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:** | ***2017.007S*** | | | | (to be completed by ICTV officers) |
| **Short title:** Rename *Melegrivirus A* as *Megrivirus A* and create 4 new species (*Megrivirus B, C, D, E*) in the genus *Megrivirus*  (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: | | | | 07 June 2017 | |
| Date of this revision (if different to above): | | | | 20 November 2017 | |

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

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

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.007S.N.v1.Megrivirus\_4sp |

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:** |
| **Turkey hepatitis virus:**  Honkavuori KS, Shivaprasad HL, Briese T, Street C, Hirschberg DL, Hutchinson SK, Lipkin WI. 2011. Novel picornavirus in turkey poults with hepatitis, California, USA. Emerg Inf Dis 17(3):480-487.  **Mesivirus:**  Phan TG, Vo NP, Boros A, Pankovics P, Reuter G, Li OTW, Wang C, Deng X, Poon LLM, Delwart E. 2013. The viruses of wild pigeon droppings. PLOS One 8(9):e72787.  **Chicken megrivirus:**  Boros A, Pankovics P, Knowles NJ, Nemes C, Delwart E, Reuter G. 2014. Comparative complete genome analysis of chicken and turkey megriviruses (family *Picornaviridae*): Long 3' untranslated regions with a potential second open reading frame and evidence of possible recombination. J Virology 88(11):6434-6443.  **Duck megrivirus:**  Liao Q, Zheng L, Yuan Y, Shi J, Zhang D. 2014. Genomic characterization of a novel picornavirus in Pekin ducks. Vet Microbiol 172:78-91.  **Harrier megrivirus:**  Boros Á, Pankovics P, Mátics R, Adonyi Á, Bolba N, Phan TG, Delwart E, Reuter G. 2017. Genome characterization of a novel megrivirus-related avian picornavirus from a carnivorous wild bird, western marsh harrier (*Circus aeruginosus*). Arch Virol. 2017 May 12. doi: 10.1007/s00705-017-3403-4. [Epub ahead of print]  **Goose megriviruses:**  Wang F, Liang T, Liu N, Ning K, Yu K, Zhang D. 2017. Genetic characterization of two novel megriviruses in geese. J Gen Virol. 2017 Apr; 98(4):607-611. doi: 10.1099/jgv.0.000720. Epub 2017 Apr 27.  **Penguin Megrivirus:**  Zell R, et al. 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. |

**Rename *Melegrivirus A* as *Megrivirus A* and create 4 new species (*Megrivirus B, C, D* & *E*) in the genus *Megrivirus***

The *Melegrivirus A* species of the genus *Megrivirus* was created on the basis of two sequences of the turkey hepatitis virus (HM751199, HQ189775) representing a single type. Now, 15 nearly complete genomes of megriviruses are available. The megriviruses have been detected in faecal/tissue samples of turkeys (*Meleagris gallopavo*), chickens (*Gallus gallus*), Pekin ducks (*Anas platyrhynchos f. domestica*), geese (*Anser spec.*), pigeons (*Columba livia*), harriers (*Circus aeruginosus*) and penguins (*Pygoscelis papua*).

All megriviruses show a similar genome layout (compare Fig. 1):

- Genome lengths range from 8541-10101 nt; the polyproteins are rather long (2485-2972 amino acids).

- There are three capsid proteins as VP0 (1AB) remains uncleaved, three to six P2 proteins and four P3 proteins. VP0 consists of c. 380-450 amino acids which is long whereas the VP3 protein has a length of only 166-181 aa.

- There are one to four 2A proteins, the last of which has a H-box/NC motif. Beside 2AH-box/NC six genetically distinct, unique 2A proteins have been identified so far.

- Other unusually long proteins are 2B (190-192 amino acids) and 3A (150-182 amino acids).

- The penguin megrivirus (MF405436) has a N-terminal extension of VP0 consistent with the assumption of a leader protein of 131 amino acids.

- The megrivirus 5'-NTR has a type IV IRES with exception of harrier megrivirus which has a type II IRES.

- The lengths of the 3'-NTR are inconsistent and ranges from 174 nt to 678 nt.

