

Virus classification and support for different stakeholders

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Stakeholders in virus classification

- ICTV members!
- The wider virology community
 - Provides the framework for understanding virus relationships
 - Inference of the evolutionary basis for shared and divergent characteristics
 - Framework for understanding origins, zoonoses and adaptive evolution
- Educators
 - Stability in virus definitions and reference
- Clinicians, Veterinarians and Phytologists
 - Aetiological agents of infectious disease
 - Somewhat agnostic of the nature of the infectious agent (bacteria, fungi, virus, viroid)
 - Requires a clear reference to the infectious agent
- Regulators of international traffic, categorisation for biosecurity
 - Agents have to be unambiguously defined
 - Require clear inclusion and exclusion criteria for reference
 - Should use internationally recognised nomenclature

Species in Virology

- Classification of animals and plants
 - Species mark the finest division possible in phenotypes
 - Biological species principle (Mayr, 1942), interbreeding capability defines species membership
 - Fundamental to shared gene pools and organism evolution
 - The term is used, but must be defined differently for asexual organisms, including bacteria and viruses.
- Virus species
 - “A species is the lowest taxonomic level in the hierarchy approved by the ICTV. A species is a monophyletic group of MGEs whose properties can be distinguished from those of other species by multiple criteria” – ICTV Rule 3.2 2023*
- Criteria include phenotype and genetic relatedness:
 - “may include, but are not limited to, natural and experimental host range, cell and tissue tropism, pathogenicity, vector specificity, antigenicity, and the degree of relatedness of their genomes or genes”*
- Species have to be monophyletic
- No intention to specify a degree of genetic similarity in species assignment
- Phenotypic properties to define species and higher taxa are optional

Is the ICTV species level adequate and appropriate?

- One virus – one species
 - Original disease-based assignment
 - One species, one pathogen
 - Arboviruses, most plant viruses



Yellow fever virus – *Orthoflavivirus flavi*
Cowpea mosaic virus – *Comovirus vignae*

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 - More often found in sequence-based classifications
 - The identity of the species insufficiently describes the pathogen



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Coxsackievirus A20

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Poliovirus type 1

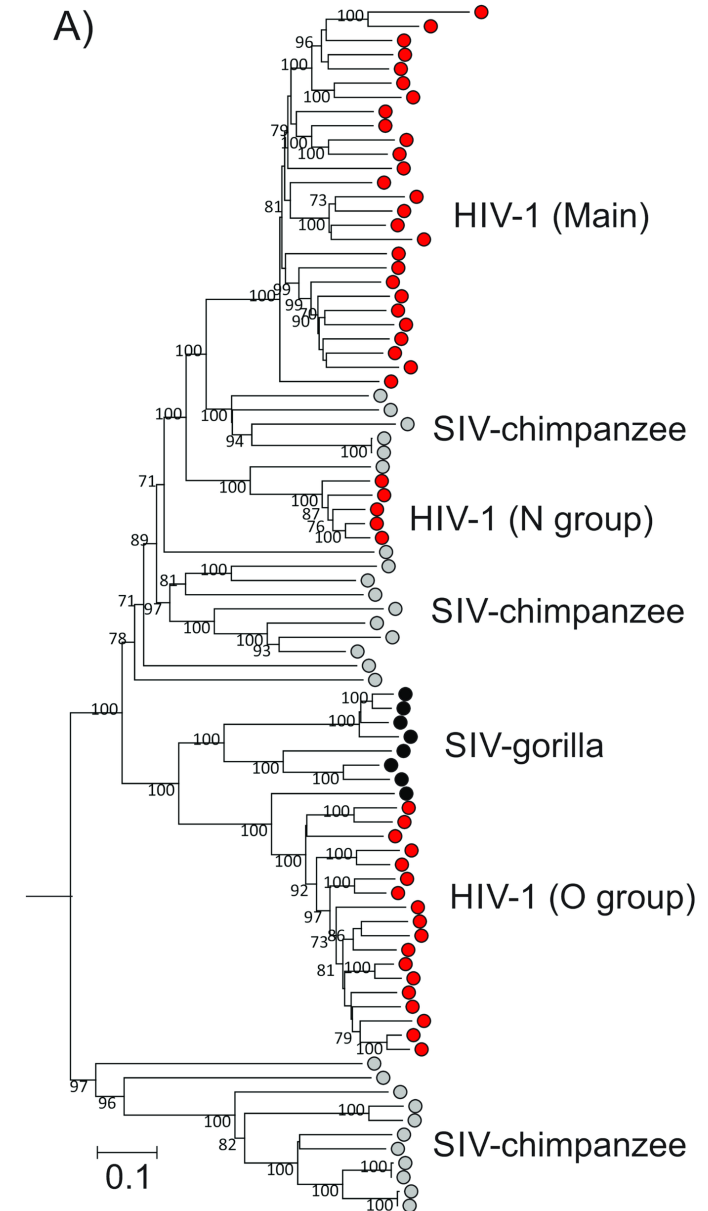
Poliovirus type 2 – *Enterovirus coxsackiepol*

