

EC55 Minutes
Meeting of the Executive Committee (EC)
International Committee on Taxonomy of Viruses (ICTV)
Wednesday 2 August - Friday 4 August, 2023
Rosensäle, Fürstengraben 27, 07743 Jena, Germany, and virtually on Zoom

Note: Agenda papers are provided in <https://ictv.global/ec/ec55>
Document names are listed in this agenda in red

EC Members

Attending in person:

F. Murilo ZERBINI (President, interim Proposals Secretary, and meeting Chair) [MZ]
Stuart G. SIDDELL (Vice-President) [SGS]
Elliot J. LEFKOWITZ (Data Secretary) [EJL]
Evelien ADRIAENSSENS (Chair, Bacterial Viruses SC) [EA]
Poliane ALFENAS-ZERBINI (Elected Member) [PA]
Bas E. DUTILH (Elected Member) [BD]
Małgorzata ŁOBOCKA (Elected Member) [ML] ('Malgosia')
David L. ROBERTSON (Elected Member) [DR]
Nobuhiro SUZUKI (Elected Member) [NS]

Attending on Zoom:

Arcady R. MUSHEGIAN (Business Secretary) [AM]
Mart KRUPOVIC (Chair, Archaeal Viruses SC) [MK]
Jens H. KUHN (Chair, Animal dsRNA and ssRNA- Viruses SC) [JK]
Luisa RUBINO (Chair, Plant Viruses SC) [LR]
Sead SABANADZOVIC (Chair, Fungal and Protist Viruses SC) [SS] ('Sejo')
Peter SIMMONDS (Chair, Animal ssRNA+ Viruses SC) [PS]
Arvind VARSANI (Chair, Animal DNA Viruses and Retroviruses SC) [AV]
María Laura GARCÍA (Elected Member) [MG]
Sandra JUNGLEN (Elected member) [SJ]
Amy LAMBERT (Elected Member) [AL]
Hanna OKSANEN (Elected Member) [HO]
Koenraad VAN DOORSLAER (Elected Member) [KVD]
Anne-Mieke VANDAMME (Elected Member) [AMV]
Donald SMITH [DS] (Attending non-member, Microbiology Society supported)

OVERVIEW OF THE TIMETABLE

Wednesday 2 August – all times CEST (Jena) = (UTC/GMT + 2 hours)

Noon-3:45pm: First session with one 15 min break

3:45pm-4:15pm: Break

4:15pm-7pm: Second session with one 15 min break

7:30pm Dinner at [Salü – Genuss am Fluss](#)

Thursday 3 August – all times CEST (Jena) = (UTC/GMT + 2 hours)

Noon-3:45pm: First session with one 15 min break

3:45pm-4:15pm: Break

4:15pm-7pm: Second session with one 15 min break

7:30pm Dinner at [Landgrafen](#) – a 20-min walk up the hill from Rosensäle, so please notify Bas and Cybille Huck (sybille.huck@uni-jena.de) if you would like to order a taxi

Friday 4 August – all times CEST (Jena) = (UTC/GMT + 2 hours)

Noon-3:45pm: First session with one 15 min break

3:45pm-4:15pm: Break

4:15pm-7pm: Second session with one 15 min break

Official business of EC55 ends

Wednesday 2 August - noon CEST

Rosensäle and <https://uni-jena-de.zoom.us/my/bedutilh>

Section 1: Introductory business, minutes and commitments

1.1 Welcome and the order of the meeting (MZ)

KVD, AMV and DS were not in attendance. PS missed C 1.5.1, joined right after; DS joined in the second half.

1.2 Amendments to Agenda (All)

JK: asked for time to discuss Study Groups - MZ will allocate time on Day 3

1.3 Review and approval of the Minutes of the EC54 Zoom Meeting held in July 2022 (AM)

[[EC54 Minutes Executive Summary for approval.pdf](#); [EC54 Minutes for approval.pdf](#)]

Approved

1.4 Matters arising (when not part of the Agenda) (all)

None

1.5 Review of Commitments (C.x.x) made at EC54 (MZ leads);

C.1.5.1 Develop a policy on the permissible forms of sequence data deposition for TPs. (SGS, BD, EJJ) [[EC55_C_1_5_1_Policy Draft.docx](#)]

