The International Committee on Taxonomy of Viruses
Taxonomy Proposal Form, 2024

Part 1a: Details of taxonomy proposals

Title:	Create a new family, *Andersonviridae* for the FelixO1-like phages (Class: *Caudoviricetes*)
Code assigned:	2024.002B

Author(s), affiliation and email address(es):

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Part 1b: Taxonomy Proposal Submission

ICTV Subcommittee:		
Animal DNA Viruses and Retroviruses	Bacterial viruses	**X**
Animal minus-strand and dsRNA viruses	Fungal and protist viruses	
Animal positive-strand RNA viruses	Plant viruses	
Archaeal viruses	General -	

List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:
Caudoviricetes Study Group

Optional – complete only if formally voted on by an ICTV Study Group:			
Study Group	**Number of members**		
	Votes in support	**Votes against**	**No vote**

Submission date:	01/06/2024

Part 1c: Feedback from ICTV Executive Committee (EC) meeting

Executive Committee Meeting Decision code:	X
A – Accept	
Ac – Accept subject to revision by relevant subcommittee chair. No further vote required	**X**
U – Accept without revision but with re-evaluation and email vote by the EC	
Uc – Accept subject to revision and re-evaluation and email vote by the EC	
Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments	
J - Reject	
W - Withdrawn	

Comments from the Executive Committee:
Corrections required to wording (figure labels) within the taxonomy proposal.

Part 1d: Revised Taxonomy Proposal Submission

Response of proposer:
The text has been corrected.

Revision date:	30/09/2024

Part 3: TAXONOMIC PROPOSAL

Name of accompanying Excel module:
2024.002B.A.v1.Andersonviridae_nf.xlsx

Taxonomic changes proposed:				
Establish new taxon	**x**	Split taxon	
Abolish taxon		Merge taxon	
Move taxon		Promote taxon	
Rename taxon		Demote taxon	
Move and rename			

Is any taxon name used here derived from that of a living person:		N
Taxon name	**Person from whom the name is derived**	**Attached** X

Abstract of Taxonomy Proposal:

Taxonomic rank(s) affected:
Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*

Description of current taxonomy:
At present the following taxa exist as floating genera in the order *Caudoviricetes*: *Felixounavirus, Kolesnikvirus, Suspvirus,* and *Mooglevirus*.

Proposed taxonomic change(s):
We propose the creation of one new family, *Andersonviridae*.
To update the genus *Felixounavirus* with 80 new species
To update the genus *Mooglevirus* with 11 new species
To add one new species to the genus *Kolesnikvirus*
To create a new genus *Daniellevirus* with two species
To create a new genus *Arnovirus* with three species

Justification:
We investigated the evolutionary relationships of 123 bacteriophages. Analysis of conserved genes revealed that these phages form a deeply branching monophyletic clade with a distance commensurate with the creation of a new family.

- **Text of Taxonomy proposal:**

Taxonomic rank(s) affected: Species, genus and family.

Description of current taxonomy:

At present the following taxa exist: The subfamily *Ounavirinae* and genera *Felixounavirus, Kolesnikvirus, Suspvirus,* and *Mooglevirus*.

Proposed taxonomic change(s):
- **A.   To update the genus *Felixounavirus* with 80 new species**
- **B.   To update the genus *Mooglevirus* with 11 new species**
- **C.   To add one new species to the genus *Kolesnikvirus***
- **D.   To create a new genus *Daniellevirus* with two species**
- **E.   To create a new genus *Arnovirus* with three species**
- **F.   To create a new family *Andersonviridae***

All our analyses reveal that the Felix-O1-like phages are part of a family which we have named *Andersonviridae* in honour of American biophysical chemist and geneticist Thomas Foxen Anderson. Unlike almost every TaxoProp submitted since the development of VIRIDIC there is not a clear distinction based upon overall DNA sequence similarity of members of the *Felixounavirus* and the *Mooglevirus*.

Demarcation criteria:

Species demarcation criteria: Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.

These values can be calculated by a number of tools, such as BLASTn [1,2] – usually calculated using intergenomic distance calculator VIRIDIC [3].

Genus demarcation criteria: In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [10]

Subfamily demarcation criteria: Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity (usually about 40-50%) and that the genera form a clade in a marker tree phylogeny. [10]

Family demarcation criteria: The family is represented by a cohesive and monophyletic group in the main predicted proteome-based clustering tools (VirClust, ViPTree, GRAViTy dendrogram, vConTACT2 network). Members of the family share a significant number of orthologous genes (the number will depend on the genome sizes and number of coding sequences of members of the family). [10]

Justification:

This assignment is in keeping with the criteria laid out in [10]

References:
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Tables, Figures:

Accession or RefSeq No/Phage name	Genus	MN270891.1_Pect_phg_Wc4	MN270892.1_Pect_phg_Wc4-1	MK290737.1_Pect_phg_Arno162	MK290738.1_Pect_phg_Arno18	OR125561.1_Erwi_phg_vB_EamM-BoyaciRG1	OR284297.1_Erwi_phg_Flfi106	OQ818707.1_Erwi_phg_Rouille	OM522317.2_Erwi_phg_Hena2	NC_041978.1_Erwi_phg_vB_EamM-M7	PP079182.1_Erwi_phg_vEam_PM_6	PP079183.1_Erwi_phg_vEam_W_25	PP079184.1_Erwi_phg_vEam_PM_27	PP079186.1_Erwi_phg_vEam_W_28	PP079185.1_Erwi_phg_vEam_PM_21	PP079187.1_Erwi_phg_vEam_S_24	MK770412.1_Salm_phg_SE5	PP278848.1_Erwi_phg_Omen	OR863359.1_Salm_phg_SeKF_13
MN270891.1_Pect_phg_Wc4		100.0	100.0	90.9	88.8	10.8	10.7	10.7	10.8	10.9	10.8	10.8	10.8	10.8	10.8	10.8	11.1	11.3	10.8
MN270892.1_Pect_phg_Wc4-1		100.0	100.0	90.9	88.8	10.8	10.7	10.7	10.8	10.9	10.8	10.8	10.8	10.8	10.8	10.8	11.1	11.3	10.8
MK290737.1_Pect_phg_Arno162		90.9	90.9	100.0	93.2	10.8	10.6	10.9	10.8	10.9	10.9	10.8	10.9	10.9	10.9	10.9	11.1	11.3	10.7
MK290738.1_Pect_phg_Arno18		88.8	88.8	93.2	100.0	10.6	10.7	10.6	10.7	10.7	10.8	10.8	10.8	10.8	10.8	10.8	11.0	10.6	10.3
OR125561.1_Erwi_phg_vB_EamM-BoyaciRG1	Kolesnikvirus	10.8	10.8	10.8	10.6	100.0	96.9	97.6	97.7	97.7	97.7	97.7	97.7	97.7	97.7	97.7	91.5	87.1	87.7
OR284297.1_Erwi_phg_Flfi106	Kolesnikvirus	10.7	10.7	10.6	10.7	96.9	100.0	98.2	98.2	98.2	98.2	98.2	98.2	98.2	98.2	98.2	90.4	87.5	86.3
OQ818707.1_Erwi_phg_Rouille	Kolesnikvirus	10.7	10.7	10.9	10.6	97.6	98.2	100.0	98.5	98.4	98.4	98.4	98.4	98.4	98.4	98.4	90.8	88.0	86.4
OM522317.2_Erwi_phg_Hena2	Kolesnikvirus	10.8	10.8	10.8	10.7	97.7	98.2	98.5	100.0	99.4	99.5	99.5	99.5	99.5	99.5	99.5	90.6	87.9	86.4
NC_041978.1_Erwi_phg_vB_EamM-M7	Kolesnikvirus	10.9	10.9	10.9	10.7	97.7	98.2	98.4	99.4	100.0	99.5	99.5	99.5	99.5	99.5	99.5	90.6	87.8	86.5
PP079182.1_Erwi_phg_vEam_PM_6	Kolesnikvirus	10.8	10.8	10.9	10.8	97.7	98.2	98.4	99.5	99.5	100.0	100.0	100.0	100.0	100.0	100.0	90.6	87.8	86.5
PP079183.1_Erwi_phg_vEam_W_25	Kolesnikvirus	10.8	10.8	10.9	10.8	97.7	98.2	98.4	99.5	99.5	100.0	100.0	100.0	100.0	100.0	100.0	90.6	87.8	86.5
PP079184.1_Erwi_phg_vEam_PM_27	Kolesnikvirus	10.8	10.8	10.9	10.8	97.7	98.2	98.4	99.5	99.5	100.0	100.0	100.0	100.0	100.0	100.0	90.6	87.8	86.5
PP079186.1_Erwi_phg_vEam_W_28	Kolesnikvirus	10.8	10.8	10.9	10.8	97.7	98.2	98.4	99.5	99.5	100.0	100.0	100.0	100.0	100.0	100.0	90.6	87.8	86.5
PP079185.1_Erwi_phg_vEam_PM_21	Kolesnikvirus	10.8	10.8	10.9	10.8	97.7	98.2	98.4	99.5	99.5	100.0	100.0	100.0	100.0	100.0	100.0	90.6	87.8	86.5
PP079187.1_Erwi_phg_vEam_S_24	Kolesnikvirus	10.8	10.8	10.9	10.8	97.7	98.2	98.4	99.5	99.5	100.0	100.0	100.0	100.0	100.0	100.0	90.6	87.8	86.5
MK770412.1_Salm_phg_SE5	Kolesnikvirus	11.1	11.1	11.1	11.0	91.5	90.4	90.8	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	100.0	91.6	92.6
PP278848.1_Erwi_phg_Omen	Kolesnikvirus	11.3	11.3	11.3	10.6	87.1	87.5	88.0	87.9	87.8	87.8	87.8	87.8	87.8	87.8	87.8	91.6	100.0	94.0

