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:** | ***2017.004S*** | (to be completed by ICTV officers) |
| **Short title:**  Create 2 new species (*Crohivirus A, Crohivirus B*) in a new genus (*Crohivirus*)(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:** 2017.004S.N.v1Crohivirus |

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:** |
| **Shrew crohivirus:**Sasaki M, Orba Y, Ueno K, Ishii A, Moonga L, Hang'ombe BM, Mweene AS, Ito K, Sawa H. 2015. Metagenomic analysis of the shrew enteric virome reveals novel viruses related to human stool-associated viruses. J Gen Virol 96:440-452.**Bat crohivirus:**Yinda CK, Zell R, Deboutte W, Zeller M, Conceicao-Neto N, Heylen E, Maes P, Knowles NJ, Ghogomu SM, Van Ranst M, Matthijnssens J. 2016. Highly diverse population of *Picornaviridae* and other members of *Picornavirales*, in Cameroonian fruet bats. BMC Genomics 18:249. |

|  |
| --- |
| **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 2 new species (*Crohivirus A, Crohivirus B*) in a new genus (*Crohivirus*)**Two novel picornaviruses, shrew crohivirus and bat crohivirus, were detected in the intestinal contents and faecal samples, respectively, of captured wild shrews in Zambia and fruit bats (*Eidolon helvum*) in Cameroon, respectively. Virus isolates are not available, but the genome sequences suggest that these viruses belong to the *Picornaviridae*. 3-4-4 genome layout (compare Figure 1):VPg+5'UTRIRES-IV[1AB-1C-1D-2A1NPG↓P/2A2H-box/NC-2B-2CHel/3A-3BVPg-3CPro-3DPol]3'UTR-poly(A)Crohivirus proteins P1 and 3CD show only low amino acid similarities with the orthologous proteins of other picornaviruses. Alignments reveal amino acid identities <40% for the 3CD protein and <34% for the P1 polyprotein (Tables 1, 2).**Features that identify crohiviruses as picornaviruses are:**(i) a typical picornavirus genome layout with a single open reading frame (ii) the presence of sequence motifs typical of picornaviruses, i.e.: three rhv-like domains (Pfam database) corresponding to VP0, VP3, VP1,  NTP-binding motif of 2CHel (GxxGxGKS, Walker A motif, and a DDxGQ motif) putative 3C proteinase catalytic triad (H, D, GxCG) RNA-dependent RNA polymerase motifs (KDELR, GxPSG, YGDD)The divergence (number of differences per site from between sequences) of the two known crohiviruses is c. 0.58 for the polyprotein, c. 0.62 for P1 and c. 0.53 for 2C+3CD. Therefore, it is justified to propose two crohivirus species.The phylogenetic tree of the 3CD protein comprising reference sequences of the *Aquamavirus/ Avihepatovirus/Avisivirus/Kunsagivirus/Pasivirus/Parechovirus* supergroup indicates that the crohiviruses are placed in a distinct branch (compare Fig. 2) [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)]. In the P1 tree, crohiviruses cluster with pasiviruses. Closest relatives of crohiviruses are parechoviruses and pasiviruses. Crohiviruses and Ljungan viruses (*Parechovirus B*) have an identical genome layout; pasiviruses, however, differ from crohiviruses by their 2A2 protein. Pasivirus 2A2 has no H-box/NC sequence motif.1. Phylogenetic analyses of the P1 and 3CD proteins reveal that crohiviruses cluster in a distinct branch. They are divergent picornaviruses related to parechoviruses and pasiviruses (Figures 2, 3):  - crohiviruses share aa identities of their capsid proteins up to 35% with parechoviruses and pasiviruses; - crohiviruses share aa identities of the conserved 3CD protein up to 40% with parechoviruses and pasiviruses; 2. Figure 1 compares the genomes of crohiviruses with those of the parechoviruses and pasiviruses. Distinctive features of crohiviruses are  - a unique 3A protein which has no homology to other picornaviruses; - a short 3'-UTR.**Origin of the new genus name:**Crohivirus: from ***Cro****cidura* ***hi****rta* (the lesser red musk shrew which hosted the first strain)**Species demarcation criteria in the new genus:**Members of a species of the genus *Crohivirus*:• share greater than 45% aa identity in the polyprotein,• share greater than 40% aa identity in P1,• share greater than 50% aa identity in 2C + 3CD,• share a common genome organization. |