Poliovirus type 3

Enterovirus C111

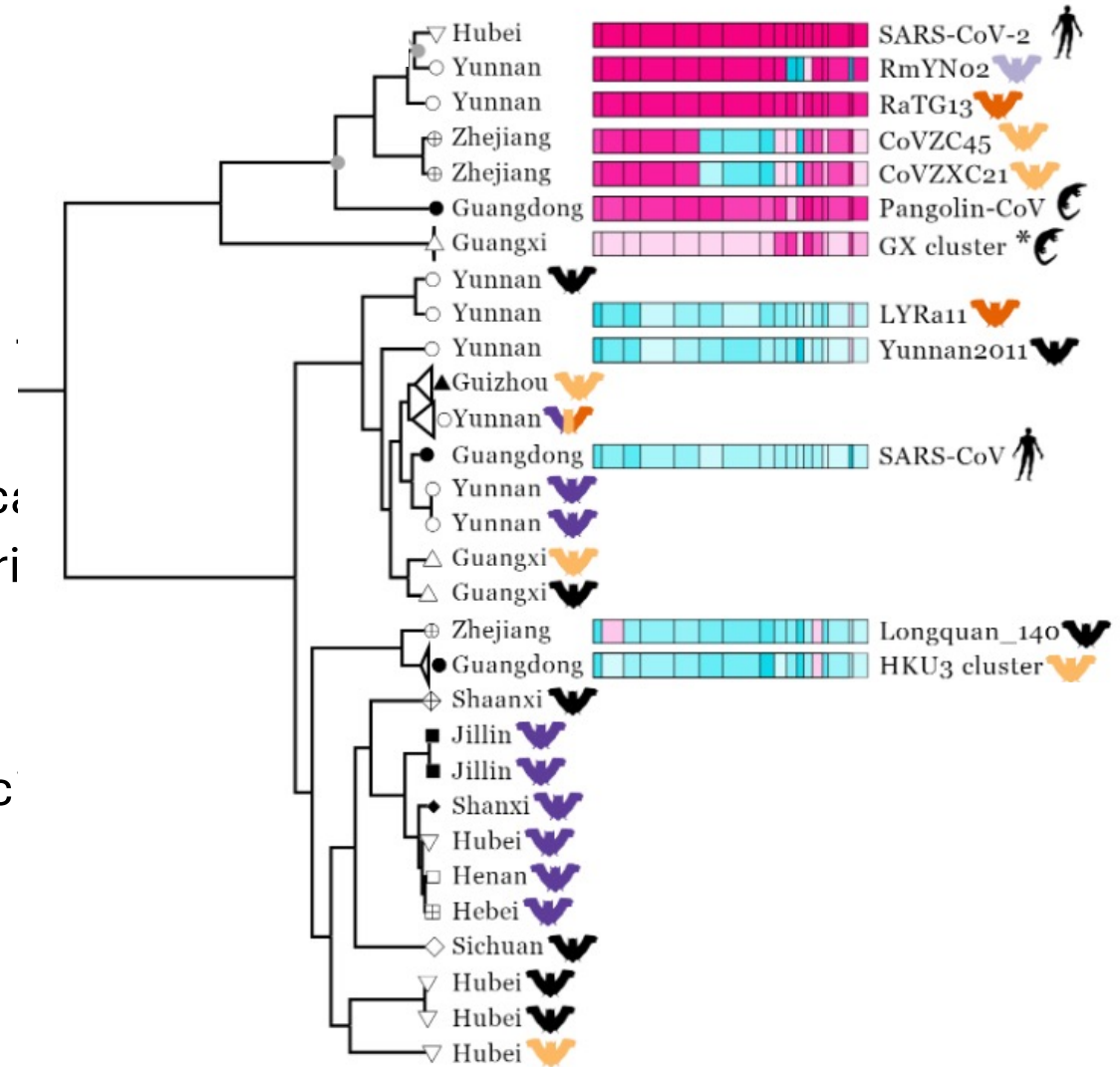
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- A recently zoonotic virus
 - Often clinically distinctive and important
 - Minimally different genetically from its animal source



Taxonomy is only one way to classify viruses

- HIV-1 and HIV-2
 - Obvious clinical and regulatory (eg. biocontainment) importance of the term HIV-1
 - Can't be represented as a species or below-species group
- SARS-CoV-2 and SARS-CoV
 - Lineages within a large clade of bat-infecting sarbecoviruses, collectively assigned to the species *Betacoronavirus pandemicum*

• Baltimore classification

- Classifies viruses by replication mechanism and genome properties
- Entirely incompatible with evolutionary origins and realm taxon assignments