Figure 1. VIRIDIC heat map of a small portion of the members of this family: VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: phg = phage; vir = virus; Esch = *Escherichia; Shig* = *Shigella;* Salm = *Salmonella,* Pect = *Pectobacterium;* Hafn = *Hafnia;* Erwi = *Erwinia;* Ente = Enterobacteria. The full VIRIDIC comparison is provided as supplementary material.
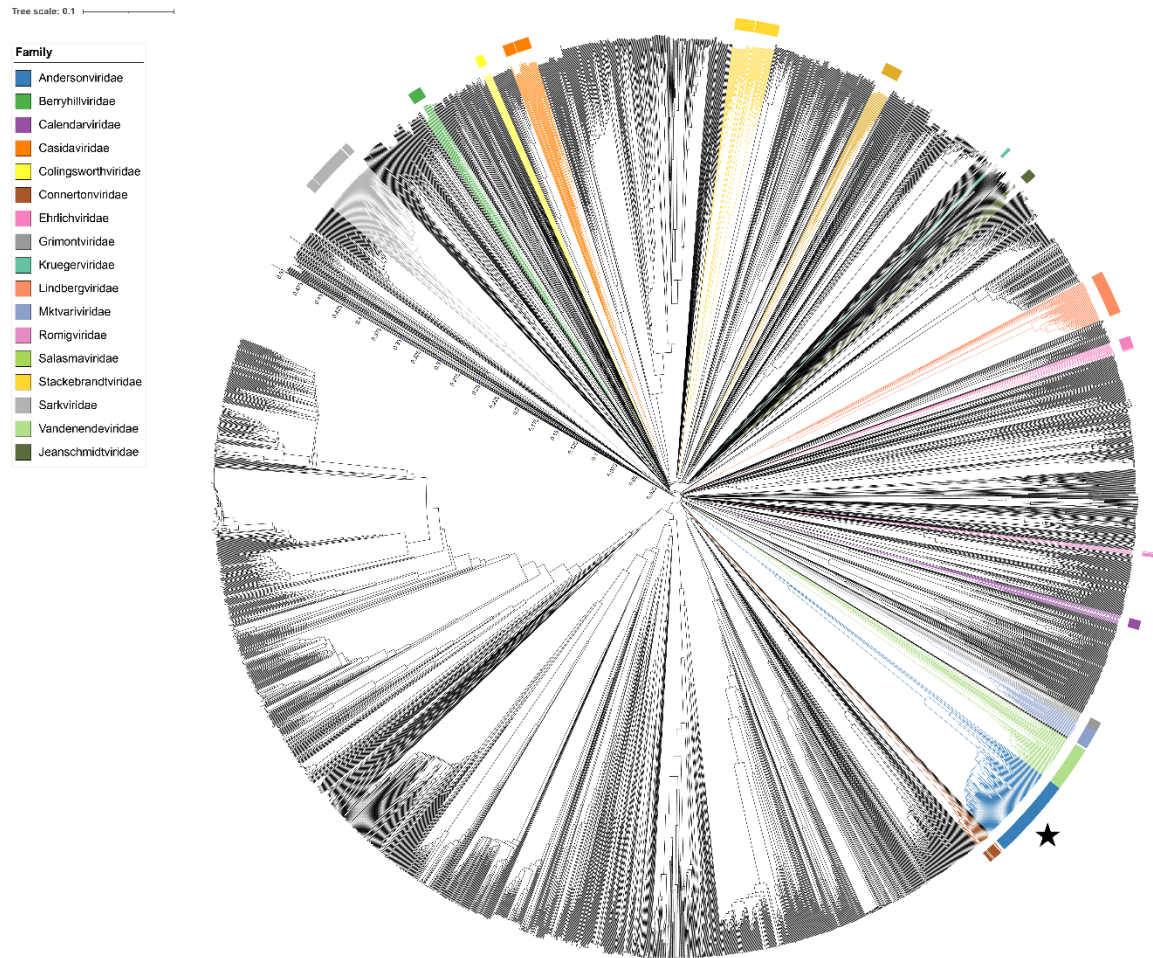
Figure 2. ViPTree [4] analysis Proteomic tree of 4,408 bacterial viruses with proposed viral families labeled by the coloured ring. The *Andersonviridae* are marked with a star symbol. The hierarchical tree was created using ViPTreeGen (version 1.1.2) [4] and annotated using iToL [15-16]. The tree is based on a dissimilarity matrix generated by pairwise tBLASTx scores between each of the genomes.

Figure 3. ViPTree [4] hierarchical tree pruned to show the proposed *Andersonviridae* alongside neighbouring clades. The proposed family is shown in grey with branches collapsed.