**Figure 1:** Genome organization of Ljungan virus (A), shrew crohivirus (B), bat crohivirus (C) and swine pasivirus (D). The open reading frames are indicated by boxes. Positions of putative aa cleavage sites and the lengths of the deduced proteins are shown. The ▼ indicates the putative 3CPro processing sites, a # the site of termination/reinitiation of RNA translation at the NPGP sequence motif. The unique 2A2 protein of swine pasivirus is shaded. The remaining proteins show significant homology.



**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 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 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Figure 3 (previous page):** 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 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 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 of 3CD Protein between Sequences**

[ 1] #AB937989\_Shrew\_crohivirus\_shrew/ZM54/Zambia/2012

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

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

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

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

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

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

[ 8] #JX491648\_Pasivirus\_A2\_PLV-CHN

[ 9] #KM259923\_Pasivirus\_A3\_swine/Zsana1/2013/HUN

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

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

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

[13] #EF067923\_Avihepatovirus\_A2\_strain\_04G

[14] #DQ256132\_Avihepatovirus\_A3\_isolate\_AP-03337

[15] #KJ000696\_Aalivirus\_A1\_duck/GL/12/China/2012

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

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

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

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

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

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

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

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

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

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

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

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

[28] #KF306267\_Limnipivirus\_B1\_CarpPV

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

[30] #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 ]

[ 1]

[ 2] 0.542

[ 3] 0.629 0.628

[ 4] 0.595 0.590 0.510

[ 5] 0.604 0.591 0.541 0.340

[ 6] 0.643 0.596 0.591 0.573 0.573

[ 7] 0.647 0.646 0.710 0.689 0.680 0.669

[ 8] 0.639 0.641 0.709 0.675 0.679 0.670 0.105

[ 9] 0.647 0.640 0.707 0.677 0.680 0.669 0.087 0.130

[10] 0.650 0.644 0.663 0.681 0.684 0.664 0.706 0.690 0.701

[11] 0.681 0.681 0.703 0.657 0.647 0.670 0.718 0.710 0.715 0.685

[12] 0.685 0.674 0.665 0.651 0.655 0.671 0.706 0.701 0.711 0.676 0.679

[13] 0.685 0.670 0.660 0.658 0.661 0.661 0.712 0.711 0.716 0.674 0.682 0.112

[14] 0.680 0.667 0.660 0.658 0.656 0.658 0.703 0.704 0.712 0.677 0.682 0.110 0.052

[15] 0.672 0.659 0.677 0.659 0.663 0.669 0.689 0.690 0.697 0.698 0.689 0.521 0.529 0.536

[16] 0.721 0.737 0.715 0.703 0.697 0.699 0.713 0.713 0.715 0.722 0.737 0.609 0.612 0.606 0.573

[17] 0.721 0.733 0.708 0.699 0.695 0.699 0.716 0.713 0.719 0.713 0.735 0.616 0.616 0.612 0.569 0.041

[18] 0.674 0.694 0.698 0.670 0.683 0.681 0.691 0.686 0.691 0.698 0.711 0.596 0.590 0.595 0.557 0.492 0.491

[19] 0.711 0.720 0.725 0.704 0.706 0.700 0.712 0.711 0.709 0.706 0.727 0.607 0.599 0.602 0.555 0.461 0.460 0.494

[20] 0.710 0.720 0.725 0.704 0.706 0.700 0.714 0.709 0.708 0.707 0.728 0.604 0.592 0.596 0.552 0.456 0.455 0.496 0.014

[21] 0.721 0.701 0.696 0.676 0.679 0.704 0.732 0.737 0.735 0.706 0.701 0.625 0.617 0.620 0.642 0.705 0.698 0.681 0.672 0.672

[22] 0.717 0.695 0.704 0.673 0.677 0.699 0.724 0.728 0.724 0.706 0.699 0.623 0.621 0.626 0.650 0.687 0.682 0.665 0.683 0.683 0.158

