

Supplementary Material

Supplementary Figures

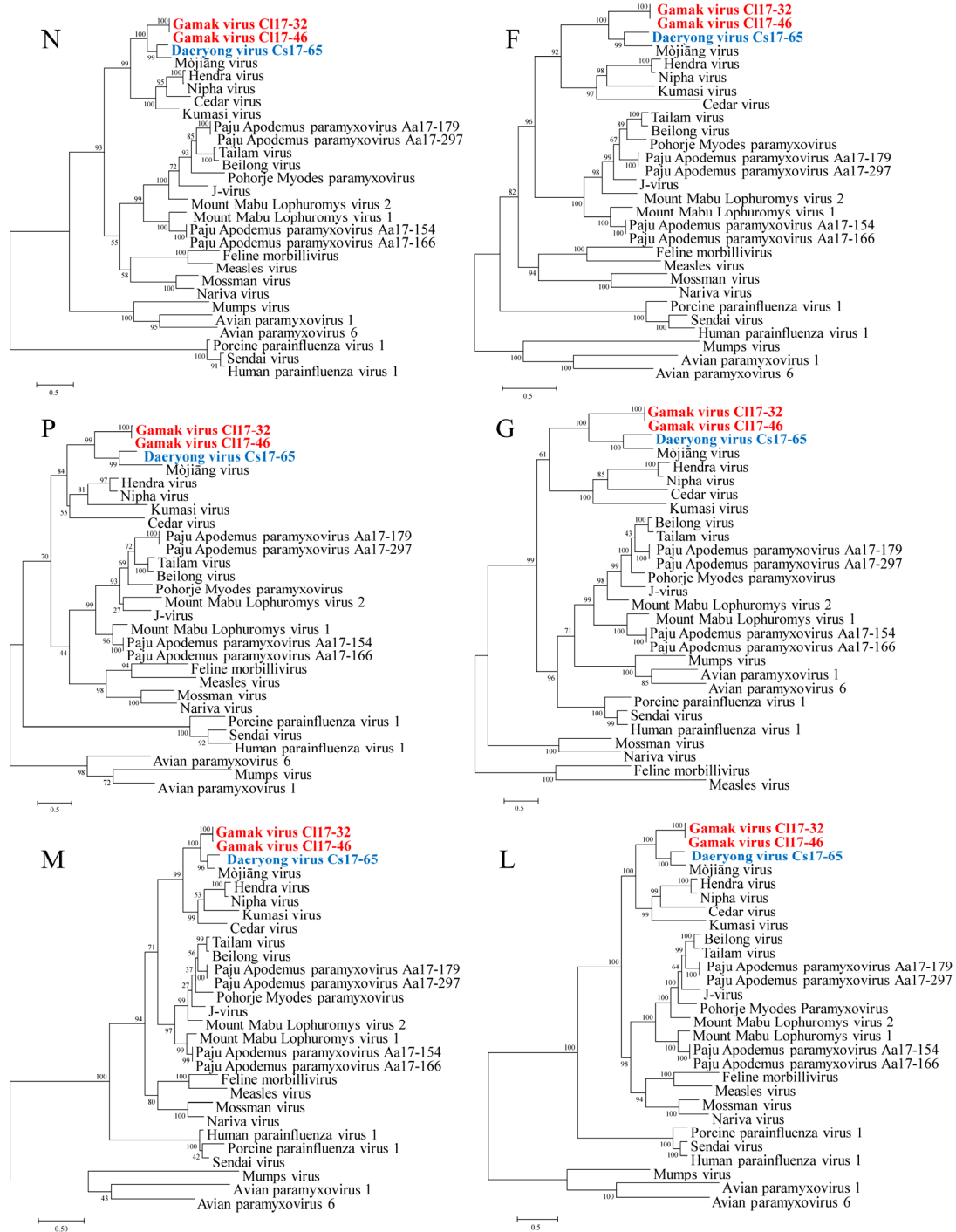


Figure S1. Phylogenetic trees using the coding sequences (CDSs) of *N*, *P*, *M*, *F*, *G*, and *L* genes of Gamak virus (GAKV) and Daeryong virus (DARV). The phylogenetic trees of orthoparamyxoviruses were generated using the maximum likelihood method with distribution models based on the *N*, *P*, *M*, *F*, *G*, and *L* proteins. Topologies were evaluated using a bootstrap analysis of 1,000 iterations. Multiple *Paramyxoviridae* strains were implemented as reference sequences for this phylogenetic inference. Red and blue bold texts indicate GAKV and DARV, respectively.

