

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create a new family, *Hirszfeldviridae*, with 22 genera, *Nosocomialisvirus, Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, Scipiovirus,* *Wenzhouvirus*, *Burnvirus*, *Ankaravirus*, *Polandvirus*, *Kenyavirus*, *Cairovirus*, *Helsinkivirus*, *Sichuanvirus*, *Pakistanvirus*, *Catovirus*, and *Theraphagusvirus,* for a group of *Acinetobacter-*specific phages (class *Caudoviricetes*) |
| **Code assigned:** | 2025.054B.Uc.v3.Hirszfeldviridae\_1nf\_21ng\_1mg\_5mrs\_46ns | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corresponding author(s)** |
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**Part 1b: Taxonomy Proposal Submission**

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| **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 |  |

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

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** | 20/06/2025 |

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

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| **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 |  |

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| **Comments from the Executive Committee:** |
| Some of the proposed species fall below 70% genus demarcation criteria. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
| All issues have been corrected in accordance with the suggestions. |

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| **Revision date:** | 23/10/2025 |

**Part 3:** **TAXONOMIC PROPOSAL**

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

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *Hirszfeldviridae* | Family name created in honor of Prof. Ludwik Hirszfeld (b. 1884, d. 1954) – Polish physician, bacteriologist, and immunologist, the founder of the Polish School of Immunology and a new scientific discipline – seroanthropology. In 1952, he established the Institute of Immunology and Experimental Therapy of the Polish Academy of Sciences in Wrocław, where the Department of Phage Therapy and the Phage Therapy Unit are located. |
| *Nosocomialisvirus* | Genus name derived from *Acinetobacter nosocomialis* – the host for Acinetobacter phage XC1 – one of the representatives of this genus. |
| *Nosocomialisvirus XC1* | Species name derived from the phage name in the GenBank database – Acinetobacter phage XC1. |
| *Nosocomialisvirus QH4* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_Aba\_QH4. |
| *Beijingvirus* | Genus name derived from Beijing – the capital city of China, where the Acinetobacter phage vB\_AbaM\_IME284, the only representative of this genus, was isolated. |
| *Beijingvirus IME284* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbaM\_IME284. |
| *Guangzhouvirus* | Genus name derived from Guangzhou – the capital and largest city of the Guangdong province in southern China, where the Acinetobacter phage vB\_AbaM\_AB3P2, the only representative of this genus, was isolated. |
| *Guangzhouvirus AB3P2* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbaM\_AB3P2. |
| *Chinavirus* | Genus name derived from China, where the Acinetobacter phage BUCT628, the only representative of this genus, was isolated. |
| *Chinavirus BUCT628* | Species name derived from the phage name in the GenBank database – Acinetobacter phage BUCT628. |
| *Pittiivirus* | Genus name derived from *Acinetobacter pittii* – the host for Acinetobacter phage vB\_ApiM\_IME-Ap7 – one of the representatives of this genus. |
| *Pittiivirus IMEAp7* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_ApiM\_IME-Ap7. |
| *Obolenskvirus A8321* | Species name derived from the phage name in the GenBank database – Acinetobacter phage A832.1. |
| *Obolenskvirus R2919* | Species name derived from the phage name in the GenBank database – Acinetobacter phage Bphi-R2919. |
| *Obolenskvirus R1888* | Species name derived from the phage name in the GenBank database – Acinetobacter phage Bphi-R1888. |
| *Obolenskvirus IME285* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbaM\_IME285. |
| *Ganjingzivirus* | Genus name derived from Ganjingzi – one of the seven districts of Dalian, Liaoning province (China), where the Acinetobacter phage vB\_AbaM\_BP10, the only representative of this genus, was isolated. |
| *Ganjingzivirus BP10* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbaM\_BP10. |
| *Guizhouvirus* | Genus name derived from Guizhou – an inland province in Southwestern China, where the Acinetobacter phage Abp95, the only representative of this genus, was isolated. |
| *Guizhouvirus Abp95* | Species name derived from the phage name in the GenBank database – Acinetobacter phage Abp95. |
| *Brutusvirus* | Genus name derived from Acinetobacter phage Brutus, the only representative of this genus. |
| *Brutusvirus Brutus* | Species name derived from the phage name in the GenBank database – Acinetobacter phage Brutus. |
| *Walailakvirus* | Genus name derived from Walailak University (Thailand), where the Acinetobacter phage vB\_AbM\_WUPSU, the only representative of this genus, was isolated. |
| *Walailakvirus WUPSU* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbM\_WUPSU. |
| *Scipiovirus* | Genus name derived from Acinetobacter phage Scipio, the only representative of this genus. |
| *Scipiovirus Scipio* | Species name derived from the phage name in the GenBank database – Acinetobacter phage Scipio. |
| *Wenzhouvirus* | Genus name derived from the Institute of Biomedical Informatics/Zhejiang Provincial Key Laboratory of Medical Genetics, Wenzhou Medical College, where the Acinetobacter phage AB1, the one of representatives of this genus, was isolated. |