SGS reviewed the document and provided the context. The goal of the policy is to make the rules, and especially their implementation, more rigorous. One key question is the requirement of one exemplar sequence that is recorded as such in VMR (more sequences may be included in VMR, including strains - but only one should be designated as the exemplar; no taxonomy should exist without such). EJJ explained the record-level handling of this. SGS brought up Hepatitis C virus, where medics are really interested in the isolates' specifics - but the whole point is that only one isolate should be the taxon exemplar. BD asked about MSL - should inclusion in it be noted in the document ("species TaxoProps, aiming at inclusion of the species in MSL"?). EJJ: generally, no, because at the TaxoProp stage a taxon is not guaranteed to become part of MSL. SGS: Switching to a more important 2nd point, the sequence of the exemplar must be deposited. It must be protein coding-complete, and TaxoProp should include an explanation of how the completeness was determined. Discussion: "coding-complete" is defined with different criteria for different virus groups. Should there be a box in the proposal that the authors should check ("have you verified that it is coding complete?") General opinion - yes. SGS continued: there must be a sentence asking authors to document their assembly and annotation method. ML: GenBank is asking for this already, so - no, this is not onerous. AV: it is in GB metadata. MK: if submitters to GB did not include this in the metadata, it may not be possible to classify the sequence. AL agreed. AV: segmented viruses are worse. JK: We want to keep a connection to the virology community - practices of characterizing viruses differ across the community, we cannot insist on what is impossible for some parts of the community. EJJ: let us ask for a link to the GB entry that does contain such assembly and annotation information. MZ: is this an amendment to ICTV Code 3.6, or is it a policy / form level? Suggested it to be a comment to a rule, pointing to the document? Agreed. Final point: "accession number is pending" is not acceptable - should provide the actual number. BD: What if someone is writing a paper and wants to name a virus? EA: They do it all the time, it should not be a logistics problem. JK: No one should propose a taxon name in a paper. AM and EA: Proposing a taxon name in a paper cannot be prohibited by ICTV; we are only controlling the adoption of official taxa

names adoption, not what people are allowed to write. SGS: will revise the document. **New C.1.5.1: revise the policy on the permissible forms of sequence data deposition for TPs and provide the text of a comment to Code 3.6**

C.1.5.2 Develop a written remit for the Bioinformatics Expert Group (BD, EJJ, MZ) **[Done]**

BD described the short document deposited in the EC55 files folder. Two papers have been published so far, stating the problems and describing the remit of the group. Worth making a written record on the mode of interaction with SGs and SCs. Who should be in the group - consensus is not to overspecify (e.g., “one bioinformatician from each subcommittee” is overspecifying). “Experts” is too self-congratulatory - change it (“Enthusiasts” for E)? **New C.1.5.2: finish the document (BD)**

C.1.5.3 Develop a virus taxonomy challenge for bioinformaticians and decide how to brand it as an ICTV activity (BD) **[Done]**

BD: The activity is ongoing - the main challenge is to find enough sequences that are not in the database. There are currently about 600 such sequences. Community interest is substantial. **New C.1.5.3. Make a decision soon (BD). Event horizon - 6 mo to 1 yr.** Who in the new EC is active in it and can report next year: SR. Already branded as ICTV - EJJ: when ready, the site will announce.

C.1.5.4 Analyze the “policy-making” activities for the last 10 years and write a report. (AL, ML, AM)

AL: the vast majority of (more than 100) decisions that may qualify as “ICTV policy” have been handled by EC within a year. Proposed to add EC54 and EC55 analysis, improve statistics, **New C.1.5.4. Produce the report (next month)**. EJJ asked for an index of policies, including the active policies and resolved issues.

C.1.5.5 Proposal withdrawal should be by consensus of the authors, and if there is no consensus, then the EC must deal with it. Make this a written policy? (MZ) **[Done]**

This is covered later in the agenda.

C.1.5.6 Naming-taxa-after-living-people policy: honoree should agree to the fact of the naming as well as the form – proposal template should state that those permissions have been obtained. (MZ, EJJ)

Question about recently deceased people - should there also be some approval, and at least some good sense of not naming the virus after a person that was killed by this virus? How about asking family members - the general feeling is that it may not be a good idea. Related: we do have a policy against naming after a current SG member - but what if the SG wants to honor their (living) member? AM: this may be an appearance of COI, should not be allowed.

C.1.5.7 Revise the TaxoProp Excel module (EJJ – open ended, includes QC and Genbank name matching?) **[Done]**

EA: asked for a lead time - EJJ should decide on when the new form is released - not too close to the deadline. Nov 1. EJJ: Is a sample proposal useful? Will work with PS to put a better one together

C.3.5.1 Explore pros and cons of starting our own journal with a professional society. (JK, AV, LR, PS).

JK: Has submitted a white paper for EC's attention; it was initially written to Springer. PS: incentives were discussed repeatedly; one important one is that this would allow publishing a TaxoProp when it is approved. AM: What are the desired features of such a journal? That it is indexed in Pubmed? EA: No, PubMed is not necessary - the paper should be citable, but doi is enough for that. AM: May we have a list of essential properties (paid, peer-reviewed, doi'ed, pubmed-indexed?) LR, JK, PS go on to discuss details. JK: precedents in microbiology societies - structured format for taxon (genome?) announcement, inexpensive (\$500 for society members, otherwise \$1000). MZ: let us restate this commitment as **C.3.5.1 Find a way to make the proposal citable with doi**. AM: what if someone on the EC disagrees? MK: part of our Journal discussion in the past was to generate revenue for ICTV - is this abandoned? MZ, BD - yes, it is abandoned - always felt this was too complicated. EYL: registering costs money, especially when there are 1000s of them each year.

C.7.2.1 Prepare TP2021.003G.U.v1.ICVCN and Statutes harmonization for EC55 (MZ, EYL, JK).

