacytorhabdovirus 1 (**Figure 3A**).  **Ipomoea betacytorhabdovirus 1 (IpoBCRV1)** was identified from an in-silico analysis of transcriptome data of sweet potato (*Ipomoea batatas*) tissues from Mpumalanga, South Africa. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of IpoBCRV1 has 12,811 nucleotides (BK064320), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of IpoBCRV1 has the highest sequence identity with that of Artemisia betacytorhabdovirus 1 (ArtBCRV1; 44.4%), while the IpoBCRV1 L protein amino acid sequence has the highest sequence identity with that of ArtBCRV1 (49.6%) [1]. Based on ML tree generated from complete L protein sequences, IpoBCRV1 is placed within a subclade of the betacytorhabdoviruses, with ArtBCRV1, Chrysanthemum betacytorhabdovirus 1 and Cucurbita betacytorhabdovirus 1 (**Figure 3A**).  **Ixeris denticulata associated rhabdovirus (IdaRV)** was identified in Maiden´s revenge (*Ixeris denticulata*) plants collected in Beijing, China. The complete genome (CG) sequence of IdaRV has 12,705 nucleotides (OQ927981) and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [8] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes. Interestingly this virus lacked the G gene (**Figure 3B**). The CG nucleotide sequence of IdaRV has the highest sequence identity with that of Rudbeckia virus 1 (RudV1; 53%), while the IdaRV L protein amino acid sequence has the highest sequence identity with that of RudV1 (57.1%) [8]. Based on ML tree generated from complete L protein sequences, IdaRV is placed within a subclade of the betacytorhabdoviruses, with RudV1 and Tagetes erecta virus 1 (**Figure 3A**).  **Justicia betacytorhabdovirus 1 (JusBCRV1)** was identified from an in-silico analysis of transcriptome data of Malabar nut (*Justicia adhatoda*) tissues from Chengalpattu, India. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of JusBCRV1 has 15,957 nucleotides (BK064321), and contains nine ORFs in the order 3’-N-X-P- P3-M-G-P6-P7-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, an accessory protein X between the N and P genes, and the accessory proteins P6 and P7 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of JusBCRV1 has the highest sequence identity with that of Nitraria betacytorhabdovirus 1 (NitBCRV1; 42.7%), while the JusBCRV1 L protein amino acid sequence has the highest sequence identity with that of NitBCRV1(47.9%) [1]. Based on ML tree generated from complete L protein sequences, JusBCRV1 is placed within a subclade of the betacytorhabdoviruses, with NitBCRV1, Populus betacytorhabdovirus 1 and rose-associated cytorhabdovirus (**Figure 3A**).  **Kobresia betacytorhabdovirus 1 (KobBCRV1)** was identified from an in-silico analysis of transcriptome data of Royle´s sedge (*Kobresia royleana*) tissues from Qinghai, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of KobBCRV1 has 14,255 nucleotides (BK064322), and contains seven ORFs in the order 3’-N-P-M-G-P5-L-P7-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the accessory protein P5 between the G and L genes, and the accessory protein P7 between the L gene and the 5´trailer (**Figure 3B**). Interestingly, this virus lacks the putative cell-to-cell movement protein gene P3 [1]. The CCG nucleotide sequence of KobBCRV1 has the highest sequence identity with that of rice stripe mosaic virus (RSMV; 48.4%), while the KobBCRV1 L protein amino acid sequence has the highest sequence identity with that of RSMV (53.1%) [1]. Based on ML tree generated from complete L protein sequences, KobBCRV1 is placed within a subclade of the betacytorhabdoviruses, with RSMV (**Figure 3A**).  **Leucadendron betacytorhabdovirus 1 (LeuBCRV1)** was identified from an in-silico analysis of transcriptome data of plate-seed cornbush (*Leucadendron platyspermum*) tissues from South Africa. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of LeuBCRV1 has 12,698 nucleotides (BK064323), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of LeuBCRV1 has the highest sequence identity with that of Schiedea betacytorhabdovirus 1 (SchBCRV1; 42.4%), while the LeuBCRV1 L protein amino acid sequence has the highest sequence identity with that of SchBCRV1 (48.1%) [1]. Based on ML tree generated from complete L protein sequences, LeuBCRV1 is placed within a subclade of the betacytorhabdoviruses, with SchBCRV1 (**Figure 3A**).  **Mango betacytorhabdovirus 1 (ManBCRV1)** was identified from an in-silico analysis of transcriptome data of mango (*Mangifera indica*) tissues from Hainan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ManBCRV1 has 13,826 nucleotides (BK064325), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of ManBCRV1 has the highest sequence identity with that of Cypripedium betacytorhabdovirus 1 (CypBCRV1; 33.8%), while the ManBCRV1 L protein amino acid sequence has the highest sequence identity with that of CypBCRV1 (37.5%) [1]. Based on ML tree generated from complete L protein sequences, ManBCRV1 is placed within a subclade of the betacytorhabdoviruses, with CypBCRV1 (**Figure 3A**).  **Morus betacytorhabdovirus 1 (MorBCRV1)** was identified from an in-silico analysis of transcriptome data of white mulberry (*Morus alba*) tissues from Hunan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of MorBCRV1 has 15,904 nucleotides (BK064326) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus has a short G gene [1]. The CCG nucleotide sequence of MorBCRV1 has the highest sequence identity with that of Phellodendron betacytorhabdovirus 1 (PheBCRV1; 44.4%), while the MorBCRV1 L protein amino acid sequence has the highest sequence identity with that of PheBCRV1 (48.7%) [1]. Based on ML tree generated from complete L protein sequences, MorBCRV1 forms a well-supported clade with those betacytorhabdoviruses that have the shorter G gene (**Figure 3A**).  **Nitraria betacytorhabdovirus 1 (NitBCRV1)** was identified from an in-silico analysis of transcriptome data of nitre bush (*Nitraria tangutorum*) tissues from Inner Mongolia, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of NitBCRV1 has 15,520 nucleotides (BK064327), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of NitBCRV1 has the highest sequence identity with that of Populus betacytorhabdovirus 1 (PopBCRV1; 62.4%), while the NitBCRV1 L protein amino acid sequence has the highest sequence identity with that of PopBCRV1 (67.8%) [1]. Based on ML tree generated from complete L protein sequences, NitBCRV1 is placed within a subclade of the betacytorhabdoviruses, with PopBCRV1 (**Figure 3A**).  **Panicum betacytorhabdovirus 1 (PanBCRV1)** was identified from an in-silico analysis of transcriptome data of Hall´s panicgrass (*Panicum hallii*) tissues from Texas, USA. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PanBCRV1 has 12,136 nucleotides (BK064328) and contains seven ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). The CCG nucleotide sequence of PanBCRV1 has the highest sequence identity with that of Colocasia bobone disease-associated virus (CBDaV; 71.4%), while the PanBCRV1 L protein amino acid sequence has the highest sequence identity with that of CBDaV (75.9%) [1]. Based on ML tree generated from complete L protein sequences, PanBCRV1 is placed within a subclade of the betacytorhabdoviruses, with CBDaV (**Figure 3A**).  **Passiflora betacytorhabdovirus 1 (PasBCRV1)** was identified from an in-silico analysis of transcriptome data of blue passionflower (*Passiflora caerulea*) tissues from China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PasBCRV1 has 13,471 nucleotides (BK064329), and contains eight ORFs in the order 3’-N-P- P3-P4-M-G-P7-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, an accessory protein P4 between the P3 and M genes, and the accessory protein P7 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of PasBCRV1 has the highest sequence identity with that of Tilia cytorhabdovirus 1 (TiCRV1; 58.2%), while the PasBCRV1 L protein amino acid sequence has the highest sequence identity with that of TiCRV1 (63%) [1]. Based on ML tree generated from complete L protein sequences, PasBCRV1 is placed within a subclade of the betacytorhabdoviruses, with TiCRV1 (**Figure 3A**).  **Peat soil associated betacytorhabdovirus 1 (PSaBCRV1)** was identified from an in-silico analysis of transcriptome data of wetland freshwater samples from Bavaria, Germany. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PSaBCRV1 has 12,663 nucleotides (BK064330), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of PSaBCRV1 has the highest sequence identity with that of maize yellow striate virus (MYSV; 50.4%), while the PSaBCRV1 L protein amino acid sequence has the highest sequence identity with that of MYSV (55%) [1]. Based on ML tree generated from complete L protein sequences, PSaBCRV1 is placed within a subclade of the betacytorhabdoviruses, with MYSV, barley yellow striate mosaic virus, maize-associated cytorhabdovirus and northern cereal mosaic virus (**Figure 3A**).  **Peat soil associated betacytorhabdovirus 2 (PSaBCRV2)** was identified from an in-silico analysis of transcriptome data of wetland freshwater samples from Alaska, USA. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PSaBCRV2 has 14,865 nucleotides (BK064331), and contains nine ORFs in the order 3’-N-P- P3-M-G-P6-P7-P8-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory proteins P6, P7 and P8 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of PSaBCRV2 has the highest sequence identity with that of Bouteloa betacytorhabdovirus 1 (BouBCRV1; 54.7%), while the PSaBCRV2 L protein amino acid sequence has the highest sequence identity with that of BouBCRV1 (60.3%) [1]. Based on ML tree generated from complete L protein sequences, PSaBCRV2 is placed within a subclade of the betacytorhabdoviruses, with BouBCRV1 (**Figure 3A**).  **Pentaphragma betacytorhabdovirus 1 (PenBCRV1)** was identified from an in-silico analysis of transcriptome data of Scaveola tussock (*Pentaphragma spicatum*) tissues from Guangxi, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PenBCRV1 has 12,983 nucleotides (BK064332), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of PenBCRV1 has the highest sequence identity with that of Begonia betacytorhabdovirus 1 (BegBCRV1; 44.3%), while the PenBCRV1 L protein amino acid sequence has the highest sequence identity with that of BegBCRV1 (48.9%) [1]. Based on ML tree generated from complete L protein sequences, PenBCRV1 is placed within a subclade of the betacytorhabdoviruses, with BegBCRV1 (**Figure 3A**).  **Phellodendron betacytorhabdovirus 1 (PheBCRV1)** was identified from an in-silico analysis of transcriptome data of Amur cork tree (*Phellodendron amurense*) tissues from Linjiang, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PheBCRV1 has 14,292 nucleotides (BK064333) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus genome has a shorter G gene than most other betacytorhabdoviruses [1]. The CCG nucleotide sequence of PheBCRV1 has the highest sequence identity with that of Dryobalanops betacytorhabdovirus 1 (DryBCRV1; 49.4%), while the PheBCRV1 L protein amino acid sequence has the highest sequence identity with that of DryBCRV1 (54.2%) [1]. Based on ML tree generated from complete L protein sequences, PheBCRV1 is placed within a subclade of the betacytorhabdoviruses, with DryBCRV1, within a well-supported clade with those betacytorhabdoviruses that have the shorter G gene (**Figure 3A**).  **Populus betacytorhabdovirus 1 (PopBCRV1)** was identified from an in-silico analysis of transcriptome data of desert poplar (*Populus pruinosa*) tissues from Lanzhou, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PopBCRV1 has 15,094 nucleotides (BK064334), and contains seven ORFs in the order 3’-N-P- P3-M-G-P6-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P6 between the G and L genes (**Figure 3B**). The CCG nucleotide sequence of PopBCRV1 has the highest sequence identity with that of Nitraria betacytorhabdovirus 1 (NitBCRV1; 62.4%), while the PopBCRV1 L protein amino acid sequence has the highest sequence identity with that of NitBCRV1 (67.8%) [1]. Based on ML tree generated from complete L protein sequences, PopBCRV1 is placed within a subclade of the betacytorhabdoviruses, with NitBCRV1 (**Figure 3A**).  **Pueraria betacytorhabdovirus 1 (PueBCRV1)** was identified from an in-silico analysis of transcriptome data of kudzu (*Pueraria montana*) tissues from Enshi, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of PueBCRV1 has 13,614 nucleotides (BK064335) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus genome has a short G gene [1]. The CCG nucleotide sequence of PueBCRV1 has the highest sequence identity with that of Glycyrrhiza betacytorhabdovirus 1 (GlyBCRV1; 43.6%), while the PueBCRV1 L protein amino acid sequence has the highest sequence identity with that of GlyBCRV1 (48.1%) [1]. Based on ML tree generated from complete L protein sequences, PueBCRV1 forms a well-supported clade with those betacytorhabdoviruses that have the shorter G gene (**Figure 3A**).  **Schiedea betacytorhabdovirus 1 (SchBCRV1)** was identified from an in-silico analysis of transcriptome data of five-stemmed schiedea (*Schiedea pentandra*) tissues from Oxford, United Kingdom. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of SchBCRV1 has 12,964 nucleotides (BK064338), and contains seven ORFs in the order 3’-N-P- P3-M-G-L-P7-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P7 between the L gene and the 5´trailer region (**Figure 3B**). The CCG nucleotide sequence of SchBCRV1 has the highest sequence identity with that of Leucadendron betacytorhabdovirus 1 (LeuBCRV1; 42.4%), while the SchBCRV1 L protein amino acid sequence has the highest sequence identity with that of LeuBCRV1 (48.1%) [1]. Based on ML tree generated from complete L protein sequences, SchBCRV1 is placed within a subclade of the betacytorhabdoviruses, with LeuBCRV1 (**Figure 3A**).  **Sesamum betacytorhabdovirus 1 (SesBCRV1).** Two strains of this virus, named SesBCRV1\_Cat and SesBCRV1\_Ses, were identified from an in-silico analysis of transcriptome data of Madagascar periwinkle (*Catharanthus roseus*) and sesame (*Sesamum indicum*) tissues from New Delhi and Kolkata, India, respectively. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of SesBCRV1\_Cat and SesBCRV1\_Ses has 13,497 (BK064337) and 13,565 nucleotides (BK064336), respectively, and contains seven ORFs in the order 3’-N-P- P3-P4-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and an accessory protein P4 between the P3 and M genes (**Figure3B**). The CCG nucleotide sequence identity of both strains of SesBCRV1 is 94.3%, while the L protein aa sequence of both strains is 99.3% identical. On the other hand, the CCG of both strains of SesBCRV1 has the highest sequence identity with that of soybean blotchy mosaic virus (SbBMV; 44.3% and 44.6%), while the L protein amino acid sequence of both strains of SesBCRV1 has the highest sequence identity with that of SbBMV (49% and 49.1%) [1]. Based on ML tree generated from complete L protein sequences, SesBCRV1 is placed within a subclade of the betacytorhabdoviruses, with SbBMV, Bemisia tabaci-associated virus 1 and cucurbit cytorhabdovirus 1 (**Figure 3A**).  **Sophora betacytorhabdovirus 1 (SopBCRV1)** was identified from an in-silico analysis of transcriptome data of Japanese pagoda tree (*Sophora japonica*) tissues from Chongqing, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of SopBCRV1 has 13,767 nucleotides (BK064339) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus genome has a shorter G gene than most betacytorhabdoviruses [1]. The CCG nucleotide sequence of SopBCRV1 has the highest sequence identity with that of goji cytorhabdovirus A (GCVA; 50.4%), while the SopBCRV1 L protein amino acid sequence has the highest sequence identity with that of GCVA (55.5%) [1]. Based on ML tree generated from complete L protein sequences, SopBCRV1 is placed within a subclade of the betacytorhabdoviruses, with GCVA, within a well-supported clade with those betacytorhabdoviruses that have the shorter G gene (**Figure 3A**).  **Trifolium betacytorhabdovirus 1 (TriBCRV1)** was identified from an in-silico analysis of transcriptome data of red clover (*Trifolium pratense*) tissues from Germany. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of TriBCRV1 has 13,511 nucleotides (BK064340), and contains eight ORFs in the order 3’-N-P- P3-M-G-P6-L-P8-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, the accessory protein P6 between the G and L genes, and the accessory protein P8 between the L gene and the 5´trailer region (**Figure 3B**). The CCG nucleotide sequence of TriBCRV1 has the highest sequence identity with that of Durio betacytorhabdovirus 1 (DurBCRV1; 52.4%), while the TriBCRV1 L protein amino acid sequence has the highest sequence identity with that of DuriBCRV1 (57.3%) [1]. Based on ML tree generated from complete L protein sequences, TriBCRV1 is placed within a subclade of the betacytorhabdoviruses, with DurBCRV1 (**Figure 3A**).  **Vicia betacytorhabdovirus 1 (VicBCRV1)** was identified from an in-silico analysis of transcriptome data of broad bean (*Vicia faba*) tissues from China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of VicBCRV1 has 12,101 nucleotides (BK064341), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes. Interestingly this virus genome lacked the G gene (**Figure 3B**). The CCG nucleotide sequence of VicBCRV1 has the highest sequence identity with that of Colocasia bobone disease associated virus (CBDaV 40.2%), while the VicBCRV1 L protein amino acid sequence has the highest sequence identity with that of CBDaV (44.7%) [1]. Based on ML tree generated from complete L protein sequences, VicBCRV1 is placed within a subclade of the betacytorhabdoviruses, with CBDaV, barley yellow striate mosaic virus, Durio betacytorhabdovirus 1, maize-associated cytorhabdovirus, maize yellow striate virus, northern cereal mosaic virus, Panicum betacytorhabdovirus 1, peat soil-associated betacytorhabdovirus 1 and Trifolium betacytorhabdovirus 1 (**Figure 3A**).  **Zanthoxylum betacytorhabdovirus 1 (ZanBCRV1)** was identified from an in-silico analysis of transcriptome data of Japanese prickly ash (*Zanthoxylum ailanthoides*) tissues from Taiwan. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ZanBCRV1 has 16,669 nucleotides (BK064342) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus genome has a shorter G gene than most other betacytorhabdoviruses [1]. The CCG nucleotide sequence of ZanBCRV1 has the highest sequence identity with that of Zanthoxylum betacytorhabdovirus2 (ZanBCRV2; 56.4%), while the ZanBCRV1 L protein amino acid sequence has the highest sequence identity with that of ZanBCRV2 (61.8%) [1]. Based on ML tree generated from complete L protein sequences, ZanBCRV1 is placed within a subclade of the betacytorhabdoviruses, with ZanBCRV2 and Zanthoxylum betacytorhabdovirus3, within a well-supported clade with those betacytorhabdoviruses that have a shorter G gene (**Figure 3A**).  **Zanthoxylum betacytorhabdovirus 2 (ZanBCRV2)** was identified from an in-silico analysis of transcriptome data of Japanese prickly ash (*Zanthoxylum ailanthoides*) tissues from Taiwan. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ZanBCRV2 has 15,584 nucleotides (BK064343) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus has a shorter G gene [1]. The CCG nucleotide sequence of ZanBCRV2 has the highest sequence identity with that of Zanthoxylum betacytorhabdovirus3 (ZanBCRV3; 65.8%), while the ZanBCRV2 L protein amino acid sequence has the highest sequence identity with that of ZanBCRV3 (71.4%) [1]. Based on ML tree generated from complete L protein sequences, ZanBCRV2 is placed within a subclade of the betacytorhabdoviruses, with ZanBCRV3, within a well-supported clade with those betacytorhabdoviruses that have a shorter G gene (**Figure 3A**).  **Zanthoxylum betacytorhabdovirus 3 (ZanBCRV3)** was identified from an in-silico analysis of transcriptome data of Japanese prickly ash (*Zanthoxylum ailanthoides*) tissues from Taiwan. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ZanBCRV3 has 16,283 nucleotides (BK064344) and contains six ORFs in the order 3’-N-P- P3-M-G-L-5’ [1] representing the five canonical rhabdovirus structural protein genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 3B**). Interestingly, this virus has a shorter G gene [1]. The CCG nucleotide sequence of ZanBCRV3 has the highest sequence identity with that of Zanthoxylum betacytorhabdovirus2 (ZanBCRV2; 65.8%), while the ZanBCRV3 L protein amino acid sequence has the highest sequence identity with that of ZanBCRV2 (71.4%) [1]. Based on ML tree generated from complete L protein sequences, ZanBCRV3 is placed within a subclade of the betacytorhabdoviruses, with ZanBCRV2, within a well-supported clade with those betacytorhabdoviruses that have a shorter G gene (**Figure 3A**).  AaCV, ArtBVRV1, BegBCRV1, BetBCRV1, BetBCVR2, BouBCRV2, ChrBCRV2, CorBCRV1, CucBCRV1, CypBCRV1, DryBCRV1, DurBCRV1, GleBCRV1, GlyBCRV1, GCVA, HepBCRV1, HowBCRV1, IpoBCRV1, IdaRV, JusBCRV1, KobBCRV1, LeuBCRV1, ManBCRV1, MorBCRV1, NitBCRV1, PanBCRV1, PasBCRV1, PSaBCRV1, PSaBCRV2, PenBCRV1, PheBCRV1, PopBCRV1, PueBCRV1, SchBCRV1, SesBCRV1, SopBCRV1, TriBCRV1, VicBCRV1, ZanBCRV1, ZanBCRV2 and ZanBCRV3 meet the demarcation criteria A and B. Thus, we propose to classify AaCV, ArtBVRV1, BegBCRV1, BetBCRV1, BetBCVR2, BouBCRV2, ChrBCRV2, CorBCRV1, CucBCRV1, CypBCRV1, DryBCRV1, DurBCRV1, GleBCRV1, GlyBCRV1, GCVA, HepBCRV1, HowBCRV1, IpoBCRV1, IdaRV, JusBCRV1, KobBCRV1, LeuBCRV1, ManBCRV1, MorBCRV1, NitBCRV1, PanBCRV1, PasBCRV1, PSaBCRV1, PSaBCRV2, PenBCRV1, PheBCRV1, PopBCRV1, PueBCRV1, SchBCRV1, SesBCRV1, SopBCRV1, TriBCRV1, VicBCRV1, ZanBCRV1, ZanBCRV2 and ZanBCRV3 in the new species *Betacytorhabdovirus aristolochiae*, *Betacytorhabdovirus artemisiae*, *Betacytorhabdovirus begoniae*, *Betacytorhabdovirus alphabetulae*, *Betacytorhabdovirus betabetulae*, *Betacytorhabdovirus bouteloae*, *Betacytorhabdovirus chrysanthemi*, *Betacytorhabdovirus coryli*, *Betacytorhabdovirus betacucurbitae*, *Betacytorhabdovirus cypripedii*, *Betacytorhabdovirus dryobalanopis*, *Betacytorhabdovirus durionis*, *Betacytorhabdovirus gleditsiae*, *Betacytorhabdovirus glycyrrhizae*, *Betacytorhabdovirus lycii*, *Betacytorhabdovirus hepaticae*, *Betacytorhabdovirus howeae*, *Betacytorhabdovirus ipomoeae*, *Betacytorhabdovirus ixeris*, *Betacytorhabdovirus justiciae*, *Betacytorhabdovirus kobresiae*, *Betacytorhabdovirus leucadendri*, *Betacytorhabdovirus mangonis, Betacytorhabdovirus mori*, *Beacytorhabdovirus nitrariae*,, *Betacytorhabdovirus panici*, *Betacytorhabdovirus passiflorae*, *Betacytorhabdovirus alphaturbaesoli, Betacytorhabdovirus betaturbaesoli, Betacytorhabdovirus pentaphragmae*, *Betacytorhabdovirus phellodendri Betaacytorhabdovirus populi*, *Betacytorhabdovirus puerariae*, *Betacytorhabdovirus schiedeae*, *Betacytorhabdovirus sesami*, *Betacytorhabdovirus sophorae*, *Betacytorhabdovirus trifolii*, *Betacytorhabdovirus viciae*, *Betacytorhabdovirus alphazanthoxyli*, *Betacytorhabdovirus betazanthoxyli*, and *Betacytorhabdovirus gammazanthoxyli*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*.  **Genus *Gammacytorhabdovirus***  The genomic organization of the gammacytorhabdoviruses is quite similar, with few exceptions (**Figure 4B**); where a common feature of all identified gammacytorhabdoviruses is the absence of the G gene, while few members also lacked the M gene, but two members have a small ORF located between the M and L genes [1]. Moreover, the observed phylogenetic relationships suggest a common evolutionary history for gammacytorhabdoviruses (**Figure 4A**) [1].  A distinctive feature of gammacytorhabdoviruses is that the intergenic spacer of their gene junctions starts with an A instead of a typical G, like for alpha- and betacytorhabdoviruses, suggesting a unique evolutionary history of these viruses [1].  The absence of the G gene, coupled with the detection of one gammacytorhabdovirus in a fungal library, raises the possibility that these viruses might be transmitted by a fungal vector rather than by arthropods, as is commonly observed in viruses classified as alpha- and betacytorhabdoviruses. This serves as another distinguishing characteristic of the gammacytorhabdoviruses. [1].  We propose that the species *Cytorhabdovirus orchidaceae,* and *Cytorhabdovirus trachyspermi* shall be moved into the genus *Gammacytorhabdovirus* and be renamed *Gammacytorhabdovirus gymnadeniae,* and *Gammacytorhabdovirus trachyspermi*.  In addition to those reassigned species, we propose the creation of 16 new species within the genus *Gammacytorhabdovirus* to accommodate the following viruses:  **Argyranthemum gammacytorhabdovirus 1 (ArgGCRV1)** was identified from an in-silico analysis of transcriptome data of Teide marguerite (*Argyranthemum tenerifae*) tissues from Chelsea, United Kingdom. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of ArgGCRV1 has 10,801 nucleotides (BK064345), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of ArgGCRV1 has the highest sequence identity with that of Lonas gammacytorhabdovirus 1 (LonGCRV1; 78.4%), while the ArgGCRV1 L protein amino acid sequence has the highest sequence identity with that of LonGCRV1 (83.8%) [1]. Based on ML tree generated from complete L protein sequences, ArgGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with LonGCRV1 (**Figure 4A**).  **Carrot gammacytorhabdovirus 1 (CarGCRV1)** was identified from an in-silico analysis of transcriptome data of carrot (*Daucus carota*) tissues from India. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CarGCRV1 has 11,730 nucleotides (BK064346), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of CarGCRV1 has the highest sequence identity with that of celery gammacytorhabdovirus 1 (CelGCRV1; 60.1%), while the CarGCRV1 L protein amino acid sequence has the highest sequence identity with that of CelGCRV1 (65.2%) [1]. Based on ML tree generated from complete L protein sequences, CarGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with CelGCRV1 and Trachyspermum ammi virus 1(**Figure 4A**).  **Celery gammacytorhabdovirus 1 (CelGCRV1)** was identified from an in-silico analysis of transcriptome data of celery (*Apium graveolens*) tissues from Zhejiang, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CelGCRV1 has 12,008 nucleotides (BK064347), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of CelGCRV1 has the highest sequence identity with that of Trachyspermum ammi virus 1 (TrAV1; 66.2%), while the CelGCRV1 L protein amino acid sequence has the highest sequence identity with that of TrAV1 (72.5%) [1]. Based on ML tree generated from complete L protein sequences, CelGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with TrAV1 and carrot gammacytorhabdovirus 1 (**Figure 4A**).  **Coptis gammacytorhabdovirus 1 (CopGCRV1)** was identified from an in-silico analysis of transcriptome data of Chinese goldthread (*Coptis chinensis*) tissues from Chongqing, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CopGCRV1 has 11,214 nucleotides (BK064348), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of CopGCRV1 has the highest sequence identity with that of Cypripedium gammacytorhabdovirus 1 (CypGCRV1; 58.2%), while the CopGCRV1 L protein amino acid sequence has the highest sequence identity with that of CypGCRV1 (64.4%) [1]. Based on ML tree generated from complete L protein sequences, CopGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with CypGCRV1 (**Figure 4A**).  **Cuscuta gammacytorhabdovirus 1 (CusGCRV1)** was identified from an in-silico analysis of transcriptome data of bigseed alfalfa dodder (*Cuscuta indecora*) tissues from the USA. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CusGCRV1 has 10,772 nucleotides (BK064349), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of CusGCRV1 has the highest sequence identity with that of Cuscuta gammacytorhabdovirus 2 (CusGCRV2; 72.8%), while the CusGCRV1 L protein amino acid sequence has the highest sequence identity with that of CusGCRV2 (78.6%) [1]. Based on ML tree generated from complete L protein sequences, CusGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with CusGCRV2 (**Figure 4A**).  **Cuscuta gammacytorhabdovirus 2 (CusGCRV2)** was identified from an in-silico analysis of transcriptome data of nevada dodder (*Cuscuta nevadensis*) tissues from California, USA. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CusGCRV2 has 10,700 nucleotides (BK064350), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of CusGCRV2 has the highest sequence identity with that of Cuscuta gammacytorhabdovirus 1 (CusGCRV1; 72.8%), while the CusGCRV2 L protein amino acid sequence has the highest sequence identity with that of CusGCRV1 (78.6%) [1]. Based on ML tree generated from complete L protein sequences, CusGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with CusGCRV1 (**Figure 4A**).  **Cypripedium gammacytorhabdovirus 1 (CypGCRV1)** was identified from an in-silico analysis of transcriptome data of slipper orchid (*Cypripedium flavum*) tissues from Sichuan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of CypGCRV1 has 10,872 nucleotides (BK064351), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of CypGCRV1 has the highest sequence identity with that of Coptis gammacytorhabdovirus 1 (CopGCRV1; 58.2%), while the CypGCRV1 L protein amino acid sequence has the highest sequence identity with that of CopGCRV1 (64.4%) [1]. Based on ML tree generated from complete L protein sequences, CypGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with CopGCRV1 (**Figure 4A**).  **Epipactis gammacytorhabdovirus 1 (EpiGCRV1)** was identified from an in-silico analysis of transcriptome data of violet helleborine (*Epipactis purpurata*) tissues from Levier, France. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of EpiGCRV1 has 11,001 nucleotides (BK064352), and contains four ORFs in the order 3’-N-P-P3-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 between the P and L genes (**Figure 4B**). The CCG nucleotide sequence of EpiGCRV1 has the highest sequence identity with that of Rhopalocnemis gammacytorhabdovirus 1 (RhoGCRV1; 54.2%), while the EpiGCRV1 L protein amino acid sequence has the highest sequence identity with that of RhoGCRV1 (60.1%) [1]. Based on ML tree generated from complete L protein sequences, EpiGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with RhoGCRV1 (**Figure 4A**).  **Fraxinus gammacytorhabdovirus 1 (FraGCRV1)** was identified from an in-silico analysis of transcriptome data of common ash (*Fraxinus excelsior*) tissues from the United Kingdom. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of FraGCRV1 has 11,521 nucleotides (BK064353), and contains six ORFs in the order 3’-N-P-P3-M-P5-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P5 between the M and L genes (**Figure 4B**). The CCG nucleotide sequence of FraGCRV1 has the highest sequence identity with that of Fraxinus gammacytorhabdovirus 2 (FraGCRV2; 66.6%), while the FraGCRV1 L protein amino acid sequence has the highest sequence identity with that of FraGCRV2 (72.4%) [1]. Based on ML tree generated from complete L protein sequences, FraGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with FraGCRV2 (**Figure 4A**).  **Fraxinus gammacytorhabdovirus 2 (FraGCRV2)** was identified from an in-silico analysis of transcriptome data of ash dieback fungi (*Hymenoscyphus fraxineus*) samples from Norfolk, United Kingdom. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of FraGCRV2 has 11,737 nucleotides (BK064354), and contains six ORFs in the order 3’-N-P-P3-M-P5-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes, and the accessory protein P5 between the M and L genes (**Figure 4B**). The CCG nucleotide sequence of FraGCRV2 has the highest sequence identity with that of Fraxinus gammacytorhabdovirus 1 (FraGCRV1; 66.6%), while the FraGCRV2 L protein amino acid sequence has the highest sequence identity with that of FraGCRV1 (72.4%) [1]. Based on ML tree generated from complete L protein sequences, FraGCRV2 is placed within a subclade of the gammacytorhabdoviruses, with FraGCRV1 (**Figure 4A**).  **Heliosperma gammacytorhabdovirus 1 (HelGCRV1)** was identified from an in-silico analysis of transcriptome data of dwarf heliosperma (*Helisoperma pusillum*) tissues from Friuli Venezia, Italy. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of HelGCRV1 has 11,579 nucleotides (BK064355), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of HelGCRV1 has the highest sequence identity with that of Silene gammacytorhabdovirus 1 (SilGCRV1; 70.4%), while the HelGCRV1 L protein amino acid sequence has the highest sequence identity with that of SilGCRV1 (76%) [1]. Based on ML tree generated from complete L protein sequences, HelGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with SilGCRV1 (**Figure 4A**).  **Hibiscus gammacytorhabdovirus 1 (HibGCRV1)** was identified from an in-silico analysis of transcriptome data of kenaf (*Hibiscus cannabinus*) tissues from Nanning, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of HibGCRV1 has 11,079 nucleotides (BK064356), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of HibGCRV1 has the highest sequence identity with that of celery gammacytorhabdovirus 1 (CelGCRV1; 50.3%), while the HibGCRV1 L protein amino acid sequence has the highest sequence identity with that of CelGCRV1 (55.6%) [1]. Based on ML tree generated from complete L protein sequences, HibGCRV1 forms a well-supported clade with other gammacytorhabdoviruses (**Figure 4A**).  **Lonas gammacytorhabdovirus 1 (LonGCRV1)** was identified from an in-silico analysis of transcriptome data of golden ageratum (*Lonas annua*) tissues from New South Wales, Australia. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of LonGCRV1 has 11,920 nucleotides (BK064357), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of LonGCRV1 has the highest sequence identity with that of Argyranthemum gammacytorhabdovirus 1 (ArgGCRV1; 78.4%), while the LonGCRV1 L protein amino acid sequence has the highest sequence identity with that of ArgGCRV1 (83.8%) [1]. Based on ML tree generated from complete L protein sequences, LonGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with ArgGCRV1 (**Figure 4A**).  **Lupinus gammacytorhabdovirus 1 (LupGCRV1)** was identified from an in-silico analysis of transcriptome data of Mantano river lupine (*Lupinus mantaoroensis*) tissues from Peru. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of LonGCRV1 has 11,196 nucleotides (BK064358), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of LupGCRV1 has the highest sequence identity with that of Cuscuta gammacytorhabdovirus 1 (CusGCRV1; 64.6%), while the LupGCRV1 L protein amino acid sequence has the highest sequence identity with that of CusGCRV1 (83.8%) [1]. Based on ML tree generated from complete L protein sequences, LupGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with CusGCRV1 and Cuscuta gammacyto~~t~~rhabdovirus 2 (**Figure 4A**).  **Rhopalocnemis gammacytorhabdovirus 1 (RhoGCRV1)** was identified from an in-silico analysis of transcriptome data of stinkhorn clubhead (*Rhopalocnemis palloides*) tissues from Yunnan, China. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of RhoGCRV1 has 11,024 nucleotides (BK064359), and contains four ORFs in the order 3’-N-P-P3-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 between the P and L genes (**Figure 4B**). The CCG nucleotide sequence of RhoGCRV1 has the highest sequence identity with that of Epipactis gammacytorhabdovirus 1 (EpiGCRV1; 54.2%), while the RhoGCRV1 L protein amino acid sequence has the highest sequence identity with that of EpiGCRV1 (60.1%) [1]. Based on ML tree generated from complete L protein sequences, RhoGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with EpiGCRV1 (**Figure 4A**).  **Silene gammacytorhabdovirus 1 (SilGCRV1)** was identified from an in-silico analysis of transcriptome data of bladder campion (*Silene vulgaris*) tissues from the Czech Republic. The coding-complete genome (CCG) sequence (partial 3’ leader and 5’ trailer) of SilGCRV1 has 11,500 nucleotides (BK064360), and contains five ORFs in the order 3’-N-P-P3-M-L-5’ [1] representing the canonical nucleocapsid (N), phosphoprotein (P), matrix protein (M) and polymerase (L) rhabdovirus structural proteins genes as well as the putative cell-to-cell movement protein gene P3 in the conserved location between P and M genes (**Figure 4B**). The CCG nucleotide sequence of SilGCRV1 has the highest sequence identity with that of Heliosperma gammacytorhabdovirus 1 (HelGCRV1; 70.4%), while the SilGCRV1 L protein amino acid sequence has the highest sequence identity with that of HelGCRV1 (76%) [1]. Based on ML tree generated from complete L protein sequences, SilGCRV1 is placed within a subclade of the gammacytorhabdoviruses, with HelGCRV1 (**Figure 4A**).  ArgGCRV1, CarGCRV1, CelGCRV1, CopGCRV, CusGCRV1, CusGCRV2, CypGCRV1, EpiGCRV1, FraGCRV1, FraGCRV2, HelGCRV1, HibGCRV1, LonGCRV1, LupGCRV1, RhoGCRV1, and SilGCRV1 meet the demarcation criteria A and B. Thus, we propose to classify these viruses in the new species *Gammacytorhabdovirus argyranthemi*, *Gammacytorhabdovirus* *dauci*, *Gammacytorhabdovirus apii, Gammacytorhabdovirus coptis, Gammacytorhabdovirus alphacuscutae, Gammacytorhabdovirus betacuscutae, Gammacytorhabdovirus cypripedii, Gammacytorhabdovirus epipactis, Gammacytorhabdovirus alphafraxini, Gammacytorhabdovirus betafraxini, Gammacytorhabdovirus heliospermae, Gammacytorhabdovirus hibisci , Gammacytorhabdovirus lonatis, Gammacytorhabdovirus lupini, Gammacytorhabdovirus rhopalocnemis,* and *Gammacytorhabdovirus silenis*, subfamily *Betarhabdovirinae*, family *Rhabdoviridae*.  **Abolish four species**  We propose to abolish the four cytorhabdovirus species *Cytorhabdovirus brassicae, Cytorhabdovirus festucae, Cytorhabdovirus sonchi and Cytorhabdovirus tritici*, due to the lack of sequence data for the four viruses. |

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| **Tables, Figures:**  **Diagrama  Descripción generada automáticamente**  **Figure 1**. Maximum-likelihood phylogenetic tree based on amino acid sequence alignments of the complete L gene of all cytorhabdoviruses reported so far constructed with the WAG + G + F model. The scale bar indicates the number of substitutions per site. Bootstrap values following 1000 replicates are given at the nodes, but only the values above 50% are shown. The recently identified viruses [1] are noted with green, red, and violet rectangles according to the proposed genus membership. Alphanucleorhabdoviruses were used as outgroup.    **Figure 2.** (A): An inset of the maximum-likelihood phylogenetic tree shown in Figure 1 was cropped to show those viruses included in the proposed genus *Alphacytorhabdovirus*. Those viruses potentially belonging to the new species are noted with green squares. (B): genomic organization of the viral sequences used in the phylogeny.    **Figure 3.** (A): An inset of the maximum-likelihood phylogenetic tree shown in Figure 1 was cropped to show those viruses included in the proposed genus *Betacytorhabdovirus*. Those viruses potentially belonging to the new species are noted with red squares. (B): genomic organization of the viral sequences used in the phylogeny.  Gráfico, Gráfico de barras  Descripción generada automáticamente  **Figure 4.** (A): An inset of the maximum-likelihood phylogenetic tree shown in Figure 1 was cropped to show those viruses included in the proposed genus *Gammacytorhabdovirus*. Those viruses potentially belonging to the new species are noted with violet squares. (B): genomic organization of the viral sequences used in the phylogeny. |