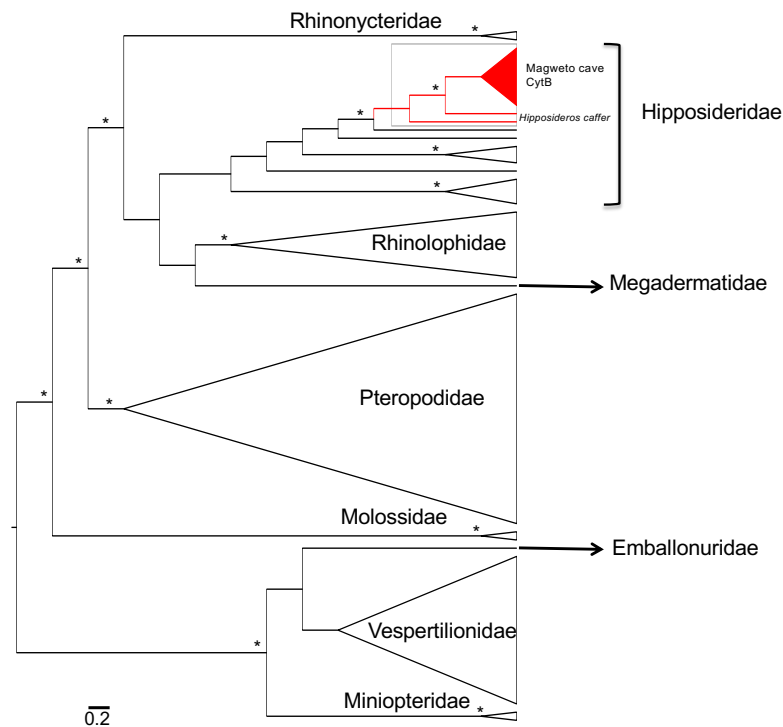


Supplementary Materials

Figure 1S:



Phylogenetic analysis of partial *CytB* sequences (550 bp). New *CytB* sequences obtained were compared to representative bat family *CytB* sequences available in the GenBank. Only Bayesian posterior probabilities are showed. Asterisks at nodes represent posterior probability $\geq 85\%$. Scale bars indicate the number of base substitutions per site. New *Hipposideros caffer* *CytB* sequences are represented by the red triangle. The following sequences have been used for this analysis: KX467590.1 *Miniopterus schreibersii*, KX467591.1 *Miniopterus magnater*, KX467593.1 *Tylonycteris pachypus*, KX467595.1 *Hypsugo albanicus*, KX467596.1 *Nyctalus plancyi*, KX467597.1 *Pipistrellus abramus*, KX467598.1 *Murina leucogaster*, KX467601.1 *Myotis laniger*, KX467611.1 *Myotis davidii*, KX467606.1 *Myotis blythii*, KX467607.1 *Myotis chinensis*, KX467608.1 *Myotis pequinus*, KX467609.1 *Myotis bombinus*, KX467605.1 *Myotis formosus*, KX467610.1 *Myotis altarium*, KX467612.1 *Myotis frater*, KX467599.1 *Myotis ricketti*, KX467600.1 *Myotis adversus*, KX467604.1 *Myotis fimbriatus*, KX467602.1 *Myotis daubentonii*, KX467603.1 *Myotis macrodactylus*, KF218429.1 *Taphozous nudiventris*, AY591536.1 *Otomops martiensseni*, AY591537.1 *Otomops martiensseni*, KX467574.1 *Megaderma lyra*, KX467575.1 *Rhinolophus pusillus*, KX467576.1 *Rhinolophus lepidus*, KX467579.1 *Rhinolophus macrotis*, KX467580.1 *Rhinolophus marshalli*, KX467582.1 *Rhinolophus rex*, KX467578.1 *Rhinolophus ferrumequinum*, KX467583.1 *Rhinolophus sinicus*, KX467577.1 *Rhinolophus affinis*, KX467581.1 *Rhinolophus pearsonii*, KX467584.1 *Hipposideros cineraceus*, KX467585.1 *Hipposideros pomona*, FJ347979.1 *Hipposideros caffer*, FJ347980.1 *Hipposideros caffer*, KX467587.1 *Hipposideros armiger*, KX467588.1 *Hipposideros larvatus*, KX467589.1 *Hipposideros pratti*, KX467586.1 *Aselliscus stoliczkanus*, KT583805.1 *Hipposideros vittatus*, KT583806.1 *Hipposideros vittatus*, KT583801.1

