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:** | ***2017.003S*** | (to be completed by ICTV officers) |
| **Short title:** Create 1 new species (*Bopivirus A*) in a new genus (*Bopivirus*)(e.g. 6 new species in the genus *Zetavirus*) |
| **Modules attached** (Modules 1, 4 and either 2 or 3 are required.  |  **1** **[x]  2 [x]  3 [ ]  4 [x]**  |
| **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) |
| **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: | 07 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: 2017.003S.N.v1.Bopivirus** |

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:** |
| **Erbovirus:****Wutz G, Auer H, Nowotny N, Grosse B, Skern T, Kuechler E**. 1996. Equine rhinovirus serotypes 1 and 2: relationship to each other and to aphthoviruses and cardiovirses. J Gen Virol 77(8):1719-1730.**bovine picornavirus:****Tokarz R, Lipkin WI**. Unpublished. |

|  |
| --- |
| **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 (*Bopivirus A*) in a new genus (*Bopivirus*)**

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

VPg+5'UTRIRES[1A-1B-1C-1D-2A1NPGP/2B-2CHel/3A-3BVPg-3CPro-3DPol]3'UTR-poly(A)

*Note:* It is unclear, whether VP0 is cleaved.

The deduced P1 and 3CD proteins show low amino acid similarities with the orthologous proteins of other picornaviruses. Alignments reveal amino acid identities >40% for the P1 and 3CD proteins.

**Features that identify bopivirus as a picornavirus are:**

Genome layout with a single open reading frame and the presence of sequence motifs typical of picornaviruses, i.e.:

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

 N1173PGP motif,

 NTP-binding motif of 2CHel (**G**1585PPGQ**GKS**, Walker A motif, and a D1634DLGQ motif)

 putative 3C proteinase catalytic triad (H, D, GF**C**C)

 RNA-dependent RNA polymerase motifs (K2408DELR, P2541SG, Y2580GDD, F2628LKR)

Phylogenetic trees of the P1 and 3CD proteins comprising reference sequences of the *Aphthovirus/ Cardiovirus/Cosavirus/Erbovirus/Hunnivirus/Mischivirus/Mosavirus/Senecavirus/Teschovirus/Torchivirus* supergroup indicate that bopivirus forms a distinct branch (compare Figs. 2, 3) [Note: the supergroup concept does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)]. Unlike the other viruses of this supergroup, bopivirus lacks a leader protein. The 2B and 3A protein lack significant homology to known proteins; a blastp search did not yield a match. The orthologous proteins show closest similarity to erboviruses.

- Phylogenetic analyses of the P1 and 3CD proteins reveal that bopivirus is a divergent picornavirus related to erboviruses of the *Aphthovirus/Cardiovirus/Cosavirus/Erbovirus/ Hunnivirus/Mischivirus/Mosavirus/Senecavirus/Teschovirus/Torchivirus* supergroup (Figures 2, 3);

 - bopivirus has no L protein compared to the other viruses of the *Aphthovirus/ Cardiovirus/ Cosavirus/Erbovirus/Hunnivirus/Mischivirus/Mosavirus/Senecavirus/Teschovirus/Torchivirus* supergroup;

 - 2B and 3A of bopivirus are unique proteins without recognizable homology to other proteins of the GenBank (negative blastp result).

 - as shown in Tables 1, 2, bopivirus shows an amino acid divergence of both the 3CD and the P1 polyprotein >60-90% to all picornaviruses.

**Origin of name:**

Bopivirus: from **bo**vine **pi**cornavirus



**Figure 1:** Genome organization of *Erbovirus A* and bopivirus. 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 # and the (assumed) site of autocatalytic cleavage of VP0 is indicated by a ¶.The lengths of the deduced proteins (as proposed by Wutz et al. 1996) are also presented.



**Figure 2:** Phylogenetic analyses of picornavirus **3CD** using Bayesian tree inference (MrBayes 3.2). Twenty-nine picornavirus sequences of the *Aphthovirus/Cardiovirus/Cosavirus/Erbovirus/Hunnivirus/ Mischivirus/Mosavirus/Senecavirus/Teschovirus/Torchivirus* supergroup were retrieved from GenBank; the newt ampivirus sequence served as outgroup [Note: the supergroup concept 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** using Bayesian tree inference (MrBayes 3.2). Thirty-three picornavirus sequences of the *Aphthovirus/Cardiovirus/Cosavirus/Erbovirus/Hunnivirus/ Mischivirus/Mosavirus/Senecavirus/Teschovirus/Torchivirus* supergroup were retrieved from GenBank; the newt ampivirus sequence served as outgroup [Note: the supergroup concept 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.