Phylogenetic trees of P1-encoding and 3CD-encoding gene regions (compare Figs. 2 and 3) reveal that all known viruses of the *Melegrivirus A1* type (HM751199, HQ189775, KF961188, KF979335) and one of the two known goose megriviruses (KY369300) are likely the result of *inter*species recombination. Inconsistent clustering of picornavirus sequences in phylogenetic trees of capsid proteins and the polymerase protein is a well-known phenomenon in picornavirology and commonly interpreted as a result of RNA recombination after infection of the host cell with two or more viruses. However, RNA recombination usually affects the types of a given picornavirus species only (*intra*species recombination). *Inter*species recombination is not normally observed in picornaviruses (except for the 5ʹ UTR region in enteroviruses). This finding necessitates a revision of the present megrivirus taxonomy.

The *Megrivirus* genus of the proposed taxonomy comprises five species (*Megrivirus A* to *E*) consistent with the five branches of the megrivirus clade in the 3CD tree (Figure 2). The 2C helicase, 3C proteinase and 3D polymerase are the most conserved picornavirus proteins and are well-suited to define a picornavirus species.

Amino acid identities of 15 megrivirus sequences: 2CHel >50%; 3CPro >33%; 3DPol >50%

In order to avoid confusion, the species *Melegrivirus A* will be renamed (proposed *Megrivirus A*) with duck megrivirus LY (KC663628) as the prototype strain. The turkey hepatitis virus will be moved to the species *Megrivirus C* which is consistent with the clustering of 2C helicase, 3C proteinase and the 3D polymerase. Interspecies recombinants should receive type designations indicating the putative donor and acceptor viruses; presently known interspecies recombinants are the turkey hepatitis viruses (strains 2993D, 00911 and B407-THV), chicken picornavirus 4 (strain 5C) and the goose megrivirus 2 (strain HN56). Their type designations should be

- A1CP-CPol for those viruses with type A1 capsid proteins and P2/P3 regions of MeV-C and

- B3CP-APol for the goose megrivirus 2 with type B3 capsid proteins and P2/P3 region of MeV-A (compare Figs. 2 and 3).

The five species of genus *Megrivirus* are distinguished by virtue of their

- sequence divergence (compare Tables 1 and 2),

- features of the 2A genome region (Fig. 1),

- presence/absence of a putative leader protein (Fig. 1),

- IRES type (Fig. 1), and

- length of 3'-NTR (Fig. 1).

**Creation of five megrivirus species requires definition of species demarcation criteria:**

- The presently known megriviruses share birds as hosts.

- The following proteins of the known megriviruses are orthologous:

• capsid proteins (VP0, VP3, VP1);

• 2AH-box/NC protein;

• 2B protein;

• 2CHel, protein;

• 3A protein;

• 3BVPg;

• 3CPro protein;

• 3DPol protein.

- Megriviruses have the longest known picornavirus genomes. The lengths of the known polyproteins vary from 2485 to 2972 aa.

- There are 1-4 2A polypeptides, the last of which with H-box/NC motif.

- The overall aa identities of the P1/2B-2C/P3 polyproteins are >45/>35/>40% (compare Table 1: divergence <55/<65/<60%). However, aa identities of the processed protein range from 28% (2A2) to 80% (3B). The overall nt identities of the P1/P2/P3 genome regions are >50/>45/>45% (compare Table 1: divergence <50/<55/<55%).

Species demarcation criteria in the new genus:

Members of a species of the genus Megrivirus:

- share greater than >55% nt identity (>50% aa identity) in the P1,

- share greater than >50% nt identity (>40% aa identity) in the 2B-2C,

- share greater than >50% nt identity (>45% aa identity) in the P3,

- share greater than >85% nt identity (>95% aa identity) in the 3CD,

- share a common genome organization including essentially the same combination of 2A proteins.



**Figure 1 (previous page):** Comparison of variants of the megrivirus genome organisation (schematic depiction). Panels A, B, D, F, G indicate the genomes of the proposed species *Megrivirus A* to *E*. The open reading frames are indicated by boxes. Positions of putative aa cleavage sites and the lengths of the deduced proteins are shown. Triangles indicate the putative processing sites. The various 2A polypeptides are indicated by different colors. With exception of 2AH-box/NC, the 2A polypeptides are unique. Presumably, turkey hepatitis virus (panel C) is an interspecies recombinant composed of capsid proteins of a megrivirus A1 donor and the polymerase of a *Megrivirus C* acceptor (A1CP-CPol). Likewise, goose megrivirus 2 (panel E) is an interspecies recombinant comprising capsid proteins of a yet unidentified *Megrivirus B* strain and the polymerase protein of *Megrivirus A* (B3CP-APol). The accession number of the penguin megrivirus is MF405436.