| *Wenzhouvirus AB1* | Species name derived from the phage name in the GenBank database – Acinetobacter phage AB1 (move from *Obolenskvirus* genus and rename to new genus). |
| *Wenzhouvirus Acb75* | Species name derived from the phage name in the GenBank database – Acinetobacter phage VB\_AB\_Acb75. |
| *Burnvirus* | Genus name derived from the Southwest Hospital, Third Military Medical University, Institute of Burn Research, where the Acinetobacter phage AbP2, the one of representatives of this genus, was isolated. |
| *Burnvirus AbP2* | Species name derived from the phage name in the GenBank database – Acinetobacter phage AbP2 (move from *Obolenskvirus* genus and rename to new genus). |
| *Burnvirus P1068* | Species name derived from the phage name in the GenBank database – Acinetobacter phage P1068. |
| *Burnvirus Arbor* | Species name derived from the phage name in the GenBank database – Acinetobacter phage Arbor. |
| *Burnvirus MRABphi22* | Species name derived from the phage name in the GenBank database – Acinetobacter phage MRABphi22. |
| *Burnvirus Aba01* | Species name derived from the phage name in the GenBank database – Acinetobacter phage HN\_Aba\_01. |
| *Burnvirus A72* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbaM\_A72. |
| *Burnvirus HZY2308* | Species name derived from the phage name in the GenBank database – Acinetobacter phage HZY2308. |
| *Burnvirus phi1092006* | Species name derived from the phage name in the GenBank database – Acinetobacter phage phi1\_092006. |
| *Burnvirus BUCT629* | Species name derived from the phage name in the GenBank database – Acinetobacter phage BUCT629. |
| *Burnvirus NJ02* | Species name derived from the phage name in the GenBank database – Acinetobacter phage NJ02. |
| *Burnvirus IME512* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbaM\_IME512. |
| *Ankaravirus* | Genus name derived from Ankara - the capital city of Turkey, where the Acinetobacter phage Ab69, the only representative of this genus, was isolated. |
| *Ankaravirus Ab69* | Species name derived from the phage name in the GenBank database – Acinetobacter phage Ab69. |
| *Polandvirus* | Genus name derived from Poland, where the Acinetobacter phage Acba\_21, the one of representatives of this genus, was isolated. |
| *Polandvirus Acba21* | Species name derived from the phage name in the GenBank database – Acinetobacter phage Acba\_21. |
| *Polandvirus YNAF* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbaM\_YNAF. |
| *Kenyavirus* | Genus name derived from Kenya, where the Acinetobacter phage vB\_Ab\_01\_KEN\_01, the only representative of this genus, was isolated. |
| *Kenyavirus 01KEN01* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_Ab\_01\_KEN\_01. |
| *Cairovirus* | Genus name derived from Cairo - the capital city of Egypt, where the Acinetobacter phage RM\_A1 and Acinetobacter phage RM\_A2, the representative of this genus, were isolated. |
| *Cairovirus RMA1* | Species name derived from the phage name in the GenBank database – Acinetobacter phage RM\_A1. |
| *Cairovirus RMA2* | Species name derived from the phage name in the GenBank database – Acinetobacter phage RM\_A2. |
| *Helsinkivirus* | Genus name derived from Helsinki - the capital city of Finland, where the Acinetobacter phage vB\_AbaM\_fThrA, the one of representatives of this genus, was isolated. |
| *Helsinkivirus fThrA* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbaM\_fThrA. |
| *Helsinkivirus AQ1* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AQ1. |
| *Sichuanvirus* | Genus name derived from the Center of Infectious Diseases, West China Hospital, Sichuan University, where the Acinetobacter phage WCHABP1, the one of representatives of this genus, was isolated. |
| *Sichuanvirus WCHABP1* | Species name derived from the phage name in the GenBank database – Acinetobacter phage WCHABP1 (move from *Obolenskvirus* genus and rename to new genus). |
| *Sichuanvirus WCHABP12* | Species name derived from the phage name in the GenBank database – Acinetobacter phage WCHABP12 (move from *Obolenskvirus* genus and rename to new genus). |
| *Sichuanvirus ZC3* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_Aba\_ZC3. |
| *Sichuanvirus 02KEN02* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_Ab\_02\_KEN\_02. |
| *Sichuanvirus SPA* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbaM-SPA. |
| *Sichuanvirus Abp9* | Species name derived from the phage name in the GenBank database – Acinetobacter phage Abp9. |
| *Pakistanvirus* | Genus name derived from Pakistan, where the Acinetobacter phage SR, the only representative of this genus, was isolated. |
| *Pakistanvirus SR* | Species name derived from the phage name in the GenBank database – Acinetobacter phage SR. |
| *Catovirus* | Genus name derived from Acinetobacter phage Cato, the only representative of this genus. |
| *Catovirus Cato* | Species name derived from the phage name in the GenBank database – Acinetobacter phage Cato. |
| *Theraphagusvirus* | Genus name derived from the Greek: *therapeia*, meaning therapy, and *phagus*, meaning the one who eats (eater). |
| *Theraphagusvirus AP22* | Species name derived from the phage name in the GenBank database – Acinetobacter phage AP22 (move from *Obolenskvirus* genus and rename to new genus). |
| *Theraphagusvirus SPB* | Species name derived from the phage name in the GenBank database – Acinetobacter phage vB\_AbaM-SPB. |