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

[ 1] #KM589358\_Bovine\_picornavirus\_isolate\_TCH6

[ 2] #X96871\_Erbovirus\_ERBV-1\_P1436/71

[ 3] #KX260141\_Erbovirus\_ERBV-2\_strain\_1228\_cg

[ 4] #AF361253\_Erbovirus\_ERBV-3\_strain\_P313/75\_cg

[ 5] #X00871\_Aphthovirus\_FMDV\_O1Kaufbeuren

[ 6] #X96870\_Aphthovirus\_ERAV\_PERV\_P2P3

[ 7] #JN936206\_BRAV-2\_H-1

[ 8] #EU236594\_BRBV-1\_EC11

[ 9] #M81861\_Cardiovirus\_EMCV-R

[10] #M20562\_Cardiovirus\_TMEV\_GDVII

[11] #JQ864242\_Boone\_cardiovirus\_1\_isolate\_rat/USA/2010

[12] #JX683808\_Boone\_cardiovirus\_2\_isolate\_rat/USA/2012

[13] #DQ641257\_Senecavirus\_A\_SVV-1\_cc/US/SVV-001

[14] #JQ814851\_Mischivirus\_A1\_M.\_schreibersii\_picornavirus\_1\_bat/China/2010

[15] #KP054278\_Mischivirus\_B1\_Bat\_picornavirus\_strain\_BatPV/V14/13/Hun

[16] #KP100644\_Mischivirus\_C1\_African\_bat\_icavirus\_A\_isolate\_TNo13

[17] #FJ438902\_Cosavirus\_HCoSV-A1

[18] #FJ438907\_Cosavirus\_HCoSV-B1

[19] #FJ438908\_Cosavirus\_HCoSV-D1

[20] #FJ555055\_Cosavirus\_HCoSV-E1

[21] #JN867758\_Cosavirus\_HCoSV\_F1\_PK5006

[22] #AF231769\_Teschovirus\_A\_PTV-1\_Talfan

[23] #JQ941880\_Hunnivirus\_A1\_HuV-A1\_cattle/HUN/2008

[24] #KX156157\_Hunnivirus\_A2\_rodent/Rn/PicoV/SX2015\_2

[25] #KM396707\_Lesavirus\_1\_isolate\_Mis101308/2012

[26] #KM396708\_Lesavirus\_2\_isolate\_Nai108015/2012

[27] #LC113907\_Porcine\_picornavirus\_Japan\_Tottori-WOL

[28] #JF973687\_Mosavirus\_A1\_mouse/M-7/USA/2010

[29] #KF958461\_Mosavirus\_A2\_strain\_SZAL6-MoV/2011/HUN

[30] #KM873611\_Torchivirus\_A1\_Tortoise\_picornavirus\_strain\_14-04

[31] #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 28 29 30 31 ]

[ 1]

[ 2] 0.596

[ 3] 0.605 0.031

[ 4] 0.605 0.036 0.029

[ 5] 0.685 0.672 0.673 0.673

[ 6] 0.674 0.643 0.643 0.637 0.531

[ 7] 0.680 0.650 0.656 0.652 0.417 0.560

[ 8] 0.698 0.664 0.664 0.664 0.399 0.545 0.412

[ 9] 0.669 0.635 0.633 0.636 0.634 0.614 0.645 0.616

[10] 0.673 0.654 0.661 0.664 0.663 0.605 0.651 0.644 0.403

[11] 0.675 0.647 0.654 0.651 0.640 0.591 0.646 0.630 0.450 0.469

[12] 0.781 0.732 0.742 0.742 0.718 0.698 0.725 0.720 0.537 0.565 0.028

[13] 0.683 0.659 0.666 0.662 0.620 0.607 0.635 0.610 0.490 0.493 0.516 0.630

[14] 0.659 0.642 0.645 0.645 0.662 0.628 0.645 0.643 0.506 0.538 0.539 0.652 0.516

[15] 0.681 0.649 0.648 0.652 0.666 0.628 0.655 0.657 0.523 0.528 0.536 0.636 0.515 0.202