MZ: this is not finished, though some progress was made. A colleague journal editor cross-checked extensively, found many loose ends. MZ committed to **C.7.2.1 revise further in 2-3 weeks (MZ) and submit for feedback**, so that would be for the next EC. JK suggested rather discussing the TP this year to make at least some progress. MZ: it is not really a proposal, and was not uploaded. EYL, MZ - it is red and blue all over, not ready for discussion. MZ: can discuss in emails. EYL - this is better discussed face to face.

C.7.3.1 Approve of a Comment to Rule 3.20 of the ICTV Code (SGS, SS)

SGS: this is part of a long-term debate, but let us discuss the comment first. "Species is the lowest taxonomic level...." is clearly about the taxon. "Species is a monophyletic group of MGE..." is about biological species - a real entity (a population). Thus, it is ambiguous, but maybe there is some utility in this ambiguity? BD: What if we just swap the two sentences? "Here is a biological entity, here is how we catch in a [taxonomic] box." JK: We may hope that people will not abandon virus names in favor of species name. AM: seconding BD's suggestion. PS: suggest "Members of a species form a monophyletic...". ML: Are there any examples of species that do NOT "form a monophyletic...? Answer from the room: no. JK: defining "species" in the code and then "biological species" in the comment, and both being different from "virus", is not helping the community. JK: incorporate this into the Code/Statutes revision discussion - for the next year. PS: the knot of issues around entity vs its taxon is not resolved anywhere in biology. Long discussion that SGS alluded to at the beginning, interrupted by AM asking: What is the action point here? JK: include into the guidance the relationship between "species" and "virus". **Postpone per JK, absorb into C.7.2.1 and its follow-up.**

C.9.7.1 Make a comment in the Code – if the tree is included in a TP, it should make a point directly relevant to this proposal (MZ)?

Into the next year **absorb into C.7.2.1 and its follow-up.**

C.11.1.1 Interim appointment of a Proposal Secretary (MZ) **[Done]**

C.11.2.1 Get IUMS VD approval of the new asynchronous election schedule (MZ) **[Done]**

Section 2: General ICTV business

2.1 Virology Division News, including difficulties with Springer Production Office (SS)

SS: Good progress - six VDN already published (one of them is obituary). 2022: annoying two-month delay in publication of two papers, different hiccups. In 2023, no such delays, but a hiccup with the change of policy at the journal (PMC deposition must be done by the authors). Collaboration with AoV should continue.

2.2 ICTV Newsletters (SGS)

SGS showed a newsletter, noted it is very template-like, not hard to update with Minutes and other supporting material in hand. EA asked for a list of tasks in the VP's portfolio. MZ: We have that, sort of, will provide to EA.

2.3 ICTV Report, JGV Profiles, Interactions with the Microbiology Society, – report of the editor-in-chief (SGS), managing editor (DS)

SGS showed a PowerPoint. Profiles: There are 109 JGV profiles, 49 got more than 17 citations and 17 over 100 citations, mean is 57 - Microbiology Society cares about citations and seems to be satisfied with the performance of Profiles. Report: the number of chapters falls behind taxonomy - one solution may be to write at a higher taxonomy level. Interim report pages are another stopgap measure. HO: should we produce Profiles from some of those? JK: Why separate Profiles and Chapters? PS: Profile is not easily updated, Chapter can be. MZ: gave examples of some of the higher-ranking taxa for which a Chapter would be extremely citable (*Caudoviricetes*).

2.4 Virus Metadata Resource (SGS)

Elliot and Donald will be taking over VMR - the problem spot is the RefSeq column. We are working to automate the process of generating and updating the VMR with each new MSL release and each new set of VMR data. This is very tedious and complex.

2.5 Interaction with NCBI/GenBank: unique virus names in the VMR; send updated VMR to NCBI before updating ICTV taxonomy (SGS)

EJL: Rob Edwards requested that NCBI taxon IDs be added to the VMR, but this turned out to be more complicated than thought initially. It is easy to get sequence-level taxon IDs, but what we really want is species-level taxon IDs. These require a much more complicated query, but we are working on it. Long technical discussion on the relationships of GenBank, RefSeq and Entrez records. The exemplars are for species, everything now has TaxID (including below species). SGS: VMR is created after ICTV Taxonomy is generated following the ratification, then 2-3 updates between releases - what of this should go to NCBI and when? EA: NCBI should be receiving (some of) those updates. EJL: a lot of the requests for name changes and comments about non-unique names are coming from Igor Tolstoy at NCBI. EA: EC efforts of making the names unique and NCBI efforts of making names in their database unique should benefit from information exchange. EJL: NCBI allows people to deposit (unique) sequences with non-unique virus names - they created this problem, they should fix it - sending them VMR means we already loaded the information in our database. We are helping NCBI though - e.g., when names change on our end. EJL bottomline: only ratified info should go to NCBI.

2.6 Preview of Nominations and Election on Day 3

MZ gave an overview. The matrix was just posted.

Section 3: Finances

3.1 Treasurer's report (MZ)

There is some money in the bank, so we paused grant requests in 2022-23 because of the pandemic. EC Zooms that saved us some money. OTOH some grant support of travel ran out. Discussion on what various sponsors require viz. justification and reports.

3.2 Grant activities, if any (all)

None

Section 4: Procedures and Policies

4.1 Conversion of all virus species names to the binomial format – the deadline is now! (More in 7.1)

MZ: pretty much this is done. EJJ: another year if we find a stray unconverted name - it will have to be corrected via a proposal.