I *Adnaviria, Duplodnaviria, Varidnaviria, Monodnaviria*

II *Monodnaviria*

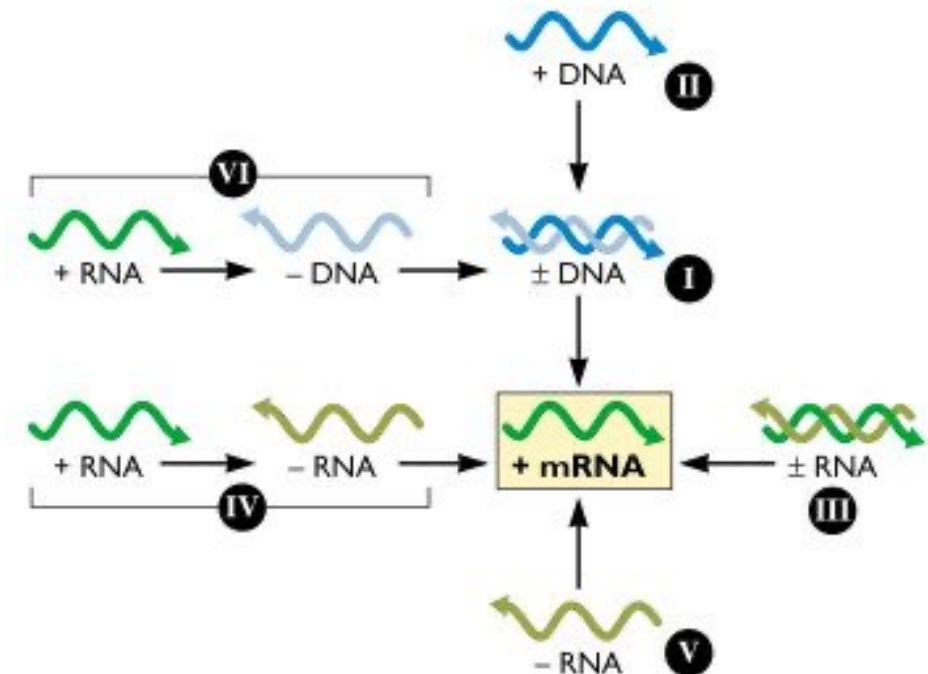
III *Riboviria*

IV *Riboviria*

V *Riboviria*

VI *Riboviria*

? *Ribozyviria*



Subspecies and other below-species classification

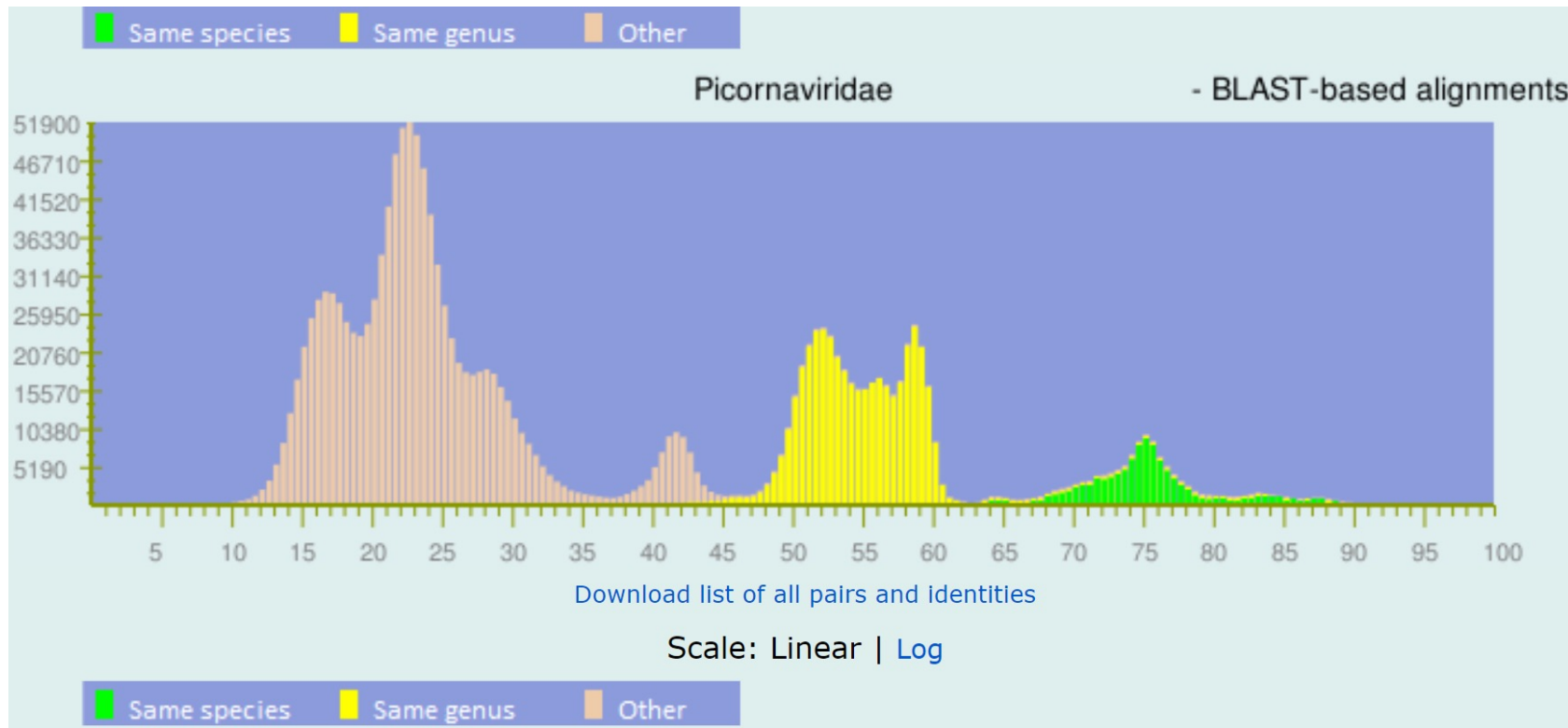
- All biological codes have one or more, optional below-species ranks
 - Zoological classification allows Latinised trinomials
 - Common and West African Chimpanzees: *Pan troglodytes troglodytes*, *P. t. verus*
 - More flexible and extensive in botany, with additional categories such as varieties
 - Subspecies: *Poa secunda* subsp. *juncifolia*
 - Varieties *Acanthocalycium klimpelianum* var. *macranthum*
 - Cultivars *Pinus nigra* 'Arnold Sentinel'
 - Two lower ranks *P. edulis* f. *flavicarpa* 'FB200'
 - Assignments are made independently of the biological species principle (but grey areas)
- The ICTV does not classify virus below the species rank
 - Assignments are formally unrecorded by the ICTV
 - Consensus on definitions, nomenclature made in the wider virology community
 - Establishing a consensus in the community and disseminating information
 - Many conflicting and outdated classification schemes

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 - **Arbitrariness of the species level assignment level**

