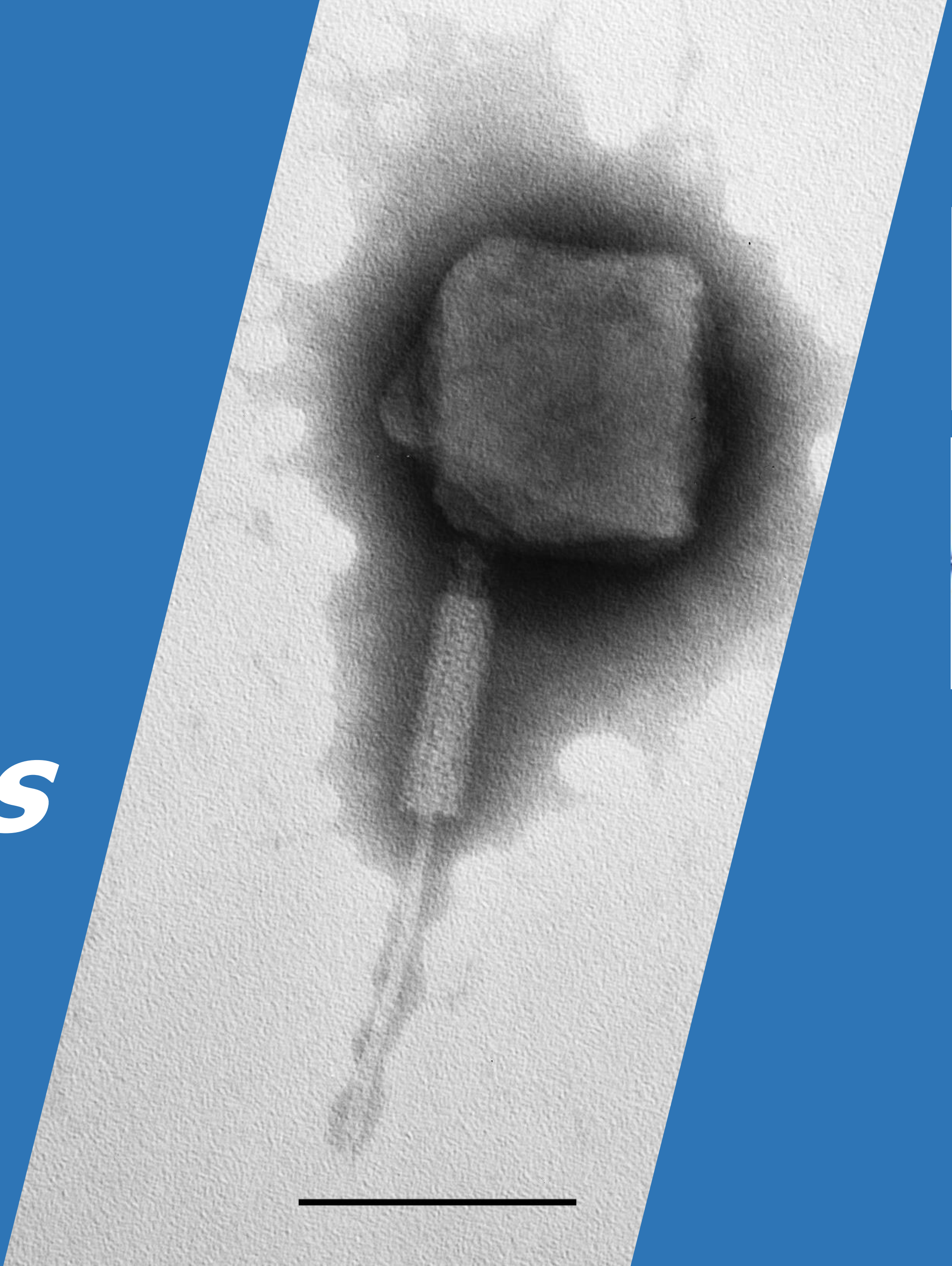
Classification of bacterial viruses in the class *Caudoviricetes*



Evelien Adriaenssens

Dann Turner

Introduction

- Classification of bacterial viruses is overseen of the ICTV Bacterial Viruses Subcommittee
- Major changes in 2021
  - Abolishment of the *Caudovirales* and the morphological families *Myoviridae*, *Siphoviridae* and *Podoviridae*
- Establishment of guidelines for genome-based classification
- New tools available to support classification, e.g.
  - INPHARED
  - GRAViTy
  - vConTACT2
  - virCLUST