4.2 Non-viral taxon names: what should and should not be italicized (SGS) [[Thines et al on italicization.pdf](#)]

SGS referred to the paper above, which asks to italicize everything. See no reason why we could not / should not italicize everything. Everyone agreed.

4.3 Statute 4.3.5 interpretation: Can an SC chair serve 2 terms, then be elected to chair another SC ?

Consensus: yes they can. No suggestion to include this into the revision.

4.4 Statute 4.3.1 correction - “no earlier than 180 days and no later than 60 days before the ICTV Plenary Meeting” in the years when there is no ICTV Plenary Meeting.

MZ: Will be included in the revision.

4.5 How to write virus names in the taxonomy proposals and VMR and how to ensure that these virus names are unique in NCBI (EA)

MZ: This was dealt with earlier.

Section 5: Data and Software

5.1 Taxonomy Database and Website (EJJ)

EJJ gave an overview of the revamped website, with the main resources now linked at the top-middle of the first page. Visual browser now supports lineage extraction, matching taxa name as one is typing, etc. Hierarchy of development priorities, notably Sequence-based Taxon Lookup. BD had many suggestions on features, but in short this is not trivial, and how to do this properly is what we hope will come out of the ICTV Taxonomy Challenge, see C.1.5.3. EJJ said - send me feedback in any form. Other important project: compiling the list of all demarcation criteria, extracted out of the approved TaxoProps.

Section 6: General taxonomy and nomenclature issues

6.1. Progress in binomial nomenclature adoption (SC chairs)

Covered.

6.2. Is there more to say about naming / not naming taxa after people?

No.

6.3. Should every species have a named virus ?

ICTV does not work with or on virus names - if there is none, do not invent one to put into the Virus name. JK: Strong opinion that absolutely there should be a name for every

classified virus species, otherwise, like bacteriologists, we will drag species' names to double up as virus names. AM: The community should be coming up with common names as they see fit. JK: Let us put pressure on the TaxoProp authors to come up with a name every time they write a proposal. Otherwise we are not serious about distinguishing virus name and species name. EA brought up metagenomes again. This discussion should continue at EC56 (agenda item).

6.4. The nomenclature of viruses and virus species – options for change (PS) [Species **name discussion document Agenda item 7 PS.pdf**]

MZ introduction - this is a complex question, let us approach it in this spirit. PS: There is a difference between the name of a physical object vs. the name of a category to which this object belongs; taxonomic name refers only to the latter. JK: In botany and zoology, people are more flexible; on the other hand, mammalogy is striving to assign a common name to every mammal species. Entomology - the same. So it is not exactly virology vs the rest of the world. More philosophically - what people do / not do vs. what is the right thing to do. BD: Only a single virion is a physical entity; "virus name", therefore, refers to a category name in practice and in principle. What people mean by "virus" I would call a "virus strain" (or other sub-species grouping). AM: What is being optimized? LR: Binomial nomenclature reform just went down, let us be easy on the community for a little while? EA: As long as it is understood what people mean, we should cut them some slack. SGS: repeating 'we are not touching your virus names' actually had a positive effect on the community. SGS: it should be more than 2 years before the next major change. ML: Medically important viruses should have sequence isolates. Then it may be easier to sort which is which. Consensus decision: sit on this - assess how the community is dealing with the transition to binomials first (meeting, diverse sub-communities - report back next year(s)).

SGS previewed some concerns, having to do with multiple proposals each. Using virus name abbreviation as a species epithet ('*Tobamovirus tmv*'-like) - LR noticed that there are only two SGs that dug their heels on this, and it is likely that even the authors of those two will change them in a year. SGS said: let EC be strict about this and return those. SS, EA, AM: We said 'free form' - our word has to be good on this. JK: If we have specific reasons to object to a name, we could name the reasons, same as with everything else in any proposal.

Thursday 3 August - noon CEST

Rosensäle and <https://uni-jena-de.zoom.us/my/bedutilh>

Discussions from Wednesday continue as needed

Section 7: General taxonomic proposals (MZ, SGS)

Total: 2

proposals are in <https://ictv.global/files/proposals/pending>, **nested under each Subcommittee folder**

2023.002G.N.V1.Proposal_withdrawal	MZ commented on the time points when a prop may be withdrawn (really, any time pre-ratification) and that prop must be stored nonetheless. EYL: can just one author withdraw? MZ: an email from the corresponding author should state that it is a unanimous solution; otherwise disagreeers may withdraw their name. 18 for Ac.
2023.003G.Rename_MSL	Discussing the meaning and usage of 'Master'. 19 for R

Section 8: Subcommittee reports and proposals

Only the proposals slated for discussion are shown. The 'species only' and in some cases 'genera and species' proposals MAY be streamlined, i.e., not formally presented and discussed. This can be done at the discretion of the SC chairs, with co-sponsorship and provided that no EC member requests a discussion. All proposals are in <https://talk.ictvonline.org/files/proposals/>, nested under each Subcommittee folder