[23] 0.741 0.735 0.746 0.745 0.731 0.727 0.743 0.743 0.732 0.752 0.741 0.741 0.740 0.740 0.728 0.748 0.746 0.720 0.736 0.734 0.734 0.742

[24] 0.740 0.750 0.739 0.729 0.716 0.728 0.752 0.744 0.741 0.748 0.738 0.723 0.713 0.717 0.734 0.756 0.750 0.724 0.737 0.735 0.731 0.739 0.524

[25] 0.735 0.719 0.720 0.727 0.703 0.699 0.734 0.721 0.716 0.732 0.741 0.737 0.742 0.736 0.730 0.731 0.737 0.727 0.743 0.743 0.733 0.735 0.576 0.575

[26] 0.743 0.748 0.714 0.697 0.701 0.711 0.746 0.746 0.742 0.732 0.744 0.724 0.719 0.719 0.738 0.753 0.750 0.721 0.739 0.738 0.764 0.762 0.685 0.684 0.666

[27] 0.706 0.711 0.686 0.691 0.689 0.707 0.755 0.749 0.747 0.711 0.670 0.715 0.716 0.715 0.711 0.746 0.740 0.719 0.745 0.739 0.722 0.727 0.769 0.789 0.768 0.775

[28] 0.697 0.718 0.696 0.678 0.681 0.689 0.728 0.727 0.727 0.710 0.665 0.725 0.724 0.721 0.716 0.758 0.756 0.728 0.758 0.758 0.731 0.731 0.774 0.776 0.750 0.783 0.561

[29] 0.720 0.702 0.705 0.659 0.671 0.703 0.736 0.741 0.743 0.703 0.672 0.713 0.715 0.716 0.716 0.758 0.753 0.734 0.741 0.737 0.710 0.710 0.766 0.788 0.761 0.775 0.569 0.490

[30] 0.812 0.823 0.824 0.822 0.813 0.822 0.818 0.816 0.813 0.827 0.820 0.807 0.800 0.803 0.811 0.817 0.815 0.826 0.815 0.814 0.829 0.829 0.840 0.840 0.820 0.828 0.825 0.819 0.809

The number of amino acid differences per site from between sequences are shown. The analysis involved 30 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].

\_\_\_ within type comparison, \_\_\_ between types/within species comparison, \_\_\_ between species/within genus comparison, \_\_\_ between genera comparison

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

[ 1] #AB937989\_Shrew\_crohivirus\_strain\_ZM54

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

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

[ 8] #JX491648\_Pasivirus\_A2\_PLV-CHN

[ 9] #KM259923\_Pasivirus\_A3\_strain\_swine/Zsana1/2013/HUN

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

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

[12] #Potamipivirus\_A1\_EelPV\_F15-05

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

[14] #EF067923\_Avihepatovirus\_A2\_Duck\_hepatitis\_virus\_2\_strain\_04G

[15] #DQ256132\_Avihepatovirus\_A3\_Duck\_hepatitis\_A\_virus\_3\_isolate\_AP-03337

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

[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] 0.624

[ 3] 0.668 0.617

[ 4] 0.648 0.578 0.511

[ 5] 0.662 0.602 0.538 0.444

[ 6] 0.681 0.624 0.602 0.599 0.622

[ 7] 0.667 0.640 0.667 0.666 0.658 0.712

[ 8] 0.659 0.642 0.671 0.666 0.667 0.700 0.175

[ 9] 0.656 0.652 0.669 0.665 0.656 0.703 0.203 0.199

[10] 0.735 0.715 0.740 0.727 0.729 0.727 0.747 0.748 0.751

[11] 0.731 0.734 0.723 0.737 0.731 0.727 0.734 0.745 0.733 0.307

[12] 0.746 0.747 0.745 0.726 0.750 0.735 0.758 0.757 0.767 0.782 0.784

[13] 0.744 0.748 0.689 0.708 0.727 0.734 0.763 0.762 0.765 0.797 0.801 0.767

[14] 0.765 0.746 0.699 0.713 0.743 0.737 0.771 0.763 0.760 0.781 0.793 0.778 0.252