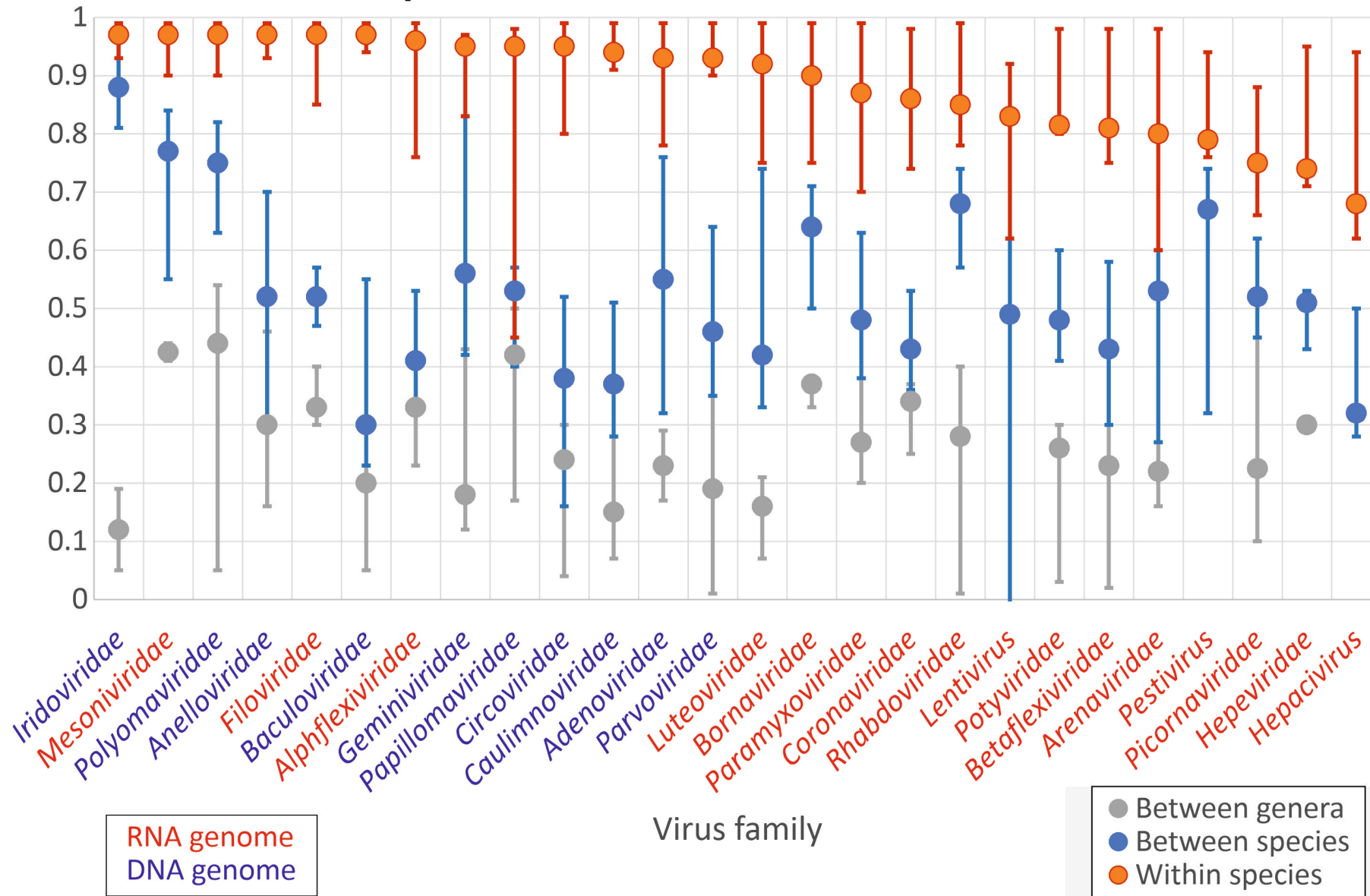
Genetic correlates of species-level classification

- When in Rome.....
 - PASC* – Pairwise similarity comparisons
 - Systematic calculation of pairwise distances between species and genera