Total: 207, including 102 for streamlining and 95 for discussion (EC54: 175/114/61; EC53: 189/132/57; EC52: 290/240/50) <order of SCs may change>

8.1 Animal viruses D (DNA and Retro) SC: 24 proposals, 10 streamlined, 14 for discussion (EC54: 9/2/7; EC53: 8/6/2; EC52: 19/16/3) (AV)

AV commented on the utility of the error-checking tool, which caught mistakes in streamlined as well as non-streamlined proposals. Described approaches to the epithet derivation. There was occasional formation like “*Heteroruevirus hominid3*”. SGS asked for time to object to this. Also “*Lentivirus humanimmunodeficiency1*”. SGS: Anellovirus sequence used in the analysis represents half of the genome - were the genomes coding complete? AV: variation in genome length, some non-conserved ORFs are often present but were not used. EYL: we request coding-complete genome with sequences backing it up - but this is nowhere in the proposal template. MK: there are limitations of this e.g. with large genomes (poxviruses); “coding complete” cannot be construed as the requirement to guarantee all ORFs. Again discussion of what to do with sequences deposited by workers not familiar with virology - metagenomics, though not only. One (the only?) solution is to create a RefSeq record with 3rd party annotation (and hope that no one changes it back, as there is no ownership of RefSeq records). AV: to answer SGS query about Proposal 005D, those have terminal redundancies indicative of the complete coverage of the circle.

SGS and JK said that fusing numbers to epithets is taking ‘binomial’ too far. JK had questions about ‘elegance’. JK: Then again, who is “the community” (suspects it is often a

small sample, may or may not be representative). BD: We committed before to intrude only when “the community” is not coming up with their own names? PS: There is a guidance document that says that species names should ideally be distinct from virus names. MZ, AV - Do not recommend an R; do Ac and even propose ways to be creative per the guidance. AV: some were last-moment submissions, and authors should have a chance.

Voted as a list - 19 for. All Ac's are to correct typos.

001D	Ac
002D	Ac
003D	Ac
004D	Ac
005D	Ac
2023.006D.N.v1.Redondoviride_2ren	Ac
007D	Ac
2023.008D.N.v1.Adenoviridae_1reng_22ns_86 rens	A
2023.009D.N.v1.Retroviridae_68rensp	Uc – improve the naming approach (not virus names verbatim)
010D	Ac
011D	A
2023.012D.N.v1.Iridoviridae_22renam	Ac
	Ac
2023.015D.N.v1.Poxviridae_ab_27sp_1g	A
	Ac
2023.017D.N.v1.Poxviridae_55renam	Ac
2023.018D.N.v1.Mulpavirales_1nf_9ng_9nsp	Ac
2023.019D.N.v1.Cirivirales_1nf_4ng_10nsp	Ac
2023.020D.N.v1.Geplafuvirales_1nf_18ng_30 nsp	Ac
2023.021D.N.v1.Rohanvirales_2nf_28ng_34ns p	Ac
2023.022D.N.v1.Ringavirales_1no_1nf_8ng_1 5nsp_v2	Ac
2023.023D.N.v1.Squillovirales_1no_1nf_42ng _67nsp_v2	Ac
2023.024D.N.v1.Gredzevirales_1no_1nf_38ng _58nsp	Ac
2023.025D.N.v1.Saturnivirales_1no_2nf_35ng _120nsp	Ac

8.2 Animal viruses M (dsRNA and ssRNA-) SC: 35 proposals, 28 streamlined, 7 for discussion (EC54: 31/19/12; EC53: 42/39/3; EC52: 29/22/7) (JK)

Most c's are typos. Comments inside the cells. 035 and the need for coding completeness. Hantavirus sequences are not consistent in that regard, only provable ones are retained upon the reorganization. SGS: *Mymonaviridae*, 16 species - accessions are to RdRp, replace them with accession to full genomes. Everything **Ac. 19 for**. Other c's are typos to correct.

2023.006M.N.v1.Bunyavirales_1nfam_1ngen_1nsp	Ac - why not in <i>Leishbuviridae</i>
2023.018M.N.v1.Paramyxoviridae_reorg	A
2023.021M.N.v1.Rhabdoviridae_24nsp_5ng_1nsf	Ac . SG vote to be added.
2023.024M.N.v1.Bunyaviricetes	Ac . Excel must be re-done. Tulip streak virus seems to be either its own family or <i>Leishbuviridae</i> - why neither? SG vote to be added.
2023.033M.N.v1.Sedoreoviridae_sprenam	Ac . SG is not functional, JK and T. Postler wrote up the names, asked SG whether they are OK, first got nothing and then last-moment 'it's OK'. SG vote to be added.
2023.034M.N.v1.Spinoreoviridae_sprenam	Ac . SG is not functional, JK and T. Postler wrote up the names etc. SG vote to be added.
2023.035M.N.v1.Hantaviridae_reorg	Ac . SG vote to be added

8.3 Animal viruses S (ssRNA+) SC: 15 proposals, 1 streamlined, 14 for discussion (EC54: 7/2/5; EC53: 8/3/5; EC52: 13/12/1) (PS)

PS: general comments: all SGs worked, received renaming suggestions, most took or modified them, some decided in favor of non-Latinized. One SG (*Astroviridae*) was non-responsive, and must be contacted again, though the renamings will be voted on. JK: saw a Latinisation attempt that was done incorrectly (should be -ense ending instead of -ensis, as virus is neutral gender). Though those that are binary non-Latin are done elegantly! But then there is the *Togaviridae* study group that went a different way - mostly, geography used verbatim. Tell the group to reconsider (JK+TP suggestions, but if not, put Rio back into rionegro).