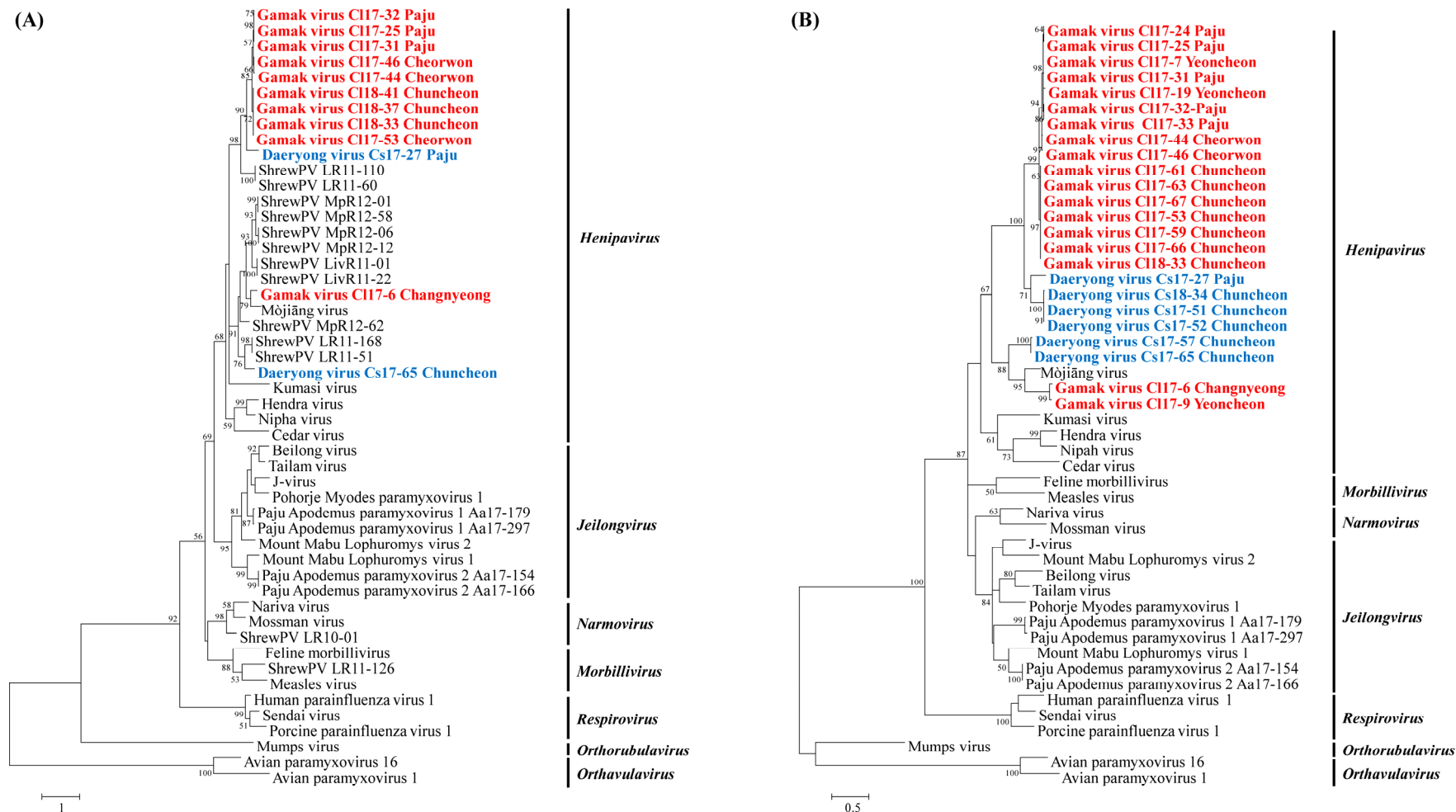


Figure S2. Phylogenetic analyses of the paramyxoviruses using partial genome sequences of L gene. Phylogenetic trees were generated using the maximum likelihood method via alignment of the rodent- and shrew-borne paramyxoviruses with other members of the *Paramyxovirinae* subfamily. Phylogenetic analysis of (A) 13,790–14,215 nt (426 bp) and (B) 14,849–15,311 nt (463 bp) of the L gene from *Henipavirus* with the corresponding region from other members of the *Paramyxovirinae* subfamily. Support for the topologies was assessed via bootstrapping for 1,000 iterations.