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| **Permission for use of names derived from a living person** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Family, genus, species  *Description of current taxonomy*:  According to the current taxonomy, the *Obolenskvirus* genus has been classified within the class *Caudoviricetes* without assignment to a family rank. Currently, the *Obolenskvirus* genus includes eight species: *Obolenskvirus AB1*, *Obolenskvirus AB2*, *Obolenskvirus AbC62*, *Obolenskvirus AbP2*, *Obolenskvirus AP22*, *Obolenskvirus LZ35*, *Obolenskvirus WCHABP1*, and *Obolenskvirus WCHABP12.*  *Proposed* *taxonomic change(s):*  Create a new family, *Hirszfeldviridae*, with 22 genera, *Nosocomialisvirus, Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, Scipiovirus,*  *Wenzhouvirus*, *Burnvirus*, *Ankaravirus*, *Polandvirus*, *Kenyavirus*, *Cairovirus*, *Helsinkivirus*, *Sichuanvirus*, *Pakistanvirus*, *Catovirus*, and *Theraphagusvirus,* for a group of *Acinetobacter-*specific phages.  We performed a genomic analysis of several *Acinetobacter*-specific phages deposited in the NCBI database, all of which have been classified within the genus *Obolenskvirus*. Based on our analysis, we propose the creation of a new family for these phages along with 22 distinct genera.   1. To create a new family, *Hirszfeldviridae*, with 22 genera. 2. To create a new genus, *Nosocomialisvirus*, with two species. 3. To create a new single species genus, *Beijingvirus*. 4. To create a new single species genus, *Guangzhouvirus*. 5. To create a new single species genus, *Chinavirus*. 6. To create a new single species genus, *Pittiivirus*. 7. To move the genus *Obolenskvirus* to new family, *Hirszfeldviridae*. 8. To create four new species in genus *Obolenskvirus*. 9. To create a new single species genus, *Ganjingzivirus*. 10. To create a new single species genus, *Guizhouvirus*. 11. To create a new single species genus, *Brutusvirus*. 12. To create a new single species genus, *Walailakvirus*. 13. To create a new single species genus, *Scipiovirus*. 14. To move *Obolenskvirus AB1* from *Obolenskvirus* genus and rename to new *Wenzhouvirus* genus with two species. 15. To move *Obolenskvirus AbP2* from *Obolenskvirus* genus and rename to new *Burnvirus* genus with 11 species. 16. To create a new single species genus, *Ankaravirus*. 17. To create a new genus, *Polandvirus*, with two species. 18. To create a new single species genus, *Kenyavirus*. 19. To create a new genus, *Cairovirus*, with two species. 20. To create a new genus, *Helsinkivirus*, with two species. 21. To move *Obolenskvirus WCHABP1* and *Obolenskvirus WCHABP12* from *Obolenskvirus* genus and rename to new *Sichuanvirus* genus with six species. 22. To create a new single species genus, *Pakistanvirus*. 23. To create a new single species genus, *Catovirus*. 24. To move *Obolenskvirus AP22* from *Obolenskvirus* genus and rename to new *Theraphagusvirus* genus with two species.   *Justification*:  After examination of 55 bacteriophages based on nucleotide sequence similarity, tblastx distances and core gene phylogeny, we propose the creation of a new family, *Hirszfeldviridae*, to accommodate 22 genera (*Nosocomialisvirus, Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, Scipiovirus, Wenzhouvirus*, *Burnvirus*, *Ankaravirus*, *Polandvirus*, *Kenyavirus*, *Cairovirus*, *Helsinkivirus*, *Sichuanvirus*, *Pakistanvirus*, *Catovirus*, and *Theraphagusvirus*). |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Family, genus, species  *Description of current taxonomy*:  According to the current taxonomy, the *Obolenskvirus* genus has been classified within the class *Caudoviricetes* without assignment to a family rank. Currently, the *Obolenskvirus* genus includes eight species: *Obolenskvirus AB1*, *Obolenskvirus AB2*, *Obolenskvirus AbC62*, *Obolenskvirus AbP2*, *Obolenskvirus AP22*, *Obolenskvirus LZ35*, *Obolenskvirus WCHABP1*, and *Obolenskvirus WCHABP12.*  *Proposed* *taxonomic change(s)*:  Create a new family, *Hirszfeldviridae*, with 22 genera, *Nosocomialisvirus, Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, Scipiovirus,*  *Wenzhouvirus*, *Burnvirus*, *Ankaravirus*, *Polandvirus*, *Kenyavirus*, *Cairovirus*, *Helsinkivirus*, *Sichuanvirus*, *Pakistanvirus*, *Catovirus*, and *Theraphagusvirus,* for a group of *Acinetobacter-*specific phages.  We performed a genomic analysis of several *Acinetobacter*-specific phages deposited in the NCBI database, all of which have been classified within the genus *Obolenskvirus*. Based on our analysis, we propose the creation of a new family for these phages along with 22 distinct genera.   1. To create a new family, *Hirszfeldviridae*, with 22 genera. 2. To create a new genus, *Nosocomialisvirus*, with two species. 3. To create a new single species genus, *Beijingvirus*. 4. To create a new single species genus, *Guangzhouvirus*. 5. To create a new single species genus, *Chinavirus*. 6. To create a new single species genus, *Pittiivirus*. 7. To move the genus *Obolenskvirus* to new family, *Hirszfeldviridae*. 8. To create four new species in genus *Obolenskvirus*. 9. To create a new single species genus, *Ganjingzivirus*. 10. To create a new single species genus, *Guizhouvirus*. 11. To create a new single species genus, *Brutusvirus*. 12. To create a new single species genus, *Walailakvirus*. 13. To create a new single species genus, *Scipiovirus*. 14. To move *Obolenskvirus AB1* from *Obolenskvirus* genus and rename to new *Wenzhouvirus* genus with two species. 15. To move *Obolenskvirus AbP2* from *Obolenskvirus* genus and rename to new *Burnvirus* genus with 11 species. 16. To create a new single species genus, *Ankaravirus*. 17. To create a new genus, *Polandvirus*, with two species. 18. To create a new single species genus, *Kenyavirus*. 19. To create a new genus, *Cairovirus*, with two species. 20. To create a new genus, *Helsinkivirus*, with two species. 21. To move *Obolenskvirus WCHABP1* and *Obolenskvirus WCHABP12* from *Obolenskvirus* genus and rename to new *Sichuanvirus* genus with six species. 22. To create a new single species genus, *Pakistanvirus*. 23. To create a new single species genus, *Catovirus*. 24. To move *Obolenskvirus AP22* from *Obolenskvirus* genus and rename to new *Theraphagusvirus* genus with two species.   *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 using several tools, such as BLASTn [1], and are typically determined with the intergenomic distance calculator VIRIDIC [2].  **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 [3].  **Family demarcation criteria:** The family is represented by a cohesive and monophyletic group in the main predicted proteome-based clustering tools (ViPTree, GRAViTy dendrogram, vConTACT2 network). Family members share a significant number of orthologous genes (the number will depend on the genome sizes and number of coding sequences of family members) [3].  *Justification*:  After examination of 55 bacteriophages we identified 22 genera and 46 species based on intergenomic nucleotide sequence similarity (Figure 1). The heirarchially clustered tblastx distance tree produced using ViPTree indicated that these genomes for a deep-branching clade (Figure 2). Comparison of 50 genomes with MMSeqs2 after reannotated with Pharokka resulted in the identification of 8 proteins conserved across all members of the proposed family (Figures 3 and 4).  We propose the creation of a new family, *Hirszfeldviridae*, to accommodate 22 genera (*Nosocomialisvirus, Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, Scipiovirus,* *Wenzhouvirus*, *Burnvirus*, *Ankaravirus*, *Polandvirus*, *Kenyavirus*, *Cairovirus*, *Helsinkivirus*, *Sichuanvirus*, *Pakistanvirus*, *Catovirus*, and *Theraphagusvirus*). |