Tree scale: 1 ⊢————┤

[MN270891] Pectobacterium phage Wc4
[MK290738] Pectobacterium phage Arno18
[MK290737] Pectobacterium phage Arno162
[MW749010] Hafnia phage vB_HpaM_SarahDanielle
[MW749004] Hafnia phage vB_HpaM_Zyzzx
[EU710883] Erwinia phage phiEa21-4
[HQ728263] Erwinia phage vB_EamM-M7
[MK770412] Salmonella phage SE5
[KT454805] Escherichia phage phiSUSP1
[KT454806] Escherichia phage SUSP2
[OQ845957] Escherichia phage pEC-M719-6WT.1
[MK562504] Enterobacteria phage CHB7
[MN850587] Escherichia phage mistaenkt
[OR892555] Escherichia phage EP1
[OR687644] Salmonella phage PC79-13
[MK562505] Shigella phage Silverhawkium
[MF158040] Shigella phage Sf13
[KT363872] Citrobacter phage Mordin
[KM236239] Citrobacter phage Moogle
[OK539913] Citrobacter phage vB_CbrM_HP1
[OP902295] Citrobacter phage BSwM KMM2
[MF327003] Shigella phage Sf14
[MF327004] Shigella phage Sf17
[OM953433] Shigella phage Henu11
[OQ031072] Shigella phage SFPB
[OP902293] Citrobacter phage BSwM KMM4
[KX377933] Escherichia phage vB_EcoM_Alf5
[MN850603] Escherichia phage pinkbiff
[LR880803] Escherichia phage Barry
[OX016465] Escherichia phage vB_Eco_Tribble
[MN850605] Escherichia phage fjerdesal
[MK962758] Shigella phage JK55
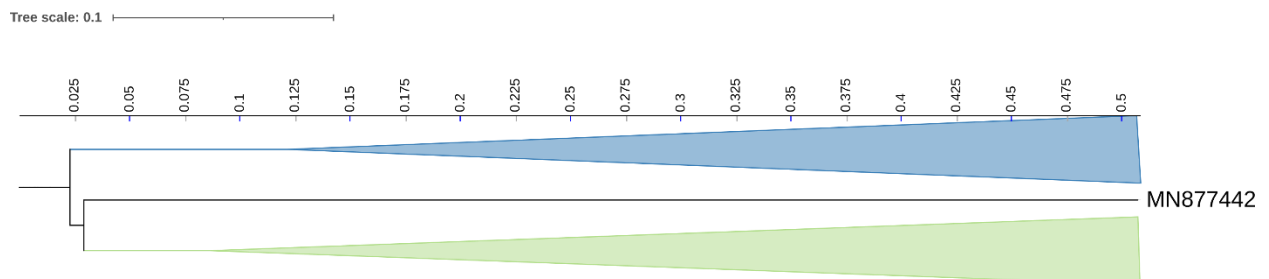[MN850644] Escherichia phage ekra
[MN850577] Escherichia phage heid
[MN850564] Escherichia phage humlepung
[MN850566] Escherichia phage garuso
[MN850636] Escherichia phage dune
[MN850637] Escherichia phage warpig
[OQ743992] Escherichia phage vB_EfeM_pEP20
[MN850633] Escherichia phage allfine
[KP143762] Salmonella phage Mushroom
[LC473039] Escherichia phage L27
[MZ327262] Salmonella phage vB_Si_DR094
[MZ327261] Salmonella phage vB_Si_35FD
[AF320576] Salmonella phage Felix01
[MN850647] Escherichia phage tootiki
[OM386661] Escherichia phage vB_EcoM_ESCO45
[MN850619] Escherichia phage finno
[MN850614] Escherichia phage adrianh
[MN850611] Escherichia phage nataliec
[MF370225] Salmonella phage ST11
[MG251391] Salmonella virus VSe11
[OK272472] Escherichia phage JLBYU28
[MW311372] Salmonella phage SEP1
[MZ501086] Escherichia phage JohannRWettstein
[MN655999] Shigella phage Z31
[ON210138] Escherichia phage EC106
[MH051914] Enterobacteria phage vB_EcoM_IME338
[OQ594353] Salmonella phage SWJM-02
[ON868915] Salmonella phage vB_SalM_SPJ41
[MN227145] Salmonella phage BPSELC-1
[MG646669] Salmonella phage BPS17W1
[OK539833] Salmonella phage vB_SenM-pSJ21
[MN481367] Salmonella phage D1-2
[OQ845959] Salmonella phage NJ12
[MW423797] Salmonella phage vB Seyj1-1
[MG646672] Salmonella phage BPS17L1
[OP172796] Escherichia phage EF202P1
[KP010413] Salmonella phage vB_SPuM_SP116
[MT409176] Salmonella phage SapYZU01
[OQ708377] Escherichia phage vB_EcoM_CRP22
[MN850635] Escherichia phage bumzen
[KF055347] Escherichia phage JH2
[MH586731] Salmonella phage Meda
[OL474141] Salmonella phage ph2-2
[OP515798] Salmonella phage MBP4696116
[MN882542] Escherichia phage JN01
[ON540300] Escherichia phage ECOH1
[LR699048] Escherichia phage VpaE1_ev035
[MN850610] Escherichia phage Andreotti
[MN850580] Escherichia phage momo
[OQ174504] Escherichia phage REP5
[MZ726791] Escherichia phage vB_EcoM_ASO1A
[OQ174507] Escherichia phage REP8
[OK272490] Escherichia phage JLBYU32
[MK524176] Escherichia phage PHB11
[MZ150758] Salmonella phage S19cd
[MW296865] Salmonella phage SP3_SHan-2021
[KX405003] Salmonella phage BPS15Q2
[MT887289] Escherichia phage SME50
[OR498728] Escherichia phage ZX4221
[MN994499] Phage NBEco005
[MH571750] Escherichia phage vB_EcoM-Ro111lw
[OP595146] Escherichia phage vB_EcoM_DE17
[MT833282] Escherichia phage vB_EcoM_Shy
[MK482688] Escherichia phage vB_EcoM_LMP25
[MW481326] Escherichia phage vB_EcoM-Pr103Blw
[MN994498] Phage NBEco004
[OL825705] Escherichia phage vB_EcoM_DE7
[ON239128] Salmonella phage OPT-SAL01
[ON855038] Salmonella phage GSP193
[OL800606] Salmonella phage vB_SAg-RPN213
[KT184313] Enterobacteria phage KhF1
[JN225449] Enterobacteriaphage UAB_Phi87
[MN850631] Escherichia phage mio
[OM386663] Escherichia phage vB_EcoM_ESCO49
[OM386664] Escherichia phage vB_EcoM_ESCO50
[KY626162] Salmonella phage Si3
[OK040806] Escherichia phage CL1
[MN850639] Escherichia phage radambza
[LR597663] Escherichia phage VpaE1_ev78
[LR597658] Escherichia phage VpaE1_ev108
[JX560968] Escherichia phage EC6
[LC739530] Escherichia phage phiWec172
[KM657822] Escherichia phage vB_EcoM-VpaE1
[OQ871555] Salmonella phage SUT_S720
[KR014248] Escherichia phage vB_EcoM_AYO145A
[MZ956763] Escherichia phage RP3
[MN850585] Escherichia phage skuden
[MN994503] Phage NBSal004
[KM092515] Escherichia phage HY02
[EU877232] Escherichia phage wV8
[KP869100] Escherichia typing phage_1