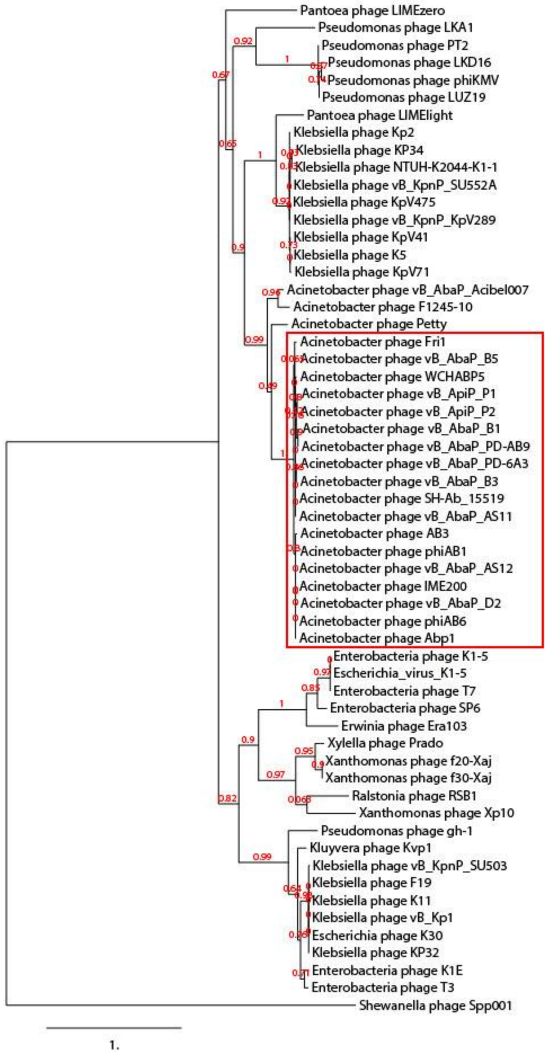
Classification Criteria

- **Species**
  - <95% sequence similarity
- **Genus**
  - >70% sequence similarity
  - Pangenome analysis for conserved ‘signature’ genes
- **Subfamily**
  - Relationships between discrete genera
  - Form clade in marker tree ML phylogeny

Nucleotide BLAST
nucleotide ▶ nucleotide

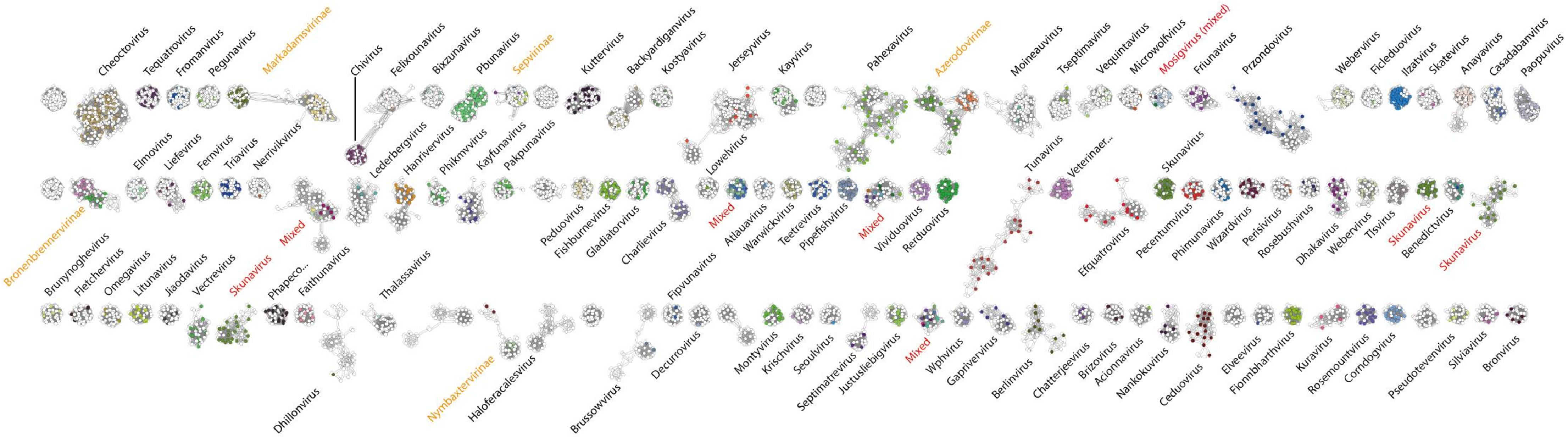
VIRIDIC **VICTOR** **ViPTree** **PHROGs**