[16] 0.672 0.642 0.647 0.651 0.655 0.604 0.642 0.639 0.515 0.552 0.561 0.682 0.545 0.454 0.457

[17] 0.711 0.675 0.670 0.675 0.628 0.628 0.642 0.627 0.598 0.594 0.594 0.711 0.588 0.607 0.602 0.614

[18] 0.692 0.685 0.682 0.686 0.625 0.629 0.644 0.628 0.605 0.617 0.621 0.735 0.607 0.611 0.624 0.618 0.304

[19] 0.706 0.670 0.667 0.667 0.634 0.623 0.637 0.626 0.601 0.610 0.609 0.701 0.593 0.601 0.602 0.609 0.337 0.315

[20] 0.712 0.666 0.666 0.666 0.637 0.616 0.639 0.626 0.609 0.616 0.614 0.707 0.605 0.619 0.623 0.627 0.344 0.334 0.224

[21] 0.708 0.691 0.687 0.688 0.633 0.626 0.653 0.629 0.617 0.610 0.608 0.727 0.606 0.604 0.607 0.623 0.331 0.360 0.361 0.370

[22] 0.664 0.661 0.657 0.657 0.669 0.663 0.700 0.670 0.658 0.663 0.692 0.771 0.653 0.660 0.674 0.667 0.682 0.685 0.680 0.677 0.679

[23] 0.687 0.666 0.667 0.669 0.679 0.682 0.694 0.687 0.657 0.664 0.691 0.766 0.669 0.651 0.672 0.667 0.709 0.716 0.699 0.698 0.721 0.575

[24] 0.698 0.672 0.673 0.673 0.674 0.684 0.696 0.687 0.658 0.664 0.685 0.766 0.672 0.660 0.669 0.665 0.710 0.717 0.701 0.705 0.718 0.575 0.095

[25] 0.680 0.683 0.688 0.684 0.667 0.653 0.663 0.669 0.656 0.657 0.680 0.778 0.639 0.662 0.679 0.656 0.669 0.685 0.676 0.664 0.671 0.562 0.498 0.497

[26] 0.693 0.681 0.681 0.681 0.666 0.666 0.676 0.674 0.657 0.658 0.684 0.784 0.645 0.651 0.666 0.653 0.664 0.688 0.678 0.673 0.683 0.578 0.505 0.510 0.252

[27] 0.716 0.707 0.708 0.708 0.674 0.678 0.681 0.681 0.676 0.678 0.673 0.773 0.665 0.661 0.677 0.679 0.671 0.678 0.686 0.679 0.676 0.645 0.559 0.553 0.570 0.565

[28] 0.687 0.691 0.692 0.695 0.664 0.640 0.669 0.674 0.660 0.657 0.675 0.764 0.668 0.653 0.669 0.659 0.679 0.683 0.683 0.680 0.696 0.699 0.689 0.689 0.688 0.692 0.685

[29] 0.688 0.695 0.700 0.697 0.668 0.647 0.665 0.665 0.666 0.660 0.688 0.767 0.674 0.667 0.673 0.662 0.682 0.689 0.698 0.689 0.702 0.701 0.686 0.692 0.689 0.692 0.678 0.187

[30] 0.671 0.675 0.683 0.686 0.673 0.650 0.657 0.659 0.640 0.630 0.647 0.742 0.637 0.643 0.647 0.644 0.685 0.655 0.666 0.671 0.670 0.695 0.692 0.689 0.685 0.672 0.635 0.598 0.590

[31] 0.810 0.822 0.824 0.819 0.835 0.821 0.817 0.823 0.814 0.838 0.826 0.858 0.820 0.820 0.836 0.824 0.813 0.815 0.819 0.806 0.807 0.802 0.811 0.814 0.806 0.795 0.813 0.828 0.833 0.827

The number of amino acid differences per site from between sequences are shown. The analysis involved 31 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 824 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

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

[ 1] #KM589358\_Bovine\_picornavirus\_isolate\_TCH6

[ 2] #X96871\_Erbovirus\_ERBV-1\_P1436-71

[ 3] #AY606988\_Erbovirus\_ERBV-1\_strain\_ERBV1.293/74\_(P1)

[ 4] #AY606998\_Erbovirus\_ERBV-2\_strain\_ERBV2.1576/99\_(P1)