Hipposideros gigas, KT583817.1 *Hipposideros commersoni*, DQ005796.1 *Triaenops persicus*, DQ005797.1 *Triaenops persicus*, KX823312.1 *Megaerops niphanae*, KX823313.1 *Cynopterus sp.*, KX823314.1 *Cynopterus sp.*, KX823317.1 *Sphaeria sblanfordi*, KX822888.1 *Eidolon helvum*, KX822889.1 *Eidolon helvum*, KX823318.1 *Macroglossus sobrinus*, KX823319.1 *Eonycteris spelaea*, KX822938.1 *Rousettus aegyptiacus*, KX822939.1 *Rousettus aegyptiacus*, KX823315.1 *Rousettus leschenaultii*, KX823311.1 *Plerotes anchietae*, KX823011.1 *Hypsignathus monstrosus*, KX823012.1 *Hypsignathus monstrosus*, KX823087.1 *Epomops franqueti*, KX823088.1 *Epomops franqueti*, KX823233.1 *Epomops buettikoferi*, KX823234.1 *Epomops buettikoferi*, KX822985.1 *Nanonycteris veldkampii*, KX822986.1 *Nanonycteris veldkampii*, KX823306.1 *Epomops dobsonii*, KX823307.1 *Epomophorus anelli*, KX823308.1 *Epomophorus crypturus*, KX823309.1 *Epomophorus labiatus*, KX823310.1 *Epomophorus minimus*, KX822798.1 *Epomophorus gambianus*, KX822810.1 *Micropteropus pusillus*, KX822797.1 *Epomophorus gambianus*, KX822809.1 *Micropteropus pusillus*.

Figure2S: Order and family of insect found in the faeces' bats. The confident value for the taxonomic identification must be equal or superior to 0.98. In green are represented values between 0.98 and 1.

ORDER	FAMILY
Lepidoptera	<i>Noctuidae</i>
Lepidoptera	<i>Pieridae</i>
Lepidoptera	<i>Erebidae</i>
Lepidoptera	<i>Geometridae</i>
Lepidoptera	<i>Gelechiidae</i>
Diptera	<i>Sepsidae</i>
Lepidoptera	<i>Crambidae</i>
Lepidoptera	<i>Oecophoridae</i>
Diptera	<i>Syrphidae</i>
Lepidoptera	<i>Sphingidae</i>
Lepidoptera	<i>Erebidae</i>
Lepidoptera	<i>Tineidae</i>
Coleoptera	<i>Scarabaeidae</i>
Diptera	<i>Empididae</i>
Hymenoptera	<i>Vespidae</i>
Hemiptera	<i>Membracidae</i>
Hymenoptera	<i>Agaonidae</i>
Lepidoptera	<i>Nymphalidae</i>
Hymenoptera	<i>Braconidae</i>
Diptera	<i>Ptychopteridae</i>
Coleoptera	<i>Cerambycidae</i>
Coleoptera	<i>Lycidae</i>
Hymenoptera	<i>Agaonidae</i>
Ephemeroptera	<i>Heptageniidae</i>
Hymenoptera	<i>Agaonidae</i>
Diptera	<i>Therevidae</i>
Hemiptera	<i>Issidae</i>

Text S3: Command lines used for bioinformatic pre-analysis

Database formatting

```
makeblastdb -in database/C-RVDBv12.2.fasta -dbtype nucl -out DB_RVDB
```