Supplementary Tables

Table S1. Sequences of primers for quantitative reverse transcription-polymerase chain reaction.

| Genes | Forward (Sense, 5'–3') | Reverse (Antisense, 5'–3') |
|------------------------------|---------------------------|----------------------------|
| <i>Human b-actin</i> | AGAGCTACGAGCTGCCTGAC | CGTGGATGCCACAGGACT |
| <i>Human GAPDH</i> | GCAAATTCCATGGCACCGT | TCGCCCCACTTGATTTTGG |
| <i>Ifnβ</i> | GTCAGAGTGGAAATCCTAAG | ACAGCATCTGCTGGTTGAAG |
| <i>Il-29</i> | CGCCTTGGAAGAGTCACTCA | GAAGCCTCAGGTCCCAATTC |
| <i>Isg15</i> | GCGAACTCATCTTTGCCAGTA | CCAGCATCTTCACCGTCAG |
| <i>Ifit2/Isg54</i> | ATCCCCCATCGCTTATCTCT | CCACCTCAATTAATCAGGCACT |
| <i>Ifit1/Isg56</i> | GGATTCTGTACAATACTAGAAACCA | CTTTTGGTTACTTTTCCCCTATCC |
| <i>Rsad2/Viperin</i> | TGCTTTTGCTTAAGGAAGCTG | TCTACTTTGCAGAACCTCACCA |
| <i>OAS-1</i> | GAAGGCAGCTCACGAAACC | AGGCCTCAGCCTCTTGTG |
| <i>Ddx58/Rig-I</i> | CAGACAGATCCGAGACACTA | TGCAAGACCTTTGGCCAGTT |
| <i>Ifih1/Mda5</i> | GAGGAATCAGCACGAGGAATAA | TCAGATGGTGGGCTTTGAC |
| <i>Il-6</i> | GCCCAGCTATGAACTCCTTCT | GCGGCTACATCTTTGGAATCT |
| GAKV RdRp | CAGTGCAGAACGAGCTCAAGCATA | TGTGTACTTATTATGGTTTCGGTTGC |

Table S2. Characteristics of *Crocidura* species infected with Gamak virus (GAKV) and Daeryong virus (DARV) and the nucleotide position of GAKV and DARV RNA obtained in this study.

| Type of Paramyxovirus | Sample | Site (City/Province) | Trapping date | Gender | Weight (g) | Vital status | Nucleotide (nt) position of Paramyxovirus RNA |
|-----------------------|------------------------|---------------------------|---------------|--------|------------|--------------|---|
| GAKV | Cl17-32 ^{a,b} | Paju/Gyeonggi | Oct. 27, 2017 | Male | 8.0 | Alive | 1–18,460 |
| | Cl17-46 ^a | Cheorwon/Gangwon | Nov. 21, 2017 | Male | 8.0 | Dead | 1–18,460 |
| | Cl17-6 | Changnyeong/Gyeongsangnam | Jun. 29, 2017 | Female | 12.5 | Dead | 13,790–14,215; 14,849–15,311 |
| | Cl17-7 | Yeoncheon/Gyeonggi | Sep. 28, 2017 | Male | 8.0 | Alive | 14,849–15,311 |
| | Cl17-9 | Yeoncheon/Gyeonggi | Sep. 28, 2017 | Male | 11.0 | Dead | 14,849–15,311 |
| | Cl17-19 | Yeoncheon/Gyeonggi | Sep. 29, 2017 | Male | 10.0 | Dead | 14,849–15,311 |
| | Cl17-24 | Paju/Gyeonggi | Oct. 19, 2017 | Male | 9.5 | Dead | 14,849–15,311 |
| | Cl17-25 | Paju/Gyeonggi | Oct. 19, 2017 | Male | 11.5 | Dead | 13,790–14,215; 14,849–15,311 |
| | Cl17-27 | Paju/Gyeonggi | Oct. 19, 2017 | Female | 5.5 | Dead | 13,790–14,215; 14,849–15,311 |
| | Cl17-31 | Paju/Gyeonggi | Oct. 27, 2017 | Male | 8.5 | Dead | 13,790–14,215; 14,849–15,311 |
| | Cl17-33 | Paju/Gyeonggi | Oct. 27, 2017 | Male | 9.0 | Alive | 13,790–14,215; 14,849–15,311 |
| | Cl17-44 | Cheorwon/Gangwon | Apr. 6, 2017 | Male | 11.0 | Dead | 13,790–14,215; 14,849–15,311 |
| | Cl17-59 | Chuncheon/Gangwon | Oct. 29, 2017 | Female | 9.5 | Dead | 14,849–15,311 |
| | Cl17-61 | Chuncheon/Gangwon | Oct. 30, 2017 | Male | 10.2 | Dead | 14,849–15,311 |