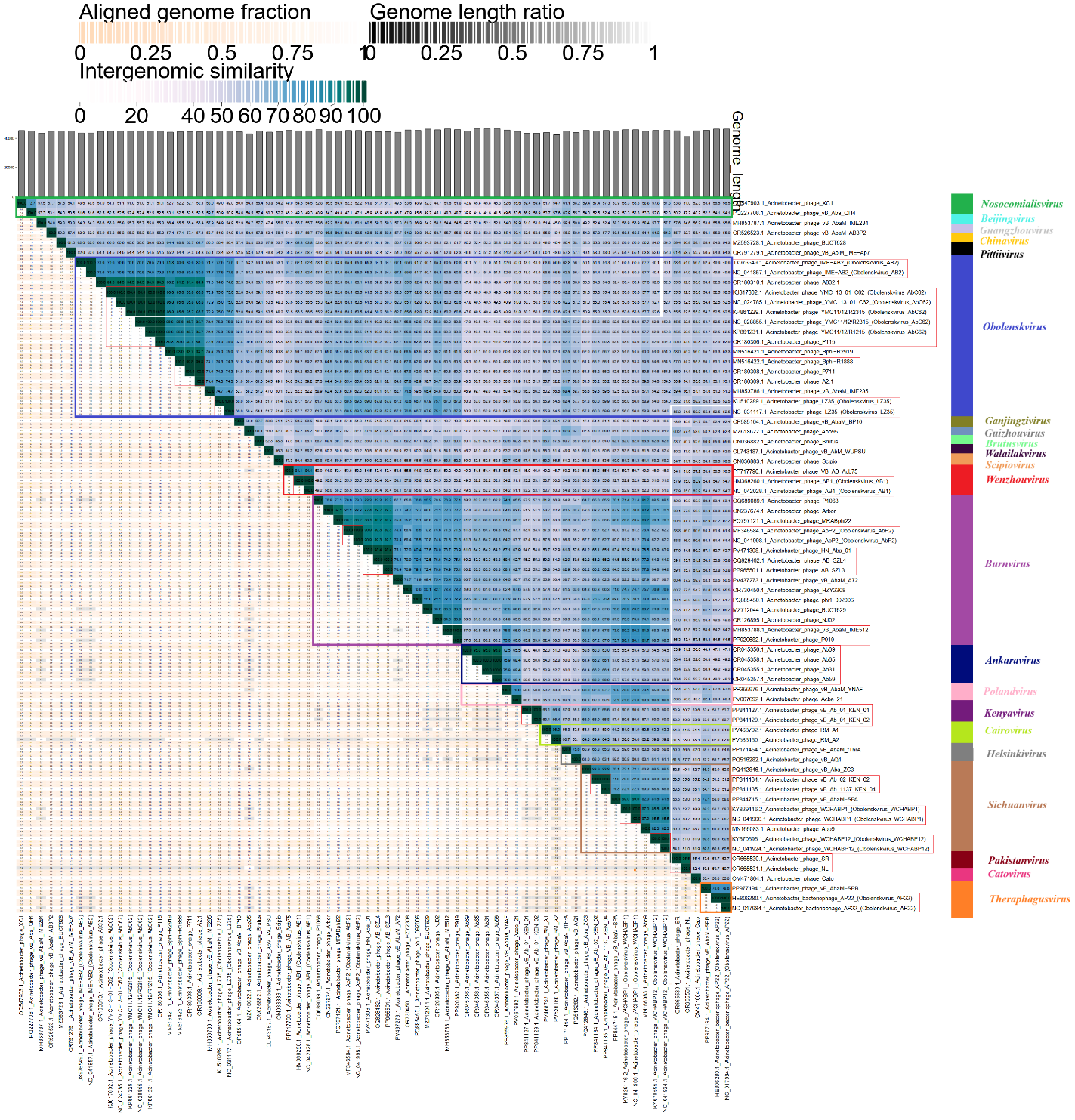
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| **References:** |
| 1. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, Marchler-Bauer A, Landrum M, Lathrop S, Lu Z, Madden TL, O'Leary N, Phan L, Rangwala SH, Schneider VA, Skripchenko Y, Wang J, Ye J, Trawick BW, Pruitt KD, Sherry ST. Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res.* 2021, 49(D1):D10-D17. 2. Moraru C, Varsani A, Kropinski AM. VIRIDIC - a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. *Viruses* 2020, 12(11):1268. 3. Turner D, Kropinski AM, Adriaenssens EM. A roadmap for genome-based phage taxonomy. *Viruses* 2021, 13(3):506. 4. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. *Bioinformatics* 2017, 33(15):2379-2380. 5. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. *J. Bacteriol.* 2002, 184(16):4529-35. 6. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. *BMC Res. Notes.* 2013, 6:140. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.054B.Hirszfeldviridae\_1nf\_21ng\_1mg\_5mrs\_46ns.xlsx | To present the proposed taxonomic changes as a comparison of new taxonomic structures. |