Betacoronavirus alizaki - first there was no permission from Ali Zaki, then later there was an email thread that responded (positively) to the wrong question, i.e., the renaming of virus, not renaming of virus species. Need to re-ask to be 100% sure he knows what he is agreeing to, and change the reason to "important contributions" rather than hinting on him being the sole discoverer. (He is in an unspecified political hot water...).

Naming after a dead discoverer is not recommended. SGS: *Betacoronavirus sarsi* is bad because it is 'about disease' but the disease evolves, so this (soon will be?) not accurate. Others did not think this was a problem - recognizable, easy to pronounce. EJJ: We absolutely need to get an agreement from a live person. But also - especially if it is a disease with a possibility of stigma, should family members with the same name also be asked for approval ???? And then how to handle the rejection - should not a SG notify the honoree about such a possibility?? Dead person - even harder: who should be consulted - under legal (who is 'next of kin' and who seems to be but is legally not) and moral (who feels unfairly

stigmatized?) obligations? The group (all but 012S and 015S) passed as **Ac 19 for, correct typos.**

2023.001S.N.v1.Caliciviridae_12sprenamed	Ac typos etc
2023.002S.N.v1.Arteriviridae_7sprenamed	Ac typos etc
2023.003S.N.v2.Picornaviridae_158sprenamed	Ac typos etc
2023.004S.N.v1.Astroviridae_22sprenamed	Ac typos etc
2023.005S.N.v1.Tetraviridae_13sprenamed	Ac typos etc
2023.006S.N.v1.Togaviridae_32sprenamed	Ac typos etc
2023.007S.N.v1.Solinviridae_2sprenamed	Ac
2023.008S.N.v1.Polycipiviridae_14sprenamed	Ac
2023.009S.N.v1.Mesoniviridae_12sprenamed	Ac
2023.010S.N.v1.Nodaviridae_9sprenamed	Ac
2023.011S.N.v1.Sarothroviridae_1sprenamed	Ac
2023.012S.N.v2.Coronaviridae_54sprenamed	secondly after 015, this one. Uc - consider different names for MERS virus (to not include Middle East reference) and SARS virus 19 for passes
2023.013S.N.v1.Nidovirales_27sprenamed	Ac
2023.015S.N.v1.Coronaviridae_2sprenamed	MZ suggested voting for Uc (provide unambiguous confirmation from Ali Zaki himself, provide permission from the next of kin of Urbani, and get SG signoff on both) 12 against - Rejected.

8.4 Plant viruses SC: 36 proposals, 11 streamlined, 25 for discussion (EC54: 22/12/10; EC53: 20/16/4; EC52: 36/33/3) (LR)

LR described the renamings, for the most part all is harmonious. Viroids - did not consult the study group, but Chair is in the next office to the SC Chair :) (*SJ leaves - total headcount is 18, will become 17 when I leave a bit later*) Discussion of the suffixes (and infixes) as related to viroids. Veering into a code issue on suffix modification. The package vote (**Ac**) **18 for passes;** *AM leaves the meeting and HO takes notes for the rest of the day. Total headcount is now 17.* Rest of the proposals were voted separately **17 for, all passed**

2023.001P.N.v1.Koshovirus_1ng_4ns	Ud , new species coming next year, thus this is too premature, consider next year, 17 for
2023.002P.N.v1.Endornaviridae_rename_sp	Ac
2023.003P.N.v1.Metaxyviridae_rename_1sp	Ac
2023.004P.N.v1.Bromoviridae_rename_sp	Uc , reconsider using the acronyms as the species epithet
2023.005P.N.v1.Bromoviridae_10nsp	Uc , reconsider using the acronyms as the species epithet, 17 for
2023.006P.N.v1.Alphasatellitidae_rename_30s p	Ac

2023.007P.S.v1.Serpentovirales_rename	Ac
2023.013P.N.v1.Potyviridae_rename_sp	Ac
2023.014P.N.v1.Geminiviridae_1ng_2nsp	A, 17 for
2023.015P.N.v2.Geminiviridae_rename_sp	Ac
2023.016P.N.v1.Virgaviridae and Benyviridae_rename_sp	Ac
2023.019P.N.v1.Solemoviridae_rename_sp	Uc reconsider using the acronyms as the species epithet
2023.020P.N.v1.Enamovirus_10nsp	Uc reconsider using the acronyms as the species epithet
2023.022P.N.v1.Poliovirus_47nsp	Uc reconsider using the acronyms as the species epithet
2023.024P.N.v1.Nanoviridae_rename_sp	Ac
2023.025P.N.v1.Alphaflexiviridae_rename_sp	Ac
2023.026P.v1.Viroids_rename_families	Uc and back to the study group to fix the nomenclature
2023.027P.N.v1.Betaflexiviridae_rename	Ac
2023.029P.N.v1.Hubsclerovirus_1ng_1nsp	Uc 17 for, reconsider using the acronyms as the species epithet
2023.030P.N.v1.Closteroviridae_rename_sp	Ac
2023.032P.N.v1.Avsunviroidae_Pospiviroidae_rename_sp	Ac
2023.033P.N.v1.Pseudoviridae_Metaviridae_rename_sp	Ac
2023.034P.N.v1.Geminiviridae_1ng_1nsp	Uc, 16 for needs an approval from the SG
2023.035P.N.v1.Tolecusatellitidae_rename	Ac
2023.036P.N.v1.Geminialphasatellitinae_rename	Ac

