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:** | ***2017.002S*** | (to be completed by ICTV officers) |
| **Short title:**  Create 1 new species (*Aalivirus A*) in new genus (*Aalivirus*)(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* SG** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: | 15/06/2017 |
| 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:** 2017.002S.N.v1.Aalivirus |

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:** |
| Wang X, Liu N, Wang F, Ning K, Li Y, Zhang D. 2014. Genetic characterization of a novel duck-origin picornavirus with six 2A proteins. J Gen Virol 95:1289-1296. |

|  |
| --- |
| **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.
 |

A novel picornavirus, duck aalivirus, was detected in the intestinal contents of diseased 4- to 5-weeks old Pekin ducks in China. A virus isolate is not available, but the genome sequence suggests that this virus belongs to the *Picornaviridae* family but has an unusual 3-8-4 genome layout (compare Figure 1):

VPg+5'UTRIRES-IV[1AB-1C-1D-2A1NPG↓P/2A2NPG↓P/2A3NPG↓P/2A4NPG↓P/2A5NTPase-2A6H-box/NC-2B-2CHel/3A-3BVPg-3CPro-3DPol]3'UTR-poly(A)

All aalivirus proteins except 2A2NPGP, 2A3NPGP, 2A4NPGP (three unique proteins, no significant similarities found in blastp searches) show homology to the orthologous proteins of avihepatoviruses but are highly divergent (Table 1). Deviant aalivirus proteins are:

- VP1 protein: C-terminal deletion of c. 50 amino acids,

- 2B protein: C-terminal extension of c. 70 amino acids,

- VPg has a length of only 22 amino acids (vs. 34 aa of avihepatoviruses).

Table 1: Comparison of 5'-, 3'-NTR und processed proteins.

|  |  |  |  |
| --- | --- | --- | --- |
| Genomeregion | *Avihepatovirus A*(duck hepatitis A virus) | *Aalivirus A*(duck aalivirus) | Amino acididentity |
| 5-UTR | 623 nt | 604 nt | n.d. |
| VP0 | 256 aa | 264 aa | 37.8% |
| VP3 | 237 aa | 234 aa | 39.9% |
| VP1 | 238 aa | 188 aa | 41.6% |
| 2A1NPGP | 20 aa | 19 aa | n.d. |
| 2A2NPGP | - | 133 aa | - |
| 2A3NPGP | - | 150 aa | - |
| 2A4NPGP | - | 131 aa | - |
| 2ANTPase | 161 aa | 169 aa | 24.5% |
| 2AH-box/NC | 124 aa | 123 aa | 35.8% |
| 2B | 119 aa | 189 aa | 49.3% |
| 2C | 333 aa | 338 aa | 50.3% |
| 3A | 93 aa | 83 aa | 31.6% |
| 3B | 34 aa | 22 aa | 26.7% |
| 3C | 181 aa | 182 aa | 46.1% |
| 3D | 453 aa | 455 aa | 48.9% |
| 3'-UTR | 317 nt | 314 nt | n.d. |

Amino acid identities of P1 polypeptide: 39.6%, of P3 polypeptide: 45.6%

See also Tables 2, 3 (Estimates of evolutionary divergence of 3CD protein and P1 polyprotein between sequences).

The phylogenetic tree of the 3CD protein comprising reference sequences of the *Aquamavirus/ Avihepatovirus/Avisivirus/Kunsagivirus/Limnipivirus/Pasivirus/Parechovirus/Potamipivirus* supergroup indicates that the aaliviruses are placed on a separate 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, aalivirus clusters with avihepatovirus but due to sequence divergence with a long branch length (Fig. 3).

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

(i) a typical picornavirus genome layout with a single open reading frame and

(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, GxCSG, YGDD)

**Distinguishing features of aaliviruses are**

- deletion of c. 50 amino acids at C-terminus of VP1

- 4 copies of 2ANPGP proteins with lengths of 19 aa, 133 aa, 150 aa, and 131 aa,

- insertion of 70 amino acids at C-terminus of 2B protein,

- low amino acid identities of 2AATPase, 2AH-box/NC, 3A, 3B compared to avihepatoviruses.

**Origin of the new genus name:**

Aalivirus: from **a**vihepatovirus/**a**visivirus-**li**ke **virus**

**Proposed abbreviation:**

AaV-A



**Figure 1:** Genome organization of duck hepatitis A virus (A) and duck aalivirus (B). 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.