Querying database

```
blastn -query 1_S1_L001_R1_001.fasta -outfmt "6 qseqid sseqid qseq qlen pident  
nident mismatch evalue " -evalue 1e-9 -out reads1_RBDB.out -db DB_RBDB -  
num_threads 6
```

Reads indexing

```
makeblastdb -in 1_S1_L001_R1_001.fasta -parse_seqids -dbtype nucl -out  
DB_reads1
```

Reads ID list creation

```
grep -i "virus_name" reads1_RBDB.out | cut -f 1 | sort -u > reads_ID
```

Reads extraction

```
blastdbcmd -entry_batch reads_ID -db DB_reads1 -dbtype nucl -out  
virus_name_reads.fasta
```

Text S4: Specific primers used to fill the gap and to confirm the presence of Dicistrovirus in the feces samples.

Big Sioux River Virus specific primers

Amplicon size: 1531 bp

BSRV-F1-30 3'-GAGTGATTAACCCGCCTTTAT-5'
BSRV-R1-1523 3'-TTCCTGTAGCCTCCGATA-5'

Amplicon size: 616 bp

BSRV-F2-529 3'-TTTAGCTGCCTTAAGCAAC-5'
BSRV-R2-1127 3'-AAGCTCGGACGAGTCCAA-5'

Acute Bee Paralysis Virus specific primers

Fragment A

Amplicon size: 623 bp

A-F1 3'-CAGGATTTTCGACAAACTTACTCA-5'
A-R1 3'-ACTCTTACTATCTAGTTCTCCCTC-5'

Amplicon size: 324 bp

A-F2 3'-GCAAAACCAACTATGAAAATTGCT-5'
A-R2 3'-TCCAGATTTACCTCGTCCTGATTCTCC-5'

Fragment B

Amplicon size: 1014 bp

B-F1 3'-TTGGGATAACTATCAAGGCCAGAAC-5'
B-R1 3'-TCACAAAGCCATTTCCAGAAGCCA-5'

Amplicon size: 748 bp

B-F2 3'-GATTCATCTTCAAATCCTAACCCTG-5'
B-R2 3'-GTTCCCATTGTTCTTCATAATC-5'

Fragment C

Amplicon size: 644 bp

C-F1 3'-TCACGTGCAGGGTCCACAGGATA-5'
C-R1 3'-CATTTGATCGTAGATGTTACGG-5'

Amplicon size: 484 bp

C-F2 3'-GTAGAAATGACGATACCATATGC-5'
C-R2 3'-TAGGTCCAATCTTAGGATTCTCA-5'

Aphid Lethal Paralysis Virus specific primers

Amplicon size: 347 bp

ALPV F1 3'-TAAGAATCCTGAACTGAAACGAC-5'
ALPV R1 3'-CGATCCTTTATCTTGTTCAGGT-5'

Amplicon size: 217 bp

ALPV F2 3'-TCTCGCCGTGCGAATTCAACT-5'
ALPV R2 3'-AGCAGGACTGTTTGTATGTC-5'

Text S5: Dicistrovirus reference strains used for the phylogenetic analyses presented in Figure 1.

KX884274 *Wuhan insect virus*
MH476202.1 *Aphis gossypii virus*
MH476203.1 *Aphis gossypii virus*
KY826434.1 *Big Sioux River virus*
KY933256.1 *Big Sioux River virus*
NC001874.1 *Rhopalosiphum padi virus*
MF535298.1 *Rhopalosiphum padi*
MF458893.1 *Aphid lethal paralysis virus*
MF458892.1 *Aphid lethal paralysis virus*
KM270560.1 *Nilaparvata lugens C virus*