**Figure 2:** Phylogenetic analyses of picornavirus **3CD** using Bayesian tree inference (MrBayes 3.2). Forty-seven picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Oscivirus/Passerivirus/Sakobuvirus/ Salivirus/Sicinivirus/Rosavirus* 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 4,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site. The accession number of the penguin megrivirus is MF405436.



**Figure 3:** Phylogenetic analyses of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Forty-seven picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Oscivirus/Passerivirus/Sakobuvirus/ Salivirus/Sicinivirus/Rosavirus* 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. The accession number of the penguin megrivirus is MF405436.

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

[ 1] #KC663628\_MeV-A2\_duck\_megrivirus\_LY

[ 2] #KY369299\_MeV-A3\_goose\_megrivirus\_W18

[ 3] #KY369300\_MeV-B3CP-APol\_Goose\_megrivirus\_HN56

[ 4] #KC876003\_MeV-B1\_mesivirus\_1\_HK21

[ 5] #KC811837\_MeV-B2\_pigeon\_mesivirus\_2\_pigeon/GALII5-PiMeV/2011/HUN

[ 6] #HM751199\_MeV\_A1CP-CPol\_hurkey\_hepatitis\_virus\_2993D

[ 7] #KF961188\_MeV-A1CP-CPol\_turkey\_megrivirus\_strain\_turkey/B407-THV/2011/HUN

[ 8] #HQ189775\_MeV-A1CP-CPol\_turkey\_hepatitis\_virus\_0091.1

[ 9] #KF979335\_MeV-A1CP-CPol\_chicken\_picornavirus\_4\_isolate\_5C

[10] #KF961186\_MeV-C1\_chicken\_megrivirus\_chicken/B21-CHV/2012/HUN

[11] #KF961187\_MeV-C1\_chicken\_megrivirus\_chicken/CHK-IV-CHV/2013/HUN

[12] #KJ690629\_MeV-C1\_chicken\_proventriculitis\_virus\_CPV/Korea/03

[13] #KF979336\_MeV-C2\_chicken\_picornavirus\_5\_27C

[14] #MF405436\_MeV-E1\_penguin\_megrivirus\_penguin/KGI-BLH-P5

[15] #KY488458\_MeV-D1\_Harrier\_picornavirus\_1\_harrier/MR-01/HUN/2014

[16] #KU977108\_Poecivirus\_BCCH-449

[17] #GU182408\_Oscivirus\_A1\_robin/Hong\_Kong/10717/2006

[18] #GU182410\_Oscivirus\_A2\_robin/Hong\_Kong/10878/2006

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 ]

[ 1]

[ 2] 0.025

[ 3] 0.022 0.010

[ 4] 0.372 0.369 0.368

[ 5] 0.378 0.375 0.373 0.016

[ 6] 0.401 0.403 0.404 0.438 0.436

[ 7] 0.405 0.407 0.409 0.436 0.434 0.019

[ 8] 0.402 0.404 0.406 0.436 0.434 0.007 0.018

[ 9] 0.407 0.406 0.410 0.439 0.437 0.016 0.030 0.018

[10] 0.408 0.404 0.409 0.444 0.442 0.025 0.034 0.024 0.015

[11] 0.405 0.401 0.406 0.438 0.436 0.024 0.030 0.022 0.013 0.007

[12] 0.406 0.402 0.406 0.440 0.438 0.027 0.036 0.025 0.016 0.007 0.006

[13] 0.405 0.406 0.407 0.438 0.436 0.021 0.031 0.019 0.010 0.015 0.015 0.013

[14] 0.315 0.318 0.315 0.349 0.350 0.413 0.417 0.410 0.414 0.413 0.408 0.409 0.408

[15] 0.496 0.490 0.495 0.518 0.524 0.526 0.528 0.526 0.525 0.523 0.525 0.526 0.526 0.484

[16] 0.554 0.558 0.557 0.563 0.565 0.577 0.575 0.577 0.577 0.575 0.575 0.576 0.574 0.573 0.529

[17] 0.633 0.629 0.629 0.624 0.625 0.625 0.628 0.625 0.625 0.623 0.625 0.624 0.623 0.610 0.624 0.647

[18] 0.628 0.626 0.628 0.627 0.629 0.625 0.626 0.625 0.625 0.621 0.623 0.622 0.621 0.621 0.624 0.667 0.203

The number of amino acid differences per site from between sequences are shown.