Subfamilies
■ Ounavirinae

Genera
■ Arnovirus
■ Daniellevirus
■ Felixounavirus
■ Kolesnikvirus
■ Mooglevirus

Figure 4. Core genome phylogeny of the proposed *Andersonviridae* family of bacterial viruses. A partitioned protein ML phylogeny was created from 5 genes present in all species of the proposed family. Alignments were performed using MAFFT in e-insi mode and trimmed using trimAl with a gap threshold of 0.5. The tree was calculated using IQ-Tree2 with 1000 ultrafast (UF) bootstrap replicates and SH-Alrt tests with -m TEST to optimise models for each alignment. The tree is rooted at the midpoint and UF bootstrap support ≥ 95% are shown. The coloured strips indicate proposed genera and subfamilies.
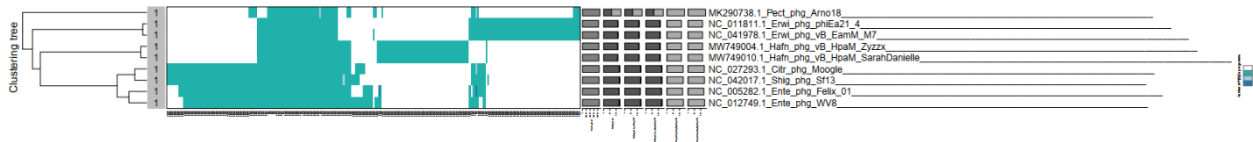
Figure 5. VirClust protein heatmap of a portion of species. At the first level, proteins are grouped based on their reciprocal BLASTP similarities into protein clusters, or PCs. At the second level, PCs are grouped based on their Hidden Markov Model (HMM) similarities into protein superclusters, or PSCs. AT the third, still experimental level, PSCs are grouped based on their HMM similarities into protein super-superclusters, or PSSCs [13].