**Figure 2:** Phylogenetic analyses of picornavirus **3CD** using Bayesian tree inference (MrBayes 3.2). Twenty-five picornavirus sequences of the *Aquamavirus/Avihepatovirus/Avisivirus/ Kunsagivirus/Limnipivirus/Pasivirus/Parechovirus/Potamipivirus* 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. The proposed name is 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:** 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/Limnipivirus/Pasivirus/Parechovirus/Potamipivirus* 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. The proposed name is 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] #KJ000696\_Aalivirus\_A1\_duck\_aalivirus\_duck/GL/12/China/2012

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

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

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

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

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

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

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

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

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

[11] #KX644936\_Bat\_kunsagivirus\_Bat/CAM/KuV-P2/2013

[12] #KY670597\_Bakunsa\_virus\_baboon/M27-KuV/1986/TAN

[13] #EU142040\_Aquamavirus\_A1\_SePV-1\_HO-02-21

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

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

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

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

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

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

[20] #KF006989\_Parechovirus\_D1\_ferret\_parechovirus\_ferret/MpPeV1/NL

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

[22] #KC843627\_Potamipivirus\_A1\_eel\_picornavirus\_F15-05

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

[24] #KF306267\_Limnipivirus\_B1\_CarpPV\_F37/06

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

[26] #KP770140\_Ampivirus\_A1\_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]

[ 2] 0.513

[ 3] 0.553 0.595

[ 4] 0.548 0.603 0.050

[ 5] 0.533 0.579 0.518 0.514

[ 6] 0.536 0.596 0.463 0.464 0.499

[ 7] 0.531 0.592 0.456 0.457 0.501 0.020

[ 8] 0.606 0.585 0.680 0.670 0.647 0.633 0.633

[ 9] 0.629 0.600 0.671 0.666 0.631 0.651 0.651 0.163

[10] 0.678 0.699 0.716 0.715 0.679 0.698 0.696 0.682 0.693

[11] 0.693 0.690 0.731 0.728 0.682 0.709 0.707 0.680 0.693 0.433

[12] 0.691 0.708 0.707 0.711 0.697 0.717 0.717 0.676 0.683 0.532 0.536

[13] 0.707 0.696 0.734 0.729 0.708 0.715 0.713 0.728 0.721 0.639 0.656 0.641

[14] 0.665 0.685 0.701 0.706 0.667 0.696 0.698 0.713 0.706 0.726 0.730 0.708 0.740

[15] 0.644 0.650 0.711 0.711 0.659 0.691 0.689 0.687 0.687 0.706 0.710 0.704 0.743 0.639

[16] 0.628 0.635 0.706 0.701 0.661 0.687 0.687 0.668 0.659 0.701 0.725 0.689 0.743 0.623 0.513

[17] 0.652 0.642 0.704 0.697 0.670 0.715 0.715 0.667 0.674 0.713 0.715 0.687 0.709 0.702 0.619 0.619

[18] 0.629 0.614 0.685 0.680 0.648 0.680 0.682 0.641 0.634 0.703 0.696 0.694 0.665 0.663 0.577 0.572 0.501

[19] 0.642 0.612 0.692 0.689 0.661 0.680 0.682 0.646 0.643 0.690 0.692 0.683 0.676 0.663 0.573 0.570 0.520 0.326

[20] 0.646 0.638 0.680 0.679 0.645 0.675 0.675 0.664 0.658 0.687 0.691 0.667 0.688 0.651 0.622 0.605 0.583 0.549 0.552

[21] 0.676 0.670 0.712 0.700 0.686 0.700 0.698 0.668 0.670 0.712 0.715 0.707 0.743 0.682 0.642 0.621 0.663 0.666 0.668 0.634

[22] 0.641 0.626 0.702 0.699 0.676 0.697 0.699 0.633 0.633 0.711 0.703 0.685 0.702 0.680 0.601 0.601 0.640 0.571 0.553 0.593 0.636

[23] 0.652 0.652 0.703 0.695 0.675 0.698 0.689 0.666 0.670 0.739 0.750 0.727 0.742 0.715 0.644 0.655 0.615 0.630 0.620 0.644 0.662 0.616

[24] 0.657 0.670 0.716 0.714 0.687 0.707 0.707 0.676 0.681 0.730 0.741 0.714 0.744 0.700 0.640 0.660 0.622 0.612 0.612 0.637 0.659 0.595 0.509

[25] 0.663 0.659 0.714 0.707 0.687 0.692 0.687 0.659 0.656 0.726 0.759 0.716 0.748 0.714 0.662 0.632 0.656 0.582 0.595 0.641 0.663 0.607 0.512 0.422

[26] 0.777 0.782 0.782 0.782 0.790 0.787 0.785 0.798 0.803 0.826 0.818 0.788 0.801 0.797 0.774 0.793 0.809 0.780 0.776 0.794 0.796 0.774 0.799 0.787 0.768

The number of amino acid differences per site from between sequences are shown. 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 582 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

1. Tamura K., Peterson D., Peterson N., Stecher G., Nei M., and Kumar S. (2011). MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Molecular Biology and Evolution 28: 2731-2739.