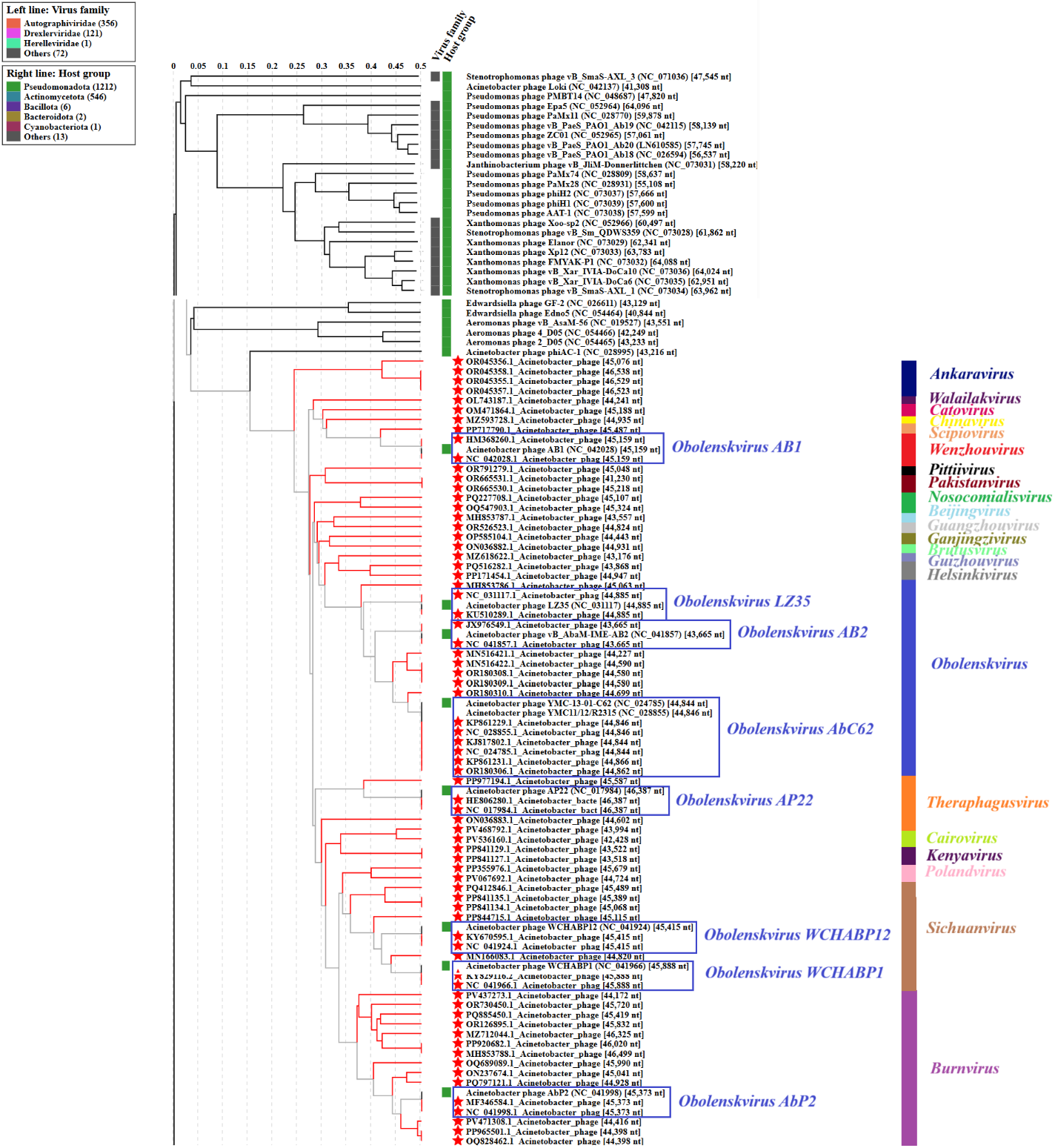
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| **Tables, Figures:** |