| | | | | | | | |
|------|----------------------|-------------------|---------------|--------|------|-------|------------------------------|
| | Cl17-63 | Chuncheon/Gangwon | Oct. 29, 2017 | Female | 8.5 | Dead | 14,849-15,311 |
| | Cl17-66 | Chuncheon/Gangwon | Oct. 31, 2017 | Female | 11.4 | Dead | 14,849-15,311 |
| | Cl17-67 | Chuncheon/Gangwon | Nov. 8, 2017 | Male | 12.4 | Dead | 14,849-15,311 |
| | Cl18-33 | Chuncheon/Gangwon | Nov. 13, 2018 | Male | 10.5 | Dead | 13,790-14,215; 14,849-15,311 |
| | Cl18-37 | Chuncheon/Gangwon | Nov. 13, 2018 | Male | 7.0 | Dead | 13,790-14,215; 14,849-15,311 |
| | Cl18-41 | Chuncheon/Gangwon | Nov. 14, 2018 | Male | 7.5 | Alive | 13,790-14,215 |
| DARV | Cs17-65 ^a | Chuncheon/Gangwon | Oct. 31, 2017 | Female | 5.1 | Dead | 1–19,475 |
| | Cs17-51 | Chuncheon/Gangwon | Sep. 28, 2017 | Male | 36.5 | Dead | 14,849-15,311 |
| | Cs17-52 | Chuncheon/Gangwon | Oct. 11, 2016 | Female | 44.5 | Dead | 14,849-15,311 |
| | Cs17-53 | Chuncheon/Gangwon | Apr. 18, 2017 | Male | 26.0 | Dead | 13,790-14,215 |
| | Cs17-57 | Chuncheon/Gangwon | Apr. 18, 2017 | Female | 28.0 | Dead | 14,849-15,311 |
| | Cs18-34 | Chuncheon/Gangwon | Oct. 16, 2018 | Female | 32.0 | Dead | 14,849-15,311 |

^a: Whole genome sequences were completely obtained.

^b: Cell culture-based isolates.

Table S3. Molecular prevalence of Gamak virus (GAKV) by region, sex, weight, and season in *C. lasiura*, the Republic of Korea from 2017 to 2018.

| Category | Number of <i>C. lasiura</i> | RNA positivity of GAKV (%) [*] |
|----------------------|--------------------------------|--|
| Region (n=94) | | |
| Gangwon | 40 | 11/40 (27.5%) |
| Gyeonggi | 52 | 9/52 (17.3%) |
| Gyeongsangnam | 2 | 1/2 (50.0%) |
| Sex (n=94) | | |
| Males | 58 | 16/58 (27.6%) |
| Females | 36 | 5/36 (13.9%) |
| Weight (n=94) | | |
| <10g (Subadults) | 54 | 11/54 (20.4%) |
| 10–20g (Adults) | 40 | 10/40 (25.0%) |
| Season (n=94) | | |
| Spring (Mar.–May) | 9 | 1/9 (11.1%) |
| Summer (Jun.–Aug.) | 2 | 1/2 (50.0%) |
| Autumn (Sep.–Nov.) | 79 | 19/79 (24.1%) |
| Winter (Dec.–Feb.) | 4 | 0/4 |
| Total | 94 | 21/94 (22.3%) |

^{*}The positive rate of GAKV RNA indicates the detection of the partial L gene (targeting pan-*Orthoparamyxovirinae* and the genera *Respirovirus*, *Morbillivirus*, and *Henipavirus*) using RT-PCR and Sanger sequencing.