[ 5] #DQ108383\_Erbovirus\_ERBV-3\_strain\_ERBV3.4442/75.acid\_stable\_(P1)

[ 6] #KX260141\_Erbovirus\_ERBV-2\_strain\_1228\_cg

[ 7] #AF361253\_Erbovirus\_ERBV-3\_strain\_P313/75\_cg

[ 8] #X00871\_Aphthovirus\_FMDV\_O1K

[ 9] #X96870\_Aphthovirus\_ERAV\_PERV

[10] #JN936206\_Aphthovirus\_BRAV-2\_H-1

[11] #EU236594\_Aphthovirus\_BRBV-1\_EC11

[12] #M81861\_Cardiovirus\_A\_EMCV-1\_R

[13] #M20562\_Cardiovirus\_B\_TMEV\_GDVII

[14] #JQ864242\_Cardiovirus\_C\_Boone\_cardiovirus\_isolate\_BCV-1

[15] #JX683808\_Cardiovirus\_C\_Boone\_cardiovirus\_isolate\_BCV-2

[16] #DQ641257\_Senecavirus\_SVV-1\_SVV-001

[17] #JQ814851\_Mischivirus\_A1

[18] #KP054278\_Mischivirus\_B1\_Bat\_picornavirus\_strain\_BatPV/V14/13/Hun

[19] #KP100644\_Mischivirus\_C\_African\_bat\_icavirus\_A\_isolate\_TNo13

[20] #FJ438902\_HCoSV-A1\_0553

[21] #FJ438907\_HCoSV-B1

[22] #FJ438908\_HCoSV-D1

[23] #FJ555055\_HCoSV-E1

[24] #JN867758\_HCoSC\_F1\_PK5006

[25] #AF231769\_Teschovirus\_PTV\_PTV1-Talfan

[26] #JQ941880\_Hunnivirus\_BHUV1/2008/HUN

[27] #KX156157\_Hunnivirus\_sp.\_rodent/Rn/PicoV/SX2015\_2

[28] #KM396707\_Lesavirus\_1\_isolate\_Mis101308/2012

[29] #KM396708\_Lesavirus\_2\_isolate\_Nai108015/2012

[30] #LC113907\_Porcine\_picornavirus\_Japan\_Tottori-WOL

[31] #JF973687\_Mosavirus\_A1\_M-7

[32] #KF958461\_Mosavirus\_A2\_strain\_SZAL6-MoV/2011/HUN

[33] #KM873613\_Torchivirus\_tortoise\_picornavirus\_strain\_9-05

[34] #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 28 29 30 31 32 33 34 ]

[ 1]

[ 2] 0.615

[ 3] 0.612 0.031

[ 4] 0.607 0.273 0.273

[ 5] 0.605 0.226 0.234 0.240

[ 6] 0.608 0.270 0.266 0.052 0.244

[ 7] 0.607 0.281 0.279 0.055 0.249 0.047

[ 8] 0.680 0.679 0.683 0.666 0.680 0.673 0.666

[ 9] 0.675 0.656 0.660 0.646 0.653 0.648 0.642 0.630

[10] 0.695 0.690 0.694 0.673 0.692 0.677 0.674 0.545 0.652

[11] 0.687 0.685 0.685 0.674 0.690 0.676 0.678 0.539 0.617 0.540

[12] 0.645 0.663 0.665 0.645 0.657 0.654 0.656 0.706 0.691 0.731 0.706

[13] 0.634 0.667 0.667 0.641 0.666 0.649 0.645 0.698 0.688 0.726 0.690 0.380

[14] 0.636 0.681 0.683 0.660 0.662 0.665 0.670 0.711 0.722 0.739 0.724 0.505 0.484

[15] 0.630 0.674 0.672 0.654 0.665 0.654 0.662 0.706 0.714 0.734 0.721 0.486 0.465 0.138

[16] 0.677 0.678 0.675 0.670 0.670 0.672 0.677 0.713 0.698 0.739 0.720 0.646 0.644 0.655 0.651

[17] 0.665 0.673 0.677 0.668 0.673 0.668 0.667 0.713 0.695 0.740 0.723 0.604 0.598 0.616 0.611 0.674

[18] 0.668 0.680 0.682 0.677 0.670 0.676 0.679 0.701 0.691 0.737 0.727 0.590 0.595 0.612 0.606 0.665 0.275