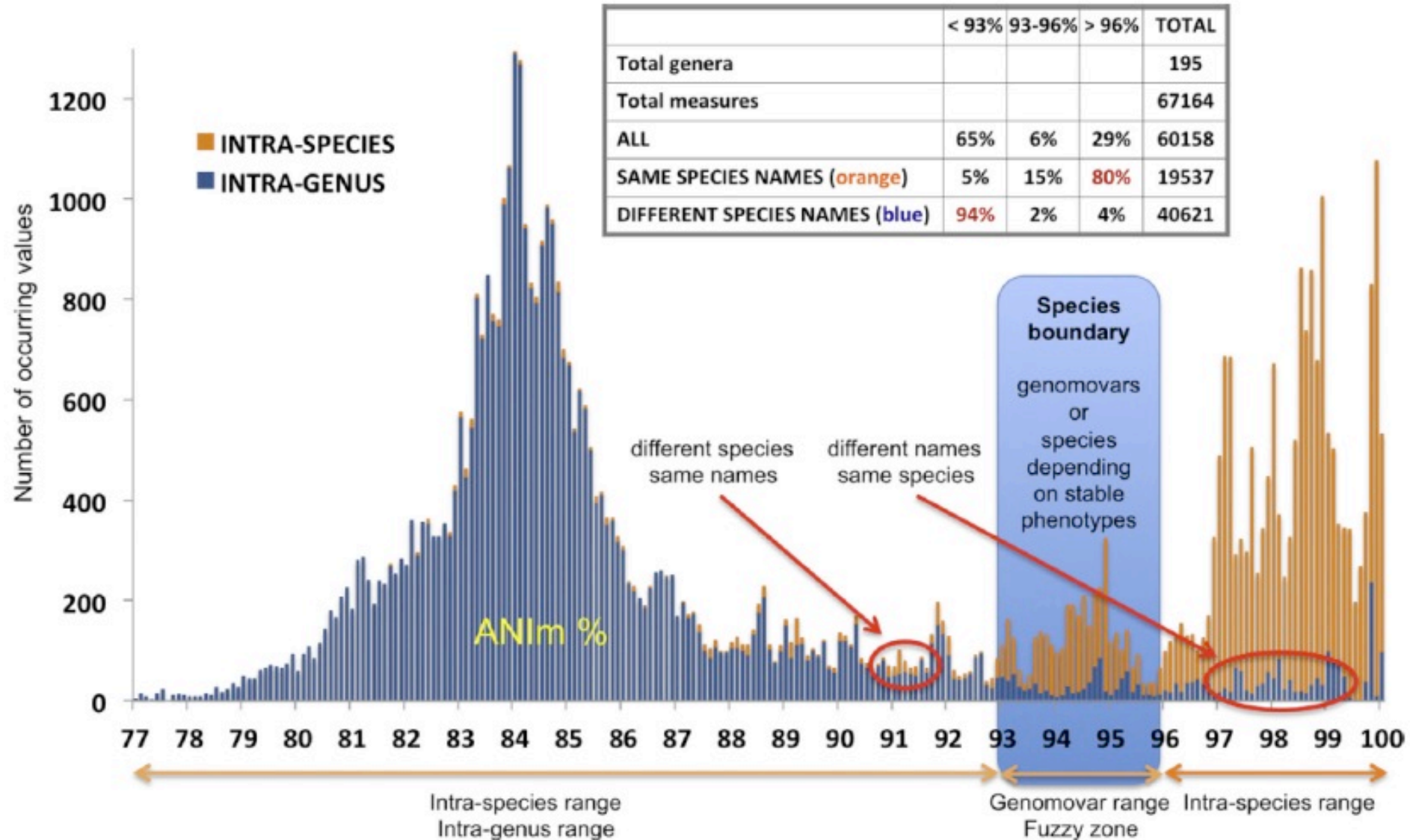
*Bao Y, Chetvernin V, Tatusova T. [Improvements to pairwise sequence comparison \(PASC\): a genome-based web tool for virus classification.](#) Arch Virol. 2014 Dec;159(12):3293-3304. doi:10.1007/s00705-014-2197-x

Pairwise similarity ranges of species and genus ranks in representative virus families



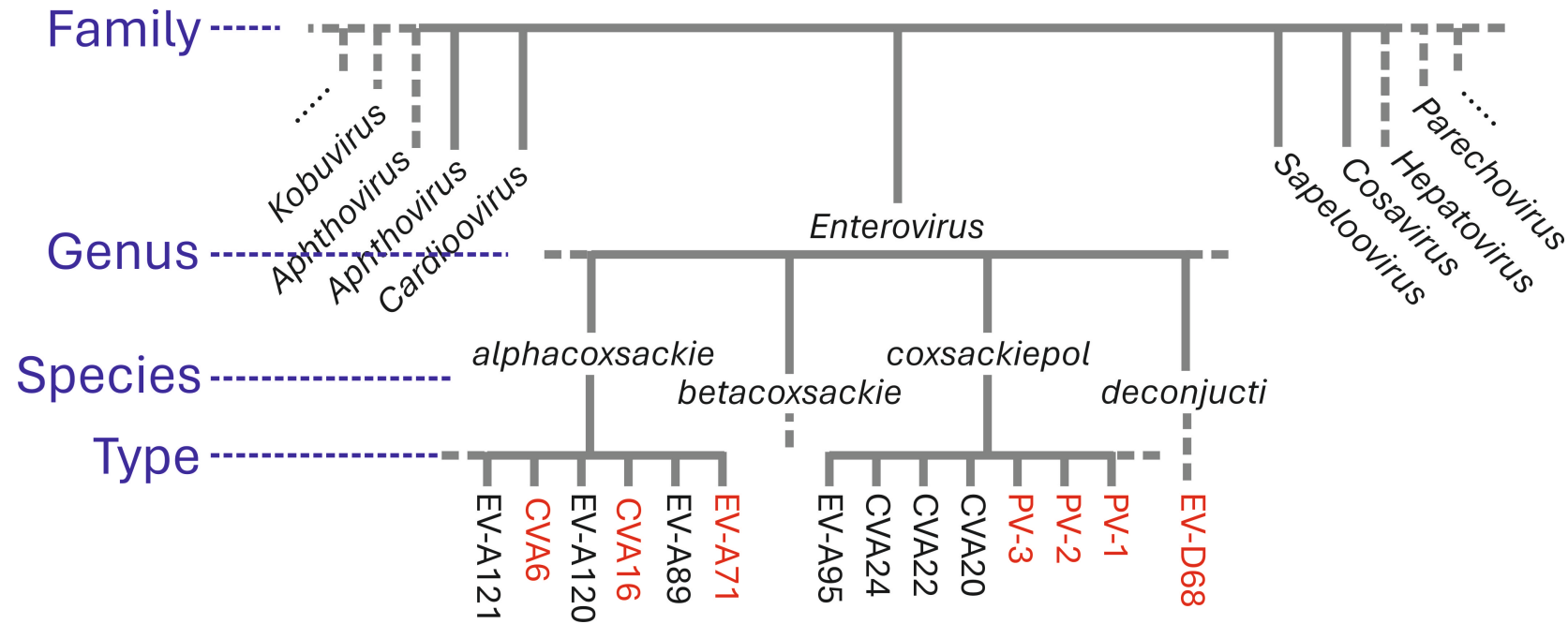
Better defined thresholds for bacterial species

