This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.009S*** | | | | (to be completed by ICTV officers) |
| **Short title:** Create 1 new species (*Shanbavirus A*) in a new genus (*Shanbavirus*)  (e.g. 6 new species in the genus *Zetavirus*) | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Roland Zell, Eric Delwart, Alexander E. Gorbalenya, Tapani Hovi, Andrew M.Q. King, Nick J. Knowles, A. Michael Lindberg, Mark A. Pallansch, Ann C. Palmenberg, Gabor Reuter, Peter Simmonds, Tim Skern, Glyn Stanway and Teruo Yamashita | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Roland Zell ([roland.zell@med.uni-jena.de](mailto:roland.zell@med.uni-jena.de)) | | | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | *Picornaviridae* Study Group | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | 02 June 2017 | |
| Date of this revision (if different to above): | | | |  | |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|  |

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.009S.N.v1.Shanbavirus |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| **Bat picornavirus BtMf-PicoV-1/SAX2011:**  **Wu Z, Yang L, Jin Q** (MOH Key Laboratory of Systems Biology of Pathogens, Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, No. 6 Rongjing East Street, Yizhuang, Beijing 100176, China) **unpublished**  **Rhinolophus affinis picornavirus 1:**  **Wu Z, Ren X, Yang L, Hu Y, Yang J, He G, Zhang J, Dong J, Sun L, Du J, Liu L, Xue Y, Wang J, Yang F, Zhang S, Jin Q**. 2012. Virome analysis for identification of novel Mammalian viruses in bat species from Chines provinces. J Virol 86(20):10999-11012. |

|  |
| --- |
| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

**Create 1 new species (*Shanbavirus A*) in a new genus (*Shanbavirus*)**

A novel bat picornavirus was detected in tissue samples of *Minopterus fuliginosus* bats in China. A virus isolate is not available, but the genome sequence suggests that this virus belongs to the *Picornaviridae*. 3-4-4 genome layout (compare Figure 1):

VPg+5'UTRIRES-II[1AB-1C-1D-2A1NPGP/2A2H-box/NC-2B-2CHel/3A-3BVPg-3CProt-3DPol]3'UTR-poly(A)

The deduced P1 and 3CD proteins show low amino acid similarities with the orthologous proteins of other picornaviruses. Alignments reveal amino acid identities >34% for 3CD and >30% for P1.

**Features that identify shanbaviruses as picornaviruses are:**

(i) a genome layout with a single open reading frame preceeded by a long 5'-NTR

(ii) the presence of sequence motifs typical of picornaviruses, i.e.:

three rhv-like domains (Pfam database) corresponding to VP0, VP3, VP1,

NPGP motif,

NTP-binding motif of 2CHel (**G**1156PPGQ**GKS**, Walker A motif, and a D1206DLGQ motif)

putative 3C proteinase catalytic triad (H1533, D1597, G1643TCG)

RNA-dependent RNA polymerase motifs (K1843DELR, P1973SG, Y2009GDD, F2058LKR)

Phylogenetic trees of the P1 and 3CD proteins comprising reference sequences of the *Aquamavirus/ Avihepatovirus/Avisivirus/Kunsagivirus/Pasivirus/Parechovirus* supergroup indicate that shanbavirus forms a distinct branch (compare Figs. 2, 3; Appendix) [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)]. Closest relative is Rhinolophus affinis picornavirus which was only partially sequenced (P1-2A). Next relatives are parechoviruses and pasiviruses which have a similar genome layout.

- Phylogenetic analyses of the P1 and 3CD proteins reveal that shanbavirus is a divergent picornavirus related to parechoviruses and pasiviruses (Figures 2, 3; Appendix):

- 2A1 and 2A2 of shanbavirus and parechoviruses share significant homology (c. 41% amino acid identity);

- 2B of shanbavirus and parechoviruses shares significant homology (c. 28-30% amino acid identity);

- protein 3A lacks recognizable homology to any other picornavirus.