\_\_\_ 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] #KC663628\_MeV-A2\_duck\_megrivirus\_strain\_LY

[ 2] #KF961188\_MeV-A1-C\_turkey\_megrivirus\_strain\_turkey/B407-THV/2011/HUN

[ 3] #HQ189775\_MeV-A1-C\_turkey\_hepatitis\_virus\_0091.1

[ 4] #KF979335\_MeV-A1-C\_chicken\_picornavirus\_4\_isolate\_5C

[ 5] #HM751199\_MeV-A1-C\_THV\_2993D

[ 6] #KY369299\_MeV-A3\_goose\_megrivirus\_isolate\_W18

[ 7] #KC876003\_MeV-B1\_mesivirus\_1\_HK21

[ 8] #KC811837\_MeV-B2\_mesivirus\_2\_strain\_pigeon/GALII5-PiMeV/2011/HUN

[ 9] #KY369300\_MeV-B3-A\_goose\_megrivirus\_isolate\_HN56

[10] #KF961186\_MeV-C1\_chicken\_megrivirus\_strain\_chicken/B21-CHV/2012/HUN

[11] #KF961187\_MeV-C1\_chicken\_megrivirus\_strain\_chicken/CHK-IV-CHV/2013/HUN

[12] #KJ690629\_MeV-C1\_chicken\_proventriculitis\_virus\_isolate\_CPV/Korea/03

[13] #KF979336\_MeV-C2\_chicken\_picornavirus\_5\_isolate\_27C

[14] #MF405436\_MeV-D1\_PenguinMegriV\_penguin/KGI-BHS-P5

[15] #KY488458\_MeV-E1\_harrier\_picornavirus\_1\_harrier/MR-01/HUN/2014

[16] #KU977108\_Poecivirus\_BCCH-449

[17] #GU182408\_Oscivirus\_A1\_turdivirus\_2\_strain\_10717

[18] #GU182410\_Oscivirus\_A2\_turdivirus\_3\_strain\_10878

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 ]

[ 1]

[ 2] 0.313

[ 3] 0.325 0.075

[ 4] 0.326 0.094 0.108

[ 5] 0.319 0.065 0.074 0.102

[ 6] 0.301 0.349 0.346 0.354 0.345

[ 7] 0.574 0.553 0.555 0.565 0.561 0.571

[ 8] 0.589 0.580 0.577 0.585 0.586 0.583 0.257

[ 9] 0.526 0.527 0.515 0.526 0.524 0.528 0.481 0.500

[10] 0.660 0.628 0.624 0.617 0.628 0.656 0.648 0.644 0.625

[11] 0.653 0.624 0.617 0.610 0.620 0.648 0.643 0.638 0.620 0.084

[12] 0.642 0.620 0.616 0.608 0.617 0.644 0.637 0.638 0.614 0.089 0.034

[13] 0.659 0.633 0.630 0.625 0.631 0.659 0.636 0.640 0.603 0.262 0.257 0.260

[14] 0.625 0.616 0.625 0.620 0.622 0.644 0.634 0.636 0.626 0.529 0.533 0.526 0.510

[15] 0.621 0.618 0.616 0.625 0.623 0.642 0.614 0.637 0.594 0.656 0.665 0.660 0.647 0.645

[16] 0.747 0.735 0.727 0.725 0.727 0.733 0.740 0.728 0.728 0.754 0.741 0.742 0.740 0.735 0.734

[17] 0.820 0.818 0.813 0.824 0.809 0.804 0.822 0.819 0.817 0.835 0.830 0.829 0.827 0.829 0.818 0.840

[18] 0.836 0.830 0.827 0.835 0.821 0.821 0.822 0.812 0.831 0.829 0.829 0.832 0.837 0.845 0.838 0.849 0.312

The number of amino acid differences per site from between sequences are shown.

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

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