R. Rosselló-Móra, R. Amann / *Systematic and Applied Microbiology* 38 (2015) 209–216

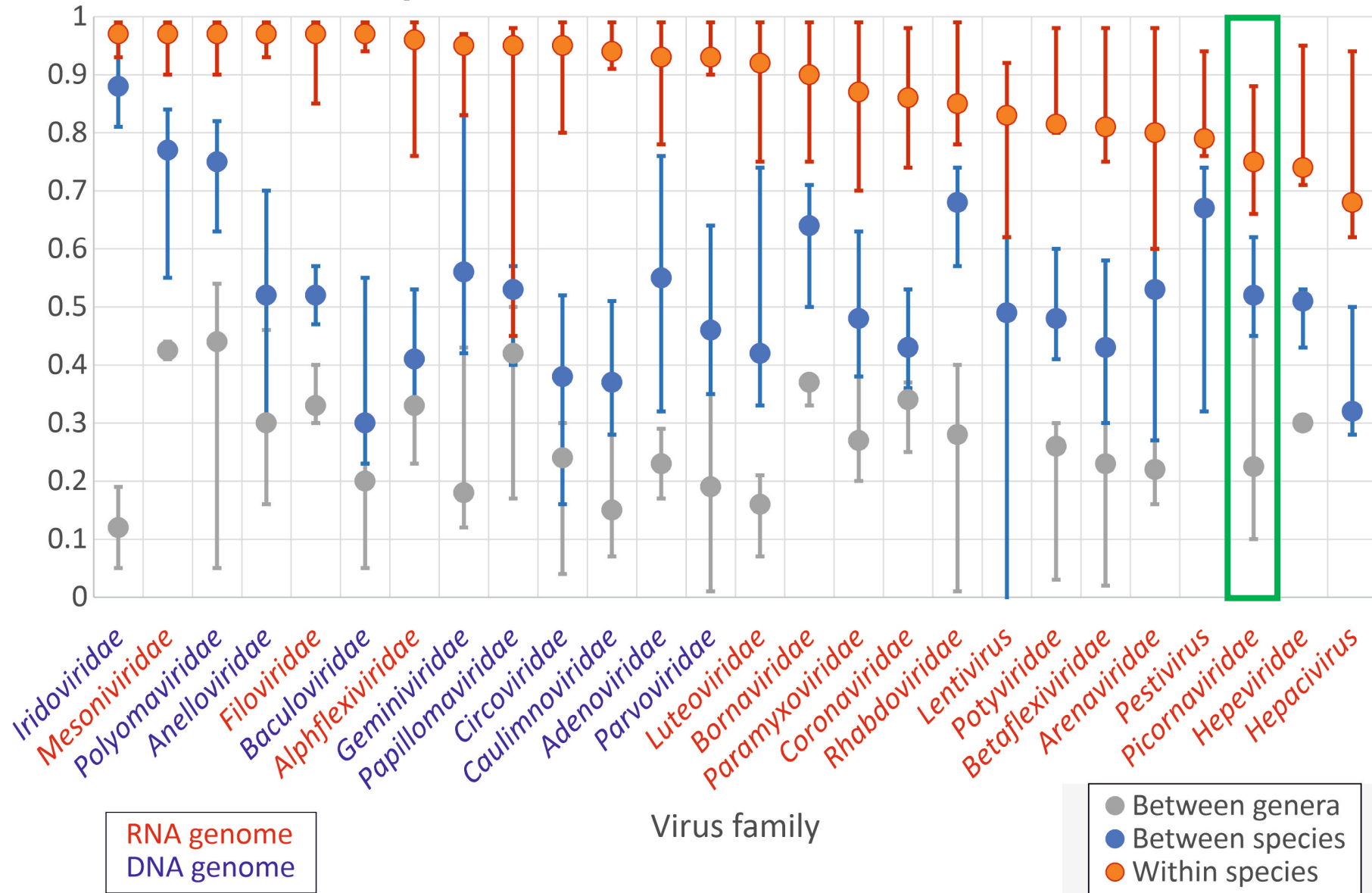


Consequences of the species level demarcation

- No defined level of genetic divergence that might define species and below-species classification levels
 - Within-species divergence of hepaciviruses is less than between-species divergence of *Iridoviridae*, *Mesoniviridae*, *Polyomaviridae* and *Rhabdoviridae*
 - Reflects historical frameworks for defining and identifying species based on distinguishable disease phenotypes
- The ICTV has no formal role in the definition of nomenclature of viruses below the species level, despite its arbitrariness