As shown in Tables 1, 2 (Appendix), shanbavirus shows an amino acid divergence of the P1 region of 71-91% to all picornaviruses; the 3CD proteins has a divergence of c. 64% compared to the crohiviruses and greater diversity (66-83%) to the other picornaviruses.

**Origin of the name:**

Shanbavirus: from **Sha**nxi **ba**t picornavirus (Shanxi Province in China, were sample was collected)

**Figure 1:** Genome organization of *Parechovirus B* and shanbavirus. The open reading frames are indicated by boxes. Positions of putative 3CPro cleavage sites are indicated by ▼, the site of termination/reinitiation of RNA translation at the NPGP sequence motif is indicated by a #. The lengths of the deduced proteins are also presented.



**Figure 2:** Phylogenetic analyses of picornavirus **3CD** using Bayesian tree inference (MrBayes 3.2). Twenty-five picornavirus sequences of the *Aquamavirus/Avihepatovirus/Avisivirus/Kunsagivirus/ Pasivirus/Parechovirus* supergroup were retrieved from GenBank; the newt ampivirus sequence served as outgroup [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)]. Presented are GenBank accession numbers, ***genus*** ***names***, *species names* and *types* (underlined). If available, common names and designations of isolates [in square brackets] are also given. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 3,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Figure 3:** Phylogenetic analyses of picornavirus **P1** capsid protein precursor using Bayesian tree inference (MrBayes 3.2). Twenty-six picornavirus sequences of the *Aquamavirus/Avihepatovirus/ Avisivirus/Kunsagivirus/Pasivirus/Parechovirus* supergroup were retrieved from GenBank; the newt ampivirus sequence served as outgroup [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)]. Presented are GenBank accession numbers, ***genus*** ***names***, *species names* and *types* (underlined). If available, common names and designations of isolates [in square brackets] are also given. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

**Table 1. Estimates of Evolutionary Divergence between 3CD Sequences**

[ 1] #KJ641698\_bat\_picornavirus\_isolate\_bat/BtMf-PicoV-1/SAX2011

[ 2] #L02971\_Parechovirus\_A1\_HPeV-1\_Harris

[ 3] #AF327920\_Parechovirus\_B1\_LV-1\_87-012

[ 4] #HF677705\_Parechovirus\_C1\_Sebokele\_virus\_1\_strain\_An\_B\_1227\_d

[ 5] #KF006989\_Parechovirus\_D1\_Ferret\_parechovirus\_strain\_ferret/MpPeV1/NL

[ 6] #KC843627\_Potamipivirus\_A1\_Eel\_picornavirus\_F15-05

[ 7] #KJ000696\_Aalivirus\_duck/GL/12/China/2012

[ 8] #DQ249299\_Avihepatovirus\_DHAV-1\_03D

[ 9] #KC465954\_Avisivirus\_A1\_strain\_turkey/M176-TuASV/2011/HUN

[10] #KC614703\_Avisivirus\_A1\_isolate\_turkey/USA/IN1/2010

[11] #KF979333\_Avisivirus\_B1\_chicken\_picornavirus\_2\_isolate\_44C

[12] #KF979334\_Avisivirus\_C1\_chicken\_picornavirus\_3\_isolate\_45C

[13] #KT880669\_Avisivirus\_C1\_Pf-CHK1/AsV

[14] #KT880667\_Orivirus\_2\_Pf-CHK1/OrV-A2

[15] #KM203656\_Orivirus\_1\_strain\_chicken/Pf-CHK1/2013/HUN

[16] #KC935379\_Kunsagivirus\_A1\_strain\_roller/SZAL6-KuV/2011/HUN

[17] #KX644936\_Kunsagivirus\_B1\_Bat\_Kunsagivirus

[18] #KY670597\_Kunsagivirus\_C1\_Bakunsa\_virus\_strain\_baboon/M27-KuV/1986/TAN\_P3