Table 1. Signature genes in the proposed *Andersonviridae* family of bacterial viruses. Genes were identified by clustering with MMSeqs2, with thresholds of 35% sequence similarity and 50% coverage.

protein cluster	No. of genomes (123 total)	Percentage of genomes present in protein cluster	Predicted gene function
1	123	100%	rIIB
2	123	100%	virion structural protein
3	123	100%	lysozyme
4	123	100%	thymidylate synthase
5	123	100%	major capsid protein
6	122	99.19%	hypothetical protein
7	122	99.19%	hypothetical protein
8	122	99.19%	hypothetical protein
9	122	99.19%	hypothetical protein
10	122	99.19%	baseplate assembly protein
11	122	99.19%	baseplate wedge subunit
12	122	99.19%	terminase, large subunit
13	122	99.19%	baseplate assembly protein
14	122	99.19%	hypothetical protein
15	122	99.19%	portal protein
16	122	99.19%	hypothetical protein
17	122	99.19%	baseplate protein
18	122	99.19%	hypothetical protein

Proposals Data:

A. **To update the genus *Felixounavirus* with 80 new species**

B. **To update the genus *Mooglevirus with* 11 new species**

C. **To add one new species to the genus *Kolesnikvirus***

D. **To create a new genus *Daniellevirus* with two species**

E. **To create a new genus *Arnovirus* with three species**

F. **To create a new family *Andersonvirida*e**

Taxonomic Proposals:

A. **To update the genus *Felixounavirus* with 80 new species**

Origin of the name of this taxon: N/A

Historical aspects: This taxon was created through Taxonomy Proposal 2009.006a-gB.A.v2.FelixO1likevirus.

Genomic characterization:

Accession No.	Exemplar	% DNA Sequence similarity (*)	Species
NC_005282.1	Enterobacteria phage Felix01	100	
ON239128.1	*Salmonella* phage OPT-SAL01	88.4	*Felixounavirus OPTSAL01*
MT409176.1	*Salmonella* phage SapYZU01	87.6	*Felixounavirus CapYZU01*
MW423797.1	*Salmonella* phage vB Seyj1-1	87	*Felixounavirus fv1*
ON868915.1	*Salmonella* phage vB_SalM_SPJ41	86.3	*Felixounavirus SPJ41*
OQ594353.1	*Salmonella* phage SWJM-02	85.8	*Felixounavirus SWJM02*
MH586731.1	*Salmonella* phage Meda	88	*Felixounavirus meda*
OK539833.1	*Salmonella* phage vB_SenM-pSJ21	86.8	*Felixounavirus pSJ21*
OQ871555.1	*Salmonella* phage SUT_S720	87.8	*Felixounavirus SUTS720*
ON855038.1	*Salmonella* phage GSP193	87.8	*Felixounavirus GSP193*
OL474141.1	*Salmonella* phage ph2-2	87.2	*Felixounavirus ph22*
OP515798.1	*Salmonella* phage MBP4696116	88.3	*Felixounavirus MBP496116*
OQ845959.1	*Salmonella* phage NJ12	87.1	*Felixounavirus NJ12*
MN227145.1	*Salmonella* phage BPSELC-1	87.6	*Felixounavirus BPSELC1*
MN481367.1	*Salmonella* phage D1-2	87.9	*Felixounavirus D12*
OL825705.1	*Escherichia* phage vB_EcoM_DE7	86.8	*Felixounavirus DE7*
MN655999.1	*Shigella* phage Z31	85.3	*Felixounavirus Z31*
OQ708377.1	*Escherichia* phage vB_EcoM_CRP22	87.6	*Felixounavirus CRP22*
MN882542.1	*Escherichia* phage JN01	87.4	*Felixounavirus JN01*
MW296865.1	*Salmonella* phage SP3_SHan-2021	86.1	*Felixaunavirus Sp3Shan2021*
OQ743992.1	*Escherichia* phage vB_EfeM_pEP20	86.7	*Felixounavirus pEP20*
MT833282.1	*Escherichia* phage vB_EcoM_Shy	86.9	*Felixounavirus shy*