**Proposals data:**

1. **To create a new family, *Hirszfeldviridae*, with 22 genera.**
2. **To create a new genus, *Nosocomialisvirus*, with two species.**
3. **To create a new single species genus, *Beijingvirus*.**
4. **To create a new single species genus, *Guangzhouvirus*.**
5. **To create a new single species genus, *Chinavirus*.**
6. **To create a new single species genus, *Pittiivirus*.**
7. **To move the genus *Obolenskvirus* to new family, *Hirszfeldviridae*.**
8. **To create four new species in genus *Obolenskvirus*.**
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19. **To create a new genus, *Cairovirus*, with two species.**
20. **To create a new genus, *Helsinkivirus*, with two species.**
21. **To move *Obolenskvirus WCHABP1* and *Obolenskvirus WCHABP12* from *Obolenskvirus* genus and rename to new *Sichuanvirus* genus with six species.**
22. **To create a new single species genus, *Pakistanvirus*.**
23. **To create a new single species genus, *Catovirus*.**
24. **To move *Obolenskvirus AP22* from *Obolenskvirus* genus and rename to new *Theraphagusvirus* genus with two species.**

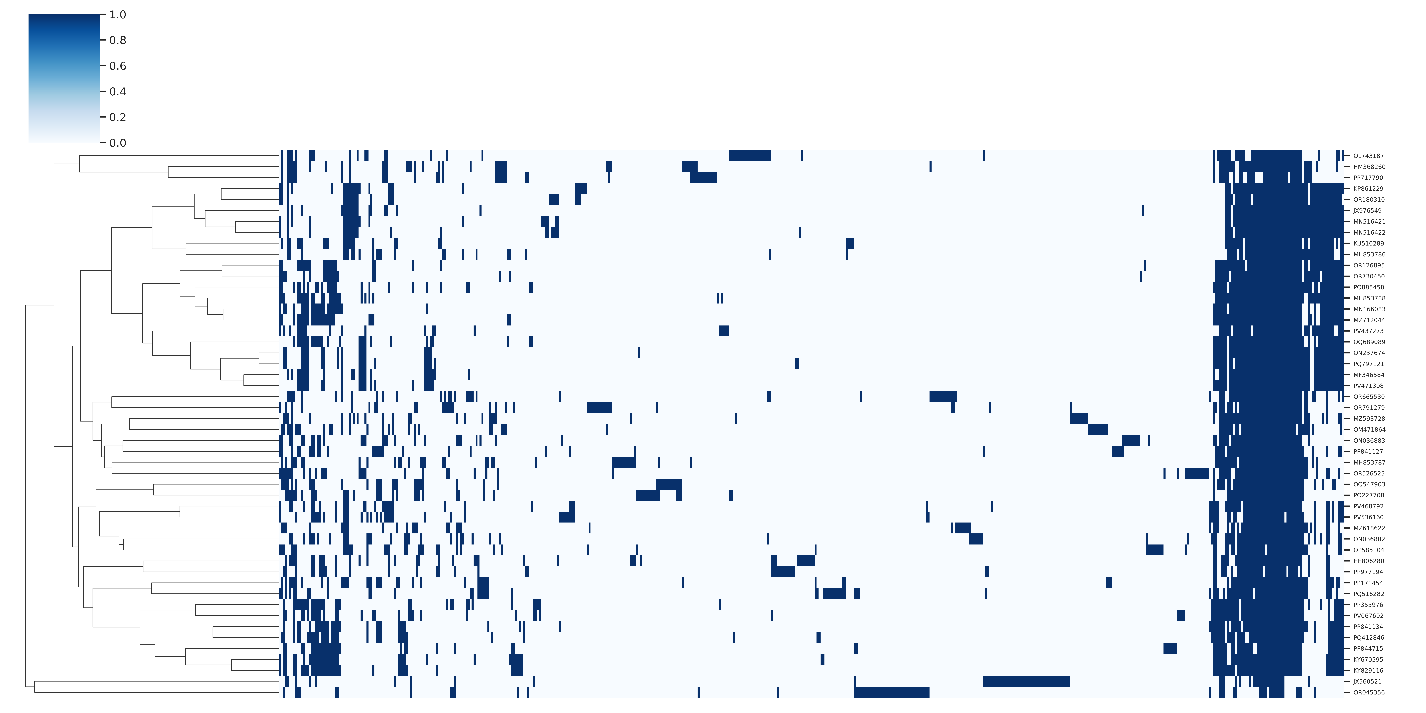


**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Phages belonging to the same species (nucleotide similarity above 95%) are marked with a red thin frame.

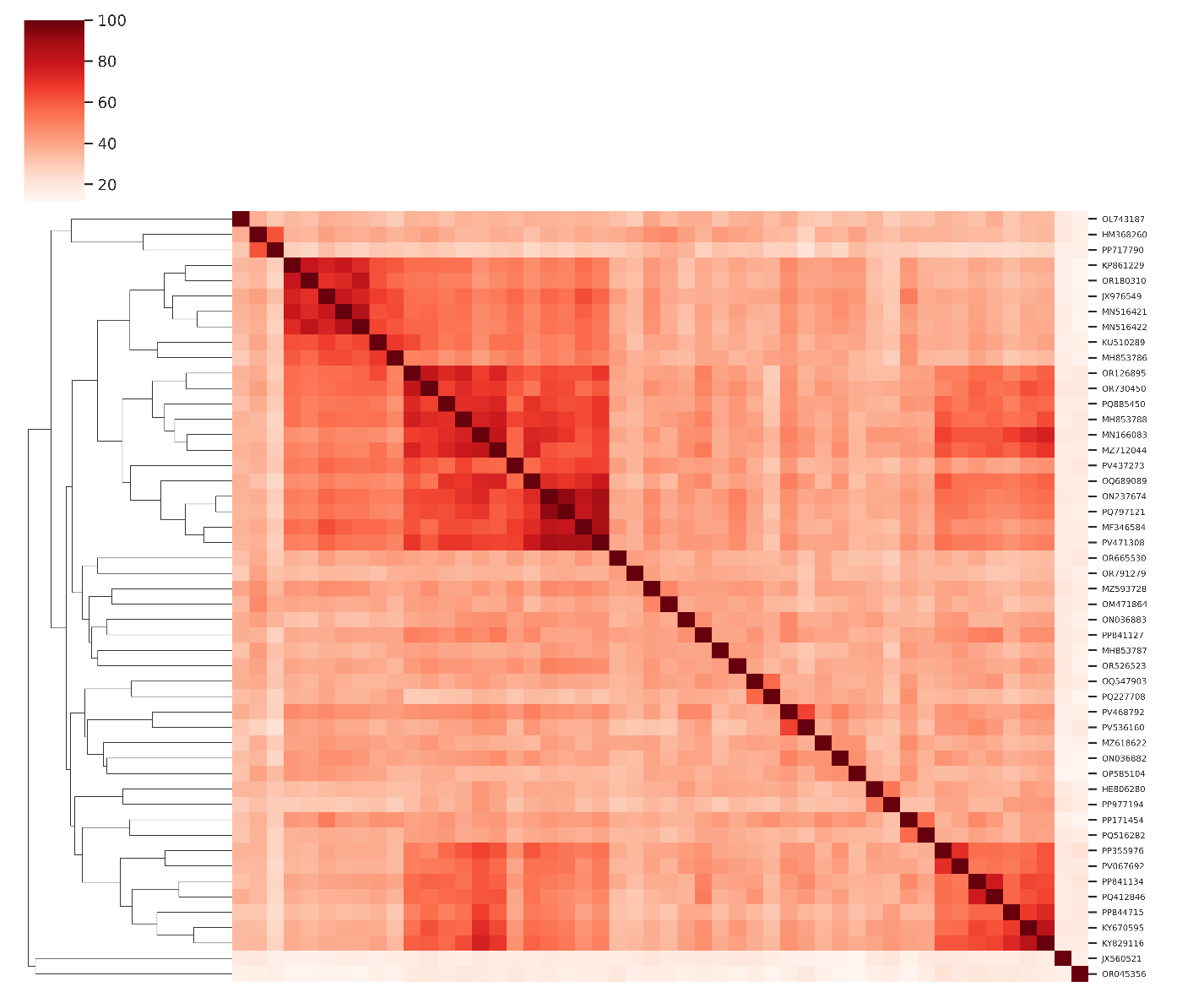


**Figure 2. ViPTree analysis\*:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [5]. The phages of interest are indicated with a **red stars**. Current species in the *Obolenskvirus* genus are marked in **blue font**.

\* The *Autographiviridae* family shown in **Figure 2** (automatically labeled by the software) is outdated. In 2025, the *Autographiviridae* family was elevated to the rank of order and renamed *Autographivirales*.