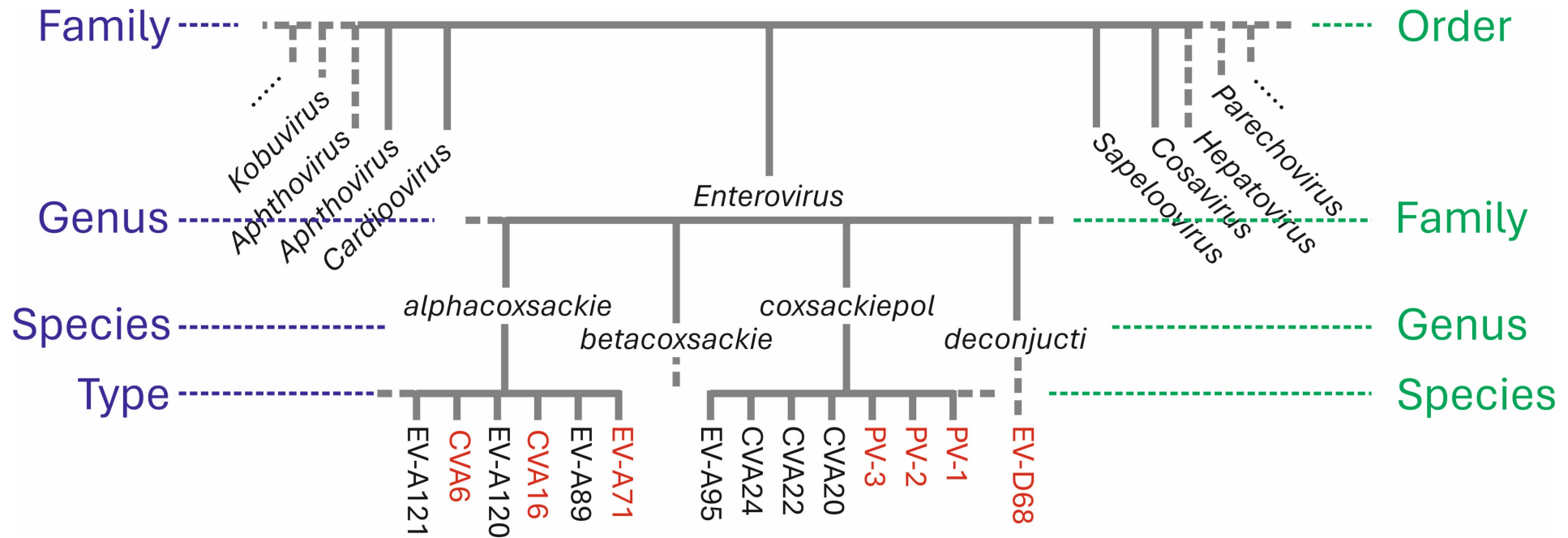


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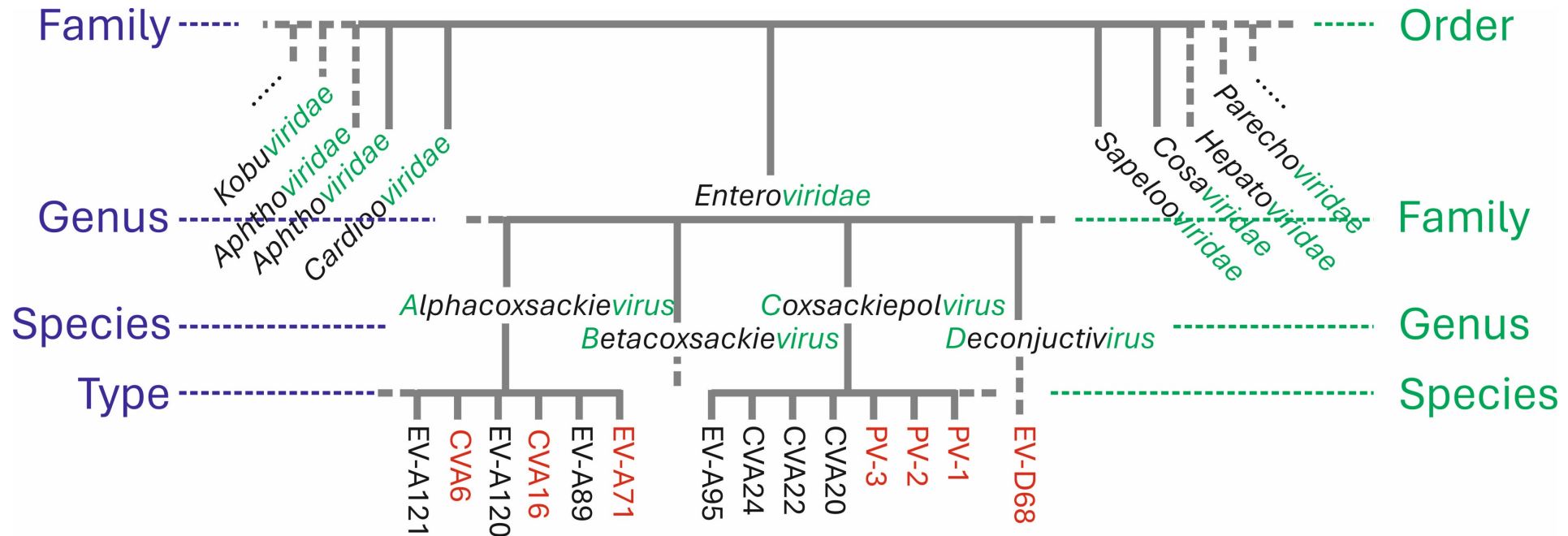
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A UK Regulatory Document



The Approved List of biological agents

Advisory Committee on Dangerous Pathogens



Family Picornaviridae		
Order Picornvirales		
Genus <i>Cardiovirus</i>		
Cardiovirus B (Saffold virus)	2	
Genus <i>Cosavirus</i>		
Cosavirus A	2	
Genus <i>Enterovirus</i>		
Enterovirus D, Human Enterovirus type 70	2	Synonyms: Coxsackievirus CA24 (A24); Enterovirus 70
Human Enterovirus A also known as Coxsackieviruses (A)	2	
Enterovirus B (which includes the sub-species Echoviruses and the coxsackieviruses)	2	
Human enterovirus C type 1 (also known as Poliovirus)	2	Poliovirus Vaccine available
Human enterovirus C type 2 (also known as Poliovirus)	3	
Human enterovirus C type 3 (also known as Poliovirus)	2	

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Genus Cardiovirus		
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Human enterovirus C type 1 (also known as Poliovirus)	2	Poliovirus Vaccine available
Human enterovirus C type 2 (also known as Poliovirus)	3	
Human enterovirus C type 3 (also known as Poliovirus)	2	