[19] 0.678 0.679 0.686 0.654 0.670 0.658 0.662 0.727 0.704 0.738 0.730 0.628 0.609 0.623 0.614 0.658 0.552 0.551

[20] 0.727 0.707 0.708 0.691 0.708 0.696 0.698 0.743 0.736 0.773 0.752 0.656 0.647 0.671 0.661 0.706 0.653 0.659 0.667

[21] 0.700 0.703 0.701 0.686 0.697 0.689 0.691 0.746 0.713 0.758 0.747 0.661 0.653 0.669 0.653 0.703 0.648 0.657 0.655 0.448

[22] 0.704 0.682 0.683 0.682 0.696 0.678 0.683 0.751 0.739 0.769 0.749 0.666 0.670 0.675 0.670 0.713 0.667 0.656 0.674 0.525 0.505

[23] 0.701 0.687 0.688 0.681 0.689 0.681 0.686 0.744 0.727 0.763 0.735 0.666 0.645 0.671 0.660 0.708 0.636 0.645 0.649 0.464 0.430 0.489

[24] 0.701 0.694 0.698 0.678 0.689 0.684 0.684 0.726 0.726 0.747 0.743 0.659 0.662 0.670 0.656 0.697 0.658 0.659 0.665 0.392 0.423 0.505 0.472

[25] 0.735 0.740 0.740 0.749 0.745 0.750 0.754 0.767 0.734 0.781 0.739 0.726 0.711 0.716 0.704 0.758 0.753 0.750 0.766 0.755 0.745 0.758 0.767 0.743

[26] 0.695 0.707 0.707 0.693 0.698 0.686 0.692 0.722 0.725 0.737 0.719 0.677 0.700 0.698 0.693 0.695 0.712 0.705 0.714 0.745 0.747 0.740 0.754 0.725 0.637

[27] 0.698 0.701 0.703 0.689 0.696 0.687 0.697 0.721 0.733 0.729 0.716 0.689 0.696 0.688 0.689 0.691 0.718 0.704 0.725 0.748 0.737 0.732 0.753 0.723 0.635 0.149

[28] 0.702 0.689 0.694 0.702 0.692 0.705 0.705 0.720 0.720 0.720 0.698 0.680 0.687 0.680 0.677 0.685 0.704 0.690 0.719 0.713 0.692 0.701 0.710 0.685 0.653 0.557 0.551

[29] 0.690 0.692 0.698 0.692 0.696 0.691 0.693 0.711 0.708 0.704 0.706 0.679 0.680 0.670 0.664 0.700 0.693 0.698 0.711 0.710 0.710 0.717 0.721 0.712 0.638 0.533 0.529 0.396

[30] 0.717 0.709 0.709 0.711 0.722 0.705 0.709 0.728 0.727 0.729 0.727 0.697 0.714 0.703 0.684 0.720 0.736 0.729 0.727 0.729 0.715 0.726 0.718 0.719 0.686 0.629 0.630 0.589 0.594

[31] 0.646 0.636 0.639 0.637 0.645 0.642 0.636 0.701 0.678 0.724 0.703 0.660 0.659 0.662 0.659 0.688 0.680 0.682 0.667 0.709 0.694 0.692 0.681 0.674 0.711 0.699 0.707 0.675 0.679 0.698

[32] 0.674 0.649 0.647 0.639 0.651 0.642 0.638 0.717 0.704 0.719 0.699 0.656 0.649 0.666 0.656 0.695 0.684 0.688 0.675 0.696 0.685 0.683 0.676 0.672 0.714 0.708 0.709 0.683 0.689 0.708 0.309

[33] 0.664 0.630 0.631 0.638 0.634 0.638 0.637 0.703 0.679 0.727 0.714 0.645 0.640 0.656 0.648 0.658 0.657 0.657 0.656 0.709 0.694 0.664 0.686 0.685 0.729 0.684 0.687 0.675 0.670 0.715 0.601 0.597

[34] 0.899 0.906 0.905 0.902 0.892 0.905 0.904 0.896 0.869 0.892 0.902 0.885 0.887 0.877 0.870 0.884 0.895 0.880 0.886 0.896 0.896 0.898 0.901 0.898 0.896 0.904 0.905 0.897 0.901 0.905 0.900 0.906 0.912

The number of amino acid differences per site from between sequences are shown. The analysis involved 34 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 1113 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].