[19] #EU142040\_Aquamavirus\_AV-A\_SePV-1\_HO-02-21

[20] #JQ316470\_Pasivirus\_A1\_swine/France/2011

[21] #AB937989\_Crohivirus\_1\_shrew/ZM54/Zambia/2012

[22] #KX644937\_Bat\_crohivirus\_clone\_Bat/CAM/CroV-P25/2013

[23] #JX134222\_Limnipivirus\_A1\_BGPV-1\_04-032

[24] #KF306267\_Limnipivirus\_B1\_CarpPV

[25] #KF183915\_Limnipivirus\_C1\_FHMPV-1\_isolate\_fhm/1/MN/USA/2010

[26] #KP770140\_Ampivirus\_A1\_strain\_NEWT/2013/HUN

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 ]

[ 1] - [0.017 ][0.018 ][0.018 ][0.018 ][0.017 ][0.017 ][0.019 ][0.017 ][0.017 ][0.017 ][0.017 ][0.017 ][0.018 ][0.017 ][0.016 ][0.015 ][0.017 ][0.017 ][0.017 ][0.018 ][0.018 ][0.017 ][0.018 ][0.018 ][0.014 ]

[ 2] 0.663 - [0.019 ][0.018 ][0.018 ][0.016 ][0.018 ][0.018 ][0.017 ][0.017 ][0.018 ][0.017 ][0.017 ][0.017 ][0.017 ][0.016 ][0.016 ][0.016 ][0.016 ][0.017 ][0.018 ][0.017 ][0.017 ][0.017 ][0.017 ][0.014 ]

[ 3] 0.681 0.510 - [0.017 ][0.018 ][0.017 ][0.018 ][0.018 ][0.017 ][0.017 ][0.017 ][0.017 ][0.017 ][0.019 ][0.019 ][0.016 ][0.016 ][0.016 ][0.016 ][0.018 ][0.018 ][0.018 ][0.017 ][0.017 ][0.017 ][0.014 ]

[ 4] 0.684 0.541 0.340 - [0.017 ][0.017 ][0.017 ][0.018 ][0.017 ][0.017 ][0.017 ][0.017 ][0.017 ][0.018 ][0.018 ][0.017 ][0.016 ][0.016 ][0.017 ][0.018 ][0.018 ][0.018 ][0.017 ][0.016 ][0.017 ][0.014 ]

[ 5] 0.664 0.591 0.573 0.573 - [0.017 ][0.018 ][0.017 ][0.016 ][0.016 ][0.017 ][0.016 ][0.016 ][0.018 ][0.018 ][0.017 ][0.017 ][0.017 ][0.016 ][0.017 ][0.018 ][0.018 ][0.016 ][0.016 ][0.017 ][0.014 ]

[ 6] 0.685 0.704 0.660 0.649 0.668 - [0.017 ][0.017 ][0.016 ][0.016 ][0.016 ][0.016 ][0.016 ][0.018 ][0.018 ][0.016 ][0.016 ][0.017 ][0.016 ][0.016 ][0.016 ][0.017 ][0.017 ][0.018 ][0.017 ][0.014 ]

[ 7] 0.700 0.682 0.666 0.666 0.679 0.697 - [0.019 ][0.019 ][0.019 ][0.018 ][0.018 ][0.018 ][0.018 ][0.018 ][0.017 ][0.016 ][0.016 ][0.017 ][0.017 ][0.018 ][0.018 ][0.016 ][0.016 ][0.017 ][0.015 ]

[ 8] 0.682 0.673 0.659 0.658 0.681 0.689 0.522 - [0.018 ][0.018 ][0.018 ][0.017 ][0.017 ][0.019 ][0.019 ][0.016 ][0.016 ][0.016 ][0.016 ][0.018 ][0.018 ][0.018 ][0.017 ][0.016 ][0.017 ][0.015 ]

[ 9] 0.725 0.720 0.704 0.702 0.711 0.746 0.573 0.610 - [0.008 ][0.020 ][0.019 ][0.019 ][0.018 ][0.017 ][0.017 ][0.016 ][0.018 ][0.016 ][0.017 ][0.018 ][0.017 ][0.016 ][0.016 ][0.016 ][0.014 ]