8.5 Fungal and Protist Viruses SC: 15 proposals, 1 streamlined, 14 for discussion (EC54: 6/1/5; EC53: 10/5/5; EC52: 5/4/1) (SS)

2023.001F.v1. Botourmiaviridae_move_renamelssp	A
2023.002F.v1.Trichomonasvirus_1nsp_spre	A
2023.003F.v1.Narnaviridae_spre	A
2023.004F.v1.Marseilleviridae_1newgen_spre	Uc, new genus name needed
2023.005F.v1.Polymycoviridae_spre	A
2023.006F.v1.Curvulaviridae_spre	A
2023.007F.v1.Ambiviricota_nphy	Ac , reconsider the naming, New phyla (Realm <i>Riboviria</i>) based on 20 isolates (experimental evidence) and more than 350 more coming in future (sequence based)
2023.009F.v1.Viropages_reorg	A , major taxonomic reorganization of the orders and families (original in 2022); 4 orders, taxonomy based on the MCP; demarcation criteria for all ranks in place;
2023.010F.v1.Phycodnaviridae_abolish19sp_spre	Ac , 19 species removed (no seq data available), remaining species were named (binominal); Naming after the chair (reason for Ac): name might be used in the epithet if the chair will resign and not be a member.
2023.011F.v1.Pimascovirales_3nf	Ac , consider the changing the names to avoid to use the same stem (e.g. Cedraviridae, Cedravirus) Refer to 3.14
2023.012.F.v1.Partitiviridae_abolish15sp_spre	Ac , 45 species were abolished, the remaining were named, reconsider names to be more pronounceable
2023.013F.v1.Deltaflexiviridae_1nsp_spre	Ac , double-checking that the correct excel submitted
2023.014F.v1.Gammaflexiviridae_spre	A
2023.015F.v1.Ghabrivirales_reorg	Ac , major reorganization of the class <i>Ghabrivirales</i> , double-checking of the excel, E.J.L.: 4 errors found; renaming of the ranks not to have the same stems at genus and family level

Vote at once on all: 17 for, all passed

8.6 Archaeal Viruses SC: 2 proposals, 0 streamlined, 2 for discussion (EC54: 4/0/4; EC53: 5/3/2) (MK)

Voted at once on all: **16 for, both passed**

2023.001A.N.v1.Archaeal_binomials	A , all archaeal species now binomial and latinized
2023.002A.N.v1.Caudoviricetes_5nf	Uc , methanogenic archaeal tailed viruses, metagenomics from gut; 5 new families, 5 species; based on virus proteomic tree; no GenBank Acc numbers available yet

8.7 Bacterial Viruses SC: 80 proposals, 61 streamlined, 19 for discussion (EC54: 96/78/18; EC53: 96/74/22; EC52: 188/153/35, including Archaeal) (EA)

61 streamlined: Some species epithets are inherited from phage names and now transferred species names, reconsider the naming - EA proposes Ac for all 61 streamlined proposals 19 for discussion:

Proposals on subfamilies, two new families, some typos - very clear ones

Major re-organizations done which has resulted in several floating taxa. Currently, waiting for more sequences, but also more analyses before creating new genera. More systematic efforts needed, but not yet in place.

three proposals (042B, 069B, 072B): GenBank files over annotated (functions annotations not supported), sequence data correct

Vote at once on all: 16 for, all passed

2023.001B.N.v1.Leviviricetes_reorg	Uc, impossible to verify the results, the trees and heatmap should be available, provide the (raw) data and trees so that the proposal can be assessed; JK comments: reanalyses and reorganizations have resulted in abolishment of genera, some of them could be retained
2023.015B.N.v1.Chimalliviridae_nf	A
2023.019B.N.v1.Daemsvirinae_nsf	Ac, taxa should be italicized; correct typos
2023.027B.N.v1.Gorskivirinae_nsf	A
2023.028B.N.v1.Grandevirales_no	Uc, problems with GenBank numbers; GenBank accession numbers should be provided. If that is not possible in time, the proposal can be deferred.
2023.029B.N.v1.Guarnerosvirinae_nsf	A
2023.033B.N.v1.Heleneionescovirinae_nsf	was streamlined as Ac
2023.036B.N.v1.Jameshumphriesvirinae_8ng	Ac, some incorrect sentences and typos; provide corrected version
2023.038B.N.v1.Johnpaulvirinae_nsf	A
2023.039B.N.v1.Jondennisvirinae_nsf	A
2023.042B.N.v1.Konodaiviridae_nf	Ac: Proposal is correct; GenBank files overannotated (functions annotations not supported); ask the proposers to address the over-annotation of the genbank file (not mandatory), ask to change the virus names in the Excel module to match the format "Genusname sp. isolate XXX"
2023.043B.N.v1.Kutznervirinae_nsf	Ac, add explanation of annotation to legends of Figs 1 and 2 so that the genera and subfamily boundaries are clear for the reader
2023.046B.N.v1.Madridviridae_nf	A
2023.048B.N.v1.Munstervirinae_nsf	A
2023.057B.N.v1.Saffermanviridae_nf	A
2023.062B.N.v1.Skurskavirinae_nsf	A
2023.063B.N.v1.Stanbayleyvirinae_nsf	A
2023.069B.N.v1.Toyamaviridae_nf	Ac, Proposal is correct; GenBank files overannotated (functions annotations not supported); ask the proposers to