Enterovirus A

Child level

EV-A seqs
EV-A71

Same level

Home
Up

Enterovirus A

Enterovirus B

Enterovirus C

Enterovirus D

Enterovirus E

Enterovirus F

Enterovirus G

Enterovirus H

Enterovirus I

Enterovirus J

Enterovirus K

Enterovirus L

Rhinovirus A

Rhinovirus B

Rhinovirus C

Unassigned EV

Prototype strains

HFMD

EV refs

Genera

Aalivirus

Ampivirus

Aphthovirus

Aquavirus

Avihepatovirus

Avisivirus

Bopivirus

Cardiovirus

Cosavirus

Crohivirus

Dicipivirus

The species **Enterovirus A** (formerly named *Human enterovirus A*) consists of 25 (sero)types: coxsackievirus A2 (CVA2), CVA3, CVA4, CVA5, CVA6, CVA7, CVA8, CVA10, CVA12, CVA14, CVA16, enterovirus A71 (EV-A71), EV-A76, EV-A89, EV-A90, EV-A91, EV-A92, EV-A114, EV-A119, EV-A120, EV-A121, EV-A122 (formerly SV19), EV-A123 (formerly SV43), EV-A124 (formerly SV46) and EV-125 (formerly BA13).

Serotype	Prototype strain	Accession no.	Known hosts*	Sequence reference
CVA2	Fleetwood	AY421760	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2004
CVA3	Olson	AY421761	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2004
CVA4	High Point	AY421762	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2004
CVA5	Swartz	AY421763	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2004
CVA6	Gdula	AY421764	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2004
CVA7	Parker	AY421765	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2004
CVA8	Donovan	AY421766	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2004
CVA10	Kowalik	AY421767	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2004
CVA12	Texas-12	AY421768	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2004
CVA14	G-14	AY421769	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2004
CVA16	G-10	U05876	<i>Homo sapiens</i>	Poyry <i>et al.</i> , 1994
EV-A71	BrCr	U22521	<i>Homo sapiens</i>	Brown & Pallansch, 1995
EV-A76	FRA91-10369	AY697458	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2005a
EV-A89	BAN00-10359	AY697459	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2005a
EV-A90	BAN99-10399	AY697460	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2005a
EV-A91	BAN00-10406	AY697461	<i>Homo sapiens</i>	Oberste <i>et al.</i> , 2005a
EV-A92	USA/GA99-RJg-7	EF667344	<i>Macaca mulatta</i> ; <i>Macaca nemestrina</i> ; <i>Cercocebus atys</i>	Oberste <i>et al.</i> , 2008
EV-A114	V13-0285/IND/2013	KU355876	<i>Homo sapiens</i>	Deshpande <i>et al.</i> , 2016
EV-A119	hu/09C13CMR	KC787153	<i>Homo sapiens</i> ; <i>Gorilla gorilla</i> ; <i>Pan troglodytes</i>	Ayukekbong <i>et al.</i> , 2013
EV-A120	MAD-2741-11	LK021688	<i>Homo sapiens</i>	Razafindratsimandresy <i>et al.</i> , 2014
EV-A121	V13-0682/IND/2013	KU355877	<i>Homo sapiens</i>	Deshpande <i>et al.</i> , 2016
EV-A122	SV19-M19s	AF326754	<i>Macaca fascicularis</i> ; <i>Macaca mulatta</i> ; <i>Macaca nemestrina</i>	Oberste <i>et al.</i> , 2007
EV-A123	SV43-OM112t	AF326761	<i>Macaca fascicularis</i>	Oberste <i>et al.</i> , 2007
EV-A124	SV46-OM22	AF326764	<i>Macaca mulatta</i> ; <i>Macaca nemestrina</i>	Oberste <i>et al.</i> , 2007
EV-A125	BA13	AF326750	<i>Papio cynocephalus</i>	Oberste <i>et al.</i> , 2007

*, *Gorilla gorilla*, gorilla; *Pan troglodytes*, chimpanzee; *Homo sapiens*, man; *Macaca mulatta*, rhesus macaque; *Macaca nemestrina*, pigtail macaque; *Macaca fascicularis*, long tailed or crab eating macaque; *Cercocebus atys*, sooty mangabey; *Papio cynocephalus*, yellow baboon.

Download all of the above publically available sequences (EMBL: [ascii](#); [fasta](#))

Enterovirus A receptors

Nishimura, Y. and Shimizu, H. (2012). Cellular receptors for human enterovirus species A. *Front. Microbiol.* 3:105. Epub 2012 Mar 27.

Is there a case for below-species taxa of viruses?

- Can existing classifications be adopted as the basis for taxon names?
- Use the flexibility of ICBN code (or an approximation) that uses designators
 - Enterovirus coxsackiopol* type 'poliovirus 2'
 - Orthobunyavirus bunyamweraense* ssp. 'Bunyamwera virus'
 - Betacoronavirus pandemicum* isolate 'SARS Coronavirus 2'
- Assignments would be based on stakeholder need
- Provides the authority and permanence of an established taxonomic framework
 - Established through community-based taxonomy proposals
 - Formal and coordinated oversight and standardisation of criteria and nomenclature
 - Recording in the Master Species List
 - Information provided in standardised form to INSDC databases
- Publication record, attribution and access to taxonomy additions and changes

Summary and questions

- A virus taxonomy serves a very wide community of scientists, clinician and regulators
- A taxonomy based on evolutionary relationships cannot reproduce all categories needed for clinical and regulatory purposes
 - The classification may be below the species level
 - The category may not be monophyletic or defined without reference to genomic relatedness
- The lack of a subspecies rank is one of several exceptions in virus taxonomy compared to the three other codes
- There is a degree of arbitrariness in where the species level is set in terms of sequence identities and biological properties
- There should be a re-examination of whether this could be reviewed with options to:
 - Re-classify species more consistently at a genomic level (95% ANI?) – this would be difficult for the virus community and may cut across useful categories
 - Extend taxonomy below species where required and justified – relatively straightforward