Roary **ProteinOrtho** **vConTACT2** **GRAVITY**



Genus level classification

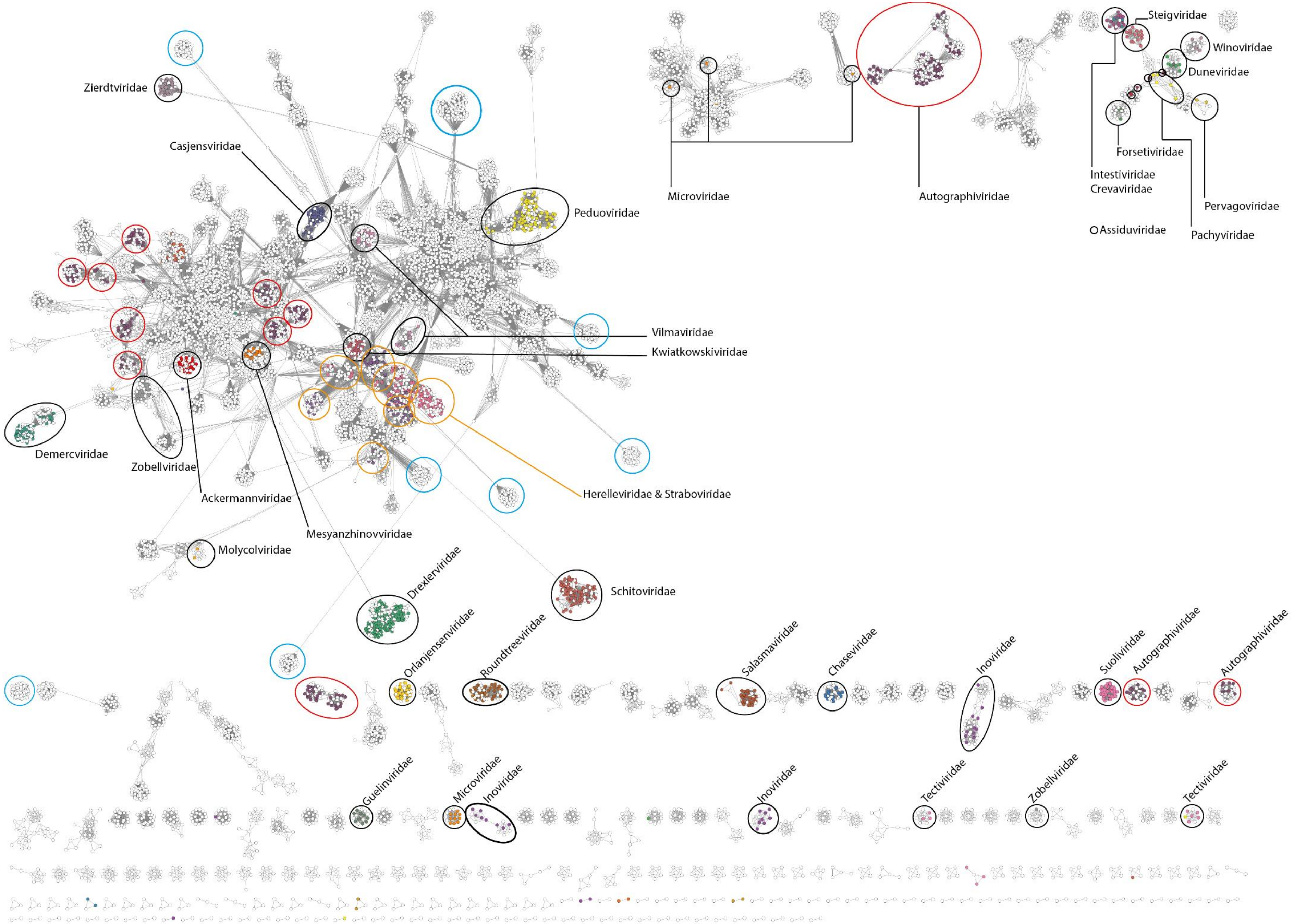
- **MASH** network analysis may allow for rapid delineation of genera, species and strains
- Ideally requires verification using a second method (e.g. **VIRIDIC**)



Partial network of bacterial viruses generated using an all-versus-all MASH analysis and visualised using Cytoscape. The clusters are *generally* concordant with genus and subfamily level assignments. (Unpublished)