[15] 0.752 0.735 0.679 0.701 0.724 0.723 0.757 0.758 0.755 0.792 0.799 0.770 0.223 0.230

[16] 0.770 0.735 0.727 0.719 0.715 0.740 0.764 0.760 0.769 0.793 0.793 0.754 0.622 0.634 0.644

[17] 0.754 0.744 0.724 0.752 0.748 0.748 0.747 0.756 0.753 0.799 0.785 0.798 0.666 0.657 0.672 0.690

[18] 0.757 0.748 0.725 0.751 0.749 0.746 0.740 0.754 0.748 0.795 0.783 0.794 0.670 0.659 0.663 0.699 0.107

[19] 0.747 0.741 0.716 0.734 0.747 0.745 0.768 0.763 0.755 0.794 0.778 0.786 0.649 0.651 0.662 0.665 0.585 0.579

[20] 0.752 0.761 0.729 0.734 0.736 0.739 0.765 0.766 0.765 0.783 0.785 0.775 0.630 0.626 0.636 0.662 0.549 0.552 0.541

[21] 0.742 0.752 0.735 0.736 0.730 0.727 0.766 0.773 0.767 0.779 0.786 0.770 0.627 0.639 0.632 0.661 0.557 0.555 0.558 0.098

[22] 0.792 0.764 0.752 0.761 0.767 0.754 0.777 0.773 0.778 0.807 0.810 0.792 0.694 0.700 0.697 0.685 0.697 0.698 0.706 0.703 0.705

[23] 0.795 0.766 0.752 0.763 0.766 0.758 0.785 0.773 0.784 0.811 0.818 0.797 0.702 0.701 0.699 0.692 0.704 0.709 0.701 0.701 0.702 0.100

[24] 0.786 0.809 0.790 0.792 0.790 0.773 0.810 0.802 0.811 0.811 0.802 0.813 0.787 0.803 0.795 0.827 0.794 0.799 0.801 0.797 0.797 0.817 0.822

[25] 0.790 0.773 0.766 0.775 0.764 0.770 0.774 0.765 0.768 0.807 0.794 0.797 0.772 0.778 0.781 0.790 0.799 0.795 0.785 0.792 0.783 0.791 0.790 0.499

[26] 0.763 0.793 0.766 0.782 0.752 0.773 0.795 0.785 0.793 0.782 0.786 0.800 0.780 0.786 0.787 0.795 0.796 0.795 0.780 0.779 0.779 0.804 0.806 0.496 0.516

[27] 0.778 0.790 0.761 0.798 0.793 0.797 0.806 0.804 0.803 0.841 0.819 0.785 0.811 0.823 0.816 0.830 0.805 0.813 0.798 0.796 0.800 0.805 0.803 0.751 0.754 0.741

[28] 0.813 0.823 0.794 0.822 0.825 0.829 0.836 0.839 0.835 0.846 0.839 0.810 0.832 0.842 0.835 0.825 0.845 0.847 0.827 0.826 0.827 0.826 0.821 0.845 0.856 0.830 0.860

[29] 0.796 0.806 0.801 0.825 0.809 0.807 0.819 0.819 0.821 0.841 0.830 0.789 0.815 0.820 0.825 0.800 0.811 0.815 0.799 0.810 0.807 0.819 0.819 0.838 0.836 0.820 0.849 0.412

[30] 0.803 0.818 0.796 0.808 0.814 0.810 0.825 0.831 0.824 0.848 0.831 0.804 0.826 0.834 0.839 0.805 0.837 0.837 0.815 0.812 0.815 0.813 0.810 0.846 0.845 0.843 0.854 0.435 0.295

[31] 0.894 0.897 0.897 0.904 0.898 0.899 0.909 0.915 0.913 0.921 0.905 0.916 0.906 0.903 0.901 0.908 0.911 0.912 0.909 0.914 0.919 0.914 0.916 0.907 0.897 0.913 0.912 0.895 0.884 0.885

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 1101 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

\_\_\_ within type comparison, \_\_\_ between types/within species comparison, \_\_\_ between species/within genus comparison, \_\_\_ between genera comparison