	address the over-annotation of the genbank file (not mandatory), ask to change the virus names in the Excel module to match the format "Genusname sp. isolate XXX"
2023.072B.N.v1.Umezonoviridae_nf	Ac , Proposal is correct; GenBank files over annotated (functions annotations not supported); ask the proposers to address the over-annotation of the Genbank file (not mandatory), ask to change the virus names in the Excel module to match the format "Genusname sp. isolate XXX"

BD proposed to include phylogenetic trees and more data to every taxonomic proposal, bioinformatics enthusiasts group is ready to help (more time tomorrow to discuss)

Friday 3 August - noon CEST

Rosensäle and <https://uni-jena-de.zoom.us/my/bedutilh>

Section 8: Subcommittee reports and proposals (continued as needed)

Continued discussion of the service proposed by BD. AM warned against offering an undefined set of services, b/c then there will be too many requests and too much abuse; the onus and responsibility of presenting the data and explaining why they are presented should be on the proposal authors. PS: are there/should there be minimal information standards? MZ: why not the Enthusiast Group write up such a guiding document to publish on the website? SS interesting question: how many erroneous / useless trees have been submitted for EC consideration since we started requiring them? SS, PS: More requirements may mean that fewer SGs will write proposals. JK reminded of the perceptions in the community (also that following instructions, even as basic as “delete blue font”, is hard). EJJ: some software development is ongoing; in the meantime - tree should be with the tree file and the alignment. Should there be a requirement for public deposition of the supporting data? EA: yes, like with the journals (EJJ supports) AV: Everyone is doing this as a volunteer service, no comparison with the journal - different incentives? BD: But people put TaxoProps into their CVs, so there should be some seriousness about their content... JK: A gap between the process as it is described to the outside and the real thing. SS: some TaxoProps contain original ideas - how they should be considered (if there is no supporting data?)
Voting: Proposal File and Help Documentation should include minimal requirements: request tree image, tree file, source alignment, metadata file, explain that they will be stored in a non-public area. **C9.1. PropSec+DataSec prepare this infrastructure (Word doc etc) 17 for**

Section 9: Optional catch-up session

Placed here in case it proves necessary to return to discussions initiated earlier.

Section 10: EC nominations and elections

10.1. Nominations Committee report

MZ reported on the NomCom activities. Debates: exact count with slots filled, or extra candidate? How to replace a candidate that is inactive?

10.2. EC Elections

NomCom will meet within a week, finalize the plan for Elected Members, vote to be organized by AM (C.11.2.1). Moving on to direct vote for SCCs - reminder that they are elected directly, do not have to be the EC members first.

AV 18 for
 HH 19 for
 JK 18 for
 MK 18 for
 DT 19 for
 SS 18 for
 LR 18 for

10.3. The order of transition to the new EC

Plenary will be arranged virtually, approvals obtained, after which the newly elected Officers and Members will be in office.

10.4. On the future arrangements with IUMS – charge to the new EC?

MZ: We remain affiliated with IUMS, but we emancipated away from their congresses for our elections. SGS commented on ICTV becoming a (UK) charity. IUMS, which has a UK office, applied for a UK charity some time ago and failed. ICTV was not prominently featured in the application as a major activity of IUMS; if it were, IUMS might have better luck - encourage IUMS to do this right?

Section 11: Future EC activities and concluding business

11.1 Arrangements for EC56 meeting (MZ)

MZ: Let us wait for the new EC to discuss this.

11.2 Review of commitments (AM)

AM: Permission to do it online, first draft within a week? [AM adds on Nov 5]

11.3 Any other business (MZ, AM)

JK: about inactive study groups. It is a de-facto state anyway that very few people do most of the work - should we abolish SGs or otherwise codify the status quo? General discussion of taxonomy, classification and the role of the community (active, passive) in this? LR noted binomial switch was seen by some as a permission to sit back and wait. BD: large interest in the community in automating some or all aspects of virus taxa definition. DS noted that every chapter that was published for the Report thus far involved an actually working study group. On the (perceived) ease or difficulty of coding this or that functionality. EA argued for doing a better job of recruiting the next generation of scientists - one can do this outside the study groups if a study group is populated (by a SG Chair) with senior traditional virologists.

Official business of EC55 concludes