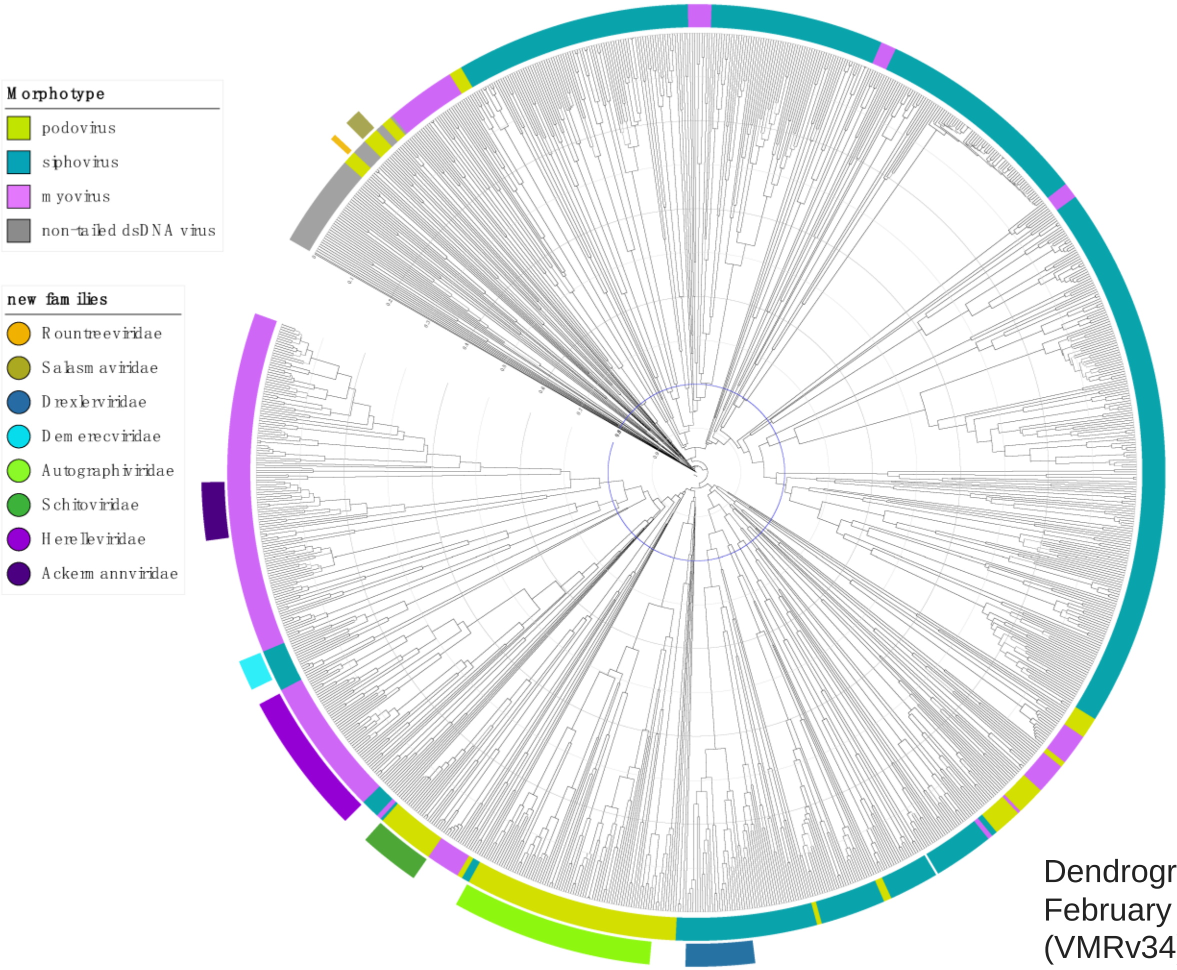
Family Level Classifcation: Global Views

- **Families** need to be cohesive and monophyletic
- Should share a significant number (how many?) of orthologous genes
- **Two** main tools available: **GRAViTy** and **vConTACT2**
- **vConTACT2** combined with the **INPHARED** pipeline
- Scripts available to map ICTV VMR data to resultant network
- A wish list:
  - Integration of nucleotide sequence similarity
  - Hierarchical clustering output of nearest neighbours based on PC content to a query genome
  - A measure of synteny



Network analysis produced using vCONTact2 with input genomes from the INPHARED pipeline (March 2022 release) and mapped against family level taxonomy of bacterial viruses. (Unpublished)

GRAViTy



- Measures of shared protein content and genome organisation
- Another wish list…
  - More frequent updates to reference database
  - Address barriers to local implementation
  - Scaling for large datasets
  - HMM recalculations

Dendrogram generated by GRAViTy (**http://gravity.cvr.gla.ac.uk**, accessed on 5 February 2021) for DB-B: Baltimore Group Ib—Prokaryotic and archaeal dsDNA viruses (VMRv34) and annotated using iTOL

Current Issues

- Classification lags significantly behind current INSDC releases
  - c. 7,000 bacterial viruses classified by BVS
  - c. 20,000 genomes in GenBank (March 2021)
- Recombination/HGT?
  - Not an evident problem for strictly lytic bacterial viruses
  - More apparent as a confounding factor for temperate viruses
- Metagenomic studies
  - How to cope with the increases in metagenome-derived information?
- A global view
  - How to assess congruity between different methods
  - Maintaining and updating source databases for bioinformatics tools

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Questions