[10] 0.717 0.715 0.700 0.700 0.709 0.743 0.569 0.617 0.041 - [0.020 ][0.019 ][0.019 ][0.017 ][0.017 ][0.017 ][0.016 ][0.018 ][0.016 ][0.017 ][0.018 ][0.017 ][0.016 ][0.016 ][0.016 ][0.014 ]

[11] 0.701 0.702 0.672 0.685 0.688 0.719 0.557 0.597 0.492 0.491 - [0.019 ][0.018 ][0.018 ][0.018 ][0.017 ][0.017 ][0.017 ][0.018 ][0.017 ][0.018 ][0.018 ][0.016 ][0.017 ][0.016 ][0.014 ]

[12] 0.709 0.726 0.705 0.703 0.704 0.735 0.555 0.607 0.461 0.460 0.494 - [0.004 ][0.017 ][0.017 ][0.016 ][0.017 ][0.017 ][0.016 ][0.016 ][0.017 ][0.017 ][0.016 ][0.016 ][0.017 ][0.014 ]

[13] 0.707 0.726 0.706 0.705 0.704 0.737 0.552 0.604 0.456 0.455 0.496 0.014 - [0.017 ][0.017 ][0.016 ][0.017 ][0.017 ][0.016 ][0.016 ][0.017 ][0.017 ][0.016 ][0.016 ][0.017 ][0.014 ]

[14] 0.710 0.705 0.680 0.682 0.708 0.705 0.642 0.625 0.705 0.698 0.681 0.672 0.672 - [0.014 ][0.016 ][0.017 ][0.017 ][0.016 ][0.017 ][0.018 ][0.018 ][0.017 ][0.017 ][0.018 ][0.014 ]

[15] 0.711 0.712 0.675 0.680 0.701 0.704 0.650 0.624 0.687 0.682 0.665 0.683 0.683 0.158 - [0.016 ][0.016 ][0.017 ][0.016 ][0.017 ][0.018 ][0.018 ][0.017 ][0.017 ][0.018 ][0.014 ]

[16] 0.755 0.744 0.743 0.729 0.727 0.745 0.728 0.741 0.748 0.746 0.720 0.736 0.734 0.734 0.742 - [0.018 ][0.018 ][0.017 ][0.017 ][0.016 ][0.015 ][0.015 ][0.016 ][0.016 ][0.013 ]

[17] 0.746 0.740 0.725 0.716 0.725 0.741 0.734 0.723 0.756 0.750 0.724 0.737 0.735 0.731 0.739 0.524 - [0.018 ][0.017 ][0.017 ][0.016 ][0.016 ][0.015 ][0.016 ][0.015 ][0.013 ]

[18] 0.734 0.722 0.726 0.708 0.697 0.736 0.730 0.737 0.731 0.737 0.727 0.743 0.743 0.733 0.735 0.576 0.575 - [0.018 ][0.017 ][0.017 ][0.017 ][0.016 ][0.016 ][0.016 ][0.014 ]

[19] 0.726 0.722 0.699 0.706 0.713 0.749 0.738 0.724 0.753 0.750 0.721 0.739 0.738 0.764 0.762 0.685 0.684 0.666 - [0.016 ][0.016 ][0.016 ][0.016 ][0.015 ][0.016 ][0.014 ]

[20] 0.704 0.706 0.687 0.678 0.665 0.716 0.690 0.707 0.713 0.716 0.691 0.712 0.714 0.732 0.724 0.743 0.752 0.734 0.746 - [0.018 ][0.018 ][0.016 ][0.016 ][0.016 ][0.015 ]

[21] 0.647 0.626 0.591 0.600 0.638 0.672 0.672 0.683 0.721 0.721 0.674 0.711 0.710 0.721 0.717 0.741 0.740 0.735 0.743 0.648 - [0.019 ][0.016 ][0.016 ][0.016 ][0.014 ]

[22] 0.640 0.622 0.579 0.582 0.591 0.673 0.659 0.673 0.737 0.733 0.694 0.720 0.720 0.701 0.695 0.735 0.750 0.719 0.748 0.648 0.542 - [0.017 ][0.017 ][0.017 ][0.014 ]