OR498728.1	*Escherichia* phage ZX4221	86.9	*Felixounavirus ZX4221*
MK524176.1	*Escherichia* phage PHB11	86.6	*Felixounavirus PHB11*
MT887289.1	*Escherichia* phage SME50	87.6	*Felixounavirus SME50*
MN994498.1	Phage NBEco004	86.9	*Felixounavirus NBEco004*
MZ150758.1	*Salmonella* phage S19cd	86.2	*Felixounavirus S19cd*
OK040806.1	*Escherichia* phage CL1	86.9	*Felixounavirus CL1*
MN994499.1	Phage NBEco005	88.4	*Felixounavirus NBEco005*
OP172796.1	*Escherichia* phage EF202P1	87.4	*Felixounavirus EF202P1*
MW481326.1	*Escherichia* phage vB_EcoM-Pr103Blw	87	*Felixounavirus Pr103Blw*
MH571750.1	*Escherichia* phage vB_EcoM-Ro111lw	88.3	*Felixounavirus Ro111lw*
OP595146.1	*Escherichia* phage vB_EcoM_DE17	86.5	*Felixounavirus DE17*
LR597663.1	*Escherichia* phage VpaE1_ev78	89.4	*Felixounavirus ev78*
KT184313.1	Enterobacteria phage KhF1	88.3	*Felixounavirus KhF1*
MK482688.1	*Escherichia* phage vB_EcoM_LMP25	87.9	*Felixounavirus LMP25*
LR699048.1	*Escherichia* phage VpaE1_ev035	87.3	*Felixounavirus ev035*
LR597658.1	*Escherichia* phage VpaE1_ev108	88.2	*Felixounavirus ev108*
MZ726791.1	*Escherichia* phage vB_EcoM_ASO1A	89.5	*Felixounavirus ASO1A*
MZ501086.1	*Escherichia* phage JohannRWettstein	88.4	*Felixounavirus johannrwettstein*
MZ956763.1	*Escherichia* phage RP3	87.1	*Felixounavirus RP3*
MN850585.1	*Escherichia* phage skuden	90.2	*Felixounavirus skuden*
MN850619.1	*Escherichia* phage finno	89.6	*Felixounavirus finno*
MN850631.1	*Escherichia* phage mio	89	*Felixounavirus mio*
MN850637.1	*Escherichia* phage warpig	89.6	*Felixounavirus warpig*
LR880803.1	*Escherichia* phage Barry	87.5	*Felixounavirus barry*
MN850577.1	*Escherichia* phage heid	87.9	*Felixounavirus heid*
OK272490.1	*Escherichia* phage JLBYU32	88.5	*Felixounavirus JLBYU32*
MN850605.1	*Escherichia* phage fjerdesal	88.3	*Felixounavirus fjerdesal*
MN850636.1	*Escherichia* phage dune	89.5	*Felixounavirus dune*
MN850603.1	*Escherichia* phage pinkbiff	89.7	*Felixounavirus pinkbiff*
OX016465.1	*Escherichia* phage vB_Eco_Tribble	87	*Felixounavirus tribble*
MN850611.1	*Escherichia* phage nataliec	89.1	*Felixounavirus nataliec*
MN850633.1	*Escherichia* phage allfine	87.3	*Felixounavirus allfine*
MN850566.1	*Escherichia* phage garuso	88.4	*Felixounavirus garuso*
MN850580.1	*Escherichia* phage momo	88.9	*Felixounavirus momo*
MN850635.1	*Escherichia* phage bumzen	88.2	*Felixounavirus bumzen*
MN850647.1	*Escherichia* phage tootiki	89	*Felixounavirus tootiki*
MN850614.1	*Escherichia* phage adrianh	89.1	*Felixounavirus adrianh*
MK962758.1	*Shigella* phage JK55	88.9	*Felixounavirus JK55*
MN850644.1	*Escherichia* phage ekra	88.6	*Felixounavirus ekra*
MZ327262.1	*Salmonella* phage vB_Si_DR094	88.7	*Felixounavirus DR094*

MN850564.1	*Escherichia* phage humlepung	90.2	*Felixounavirus humlepung*
MN850639.1	*Escherichia* phage radambza	89.9	*Felixounavirus radambza*
OQ174507.1	*Escherichia* phage REP8	86.5	*Felixounavirus REP8*
OQ174504.1	*Escherichia* phage REP5	86.6	*Felixounavirus REP5*
OK272472.1	*Escherichia* phage JLBYU28	87.2	*Felixounavirus JLBYU28*
MZ327261.1	*Salmonella* phage vB_Si_35FD	87.9	*Felixounavirus fv35FD*
LC473039.1	*Escherichia* phage L27	88.2	*Felixounavirus L27*
MN994503.1	Phage NBSal004	89	*Felixounavirus NBSal004*
ON540300.1	*Escherichia* phage ECOH1	85.1	*Felixounavirus ECOH1*
MN850610.1	*Escherichia* phage Andreotti	87.9	*Felixounavirus andreotti*
MF370225.1	*Salmonella* phage ST11	95	*Felixounavirus ST11*
MG251391.1	*Salmonella* virus VSe11	90.9	*Felixounavirus VSe11*
OM386661.1	*Escherichia* phage vB_EcoM_ESCO45	85.7	*Felixounavirus ESCO45*
OM386663.1	*Escherichia* phage vB_EcoM_ESCO49	88.2	*Felixounavirus ESCO49*
OM386664.1	*Escherichia* phage vB_EcoM_ESCO50	87.5	*Felixounavirus ESCO50*
ON210138.1	*Escherichia* phage EC106	84	*Felixounavirus EC106*
LC739530.1	*Escherichia* phage phiWec172	86.7	*Felixounavirus Wec171*
MH051914.1	Enterobacteria phage vB_EcoM_IME338	83.1	*Felixounavirus IME338*
MW311372.1	*Salmonella* phage SEP1	84.4	*Felixounavirus SEP1*

(*) determined using VIRIDIC [3]

B. **To update the genus *Mooglevirus* with 11 new species**

Origin of the name of this taxon: N/A

Historical aspects: This taxon was created through Taxonomy Proposal 2016.031a-rB.A.v2.Ounavirinae