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

**Table 2. Estimates of Evolutionary Divergence 0f P1 Polyprotein between Sequences**

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

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

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

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

[ 5] #KF979333\_Avisivirus\_B1\_chicken\_picornavirus\_2\_44C

[ 6] #KF979334\_Avisivirus\_C1\_chicken\_picornavirus\_3\_45C

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

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

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

[10] #KC935379\_Kunsagivirus\_1\_roller/SZAL6-KuV/2011/HUN

[11] #KX644936\_Bat\_kunsagivirus\_BAT/CAM/KuV-P2/2013

[12] #KY670597\_Bakunsa\_virus\_baboon/M27-KuV/1986/TAN

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

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

[15] #AB937989\_Crohivirus\_shrew/ZM54/Zambia/2012

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

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

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

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

[20] #KF006989\_Parechovirus\_D1\_ferret\_parechovirus\_isolate\_MpPeV1

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

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

[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\_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] 0.621

[ 3] 0.691 0.667

[ 4] 0.700 0.671 0.107

[ 5] 0.663 0.653 0.585 0.579

[ 6] 0.668 0.648 0.555 0.558 0.556

[ 7] 0.669 0.644 0.564 0.562 0.569 0.125

[ 8] 0.697 0.703 0.713 0.714 0.711 0.717 0.717

[ 9] 0.691 0.697 0.703 0.705 0.718 0.720 0.720 0.100

[10] 0.828 0.789 0.785 0.788 0.806 0.800 0.797 0.816 0.812

[11] 0.792 0.756 0.798 0.791 0.806 0.790 0.781 0.788 0.791 0.497

[12] 0.797 0.764 0.789 0.787 0.790 0.777 0.777 0.808 0.808 0.496 0.516

[13] 0.816 0.795 0.798 0.807 0.792 0.786 0.790 0.801 0.809 0.761 0.753 0.740

[14] 0.782 0.772 0.753 0.748 0.770 0.776 0.777 0.795 0.790 0.803 0.775 0.803 0.802

[15] 0.775 0.742 0.752 0.753 0.760 0.762 0.753 0.787 0.785 0.795 0.795 0.784 0.790 0.697

[16] 0.767 0.759 0.764 0.770 0.763 0.785 0.773 0.786 0.786 0.820 0.778 0.797 0.791 0.679 0.626

[17] 0.740 0.705 0.735 0.733 0.733 0.746 0.749 0.778 0.777 0.802 0.775 0.774 0.766 0.698 0.708 0.670

[18] 0.736 0.722 0.763 0.764 0.760 0.740 0.745 0.780 0.776 0.793 0.783 0.795 0.809 0.699 0.691 0.641 0.515

[19] 0.731 0.728 0.757 0.757 0.760 0.742 0.740 0.782 0.783 0.795 0.770 0.773 0.794 0.699 0.709 0.672 0.536 0.432

[20] 0.740 0.742 0.759 0.752 0.769 0.754 0.733 0.767 0.767 0.786 0.772 0.784 0.795 0.736 0.730 0.681 0.615 0.608 0.632

[21] 0.781 0.785 0.785 0.780 0.784 0.773 0.774 0.793 0.792 0.816 0.800 0.771 0.826 0.770 0.763 0.757 0.770 0.732 0.748 0.751

[22] 0.791 0.788 0.780 0.775 0.772 0.783 0.791 0.801 0.797 0.796 0.786 0.776 0.802 0.757 0.747 0.765 0.748 0.746 0.755 0.753 0.307

[23] 0.754 0.764 0.789 0.785 0.786 0.766 0.767 0.805 0.798 0.806 0.793 0.801 0.775 0.773 0.766 0.762 0.765 0.743 0.765 0.756 0.793 0.794

[24] 0.815 0.809 0.841 0.836 0.835 0.840 0.838 0.820 0.827 0.843 0.831 0.831 0.868 0.832 0.804 0.815 0.808 0.825 0.829 0.831 0.846 0.830 0.817

[25] 0.797 0.803 0.820 0.820 0.827 0.833 0.827 0.818 0.819 0.843 0.825 0.825 0.844 0.825 0.786 0.799 0.818 0.825 0.811 0.819 0.854 0.842 0.798 0.410

[26] 0.812 0.814 0.844 0.841 0.837 0.822 0.826 0.820 0.827 0.844 0.823 0.826 0.847 0.830 0.797 0.818 0.810 0.815 0.816 0.824 0.852 0.839 0.810 0.430 0.298

[27] 0.909 0.916 0.911 0.919 0.904 0.912 0.915 0.923 0.920 0.912 0.934 0.924 0.910 0.925 0.911 0.923 0.918 0.919 0.921 0.916 0.910 0.909 0.918 0.921 0.915 0.926

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 1168 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

1. Tamura K., Peterson D., Peterson N., Stecher G., Nei M., and Kumar S. (2011). MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Molecular Biology and Evolution 28: 2731-2739.

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