NC003924.1 *Cricket paralysis virus*
KP974706.1 *Cricket paralysis virus*
AF014388.1 *Drosophila C virus*
NC001834.1 *Drosophila C virus*
MH310078.1 *Hypsignathus monstrosus dicistrovirus*
KU169878.1 *Anopheles C virus*
NC029052.1 *Goose dicistrovirus isolate*
KF500001.1 *Formica exsecta virus*
NC023021.1 *Formica exsecta virus*
KY465696.1 *Israeli acute paralysis virus*
KF500001.1 *Israeli acute paralysis virus*
KF956377.1 *Kashmir bee virus*
AF486073.2 *Acute bee paralysis virus isolate*
AF178440.1 *Triatoma virus*
NC003783.1 *Triatoma virus*
NC003779.1 *Plauti astali intestine virus*
AB006531.1 *Plauti astali intestine virus*
NC003782.1 *Himetobi P virus*
KM270559.1 *Himetobi P virus*
MH267694.1 *Black queen cell virus isolate*
MH267693.1 *Black queen cell virus isolate*
NC008029.1 *Homalodisca coagulata virus*
KT207917.1 *Homalodisca coagulata virus*
JX094350.1 *Taura syndrome virus*
NC003005.1 *Taurus yndrome virus*
NC018570.2 *Macrobrachium rosenbergii Taihu virus*
HQ113110.2 *Macrobrachium rosenbergii Taihu virus*
NC014793.1 *Mud crab dicistrovirus*
HM777507.1 *Mud crab dicistrovirus*
AY634314.1 *Solenopsis invicta virus*
KY973643.1 *Human Blood-associated Dicistrovirus*
MH536109 *Human Dicistrovirus*
MH536110 *Human Dicistrovirus*
KX588249.1 *Aphis glycines virus*

Table S6: Amino acid identities between *BSRV*, *AGV*, *WIV* and *AGLV*

ORF-1 and ORF-2 Amino acid identities between *BSRV*, *AGV*, *WIV* and *AGLV* are showed. Species demarcation criteria within the *Cripavirus* genus is amino acid identities of the capsid protein (ORF-2) above 90%.

	BSRV CR026	BSRV P7	BSRV S36	BSRV S32	BSRV S28	BSRV S19	BSRV P4	BSRV P9	BSRV S42	BSRV S37	BSRV P5	AGV NZ	AGV AB	AGV RZ	WIV	AGLV
BSRV CR026	-	96	96	96	96	96	96	96	96	96	96	98	98	98	98	92
BSRV P7	96	-	100	100	100	100	100	100	100	100	100	96	96	96	96	91
BSRV S36	96	100	-	100	100	100	100	100	100	100	100	96	96	96	96	91
BSRV S32	96	100	100	-	100	100	100	100	100	100	100	96	96	96	96	91
BSRV S28	96	99	100	100	-	100	100	100	100	100	100	96	96	96	96	91
BSRV S19	96	100	100	100	100	-	100	100	100	100	100	96	96	96	96	91
BSRV P4	96	100	100	100	100	100	-	100	100	100	100	96	96	96	96	91
BSRV P9	96	99	100	100	100	100	100	-	100	100	100	96	96	96	96	91
BSRV S42	96	100	100	100	99	100	100	99	-	100	100	96	96	96	96	91
BSRV S37	96	100	100	100	100	100	100	100	100	-	100	96	96	96	96	91
BSRV P5	96	100	100	100	100	100	100	100	100	100	-	96	96	96	96	91
AGV	87	87	87	87	87	87	87	87	87	87	87	-	100	100	99	92
AGV NZ	87	87	87	87	87	87	87	87	87	87	87	98	-	100	100	99
AGV AB	88	87	88	88	88	88	88	88	87	88	88	98	100	-	100	92
AGV RZ	87	87	88	87	88	88	87	87	87	88	87	99	100	100	100	92
WIV	91	91	91	91	91	91	91	91	91	91	91	89	89	90	89	-
AGLV	91	91	91	91	91	91	91	91	91	91	91	89	89	90	89	100
	Capsid protein															

ORF-1