Table S4. Molecular prevalence of Daeryong virus (DARV) by region, sex, weight, and season in *C. shantungensis*, the Republic of Korea from 2017 to 2018.

| Category | Number of <i>C. shantungensis</i> | RNA positivity of DARV (%)* |
|----------------------|--------------------------------------|--------------------------------|
| Region (n=21) | | |
| Gangwon | 10 | 5/10 (50.0%) |
| Gyeonggi | 11 | 0/11 |
| Gyeongsangnam | 0 | 0/0 |
| Sex (n=21) | | |
| Males | 9 | 1/9 (11.1%) |
| Females | 12 | 4/12 (33.3%) |
| Weight (n=21) | | |
| <5g (Subadults) | 14 | 3/14 (21.4%) |
| 5–9g (Adults) | 5 | 2/7 (28.6%) |
| Season (n=21) | | |
| Spring (Mar.–May) | 2 | 0/2 |
| Summer (Jun.–Aug.) | 0 | 0/0 |
| Autumn (Sep.–Nov.) | 19 | 5/19 (26.3%) |
| Winter (Dec.–Feb.) | 0 | 0/0 |
| Total | 21 | 5/21 (23.8%) |

*The positive rate of DARV RNA indicates the detection of the partial L gene (targeting pan-*Orthoparamyxovirinae* and the genera *Respirovirus*, *Morbillivirus*, and *Henipavirus*) using RT-PCR and Sanger sequencing.

Table S5. Genome coverage of consensus sequences for Gamak virus using next-generation sequencing (SISPA-based MiSeq) method.

| NGS method | Origin | Strains | Total reads | Read mapped to reference/Total reads (%) | Crocidura paramyxoviruses | |
|----------------------|--------|----------------------|-------------|---|-----------------------------|--------------------|
| | | | | | Read mapped to reference | Depth of coverage* |
| SISPA-based MiSeq | Kidney | Cl17-46 ^a | 245,846 | 1.468 | 3,608 | 28.703 |

*Depth of coverage was calculated using the number of mapped reads [(average read length × number of reads that matched the reference)/(reference genome size)].

^a: Gamak virus 18,460 nt

SISPA: sequence-independent, single-primer amplification

Table S6. Genome coverage of consensus sequences for Gamak and Daeryong viruses using next-generation sequencing (RNA-Seq based HiSeq) method.

| NGS method | Origin | Strains | Total reads | Read mapped to reference/Total reads (%) | Crocidura paramyxoviruses | |
|------------------------|--------|----------------------|-------------|---|-----------------------------|--------------------|
| | | | | | Read mapped to reference | Depth of coverage* |
| RNA-Seq based HiSeq | Vp | Cl17-32 ^a | 83,500,574 | 17.699 | 14,779,024 | 80665.238 |
| | Kidney | Cl17-46 ^a | 72,742,132 | 0.009 | 6,497 | 35.356 |
| | | Cs17-65 ^b | 83,682,946 | 0.061 | 50,987 | 278.016 |
| Total | | | 239,925,652 | 6.184 | 14,836,508 | 80,978.61 |

*Depth of coverage was calculated using the number of mapped reads [(read length × number of reads that matched the reference)/(reference genome size)].

Vp: Cell culture-based isolates

^a: Gamak virus 18,460 nt

^b: Daeryong virus 19,475 nt

Table S7. Sequences of intergenic regions (IGRs) and transcriptional stop and start signals of Gamak virus.

| Genes | Gene stop | IGR | Gene Start |
|------------------------|------------|-----|------------|
| /N | | CTT | AAGAATCAAA |
| N/P | TTAAGAAAAA | CTT | AAGAATCAAA |
| P/M | TTAAGAAAAA | CTT | AAGAGTCAAA |
| M/F | TTAGAAAAAA | CTT | AAGAATCAAA |
| F/G | TTAAGAAAAA | CTT | AAGAATCAAA |
| G/L | TTAAGAAAAA | CTT | AAGAATCAAA |
| L/ | TTAAGAAAAA | CTT | |
| Consensus sequences | TTARRAAAAA | CTT | AAGARTCAAA |

