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:** | ***2017.008S*** | (to be completed by ICTV officers) |
| **Short title:** Create 1 new species (*Orivirus A*) in a new genus (*Orivirus*)(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:** 2017.008S.N.v1.Orivirus |

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:** |
| Boros A, Pankovics P, Adonyi A, Phan TG, Delwart E, Reuter G. 2014. Genome characterization of a novel chicken picornavirus distantly related to the members of genus *Avihepatovirus* with a single 2A protein and a megrivirus-like 3' UTR. Inf. Genet. Evol. 28:333-338.Boros A, Pankovics P, Adonyi A, Fenyvesi H, Day JM, Phan TG, Delwart E, Reuter G. 2015. A diarrheic chicken simultaneously co-infected with multiple picornaviruses: Complete genome analysis of avian picornaviruses representing up to six genera. Virology 489:63-74. |

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

Two novel picornaviruses, orivirus 1 and 2, were detected in cloacal samples of diseased chickens in Hungary. Virus isolates are not available, but the genome sequences suggest that these viruses belong to the *Picornaviridae*. 3-3-4 genome layout (compare Figure 1D):

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

Orivirus proteins P1, 2C and 3CD show only low amino acid similarities with the orthologous proteins of other picornaviruses (Boros et al., 2014). Alignments reveal amino acid identities ranging from:

P1: 11.3-28.7%,

2CHel: 19.1-40.1%,

3DPol: 19.6-40.8% (Data from Boros et al., 2014).

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

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

(ii) a long 5'-NTR with type II IRES

(iiI) 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 (**G**1057SAGA**GKS**, Walker A motif, and a D1105DFGQ motif)

 putative 3C proteinase catalytic triad (H1378, D1431, G1482DCG)

 RNA-dependent RNA polymerase motifs (K1667DELR, G1795MCSG, Y1831GDD, Q1916LKS)

Phylogenetic trees of the P1 and 3CD proteins comprising reference sequences of the *Aquamavirus/Avihepatovirus/ Avisivirus/Kunsagivirus/Pasivirus/Parechovirus* supergroup indicate that the oriviruses are placed in a distinct branch (compare Figs. 2 and 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)]. Closest relatives are avihepatoviruses, avisiviruses, kunsagiviruses and duck aalivirus. These viruses, however, have different genome layouts.

1. Phylogenetic analyses of the P1 and 3CD proteins reveal that oriviruses are divergent picornaviruses related to avihepatoviruses, avisiviruses, kunsagiviruses and the duck aalivirus (Figures 2 and 3):

 - the conserved picornavirus proteins P1, 3C and 3D proteins share aa identities up to 41%;

 - the sequence similarity of the remaining proteins is lower;

 - proteins 2A, 2B, 3A lack recognizable homology to the respective proteins of the members of the *Aquamavirus/Avihepatovirus/Avisivirus/Kunsagivirus/Pasivirus/Parechovirus* supergroup;

 - the genomes of the oriviruses share less homology with the other picornaviruses.

2. Figure 1 compares the genomes of oriviruses with those of the kunsagiviruses, avisiviruses, avihepatoviruses and duck aalivirus. Distinctive features of oriviruses are

 - the short length of the deduced polyprotein (only 1974 aa),

 - a unique 2A protein which has no homology to other picornaviruses.

As shown in Tables 1 and 2, oriviruses show a an amino acid divergence of the 3CD protein of c. 62% compared to *Avihepatovirus A* and greater diversity (64-83%) to the other picornaviruses; the P1 region shows a divergence greater 68% to all picornaviruses. There are two known types of oriviruses sharing 90% amino acid identity of their P1 region.

**Origin of name:**

Orivirus: from **Or**osháza (town in Hungary where the cloacal sample was taken)



**Figure 1:** Genome organization of duck hepatitis A virus (A), roller kunsagivirus (B), chicken avisivirus (C) and chicken orivirus (D). The open reading frames are indicated by boxes. Positions of putative aa cleavage sites and the lengths of the deduced proteins of orivirus are shown as proposed by Boros et al. (2014). Arrows (↓) indicate the putative processing sites. Non-structural proteins necessary for virus replication are shaded.