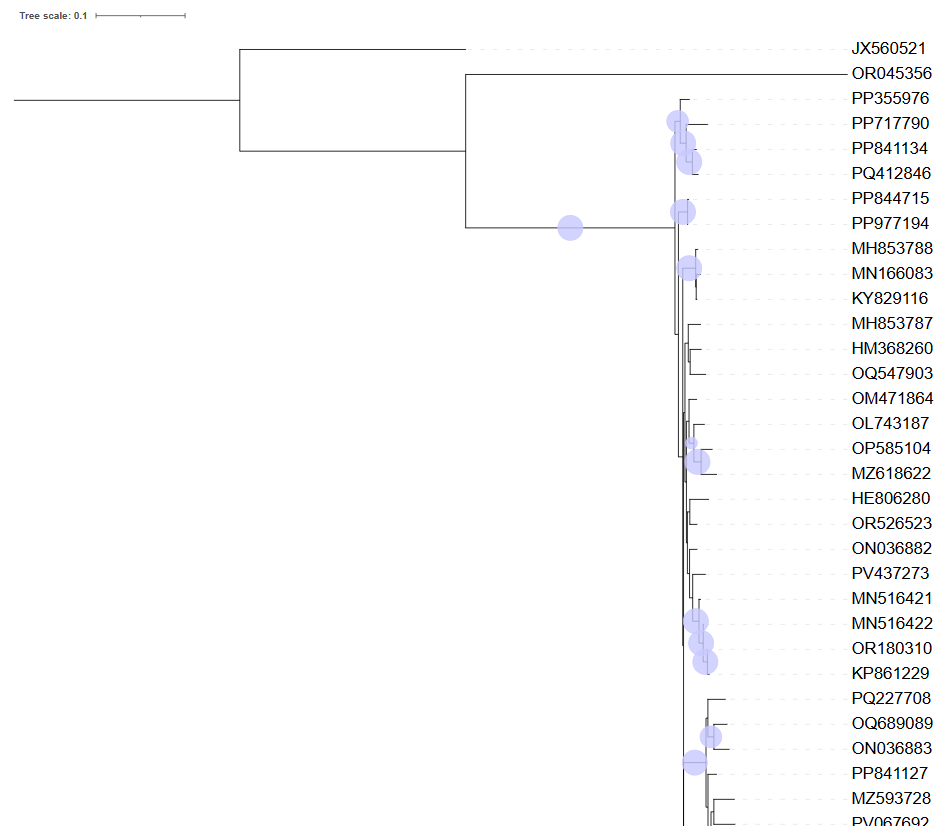
**Figure 3.** Presence-absence matrix of protein clusters by genome. Rows and columns were heirarchically clustered using the complete method. Rows represent individual genomes with columns representing protein clusters. Vertical blue bars denote the presence of protein clusters in each genome.

****

**Figure 4.** Heatmap of Jaccard similarity calculated from the percentage of shared protein clusters between genomes. PV067699 is included as an outlier.

**Table 1.** Conserved proteins in the family *Hirszfeldviridae.*

|  |  |
| --- | --- |
| **Protein cluster** | **Putative function** |
| 1 | Baseplate hub protein |
| 2 | Baseplate wedge subunit |
| 3 | Structural protein |
| 4 | Baseplate spike protein |
| 5 | Hypothetical protein |
| 6 | Virion structural protein |
| 7 | Baseplate wedge subunit |
| 8 | Hypothetical protein |

**Figure 5.** Partition maximum likelihood phylogeny of the eight conserved proteins, inferred with IQTree2. The circles represent UFBoot support of ≥95%.

1. **To create a new family, *Hirszfeldviridae*, with 22 genera.**

After examination of 55 bacteriophages based on nucleotide sequence similarity, tblastx distances and core gene phylogeny, we propose the creation of a new family, *Hirszfeldviridae*, to accommodate 22 genera; *Nosocomialisvirus, Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, Scipiovirus,* *Wenzhouvirus*, *Burnvirus*, *Ankaravirus*, *Polandvirus*, *Kenyavirus*, *Cairovirus*, *Helsinkivirus*, *Sichuanvirus*, *Pakistanvirus*, *Catovirus*, and *Theraphagusvirus*.

1. **To create a new genus, *Nosocomialisvirus*, with two species.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage XC1 (selected as the reference genome)** | **OQ547903.1** | **OQ547903** | **45,324** | **37.4** | **84** | **100.0** | **100.00** |
| Acinetobacter phage vB\_Aba\_QH4 |  | PQ227708 | 45,107 | 37.3 | 84 | 73.7 | 80.95 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Beijingvirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage vB\_AbaM\_IME284 |  | MH853787 | 43,557 | 38.3 | 84 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Guangzhouvirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage vB\_AbaM\_AB3P2 |  | OR526523 | 44,824 | 37.8 | 94 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Chinavirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage BUCT628 |  | MZ593728 | 44,935 | 37.5 | 86 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Pittiivirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage vB\_ApiM\_IME-Ap7 |  | OR791279 | 45,048 | 37.9 | 92 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To move the genus *Obolenskvirus* to new family, *Hirszfeldviridae*.**

After examining bacteriophages based on nucleotide sequence similarity, tblastx distance, and core gene phylogeny, we proposed to include the genus *Obolenskvirus* in a newly proposed family, *Hirszfeldviridae*.