Table S8. Sequences of intergenic regions (IGRs) and transcriptional stop and start signals of Daeryong virus.

| Genes | Gene stop | IGR | Gene Start |
|------------------------|------------|-----|------------|
| /N | | CTT | AGGACTCAGG |
| N/P | TTATAAAAAA | CTT | AGGATGCAAG |
| P/M | TTAAGAAAAA | CTT | AGGGGTAAAG |
| M/F | TTAAAGAAAA | CTT | AGGACGTCAA |
| F/G | TTATAAAAAA | CTT | AGGGGTCAAG |
| G/L | TTAAGAAAAA | CTT | AGGTGCAATG |
| L/ | ATATAAAAAA | CTT | |
| Consensus sequences | WTAWRRAAAA | CTT | AGGDBBHMDR |

Table S9. Amino acid similarities of GAKV and DARV with other viruses in *Paramyxoviridae*.

| Genus | Virus | GAKV | | | | | | DARV | | | | | |
|-------------------------|-------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | | N | P | M | F | G | L | N | P | M | F | G | L |
| <i>Henipavirus</i> | GAKV | 98.7 | 96.3 | 99.4 | 99.1 | 99.4 | 98.5 | 57.9-60.1 | 30.7-31.3 | 76.8 | 57.5-57.7 | 28.8-28.9 | 62.9 |
| | DARV | 57.9-60.1 | 30.7-31.3 | 76.8 | 57.5-57.7 | 28.8-28.9 | 62.9 | - | - | - | - | - | - |
| | HeV | 47.0-48.1 | 22.7-23.0 | 60.1-60.4 | 39.7 | 17.4 | 52.0-52.1 | 46.4 | 22.0 | 59.5 | 39.0 | 18.4 | 51.9 |
| | NiV | 47.7-48.7 | 23.9-24.2 | 59.5-59.8 | 40.3 | 17.8 | 52.4 | 46.6 | 18.7 | 59.3 | 39.9 | 18.3 | 52.2 |
| | MojV | 58.4-58.6 | 27.4-29.0 | 80.3-80.6 | 56.9-57.1 | 29.9 | 62.3-62.4 | 69.6 | 36.0 | 83.1 | 67.3 | 49.3 | 74.1 |
| | CedV | 45.7 | 19.1-19.4 | 57.5 | 33.4 | 16.9 | 49.4-49.5 | 45.7 | 19.0 | 57.8 | 34.1 | 17.3 | 49.8 |
| | KV | 46.1 | 25.6-25.7 | 56.9 | 38.3 | 16.3 | 49.0-49.3 | 46.1 | 19.3 | 58.9 | 39.2 | 18.3 | 49.2 |
| <i>Jeilongvirus</i> | PAPV-1 | 34.7-35.4 | 18.3 | 55.3 | 37.9-38.4 | 18.6 | 49.6 | 36.4 | 20.4-21.4 | 53.5 | 36.8-37.0 | 19.9 | 49.0-49.2 |
| | PAPV-2 | 33.3-34.6 | 21.4-22.9 | 57.2-57.4 | 35.5-35.7 | 17.1-17.3 | 49.7 | 34.9-35.8 | 20.0 | 56.0-56.2 | 35.8-35.9 | 17.8 | 50.7-50.8 |
| | TaiV | 34.7-34.9 | 19.4-19.6 | 53.5 | 37.5-37.7 | 18.4 | 48.7-48.8 | 36.6 | 17.3 | 53.2 | 35.5 | 18.6 | 49.5 |
| | BeiV | 34.7-35.4 | 18.5-19.4 | 55.0 | 38.4-38.6 | 18.6 | 48.7-48.8 | 36.2 | 14.3 | 54.1 | 35.3 | 19.2 | 49.0 |
| | JV | 33.7 | 18.6-18.8 | 52.9 | 37.3-37.5 | 17.9 | 48.6-48.8 | 36.0 | 20.4 | 52.6 | 36.2 | 20.5 | 48.7 |