[23] 0.710 0.682 0.692 0.689 0.702 0.670 0.711 0.714 0.746 0.740 0.719 0.745 0.739 0.722 0.727 0.769 0.789 0.768 0.775 0.755 0.706 0.711 - [0.018 ][0.018 ][0.014 ]

[24] 0.709 0.697 0.678 0.681 0.688 0.663 0.716 0.725 0.758 0.756 0.728 0.758 0.758 0.731 0.731 0.774 0.776 0.750 0.783 0.728 0.697 0.718 0.561 - [0.017 ][0.014 ]

[25] 0.700 0.703 0.659 0.669 0.701 0.670 0.716 0.713 0.758 0.753 0.734 0.741 0.737 0.710 0.710 0.766 0.788 0.761 0.775 0.738 0.720 0.702 0.569 0.490 - [0.014 ]

[26] 0.828 0.819 0.821 0.812 0.827 0.820 0.811 0.807 0.817 0.815 0.826 0.815 0.814 0.829 0.829 0.840 0.840 0.820 0.828 0.816 0.812 0.823 0.825 0.819 0.809 - .

The number of amino acid differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 26 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. There were a total of 838 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

**Table 2. Estimates of Evolutionary Divergence between P1 Sequences**

[ 1] #KJ641698\_bat\_picornavirus\_isolate\_bat/BtMf-PicoV-1/SAX2011

[ 2] #JQ814853\_Rhinolophus\_affinis\_picornavirus\_1

[ 3] #L02971\_Parechovirus\_A1\_HPeV-1\_Harris

[ 4] #AF327920\_Parechovirus\_B1\_LV-1\_87-012

[ 5] #HF677705\_Parechovirus\_C1\_Sebokele\_virus\_1\_An/B/1227/d

[ 6] #KF006989\_Parechovirus\_D1\_Ferret\_parechovirus\_isolate\_MpPeV1

[ 7] #AB937989\_Crohivirus\_strain\_ZM54

[ 8] #KX644937\_Bat\_crohivirus\_clone\_Bat/CAM/CroV-P25/2013

[ 9] #JQ316470\_Pasivirus\_1\_swine/France/2011

[10] #KM203656\_Orivirus\_1\_strain\_chicken/Pf-CHK1/2013/HUN

[11] #KT880667\_Orivirus\_2\_Pf-CHK1/OrV-A2

[12] #DQ249299\_Avihepatovirus\_A1\_DHAV-1\_03D

[13] #KJ000696\_Aalivirus\_A1\_duck\_picornavirus\_GL/12

[14] #KC465954\_Avisivirus\_A1\_strain\_turkey/M176-TuASV/2011/HUN

[15] #KC614703\_Avisivirus\_A1\_isolate\_turkey/USA/IN1/2010

[16] #KF979333\_Avisivirus\_B1\_Chicken\_picornavirus\_2\_isolate\_44C

[17] #KF979334\_Avisivirus\_C1\_Chicken\_picornavirus\_3\_isolate\_45C

[18] #KT880669\_Avisivirus\_C1\_Pf-CHK1/AsV

[19] #KC935379\_Kunsagivirus\_A1\_strain\_roller/SZAL6-KuV/2011/HUN

[20] #KX644936\_Kunsagivirus\_B1\_bat\_kunsagivirus

[21] #KY670597\_Kunsagivirus\_C1\_Bakunsa\_virus\_baboon/M27-KuV/1986/TAN

[22] #EU142040\_Aquamavirus\_A\_SePV-1\_HO-02-21

[23] #KC843627\_Potamipivirus\_A1\_EelPV\_F15-05

[24] #JX134222\_Limnipivirus\_A1\_Bluegill\_picornavirus\_isolate\_04-032

[25] #KF306267\_Limnipivirus\_B1\_Carp\_picornavirus\_1\_isolate\_F37/06

[26] #KF183915\_Limnipivirus\_C1\_Fathead\_minnow\_picornavirus\_isolate\_fhm/1/MN/USA/2010

[27] #KP770140\_Ampivirus\_A1\_strain\_NEWT/2013/HUN

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 ]