1. **To create four new species in genus *Obolenskvirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage IME-AB2**  **(*Obolenskvirus AB2*; reference genome)** | **JX976549.1 = NC\_041857.1** | **JX976549** | **43,665** | **37.5** | **82** | **100.0** | **100.00** |
| Acinetobacter phage YMC11/12/R2315 (*Obolenskvirus AbC62*) | KP861229.1 = NC\_028855.1 | KP861229 | 44,846 | 37.6 | 85 | 79.5 | 90.24 |
| Acinetobacter phage LZ35 (*Obolenskvirus LZ35*) | KU510289.1 = NC\_031117.1 | KU510289 | 44,885 | 37.9 | 83 | 77.5 | 86.59 |
| Acinetobacter phage A832.1 |  | OR180310 | 44,699 | 37.8 | 86 | 78.6 | 90.24 |
| Acinetobacter phage Bphi-R2919 |  | MN516421 | 44,227 | 37.8 | 80 | 81.8 | 90.24 |
| Acinetobacter phage Bphi-R1888 |  | MN516422 | 44,590 | 37.9 | 78 | 80.6 | 85.37 |
| Acinetobacter phage vB\_AbaM\_IME285 |  | MH853786 | 45,063 | 37.9 | 85 | 74.7 | 87.80 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Ganjingzivirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage vB\_AbaM\_BP10 |  | OP585104 | 44,443 | 37.3 | 88 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Guizhouvirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage Abp95 |  | MZ618622 | 43,176 | 37.8 | 57 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Brutusvirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage Brutus |  | ON036882 | 44,931 | 37.4 | 86 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Walailakvirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage vB\_AbM\_WUPSU |  | OL743187 | 44,241 | 37.2 | 83 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Scipiovirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage Scipio |  | ON036883 | 44,602 | 37.6 | 81 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To move *Obolenskvirus AB1* from *Obolenskvirus* genus and rename to new *Wenzhouvirus* genus with two species.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage AB1 (selected as the reference genome)** | **HM368260.1 = NC\_042028.1** | **HM368260** | **45,159** | **37.7** | **85** | **100.0** | **100.00** |
| Acinetobacter phage VB\_AB\_Acb75 |  | PP717790 | 45,487 | 38.0 | 42 | 84.1 | 47.06 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To move *Obolenskvirus AbP2* from *Obolenskvirus* genus and rename to new *Burnvirus* genus with 11 species.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage AbP2 (selected as the reference genome)** | **MF346584.1 = NC\_041998.1** | **MF346584** | **45,373** | **37.8** | **88** | **100.0** | **100.0** |
| Acinetobacter phage P1068 |  | OQ689089 | 45,990 | 37.4 | 102 | 79.0 | 88.64 |
| Acinetobacter phage Arbor |  | ON237674 | 45,041 | 37.4 | 83 | 83.8 | 88.64 |
| Acinetobacter phage MRABphi22 |  | PQ797121 | 44,928 | 37.9 | 83 | 88.7 | 88.64 |
| Acinetobacter phage HN\_Aba\_01 |  | PV471308 | 44,416 | 37.9 | 85 | 90.9 | 94.32 |
| Acinetobacter phage vB\_AbaM\_A72 |  | PV437273 | 44,172 | 37.7 | 90 | 78.4 | 81.82 |
| Acinetobacter phage HZY2308 |  | OR730450 | 45,720 | 37.9 | 87 | 68.4 | 80.68 |
| Acinetobacter phage phi1\_092006 |  | PQ885450 | 45,419 | 37.6 | 101 | 76.5 | 85.23 |
| Acinetobacter phage BUCT629 |  | MZ712044 | 46,325 | 37.6 | 89 | 70.8 | 81.82 |
| Acinetobacter phage NJ02 |  | OR126895 | 45,832 | 37.9 | 86 | 74.6 | 82.95 |
| Acinetobacter phage vB\_AbaM\_IME512 |  | MH853788 | 46,499 | 37.6 | 91 | 71.6 | 86.36 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Ankaravirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage Ab69 |  | OR045356 | 45,076 | 38.0 | 159 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new genus, *Polandvirus*, with two species.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage Acba\_21 (selected as the reference genome)** | **PV067692.1** | **PV067692** | **44,724** | **37.8** | **85** | **100.0** | **100.00** |
| Acinetobacter phage vB\_AbaM\_YNAF |  | PP355976 | 45,379 | 37.6 | 85 | 78.9 | 85.88 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Kenyavirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage vB\_Ab\_01\_KEN\_01 |  | PP841127 | 43,518 | 37.8 | 91 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new genus, *Cairovirus*, with two species.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage RM\_A1 (selected as the reference genome)** | **PV468792.1** | **PV468792** | **43,994** | **38.0** | **84** | **100.0** | **100.00** |
| Acinetobacter phage RM\_A2 |  | PV536160 | 42,428 | 37.8 | 84 | 86.0 | 89.29 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new genus, *Helsinkivirus*, with two species.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage vB\_AbaM\_fThrA (selected as the reference genome)** | **PP171454.1** | **PP171454** | **44,947** | **37.6** | **98** | **100.0** | **100.00** |
| Acinetobacter phage vB\_AQ1 |  | PQ516282 | 43,868 | 37.4 | 103 | 75.6 | 78.57 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To move *Obolenskvirus WCHABP1* and *Obolenskvirus WCHABP12* from *Obolenskvirus* genus and rename to new *Sichuanvirus* genus with six species.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter phage WCHABP1 (selected as the reference genome)** | **KY829116.2 = NC\_041966.1** | **KY829116** | **45,888** | **37.6** | **89** | **100.0** | **100.00** |
| Acinetobacter phage WCHABP12 | KY670595.1 = NC\_041924.1 | KY670595 | 45,415 | 37.6 | 88 | 85.5 | 94.38 |
| Acinetobacter phage vB\_Aba\_ZC3 |  | PQ412846 | 45,489 | 37.3 | 88 | 72.1 | 84.27 |
| Acinetobacter phage vB\_Ab\_02\_KEN\_02 |  | PP841134 | 45,068 | 37.7 | 90 | 72.0 | 82.02 |
| Acinetobacter phage vB\_AbaM-SPA |  | PP844715 | 45,115 | 37.4 | 70 | 89.0 | 75.28 |
| Acinetobacter phage Abp9 |  | MN166083 | 44,820 | 37.7 | 81 | 87.0 | 83.15 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Pakistanvirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage SR |  | OR665530 | 45,218 | 38.0 | 87 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To create a new single species genus, *Catovirus*.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Acinetobacter phage Cato |  | OM471864 | 45,188 | 37.4 | 85 | 100.0 | 100.0 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

1. **To move *Obolenskvirus AP22* from *Obolenskvirus* genus and rename to new *Theraphagusvirus* genus with two species.**

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (bp) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| **Acinetobacter bacteriophage AP22 (selected as the reference genome)** | **HE806280.1 = NC\_017984.1** | **HE806280** | **46,387** | **37.7** | **89** | **100.0** | **100.00** |
| Acinetobacter phage vB\_AbaM-SPB |  | PP977194 | 45,587 | 37.7 | 70 | 78.6 | 66.29 |

(\*) determined using VIRIDIC [2]

(\*\*) determined using CoreGenes 3.5 [6]

**Conclusion:** On the basis of DNA and protein similarity, *Hirszfeldviridae* is a cohesive family.