| | MMLV-1 | 35.6-36.0 | 22.1-22.5 | 56.0 | 34.8-35.0 | 20.3-20.6 | 49.1-49.3 | 35.3 | 18.4 | 57.5 | 36.8 | 18.4 | 49.9 |
| | MMLV-2 | 33.9 | 20.9-22.5 | 57.1-57.4 | 38.3 | 19.7 | 50.3-50.4 | 36.2 | 19.5 | 53.8 | 37.2 | 17.8 | 50.5 |
| <i>Morbillivirsu</i> | PMPV-1 | 34.8-35.0 | 21.6-22.8 | 54.7 | 36.0 | 19.7 | 49.2-49.3 | 35.0 | 18.5 | 52.9 | 35.1 | 19.1 | 50.5 |
| | FeMV | 31.8 | 17.7-17.9 | 45.4 | 32.2 | 12.4 | 45.2-45.3 | 32.2 | 18.5 | 46.0 | 32.8 | 9.7 | 45.7 |
| <i>Narmovirus</i> | MV | 31.2-31.6 | 16.8-17.4 | 46.0 | 31.8 | 12.3 | 46.9-47.1 | 32.4 | 18.1 | 46.6 | 32.1 | 10.9 | 46.7 |
| | MossV | 34.8-35.2 | 12.7-14.6 | 48.2 | 29.9 | 13.8 | 47.4-47.5 | 36.2 | 19.2 | 48.2 | 32.6 | 13.5 | 48.1 |
| <i>Respirovirus</i> | NarV | 36.2-36.4 | 14.7-15.7 | 49.4 | 29.0 | 14.0-14.2 | 46.3-46.4 | 36.4 | 16.7 | 49.1 | 30.6 | 12.9 | 46.3 |
| | PPIV-1 | 20.0 | 11.1-11.5 | 34.3 | 25.9 | 19.1 | 37.5-37.9 | 18.3 | 7.8 | 34.7 | 26.9 | 18.6 | 39.6 |
| <i>Orthorubulavirus</i> | SenV | 19.5 | 12.0-12.3 | 34.6 | 26.4-26.5 | 18.4-18.6 | 36.7-37.4 | 20.6 | 9.7 | 34.4 | 27.5 | 19.8 | 38.6 |
| | HPIV-1 | 19.5-19.8 | 11.4-12.7 | 35.8 | 25.8-25.9 | 18.3 | 36.8-37.3 | 20.0 | 13.6 | 33.5 | 26.2 | 18.1 | 39.5 |
| <i>Orthoavulavirus</i> | MuV | 24.5 | 9.4-12.1 | 17.9 | 25.8-25.9 | 13.4 | 27.2-27.3 | 25.7 | 10.3 | 17.6 | 25.1 | 13.1 | 26.3 |
| <i>Metaavulavirus</i> | APMV-1 | 27.4-27.6 | 17.5 | 19.6 | 24.6-24.8 | 15.3 | 24.9 | 25.3 | 17.7 | 19.4 | 26.9 | 13.5 | 26.0 |
| | APMV-6 | 26.7-27.1 | 13.0-14.0 | 22.3 | 25.2 | 15.5 | 25.8-26.8 | 27.5 | 10.2 | 22.5 | 28.2 | 15.2 | 26.7 |

Similarities are indicated per protein and are expressed as percentages. GAKV, Gamak virus; DARV, Daeryong virus; HeV, Hendra virus; NiV, Nipah virus; MojV, Mòjiāng virus; CedV, Cedar virus; KV, Kumasi virus; PAPV-1, Paju Apodemus paramyxovirus 1; PAPV-2, Paju Apodemus paramyxovirus 2; TaiV, Tailam virus; BeiV, Beilong virus; JV, J-virus; MMLV-1, Mount Mabu Lophuromys virus 1; MMLV-2, Mount Mabu Lophuromys virus 2; PMPV-1, Pohorje Myodes paramyxovirus 1; FeMV, Feline morbillivirus; MeV, Measles virus; PPIV-1, Porcine parainfluenza virus 1; SenV, Sendai virus; HPIV-1, Human parainfluenza virus 1; MuV, Mumps virus; APMV-1, Avian paramyxovirus 1; APMV-6, Avian paramyxovirus 6.