[ 1] -

[ 2] 0.307 -

[ 3] 0.738 0.718 -

[ 4] 0.724 0.738 0.514 -

[ 5] 0.722 0.723 0.538 0.444 -

[ 6] 0.729 0.725 0.602 0.598 0.622 -

[ 7] 0.737 0.724 0.666 0.648 0.660 0.682 -

[ 8] 0.714 0.728 0.613 0.577 0.603 0.630 0.621 -

[ 9] 0.747 0.730 0.669 0.669 0.665 0.720 0.665 0.637 -

[10] 0.798 0.805 0.755 0.762 0.764 0.761 0.792 0.771 0.791 -

[11] 0.795 0.798 0.753 0.762 0.765 0.757 0.789 0.763 0.783 0.100 -

[12] 0.800 0.800 0.696 0.713 0.724 0.739 0.744 0.748 0.759 0.701 0.693 -

[13] 0.790 0.790 0.726 0.713 0.711 0.741 0.767 0.744 0.758 0.691 0.684 0.615 -

[14] 0.797 0.786 0.725 0.752 0.746 0.746 0.753 0.745 0.746 0.707 0.700 0.665 0.688 -

[15] 0.795 0.784 0.728 0.754 0.749 0.744 0.756 0.749 0.740 0.712 0.701 0.668 0.697 0.107 -

[16] 0.799 0.782 0.721 0.743 0.750 0.750 0.749 0.740 0.759 0.701 0.707 0.648 0.662 0.585 0.579 -

[17] 0.780 0.790 0.736 0.737 0.734 0.745 0.748 0.762 0.758 0.707 0.711 0.641 0.664 0.555 0.558 0.555 -

[18] 0.776 0.791 0.740 0.742 0.730 0.732 0.737 0.752 0.759 0.711 0.714 0.637 0.666 0.564 0.562 0.568 0.125 -

[19] 0.803 0.791 0.786 0.789 0.786 0.774 0.779 0.809 0.807 0.811 0.808 0.790 0.825 0.791 0.795 0.796 0.795 0.794 -

[20] 0.804 0.790 0.766 0.771 0.762 0.772 0.786 0.771 0.769 0.789 0.793 0.772 0.797 0.799 0.792 0.784 0.789 0.785 0.499 -

[21] 0.780 0.782 0.762 0.780 0.754 0.773 0.758 0.792 0.795 0.801 0.801 0.780 0.794 0.792 0.790 0.773 0.777 0.780 0.496 0.516 -

[22] 0.839 0.812 0.764 0.798 0.795 0.794 0.784 0.790 0.808 0.808 0.810 0.811 0.827 0.808 0.819 0.794 0.799 0.802 0.753 0.757 0.747 -

[23] 0.792 0.793 0.742 0.730 0.748 0.734 0.740 0.750 0.753 0.798 0.795 0.768 0.757 0.803 0.799 0.792 0.777 0.778 0.808 0.798 0.797 0.788 -

[24] 0.845 0.835 0.798 0.824 0.825 0.832 0.818 0.829 0.837 0.827 0.833 0.829 0.822 0.848 0.848 0.833 0.836 0.836 0.854 0.859 0.839 0.858 0.810 -

[25] 0.839 0.827 0.800 0.826 0.809 0.809 0.795 0.810 0.820 0.828 0.827 0.811 0.801 0.815 0.819 0.805 0.815 0.815 0.847 0.845 0.827 0.845 0.791 0.412 -

[26] 0.850 0.832 0.797 0.812 0.814 0.811 0.803 0.824 0.833 0.819 0.822 0.825 0.806 0.838 0.839 0.821 0.818 0.822 0.855 0.849 0.846 0.852 0.804 0.435 0.295 -

[27] 0.909 0.907 0.902 0.906 0.900 0.904 0.890 0.905 0.920 0.920 0.916 0.906 0.912 0.910 0.910 0.911 0.914 0.918 0.903 0.888 0.902 0.912 0.913 0.888 0.879 0.881 -

The number of amino acid differences per site from between sequences are shown. The analysis involved 27 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. There were a total of 1094 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].