**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 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 Proteins between Sequences**

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

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

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

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

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

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

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

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

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

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

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

[12] #KY670597\_Kunsagivirus\_C1\_bakunsavirus\_strain\_baboon/M27-KuV/1986/TAN\_P3

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

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

[15] #AB937989\_Crohivirus\_1\_strain\_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\_strain\_An\_B\_1227\_d

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

[21] #KJ641698\_bat\_picornavirus\_isolate\_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

[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] -

[ 2] 0.158 -

[ 3] 0.648 0.642 -

[ 4] 0.618 0.623 0.535 -

[ 5] 0.686 0.703 0.571 0.619 -

[ 6] 0.679 0.695 0.567 0.628 0.041 -

[ 7] 0.665 0.680 0.557 0.599 0.492 0.491 -

[ 8] 0.683 0.672 0.554 0.612 0.461 0.460 0.494 -

[ 9] 0.681 0.670 0.552 0.611 0.456 0.455 0.496 0.014 -

[10] 0.746 0.743 0.717 0.742 0.750 0.749 0.718 0.735 0.734 -

[11] 0.741 0.740 0.729 0.732 0.756 0.752 0.724 0.743 0.742 0.518 -

[12] 0.740 0.738 0.728 0.736 0.738 0.742 0.735 0.744 0.744 0.583 0.583 -

[13] 0.765 0.768 0.737 0.729 0.752 0.749 0.720 0.739 0.737 0.691 0.698 0.673 -

[14] 0.733 0.743 0.695 0.717 0.716 0.717 0.695 0.714 0.717 0.767 0.758 0.742 0.751 -

[15] 0.722 0.727 0.674 0.693 0.722 0.721 0.676 0.710 0.708 0.750 0.746 0.737 0.743 0.648 -

[16] 0.698 0.705 0.661 0.680 0.737 0.734 0.695 0.721 0.721 0.740 0.765 0.731 0.748 0.661 0.542 -

[17] 0.713 0.709 0.684 0.676 0.721 0.715 0.704 0.727 0.727 0.753 0.757 0.731 0.723 0.711 0.626 0.621 -

[18] 0.678 0.682 0.664 0.661 0.704 0.700 0.673 0.705 0.707 0.749 0.736 0.730 0.699 0.691 0.591 0.578 0.510 -

[19] 0.683 0.683 0.664 0.658 0.703 0.700 0.685 0.704 0.705 0.734 0.740 0.711 0.708 0.684 0.600 0.581 0.539 0.340 -

[20] 0.704 0.709 0.679 0.681 0.710 0.707 0.686 0.704 0.704 0.741 0.738 0.706 0.711 0.671 0.638 0.593 0.591 0.571 0.574 -

[21] 0.695 0.700 0.693 0.684 0.727 0.717 0.712 0.712 0.710 0.748 0.754 0.749 0.760 0.717 0.681 0.668 0.688 0.695 0.702 0.687 -

[22] 0.698 0.701 0.696 0.685 0.745 0.743 0.717 0.732 0.733 0.746 0.741 0.736 0.752 0.719 0.671 0.672 0.703 0.658 0.649 0.668 0.680 -

[23] 0.722 0.719 0.712 0.710 0.749 0.744 0.721 0.747 0.740 0.767 0.787 0.769 0.776 0.763 0.711 0.718 0.685 0.695 0.695 0.710 0.706 0.670 -

[24] 0.730 0.730 0.719 0.729 0.759 0.758 0.732 0.761 0.761 0.771 0.776 0.760 0.784 0.739 0.697 0.724 0.697 0.685 0.687 0.699 0.728 0.663 0.561 -

[25] 0.710 0.708 0.716 0.717 0.760 0.755 0.737 0.744 0.741 0.767 0.790 0.760 0.776 0.750 0.725 0.703 0.707 0.663 0.673 0.710 0.724 0.670 0.569 0.490 -

[26] 0.830 0.832 0.812 0.807 0.814 0.812 0.823 0.812 0.810 0.848 0.841 0.824 0.829 0.830 0.815 0.827 0.818 0.812 0.804 0.827 0.812 0.819 0.826 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 841 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