Genomic characterization:

Accession or RefSeq No.	Exemplar	% DNA Sequence similarity (*)	Species
NC_027293.1	*Citrobacter* phage Moogle	100	
MK562505.1	*Shigella* phage Silverhawkium	79.8	*Mooglevirus Silverhawkium*
OP902293.1	*Citrobacter* phage BSwM KMM4	84.5	*Mooglevirus KMM4*
OQ031072.1	*Shigella* phage SFPB	83.4	*Mooglevirus SFPB*
OM953433.1	*Shigella* phage Henu11	83.6	*Mooglevirus Henu11*
OP902295.1	*Citrobacter* phage BSwM KMM2	84.5	*Mooglevirus KMM2*

OK539913.1	*Citrobacter* phage vB_CbrM_HP1	90.2	*Mooglevirus HP1*
OQ845957.1	*Escherichia* phage pEC-M719-6WT.1	76.9	*Mooglevirus M7196WT1*
MK562504.1	Enterobacteria phage CHB7	75.2	*Mooglevirus CHB7*
OR892555.1	*Escherichia* phage EP1	75.6	*Mooglevirus EP1*
MN850587.1	*Escherichia* phage mistaenkt	76.0	*Mooglevirus mistaenkt*
OR687644.2	*Salmonella* phage PC79-13	74.2	*Mooglevirus PC7913*

(*) determined using VIRIDIC [3]

C. **To add one new species to the genus *Kolesnikvirus***

Origin of the name of this taxon: N/A

Historical aspects: This taxon was created through Taxonomy Proposal 2016.031a-rB.A.v2.Ounavirinae

Genomic characterization:

Phage name	INSDC	Size (kb)	Protein	Overall % DNA sequence identity (*)	Overall % homologous proteins (**)
Erwinia phage phiEa21-4	EU710883.1	84.6	118	100	100
Salmonella phage SE5	MK770412.1	84.6	115	94.2	94.9

(*) determined using VIRIDIC [3]
(**) determined using CoreGenes 3.5 [6]

D. **To create a new genus *Daniellevirus* with two species**

Origin of the name of this taxon: The name of this taxon derived directly from the name of its first isolate *Hafnia* phage vB_HpaM_SarahDanielle

Historical aspects: This lytic myovirus was isolated against *Hafnia paralvei*

Genomic characterization:

Phage name	INSDC	Size (kb)	Protein	Overall % DNA sequence identity (*)	Overall % homologous proteins (**)
Hafnia phage vB_HpaM_SarahDanielle	MW749010.1	86.2	119	100	100
Hafnia phage vB_HpaM_Zyzzx	MW749004.1	85.9	117	84.1	94.1

(*) determined using VIRIDIC [3]
(**) determined using CoreGenes 3.5 [6]

E. **To create a new genus *Arnovirus* with three species**

Origin of the name of this taxon: The name of this taxon derives from the name of one of the first isolates *Pectobacterium* phage Arno18

Historical aspects: This phage was isolated from the Arno river in Italy using *Pectobacterium carotovorum* subsp. *carotovorum* F18 as the host bacterium

Genomic characterization:

Phage name	INSDC	Size (kb)	Protein	Overall % DNA sequence identity (*)	Overall % homologous proteins (**)
Pectobacterium phage Arno18	MK290738.1	91.7	147	100	100
Pectobacterium phage Wc4	MN270891.1	92.0	145	88.8	89.1
Pectobacterium phage Arno162	MK290737.1	91.7	146	93.2	93.5

(*) determined using VIRIDIC [3]
(**) determined using CoreGenes 3.5 [6]

F. **To create a new family *Andersonviridae* for these taxa.**

Origin of the name of this taxon: This taxon was named in honour of American biophysical chemist and geneticist Thomas Foxen Anderson (b. 1911 Manitowoc, WI, USA; d. 1991, Philadelphia, PA). "Anderson enrolled the California Institute of Technology from which he received his bachelor's degree and doctorate in 1932 and 1936, respectively. "He joined the faculty of the University of Pennsylvania in 1942, where he was named a professor of biology in 1958. He left the university in 1977 when he became director of the Fox Chase Cancer Center's postdoctoral training program for basic research. He retired in 1983. He pioneered use of the electron microscope to study viruses. His research produced insights of how viruses infect cells, methods of their reproduction and how they alter the cells they infect."
https://en.wikipedia.org/wiki/Thomas_F._Anderson

Photograph by John Heinsinger

(Photo copied from: https://nap.nationalacademies.org/read/11522/chapter/4)

Rationale: While they infect different host the members of these genera all exhibit similarities at the DNA, proteome and phylogenetic levels. The members of the *Felixounavirus* predominantly infect *Escherichia* and *Salmonella* species; Moogleviruses are specific for *Shigella* and *Citrobacter* species while *Kolesnikvirus* infect *Erwinia* strains.