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

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

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

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

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

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

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

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

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

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

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

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

[12] #KY670597\_Kunsagivirus\_C1\_bakunsavirus\_baboon/M27-KuV/1986/TAN

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

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

[15] #AB937989\_Crohivirus\_strain\_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\_Eel\_picornavirus\_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] 0.100 -

[ 3] 0.694 0.686 -

[ 4] 0.700 0.693 0.618 -

[ 5] 0.706 0.698 0.691 0.665 -

[ 6] 0.710 0.700 0.700 0.668 0.107 -

[ 7] 0.703 0.707 0.667 0.651 0.585 0.579 -

[ 8] 0.710 0.712 0.668 0.642 0.555 0.558 0.555 -

[ 9] 0.708 0.711 0.669 0.638 0.564 0.562 0.568 0.125 -

[10] 0.821 0.816 0.833 0.792 0.794 0.798 0.799 0.796 0.795 -

[11] 0.797 0.798 0.795 0.776 0.800 0.794 0.787 0.790 0.786 0.499 -

[12] 0.809 0.807 0.796 0.781 0.794 0.793 0.776 0.778 0.781 0.496 0.516 -

[13] 0.802 0.805 0.828 0.813 0.805 0.813 0.794 0.796 0.799 0.751 0.755 0.745 -

[14] 0.791 0.785 0.766 0.765 0.749 0.743 0.766 0.767 0.768 0.803 0.768 0.794 0.807 -

[15] 0.793 0.790 0.770 0.750 0.753 0.756 0.752 0.751 0.740 0.779 0.783 0.756 0.781 0.678 -

[16] 0.772 0.770 0.743 0.753 0.747 0.751 0.746 0.763 0.753 0.809 0.770 0.790 0.790 0.656 0.620 -

[17] 0.762 0.762 0.734 0.697 0.730 0.731 0.722 0.736 0.742 0.789 0.769 0.767 0.762 0.673 0.677 0.626 -

[18] 0.772 0.770 0.720 0.711 0.757 0.757 0.744 0.738 0.743 0.790 0.771 0.783 0.801 0.684 0.661 0.597 0.512 -

[19] 0.769 0.770 0.718 0.726 0.751 0.753 0.752 0.735 0.732 0.789 0.764 0.756 0.793 0.679 0.672 0.621 0.539 0.444 -

[20] 0.767 0.764 0.743 0.738 0.755 0.753 0.755 0.750 0.736 0.776 0.770 0.770 0.798 0.729 0.696 0.643 0.601 0.599 0.624 -

[21] 0.800 0.798 0.790 0.797 0.796 0.794 0.793 0.781 0.780 0.808 0.813 0.783 0.832 0.758 0.750 0.731 0.753 0.727 0.737 0.732 -

[22] 0.809 0.802 0.793 0.797 0.783 0.781 0.776 0.784 0.789 0.798 0.798 0.788 0.810 0.745 0.737 0.744 0.738 0.743 0.743 0.733 0.307 -

[23] 0.807 0.802 0.762 0.767 0.801 0.797 0.786 0.775 0.775 0.810 0.798 0.797 0.789 0.762 0.758 0.759 0.748 0.726 0.750 0.734 0.792 0.794 -

[24] 0.824 0.831 0.824 0.826 0.848 0.848 0.833 0.837 0.835 0.854 0.858 0.838 0.861 0.835 0.814 0.823 0.793 0.821 0.825 0.826 0.847 0.840 0.814 -

[25] 0.823 0.824 0.799 0.811 0.815 0.819 0.804 0.815 0.813 0.848 0.844 0.826 0.849 0.817 0.796 0.803 0.800 0.825 0.809 0.806 0.844 0.832 0.792 0.412 -

[26] 0.814 0.819 0.805 0.824 0.839 0.839 0.820 0.818 0.821 0.855 0.851 0.848 0.854 0.827 0.804 0.816 0.796 0.809 0.814 0.808 0.851 0.835 0.808 0.435 0.295 -

[27] 0.917 0.915 0.908 0.905 0.912 0.914 0.909 0.914 0.917 0.910 0.898 0.910 0.911 0.913 0.897 0.908 0.900 0.904 0.898 0.902 0.920 0.908 0.913 0.895 0.884 0.885 -

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 27 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. Evolutionary analyses were conducted in MEGA5 [1].

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

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